EBERHARD KARLS
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TÜBINGEN

eseb
European Society for Evolutionary Biology

Tübingen 2011
13th Congress of the European Society for Evolutionary Biology

All Abstracts

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Scientific Programme Overview

		early	late	
SUN 21	morning	Plenaries (Sy 00)	General sessions (Sy 30)	
	afternoon	Sy 01, 05, 08, 11, 15, 21, 22, 25, 27	Sy 01, 05, 08, 11, 15, 21, 22, 25, 27	Regular posters A
MON 22	morning	Plenaries (Sy 00)	General sessions (Sy 30), Outreach Symposium (Sy 31)	
	afternoon	Sy 01, 03, 05, 08, 13, 20, 21, 22, 23	Sy 01, 03, 12, 13, 14, 19, 20, 21, 23	Regular posters B
TUE 23	morning	Plenaries (Sy 00)	JMS-Laureate (Sy 00) *ESEB Member meeting*	
	afternoon	Sy 01, 02, 04, 06, 09, 14, 23, 24, 28	Sy 02, 04, 06, 09, 14, 23, 24, 26, 28	Regular posters C
WED 24	morning	Sy 02, 06, 07, 10, 16, 17, 18, 26, 29	Sy 02, 06, 07, 10, 16, 17, 18, 26, 29	
	afternoon	General sessions (Sy 30)	Presidential address (Sy 00) Prizes and closing session	*Farewell party*

Symposia Overview

Plenaries (Room N6 *live*, N7 & N5 *video*)
Plenary talks, JMS Laureate, Presidential address
Invited: Duur Aanen, Julie Etterson, Johannes Krause, Anna Qvarnström, Michael Ruse, Michael Siva-Jothy, Rowan Barrett, Brian Charlesworth

Sy 31 Outreach Symposium (Room N5)
Invited: Joseph Carroll, Esben Andersen, Michael Blume, Frank Ryan
Organizers: Thomas D'Souza, Daniel Dreesmann

Sy 01 (Room N7)
Microbe/macrobe experimental evolution
Invited: Graham Bell, Richard E Lenski, Tadeusz Kawecki
Organizers: Rhonda R Snook, Nick Colegrave, Thomas U Berendock, Oliver Kaltz, Stéphanie Bedhomme, Santiago F Elena

Sy 02 (Room N6)
Coevolution from parasitism to mutualism
Invited: Greg Hurst, Jukka Jokela
Organizers: Michael Brockhurst, Britt Koskella

Sy 03 (Room N5)
Evolution and human disease
Invited: Stephen Stearns , David Haig , Bernard Crespi
Organizers: Sean G Byars, Jacobus J Boomsma

Sy 04 (Room N1)
Cooperation and virulence
Invited: Sam Brown, William Hughes
Organizers: Rolf Kuemmerli, Adin Ross-Gillespie

Sy 05 (Room N3)
Mutualism: Causes and consequences
Invited: Nancy Moran, Ulrich Mueller
Organizers: Christian Kost, Martin Kaltenpoth

Sy 06 (Room N5)
Speciation by natural versus sexual selection
*Invited:*A ndrew Hendry, Maria Servedio, Martine Maan, Erik Svensson
Organizers: Allan Debelle, Claudius Kerth

Sy 07 (Room N0)
Fossils and evolutionary biology
Invited: Walter G Joyce, Krister T Smith
Organizers: Hervé Bocherens

Sy 08 (Room N0)
Predicting macroevolution from microevolution
Invited: Emma Goldberg, Oliver Pybus
Organizers: Gavin Thomas, Rob Freckleton

Sy 09 (Room N0)
Polyploid ecological genomics
Invited: Brian Husband, Jonathan Wendel
Organizers: Christian Parisod, Malika L Ainouche

Sy 10 (Room N4)
Causes of epistasis
Invited: Roy Kishony, Dan Weinreich
Organizers: Arjan GM de Visser, Santiago F Elena

Sy 11 (Room N2)
Non-genetic inheritance and evolution
Invited: Troy Day, Alex Badyaev
Organizers: Tobias Uller, Heikki Helanterä

Sy 12 (Room N0)
Plant epigenetics
Invited: Vincent Colot, Koen Verhoeven
Organizers: Joop Ouborg, Oliver Bossdorf

Sy 13 (Room N4)
Evolution outside of the nucleus
Invited: Ron Burton, David McCauley
Organizers: Maurine Neiman, Dan Sloan, Doug Taylor

Sy 14 (Room N3)
Family interactions
Invited: Allen Moore, Mathias Kölliker
Organizers: Reinmar Hager, Per T Smiseth

Sy 15 (Room N5)
Division of labour
Invited: Richard Michod
Organizers: Claus Rueffler, Sergey Gavrilets

Sy 16 (Room N2)
Viviparity, placentation and conflict
Invited: Derek Wildman, David Reznick
Organizers: Isabella Capellini, Robert Barton

Sy 17 (Room N3)
Novel techniques in behavioural ecology
Invited: Tracey Chapman, Michal Polak
Organizers: Amanda Bretman, Thomas Price

Sy 18 (Room N1)
Perceptual manipulation and mimicry
Invited: Rebecca Fuller, Steve Johnson
Organizers: Martin H Schaefer, Florian Schiestl

Sy 19 (Room N9)
Evolution of chirality
Invited: Spencer Barrett, Rich Palmer
Organizers: Menno Schilthuizen, Barbara Gravendeel

Sy 20 (Room N1)
Chemical communication
Invited: Mark Blows, Jane Hurst
Organizers: Ally Harari, Tamar Keasar

Sy 21 (Room N6)
Evolutionary ecological genomics
Invited: Michael Pfrender, Ilkka Hanski
Organizers: Luisa Orsini, Christophe Eizaguirre

Sy 22 (Room N9)
Environment, G matrices and adaptation
Invited: Steve Chenoweth, Johanna Schmitt
Organizers: Matthew Robinson, Andrew Beckerman

Sy 23 (Room N2)
Climate change and evolution
Invited: Juha Merilä, Ary Hoffmann
Organizers: Klaus Fischer, Stephanie S Bauerfeind, Wolf U Blanckenhorn

Sy 24 (Room N9)
Adaptation in large populations
Invited: Nick Barton, Joachim Hermisson
Organizers: Nicolas Bierne, Denis Roze

Sy 25 (Room N1)
Evolutionary systems biology
Invited: Jennifer Reed, Andreas Wagner
Organizers: Laurence Loewe, Orkun Soyer

Sy 26 (Room N7)
Parallel evolution
Invited: Hopi E Hoekstra, Louis Bernatchez
Organizers: Walter Salzburger, Moritz Muschick

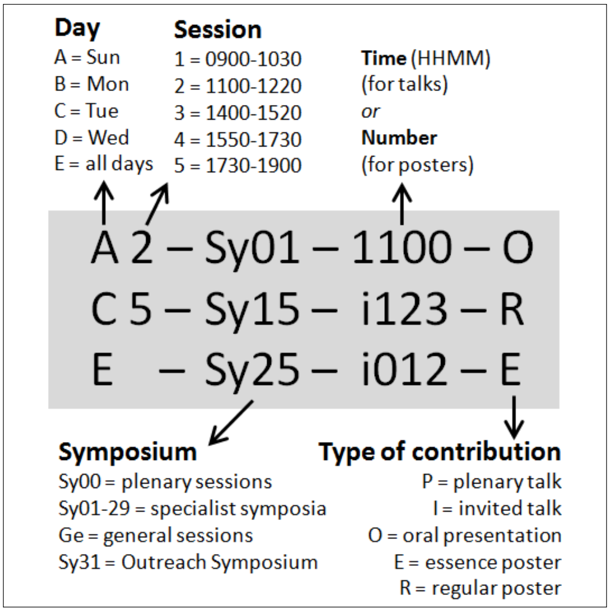
Sy 27 (Room N4)
Selective sweeps
Invited: Luis-Miguel Chevin, Wolfgang Stephan
Organizers: Kristan Schneider, Yuseob Kim

Sy 28 (Room N4)
Functional population genomics
Invited: Axel Meyer, Chris Jiggins
Organizers: Jay F Storz, Jeffrey M Good

Sy 29 (Room N9)
Can drift facilitate adaptive evolution?
Invited: Joanna Masel, Merijn Salverda
Organizers: Bas Zwaan, Arjan de Visser

Sy 30 General Sessions (Room N2 - N7)
Behaviour, Life-history, Population ecology, Development, Disease and immunity, Evolutionary genetics, Human impact, Inbreeding, Evolution of sex, Primates
Organizers: Local scientific committee

Explanation of the contribution ID



Day
A = Sun
B = Mon
C = Tue
D = Wed
E = all days

Session
1 = 0900-1030
2 = 1100-1220
3 = 1400-1520
4 = 1550-1730
5 = 1730-1900

Time (HHMM)
(for talks)
or
Number
(for posters)

A 2 – Sy01 – 1100 – O
C 5 – Sy15 – i123 – R
E – Sy25 – i012 – E

Symposium
Sy00 = plenary sessions
Sy01-29 = specialist symposia
Ge = general sessions
Sy31 = Outreach Symposium

Type of contribution
P = plenary talk
I = invited talk
O = oral presentation
E = essence poster
R = regular poster

Plenaries

Room N6 (live), N7 & N5 (video)

Duur Aanen

Rowan Barrett

Brian Charlesworth

Julie Etterson

Johannes Krause

Anna Qvarnström

Michael Ruse

Michael Siva-Jothy

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

SUN 21 AUG at 0950 - Room N6 *(live)*, N7 & N5 *(video)*
Plenary talk *A1-Sy00-0950-P*

Plenaries

The evolution of cooperation in mushrooms

Aanen DK[1]
[1]Wageningen University, Laboratory of Genetics, Wageningen, Netherlands

Summary statement:

Mushroom-forming fungi engage in ecologically important mutualisms and have a highly interesting social and sex life making them excellent models to study evolution of cooperation.

Abstract:

Conflicts between levels of selection have often been resolved decisively in favour of the higher level. For example, the germ-soma separation of most animals makes most cancers evolutionarily dead ends. This is different for fungi, where each cell is a ‘hopeful reproductive’. Therefore, fast-dividing cells or nuclei, analogous to cancer, potentially have an evolutionary future. This makes mushrooms ideal to study conflicts between levels of selection.
An important characteristic of fungi is their ability to fuse. Experiments with mutualistic fungi cultivated by termites demonstrate the benefit of mycelial fusion. Termite farmers exploit this fusion benefit by inoculating a high density of monoculture spores, which fuse upon germination. The benefit of fusion leads to a paradox (Crozier, 1986): if fusion is beneficial, how can we understand the extensive allorecognition diversity observed in nature, which restricts somatic fusion to close relatives? We show that nuclear parasitism can create the selective conditions for extensive allorecognition diversity, solving ‘Crozier’s paradox’.
In contrast to restricted occurrence of somatic fusion, virtually unrestricted fusion occurs among genetically unrelated mycelia in the sexual stage. This leads to a mycelial mosaic with two nuclei per cell. In most mushrooms, competition among genetically different nuclei is repressed by strictly coupling nuclear and cell division. I discuss experimental evidence for two remaining sources of lower-level selection, one resulting from sexual conflict due to multiple mating and one from mutation towards female-sterility giving an initial one-and-a-half fold within-mycelium selective advantage.

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TUE 23 AUG at 1100 - Room N6 *(live)*, N7 & N5 *(video)*
Plenary talk *C2-Sy00-1100-P*

Plenaries
John Maynard Smith Prize Laureate

The genetics of adaptation to changing environments

Barrett RDH[1]
[1]Harvard University, Organismic and Evolutionary Biology, Cambridge, United States

Summary statement:

The genetics of adaptation: combining theory, lab and field studies to understand the mechanisms that drive ecological and evolutionary responses to changing environments.

Abstract:

Human activities are resulting in extensive worldwide changes to ecosystems, with both ecological and evolutionary consequences. Understanding the process of adaptation to changing environments requires integrative studies that combine approaches from population genetics, evolutionary ecology and molecular biology. Here, I present theoretical, laboratory and field studies with microbes and fish that help to determine the genetic basis, ecological mechanisms, and evolutionary effects of rapid adaptation to changing environments. The work involves direct measures of natural selection acting at the molecular level, thus providing crucial information on the functional links among genotype, phenotype, and fitness. This research is helping to identify some of the primary mechanisms that are likely to drive adaptation to global environmental change.

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WED 24 AUG at 1550 - Room N6 *(live)*, N7 & N5 *(video)*
Plenary talk *D4-Sy00-1550-P*

Plenaries
Presidential address

How population genomics can solve a lot of our problems

Charlesworth B[1]
[1]University of Edinburgh, Institute of Evolutionary Biology, Edinburgh, United Kingdom

Summary statement:

Molecular population genetics is providing powerful tools for using these datasets to answer some classical problems. Examples of these problems, and steps towards solving them, will be reviewed.

Abstract:

Datasets on DNA sequence polymorphism and interspecies divergence for multiple loci, or even whole genomes, are becoming increasingly available. At the same time, statistical population genetics is providing powerful tools for using these datasets to answer some of the classical questions of evolutionary genetics. These include the extent to which natural selection, as opposed to genetic drift, has caused the fixation of mutations that distinguish related species, and the frequency distribution of the effects on fitness for newly arisen favourable and deleterious mutations. In addition, the extent to which patterns of polymorphism and divergence are affected by genetic linkage among the sites involve can be examined by these methods. Work on these problems by my own group will be reviewed, in the context of recent advances in the field as a whole.

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MON 22 AUG at 0910 - Room N6 *(live)*, N7 & N5 *(video)*
Plenary talk *B1-Sy00-0910-P*

Plenaries

Evolution of plant populations in response to climate change: Case studies from the Great Plains of the United States

Etterson JR[1]
[1]University of Minnesota Duluth, Department of Biology, Duluth, United States

Summary statement:

Two case studies are presented that examine potential adaptive responses to climate change in two plant species, a diploid annual pea and a polyploid perennial herb

Abstract:

Will natural populations attain evolutionary rates that match the rate of climate change? The magnitude of evolutionary response that will occur in any given population depends critically upon the genetic architecture of traits that are the targets of selection. In this seminar, I will present quantitative genetic approaches that I have used to predict potential adaptive responses to climate change in two plant species, a diploid annual pea, Chamaecrista fasciculata, and a polyploid perennial herb, Solidago altissima. In the case study of C. fasciculata, I characterized the genetic architecture of three Great Plains populations in field conditions that simulate the warmer and more arid climates predicted by global climate models. Predicted rates of evolutionary response are much slower than the predicted rate of climate change. In the case study of S. altissima, I examine the impact of polyploidy on adaptation to climate change in a species that is polymorphic for diploid, tetraploid and hexaploid cytotypes. This research explicitly tests the assumption that the larger genomes of polyploids allow them to evolve faster or in novel directions compared to their diploid progenitors. In this work I am comparing the rate of response to artificial selection on timing of flowering in diploid and tetraploid plants exposed to current levels of precipitation and drought conditions similar to those predicted for the future. Results from this research will increase our understanding of the nature of genetic variation in polyploid taxa that may be selected upon and may ultimately increase the persistence of populations in the face of climate change.

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TUE 23 AUG at 0950 - Room N6 ***(live)*****, N7 & N5** ***(video)***
Plenary talk *C1-Sy00-0950-P*

Plenaries

What makes us human: Insights from sequencing extinct hominin genomes?

Krause J[1]
[1]University of Tuebingen, Institute for Archaeological Sciences, Tuebingen, Germany

Summary statement:

We present the genome sequence of the Neandertal and an only recently described Siberian hominin the Denisovan. Both genomes show evidence of gene flow with modern human populations.

Abstract:

A genetic comparison between modern humans and their extinct relatives could both address the relationship between us and them and offer the possibility to identify genetic changes that happened specifically on the human lineage. Furthermore it may allow identifying and understanding the evolutionary history of genes and positions in the modern human genome that experienced recent positive selection after divergence of modern humans and their extinct relatives. Using a combination of high-throughput DNA sequencing technologies and multiple improvements in ancient DNA retrieval, library construction and targeted library enrichments, the Leipzig laboratory has recently, in collaboration with several groups, completed a first version of the Neandertal genome as well as a genome sequence of an extinct hominin discovered in the Altai mountains in southern Siberia named Denisovan. The analysis of both the Neandertal and Denisovan genome revealed evidence of geneflow between certain modern human populations and both extinct hominins. From the analysis of the data we were furthermore able to draw conclusion about diversity within and among the extinct hominins and by scanning the human genome for regions of positive selection using the Neandertal and Denisovan genome, we identified several strong candidate genes involved in diet, cognitive traits, and skeletal morphology that were potentially selected on the modern human lineage.

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TUE 23 AUG at 0910 - Room N6 *(live)*, N7 & N5 *(video)*
Plenary talk *C1-Sy00-0910-P*

Plenaries

Speciation – how difficult can it be?

Qvarnström A[1]
[1]Uppsala University, Ecology and Genetics, Uppsala, Sweden

Summary statement:

Debated issues will form starting points for some excursions into recent studies on speciation. I conclude that divergence is easy but co-existence difficult.

Abstract:

Interest in ecological speciation is growing, as evidence showing that natural selection can lead to rapid divergence between subpopulations accumulates. However, whether and how ecological divergence can lead to the build up of reproductive isolation remains under debate. How does adaptation to the environment generate reproductive isolation? Does the relative roles of natural and sexual selection change during the advancement of the speciation process? Can ecological speciation occur despite homogenizing gene flow? Is genetic incompatibility really the end point or can selection make populations compatible again? These questions will form the starting points of some excursions into recent studies of speciation displayed in this talk. For example, research on hybridizing Ficedula flycatchers will be used to illustrate how the combination of ecological and genomic studies can be used to investigate how sensitive divergence is to gene flow. Another key issue that I will discuss is why a life history perspective can be useful in the context of predicting interactions between natural and sexual selection. I conclude that divergence is easy but co-existence difficult.

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MON 22 AUG at 0950 - Room N6 *(live)*, N7 & N5 *(video)*
Plenary talk *B1-Sy00-0950-P*

Plenaries

What, if anything, does a historian and philosopher have to say to real scientists?

Ruse M[1]
[1]Florida State University, Program in the History and Philosophy of Science, Tallahassee, United States

Summary statement:

Should real working scientists take notice of the history & philosophy of science? By looking at evolution, I shall argue that there is a value in the history & philosophy of science.

Abstract:

I am a historian and philosopher of science, specializing in evolutionary theory. I have written many articles and over twenty books on my subject, one that I enjoy immensely. I feel that what I am doing is interesting and I would like to think that others might also find my ideas interesting. I do think about practical implications, but they are generally in the field of education. I have been much involved in the fight in the USA against Creationism, and I believe that my scholarly work has paid dividends. But I hardly ever think about whether my work has any implications for the practice of science. I know that scientists read my work, but I don't write for them as scientists, rather as people who might find my work interesting. Am I short-sighted, am I selfish, am I putting myself down? In this talk, given that my audience will be made up of scientists, I want to ask if what I do really does have implications for the working scientist. In other words, should you put my work on the reading lists of your students?

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SUN 21 AUG at 0910 - Room N6 *(live)*, N7 & N5 *(video)*
Plenary talk *A1-Sy00-0910-P*

Plenaries

Sex, trauma and disease: Female responses to male inflicted mating injury in cimicids

Siva-Jothy MT[1]
[1]University of Sheffield, Animal & Plant Sciences, Sheffield, United Kingdom

Summary statement:

Female bed bugs are traumatically inseminated during mating. I examine and discuss the anatomical, behavioural and physiological responses that have evolved as a consequence.

Abstract:

Male cimicids are obligate traumatic inseminators despite the fact the female has a fully functional reproductive tract. Mating is under male control, occurs multiply during each mating episode and involves non-sterile trauma. Females are therefore faced with a range of potential fitness reducing consequences. I will present data which sheds light on these consequences and identifies novel responses by females to the mating-associated immune-insults they receive.

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Outreach Symposium

Talks: *Room N5*

Invited Speakers:

Joseph Carroll, Esben Andersen, Michael Blume, Frank Ryan

Organizers:

Thomas D‘Souza, Daniel Dreesmann

Description:

The outreach symposium “Evolution – more than biology” addresses applications of evolutionary approaches in disciplines that, at first sight, have little in common with evolutionary biology. The four invited speakers of the symposium will cover society-relevant topics such as evolution of religion and religiousness, evolutionary medicine, evolutionary economics and evolutionary literary study.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

This symposium is funded by the Volkswagen Foundation

MON 22 AUG at 1140 - Room N5
Invited talk *B2-Sy31-1140-I*

Outreach Symposium

Evolutionary economics and evolutionary biology

Andersen ES[1]
[1]Aalborg University, Business and Management, Aalborg, Denmark

Summary statement:

This paper presents modern evolutionary economics in a way that emphasises its relationships with evolutionary biology.

Abstract:

Darwin derived much inspiration from economic theories of population and of the gradual and competitive process of division of labour. And a naive type of old evolutionary economics used inspiration from Darwin and Spencer. The link was for a while broken when the increasing level of formality within economics led from Homo sapiens to a model of a perfectly rational and informed “Homo Economicus”. Later, evolutionary game theory has combined within behavioural and experimental economics to bring real life back to economics. For instance, it has been demonstrated that people interpret economic situations in terms of three types of game: simple games of exchange where the parties are striving to increase their utility, games of distribution where equal shares are demanded, and games of collaboration that are upheld by the ”altruistic” punishment of defective behaviour. The development within biology of evolutionary methods of statistics and formal models has helped evolutionary economics to analyse the evolution of systems of behavioural rules and technologies. This development started as basic research, but we see the emergence of studies within organisation science, finance, industrial dynamics, economic geography, development studies, and environmental economics. We still need answers to two questions: How can we use some sort of “generalised Darwinism” without turning to empty formalisms and without loosing understanding of the radical differences between biological and economic evolution? How can we use the results of behavioural evolutionary economics without loosing our focus on the highly complex processes of economic evolution?

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MON 22 AUG at 1200 - Room N5
Invited talk *B2-Sy31-1200-I*

Outreach Symposium

Evolutionary Studies of Religiosity and Religions, started by Charles Darwin

Blume M[1]
[1]University of Jena, Study of Religion, Jena, Germany

Summary statement:

Although he underestimated the role of women and cooperative breeding, core theories developed by Darwin on evolution of religiosity turn out to be surprisingly farsighted and viable.

Abstract:

For more than a century, evolutionary studies and religious mythologies have been debated primarily in opposition to each other. But during the last decade, empirical and interdisciplinary studies about the evolution of religiosity - understood as the (neuro-)biological tendencies to assume the existence of superempirical agents such as ancestors, spirits, angels, gods or God - emerged, connected and flourished. Firmly based on methodological agnosticism, they brought about new insights, experiments, studies and hypotheses concerning the biological trait and its various cultural expressions. And this approach towards an evolutionary understanding of religion turns out to be not entirely new: Charles Darwin, who studied theology, devoted a subchapter and some dispersed sentences of his eminent "Descent of Man, and Selection in Relation to Sex" (1871) to the emergence of religious beliefs and their evolutionary effects. And he could draw on even older works such as David Hume's "The Natural History of Religion" (1757). In this lecture, Darwin's core definitions and hypotheses about the evolution of religiosity and religions are introduced and tested against contemporary data and knowledge in the field.

mi.blume@email.de

MON 22 AUG at 1100 - Room N5
Invited talk *B2-Sy31-1100-I*

Outreach Symposium

The Historical Position of Literary Darwinism

Carroll JC[1]
[1]University of Missouri, St. Louis, United States

Summary statement:

I locate Literary Darwinism in the history of science and specify ways it can contribute to the formation of a biologically grounded theory of culture.

Abstract:

I locate evolutionary literary study in a sequence of paradigm formations beginning with Charles Lyell's creation of a paradigm for geology about 200 years ago. Lyell's geological theory was a necessary precondition for Darwin's theory of evolution by means of natural selection—the foundation of modern evolutionary biology. After a hiatus of about a century, Darwin's biological paradigm provided the framework for modern research into the biological basis of human nature. That research, in turn, provides the basis for evolutionary studies in the humanities, now about two decades in the making. The paradigm for the evolutionary human sciences ("evolutionary psychology") is itself still incomplete. In recent years, evolutionists have been developing more adequate ideas of cooperative group living and flexible general intelligence, but they have not yet fully incorporated the idea of the "imagination" in their conception of human nature. As a result, their conceptions of "culture" remain rudimentary. Literary Darwinists have assimilated the evolutionary psychologists' findings about human nature, and they can in turn offer illumination to psychologists about the adaptive functions of the imagination. A comprehensively adequate model of human nature is now within our reach, and it is already possible to delineate a basic analytic structure for "biocultural critique," that is, for literary interpretation from an evolutionary perspective. I diagram a working model of human nature and a working model for biocultural critique.

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MON 22 AUG at 1120 - Room N5
Invited talk *B2-Sy31-1120-I*

Outreach Symposium

Defining and developing the concept of viral symbiosis in evolutionary biology in general and in human evolution in particular.

Ryan FP[1]
[1]University of Sheffield, Medicine/ Animal and Plant Sciences, Sheffield, United Kingdom

Summary statement:

There is growing evidence that viral symbiosis has contributed broadly to the evolution of life, and to human evolution in particular. It offers major scope for new research.

Abstract:

The synthesis of Darwinian natural selection, mutation and Mendelian genetics has contributed greatly to our understanding of evolutionary change. Meanwhile increasing knowledge of other mechanisms, such as symbiogenesis, hybridogenesis, horizontal gene transfer in prokaryotes, epigenetics, and events specific to evolutionary development, with natural selection operating in different ways and at various levels, have widened our horizons to a diversity of evolutionary possibilities. Viruses are genetic parasites long familiar as the cause of endemic and epidemic diseases. Over the last decade or so we have become increasingly aware of a wider role for viruses, possibly in the origins of life itself and certainly in its subsequent evolution to biodiversity as we see it today. This relatively new, but growing, field has major implications for our understanding of life, ecology, human and veterinary medicine, and agriculture. This has led to an expansion of novel research extending across all of the biological and applied fields. It has been assisted, at molecular level, by whole genomic sequencing, which has revealed extensive viral endogenization in prokaryotes and eukaryotes, including all animals and plants that have been studied to date. In particular, this is illustrated by the growing understanding of the viral role in human evolution. Some 8% of the human genome consists of human endogenous retroviruses, or HERVs, and, if we extend this to LINEs and SINEs, virus-linked legacy amounts to roughly half of the human DNA. Where this was previously dismissed as “junk DNA”, there is growing evidence that HERVs, and related genetic sequences, have made a major contribution to human evolution, and are playing important roles in human embryology, reproduction and day-to-day physiology. This is a relatively new field with considerable scope for novel multidisciplinary research.

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Symposium 1

Microbe/macrobe experimental evolution

Talks: *Room N7*

***Essence posters**: Upper floor lecture hall centre HZ*

***Regular posters**: Upper floor campus canteen Mensa*

Invited Speakers:

Graham Bell, Richard E Lenski, Tadeusz Kawecki

Organizers:

Rhonda R Snook, Nick Colegrave, Thomas U Berendock, Oliver Kaltz, Stéphanie Bedhomme, Santiago F Elena

Description:

Experimental evolution (EE) is a tool that has provided advances in understanding fundamental evolutionary questions in real time. The symposium goals are to (i) illustrate the diversity of uses of EE encompassing both microbial and macrobial systems and/or (ii) to highlight how emerging next generation techniques can be combined with EE for greater understanding of the genetic basis of evolution.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy01-i001-R*

Symposium 1
Microbe/macrobe experimental evolution

Using experimental evolution to investigate X-linked sexually antagonistic genetic variation in Drosophila melanogaster

Abbott JK[1], Morrow EH[1], Innocenti P[1], Chippindale AK[2]
[1]Uppsala University, Department of Ecology and Genetics, Uppsala, Sweden, [2]Queen's University, Biology Department, Kingston, Canada

Summary statement:

Male-limited X-chromosome evolution results in changes in expression level in genes associated with metabolism, locomotory activity, and male courtship activity.

Abstract:

Previous results have shown that when replicate populations of Drosophila melanogaster were exposed to many generations of male-limited (ML) experimental evolution, this resulted in masculinization of the phenotype in both sexes and an increase in fitness in ML males relative to control males, but a decrease in ML female fitness relative to control females. Theoretical and empirical evidence that the X-chromosome should be a hotspot for sexually antagonistic genetic variation, but the relative contributions of the X and autosomes to altered phenotype and fitness could not be determined in the original ML experiment. I have therefore carried out novel experimental evolution protocol where the X chromosome experiences male-limited expression, but the autosomes are expressed in both sexes. I have found the expected increase in male fitness as a result of male-limited X-chromosome (MLX) evolution, but there has been no concurrent decrease in female fitness. This may be due to dominance effects on the X, since X-linked sexually antagonistic genetic variation favouring males is expected to evolve to be recessive in females. I have also investigated differences in gene expression between MLX and control groups and found that MLX individuals have changed gene expression levels in genes associated with metabolism, locomotory activity, and male courtship activity. This is consistent with previous research suggests that locomotory activity is a sexually antagonistic trait with a substantial portion of the additive genetic variance located on the X chromosome.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy01-i002-R*

Symposium 1
Microbe/macrobe experimental evolution

The cost of codon usage bias and how to overcome it

Amorós Moya D[1], D'Auria G[2], Bedhomme S[3], Bravo IG[2,4]
[1]University Münster, Institute for Evolution and Biodiversity, Münster, Germany, [2]Centre for Public Health Research (CSISP), Genomics and Health, Valencia, Spain, [3]Instituto de Biología Molecular y Celular de Plantas (CSIC-UPV), Evolutionary Systems Virology Group, Valencia, Spain, [4]Catalan Institute of Oncology (ICO), Infection and Cancer Unit, L'Hospitalet de Llobregat, Spain

Summary statement:

Codon usage bias is not an obstacle for gene fixation upon HGT: fitness cost associated to mal-adaptation can be overcome through compensatory evolution.

Abstract:

Non-optimal codon usage decreases gene translation efficiency, potentially leading to a fitness cost. This cost is thought to be important in determining the success of horizontal gene transfer (HGT).We have mimicked a HGT event and measured for the first time the fitness cost associated with codon usage bias. We also used experimental evolution to evaluate the potential for adaptation and eventually fixation of transferred genes.
Specifically, we used three versions of an antibiotic resistance gene, each version encoding for the same protein but differing in its codon usage adaptation to the recipient organism (E. coli). Codon usage mal-adaptation results in an important cost: bacteria carrying genes with a suboptimal codon usage are ten to twenty times more sensitive to antibiotic than those with the optimal version. After 1000 generations of experimental evolution under antibiotic selective pressure, this fitness cost has been overcome by fixation of both in cis changes in the gene promoter and in trans changes in the host bacterial genome, gene silencing and gene lost. No mutations in the coding sequence of the gene have been found. Some of the changes are shared among bacterial lines and constitute experimental evidence for convergent molecular adaptive evolution. Further, pyrosequencing analysis shows hints of plasmid/cell/population multilevel selection.
These results suggest that the initial high fitness cost of non-optimal codon usage is a minor obstacle to gene fixation upon HGT and that the rapid evolution of regulatory mechanisms is of a great importance in the adaptation to new environmental and genetic situations.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy01-i001-E*

Symposium 1
Microbe/macrobe experimental evolution

The effects of ecological opportunity and resource competition on the evolution of genomic diversity

Bailey SF[1], Rodrigue N[2], Kassen R[1]
[1]University of Ottawa, Department of Biology, Ottawa, Canada, [2]Agriculture and Agri-Foods Canada, Ottawa, Canada

Summary statement:

We examine the genomes of Pseudomonas fluorescens populations experimentally evolved in environments ranging in ecological opportunity and the potential for resource competition.

Abstract:

Ecological opportunity and resource competition are thought to drive the dynamics of adaptation and diversification. Abundant opportunity leads to divergent selection which, in combination with competition for those opportunities, can generate disruptive selection leading to faster and more extreme adaptive differentiation. To test the effects of these ecological factors, we allowed populations of Pseudomonas fluorescens to evolve in environments that varied in both ecological opportunity and the potential for resource competition. We varied ecological opportunity by changing the number of distinct carbon resources available, and varied the potential for resource competition to drive disruption selection by providing those resources in either mixtures, or spatially distinct patches with dispersal. Isolates from generation 1000 were then assayed on a range of carbon sources in order to estimate phenotypic diversity, and the population genomes were sequenced. We report the effects of ecological opportunity and resource competition on the evolution of both phenotypic and genomic diversity.

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MON 22 AUG at 1650 - Room N7
Oral presentation *B4-Sy01-1650-O*

Symposium 1
Microbe/macrobe experimental evolution

Adaptation and the evolution of sex in facultative sexual rotifers

Becks L[1,2], Agrawal AF[1]
[1]University of Toronto, Ecology and Evolutionary Biology, Toronto, Canada, [2]University of Cologne, General Ecology, Cologne, Germany

Summary statement:

In experiments with a facultatively sexual rotifer, populations adapting to novel environments evolve higher rates of sex due to a long-term advantages.

Abstract:

One of the oldest and most enduring hypotheses for the evolution of sex is based on the idea that sexual reproduction facilitates adaptation. While previous empirical work showed that sexual reproduction can accelerates adaptation, evidence that sex can evolve during times of adaptation is still lacking. Using facultatively sexual rotifers, we present direct experimental evidence that adaptation can drive the evolution of sex itself. We find that sex is favoured in novel environments. Rates of sex evolved within adapting populations to higher levels, but declined when populations were close to their fitness optimum. We found a similar, but consistent decline in the control populations that stayed in the environment they previously were adapted to. We link these changes in the rate of sex to their underlying population genetic mechanisms by experimentally inducing sex in a subsample of the populations. Specifically, we find that long-term advantages of sex became large in populations adapting to novel environments, but not in control populations. Compared to non-adapting control populations in which sex is disfavoured, we find that sex has both a larger long-term advantage and a smaller short-term disadvantage in adapting populations.

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MON 22 AUG at 1440 - Room N7
Invited talk ***B3-Sy01-1400-I***

Symposium 1
Microbe/macrobe experimental evolution

The multifarious response to uniform natural selection

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Summary statement:

Evolution is an historical process with a wide range of potential outcomes when a population is exposed to a novel stress.

Abstract:

Radical change in the conditions of life will usually cause extinction, but populations may sometimes evolve a novel suite of adaptations. I report an experiment in which the green alga Chlamydomonas, which is normally a photoautotroph, was cultured in the dark as a heterotroph. The surviving lines document three leading features of adaptive evolution in novel and stressful environments:
(a) the range of direct response;
(b) the range of antagonistic response in the ancestral environment;
(c) the range of incidental response with respect to characters not directly associated with adaptation.
Each line exhibited a unique combination within some constrained set of attributes.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy01-i003-R*

Symposium 1
Microbe/macrobe experimental evolution

Intralocus sexual conflict over lifespan and aging in the seed beetle

Berg EC[1], Maklakov AA[1]
[1]Uppsala University, Department of Animal Ecology, Uppsala, Sweden

Summary statement:

We used artificial selection on male lifespan and sex-specific fitness assays to expose the role of intralocus sexual conflict over aging in a beetle.

Abstract:

Males and females have different routes to successful reproduction resulting in sex differences in lifespan and age-specific allocation of reproductive effort. Theory suggests that while the tradeoff between current and future reproduction is often resolved differently by males and females, both sexes can be constrained in their ability to reach their sex-specific optima due to intersexual genetic correlation (i.e. intralocus sexual conflict). Such genetic conflicts may have profound implications for sex-specific trait evolution, but their role in aging remains largely unresolved. We examined this question in the seed beetle, Callosobruchus maculatus, a model system for studying sex differences in genetic architecture of lifespan and aging. Previous studies suggest that male C. maculatus maximize their fitness by high reproductive investment early in life ("live-fast-die-young" strategy), while females optimize their reproductive output by conserving energy for future reproduction. Using a genetically heterogeneous stock population, we selected on male longevity for five generations to create replicate long-life lines (n = 4) that lived on average 22% longer than short-life lines (n = 4). We then performed comprehensive assays of longevity, aging and lifetime reproductive success for males and females under the conditions that reflected recent evolutionary history of these populations. In this paper we will discuss the results of these assays, which provide a direct experimental test of the role of intralocus conflict in the evolution of lifespan and aging.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy01-i004-R*

Symposium 1
Microbe/macrobe experimental evolution

Adaptation to a novel environment can promote outcrossing and maintenance of mixed mating in a preferentially self-fertilizing species

Carvalho SNL[1], Teotonio H[1]
[1]Instituto Gulbenkian de Ciencia, Evolutionary Genetics Group, Oeiras, Portugal

Summary statement:

Intra-individual sexual selection might be an important mechanism for the evolution of mating systems that has been unaccounted for in most theoretical models insofar.

Abstract:

While the role of mating systems on evolutionary adaptation has been widely studied, adaptive explanations for the evolution of mating systems themselves and more specifically for the existence of mixed mating systems has received less attention.
We performed experimental evolution on two sets of populations of the nematode Caenorhabditis elegans differing in their breeding system: androdioecy (coexistence of males and self-fertilizing hermaphrodites) and dioecy (males and females). Because males are produced by cross-fertilization, the androdioecious system could evolve towards selfing, outcrossing or mixed mating by changes in the relative proportions of self- and cross-fertilization events. Dioecious populations provided the standard for full outcrossing.
Androdioecious populations exhibited intermediate levels of crossing (50%) throughout 100 generations of experimental evolution, a rate several orders of magnitude higher than outcrossing rates estimated for natural populations based on molecular markers.
Measurements of reproductive output and viability of hermaphrodites under conditions of selfing and outcrossing and measurements of the same phenotypes in females reveal similar phenotypic evolution between the females and outcrossed hermaphrodites and significant lower phenotypic change of hermaphrodites under conditions of selfing.
Altogether, our results suggest the action of opposing selective forces between male and female reproduction components within hermaphrodites.

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TUE 23 AUG at 1500 - Room N7
Oral presentation *C3-Sy01-1500-O*

Symposium 1
Microbe/macrobe experimental evolution

High mortality leads to slower aging

Chen H-Y[1], Maklakov A[1]
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Summary statement:

Our results show that longer lifespan and lower late-life mortality rates evolve under high condition-dependent mortality challenging the classic aging theory.

Abstract:

Aging is a phenomenon that affects nearly all organisms, but why and how aging evolves is still unclear. The classic theory predicts that high extrinsic mortality should lead to accelerated aging because the strength of selection declines with age. Consequently, deleterious mutations that show effects at late age, or pleiotropic mutations that are beneficial at young age but deleterious at late age, would rise in frequency. However, mortality in nature is likely to be condition-dependent and recent theory suggests that condition-environment interactions may result in the evolution of decelerated aging under high extrinsic mortality. Environmental stress, as a source of extrinsic mortality, can select for decreased susceptibility to the stress, resulting in prolonged lifespan and decelerated aging in a population. There is strong evidence suggesting that genes involved in stress resistance can prolong lifespan but studies of the evolution of lifespan and aging under condition-dependent selection are currently lacking. Here, we subject the nematodes Caenorhabditis remanei to experimental evolution under four life-history regimes for twelve generations: 1) High Random Mortality; 2) Low Random Mortality; 3) High Condition-dependent Mortality and 4) Low Condition-dependent Mortality. We confirmed the classic prediction by showing the evolution of shorter lifespan under High Random Mortality. Remarkably, we show that longer lifespan and lower late-life mortality rates evolve under High Condition-dependent mortality supporting the novel theory. These results challenge the classic theory and suggest that the source of mortality plays a key role in the evolution of aging.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy01-i002-E*

Symposium 1
Microbe/macrobe experimental evolution

Experimental approach to the study of fisheries induced evolution

Diaz Pauli B[1], Utne Palm AC[1], Reznick DN[2], Heino M[1,3,4]
[1]University of Bergen, Department of Biology, Bergen, Norway, [2]University of California, Riverside, Department of Biology, Riverside, United States, [3]Institute of Marine Research, Bergen, Norway, [4]International Institute for Applied Systems Analysis, Laxenburg, Austria

Summary statement:

We carry out an experimental evolution study to assess the effects of size-selective fishing on life-history traits of the model species Poecilia reticulata.

Abstract:

Fishing is a selective process. Fish with the most desirable characteristics are captured and removed from the population, thus reducing the chance that these fish pass their genes to next generations. Fishing is commonly size-selective, removing the bigger and economically more valuable individuals, but it also selects other life-history traits, morphologies and behaviours. Increased mortality favours fast life histories; active fishing gear favours fish that are good at either escaping or hiding and, passive gears, such as gillnets, may favour altered body shapes and lesser activity. Therefore, given a genetic basis of the phenotypic variation, fishing can cause evolution towards a less sustainable and profitable populations.
To assess the effects of fishing on populations we carry out an experimental evolution study. Experimental populations of Trinidadian guppies, Poecilia reticulata, are harvested every sixth week, removing big individuals (positive size selection), small individuals (negative size selection) or a uniform random proportion of individuals (no size selection). The experimental selection started in October 2010; here we present the (initial) responses of the populations to the selection regimes with regards to their size distribution, size at maturation and population dynamics.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy01-i003-E*

Symposium 1
Microbe/macrobe experimental evolution

Effects of low oxygen adaptation on sperm-offence and sperm-defence in Drosophila melanogaster

Dobler R[1], Charette M[2], Reinhardt K[1], Rundle HD[2]
[1]University of Tübingen, Institute for Evolution and Ecology, Tübingen, Germany, [2]University of Ottawa, Department of Biology and Centre for Advanced Research in Environmental Genomics, Ottawa, Canada

Summary statement:

We assessed the effects of adaptation 1) on sperm performance in different environments (GxE) and 2) on time dynamics of sperm competition abilities.

Abstract:

The interaction between genotypes and environment can have strong effects on survival and fitness of individuals. However, little is known about the effects of different environments on the interaction between sperm and egg. Adaptation to different environments may lead to changes in male and female physiology (e.g., internal pH or O2-saturation) and hence alter the metabolism of sperm and egg. Differences in gamete viability of individuals from different environment in different environments may not be immediate (i.e., within the first hours after mating), but may only be detectable after several hours or days. We selected lines of fruit flies (Drosophila melanogaster) for over 40 generations in a low oxygen (hypoxic) environment (5% O2) to test effects of adaptation on male fitness. We assessed the sperm-offence and sperm-defence abilities of hypoxy-adapted and non-adapted males over six days when mated to control females in either a hypoxic or a normal environment. We expect 1) to find an interaction between the male type (i.e., hypoxy-adapted or non-adapted) and the mating environment and 2) that sperm-offence and sperm-defence abilities change differently over time in hypoxy-adapted and non-adapted males, respectively.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy01-i005-R*

Symposium 1
Microbe/macrobe experimental evolution

Ecological factors determine the cost of cooperation and selection for cheats in bacterial metapopulations

Dumas Z[1], Kümmerli R[1,2]
[1]EAWAG, Environmental Microbiology, Dübendorf, Switzerland, [2]ETH Zürich, Department of Environmental Sciences, Zürich, Switzerland

Summary statement:

We show that patchy resource distribution and increased public goods durability contribute to the evolutionary stability of cooperation in a bacterium

Abstract:

The bacterium Pseudomonas aeruginosa releases pyoverdin into the environment to scavenge insoluble or host-bound iron. Pyoverdin is a public good that can be shared among neighbouring cells. Consequently, pyoverdin producers are vulnerable to exploitation by pyoverdin-deficient mutants (cheats) that reap the benefit without paying the costs. Indeed, selection for cheats has been observed in laboratory studies, but contrasts with observations from natural environments where pyoverdin producers persist. To understand this discrepancy, we compared the strengths of selection for cheats in four patch-structured metapopulations differing in the following conditions: (1) all patches were strongly iron limited; (2) half the patches received low iron supplements, which mirrors localized increased iron availability as occurring in damaged host tissues; (3) half the patches inherited some pyoverdin from previous generations, which considers that pyoverdin can be durable and recyclable across generations; and (4) a combination of the second and third treatment. We show that all conditions were iron-limited, but investment into pyoverdin and thereby its production cost gradually decreased from treatment (1) to (4). This cost reduction impacted selection for cheats, which was strong under high iron limitation, but significantly weaker when iron or pyoverdin was supplemented. No selection for cheats occured in treatment (4), where pyoverdin over-producers were favoured. Our findings indicate that patchy iron distribution and pyoverdin durability, two important components of P. aeruginosa ecology, significantly contribute to the maintenance of cooperative pyoverdin production in nature.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy01-i006-R*

Symposium 1
Microbe/macrobe experimental evolution

Temperature increase affects virulence in a Paramecium-Caedibacter system

Dusi E[1], Krenek S[1], Schrallhammer M[1], Berendonk TU[1]
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Summary statement:

Short term temperature increase has a direct effect on parasite virulence in different host life stages.

Abstract:

Host-parasite coevolution is driven by a variety of factors, including extrinsic and intrinsic components. One of the main forces in host-parasite interactions is parasite virulence, the fitness reduction of the host caused by the parasite. Abiotic environmental changes like increasing temperature affect both parasite and host and are able to modify the coevolutionary dynamics, especially virulence evolution, in short and long term. To determine the short-term effect of increasing temperature on virulence, we used the bacterial parasite Caedibacter taeniospiralis harboured within the cytoplasm of the unicellular eukaryote Paramecium tetraurelia. Caedibacter taeniospiralis is an obligate intracellular parasite, which does not shift its transmission mode from vertical to horizontal, but rather transmits mainly vertical. In our experiments, we compared the host growth rate and its carrying capacity in different temperature treatments including the host optimum and a host stress temperature. In response to a short term temperature increase, we found differences in virulence affecting both host life stages. In the future we will compare the data of the short term experiment with the subsequent long term treatment.

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MON 22 AUG at 1630 - Room N7
Oral presentation *B4-Sy01-1630-O*

Symposium 1
Microbe/macrobe experimental evolution

Fitness associates sex and the costs of competence in long-term evolved populations of Streptococcus pneumoniae

Engelmoer DJP[1], Donaldson I[1], Bergman C[1], Rozen DE[1]
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Summary statement:

Costs of recombination in long-term evolved S. pneumoniae are mitigated by periodic stress, which is reflected in fitness, rates of recombination and genome changes.

Abstract:

Recombination plays a central role in shaping the structure of bacterial genomes. Less clear are the benefits that recombination provides to evolving bacterial populations. Recombination can increase the rate of adaptation by combining beneficial mutations and slow the rate of Muller's Ratchet. Alternatively, by breaking up combinations of beneficial alleles, recombination can be costly, in addition to its likely metabolic cost. Bacterial transformation is part of a broader change in cell state called competence. Competence is often induced under changing or stressful conditions, suggesting that benefits of transformation apply only to certain environmental conditions. Such conditional benefits are encapsulated in the fitness-associated-sex (FAS) hypothesis, which predicts that recombination is favoured during conditions when the fitness of the organism is low. To test this hypothesis we evolved sexual and asexual strains of the naturally competent bacterium S. pneumoniae in benign or periodically stressful conditions for 1,000 generations. We find that in a benign environment competence has a fitness cost and evolved recombining lines are less fit than their asexual counterparts. However, consistent with FAS this cost is mitigated when populations are exposed to periodic stress. In addition, while stressed populations retain wild-type recombination rates, this is dramatically reduced in strains evolved in benign conditions. Whole genome re-sequencing of all evolved lines will illuminate the mechanistic basis of these results. Our data highlight the context dependence of costs and benefits of bacterial transformation and support predictions of the FAS hypothesis.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy01-i007-R*

Symposium 1
Microbe/macrobe experimental evolution

Recombination reduces the rate of Muller's ratchet in the bacterium Streptococcus pneumoniae

Evans BA[1], Rozen D[1]
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Summary statement:

We provide the first evidence that bacterial sex can serve to reduce the fixation rate of deleterious mutations.

Abstract:

Quantifying the costs and benefits of sex and recombination remain a central problem in evolutionary biology. One hypothesised benefit of recombination is that it reduces the fixation rate of deleterious mutations. Here we test this hypothesis by examining the effects of recombination on the rate of fitness decline due to Muller's ratchet in the naturally competent bacterium Streptococcus pneumoniae, by incorporating recombination into a classic mutation accumulation experimental design.

Forty S. pneumoniae lines derived from a common ancestor were passaged through daily bottleneck transfers of a single cell. Half of these lines were maintained asexually, while the rest were randomly paired twice weekly and induced to recombine by natural transformation. The experiment ran for approximately 1500 generations, comprising approximately 100 single cell bottlenecks and, in the case of the recombining treatment, 30 rounds of induced recombination.

We find that in both the recombining and the non-recombining treatments, lines had decreased exponential growth rates (RGRs) relative to the ancestor. Consistent with the idea that recombination slows Muller's ratchet, the mean reduction in RGR of the recombining lines was significantly less than that of the non-recombining lines. However, we find no difference in variation in RGR among lines across treatments. Genome re-sequencing of all endpoint lines is being used to estimate treatment-specific mutation rates and the rate that mutations are removed by recombination. These data provide the first evidence that bacterial sex can serve to reduce the fixation rate of deleterious mutations.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy01-i008-R*

Symposium 1
Microbe/macrobe experimental evolution

Trade-offs shape the evolution of virulence in the vector-borne insect pathogen Xenorhabdus nematophila

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Summary statement:

The virulence of the bacterium Xenorhabdus nematophila increases its vector parasitic success but its survival during dispersal.

Abstract:

Our current understanding on how pathogens evolve rely on the hypothesis that pathogens´ transmission is traded-off against host exploitation. This central idea originates from a thirty years old mathematical model. But the main assumption it relies on, i.e. the idea that pathogens contagiousness increases with virulence while preserving host survival can enhance transmission, has received little empirical support.
Here we applied the experimental evolution protocol on Xenorhabdus nematophila a hyper-virulent bacterial insect pathogen. We produced 20 bacterial lineages that have different virulences towards their insect host. In nature Xenorhabdus nematophila is transmitted by a nematode vector, Steinernema carpocapsae, which reproduces in the insects that have been killed by the bacteria it carries. We found that nematode parasitic success increases with bacteria virulence, but that their survival during dispersal decreases with the number of bacteria they carry. Other bacterial traits, such as production of the haemolytic protein xaxAB, have a strong impact on nematodes reproduction. We then estimated pathogens´ fitness, which we divided into one parasitic component and one dispersal component. We found that the number of bacteria nematodes carry positively influences the parasitic component of fitness but negatively impacts the dispersal component. These results demonstrate the potential for a trade-off between host exploitation and transmission in Xenorhabdus nematophila. They therefore both support the trade-off theory of pathogen evolution and suggests that it can apply to pathogens that are hypervirulent and vector transmitted.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy01-i009-R*

Symposium 1
Microbe/macrobe experimental evolution

The ecology and genetics of Pseudomonas fluorescens ´Fuzzy Spreaders´ evolving in spatially structured microcosms

Ferguson GC[1], Rainey PB[1,2]
[1]Massey University Auckland, Institute for Advanced Study, Auckland, New Zealand, [2]Max Planck Institute for Evolutionary Biology, Plön, Germany

Summary statement:

Precisely how FS interacts with WS and SM types at the air-liquid interface, along with the genetic basis of the phenotype, is the focus of current investigations.

Abstract:

When propagated in a spatially structured environment, the bacterium Pseudomonas fluorescens SBW25 rapidly diversifies into a range of niche specialist genotypes. “Smooth” (SM) types colonize the broth phase of static cultures; “wrinkly spreader” (WS) types colonize the air-liquid interface in the form of a mat, via the over-expression of an acetylated cellulose-like polymer; and fuzzy spreaders (FS) form large, spreading colonies with a “fuzzy” appearance and appear to occupy the floor of the microcosm. While the WS type is well characterised, little is known about the ecology and genetics of the FS type. Closer inspection of FS growth within spatially structured microcosms revealed interesting ecological interactions between the three dominant emergent types: FS isolates observed over time initially began growth at the air-liquid interface, with clumps of cells attempting to spread as a biofilm but ultimately falling to the microcosm floor. This pattern of growth would suggest that FS competes with WS for occupancy of a similar niche. FS performs very poorly in competition with WS for this niche; however, it repeatedly arises and increases in frequency whenever spatially structured microcosms are seeded with an ancestral type, suggesting that either it occupies a subtly different niche to either WS or SM, or is maintained as a consequence of negative frequency-dependent interactions between the other two types. We have located the causal mutation of the FS phenotype and uncovered a surprising genetic link between the FS and WS phenotypes: reconstruction of the FS mutation in WS creates a mutant unable to form a strong mat at the air-liquid interface.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy01-i010-R*

Symposium 1
Microbe/macrobe experimental evolution

Evolution in species assemblages

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Summary statement:

We used bacterial assemblages to determine the effects of species richness on evolutionary responses to changing environments in the beech tree-hole laboratory system.

Abstract:

A key task for understanding the dynamics of living systems, and for predicting the impacts of human activities on those systems, is to understand how ecosystems respond to environmental change. Two types of responses and their interactions can be considered: ecological (differences in community structure) and evolutionary (genotypic changes within species). We tested whether ecological interaction in communities tend to increase, decrease of not affect the amount of evolution within component species. Using an assemblage of bacteria isolated from tree-holes of beech (Fagus sylvatica), we assembled random mixtures of species and exposed them to environmental change, in terms of a shift in pH and resource type in turn. Growth rate comparison of ancestral and evolved isolates (from monoculture and polyculture background) showed significant differences among clones that survived in experimental communities. Many showed a differential response based on which other species was present in the mix. These results demonstrate that species richness and composition can influence the adaptive responses of species to environmental change. The results will generate new conceptual understanding of the interaction between ecological and evolutionary processes in ecosystems facing environmental change.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy01-i011-R*

Symposium 1
Microbe/macrobe experimental evolution

Less-diversifying genotypes in a bacterial adaptive radiation: generalists?

Flohr RCE[1], Rainey PB[2], Beaumont HJE[1]
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Summary statement:

Experimental adaptive radiation of Pseudomonas fluorescens can be suppressed by the emergence of genotypes that appear to use a generalist strategy.

Abstract:

Aim: Adaptive radiation is a key mechanism for the evolution of biological diversity, but experimental insight into the factors that shape it is still limited. Here we present results from an ongoing experiment that seeks insight into the role of organismal factors.
Methods: Experimental populations of the bacterium Pseudomonas fluorescens readily diversify into several niche specialist genotypes that coexist in a spatially structured environment. We use a previously described selection regime to obtain genotypes with a reduced capacity to diversify and examine the ecological and genetic causes using a suite of competition experiments and a genomic selection cassette that allows detection of evolved niche specialists at low frequencies.
Results: Preliminary analysis of a less-diversifying genotype that emerged early in the selection experiment revealed that it does give rise to niche specialists by mutation, but that these reach only very low frequencies not detectable without the selection cassette. Pairwise comparison of the competitive abilities of the less-diversifying and two opposing niche-specialist genotypes indicated that invading niche specialists are suppressed more by the less-diversifying type than by each other.
Conclusions: These preliminary results suggest that the reduced capacity to diversify is due to a generalist strategy of the ancestor. The possibility of generalists in this model adaptive radiation sheds new light on how evolvability and ecological opportunity interact to shape adaptive radiations.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy01-i004-E*

Symposium 1
Microbe/macrobe experimental evolution

Adaptation of Escherichia coli to the mammalian gut

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[1]Instituto Gulbenkian de Ciência, Oeiras, Portugal

Summary statement:

High rate of adaptive mutations and pervasive clonal interference in E. coli adapting to the mammalian gut.

Abstract:

Organisms adapt through mutations that are random with respect to their needs. Adaptation depends on the mutation rate, the genotype and the nature of the environment. A great deal of our understanding of the process of adaptation comes from studying the dynamics of adaptation of microbial populations in in vitro experimental evolution settings. An important phenomena that has been recurrently observed in microbial populations undergoing adaptive evolution to laboratory conditions is named clonal interference. This phenomenon is expected to occur whenever the mutational input to novel beneficial mutations is high, which is more likely in large populations. Clonal interference is characterized by the simultaneous competition of clones carrying different adaptive mutations and its effect will lead to dynamics of adaptation very different from those expected under more classical models where single adaptive mutations increase in frequency towards fixation one at a time - the classical single selective sweep model. The patterns of molecular variation and evolution are also different under clonal interference and adaptive evolution will be characterized by the fixation of stronger effect mutations, because those are the ones most likely to win the intense competition that takes place under clonal interference. It is not known if this theoretical predicted and in vitro tested phenomenon takes place in more natural conditions. Here we study adaptation of Escherichia coli to its natural environment: the mammalian gut. Using a classical mice colonization system we show that the rate of mutation to new beneficial alleles is very high and that clonal interference is pervasive.

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SUN 21 AUG at 1500 - Room N7
Oral presentation *A3-Sy01-1500-O*

Symposium 1
Microbe/macrobe experimental evolution

Experimental evolution of bet hedging in Neurospora crassa provides support for the geometric-mean fitness principle

Graham JK[1], Smith ML[2], Simons AM[1]
[1]Carleton University, Department of Biology, Ottawa, Canada, [2]Carleton University, Department of Biology & Institute of Biochemistry, Ottawa, Canada

Summary statement:

N. crassa was subjected to experimental selection in lines differing in unpredictability. Spore dormancy fraction evolved as predicted by bet-hedging theory developed for plants.

Abstract:

The geometric-mean principle states that natural selection will result in traits that maximize fitness over the long term even if they are disadvantageous over the short term. However, no direct empirical test of the geometric-mean principle exists. Cohen's classic model of the evolution of seed dormancy as bet hedging in angiosperms offers a simple and direct test: the geometric-mean fitness is maximized by the evolution of dormancy proportional to the frequency of "bad years", including for bad-year frequencies < 0.5 (i.e. a good year is expected). Here, in an experimental test of the geometric-mean principle, we allow ascospore dormancy fraction in the fungus Neurospora crassa to evolve under five selection regimes that differ in the frequency of bad years (0, 0.2, 0.3, 0.4, 0.5). Final dormancy fractions across the five selection lines are consistent with Cohen's predictions, and evolved both upward and downward from a range of starting dormancy fractions in 12 genetic crosses. Our experimental results provide direct evidence that fluctuating selection acts to increase the geometric-mean fitness.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy01-i005-E*

Symposium 1
Microbe/macrobe experimental evolution

Evolved resistance of Staphylococcus aureus and Staphylococcus epidermidis to the cationic antimicrobial peptide, pexiganan

Habets M[1], Brockhurst MA[1]
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Summary statement:

Our data will provide essential insight into the mechanism of resistance for a novel class of antibiotics.

Abstract:

Cationic antimicrobial peptides (AMP) of the innate immune system provide a first line of defense against intruding microorganisms. These peptides are seen as a potential weapon against increasingly antibiotic -resistant microbes, and are being developed into drugs. The presumption is that resistance to these AMPs is difficult to evolve; however, it has been shown previously that against one of these novel antibiotics, pexiganan, resistance arises in both Escherichia coli and Pseudomonas fluorescens within 700 generations. As pexiganan will be introduced as a drug against infections of foot ulcers, if/when approved by the FDA, it will thus be necessary to examine whether bacteria responsible for these infections are also capable of evolving rapid resistance. Staphylococcus aureus and Staphylococcus epidermidis are a common cause for infections of foot ulcers in diabetics. We have examined the emergence of resistance by transferring six populations of each species every 48 hours to increasing concentrations of pexiganan. Reduced susceptibility has rapidly arisen in S. aureus and S. epidermidis and we are examining its associated costs. Whole genome sequencing of evolved lines will illuminate the mechanistic basis of resistance. In addition, we will test whether compensation occurs for costly resistance mutations when resistant strains are grown in the absence of the drug. Our data will provide essential insight into the mechanism of resistance for this novel class of antibiotics.

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MON 22 AUG at 1500 - Room N7
Oral presentation *B3-Sy01-1500-O*

Symposium 1
Microbe/macrobe experimental evolution

Antagonistic coevolution between clones of the social amoeba Dictyostelium discoideum

Hollis B[1,2]
[1]University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland, [2]Florida State University, Department of Biological Science, Tallahassee, United States

Summary statement:

An experimental evolution approach with social amoebae reveals changes in the magnitude of "cheating" by different clones within only 10 social generations.

Abstract:

Social groups face a fundamental problem of overcoming selfish individuals capable of destroying cooperation. The social amoeba Dictyostelium discoideum has emerged as a model system in the study of cooperation and conflict. These amoebae live as solitary haploid cells, reproducing until resources are scarce and then aggregating to form a slug that later develops into a fruiting body. There is evidence that some clones (“cheaters”) contribute disproportionately to the viable spores that will be dispersed while avoiding the dead stalk cell fate. It remains unclear if this cheating is actually the product of selection favoring cheaters and represents an adaptation. Relatedness is high in fruiting bodies collected from the wild, suggesting that the conflict demonstrated in the lab may be rare in nature and “cheating” may actually result from pleiotropic effects of divergent genes. Here I report the results of an experimental evolution study lasting ten social generations that was designed to test whether clones of Dictyostelium discoideum will evolve to exploit other clones in the laboratory. When two clones (one GFP-labeled and one wild type) were allowed to develop together and coevolve over the course of the experiment, one of the clones reliably increased its representation in the spores relative to control clones that had never been in the presence of one another. This exploitation was even greater when an experimental manipulation was used to prevent one competing clone from coevolving. Taken together, these results indicate strong antagonism between clones and ample genetic variation for cheating upon which natural selection can act.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy01-i012-R*

Symposium 1
Microbe/macrobe experimental evolution

Genes in conflict: Effects of experimental sexual selection on post-mating molecular interactions in Drosophila pseudoobscura females

Immonen E[1], Snook RR[2], Ritchie MG[1]
[1]University of St Andrews, Centre for Evolution, Genes and Genomics (CEGG), St Andrews, United Kingdom, [2]University of Sheffield, Animal & Plant Sciences, Sheffield, United Kingdom

Summary statement:

Experimentally evolved populations of D. pseudoobscura subjected to different sexual selection regimes were used to identify mating responsive genes under antagonistic selection.

Abstract:

It is now well established that promiscuity can generate sexual conflict resulting in antagonistic selection between the sexes, but more knowledge of the molecular processes and genes evolving under antagonistic selection is required. Previous studies have focused on post-mating gene expression changes in females in order to identify the molecular components of male-female interactions. However, which of the changes associated with mating are targeted by antagonistic selection is still poorly understood. We used experimentally evolved populations of D. pseudoobscura to address this question. Populations were subjected to either an enforced monogamy (M) treatment, which eliminates sperm competition, or an elevated promiscuity (E) treatment with intensified sperm competition and the opportunity for sexual conflict. We compared the gene expression profiles of M and E females as a response to mating with either M or E males, as well as of virgin females, in order to disentangle the effects of mating from those of the sexual selection regime. The differentially expressed genes and molecular pathways involved will be discussed.

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SUN 21 AUG at 1710 - Room N7
Oral presentation *A4-Sy01-1710-O*

Symposium 1
Microbe/macrobe experimental evolution

High genetic diversity accelerates adaptive radiation in microbial microcosms

Jousset A[1], Merker M[1], Eisenhauer N[2], Scheu S[1]
[1]Georg-August University Göttingen, Göttingen, Germany, [2]University of Minnesota, Department of Forest Resources, St. Paul, United States

Summary statement:

Genetic recombination improves the fitness of Pseudomonas fluorescens in presence of complex competitor communities, showing that biodiversity may accelerate evolution

Abstract:

Adaptive radiation is a central element of bacterial fitness and biodiversity. Diversification usually is assumed to result from natural selection of randomly occurring mutants. However, the underlying mutation process is by no means passive. Bacteria possess enzymes like site-specific recombinases controlling genomic rearrangement and therefore diversification processes. We used model Pseudomonas fluorescens communities to investigate the regulation of recombinases and their role in bacterial fitness in mixed communities. We used a recombinase deficient mutant to follow the role of recombination for bacterial fitness in bacterial communities of increasing richness and mean genotypic dissimilarity. Further, we followed the expression of XerD a recombinase required for phenotypic radiation. We show that the expression of XerD is upregulated if carbon resources are becoming limiting. Similarly, XerD was overexpressed at high community diversity, presumably due to niche pre-emption resulting in resource limitation. Recombination strongly increased bacterial fitness in diverse communities, which corresponded to a spread of new phenotypic variants. However, the XerD deficient mutant performed better at low diversity, suggesting that the generation of new phenotypes is costly in absence of selective pressure. The results indicate that flexible expression of the factors driving diversification is of prime importance for bacterial fitness in diverse communities. Moreover, the high expression of recombinases at high diversity indicates that diverse communities may evolve faster than less diverse ones, and therefore adapt faster to varying environmental conditions.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy01-i006-E*

Symposium 1
Microbe/macrobe experimental evolution

Reverse evolution: selection against costly resistance in disease-free microcosm populations of Paramecium caudatum

Kaltz O[1], Duncan AB[1], Fellous S[1]
[1]Université Montpellier 2, Institut des Sciences de l'Evolution (ISEM), UMR 5554, Montpellier, France

Abstract:

Costs of parasite resistance arise if genes conferring resistance reduce fitness in the absence of parasites. Thus, parasite-mediated selection should lead to increased resistance and a correlated decrease in fitness, whereas relaxed parasite-mediated selection should lead to reverse evolution of increased fitness and a correlated decrease in resistance. We tested this idea in experimental populations of the freshwater protozoan Paramecium caudatum and the parasitic bacterium Holospora undulata. After 8 years, resistance to infection and asexual reproductive rate were compared among paramecia from (i) infected populations, (ii) uninfected naive control populations and (iii) previously infected, now parasite-free (= recovered) populations. Paramecia from infected populations were more resistant (+12%), but had lower reproductive rates (-15%) than paramecia from naive populations, indicating an evolutionary trade-off between resistance and fitness. Recovered populations showed the same average reproductive rates as naive populations; however, resistance of recently recovered populations was similar to paramecia from infected populations, while longer recovered populations were as susceptible as naïve populations. This suggests a weak trade-off between resistance and fitness, allowing fitness to be regained, without complete loss of resistance. Thus (co)evolution with parasites can leave a genetic signature in a population, even when the parasite has disappeared for many generations.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy01-i013-R*

Symposium 1
Microbe/macrobe experimental evolution

The genomic architecture of adaptation in Drosophila melanogaster

Kapun M[1], Orozco-terWengel P[1], Kofler R[1], Nolte V[1], Schlötterer C[1]
[1]Vetmeduni Wien, Institut für Populationsgenetik, Wien, Austria

Summary statement:

We find evidence for positive selection on the genomic level by an experimental evolution approach in Drosophila melanogaster.

Abstract:

Aims: Understanding rates and patterns of positive selection is one of the most debated questions in evolutionary biology. Using a laboratory natural selection experiment and next generation sequencing, we are trying to find traces of positive selection on the genomic level in Drosophila melanogaster.
Methods: We performed a natural laboratory selection experiment by exposing replicate populations of D. melanogaster, which were collected in northern Portugal, to a novel environment (laboratory culture conditions at 28°C respectively) for more than 30 discrete generations. Using pooled sequencing, we determined the genome-wide allele frequencies for three different time points: start of the experiment, after 15 and 30 generations.
Results: We show that a large number of SNPs are affected by selection already after 15 generations, with pronounced excess on 3R. Consistent with previous results, we found none of the selected SNPs to be fixed by selection.
Conclusions: We noted that most of the selected changes occurred within 15 generations suggesting that the selective response is very high, but plateaus quickly. We will discuss several evolutionary scenarios that could explain our observations.

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TUE 23 AUG at 1400 - Room N7
Invited talk *C3-Sy01-1400-I*

Symposium 1
Microbe/macrobe experimental evolution

Experimental evolution of tolerance to chronic malnutrition in Drosophila: From life history to genomics

Kawecki TJ[1], Vijendravarma RK[1]
[1]University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland

Summary statement:

After >100 generations of evolution under nutritional stress fruit flies evolve changes in life history, growth pattern, behavior and gene expression patterns.

Abstract:

Many animal populations are periodically faced with insufficient food abundance or quality, and thus should have evolved adaptations that reduce the fitness consequences of malnutrition. We are using experimental evolution to study adaptation to chronic larval malnutrition in Drosophila melanogaster. Every generation the larvae of our experimental populations must complete development on nutritionally diluted food, which in non-adapted populations leads to 20 % reduction in viability, three-fold longer larval development, and adult weight reduced by half. We will summarize the changes in life history, growth pattern, immunity, behavior and gene expression patterns associated with adaptation to these extreme conditions. We will also address to what degree plastic responses to nutritional stress predict evolutionary responses.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy01-i014-R*

Symposium 1
Microbe/macrobe experimental evolution

Co-evolutionary arms race between public good cooperators and cheaters in a pathogenic bacterium

Kuemmerli R[1,2]
[1]Swiss Federal Institute of Aquatic Science & Technology (EAWAG), Environmental Microbiology, Dübendorf, Switzerland, [2]Swiss Federal Institute of Technology Zurich, Department of Environmental Sciences, Zurich, Switzerland

Summary statement:

Using a public good trait, I demonstrate an evolutionary arms race between bacterial cooperators (to escape exploitation) and cheaters (to optimize exploitation).

Abstract:

The opportunistic pathogen Pseudomonas aeruginosa releases pyoverdin into the environment to scavenge host-bound iron, making it available for metabolism. Pyoverdin represents a public good that can be used by other bacteria in the vicinity. Public good cooperators are vulnerable to cheating by individuals that no longer contribute, but still benefit from the contributions made by cooperators. However, it is unknown whether cooperators and cheaters can show adaptive responses to the presence of the other type, and whether these responses would result in an evolutionary arms race between cooperators (to escape exploitation) and cheaters (to increase exploitation efficiency). To tackle this question, I serially transferred mixed populations of cooperators and cheaters to fresh media, and monitored their frequency across 120 generations of experimental co-evolution. I found strong support for a co-evolutionary arms race:
(1) There were high temporal fluctuations in the relative frequencies of cooperators and cheaters, which significantly differed from the continuous cooperator decrease expected in the absence of co-evolution;
(2) trans-generational fitness assays revealed that cooperators escaped exploitation by cheaters from the past, but were highly vulnerable to cheaters from the future.
Finally, I sequenced evolved strains at candidate loci coding for genes involved in the production, uptake, and regulation of pyoverdin to shed light on the genetic basis of the observed arms race.

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SUN 21 AUG at 1550 - Room N7
Oral presentation *A4-Sy01-1550-O*

Symposium 1
Microbe/macrobe experimental evolution

Experimental multihost evolution of Tobacco etch virus and role of historical contengencies in evolution

Lafforgue G[1], Elena SF[1], Bedhomme S[1]
[1]IBMCP (CSIC), Valencia, Spain

Summary statement:

We evaluate the specificities of differents evolutionary history in differents host of a initial TEVclone. Do we have a signature of antagonistic pleiotropy and local adaptation?

Abstract:

In the context of extension of the host range, a virus can recurrently be submitted to the selection pressures of a new host or to the selection pressures of various alternating hosts, depending on the ecological conditions. We were interested in (1) understanding the different strategies of adaptation that can result from these two situations, and (2) analyzing the importance of historical contingencies in the context of adapation to a new host.

In a first experimental evolution phase, we started from an infective clone of the Tobacco etch virus (TEV) and derived experimental lines, transferred either on the same host at each transfer (specialist lines) or on alternative host (generalist lines) in a first time. We used four different hosts, derived ten replicates of the four specialist populations and of three generalist populations. In a second experimental evolution phase, the lines with the seven different evolutionary histories were serial transferred on the same host.

After each of two experimental evolution phases, we used a complete crossed design to evaluate the infectivity and the virulence of all the evolved virus lineages on the four hosts. These data allowed us to look for the signature of antagonistic pleiotropy and of local adaptation after the first phase and we were also able to evaluate how the specificities of each evolutionary history faded out during evolution on the same host. We also acquired the consensus sequences of the 70 evolved lineages after each phase and analysed the host specificity and the history,specificity of the mutations accumulated in each lineage, after each step.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy01-i016-R*

Symposium 1
Microbe/macrobe experimental evolution

Evolutionary trade-off between two consolidated memory phases in Drosophila

Lagasse F[1], Preat T[2], Mery F[1]
[1]LEGS CNRS, Gif sur Yvette, France, [2]ESPCI CNRS, Paris, France

Summary statement:

Artificial selection of memory in Drosophila suggests an evolutionary trade-off between the two forms of memory phases and flies lifespan are differently affected by the selection.

Abstract:

Memory is a complex and dynamic process composed of different phases. Its evolution under natural selection likely depends on a balance between fitness benefits and costs. Learning and memory capacities trade-off with other fitness related traits. However, very little is known about the pattern of genetic correlations among different memory phases. In Pavlovian aversive olfactory conditioning in Drosophila, two separate forms of consolidated memory phases can be formed: Anesthesia Resistant Memory (ARM) and Long Term Memory (LTM). In recent years, several studies have focused on the neurological differences between these long-lasting memories types, but how they evolved and are maintained remains unknown. We performed two independent artificial selections on ARM and LTM. After 23 generations, lines selected for improved ARM or LTM had higher memory scores than respective control lines 24h after massed or spaced conditioning respectively. Surprisingly, compared to control lines, lines selected for improved ARM had lower 24h memory scores when subjected to spaced conditioning and lines selected for improved LTM had lower 24h memory scores when subjected to massed conditioning. We believe this is the first evidence of an evolutionary symmetrical trade-off between two memory phases for the same learning task. Moreover, selection for improved LTM shortens lifespan whereas selection for improved ARM does not affect flies' longevity which suggests a constitutive cost of LTM selection on fitness. Such trade-offs may have important impacts on the evolution of cognitive capacities and help explain why evolution has maintained two consolidated memory phases.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy01-i017-R*

Symposium 1
Microbe/macrobe experimental evolution

The Effects of Herbicide Cycling on the Evolution of Resistance in Chlamydomonas reinhardtii

Lagator M[1], Vogwill T[1], Colegrave N[2], Neve P[1]
[1]The University of Warwick, School of Life Sciences, Coventry, United Kingdom, [2]The University of Edinburgh, School of Biological Sciences, Edinburgh, United Kingdom

Summary statement:

We investigated the merits of herbicide cycling as a method of retarding the evolution of resistance and its effects on the fitness of the evolved strains of C. reinhardtii.

Abstract:

Evolution of herbicide resistance in naturally occurring plant populations is a major problem facing modern agriculture. Cycling between herbicides with different modes of action has been proposed as a means of retarding or even preventing the evolution of resistance. The efficacy of herbicide cycling has been demonstrated in theoretical models, but rarely empirically. It has been generally accepted that herbicide rotation hampers the evolution of resistance.
We experimentally evolved populations of Chlamydomonas reinhardtii in the presence of growth inhibitory concentrations of three herbicides with distinct modes of action. Different populations were exposed to a weekly, biweekly and tri weekly cycling between all three possible pairings of herbicides; to a weekly and biweekly cycle between all three; as well as continuously to each of the three herbicides.
We present data showing that the effects of herbicide rotation do not always act against the evolution of resistance. Indeed, we show that in some cases rotation can increase the rates of herbicide resistance evolution, as well as lead to a more generalist response and wider cross-resistance patterns. These generalist resistant strains exhibited higher fitness in the presence of herbicides and a higher cost in the ancestral environment. The outcomes of herbicide cycling regimes will ultimately depend on a large number of factors and prior knowledge of these will be required before advocating effective strategies for delaying evolution of herbicide resistance.

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SUN 21 AUG at 1400 - Room N7
Invited talk *A3-Sy01-1400-I*

Symposium 1
Microbe/macrobe experimental evolution

Phenotypic and genomic evolution in a 50,000-generation experiment with bacteria

Lenski R[1]
[1]Michigan State University, Department of Microbiology and Molecular Genetics, East Lansing, United States

Summary statement:

This talk will provide an overview of phenotypic and genomic changes in evolving E. coli populations during a 50,000-generation experiment.

Abstract:

Evolution is an on-going process, and therefore it can also be studied experimentally in those organisms with short generations. To that end, 12 initially identical populations of Escherichia coli have been propagated in a simple environment since 1988. Two goals of this long-term experiment have been to characterize the dynamics of evolutionary change and examine the reproducibility of outcomes. We have measured adaptation by natural selection, documented increased specialization over time, observed the rise of mutator phenotypes, and even seen the origin of a function that transcends the usual definition of E. coli as a species. We have pursued various approaches to discover the mutations responsible for these changes, including several that affect global regulatory networks. We have also sequenced complete genomes to find all of the mutations in temporal series of clones from some populations. These genomic data provide new insights into the coupling of phenotypic and genomic evolution, and into the role of complex mutations in the origin of new functions.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy01-i018-R*

Symposium 1
Microbe/macrobe experimental evolution

Experimental evolution of antibiotic resistance in Pseudomonas aeruginosa

MacLean C[1]
[1]University of Oxford, Zoology, Oxford, United Kingdom

Summary statement:

To study antibiotic resistance, we use experimental evolution in the P.aeruginosa. Resistance evolution is driven by the interaction between ecology and molecular biology.

Abstract:

The evolution of antibiotic resistance in pathogenic bacteria has emerged as an important health problem by raising the mortality rates and economic costs associated with bacterial infections. To study the underlying evolutionary processes driving antibiotic resistance, we use experimental evolution of rifampicin resistance in the pathogenic bacterium Pseudomonas aeruginosa. Using highly replicated short-term selection experiments, we challenge hundreds of populations of Pseudomonas with adapting to rifampicin. The genetics and biochemistry of rifampicin resistance have been exquisitely characterized, making it possible to determine the underlying genetic and biochemical basis of variation in fitness among mutations at a large scale. First, we will demonstrate how this approach can be used to determine how the molecular mechanisms of resistance interact with the ecological and genetic context in which resistance evolves to determine the fitness benefits and costs of resistance mutations. Second, we will demonstrate how the molecular basis of resistance and the ecological context in which resistance evolves interact to determine the rate and dynamics of resistance evolution. Our work highlights the importance of developing an interdisciplinary approach to the study of evolution that combines ecology and molecular biology into the same evolutionary framework.

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SUN 21 AUG at 1610 - Room N7
Oral presentation *A4-Sy01-1610-O*

Symposium 1
Microbe/macrobe experimental evolution

Does evolution in temporally-varying environments require specific adaptations?

Magalhães S[1], Cailleau A[2], Blanchet E[2], Olivieri I[2]
[1]Centro de Biologia Ambiental, Lisboa, Portugal, [2]Institut des Sciences de l'Evolution de Montpellier, Montpellier, France

Summary statement:

Herbivorous spider mites evolving in an alternating environment are better adapted to that environment than to each environment separately.

Abstract:

Adaptation to environments that vary in time may be composed of a combination of the adaptations pertaining to each environment separately. Alternatively, there may be adaptations that are specific to the alternation itself. To test this, we performed experimental evolution of a cucumber-adapted population of herbivorous spider mites on two novel host plants, tomato and pepper. Five replicate lines evolved during 40 generations in homogeneous environments, where all generations were exposed to the same host plants, or in a temporally varying environment, where each plant was provided in alternating generations. Subsequently, we crossed either two lines evolving in each homogeneous environment of the same plant (tomato line (T)1 * T 2 and pepper line (P)1 * P2) , two lines evolving in the alternating environment (alternating line (A)1 * A2), or one T and one P line (T*P). We measured the performance (fecundity and survival) of each of these crosses in homogeneous environments (tomato or pepper) or in an alternating regime of tomato and pepper. Alternation was done every three days or at each generation. We found that, in homogeneous environments, A lines performed either worse than both T and P lines, or not differently from their average performance. However, in alternating environments, A lines performed sometimes better than both T and P lines. We can thus conclude that specific adaptations to an alternating environment evolved in the A lines.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy01-i019-R*

Symposium 1
Microbe/macrobe experimental evolution

Life cycle choices: lag phase evolution in stochastic environments

Magennis M[1,2], Allen RJ[2], Dawson A[2], MacPhee CE[2], Poon WCK[2], Colegrave N[1]
[1]University of Edinburgh, Institute of Evolutionary Biology, Edinburgh, United Kingdom, [2]University of Edinburgh, SUPA and School of Physics and Astronomy, Edinburgh, United Kingdom

Summary statement:

We are investigating lag phase evolution in bacteria adapted to predictable laboratory environments and to unpredictable stochastic conditions approximating natural environments.

Abstract:

During the life cycle of bacteria, the lag phase is a pre-growth step when cells prepare the molecular machinery necessary for growth in new environments. The smaller the environmental change, the shorter the adjustment period to the novel conditions and this is expressed phenotypically as a shorter lag phase.

In laboratory selection experiments, as bacteria adapt to conditions, their lag phase may shorten. The organisms may be capable of anticipating the time that they will move into the new environment, thus requiring less time in lag once they move environments. A shorter lag phase enables quicker growth and provides a selective advantage over slower-growing cells. However, it is not known why bacteria in nature have retained a lag phase. One possible explanation is that laboratory environmental conditions are static i.e. cells are transferred to media of the same composition at a regular time interval, whereas in nature the environmental conditions vary randomly and bacteria are unable to anticipate the changes.

We are investigating lag phase evolution in bacteria adapted to predictable laboratory environments and to unpredictable stochastic conditions approximating natural environments. We hypothesise that in a stochastic environment, the conditions cannot be predicted and minimising the lag phase may not be possible. We are also interested in how the lag phase relates to the rest of the growth cycle. These results will increase our understanding of the evolution of growth processes of bacteria.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy01-i020-R*

Symposium 1
Microbe/macrobe experimental evolution

Experimental removal of sexual selection reveals adaptations to polyandry in both sexes

Martin OY[1]
[1]ETH Zürich, Institute for Integrative Biology (IBZ), Zürich, Switzerland

Summary statement:

Beetles of both sexes evolving experimentally under polyandry out-perform monogamous counterparts in polyandrous contexts but not when maintained monogamously.

Abstract:

The evolutionary interests of males and females are often opposed, except under strict genetic monogamy when sexual conflict and sexual selection are absent. Polyandry is very widespread, so conflict between the sexes is frequently unavoidable, with impacts on multiple facets of reproduction. Precise knowledge of the consequences of adapting to the presence of sexual selection is critical to understanding the evolution of polyandry. Here an experimental evolution approach is applied to Tribolium castaneum to assess adaptations in both sexes to polyandry and presence of sexual selection/conflict. Specifically, male and female reproductive success (RS) and male paternity success are assessed for individuals from monogamous versus polyandrous selection lines. Experimental animals were subjected to monogamous versus polyandrous test regimes to assess how selection history determines male and female RS and whether animals from contrasting backgrounds are better adapted to their accustomed context. Under polyandry, both males and females from the polyandrous regime had greater RS than monogamous counterparts. In contrast, beetles from polyandrous and monogamous regimes did not differ in RS if maintained monogamously. This suggests that in both sexes adaptations to polyandry provide benefits only in the presence of sexual selection. Overall, these findings show that differential sexual selection intensity, achieved here through mating system (monogamy versus polyandry), can profoundly affect reproductive fitness in both sexes. Future efforts will aim to pinpoint precise mechanisms responsible for determining reproductive success and assess divergence in further traits.

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SUN 21 AUG at 1630 - Room N7
Oral presentation *A4-Sy01-1630-O*

Symposium 1
Microbe/macrobe experimental evolution

Experimental evolution of a plant pathogen into a legume symbiont

Masson-Boivin C[1], Capela D[1], Tasse L[1], Cruveiller S[2], Chane-Woon-Ming B[2], Guan S[1], Gris C[1], Marchetti M[1], Médigue C[2], Batut J[1]
[1]INRA, Castanet-Tolosan, France, [2]Genoscope, Evry, France

Summary statement:

Experimental evolution of a plant pathogen towards legume symbionts and analysis of genome modifications using genome resequencing.

Abstract:

Legumes and bacteria collectively known as rhizobia cooperate in a nitrogen-fixing symbiosis of major ecological importance that occurs on all continents and accounts for a fourth of the nitrogen fixed annually on earth. Rhizobia are a rare example of phylogenetically disparate bacteria that have achieved the same complex biological function, raising fascinating questions regarding their evolution. Ample evidence indicates that horizontal transfer of symbiotic plasmids/islands has played a crucial role in rhizobia evolution. However, adaptive mechanisms that allow the recipient genomes to express symbiotic traits are unknown.

We have launched the experimental evolution of a plant pathogen into legume symbionts using a "design then evolve" strategy. We transferred the symbiotic plasmid of the Mimosa symbiont Cupriavidus taiwanensis into the phytopathogen Ralstonia solanacearum, generating a non-nodulating and still pathogenic chimera, that was subsequently evolved towards legume symbionts using serial plant-bacteria cocultures. 9 independent lineages have been derived from three ancestral nodulating clones. Phenotypic analysis of evolved clones showed that all have acquired intracellular infection ability, whereas the wild-type R. solanacearum is strictly extracellular. Resequencing of evolved clones allowed identifying two types of adaptive mutations in the hrpG-controlled virulence pathway of R. solanacearum that are crucial for the transition from pathogenicity towards mutualism. Our findings predict that natural selection of adaptive changes in the legume environment following horizontal transfer has been a major driving force in rhizobia evolution and diversification.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy01-i007-E*

Symposium 1
Microbe/macrobe experimental evolution

Clinal differentiation of polygenic traits: How much is it expressed in a novel environment and what are the outcomes of adaptation?

Matos MM[1], Fragata I[1], Simões P[1], Bárbaro AM[1], Cunha M[1], Lima M[1], Kellen B[1], Santos J[1]
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Summary statement:

The ‘catch 22’ of clinal variation of polygenic traits and how we can fly out of it.

Abstract:

Clinal variation provides strong evidence for the role of local adaptation in the differentiation of populations. There are many examples of latitudinal clines in Drosophila, involving inversions, body size, developmental time, stress resistance, etc. But there are also disparities in the literature, in particular for physiological and life-history traits. While inversions can be characterized directly, polygenic traits are affected by the environment, due to plasticity. This implies that populations have to be analysed after some generations in a common environment. . Nevertheless, genotype-by-environment interactions may also affect the pattern of differentiation between populations, limiting extrapolations to genetic differences in the natural environment – a typical ‘catch 22’.This may explain part of the disparities between studies. Another source of contrast may be the number of generations populations spent in the laboratory before analysis. Studying the evolution of populations from contrasting latitudes in a common environment, periodically assayed in different conditions (e.g. temperatures) will provide important information related with these issues. This study analyses how populations of Drosophila subobscura from three contrasting European latitudes evolve in a common, laboratorial environment for a set of physiological, behavioural and life-history traits. Will they express a clinal pattern at an early generation, ‘mimicking’ the expected pattern in nature? If so, how dependent is this pattern on the assayed conditions (e.g. temperature)? Finally, will populations converge during laboratory evolution?

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy01-i021-R*

Symposium 1
Microbe/macrobe experimental evolution

Adaptive landscapes in evolving populations of Pseudomonas fluorescens

Melnyk AH[1], Kassen R[1]
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Summary statement:

This is an experimental study on the underlying adaptive landscape of 2 simple laboratory environments as inferred from adaptation of multiple replicate strains of P. fluorescens.

Abstract:

The repeatability of adaptive evolution depends on the ruggedness of the underlying adaptive landscape. We contrasted the relative ruggedness of adaptive landscapes across two environments by measuring the variance in fitness and metabolic phenotype within and among genetically distinct strains of Pseudomonas fluorescens in two environments differing only in the carbon source provided (glucose vs. xylose). Fitness increased in all lines, plateauing in one environment but not the other. The pattern of variance in fitness among replicate lines was unique to the selection environment; it increased over the course of the experiment in xylose but not in glucose. Metabolic phenotypes displayed two results: (1) populations adapted via changes that were distinctive to their selection environment, and (2) endpoint phenotypes were less variable in glucose than in xylose. These results indicate that although the response to selection is highly repeatable at the level of fitness, the underlying genetic routes taken were different for each environment and more variable in xylose. We suggest that this reflects a more rugged adaptive landscape in xylose compared to glucose. Our study demonstrates the utility of using replicate selection lines with different evolutionary starting points to try and quantify the relative ruggedness of adaptive landscapes.

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MON 22 AUG at 1710 - Room N7
Oral presentation *B4-Sy01-1710-O*

Symposium 1
Microbe/macrobe experimental evolution

Experimental evolution exposes male and female responses to sexual conflict and inbreeding in the red flour beetle

Millard AL[1]
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Summary statement:

Experimetal evolution techniques provide powerful evidence for the relative role of sexual selection, sexual conflict and inbreeding in the red flour beetle.

Abstract:

Utlising experimental evolution techniques in the red flour beetle Tribolium castaneum has allowed the parallel exploration of a number of trait responses by direct experimental manipulation of sexual selection and inbreeding. Fifty generations of sex ratio manipulation has led to evolved populations in which males from male bias populations display increased competitive capacity by mating faster and more often than their counterparts from female bias populations. Concurrent assays of female reproductive fitness showed that females raised in female bias populations showed a decrease in fitness when mated with multiple males. Females raised in the parallel male bias populations were able to resist deleterious effects of multiple mating, providing direct evidence for the presence of sexual conflict in this system. We have also used this system to investigate the advantages of multiple mating under inbreeding by using experimental evolution to create multiple replicate inbred lines of 8 generations of sib-sib matings. Reduced female reproductive fitness was found in inbred lines, yet enforced polyandry rescued female fitness to the level of outbred females. Subsequent behavioural assays have shown that inbred females have in fact developed more polyandrous behaviour in response to inbreeding, providing direct evidence for the evolution of polyandry as a mechanism of inbreeding avoidance.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy01-i008-E*

Symposium 1
Microbe/macrobe experimental evolution

Coevolution between the red flour beetle Tribolium castaneum and Bacillus thuringiensis bacteria ‐ are infection routes relevant?

Milutinovic B[1], Kurtz J[1]
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Summary statement:

Different routes of infection (septic wounding or oral infection) might be relevant for host-parasite coevolution in the red flour beetle T. castaneum and Bacillus thuringiensis.

Abstract:

Host-parasite interactions come with extremely high selection pressures and rapid adaptations might thus be observed in both antagonists (Red Queen Dynamics). In our experiments, we are using the red flour beetle Tribolium castaneum and its bacterial microparasite Bacillus thuringiensis to investigate the mechanisms involved in reciprocal adaptation. In this context, the outcome of the interaction between hosts and parasites might dependent on the respective host and parasite populations (genotype interactions), but also on the realized route of infection. We thus set out to compare the infectivity of a range of B. thuringiensis strains in several host populations with different experimental infection routes in the laboratory. The oral route is normally viewed as the natural way of infection. B. thuringiensis bacteria can be highly abundant in the natural environment, where they mostly persist as spores. During the sporulation phase these bacteria produce insecticidal δ-endotoxins which are specific to different orders of insects and are activated in the gut where they cause damage to the host tissue. On the other hand, beetles collected from natural habitats often show multiple injuries, suggesting that septic wounding could also be a relevant way of infection. Whether or not oral way of infection also shows specificity is not yet known. So far we observed strong differences in the host survival between the two routes of infection. Beetle populations differed in their susceptibility upon oral and septic infection. This may suggest that host-parasite coevolution in different populations might also depend on the prevailing route of infection and its associated specificity.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy01-i022-R*

Symposium 1
Microbe/macrobe experimental evolution

Mutation rates and intra-specific divergence of the genome of the nematode Pristionchus pacificus

Molnar RI[1], Sommer RJ[1]
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Summary statement:

Genetic variation in wild type isolates and mutation rate estimates from MA lines guide us into obtaining first insights into minimal divergence times in Pristionchus pacificus.

Abstract:

Evolutionary reconstruction of the natural history of an organism benefits from studies of mutational processes as the source of natural variation. The nematode Pristionchus pacificus has been established as a model system in evolutionary developmental biology for comparison to Caenorhabditis elegans. P. pacificus has a well-defined association with scarab beetles, the ecology and phylogeny are well known and recent studies on LaRéunion Island provide a case study to link population genetics with ecology and evo-devo. We assess the genome evolution of P. pacificus using the mutation accumulation (MA) lines approach to study spontaneous mutation rates in the mitochondrial genome and representative microsatellite markers. The major aim is to relate genetic variation in wild isolates to the mutation rate estimates from the MA lines in order to obtain first insight into minimal divergence times in P. pacificus. Mitochondrial DNA analysis reveals an unusual suppressor tRNA for the codon UAA that has most likely influenced the spectrum of observable mutations in the MA lines. With a mitochondrial mutation rate of 7.6×10-8 per site per generation, we calculated the minimum time to the most recent common ancestor at 105 to 106 generations between nine representative isolates of the species (Molnar et al. 2011). Similarly, microsatellite markers are used to robustly provide minimal divergence time estimates for 30 closely related strains from LaRéunion. The combination of mutation rate analysis with intra-specific divergence provides a powerful tool for the reconstruction of the natural history of P. pacificus.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy01-i009-E*

Symposium 1
Microbe/macrobe experimental evolution

Mutation accumulation studies of green algae

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Summary statement:

Mutation accumulation studies will allow us to determine the distribution of fitness effects of mutations and the extent of synergistic epistasis.

Abstract:

We are combining the advantages of using microbes to study evolution (e.g. short generation times and large scale replication) with the latest whole genome sequencing techniques, in order to address a key question in population genetics - the nature of new mutational variation. We are bottlenecking several strains of the green alga Chlamydomonas reinhardtii, and other species of green algae, to a single cell under conditions of relaxed natural selection for several hundred generations. This approach will allow all but the most strongly deleterious mutations to accumulate. We will test for changes in various components of fitness in multiple environments using growth rate assays and competitions. From these data we will infer the distribution of fitness effects of mutations (DEM) from the distribution of fitnesses of different replicates. We will also infer the extent of synergistic epistasis. We plan to sequence the whole genome of several lines before and after the mutation accumulation experiment. The sequence data will allow us to estimate the mutation rate per site per generation (u), and comparison between species and strains of the starting populations will allow molecular estimates for the DEM of natural populations which can be compared to the phenotypic estimates from the laboratory.

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SUN 21 AUG at 1440 - Room N7
Oral presentation *A3-Sy01-1440-O*

Symposium 1
Microbe/macrobe experimental evolution

Toward masculinity in mushrooms by experimental evolution

Nieuwenhuis BPS[1], Aanen DK[1]
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Summary statement:

Forcing hermaphroditic mushroom fungi to mate in the male role in an experimental evolution setup leads to increased competitve male ability, without reduction in female function.

Abstract:

Sexually antagonistic selection may lead to suboptimal sex roles. We studied this potential conflict between the sexual roles in a mushroom-forming fungus, which has a hermaphroditic life cycle. This life cycle starts with a haploid mycelium that during mating donates its nucleus type to another mycelium (male function) and simultaneously receives the nucleus type of the latter (female function). We performed an evolution experiment to select for increased masculinity, i.e. for success as a nucleus donor, and tested for trade-offs with female traits for 20 initially identical lines. We serially passed the evolving nuclei through a not-coevolving receiving mycelium for 20 sexual generations. Most of the evolved lines showed a dramatic increase in competitive fitness in the male role relative to the ancestral strain (for some lines up to 100-fold). All evolved lines were still capable to accept a nucleus, i.e. were still functional as female; furthermore, we did not see reduced performance of the somatic growth phase. One of the 20 lines had evolved strongly increased spore production. Genetic analysis showed that this trait segregated with one of the mating type loci, indicating close linkage. Altogether, we did not find clear trade-offs between the male and female traits we measured. This is consistent with the notion that the male function in fungi, i.e. the donation of a nucleus, is essentially cost free.

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MON 22 AUG at 1550 - Room N7
Oral presentation *B4-Sy01-1550-O*

Symposium 1
Microbe/macrobe experimental evolution

Horizontal gene transfer alleviates the inhibitory effect of microbial diversity on resistance evolution

Perron GG[1], Lee A[2], Wang Y[3], Huang W[3], Barraclough TG[2]
[1]Harvard University, FAS Center for Systems Biology, Cambridge, United States, [2]Imperial College London, Ascot, United Kingdom, [3]Sheffield University, Sheffield, United Kingdom

Summary statement:

To our knowledge, this study presents the first experimental evidence for the evolutionary benefits of horizontal gene transfer in diverse microbial populations.

Abstract:

Horizontal transfer of antibiotic resistance genes is believed to explain the frequency of antibiotic resistance among pathogenic bacteria. Despite extensive evidence from retrospective sequence analyses, experimental evidence for the benefits of horizontal gene transfer (HGT) is lacking. Using experimental populations of the soil bacterium, Acinetobacter baylyi, we show that HGT can alleviate the inhibitory effect that emerges from microbial diversity on resistance evolution. We first demonstrate that the presence of different antibiotic-resistant genotypes in mixtures of bacteria inhibits the evolution of de novo multidrug-resistant genotypes; multidrug-resistance evolves readily in the same antibiotic-resistance bacteria when grown in monocultures. Comparing evolution in the transformable wildtype and in a genetically engineered strain that lacked the ability to incorporate exogenous DNA, we show that HGT not only alleviated this inhibitory effect, but also favoured the rapid evolution of multidrug-resistance in the bacterial mixtures. Also, by adding treatments of naked DNA to experimental populations of the bacterium, we identified the genetic mechanism promoting resistance evolution. The addition of naked DNA harbouring a resistant gene promoted adaptation of the transformable wildtype strain, whilst the addition of susceptible naked DNA did not favour resistance evolution. Given that most microbial communities are extremely diverse, our results show that the benefits of HGT depend on levels of genetic diversity directly present in the surrounding of the bacteria and proposed a new mechanism to explain the maintenance of HGT in bacterial populations.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy01-i024-R*

Symposium 1
Microbe/macrobe experimental evolution

Experimental evolution of protection against a toxic fungus in Drosophila larvae

Rohlfs M[1], Trienens M[1]
[1]Georg-August Universität, J.F. Blumenbach Institute of Zoology and Anthropology, Göttingen, Germany

Summary statement:

Drosophila larvae evolve tolerance of rather than resistance to a fungal competitor, which positively correlates with reduced sensitivity to the fungal chemical defense system.

Abstract:

In analogy to the evolution of internal immunological countermeasures against parasitic microorganisms, animals are expected to be selected for the employment of external defense mechanisms to achieve immunity against noxious microbes. We tested this idea by subjecting replicated populations of Drosophila melanogaster larvae to the lethal impact of their fungal competitor Aspergillus nidulans. In line with our expectation, insects from fungal selected populations evolved enhanced survival when exposed to the noxious mold. Mutualistic yeast communities provided a general benefit to both fungal selected and unselected control populations but did not remediate evolved differences caused by the selection regimes. Increased protection in the fungal selected insect populations positively correlated with reduced sensitivity to the extremely toxic fungal compound Sterigmatocystin. In contrast to our expectation that Drosophila larvae evolve increased resistance which in turn reduces fungal fitness, larvae from fungal selected populations were not better at suppressing fungal growth. Rather, we observed a trend towards a less detrimental effect on A. nidulans colony expansion when fungi were confronted with larvae from fungal selected populations (compared to the effect of unselected control larvae). Thus, tolerance rather than resistance mechanisms appear to be favored when Drosophila larvae are exposed to the selective pressure of detrimental but non-parasitic microbes.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy01-i025-R*

Symposium 1
Microbe/macrobe experimental evolution

Host-parasite local adaptation after experimental coevolution of Caenorhabditis elegans and its microparasite Bacillus thuringiensis

Schulte RD[1], Schulenburg H[2]
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Summary statement:

We detected different host-parasite local adaptation patterns in single populations which experimentally coevolved. Crucial was the comparison with evolved control populations.

Abstract:

Coevolving hosts and parasites can adapt to their local antagonist. In studies on natural populations, the observation of local adaptation patterns is thus often taken as indirect evidence for coevolution. Based on this approach, coevolution was previously inferred from an overall pattern of either parasite or host local adaptation. Many studies, however, failed to detect such a pattern. One explanation is that the studied system was not subject to coevolution. Alternatively, coevolution occurred, but remained undetected because it took different routes in different populations. In some populations it is the host that is locally adapted, whereas in others it is the parasite, leading to absence of an overall local adaptation pattern. We here test for overall as well as population-specific patterns of local adaptation using experimentally coevolved populations of the nematode Caenorhabditis elegans and its bacterial microparasite Bacillus thuringiensis. Importantly, we assessed the importance of random interaction effects using control populations that evolved in the absence of the respective antagonist. Our results demonstrate that experimental coevolution produces distinct local adaptation patterns in different replicate populations, including host, parasite or absence of local adaptation. Our study thus provides experimental evidence of the predictions of the geographic mosaic theory of coevolution, i.e. that the interaction between parasite and host varies across populations. It furthermore shows the value of experimental evolution for studies of local adaptation.

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SUN 21 AUG at 1650 - Room N7
Oral presentation *A4-Sy01-1650-O*

Symposium 1
Microbe/macrobe experimental evolution

Genomic analysis of Bacillus thuringiensis parasites coevolved with a Caenorhabditis elegans host

Sheppard A[1], El Masri L[1,2], Brzuszkiewicz E[3], Branca A[4], Saebelfeld M[1], Barann M[5], Behrens S[4], Bornberg-Bauer E[4], Daniel R[3], Liesegang H[3], Rosenstiel P[5], Schulenburg H[1]
[1]Christian Albrechts University of Kiel, Evolutionary Ecology and Genetics, Zoological Institute, Kiel, Germany, [2]University of Tuebingen, Animal Evolutionary Ecology, Institute of Evolution and Ecology, Tuebingen, Germany, [3]Georg-August-University of Goettingen, Goettingen Genomics Laboratory, Institute of Microbiology and Genetics, Goettingen, Germany, [4]Westfaelische Wilhelms University Muenster, Evolutionary Bioinformatics, Institute for Evolution and Biodiversity, Muenster, Germany, [5]Christian-Albrechts University of Kiel, Institute of Clinical Molecular Biology, Kiel, Germany

Summary statement:

We use next generation sequencing technologies to investigate the underlying genetic basis of experimental host-parasite coevolution.

Abstract:

We study experimental host-parasite coevolution using the nematode Caenorhabditis elegans and the pathogenic bacterium Bacillus thuringiensis. The host and parasite were allowed to coevolve for 28 host generations (coevolution treatment). In parallel, the parasite was allowed to adapt to a non-evolving host (one-sided adaptation treatment), as well as in host-free conditions (control treatment). Each of the three experimental evolution conditions resulted in a different outcome: i) parasites from the coevolution treatment maintained high levels of virulence, ii) parasites from the control treatment lost virulence, and iii) parasites from the one-sided adaptation treatment were varied, with some populations showing high levels of virulence and some low levels of virulence. Remarkably, in all cases, low virulence was correlated with biofilm formation, while highly virulent populations did not form biofilms. We are combining sequencing data from two different next generation platforms (454 and SOLiD) and conventional Sanger sequencing to obtain whole genome sequences of the starting strains and a number of evolved clones of B. thuringiensis. In parallel, at the population level , we are analysing specific genes that are most likely to be under selection during the experiment, to determine patterns of change over time. Here we focus on central regulators affecting virulence and life-history traits, as well as toxins known to be involved in pathogenicity. The genomic changes identified will be presented in relation to the phenotypic changes that occurred during the evolution experiment and in the broader context of host-parasite coevolutionary theory.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy01-i010-E*

Symposium 1
Microbe/macrobe experimental evolution

Evolution of molecular markers under age-specific selection in the seed beetle

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Summary statement:

Analysis of 6 molecular markers shows that long-term age-specific selection resulted in significant divergence of seed beetle laboratory populations.

Abstract:

The distribution of allelic variation at 5 microsatellite loci and a 658bp long fragment at the 5' end of the mitochondrial gene cytochrome c oxidase subunit I (COI), frequently used for species identification ("DNA barcoding"), were analyzed in eight laboratory populations of seed beetle (Acanthoscelides obtectus) subjected to long-term selection for either early (E) or late (L) reproduction. The hierarchical population structure, which included two selection regimes and four replicate populations within each regime, allowed disentangling the effects of selection – responsible for the divergence between the E and L regimes – from stochastic effects – leading to difference between replicate populations. The estimated FST values of 0.46 and 0.42 for microsatellites and COI gene, respectively, between the E and L selection regimes indicated that these molecular markers were associated with the imposed selection regimes. The observed genetic divergence among replicate populations within selection regimes was also significant; FSC for microsatellites amounted 0.05 and for the COI gene 0.18. Comparison of population pairwise estimates of FST and RST for microsatellites showed a larger values of RST than FST, especially when the E and L populations were compared. Microsatellite results indicate that, besides selective sweep effects on these neutral markers, the stepwise mutations are important cause of the observed population divergence in laboratory evolution of the seed beetle. Higher haplotype diversity in the E compared with L populations implies stronger selection for genes involved in the late-life fitness traits than in early fitness components.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy01-i011-E*

Symposium 1
Microbe/macrobe experimental evolution

Using microbes to study the evolutionary ecology of dispersal

Taylor TB[1], Buckling A[1]
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Summary statement:

Using the pathogenic bacteria Pseudomonas aeruginosa to study the evolutionary ecology of dispersal, focusing on the role of social interactions and kin competition.

Abstract:

Understanding dispersal is a central aim of evolutionary ecology. Theoretical analyses of dispersal have been crucial in identifying key variables which contribute to its evolution and maintenance, but empirical data is lagging drastically behind. Microbes offer a powerful model system on which ecological and evolutionary theory can be experimentally tested with controlled and replicable experiments, and with the convenient malleability of selective pressures and bacterial genomics. I outline empirical work, using the pathogenic bacteria Pseudomonas aeruginosa, focusing on the role of social interactions and kin competition in the evolutionary ecology of dispersal.

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MON 22 AUG at 1440 - Room N7
Oral presentation *B3-Sy01-1440-O*

Symposium 1
Microbe/macrobe experimental evolution

The evolution of macroorganisms from microbes

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Summary statement:

We show that phenotypic hallmarks of multicellularity can evolve rapidly under the appropriate selective conditions.

Abstract:

We show that complexity can evolve extraordinarily rapidly under the appropriate selective conditions. In as little as 30 days, multicellular protoindividuals can evolve that have complex phenotypes and the beginnings of determinate reproductive life histories. Using a single ancestral genotype, we initiated ten replicate populations that were propagated for 60 days on a daily serial transfer regime. Using gravitational selection, we observed rapid increases in the settling of cells over the course of selection. After 60 transfers, nine populations were dominated by multicellular protoindividuals with spherical 'snowflake' phenotypes consisting of multiple attached cells. The heritability of the snowflake phenotype was confirmed by fragmenting a snowflake into individual cells using lyticase, and observing their growth into new snowflakes via time-lapse microscopy. The snowflake phenotype has ~50% fitness advantage over individual cells under the selection conditions, but suffers a fitness cost in the absence of centrifugal selection. Time-lapse microscopy of growth from individual cells shows that attachment results from adhesion after cell division, not aggregation. Reproduction occurs by the formation of daughter protoindividuals released sequentially. Propagule production begins only after a protoindividual reached a threshold size, i.e., after a "juvenile phase"; propagules, though not unicellular, were consistently smaller than the parent. The resulting multicellular group reproduces and responds to selection as an individual. Cooperation is promoted, as groups consist of highly related cells, thereby reducing conflict among the component cells.

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TUE 23 AUG at 1440 - Room N7
Oral presentation *C3-Sy01-1440-O*

Symposium 1
Microbe/macrobe experimental evolution

Adaptive changes in size-selectively exploited zebrafish (Danio rerio) populations

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Summary statement:

After five generations of size-selective harvesting in zebrafish, the fish selected for small body size were significantly smaller than fish selected for large body size.

Abstract:

Pronounced size-selectivity together with substantial mortality rates suggest the potential for fisheries-induced evolutionary changes in average growth rate and productivity in exploited stocks. We subjected experimentally wild zebrafish populations for size-selective mortality over five generations in order to understand how various phenotypic traits change over time under substantial selection pressure. Fish were harvested according to body length and three selection regimes were established: selection for large body size, random body size and small body size. After five generations of selection, fish selected for small body size were significantly smaller than fish selected for large or random body size. Despite the fact that body size of the spawners differed significantly between the large and small size selected fish, there were no differences in reproductive output between the groups. However, the offspring of fish selected for large body size had higher growth rate than the offspring of fish selected for small body size. In addition to phenotypic changes, genetic changes were studied by using non-neutral markers (SNPs) to detect signs of possible evolutionary changes in response to the experimental selection. In doing so, we aim at contributing to fundamental understanding of the evolution of adaptive traits due to size-selective mortality.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy01-i026-R*

Symposium 1
Microbe/macrobe experimental evolution

Adaptation to larval malnutrition alters foraging behaviour in Drosophila melanogaster larvae

Vijendravarma RK[1], Narasimha S[1], Kawecki TJ[1]
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Summary statement:

We conclude that adaptation to malnutrition involves chages in the larval foraging behavior and that foraging starergies in populations may reflect the environment they evolved in.

Abstract:

Adaptation to malnutrition is likely to involve behavioral changes in relation to food acquisition. Here we assay Drosophila melanogaster populations adapted to chronic larval malnutrition for their foraging behaviour. In Drosophila, naturally occurring behavioral polymorphism in foraging path lengths is attributed to the foraging locus. Larvae with the forR (rover allele), have significantly longer foraging path lengths on a yeast paste than do those homozygous for the fors (sitter allele). However, no difference in the general activity of these variants is observable, in the absence of food. We found that adaptation to larval nutritional stress alters the foraging path-length phenotype. Replicate populations that were selected for increased tolerance to juvenile nutritional stress exhibited sitter phenotype, when compared to the unselected control populations. A quantitative complementation assay suggested that these changes resulted from alterations in the frequency of forR allele in the selected populations. These results suggest that the adapted populations could have evolved sitter phenotype to conserve energy.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy01-i027-R*

Symposium 1
Microbe/macrobe experimental evolution

The experimental evolution of herbicide-resistance in Chlamydomonas reinhardtii

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[1]University of Warwick, School of Life Sciences, Warwick, United Kingdom, [2]University of Edinburgh, School of Biological Sciences, Edinburgh, United Kingdom

Summary statement:

Characterising the dynamics of herbicide-resistance evolution in the model organism, Chlamydomonas reinhardtii.

Abstract:

The evolution of herbicide-resistant weeds is a major threat to global food security, with resistance having already evolved in over 200 species of plant. However the majority of work to date has focussed on characterising the molecular end-points of the evolution of herbicide-resistance, rather than focussing on the dynamics and selective forces which drive it. To remedy this, we are developing a model system to study the evolution of herbicide-resistance in real-time by experimental evolving the unicellular chlorophyte Chlamydomonas reinhardtii. Similar to the patterns observed in higher plants, we have found that there are pronounced differences between different herbicide modes of action in the rates, pleiotropic fitness-costs and mechanisms of resistance evolution. Furthermore, when comparing across multiple herbicides, we have discovered a counterintuitive positive correlation between the maximum growth rate in the presence and absence of herbicides. We have also found a negative correlation between a strain's maximum growth rate in the absence of any herbicides and the number of herbicides a strain is resistant to, but no significant correlation between growth in the presence of herbicides and the number of herbicides a strain is resistant to. We have also begun to use this system to study the potential of management options to delay the evolution of resistance.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy01-i028-R*

Symposium 1
Microbe/macrobe experimental evolution

Evolution towards earlier maturation in Daphnia pulex after an introduction of an alien predator

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Summary statement:

We look for evidence of predator-induced evolution in Daphnia pulex following an introduction of perch. Preliminary results indicate a genetic decrease in age at maturation.

Abstract:

Size-selective predation shapes populations and induces changes in life-history traits. If small individuals are targeted, selection might favor faster growth to escape the vulnerable size range, whereas if large individuals are targeted, earlier maturation is likely to evolve. Here we look for evidence of predator-induced evolution in Daphnia pulex following an illegal introduction of an alien predator (European perch, Perca fluviatilis) to a Norwegian lake that naturally hosted no planktivorous fish. We hypothesize that the shift in predation pressure favors early-maturing clones, as the perch targets large Daphnia. Field data show that the average size of mature individuals has decreased significantly and we are interested to see if this observed pattern implies genetic change. We experimentally raised clones collected the year before introduction and 3 years after to study the potential genetic changes in size and age at maturation. Preliminary results indicate a genetic decrease in age at maturation, hence a selection towards earlier maturation caused by the introduced predator.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy01-i012-E*

Symposium 1
Microbe/macrobe experimental evolution

Evolutionary genetics of predatory behavior in the nematode Pristionchus pacificus

Weller AM[1], Sommer RJ[1]
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Summary statement:

P. pacificus can feed on bacteria or other nematodes. Predatory behavior of a lab strain was lost due to a point mutation after 4 years of culture on a bacterial food source.

Abstract:

Pristionchus pacificus, a model nematode in evolutionary biology, is an omnivore and feeds on bacteria as well as other nematodes. All P. pacificus strains tested kill and feed on C. elegans in laboratory assays with the exception of the reference strain PS312. By thawing and testing frozen backups of this strain it was discovered that it once exhibited predatory behavior but completely lost this trait in culture between 1997 and 2002.

Crossing experiments revealed a clear Mendelian inheritance pattern of the ability to kill prey, suggesting a recessive single-locus change. The complete genome of PS312 (1997) was sequenced by Illumina technology and compared to the established sequence of PS312 (2004), uncovering approximately 1000 single nucleotide polymorphisms (SNP). We found two candidate genes on chromosome 3 by employing a SNP-mapping approach. Final proof of the gene determining the killer phenotype will be brought by injection of a transformation marker into PS312 (2004).

Additionally, investigations of the evolutionary history of this behavior across the genus Pristionchus will be discussed.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy01-i029-R*

Symposium 1
Microbe/macrobe experimental evolution

The dynamics of mutation rate evolution in a long-term experiment with Escherichia coli

Wielgoss S[1], Barrick JE[2], Tenaillon O[3], Dittmar J[4], Chane-Woon-Ming B[5], Cruveiller S[5], Médigue C[5], Lenski RE[4], Schneider D[1]
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Summary statement:

We demonstrate that whole genome re-sequencing data derived from long-term evolution experiments provide a powerful way to directly infer mutations rates from a reliable phylogeny.

Abstract:

The application of next-generation sequencing technologies to evolution experiments allows for a rapid and efficient screening of available long-term lineages. The coupling of the precise history of whole genomic changes with fitness measures between evolved and ancestral individuals represents an immensely important step towards a quantitative understanding of adaptation. During the longest-running evolution experiment using Escherichia coli, twelve independent populations have been propagated for more than 40,000 generations. At regular time intervals, both population and clonal samples have been cryo-conserved and provide us with a remarkable fossil record. Unlike ordinary fossils however, ancestral and evolved populations can be revivified and directly compared to one another at both the phenotypic and genomic level. Here, we analyzed the genome sequences of several clones isolated over the entire course of the evolution experiment and inferred their phylogeny rooted in the ancestor. We statistically evaluated the average genetic distance across time, and compared the values to the degree of divergence among clones at each time-point. Results indicated a remarkable dynamics of mutation rates, and genomic evolution became manifest in marked changes of the mutational spectra. We subsequently inferred precise point mutation rates from the phylogeny to calculate the time-points of emergence of the underlying mutational events.

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MON 22 AUG at 1610 - Room N7
Oral presentation *B4-Sy01-1610-O*

Symposium 1
Microbe/macrobe experimental evolution

Insights into the genetics of adaptation and pleiotropy from experimentally evolved antibiotic resistance in Pseudomonas aeruginosa

Wong A[1], Kassen R[1]
[1]University of Ottawa, Biology, Ottawa, Canada

Summary statement:

We have investigated the genetics of adaptation and its costs using whole-genome sequencing of bacterial populations evolved in the presence of the antibiotic ciprofloxacin.

Abstract:

Pleiotropy is a central feature of most theoretical accounts of adaptation, and can have important consequences for the extent, rate, and direction of adaptive evolution. Microbial experimental evolution, in combination with next-generation sequencing technologies, offers a unique opportunity to investigate the genetic underpinnings of pleiotropy during adaptation. We have evolved resistance to the antibiotic ciprofloxacin in multiple, initially isogenic populations of Pseudomonas aeruginosa, an important pathogen of cystic fibrosis (CF) patients. In this context, pleiotropy is measured as the cost of adaptation – that is, the resistant population´s fitness in the absence of antibiotic. Costs of adaptation were highly environment-dependent: Substantial costs were realized in most culture media, but no costs were observed for populations evolved in an environment that mimics the CF lung with respect to nutritional composition and viscosity. In order to investigate the genetic basis of adaptation - and of the costs of adaptation - in these populations, we have conducted whole-genome sequencing of genotypes isolated from both resistant- and non-resistant populations. In addition to mutations in known mediators of ciprofloxacin resistance, we find putative novel targets of resistance, as well as mutations likely involved in adaptation to culture conditions. Further studies will allow us to determine the effects of individual mutations on both adaptation and on the costs of adaptation. This work will contribute to our understanding of how costs arise during the early stages of adaptation, and of how these costs are modified with subsequent adaptive steps.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy01-i030-R*

Symposium 1
Microbe/macrobe experimental evolution

Experimental evolution of bacteria under the selection of protozoans and phages

Zhang J[1], Örmälä A-M[2], Laakso J[2], Mappes J[1]
[1]University of Jyväskylä, Jyväskylä, Finland, [2]University of Helsinki, Helsinki, Finland

Summary statement:

Evolution experiments with bacteria-protozoans-phages co-culture indicate that phage infection could accelerate the evolution of the amoeba-resistant bacterial mutants.

Abstract:

Protozoa and phages are major causes of bacterial mortality in the environment. Predation induced evolution of bacterial traits and viral gene transfer can also influence the evolution of bacterial virulence. To study how bacterial traits evolve in response to enemies, insect pathogen Serratia marcescens strain DB11 was cultured with predatory protozoa, amoeba and ciliates, and parasitic phages for 8 weeks. We measured the temporal population dynamics of the predators and prey, as well as evolved bacterial traits such as biofilm formation, anti-predatory defenses and phage resistance. We found that ciliates are most efficient in reducing bacterial density in the open water phase and least efficient in inhibiting biofilm formation. In contrast, phages are the least efficient in reducing bacterial density in the open water, and amoeba reduced mostly the amount of biofilm. There are also interactions between enemies. In treatment with all enemies, the amoeba population sizes were relatively very small after one week. In this group, the density of highly amoeba-resistant bacteria peaked at week 3. The results indicate that phage infection could accelerate the evolution of the amoeba-resistant mutants. The mechanisms are not yet known but will be studied by comparing amoeba-resistant mutants originated from different treatments. Also the impact of bacterial evolution on virulence will be studied with Drosophila intestinal infection model.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy01-i031-R*

Symposium 1
Microbe/macrobe experimental evolution

Levels of ethanol typical of fermenting fruits can generate sexual selection for ethanol resistance in Drosophila melanogaster

Zhu J[1], Fry JD[1]
[1]University of Rochester, Biology, Rochester, United States

Summary statement:

Variation among D. melanogaster populations in ability to survive unnaturally high ethanol doses may be a byproduct of selection for behavioural resistance to lower natural doses.

Abstract:

Ethanol is a natural component of the decaying fruit on which D. melanogaster feeds and breeds in the wild. Resistance to being killed or knocked down by high doses of ethanol shows clinal variation on multiple continents in this cosmopolitan species, indicating that resistance, or something correlated with it, is under selection. However, ethanol concentrations in fermenting fruits are usually too low to cause larval or adult mortality, suggesting that something other than mortality at high concentrations is responsible for the clinal variation. One possibility is that ethanol exerts selection by perturbing behavior, with resistance to being killed by high ethanol concentrations having evolved as a correlated response to selection for behavioral insensitivity to lower natural concentrations. We examined the effect of a non-lethal dose of ethanol, comparable to that obtained by feeding on fermenting fruit, on the competitive mating success of males from two populations spanning the natural range of ethanol resistance. Ethanol significantly reduced mating success of males from the ethanol-sensitive population, but had no effect on mating success of males from the ethanol-resistant population. Furthermore, when a population formed by hybridizing the two populations was selected for mating competitiveness in the presence of low levels of ethanol, increased resistance to being killed by a high concentration evolved as a correlated response. Thus, variation among natural populations in resistance to unnatural high concentrations of ethanol could be partly the result of sexual selection for resistance to natural low concentrations.

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Symposium 2

Coevolution from parasitism to mutualism

Talks: *Room N6*

Essence posters*:* Upper floor lecture hall centre *HZ*

Regular posters*:* Upper floor campus canteen *Mensa*

Invited Speakers:

Greg Hurst, Jukka Jokela

Organizers:

Michael Brockhurst, Britt Koskella

Description:

Predicting transitions across the parasitism-mutualism continuum, from highly virulent pathogens to beneficial endosymbionts, requires both a thorough theoretical understanding and detailed empirical testing using a number of systems. This symposium will address new experimental and theoretical approaches to the study of host-symbiont coevolution across the parasitism-mutualism continuum, with a focus on developing a unified conceptual framework.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster ***B5-Sy02-i001-R***

Symposium 2
Coevolution from parasitism to mutualism

Co-evolutionary dynamics between transposons and their hosts in self- and cross-pollinating Capsella

Ågren JA[1], Platts AE[2], Wright SI[1]
[1]University of Toronto, Toronto, Canada, [2]McGill University, Montreal, Canada

Summary statement:

The effect of host mating system on the co-evolution between transposons and their hosts is illustrated using genome and expression data in self- and cross-pollinating Capsella.

Abstract:

A significant portion of many genomes is made up of 'selfish' or 'parasitic' genetic elements. These are stretches of DNA that gain a transmission advantage relative to other genetic elements, in spite of having no or deleterious effects on the host organism's fitness. The mobile transposable elements (TEs) are often considered to be the most successful of these genomic parasites. Despite being the single largest contributor to most genomes, the factors governing the co-evolutionary dynamics with their hosts remain elusive. Population genetic theory suggest that host mating systems should have a significant impact on this dynamic, due to differences in selective pressures on elements and hosts. Lower effective population size (Ne) and recombination rate in selfers has led to the prediction of higher TE accumulation in selfing compared to outcrossing species. On the other hand, theoretical modelling predicts that when selection is mainly due to TE-mediated ectopic recombination, outcrossers should accumulate higher TE-levels. Additionally, self-regulated transposition should be more likely to evolve in highly selfing species. Here, recent results from studies on a combination of genome and expression data from the selfer Capsella rubella and its close outcrossing relative Capsella grandiflora are presented. The results are used to discuss how examining mating system illuminates the co-evolutionary arms race between transposons and their hosts.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy02-i002-R*

Symposium 2
Coevolution from parasitism to mutualism

Dynamic Wolbachia infections in Acromyrmex leaf-cutting ants: do strains compete within hosts and might they be mutualists?

Andersen SB[1], Boye M[2], Boomsma JJ[1]
[1]University of Copenhagen, Centre for Social Evolution, Department of Biology, Copenhagen, Denmark, [2]Technical University of Denmark, National Veterinary Institute Division of Veterinary Diagnostics and Research, Copenhagen, Denmark

Summary statement:

Conflict between multiple Wolbachia strains in Acromyrmex ants appears resolved in adults by segregation & extracellular location in the gut lumen suggests novel symbiont function.

Abstract:

Wolbachia alpha-proteo bacteria are found as intracellular symbionts in many insects and the effects of infections on the host span the entire spectrum from parasitism to mutualism. Also ants are often infected with Wolbachia, but the consequences for these social insect hosts are typically not well understood. Multiple Wolbachia strains have been identified in Acromyrmex leaf-cutting ants, leading to interesting questions about possible conflict unless strains would be segregated in different tissues or some of them would have evolved to be mutualists. We did a detailed study to shed light on the infection dynamics across the larval, pupal and adult-worker life-stages, using quantitative PCR, fluorescent in situ hybridization, and laser capture microdissection. Infection levels of 100 % across all sampled colonies and an increase in bacterial density with host age suggests that sterile workers are not evolutionary dead ends for the bacteria. Comparison of colonies with multiple vs. single infections suggests that different strains may compete in immature individuals where they might occupy the same tissue niche. This conflict appears to be resolved in adult hosts where the suppressed strain proliferates extracellularly in the gut lumen. This unusual location suggests a previously unrecognized role for Wolbachia as a possibly mutualistic symbiont of leaf-cutting ants.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy02-i003-R*

Symposium 2
Coevolution from parasitism to mutualism

Virus infection suppresses Nicotiana benthamiana adaptive phenotypic plasticity

Bedhomme S[1], Elena SF[1,2]
[1]IBMCP, Valencia, Spain, [2]The Santa Fe Institute, Santa Fe, United States

Summary statement:

Two potyviruses (TEV and TuMV) drastically suppress the shade avoidance syndrome, the plant-specific phenotypic plasticity in response to competition.

Abstract:

Competition and parasitism are two important selective forces that shape life-histories, migration rates and population dynamics. Recently, it has been shown in various pathosystems that parasites can modify intraspecific competition, thus generating an indirect cost of parasitism. Here, we investigated if this phenomenon was present in a plant-potyvirus system using two viruses of different virulence (Tobacco etch virus and Turnip mosaic virus). Moreover, we asked if parasitism interacted with the shade avoidance syndrome, the plant-specific phenotypic plasticity in response to intraspecific competition. Our results indicate that the modification of intraspecific competition by parasitism is not present in the Nicotiana benthamiana – potyvirus system and suggests that this phenomenon is not universal but depends on the peculiarities of each pathosystem. However, whereas the healthy N. benthamiana presented a clear shade avoidance syndrome, this phenotypic plasticity totally disappeared when the plants were infected with TEV and TuMV, very likely resulting in a fitness loss and being another form of indirect cost of parasitism. This result suggests that the suppression or the alteration of adaptive phenotypic plasticity might be a component of virulence that is often overlooked.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy02-i004-R*

Symposium 2
Coevolution from parasitism to mutualism

The expression of virulence in mixed-infections: the role of relative virulence and dose

Ben-Ami F[1], Routtu J[2], Ebert D[2]
[1]Tel Aviv University, Zoology, Tel Aviv, Israel, [2]University of Basel, Zoological Institute, Basel, Switzerland

Summary statement:

Virulent parasite strains of Daphnia magna compensate for their inferior lifetime transmission success through superior competitiveness, regardless of their relative dose..

Abstract:

Multiple infections of the same host by different strains of the same microparasitic species are commonly observed in natural populations. When parasites cannot be cultured, studies of multiple infections often employ isolates of unknown genetic composition (i.e., samples from infected hosts that may contain multiple strains). As a result, potentially complex interactions among the strains within the isolates cannot be controlled experimentally, which may result in incorrect conclusions with regards to the expression of virulence and parasite transmission. In the present study we examined the competitive outcome of multiple infections, using a single clone of the waterflea Daphnia magna, and two strains and three isolates of its semelparous endoparasite Pasteuria ramosa. We exposed individual Daphnia to single infection treatments and to simultaneous multiple infection treatments with mixtures of 90:10, 10:90 and 50:50. Virulence was assessed by monitoring host mortality. Parasite spore production was used as a measure of parasite fitness. We found that in single infections, Pasteuria clones were less virulent than Pasteuria isolates and produced more spores than the isolates. Under simultaneous multiple infections, when a higher dosage of the less virulent strain was present (90:10), spore production was higher than it was when the two strains were in equal or opposite proportions. Despite these higher sporeloads, the more virulent parasite in the mixture always dominated the intra-host competition. Our results suggest that less virulent strains may easily be replaced by more virulent strains during multiple infections, regardless of the initial inoculation.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy02-i005-R*

Symposium 2
Coevolution from parasitism to mutualism

Time travel and patterns of adaptation

Blanquart F[1], Gandon S[1]
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Summary statement:

The general framework developed shows how the temporal and spatial heterogeneity of selection translate into the result of time shift and local adaptation experiments.

Abstract:

Understanding and predicting the dynamics of adaptation in a changing world is one of the main challenges of theoretical evolutionary biology. Time shift experiments, which involve measuring the fitness of a population transplanted to its past and future environments, have emerged as a promising tool to this end. Here we analyze the patterns of adaptation that result from general models of temporally variable environments. We show that the result of a time-shift experiment crucially depends on the properties of the change in the environment, and specifically of the temporal autocorrelation of the environmental change. We use this general framework to discuss how the study of patterns of adaptation in time (time-shift experiments) and space (local adaptation experiments) could help infer some information about the temporal and spatial heterogeneity in selection. In the context of species interactions, these patterns of adaptation can be used to study the underlying models of coevolution. In particular, in the context of host-parasite interactions, we discuss the relevance of these patterns of adaptation to distinguish between frequency dependent "red queen" dynamics and arms race dynamics.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy02-i001-E*

Symposium 2
Coevolution from parasitism to mutualism

Mycoparasitic fungi in the Epichloë-Puccinellia association: Identification and distribution in space

Bogdanowicz AM[1], Ryszka P[2], Turnau K[2], Górzyńska K[1], Lembicz M[1]
[1]Adam Mickiewicz University, Department of Plant Taxonomy, Poznan, Poland, [2]Jagiellonian University, Institute of Environmental Sciences, Krakow, Poland

Summary statement:

Our study shows that Epichloë stromata provide habitat for other fungi that may inhibit the production of ascospores by the Epichloë fungus and the infection of other plants.

Abstract:

The fungus Epichloë typhina (Clavicipitaceae: Ascomycota) is a parasite of numerous grass species. The fungal stromata enclose grass shoots suppressing their further development and, as a result, limiting the flowering and seed production of an infected plant. This disease is known as „choke disease”. Our study shows that Epichloë stromata also provide habitat for other fungi that may inhibit the production of ascospores by the Epichloë fungus and, thus, the infection of other plants. We studied the occurrence of mycoparasitic fungi on the stromata of Epichloë typhina, in five E. typhina-infected populations of the grass Puccinellia distans. The primer pair ITS1F (Gardes and Bruns 1993) and ITS4 (White et al. 1990) was used to amplify the ribosomal cassette consisting of SSU, ITS1, 5.8S, ITS2 and LSU rDNA. We found that 37 DNA sequences were present. BLAST search revealed best matches belonging to several groups of ascomyceteous fungi. Among them, 14 sequences were matched to Epichloë/Neotyphodium group, 3 to Bionectria/Clonostachys group and 20 to Microdochium. However, a phylogenetic analysis showed clustering of all obtained sequences into one monophyletic group. The highest percentage of E. typhina stromata inhabited by mycoparasitic fungi was shown in the grass populations occurring in the habitats with the lowest salinity. We use the obtained results to explain the formerly discovered by us differentiation in the production of the mature, i.e., containing ascospores, E. typhina stromata in the space.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy02-i007-R*

Symposium 2
Coevolution from parasitism to mutualism

Learning effects and transient dynamics revealed by a long-term time-shift perspective of host-parasite coevolution

Decaestecker E[1,2], Raeymaekers JA[3], De Gersem H[4]
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Summary statement:

Host-parasite coevolution model and long-term time-shift experiment incorporating learning effects through transient dynamics.

Abstract:

Hosts mostly do not evolve as fast as their parasites, yet, adaptive genetic changes do occur upon infection. An important aspect of these adaptations is that there is selection in the hosts for alternative defense mechanisms, other than the prevailing ones to which the fast evolving parasites are already adapted. This type of arms races are known as 'Red Queen' dynamics. The analyses of mathematical models of coevolution confirm that these dynamics are caused by negative frequency dependent selection in which the parasite often has a greater evolutionary potential than its host. These models assume that amplitudes of long-term fitness dynamics remain constant through time. Here, we argue that coevolutionary models need to incorporate learning effects through transient dynamics resulting in dampened cycles of infectivity through time. This statement is corroborated by a long-term time-shift experiment modifying current insights into the dynamics of these antagonistic interactions.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy02-i008-R*

Symposium 2
Coevolution from parasitism to mutualism

Behavioural switch between host protection and host induced-death during parasite ontogeny in an acanthocephalan-amphipod system: challenging the parasitism-mutualism continuum

Dianne L[1], Rigaud T[1], Perrot-Minnot M-J[1]
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Summary statement:

We confirmed a model predicting that an optimal parasitic strategy for trophically-transmitted parasites is first to be mutualistic and then virulent.

Abstract:

Many trophically-transmitted parasites with complex life cycle manipulate their intermediate host behaviour in ways facilitating their transmission to final host by predation. However, a recent theoretical model predicts that an optimal parasitic strategy would be to protect the intermediate host from predation when parasites are non infective, before switching to predation facilitation when the infective stage is reached. We tested this hypothesis experimentally in the fish acanthocephalan parasite Pomphorhynchus laevis using the amphipod Gammarus pulex as intermediate host. As predicted, gammarids parasitized by the non-infective stage of P. laevis hid significantly more under refuges and were less preyed upon than uninfected ones. To our knowledge, this is the first study showing that such behavioural changes do indeed increase host survival, a necessary criterion to assign an adaptive value to this protective strategy. A switch towards enhanced vulnerability to predation was also found when P. laevis reached the stage infective to its final host. In addition, we investigated intraspecific conflict between coinfecting infective and non-infective stages of P. laevis. We found that behavioural manipulation was weakened in gammarids infected with mixed larval stages. Coinfecting infective and non-infective larvae both suffered competition, potentially resulting in delayed transmission and increased risk of mortality respectively. Both studies raised interesting questions about mechanisms underlying manipulation, and consequences of such strategies on host fitness.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy02-i009-R*

Symposium 2
Coevolution from parasitism to mutualism

Experimental evidence of a virulence-transmission trade-off in a plant virus

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Summary statement:

Experimental data supporting the virulence-transmission trade-off hypothesis

Abstract:

The transmission-virulence trade-off hypothesis is one of the few adaptive explanations of virulence evolution currently proposed. This hypothesis assumes that there is an overall positive correlation between parasite transmission and virulence. The trade-off occurs if transmission is a saturating function of virulence. Virulence may then evolve to an intermediate optimal level because beyond that level there is a trade-off with transmission. A positive correlation between each of these traits and within-host growth is often suggested to underlie the relationship between virulence and transmission.

There are few experimental studies that test this hypothesis. We infected Brassica rapa plants with twenty natural isolates of Cauliflower mosaic virus (CaMV) and then estimated three traits: transmission rate (i.e. number of infected plants after aphid transmission), virulence (symptom severity and leaf area compared to a non-infected control) and viral accumulation (viral DNA by quantitative PCR).

As predicted by the trade-off hypothesis, we observed a positive correlation between the rate of transmission and virulence. Moreover, in agreement with the trade-off hypothesis, a saturating model fits the data better than a linear model. However, our results on viral accumulation do not support the hypothesis that this trait is responsible for the correlation between transmission and virulence.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy02-i010-R*

Symposium 2
Coevolution from parasitism to mutualism

Evolution of transmission mode in obligate symbionts

Drown DM[1], Zee PC[1], Brandvain Y[1,2], Wade MJ[1]
[1]Indiana University, Department of Biology, Bloomington, United States, [2]University of California, Davis, Department of Evolution and Ecology, Davis, United States

Summary statement:

We find little opportunity for indirect selection to drive the evolution of vertical transmission from an ancestral state of horizontal transmission.

Abstract:

Associations between hosts and symbionts are a ubiquitous feature of nature. The mode of infection of symbionts ranges widely, from wholly vertical transmission from parents to offspring at one extreme to wholly horizontal (contagious) transmission from others within a population at the other. Here, we explore the evolutionary forces that might affect a change from an ancestral state of horizontal transmission to a derived state of vertical transmission. We find that, in the absence of epistasis for fitness between host and symbiont genes, statistical genetic associations between host and symbiont created by vertical transmission are quickly broken down by even very limited amounts of horizontal transmission. Thus, there is limited opportunity for indirect selection to drive the evolution of a vertical transmission modifier without invoking direct fitness benefits to the host-symbiont combination. We explore different models of fitness epistasis between host and symbiont, wherein some host-symbiont combinations have higher fitness than others for both species. We find that only certain models generate the appropriate conditions for vertical transmission to evolve. We explore additional stochastic forces with an individual-based simulation of our model and find that mutation has a significant role in increasing the probability of fixation of strong vertical transmission modifiers. Our model results have direct implications for the dynamics of host-symbiont coevolution such as the evolution of virulence.

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WED 24 AUG at 1120 - Room N6
Oral presentation *D2-Sy02-1120-O*

Symposium 2
Coevolution from parasitism to mutualism

Zooming into interspecific interactions to better understand coevolution dynamics

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Summary statement:

The study of individual steps of the infection process reveals a key force behind coevolutionary cycles that conforms to theoretical model assumptions.

Abstract:

Interspecific interactions, such as mutualism and parasitism, consist of a sequence of steps, each critical for the success of the interplay. Studies of interspecific interactions rarely take into account the fact that different steps might be influenced by different factors and might, therefore, make different contributions to shaping coevolution. Using the Daphnia magna – Pasteuria ramosa system, one of the rare examples of host-parasite interaction where coevolution in nature has been documented, we identified the sequence of steps, and tested the role of genetic and environmental factors in two of them. Hosts of different genotypes, genders and species were able to activate endospores of all parasite clones in different test environments. This suggests that the activation cue is phylogenetically conserved and that this step can be ruled out as a major factor in coevolution. We next established that the parasite attachment to the host body occurs onto the oesophagus independently of host species, gender and environmental conditions, but depends on the combination of host-parasite genotypes resulting in a binary pattern of infection (success/failure). This step can explain host population structure and could be a key force behind coevolutionary cycles. Our results also suggest that this step has one of the most ancient polymorphism for resistance recorded in animals (ca 100 million years). Our approach reveals that even if empirical data suggest quantitative outcomes of infection, when individual steps are concerned these outcomes are mostly binary – as assumed in theoretical models of host parasite interactions.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5 -Sy02 -i006 -R*

Symposium 2
Coevolution from parasitism to mutualism

The direct fitness effects of male-killer infection on female hosts

Elnagdy S[1,2], Majerus MEN[1]
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Summary statement:

Our finding led to the conclusion that the host-male-killer relationship is a mutual-interaction based relationship.

Abstract:

Hurst (1991) argued that male-killing bacteria invasion among host populations vary according to male-killing evolutionary parameters. These parameters are vertical transmission efficiency of the male-killer, a direct fitness effect of having male-killing bacteria on infected females, the rate of inbreeding, the consequential inbreeding depression and the fitness compensation that accrues to infected female offspring as an indirect consequence of male death. In this study, the direct fitness effect of infection on females was assessed in five species of coccinellid with four types of bacteria. A range of fitness parameters were assessed in infected and uninfected matrilines. In all systems investigated, the results obtained across all systems varied both in respect of the parameters affected and the direction of effects. This finding led to the conclusion that the host-male-killer relationship is a mutual-interaction based relationship.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy02-i011-R*

Symposium 2
Coevolution from parasitism to mutualism

Looking for the molecular basis of local host adaptation to a specific macroparasite

Erin N[1], Samonte-Padilla IE[1], Milinski M[1], Kalbe M[1]
[1]Max Planck Institute for Evolutionary Biology, Department of Evolutionary Ecology, Plön, Germany

Summary statement:

Comparison of immune gene expression in three-spined sticklebacks, experimentally infected with sympatric and allopatric isolates of the tapeworm Schistocephalus solidus.

Abstract:

Coevolution between hosts and parasites can drive evolutionary change in the interacting organisms, yet much remains to be discovered about the underlying mechanisms. Here, we investigated experimentally the genetic basis of host resistance and parasite virulence by using sympatric (coevolved) and allopatric (non-coevolved) combinations of three-spined sticklebacks (Gasterosteus aculeatus) and its specific tapeworm parasite Schistocephalus solidus. The strong phenotypic differences observed in reciprocal infection experiments using Norwegian and German populations of this host-parasite system suggest different resistance/virulence strategies for the coevolved and non-coevolved systems. We compared differential expression of immunologically relevant genes in the different host-parasite combinations to try and establish the molecular mechanisms underlying the infection phenotypes.

We dissected the fish 5, 7 and 9 weeks after exposure to S. solidus infective stages and took host tissue samples from immunologically-relevant organs. Candidate genes conferring resistance or tolerance to the host were identified by a classical gene search approach from available genomic and transcriptomic data from three-spined stickleback. A total of 8 genes responsible for mounting the innate and adaptive response against the parasite were found and the difference in their gene expression was verified by qPCR.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy02-i012-R*

Symposium 2
Coevolution from parasitism to mutualism

Antagonistic pair-wise interactions are weakened in multi-enemy communities

Friman V-P-[1], Buckling A[1,2]
[1]University of Oxford, Department of Zoology, Oxford, United Kingdom, [2]University of Exeter, Biosciences, Penryn, United Kingdom

Summary statement:

The strength of antagonistic pair-wise interactions are weakened in the multi-enemy communities resulting in less evolved hosts and parasites.

Abstract:

Pairwise evolutionary interactions can differ dramatically depending on the presence of other interacting species. It is generally predicted that strength of defence against any given enemy is weakened in the presence of multiple enemies if the defence mechanisms are not positively correlated. We tested this hypothesis by coevolving Pseudomonas fluorescens SBW25 bacterium and its parasitic phage in the absence and presence of protist predator Tetrahymena thermophila. We found that bacterial defence against protist (formation of large, inedible cell aggregations) evolved stronger in the absence of phage. Similarly, bacterial mean resistance against sympatric contemporary phage, and phage infectivity in general, evolved higher in the absence of protist. Two mechanisms are likely to be important in explaining this result: reduced pair-wise encounter rates between bacteria and its enemies and trade-offs between defensive adaptations against each enemy. Consistent with both explanations, we found that protist reduced bacterial and phage population sizes (but not vice versa), and that the resistance against phages was traded off with the defence against protists in the two-enemy community. These results suggest that antagonistic pair-wise interactions are weakened in multi-enemy communities and that the evolutionary responses against enemies are likely to be predictably altered as community complexity increases.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy02-i013-R*

Symposium 2
Coevolution from parasitism to mutualism

Multidimensional trait space favors victims in exploiter-victim coevolutionary arms races

Gilman RT[1], Nuismer SL[2]
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Summary statement:

We use mathematical models to show that victim species are favored in coevolutionary arms races when species-species interactions depend on multiple, potentially correlated traits.

Abstract:

Parasites often have larger population sizes and shorter generation times than their victims, which suggests that parasites should have an advantage in coevolutionary arms races. How victim species are able to maintain defenses against rapidly evolving parasites remains poorly understood. Most models of coevolution have assumed that the interaction rate between species is governed by a single pair of coevolving traits, one in each species. Here, we introduce a model that allows species-species interactions to depend on multiple coevolving traits. We show that victim species are favored as the number of traits governing species-species interactions increases, and as the genetic correlation between traits within species increases. We introduce the concept of maximum evolutionary escape rate, which can be estimated from the G-matrices of both species. Our study offers insight into how victim species are able to persist in the face of parasite onslaught, and offers a framework for studying coevolutionary dynamics in both exploitative and mutualist systems.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy02-i002-E*

Symposium 2
Coevolution from parasitism to mutualism

Fly-fungus interaction in wild grass: Deviations from the mutualistic pattern

Górzyńska K[1], Lembicz M[1], Olszanowski Z[2], Leuchtmann A[3]
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Summary statement:

Results of our study are contrary to previous reports regarding the interaction between Epichloë fungi and Botanophila flies as mutualistic.

Abstract:

During the course of evolution, some species of Botanophila (Diptera: Anthomyiidae) developed an interaction with fungi of the genus Epichloë, which endophytically infect grasses and form sexual fruiting structures (stromata) that prevent seed production (choke disease). Since Epichloë fungi are heterothallic, for sexual reproduction their spermatia must be transferred between stromata of opposite mating types. For transfer of spermatia, the Epichloë depends on flies of the genus Botanophila that use fungal stromata as a source of food and as a convenient place to lay eggs. Although hatching larvae consume part of the perithecia, the fungus clearly profits from an association that is considered to be mutualistic.
The presence of Botanophila species was noted in four populations of the non-agricultural grass Puccinellia distans that were infected with the fungus E. typhina. During the seven-year field observation, Botanophila flies were present every year in only one population of P. distans and number of fly-infested stromata differed considerably with year and site. Among all collected stromata, 90.8% were fertilised but only 20.8% of them showed signs of fly visitation.
Our results are contrary to previous reports regarding the fly-fungus interaction as mutualistic. A high proportion of fertilised stromata without indication of fly visitation suggests the presence of more than one mechanisms of cross-fertilisation in this system. Besides the flies acting as vector, cross-fertilisation may be facilitated by direct contact of stromata or by ascosporic fertilisation. Moreover, the presence of another unknown vector can not be excluded.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy02-i003-E*

Symposium 2
Coevolution from parasitism to mutualism

Collateral adaptations of parasites are often overlooked: enhanced immunity of avian brood parasites

Hahn C[1], Erf G[2], Igl L[3], Burnett J[2]
[1]US Geological Survey, Patuxent Wildlife Research Center, Laurel, United States, [2]University of Arkansas, Department of Poultry Science, Fayetteville, United States, [3]US Geological Survey, Northern Prairie Research Center, Jamestown, United States

Summary statement:

Collateral adaptations are overlooked but essential aspects of coevolution, like the enhanced immunity of New World cowbirds, extreme host-generalist brood parasites.

Abstract:

An overlooked aspect of host-parasite coevolution is selection on parasite traits collateral to the host's principal defenses but essential to the parasite's success. Accurately characterizing a coevolutionary system requires a broad consideration of relevant traits. Enhanced immunity is an adaptation characteristic of the New World cowbirds, a genus including extreme host-generalists that lay their eggs in the nests of > 225 different host species. Traditionally, coevolutionary studies of avian brood parasites focused on traits like egg mimicry or behavioral aggressiveness of parasite nestlings. We have previously shown that several cowbird species also have an adaptive 'portfolio' of immune defenses that protect against exposure to species-specific microbes and parasites in the diverse host environments exploited. We will present new data on immune factors in eggs of brown-headed cowbirds, a combination of enhanced and typical components suited to the diverse infections that threaten young brood parasites. We compared concentrations of maternal antibodies, lysozymes, and albumen volume in eggs of the cowbird and a related, non-parasitic species. Cowbird eggs had significantly higher levels of lysozymes, immune substances effective against most Gram positive bacteria. Cowbird eggs also had higher levels of albumen, which keeps the egg free of infection through mucosal antibodies, formed in response to pathogens entering the female's respiratory, digestive, and reproductive tract. This particular combination of immune defenses reflects the parasite´s adaptations to the host´s niche.

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TUE 23 AUG at 1500 - Room N6
Oral presentation *C3-Sy02-1500-O*

Symposium 2
Coevolution from parasitism to mutualism

Host-parasite coevolutionary arms races give way to fluctuating selection

Hall A[1], Scanlan P[1], Morgan A[1], Buckling A[1,2]
[1]University of Oxford, Oxford, United Kingdom, [2]University of Exeter, Penryn, United Kingdom

Summary statement:

We used phenotypic and genetic data from coevolving communities of bacteria and bacteriophage to study coevolutionary dynamics over time.

Abstract:

Host-parasite coevolution is a key driver of biological diversity and parasite virulence, but its effects depend on the nature of coevolutionary dynamics over time. We used phenotypic data from coevolving populations of the bacterium Pseudomonas fluorescens SBW25 and parasitic phage SBW25Φ2, and genetic data from the phage tail-fibre gene (implicated in infectivity evolution) to show that arms race dynamics, typical of short-term studies, decelerate over time. We attribute this effect to increasing costs of generalism for phages and bacteria with increasing infectivity and resistance. By contrast, fluctuating selection on individual host and parasite genotypes was maintained over time, becoming increasingly important for the phenotypic properties of parasite and host populations. Given that costs of generalism are reported for many other systems, arms races may generally give way to fluctuating selection in antagonistically coevolving populations.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy02-i014-R*

Symposium 2
Coevolution from parasitism to mutualism

Multiple non-congruent colonizations of oceanic islands reveal dynamics of codiversification in a pollinating seed-predation mutualism between Glochidion trees and Epicephala moths

Hembry DH[1], Kawakita A[2], Gurr NE[3], Schmaedick MA[3], Baldwin BG[4], Gillespie RG[1]
[1]University of California, Berkeley, Department of Environmental Science, Policy, and Management, Berkeley, United States, [2]Kyoto University, Center for Ecological Research, Otsu, Japan, [3]American Samoa Community College, Pago Pago, American Samoa, [4]University of California, Berkeley, Jepson Herbarium and Department of Integrative Biology, Berkeley, United States

Summary statement:

Phylogenetic analysis of a pollinating seed-predation mutualism reveals strong phylogenetic discordance and asymmetric specialization, in contrast to previous studies

Abstract:

Coevolution is frequently invoked as a process responsible for much of the generation and maintenance of biological diversity on earth, but the manner in which coevolving clades diversify on macroevolutionary scales remains obscure, particularly in mutualistic systems. Here we examine the mutualism between Glochidion trees (Phyllanthaceae) and Epicephala moths (Lepidoptera: Gracillariidae) on the oceanic islands of Eastern Polynesia (central south Pacific). The Glochidion-Epicephala mutualism is similar to the fig-fig wasp and yucca-yucca moth mutualisms in that Epicephala actively pollinate their host plants but also oviposit in flowers so that their larvae may feed on a subset of the developing seeds. Phylogenetic analysis shows that both Glochidion (23 endemic species) and Epicephala have colonized these islands twice from the west, but that the colonizations are not phylogenetically congruent. In particular, two colonizations by Epicephala are associated with a single colonization by Glochidion. One of these Epicephala clades has diversified into numerous geographically delimited endemic morphospecies, but the other, apparently younger clade consists of a single undescribed Epicephala morphospecies that is associated with 11 species of Glochidion across three archipelagoes. Our results are in contrast to the long-standing paradigm of high host specificity in pollinating seed-predation mutualisms and indicate that patterns of host associations in these systems are dynamic over evolutionary timescales.

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WED 24 AUG at 0910 - Room N6
Invited talk ***D1-Sy02-0910-I***

Symposium 2
Coevolution from parasitism to mutualism

From parasite to commensal in five years: Host suppression and the rapid loss of sex ratio distortion by Wolbachia in Samoan H. bolina

Hurst G[1], Hornett E[1], Charlat S[2], Moran B[1], Reynolds L[1], Wedell N[3], Jiggins C[4]
[1]University of Liverpool, Institute of Integrative Biology, Liverpool, United Kingdom, [2]University Bern Claude Bernard, Lyon, France, [3]University of Exeter in Cornwall, Falmouth, United Kingdom, [4]University of Cambridge, Zoology, Cambridge, United Kingdom

Summary statement:

We detail a rapid switch in the nature of a symbiotic interaction in natural populations, with evolution from parasitic to benign in less than five years.

Abstract:

Maternally Inherited microbes of arthropods are in an interesting evolutionary position. Being inherited, they are selected to favour the survival and reproduction of their female host, and do so in ways that include providing natural enemy protection to their host. Being barred for transmission through the male line, they are also selected to manipulate female reproduction, which they do through biasing host sex ratios. They thus span the parasitism-mutualism continuum. In this talk, we outline the process of movement along the parasitism-mutualism continuum in the symbiosis between H. bolina and its Wolbachia symbiont in natural populations. A selective sweep of a suppressor of male-killer activity in the butterfly genome has altered the symbiosis from one of strong conflict between parties to one that is relatively benign. The sweep is observed in real time - from 2000 to 2006- through both phenotype and via effects on genetic variation through hitchhiking. Both measures bear testament to the rapid changes that can occur in the direction of symbiotic interactions in natural populations.

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TUE 23 AUG at 1400 - Room N6
Invited talk *C3-Sy02-1400-I*

Symposium 2
Coevolution from parasitism to mutualism

Co-evolutionary dynamics in natural host-parasite populations: Long-term research on parasite hypothesis for sex

Jokela J[1]
[1]Institute of Integrative Biology (IBZ), Eawag, Department of Aquatic Ecology, Dübendorf, Switzerland

Summary statement:

Long-term studies are needed for understanding the dynamics of host-parasite coevolution, especially when parasites are expected to select for genetic diversity in the host.

Abstract:

I will outline the results of a long-term research project addressing the importance of host-parasite coevolution for maintenance of sexual reproduction. Since 1994 we have been following a mixed population of sexual and asexual Potamopyrgus antipodarum snails in New Zealand. The most common parasite in the system is a highly virulent trematode that is suggested to drive a depth-specific cline in the proportion of sexual snails in the population. Sexuals are more common in shallow habitats of the lake where also the risk for parasite infection is higher, while the asexuals are more common in the deep. Using genetic markers we have been able to follow dynamics of clonal lineages in the population and can now associate the fluctuations in clone frequencies to parasite coevolution. The predictions of the parasite hypothesis for sex state that successful clonal lineages should be checked by coevolving parasites as the lineage becomes common. Evidence supporting this hypothesis is accumulating in this particular time series, but the empirical results also show complexity that may have many explanations. I will show the latest results from this study and use it to discuss broader implications of these results for importance of host-parasite coevolution for maintenance of genetic diversity, and what is required for refining our understanding of the coevolutionary process.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy02-i016-R*

Symposium 2
Coevolution from parasitism to mutualism

Microbiota and Tribolium castaneum – everlasting love?

Joop G[1], Mitschke A[1], Rosenstiel P[2], Schulenburg H[1]
[1]Christian-Albrechts-Universität Kiel, Evolutionary Ecology and Genetics, Zoological Institute, Kiel, Germany, [2]Institute of clinical molecular Biology, Christian-Albrechts-Universität Kiel, Kiel, Germany

Summary statement:

Beetle´s external secretion has the potential to shape and maintain the environment, thereby to manipulate the microbial diversity in flour or gut in favor of mutualistic microbes.

Abstract:

Tribolium beetles secrete Quinones into their flour environment. Quinones show broad antimicrobial activity and therefore can be considered as an "external" immune defence on the one hand, protecting from pathogens. On the other hand, some microbes and beetles might have a mutualistic relationship as well. Therefore, Quinones also have the potential to shape and maintain the beetle´s environment, and by this manipulate the microbial diversity in the flour and in the beetle gut in favor of mutualistic microbes. Here we present results of a metagenomic analysis using 454 pyrosequencing designed to identify bacteria and fungi present in different beetle lines. Some of these lines were collected only recently while others have been maintained in the lab for decades. If the Quinones indeed help to shape the beetles´ microbiota, we expect only small differences in the composition of mutualistic species found in the different beetle lines.

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TUE 23 AUG at 1440 - Room N6
Oral presentation *C3-Sy02-1440-O*

Symposium 2
Coevolution from parasitism to mutualism

Direct evidence for the Red Queen Hypothesis: Antagonistic coevolution with a parasite increases host recombination frequency

Kerstes NAG[1], Bérénos C[2], Wegner M[3,4], Schmid-Hempel P[1]
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Summary statement:

Coevolution with a parasite led to higher recombination rates in a host. As we can exclude alternative explanations, this result indicates the presence of Red Queen dynamics.

Abstract:

One of the largest remaining challenges in evolutionary biology is to understand the maintenance of meiotic recombination. As recombination breaks down successful genotypes, it is thought to be selected for only under very limited conditions. One of the hypotheses to explain the maintenance of recombination is the Red Queen Hypothesis (RQH). The RQH predicts an advantage of recombination for hosts when they are coevolving with parasites. Parasites can rapidly adapt to their hosts, and recombination can help the host escape from their parasites by constantly creating new, rare genotypes. We conducted a long-term coevolution experiment with the red flour beetle Tribolium castaneum and its microsporidian parasite Nosema whitei. We experimentally show that the recombination frequency of the host has increased after 11 generations of coevolution with its parasite. It was found that coevolving populations had higher levels of heterozygosity and allelic diversity than control populations, and that overdominance seems not to be able to explain the advantage of the more genetically divers state. Furthermore, we showed that resistance harbored a substantial epistatic component at the beginning of the experiment, which might contribute to maintenance of recombination if non-additive genetic architecture is also maintained during coevolution. Based on these findings, we believe that Red Queen mechanisms were acting in our experiment, and that the RQH cannot be discarded as one of the possible answers to the big question of recombination.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy02-i017-R*

Symposium 2
Coevolution from parasitism to mutualism

Diversity and field dynamics of gut microbiota in Central European bumblebee hosts: Evidence for coevolution

Koch H[1], Schmid-Hempel P[1]
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Summary statement:

We found a distinct and species poor community of gut bacteria in central European bumblebees and provide details on the seasonal dynamics of these bacteria in Bombus terrestris.

Abstract:

Animals are hosts to diverse bacterial communities in their gut. The members of these communities can range from obligate mutualists to deadly parasites. Recent studies have indicated the existence of a distinct and relatively species poor gut microbiota in honeybees, which is apparently absent in solitary bees, but shared to some degree with bumblebees. We are presenting a detailed look at these bacterial communities in Central European bumblebee species, comparing 6 species from 3 localities. Using a combined approach of 16S TRFLP-profiles and clone libraries, we identified a surprisingly simple and conserved microbiota across these species and localities. However, we also find strong support for significant differences of microbiota between host species. Furthermore, one member of the Betaproteobacteria was found to have distinct phylotypes in different bumblebee and honeybee host species, suggesting a pattern of coevolution with their bee hosts. To understand the dynamics of these gut bacteria in the field, we sampled Bombus terrestris colonies over the course of a season, looking at changes during colony development and correlations with parasite infection. We also compare the within colony variation to the between colony variation of gut microbiota and checked the bacteria present in gynes originating from these colonies, to look at the role of sociality in transmission.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy02-i004-E*

Symposium 2
Coevolution from parasitism to mutualism

Parasite-mediated inter- and intra-sexual selection, sexual signaling and personality evolution in the common minnow Phoxinus phoxinus

Lai Y-T[1], Kekäläinen J[1], Kortet R[1]
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Summary statement:

In this research plan, a series of experiments has been conducted to examine the influence of parasite infection in minnows. Latest results will be presented in the presentation.

Abstract:

Parasite-mediated sexual selection predicts that parasites facilitate sexual selection by influencing the presentation and evolution of secondary sexual signals of their host. Parasites may also influence host behaviors to increase the likelihood to complete their own life cycles, thus in turn increase the mortality of hosts with low parasite avoidance behaviors. If the parasite avoidance behaviors are inheritable and related to the personalities of hosts, the increase of selection pressure by parasitism to hosts with particular personalities could be seen as parasite-mediated personality evolution. In previous studies, sexual selection and sexual signaling of common minnow Phoxinus phoxinus have been noted, and the linking between sexual signaling, dominance and reproductive success of males has been examined. Moreover, parasite infection and parasite ecology in minnows have been surveyed. However, although it has been shown recently that the intensity of parasite infection may associate with dominance and sexual signaling, the relationship and potential mechanisms of the linkage have little been investigated. Similarly, although the influence of parasitism in behavioral syndromes of minnows has been noted, the influence of parasitism in personality evolution of minnows has never been investigated. In this research plan, based on results in previous studies and my finding in 2010, a series of experiments has been conducted to clarify the ambiguous parts of the sexual selection system previously demonstrated, and examine the influence of parasite infection in behavior traits and personalities in minnows. Latest results will be presented and discussed in the presentation.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy02-i018-R*

Symposium 2
Coevolution from parasitism to mutualism

Daphnia-symbiont community structure under different productivity regimes

Lange B[1], Muylaert K[1], Decaestecker E[1]
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Summary statement:

Productivity regime affects Daphnia-symbiont community structure.

Abstract:

Daphnia-symbiont community structure under different productivity regimes.The freshwater crustacean Daphnia magna inhabits ponds and lakes which differ substantially in productivity levels. This is a consequence of agricultural fertilisation and major differences between habitat structures. A taxonomically diverse group of symbionts lives in and on D. magna. We tested in an experimental approach if productivity can influence the symbiont community within a period of two months. It was found that epibionts were strongly affected by productivity changes while parasites were not. Our results show that productivity changes have an instant effect on the symbiont community of D. magna. Thus, agricultural fertilisation leads to secondary effects on biodiversity which can easily be overlooked.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy02-i005-E*

Symposium 2
Coevolution from parasitism to mutualism

Food plant specialization of a seed predator

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Summary statement:

Food plant specialization of Lygaeus equestris (Heteroptera) was studied by conducting feeding trials and a mass-selection experiment.

Abstract:

Aims: Food plant specialization is an important factor contributing to the enormous biodiversity of insects. Lack of genetic variation in food plant utilization and trade-offs (i.e. negative genetic correlations) between performances of insect herbivores on different food plant species may constrain their specialization. Our aim was to study food plant specialization of Lygaeus equestris (Heteroptera), which most commonly feeds on Vincetoxicum hirundinaria, but occasionally also on several alternative food plant species.
Methods: We conducted feeding trials in laboratory using seeds of V. hirundinaria and three alternative food plant species. In a mass-selection experiment we maintained selection lines of L. equestris for about fifteen generations on seeds of four food plant species to investigate evolution of food plant specialization.
Results: Although there was genetic variation in the performance of L. equestris on different food plant species, the bugs performed better on V. hirundinaria compared to alternative hosts. Ecological factors rather than genetic constrains determine the level of specialization. The mass-selection experiment will provide more detailed data on the costs and constrains, and the evolution of food plant specialization.
Conclusions: Understanding the factors that constrain specialization or enhance alternative food plant utilization are central for the coevolutionary dynamics between interacting species such as L. equestris and V. hirundinaria.

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TUE 23 AUG at 1610 - Room N6
Oral presentation *C4-Sy02-1610-O*

Symposium 2
Coevolution from parasitism to mutualism

Behavioural resistance against a protozoan parasite in the monarch butterfly

Lefèvre T[1], de Roode J[1]
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Summary statement:

We studied butterflies behavioral defenses against a protozoan parasite. While larvae were unable to avoid the parasite or feed on therapeutic plants, infected females laid their eggs on antiparasitic plants

Abstract:

Parasites pose a serious threat to host fitness, and natural selection should favour host traits that reduce infection or disease symptoms. One way in which hosts may protect themselves against parasitism is through altered behaviours, but such defences have been much less studied than other forms of parasite resistance. We studied whether monarch butterflies (Danaus plexippus L.) use altered behaviours to protect themselves and their offspring against the protozoan parasite Ophryocystis elektroscirrha . In particular, we studied whether (1) monarch larvae can avoid contact with infectious parasite spores; (2) whether larvae preferentially consume therapeutic food plants when given a choice or increase the intake of such plants in the absence of choice; and (3) whether female butterflies preferentially lay their eggs on medicinal plants that make their offspring less sick. We found that monarch larvae were unable to avoid infectious parasite spores. Larvae were also not able to preferentially feed on therapeutic food plants or increase the ingestion of such plants. However, infected female butterflies preferentially laid their eggs on food plants that reduce parasite growth in their offspring. Our results suggest that animals may use altered behaviours as a protection against parasites, and that such behaviours may be limited to a single stage in the host-parasite life cycle. Our results also suggest that animals may use altered behaviours to protect their offspring instead of themselves. Thus, our study indicates that an inclusive fitness approach should be adopted to study behavioural defences against parasites.

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WED 24 AUG at 1100 - Room N6
Oral presentation *D2-Sy02-1100-O*

Symposium 2
Coevolution from parasitism to mutualism

On the equivalence of host local adaptation and parasite maladaptation: An experimental test in the great tit - hen flea system

Lemoine M[1,2], Doligez B[2], Richner H[1]
[1]University of Bern, Evolutionary Ecology, Bern, Switzerland, [2]University of Lyon, Department of Biometry and Evolutionary Biology, Villeurbanne, France

Summary statement:

A test of local adaptation in the great tit-hen flea system suggested that both hosts and parasites could be locally maladapted due to a possible resistance-tolerance trade-off.

Abstract:

In heterogeneous environments, host-parasite coevolution may lead to either host or parasite local adaptation. Using reciprocal infestations over many populations, we tested local adaptation in the great tit-hen flea system. Flea reproductive success was lower on local compared to foreign hosts, revealing flea local maladaptation. Host reproductive success was intermediate between controls and foreign fleas when breeding with local fleas, suggesting host local adaptation although the non-significance between local and foreign infestations does not allow to exclude the absence of local adaptation. In contrast, fledglings were heavier and larger when reared with foreign compared to local fleas, which could also indicate host local maladaptation if offspring fitness depends mainly on size. Our results therefore challenge the traditional view that parasite local maladaptation equals host local adaptation. The differences in fledgling morphology suggest that flea origin affects host resource allocation between nestling growth and defence against parasites (a resistance-tolerance trade-off). Identifying the relevant fitness measures for both species remains necessary to understand the local adaptation patterns observed here.

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TUE 23 AUG at 1550 - Room N6
Oral presentation *C4-Sy02-1550-O*

Symposium 2
Coevolution from parasitism to mutualism

Genetic and epidemiological spatial structuring and the evolution of parasite prudence and host resistance

Lion S[1], Débarre F[1], van Baalen M[2], Gandon S[1], Boots M[3]
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Summary statement:

I synthesize theoretical results in spatial evolutionary epidemiology to discuss how genetic and epidemiological structures may shape selective pressures on host and parasites.

Abstract:

Recent theoretical and empirical studies have suggested that parasites should be expected to be more ´prudent´ (less harmful and slower transmitting) when infection occurs locally. Kin selection has been shown to be a key driver of the evolution of parasite prudence: by exploiting their host supply more prudently, parasites reduce the level of local kin competition experienced by related parasites. However, demographic or epidemiological processes can alter or even reverse the selective pressures faced by parasites. My aim is to tie together the conceptual insights of inclusive fitness theory and of spatial epidemiology to discuss to what extent the interplay between genetic and epidemiological structuring may shape selective pressures on host and parasites. I will articulate this presentation around three main results. First, I present results showing that demographic turnover is needed for local interactions to select for prudence in the susceptible-infected models that have been the focus of previous studies. Importantly, this may cause virulence to be maximised at intermediate parasite dispersal. Second, in diseases with little demographic turnover (as typical of many human diseases), our results suggest that only parasites causing diseases with long-lived immunity are likely to be prudent in space. Finally, I present related results obtained in an evolutionary model of host resistance that demonstrate that increasing disease-induced host mortality may also be a strategy of host defense. I conclude by discussing the perspectives to integrate these results into a synthetic framework for the co-evolution of hosts and parasites in a spatial ecological context.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy02-i006-E*

Symposium 2
Coevolution from parasitism to mutualism

Microbial inhibition and immune response specificity in the ant, Formica exsecta

Luhtasela-El Showk HK[1], Sundström L[1]
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Summary statement:

The function of the innate immunity of an ant was tested. Responses were induced by injection, specificity was absent and inbreeding affected the response under certain conditions.

Abstract:

Insect societies are a special case in the evolution of host-pathogen interactions. They provide a stable environment where the potential hosts are closely related and occur in high densities, conditions which promote the spread of pathogens. It can therefore be expected that social insect colonies are under constant immune challenge. Even so, social insects are successful in terms of diversity, distribution and ecological dominance. The colony´s defences range from division of labour to individual immune defences. In addition to physical barriers, the individual immune response consists of cellular and humoral defences. The cellular component involves e.g. phagocytosis and encapsulation, while the humoral defence consists of circulating defence molecules, such as antimicrobial peptides. My study focuses on the inducibility and specificity of the humoral immune response in the ant Formica exsecta. To test this, I challenged ants with 4 bacterial species, 2 gram-positive and 2 gram-negative, by injecting heat-killed bacteria into the ants´ abdomens. After injection, hemolymph was extracted and used to test the difference in the growth-inhibiting effects of the antibacterial peptides on bacterial cultures. The diameters of the resulting inhibition zones were used as a proxy for the strength of the immune response. The response against the gram-positive species was induced by injection itself, whereas no such response was seen against the gram-negative bacteria. No specificity was found. The degree of inbreeding of the colony had a negative effect on the presence of an immune response in colonies without mites, whereas no such effect was observed in colonies with mites.

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TUE 23 AUG at 1630 - Room N6
Oral presentation *C4-Sy02-1630-O*

Symposium 2
Coevolution from parasitism to mutualism

Natural selection in an artificial world: the evolution of parasite life-history and virulence on intensive farms

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Summary statement:

High host density, short host lifespan and frequent drug use may select for fast-growing and more virulent parasites: the example of the salmon louse Lepeophteirus salmonis.

Abstract:

Intensive farming creates conditions for parasite growth and transmission drastically different from what parasites experience in wild host populations and may therefore alter selection on various traits, such as life-history traits and virulence. Although recent epidemic outbreaks highlight the risks associated with intensive farming practices, most work has focused on reducing the short-term economic losses imposed by parasites, such as application of chemotherapy. Most of the research on parasite virulence evolution has been conducted using laboratory model systems, often unrelated to economically important systems. Here, based on current theory of virulence evolution, we will discuss the extent to which intensive farming practices may select for fast-growing, early-transmitted, and hence probably more virulent parasites. We will present recent empirical evidence indicating that parasite life history and virulence may be evolving as a consequence of intensive farming practices and suggest lines for future research in this area.

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WED 24 AUG at 1010 - Room N6
Oral presentation *D1-Sy02-1010-O*

Symposium 2
Coevolution from parasitism to mutualism

Going large: Coevolution across the parasitism-mutualism border in superorganisms and their macrosymbionts

Nash DR[1]
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Summary statement:

Social insect colonies face attack by social parasites and benefit from mutualistic symbionts. Here I compare their coevolution to classic host-endosymbiont-pathogen systems.

Abstract:

One of the major transitions in evolution is that to eusocial colonies from individual organisms. Although the parallels are not exact, social insect colonies can be regarded as superorganisms, which like any other organism gather and store resources to enhance their own reproductive fitness. Many other organisms act as “social symbionts” within these superorganisms, ranging from social parasites that exploit the colonies’ resources to mutualistic symbionts that enable the colony to obtain resources that are otherwise unavailable. Over the last decade there have been major advances in the understanding of the coevolution of social insects and their symbionts, which have both been inspired by and can shed light on studies of coevolution in more traditional host-symbiont systems. Using examples from the associations between ant colonies and their symbionts, I here give an overview of coevolution across the mutualism-parasitism continuum and the parallels with and differences from coevolution of pathogens, endosymbionts and their hosts.

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WED 24 AUG at 1200 - Room N6
Oral presentation *D2-Sy02-1200-O*

Symposium 2
Coevolution from parasitism to mutualism

Symbiont-mediated immunity and host genotype in an insect-pathogen interaction

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Summary statement:

Pea aphids are protected from fungi by endosymbiotic bacteria. Here we investigate features of the aphid immune response to fungus, and how it is altered by protective symbionts.

Abstract:

A diversity of organisms are associated with microbial partners that shape their hosts´ ability to combat disease, but fundamental questions remain about these multi-species interactions. Here we look at the interaction between a pea aphid host, an aphid fungal pathogen, and protective symbiotic bacteria. Pea aphids are frequently cited as an example of the great deal of variation in susceptibility to pathogens that exists among hosts. However, recent work suggests that some of this variation is due to the presence of symbionts rather than host genotype. For example, the facultative symbiont Regiella insecticola protects pea aphids from several species of fungal pathogens. In addition, genome annotation revealed several genes and pathways found in other insects studied to date that are missing in pea aphids, potentially because of the intimate association between aphids and symbionts. We are therefore working to answer several questions about this system. First, it is not clear whether aphids mount an immune response to fungal pathogens and whether this response varies among individuals, and so we conduct cost-of-immunity assays and infection experiments with fungal pathogens on aphid clonal lines with and without symbionts. Second, we have little understanding of how or whether investment in immune responses changes in the presence of protective microbes, and so we explore how pea aphids differentially respond to immune challenges in the presence and absence of protective partners. Symbionts can influence the population dynamics of many pest-insects, and are important for human health, and thus this research provides insight into an important coevolutionary interaction.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy02-i007-E*

Symposium 2
Coevolution from parasitism to mutualism

Parasitisation and reproductive investment in three-spined sticklebacks, Gasterosteus aculeatus

Rahn AK[1], Bakker TCM[1]
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Summary statement:

Different parasites and their effects on the expression of several reproductive traits in the three-spined stickleback, Gasterosteus aculeatus, are compared.

Abstract:

Reproductive traits that are influenced by parasitic infections might serve as indicators for an individual’s ability to resist infections and inherit this quality to future generations. According to the Hamilton-Zuk hypothesis this can make parasitism a driving force in sexual selection. Male three-spined sticklebacks, Gasterosteus aculeatus, exhibit various reproductive traits that are known to be under sexual selection. Those traits include, among others nuptial coloration and courtship behaviour. Examined here is male investment in reproductive traits of naturally infected sticklebacks in relation to the fish’s parasitic status.

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TUE 23 AUG at 1710 - Room N6
Oral presentation *C4-Sy02-1710-O*

Symposium 2
Coevolution from parasitism to mutualism

Within-host competition determines reproductive success of temperate bacteriophages

Refardt D[1]
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Summary statement:

Little is known about the role of multiple infections in bacteriophage ecology. I staged a round robin tournament for phages of E. coli and found strong competitive interactions.

Abstract:

Within-host competition between parasites is frequently invoked as a major force for parasite evolution, yet quantitative studies on its extent in an organismal group are lacking. Temperate bacteriophages are diverse and abundant parasites of bacteria, distinguished by their ability to enter a facultative dormant state in their host. Bacteria can accumulate multiple phages that may eventually abandon dormancy in response to host stress. Host resources are then converted into phage particles, whose release requires cell death. To study within-host competition between phages, I used the bacterium Escherichia coli and eleven lambdoid phages to construct single and double lysogens. Lysogenic bacterial cultures were then induced and time to host cell lysis and productivity of phages was measured. In double lysogens, this revealed strong competitive interactions as in all cases productivity of at least one phage declined. The outcome of within-host competition was often asymmetrical, and phages were found to vary hierarchically in within-host competitive ability. In double infections, the phage with the shorter lysis time determined the timing of cell lysis, which was associated with a competitive advantage when time differences were large. The results emphasize that within-host competition greatly affects phage fitness and that multiple infections should be considered an integral part of bacteriophage ecology.

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TUE 23 AUG at 1650 - Room N6
Oral presentation *C4-Sy02-1650-O*

Symposium 2
Coevolution from parasitism to mutualism

An offer you cannot refuse: the threat of retaliation from a pathogen can select for down-regulation of immune response in its host

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Summary statement:

I use a coevolutionary model to demonstrate that pathogen with plastic virulence can threaten their hosts into down-regulating their immune response.

Abstract:

Retaliation by cuckoos and other brood parasites against the nests of those hosts who eject parasitic eggs, has been likened to the human ‘mafia behaviour’. Although this strategy relies on the cognitive abilities of both the host and the parasite, I show that the analogy can be extended to pathogens that exhibit phenotypic plasticity in response to changes in their host’s immune activity. Previous models for the coevolution of host defences and pathogen virulence have assumed that both traits remain constant for the duration of infection. However, physiological constraints often delay the full activation of the immune response. Given intrinsic costs of immune activation, I show that natural selection can lead to (i) an optimum in the host’s rate of immune activation and (ii) differential levels of pathogen virulence before and after immune activation. The combination of these two mechanisms in a coevolutionary model leads naturally to a situation akin to ‘mafia behaviour’: hosts are forced to down-regulate their immune response to minimise exposure to high virulence. There is even an evolutionarily stable strategy with no activation of the immune response, so that retaliation is not implemented. In other words, pathogens can evolve a strategy of ‘threatening’ the host with high virulence which results in host with no immune response. This simple coevolutionary model shows that introducing a delay in the activation of the immune response can shift an antagonistic host-pathogen system to a quasi-commensal interaction with low virulence and low defences.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy02-i020-R*

Symposium 2
Coevolution from parasitism to mutualism

Inbreeding effects in the parasitic trematode Diplostomum pseudospathaceum

Rieger JK[1], Haase D[1], Reusch TBH[1], Kalbe M[2]
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Summary statement:

Diplostomum pseudospathaceum produced by outcrossing were generally fitter than inbred ones. Fitness was highly dependent on genotypic compatibility.

Abstract:

The origin and maintenance of complex life cycles in parasites are still a matter of debate. Endosymbiotic and free-living stages, sexual and asexual reproduction, as well as multiple host switches are common in parasitic organisms. Alternating between clonal and recombinant stages may give parasites the efficiency of asexual reproduction while lowering the risk of deleterious effects caused by inbreeding. Here we study the effects of inbreeding in the digenean trematode Diplostomum pseudospathaceum on infection success in its two intermediate hosts, the freshwater snail Lymnaea stagnalis and the threespined stickleback Gasterosteus aculeatus. Single trematode clones and combinations of two different clones were allowed to reproduce sexually using herring gulls as definitive hosts. The hatched larvae were used to assess the proportion of selfed and outcrossed miracidia by microsatellite typing. These results were matched with hatch rates and infection success of inbred and outcrossed trematodes in both intermediate hosts. While parasite clones had a tendency to outcross, given the chance, some combinations appeared to be more successful than others, indicating the importance of genotypic compatibility.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy02-i008-E*

Symposium 2
Coevolution from parasitism to mutualism

Understanding the molecular basis of local adaptation in the coevolving host-parasite model system, Schistocephalus solidus and Gasterosteus aculeatus viewed from the parasite side

Samonte-Padilla IE[1], Kalbe M[2], Erin N[2], Mahesh P[2], Manfred M[2]
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Summary statement:

Local adaptation (LA) in sympatric and allopatric combinations of our host-parasite model system, Gasterosteus aculeatus and Schistocephalus solidus was investigated in this study.

Abstract:

The Red Queen Hypothesis describes an evolutionary arms race between hosts and parasites, in which both partners continuously have to adapt to each other in order to maintain their own fitness. Local adaptation (LA) in host-parasite interaction is often used as a kind of snapshot to study the potential range of mutual specialization of these antagonistic partners. However, studies on the underlying genetic basis of LA usually concentrate on the host side. In this study, our focus is on the tapeworm Schistocephalus solidus and we aimed to identify genes responsible for LA and compare their expression in sympatric and allopatric combinations with its specific vertebrate intermediate host, the three-spined stickleback, Gasterosteus aculeatus, originating from Norway and Germany. Worms from different infection treatments were collected 5, 7, and 9 weeks post infection and representative worm from each group was used to construct digital gene expression (DGE) libraries composed of 26-bp tags sequenced from the 3’end of the transcripts. Also, two normalized transcriptomic libraries of the two worm populations were built to serve as template for gene identification. Candidate genes for LA were identified from the 12 DGE libraries using EDGE-R software and the difference in their quantitative expression in the different infection timepoints was measured by qPCR.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy02-i021-R*

Symposium 2
Coevolution from parasitism to mutualism

Virulence and transmission in European blue butterflies and their ant partners

Schär S[1], Ugelvig LV[2], Nash DR[1]
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Summary statement:

This study aims to test the theory of an association between virulence and transmission in five European blue butterfly species and their ant partners.

Abstract:

The association between virulence and transmission is well known from epidemiology. However, this theory has not been applied to many other host-parasite systems so far. This study tries to test this hypothesis in social insects and their socially parasitic insect partners, and extends it to mutualistic partners (with “negative virulence”). The butterfly family Lycaenidae and the subfamily of the blues (Polyommatinae) in particular, have a wide spectrum of interactions with ants, ranging from no associations to facultative or even obligate interactions. Caterpillars that interact with ants in a mutualistic way generally feed them with honeydew from their dorsal nectary organ, and in return receive protection from predators and parasitoids. At the other end of the spectrum are the species of the genus Maculinea (the large blues) that exploit ants of the genus Myrmica. They spend most of their life inside the ant nest, where they live as social parasites. Two different host exploitation strategies can be found within that genus, a “cuckoo” feeding strategy and a predatory feeding strategy, considered to be more virulent. This study investigates the dispersal strategies of five European polyommatine species (Vacciniia optilete, Plebejus argus, Glaucopsyche alexis, Maculinea alcon and M. arion) with respect to their different life history strategies and associations with ants in southern Scandinavia, using direct (mark-release-recapture experiments) and indirect (genetic) measures of dispersal in a regional and local scale as well as literature surveys.

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WED 24 AUG at 0950 - Room N6
Oral presentation *D1-Sy02-0950-O*

Symposium 2
Coevolution from parasitism to mutualism

Evolution of symbiosis-specific characteristics and the horizontally acquired killer trait in two distantly related intracellular bacteria of Paramecium

Schrallhammer M[1,2,3], Petroni G[2], Görtz H-D[3], Berendonk TU[1]
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Summary statement:

Despite similarities in expression of the killer trait Caedibacter species revealed surprising differences in host range and preference for intracellular compartments of Paramecium.

Abstract:

Certain Paramecium strains harbour intracellular bacteria of the genus Caedibacter. These are obligate intracellular bacteria which parasitize their host cell for survival and reproduction. The presence of Caedibacter bacteria refers the Paramecium host the so-called killer trait. Caedibacter-harbouring paramecia release toxic particles which lead to the death of Caedibacter-free paramecia, thus killer paramecia gain a competitive advantage. The released particles are Caedibacter cells that bear an unusual structure termed R-body (Refractile body).

Despite morphological and functional similarities, it was shown that at least Caedibacter taeniospiralis (Gammaproteobacteria) and Caedibacter caryophilus (Alphaproteobacteria) are not phylogenetically closely related, belonging to different phyla of Proteobacteria. A horizontal gene transfer of the genetic determinants involved in R-body production and expression of the killer trait is the most likely explanation for the occurring of such a complex trait in far related organisms. Here we address the question if other aspects of Caedibacter lifestyle, in particular host specificity and sub-cellular localization, are consistent among the different species. Different strains of C. taeniospiralis and C. caryophilus harboured by Paramecium strains of different geographic origins were characterized by phylogenetic reconstructions and fluorescence in situ hybridizations to visualize the sub-cellular localization within the host cell. Despite the similarities in expression of the killer trait, Caedibacter species revealed surprising differences in other aspects of their lifestyle.

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WED 24 AUG at 1140 - Room N6
Oral presentation *D2-Sy02-1140-O*

Symposium 2
Coevolution from parasitism to mutualism

Experimental test of the consequences of host-parasite co-evolution

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Summary statement:

Using experimental evolution, host-parasite co-adaptation is shown to have manifold evolutionary consequences that differ from those caused by one-sided adaptation

Abstract:

Parasites grow, exploit and shelter upon hosts, thus decreasing their fitness. They select for the evolution of more resistant hosts, which reciprocally selects for more virulent parasites, potentially leading to a co-evolutionary arms race. Here, we specifically evaluated for the first time in a single experiment the importance of reciprocal co-evolution in comparison to one-sided adaptation, where either only the host or only the parasite was allowed to adapt to a non-changing antagonist. Our analysis is based on experimental evolution of the model nematode host Caenorhabditis elegans and its microparasite Bacillus thuringiensis. Our results demonstrate that the different selective pressures vary in their effect on the evolution of host defenses, parasite pathogenicity, the associated life history trade–offs and the exact infection dynamics. We additionally discovered an effect on the parasite´s "social" interactions: Biofilm formation is specifically disfavoured in response to coevolution, whereas it is strongly favoured under control conditions, while one-sided adapted populations expressed both phenotypes. Our study emphasizes the multifaceted consequences of reciprocal selective pressures during host-parasite coevolution.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy02-i022-R*

Symposium 2
Coevolution from parasitism to mutualism

Bacterial species associated with Drosophila simulans and Drosophila melanogaster in the wild and in the laboratory

Staubach F[1], Bergland AO[1], Baines JF[2], Petrov D[1]
[1]Stanford University, Stanford, United States, [2]Max Planck Institute for Evolutionary Biology, Ploen, Germany

Summary statement:

Bacterial communities associated with Drosophila seem to vary by species and food source.

Abstract:

Microbes have been identified as important interaction partners of a variety of insects including aphids, ants, bee wolfs and many others. These interactions range across the spectrum of possible relationships between host and microbe from mutualistic symbiosis to pathogenicity. We have initiated a study of microbial flora associated with Drosophila, hoping to employ the wide arsenal of genetic tools available in D. melanogaster to start gaining insight into the nature of bacterial communities living in association with insects. To identify key bacterial species associated with Drosophila, we have collected bacterial 16S 454 sequencing data from wild caught and lab-reared flies. Preliminary analysis reveals greater taxonomic diversity in the bacterial flora than previously reported. Differences between microbial communities from wild D. melanogaster and D. simulans pairs each collected from a single fruit seem to be persistent in lab stocks of these species, suggesting a genetic component influencing the bacterial communities.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy02-i009-E*

Symposium 2
Coevolution from parasitism to mutualism

Resolving the basis of genotype by genotype interactions between plants and their symbionts

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Summary statement:

QTL mapping of Genotype*Genotype interactions informs the mechanistic basis of coevolutionary genetic variation.

Abstract:

Recent studies have found evidence of genotype by genotype (G x G) interactions in the symbiosis between the legumes and their associated rhizobia. Depending on the genotype of each partner, the interaction can shift from mutualism to mild parasitism. However, it is unknown which genetic regions affect the ecological outcome of this symbiosis or the contribution of sequence variation at known nodulation genesTo investigate these questions, we performed a large quantitative trait loci (QTL) mapping experiment using the model legume, Medicago truncatula. Replicates of 178 recombinant inbred lines were grown in the greenhouse with one of two strains of rhizobia, representing two unique genotypes. Six phenotypic traits were recorded on 2078 plants, and the data were subsequently analyzed for QTLs and QTL x rhizobial strain interactions. The results of this experiment provide insights into specific regions of the M. truncatula genome that affect the outcome of the legume-bacteria relationship.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy02-i023-R*

Symposium 2
Coevolution from parasitism to mutualism

A comparison of genetic population structure in two host-parasite systems (Myotis bechsteinii - Spinturnix bechsteini and Myotis myotis - Spinturnix myoti)

van Schaik J[1], Kerth G[2]
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Summary statement:

Here we compare host and parasite genetic population structure in two systems, and suggest that hosts adapt their social organization to minimize parasite local adaptation.

Abstract:

Aims: It is well known that parasites can alter host physiology, ecology, behavior, and population dynamics and thereby have a considerable influence on host fitness. Moreover, previous studies have shown that host social structure and population dynamics strongly influence the diversity and abundance of ectoparasites. However, in vertebrate host systems with their often complex and variable social systems it is difficult to accurately characterize the dynamics of host- parasite relationships. As a consequence, the effect of different forms of host social systems on the genetic co-variation of either host or parasite has rarely been empirically investigated in free-ranging vertebrates.
Methods: In this study, we analyzed the spatial and temporal population structure of two ectoparasitic mites (Spinturnix bechsteini and Spinturnix myoti) using mtDNA and newly developed microsatellite loci and compared them to the genetic structure of their hosts, the Bechstein's bat (Myotis bechsteinii) and the greater mouse eared bat (Myotis myotis).
Results: Our results suggest that, in S. bechsteini, seasonal bottlenecks and limited dispersal result in substantial local differentiation but long-range genetic similarity. In S. myoti, where bottlenecks are less severe, local genetic population structure was radically different, yet long-range genetic similarity was once again present.
Conclusions: We suggest that host social organization is optimized to minimize the opportunity for parasite local adaptation, thereby maintaining an advantage for the host in the evolutionary arms race despite it longer generation times compared to the parasite.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy02-i024-R*

Symposium 2
Coevolution from parasitism to mutualism

Phylogenetics of specialist herbivore butterflies

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Summary statement:

Phylogeny of butterfly sister genera rejects effect of host range size on insect herbivore diversification, but suggests an evolutionary trend in host switch direction

Abstract:

Butterflies in the African sister genera Harma and Cymothoe (Nymphalidae) are known to be specialist herbivores. Harma is monospecific, while Cymothoe comprises 74 species. Janz, Nylin and Wahlberg (2006) hypothesise that this contrast in net diversification is explained by a difference in larval host range size: Harma larvae feed only on Achariaceae; in Cymothoe some species feed on the same Achariaceae species while others feed on species of Rinorea (Violaceae). This hypothesis predicts an elevated diversification rate after host range expansion, but to date no species-level phylogenetic analysis of the two genera has been published to test this. We present the first molecular phylogenetic tree of Harma and Cymothoe, based on 45 samples and covering 60% of all species. We analysed mtDNA coi and nDNA gapdh, rps5, wingless, and idh sequences using nucleotide and codon evolutionary models. Results confirm a rapid diversification of the genus Cymothoe and suggest three independent host switches from Achariaceae to Rinorea within Cymothoe. Diversification rates within Cymothoe do not correlate with these switching events, however, rejecting the hypothesis of Janz et al (2006). Convergent evolution of Rinorea-feeding in three independent Cymothoe clades and the absence of reversals from Rinorea back to Achariaceae may indicate an evolutionary advantage of Rinorea associations for Cymothoe herbivores.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy02-i010-E*

Symposium 2
Coevolution from parasitism to mutualism

How to maximize reproduction without killing my host: Infestation balance between a weevil and the Hollyhock

Wilhelm G[1]
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Summary statement:

To investigate fitness components in the relationship between Alcea rosea and the weevil Rhopalapion longirostre and to document interactions we used multivariate statistics.

Abstract:

To investigate fitness components in the relationship between the host plant Common Hollyhock, Alcea rosea (Linnaeus 1758) (Malvaceae) and the parasitic weevil Rhopalapion longirostre(Olivier 1807) (Coleoptera, Curculionoidea, Apioninae), we used multivariate statistics (i.e., principle components analysis and path analysis). We focused on egg deposition by the females into appropriate flower buds of the host plant and on activities of the larvae, such as the choice for seeds for consumption, the preparation of seed chambers as a site for pupation, as well as the construction of escape holes through which the adults later emerge.
Our analyses revealed that the optimal conditions for successful development of the weevil depended on the availability of seed capsules which were characterized by a high number of well-developed seeds, few undeveloped and few spoiled seeds. The high number of larvae, pupae and not-emerged adults found in the seed capsules corresponds with the successful emergence of adults. The reproductive success of the host plant is partly guaranteed by a high number of seed chambers and many well developed seeds. Furthermore, the extended blooming period of Alcea rosea serves as an emergency strategy by developing buds early or late in the season that cannot become entangled in the life cycle of Rhopalapion longirostre.

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Symposium 3

Evolution and human disease

Talks: *Room N5*

Essence posters*:* Upper floor lecture hall centre *HZ*

Regular posters*:* Upper floor campus canteen *Mensa*

Invited Speakers:

Stephen Stearns, David Haig, Bernard Crespi

Organizers:

Sean G Byars, Jacobus J Boomsma

Description:

This symposium highlights the relevance of recent evolutionary research for issues of human health and disease, including evidence that our phenotypes are mismatched to our modern environment, the increasing knowledge about genetic conflicts and imprinting during pregnancy, childhood and adolescence, and the emerging data on medically significant traces of selection on reproductive life histories.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy03-i001-R*

Symposium 3
Evolution and human disease

Risk factors for the evolutionary emergence of pathogens

Alexander H[1,2], Day T[2]
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Summary statement:

Newly introduced pathogens pose a challenge to public health. We use a mathematical model to explore host- and pathogen-based factors contributing to the risk of an epidemic.

Abstract:

Recent outbreaks of novel infectious diseases (e.g. SARS, influenza H1N1) have highlighted the threat of cross-species pathogen transmission. When first introduced to a species, a pathogen is likely poorly adapted to its new host and can only escape extinction in this host population through evolutionary change. Theoretical arguments and empirical studies have suggested various factors to explain why some pathogens emerge and others do not. These factors include host contact structure, pathogen adaptive pathways, and mutation rates. We develop a stochastic mathematical model for the between-host spread of an introduced pathogen as it evolves. We use a network-based framework to separate host contact patterns from pathogen transmissibility, and allow for arbitrary adaptive pathways among a set of pathogen strains. This approach leads to novel predictions regarding the impact of hypothesized risk factors. We find that pathogen fitness depends on the host population in which it circulates, and the “riskiest” contact distribution and adaptive pathway depend on initial transmissibility. The probability of emergence is sensitive to mutation probabilities and the number of adaptive steps required to reach a well-adapted strain. The possibility of large adaptive steps (e.g. simultaneous point mutations or recombination) dramatically increases emergence risk. In most situations, increasing overall mutation probability increases the risk of emergence; however, notable exceptions arise when we account for the possibility of deleterious as well as adaptive mutations.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy03-i002-R*

Symposium 3
Evolution and human disease

Multiple mechanisms drive the evolution of papillomaviruses: The fuzzy connection between viral genotype and the multiple phenotypic manifiestations of papillomavirus infections

Bravo IG[1,2], Göker M[3], Stamatakis A[4], Bininda Emonds ORP[5], Nindl I[6,7], Gottschling M[8]
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Summary statement:

Infections by certain PVs cause cancer while other give rise to benign transformation. The evolutionary history of PVs can provide hints to explain such phenotypic diversity.

Abstract:

One out of five cases of cancers in humans is related to infection by different agents, and Papillomaviruses (PVs) account for more than 30% of this cancer burden. Research on PV biology relies historically on a number of assumptions, including strict host specificity, tissue tropism and coevolution between viruses and hosts. We have constructed robust phylogenies of both hosts and viruses and analised congruence between both reconstructions by applying a battery of tests that include topological and branch-length comparisons. We estimate that codivergence accounts for 30% of the evolutionary events needed to reconcile the evolutionary histories of PVs and their hosts. Further time analyses suggest that the scenario that best describes the evolution of PVs is an early radiation that gave rise to the major PV lineages, prior to the divergence of the ancestral mammalian hosts, followed by independent codivergence between viruses within each of the major PV clades and their hosts. We conclude that intra-host duplication, lineage sorting, recombination, colonization of new niches, and host switch play further significant roles in the evolution of PVs. The implications of these mechanisms for the appearance and evolution of the oncogenic phenotype of certain PV infections need to be explored.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy03-i003-R*

Symposium 3
Evolution and human disease

The application of the Generalized Linear Model (GLM) to detect the main variables involved in liver damage caused by HCV/HIV coinfection

Castro JA[1,2], Matas M[1,2], Cifuentes C[3], Payeras A[3], Bassa A[3], Homar F[3], López-Labrador FX[4,5,6], Moya A[4,5,6], Picornell A[1,2], Ramon MM[1,2]

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Summary statement:

GLM applied to hepatitis C virus (HCV) / Human Immunodeficiency virus-1 (HIV-1) co-infectected patients to associate liver damage and characteristics of the patients and virus

Abstract:

We have carried out an study in patients with hepatitis C virus (HCV) / Human Immunodeficiency virus-1 (HIV-1) co-infection in order to associate liver damage and disease with demographics and clinical characteristics of the patients (i.e. sex, age, alcohol intake, time from infection, method of transmission, disease stage, biochemical parameters, antirretroviral treatment) and with the genetic variability of HCV (viral subtypes and nucleotide sequencing of the NS5B region). This is an extension of a previous study based in HCV Core region sequencing, including more patients and new analysis procedures. The genetic variability of HCV is well-studied because chronic infection is the most important cause of advanced and end-stage liver disease leading to liver transplantation world-wide. However, comprehensive analyses of both patient and virus characteristics are scarce. We followed the statistical generalized linear model (GLM) methodology in a similar way as used by Szmaragd et al. (2005) and Matas et al. (2010). The degree of liver disease was measured indirectly by means of the indexes, APRI, Forns and FIB-4, due to the lack of protocol liver biopsies. HCV genetic variability was studied by sequencing the NS5B region and the reconstructions of consensus maximum-parsimony phylogenetic trees. Our analysis identifies a reduced number of variables (both from the virus and from the host) as implicated in liver damage, such as the method of transmission, age, GGT, alcohol intake and AST/ALT ratio, and distinct HCV phylogenetic clades.

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MON 22 AUG at 1440 - Room N5
Invited talk *B3-Sy03-1440-I*

Symposium 3
Evolution and human disease

Where Darwin meets Freud: Genomics, evolution and psychopathology of the social brain

Crespi B[1]
[1]Simon Fraser University, Dept. of Biosciences, Burnaby, B. C., Canada

Summary statement:

I develop and test hypotheses for the evolutionary-genomic underpinnings of autism spectrum and psychotic-affective spectrum conditions.

Abstract:

Human disease risks have evolved. I integrate theory and data from comparative primatology, inclusive fitness theory, psychiatric genetics, gene coexpression, and developmental psychology to develop and test hypotheses for the evolutionary-genomic underpinnings of autism spectrum and psychotic-affective spectrum conditions. The primary hypothesis emerging from the analyses focuses on autism and psychotic-affective conditions as diametrical disorders mediated by opposite, extreme alterations to the development of human-elaborated social-brain and sexual-brain phenotypes. By this hypothesis, social-brain architecture develops predominantly in the context of mother-child interactions, whereby early, basic attachment, underlain in part by paternally-expressed imprinted genes, serves as a scaffold for development of the highly-social, neocortical brain, underlain in part by maternally-expressed imprinted genes. More generally, the human social brain may be under-developed in childhood, manifest as autism spectrum conditions, or become selectively, relatively over-developed usually in adolescence, resulting in psychotic-affective spectrum conditions. Cognitive and affective variation between females and males strongly modulates liability to these conditions, such that major epidemiological and phenotypic features of autism and psychotic-affective conditions can be predicted from interactions between a male-female continuum and a maternal-paternal imprinting bias continuum. This conceptual framework makes novel, testable predictions with direct implications for psychological and pharmacological therapy, human evolution, and human brain development.

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MON 22 AUG at 1420 - Room N5
Invited talk *B3-Sy03-1420-I*

Symposium 3
Evolution and human disease

Genomic imprinting, helpers at the nest, and age at menarche

Haig D[1]
[1]Harvard University, Department of Organismic and Evolutionary Biology, Cambridge, United States

Summary statement:

When parents divorce, future sibs will be halfsibs rather than fullsibs. Therefore, age at sexual maturation is expected to be sensitive to cues of partner change.

Abstract:

Genomic imprinting is predicted to influence behaviors that affect asymmetric kin (individuals to whom an actor has different degrees of matrilineal and patrilineal kinship). Effects of imprinted genes are not predicted in interactions with non-relatives nor with symmetric kin (individuals who are equally related to the actor’s maternally- and paternally-derived alleles) unless the genes also have pleiotropic effects on interactions with asymmetric kin. Long-term mating-bonds are common in many cultures but the dissolution of marriages (as a result of divorce or death of a partner) has always, and everywhere, affected a significant proportion of the population. Divorce is associated with predictable changes in patterns of relatedness for the children of former marriages. As long as a couple remain together, their mutual offspring are full-sibs and symmetric kin of existing offspring. But, once parents change partners, subsequent offspring are half-sibs and asymmetric kin of existing offspring. Therefore, a child’s innate dispositions toward parents and younger sibs are expected to be sensitive to whether or not its parents remain together and these dispositions may be particularly sensitive to influences of imprinted genes after parental separation. Girls are reported to enter puberty and begin reproduction earlier when raised in households in which their biological father is absent. This may, in part, reflect a reduced disposition to help raise younger brothers and sisters when these are half-sibs rather than full-sibs.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy03-i001-E*

Symposium 3
Evolution and human disease

Predicitve adaptive response: Modelling the life history of Bicyclus anynana

Heuvel JVD[1], Brakefield P[2], Zwaan B[3], Kirkwood T[4], Shanley D[4], Saastamoinen M[5]
[1]Leiden University, Leiden, Netherlands, [2]Cambridge University, Cambridge, United Kingdom, [3]Wageningen University, Wageningen, United Kingdom, [4]University of Newcastle, Newcastle, United Kingdom, [5]University of Helsinki, Helsinki, Finland

Summary statement:

This model shows how nice the integration can be of a evo-devo model such as Bicyclus anynana can be used for ageing research such as the sutdy of the predictive adaptive response.

Abstract:

Individuals of the tropical butterfly Bicyclus anynana live in a predictable environment in which the dry season is always followed by a wet season. Experiments have shown that individuals alter allocation strategies which affect fecundity and lifespan in response to cues perceived during the late larval stage. We built an energy allocation model of the life history of B. anynana to test whether this response might be adaptive in field conditions. Individuals are represented as states known to influence the biological decisions. Life history decisions are made for size at pupation, allocation to thorax, abdomen and fat body and optimal adult behavior and allocation to repair which influence traits such as size and body composition. The environment between seasons differed in temperature, number of high quality patches and predatory pressure. In the model three generations of butterflies emerged. Two generations are considered wet season morphs, the other the dry season morph. The dry season morphs were longer lived, larger and had a higher fat content and allocated more to repair. When individuals were stressed as larvae because they were in a bad patch, they allocated more to thorax to be able to fly to a good patch to reproduce. This only happens in the wet season morphs. In the experimental setup the wet season morph individuals coped better forced flight when they were starved as larvae compared to when they had an optimal larval period. In our model we showed that the known biology of B. anynana did evolve. Also allocation patterns differed for individuals that had experienced food of different quality as larvae.

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MON 22 AUG at 1610 - Room N5
Oral presentation *B4-Sy03-1610-O*

Symposium 3
Evolution and human disease

Offspring health benefits from pregnancy-induced hypertension may explain why preeclampsia still exists

Hollegaard B[1], Byars SG[1], Lykke J[2], Boomsma JJ[1]
[1]University of Copenhagen, Centre for Social Evolution, Department of Biology, Copenhagen, Denmark, [2]Hvidovre Hospital, Department of Gynecology and Obstetric Care, Hvidovre, Denmark

Summary statement:

Offspring health benefits from pregnancy-induced hypertension may explain why preeclampsia still exists.

Abstract:

We have tested the hypothesis formulated by David Haig (Haig 1993, 2000) that pregnancy complications related to elevated blood pressure and preeclampsia should not have persisted throughout evolutionary history if they would not also have incurred fitness benefits. In particular, Haig suggested that paternal genes expressed in the fetus may manipulate maternal blood pressure to secure a higher provisioning rate. We used the Registries of the Danish National Health system to analyse a data set encompassing > 1,800,000 births over the time span 1977-2007. After excluding all cases where confounding disease variables might have affected the results, we used a sample of 637,790 singleton births for which we related maternal pregnancy diagnoses (for each of the trimesters and for the periods before and after completion of placental growth at week 22) with the probability of children to be diagnosed with 14 common disease categories. We found consistent evidence that pregnancy induced hypertension (PIH) is correlated with offspring health benefits during childhood and adolescence, provided it does not persist. When PIH continued after week 22 in the pregnancy, with the possibility of causing leaking kidneys (proteinurea) and preeclampsia, these offspring health benefits were no longer observed; instead the children born to mothers with persistent and increasing pregnancy complications suffered consistently enhanced risks of being diagnosed with disease during childhood and adolescence.

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MON 22 AUG at 1630 - Room N5
Oral presentation *B4-Sy03-1630-O*

Symposium 3
Evolution and human disease

A plague on both your houses: The intersection of infectious disease, city dwelling and religious belief

Hughes D[1], Trinitapoli J[2], Jenkins P[3]
[1]Penn State University, Center for Infectious Disease Dynamics, State College, United States, [2]Penn State University, Department of Sociology & Crime, Law and Justice, State College, United States, [3]Penn State University, Department of History and Religious Studies, State College, United States

Summary statement:

Cultural evolution, particularly diversity among religious beliefs, shapes infectious disease dynamics in cities.

Abstract:

Religious beliefs are supposedly anathema to evolutionary biology and for most researchers this would extend to the topic of this symposium. But in the case of infectious diseases, religious belief is critical to understanding disease dynamics because the multiple origins of monotheistic systems during the Axial age (800-200 BCE) exactly parallels the emergence of highly virulent diseases capable of killing up to two-thirds of a population. Using a combined evolutionary, historical, theological and demographic framework we examine all major epidemics over the last 3,500 years. Focusing first on extreme altruism (caring for non-related infectious individuals at significant risk of death) we show that this behavior is strongly dependent on the type of religion practiced during an epidemic. Further, epidemics catalyze change giving (cultural)fitness advantages to one belief over another (e.g. the Antonine and Cyprian Plagues of Rome). We also show how the increasing evidence of germ theory shaped theology (notably 9th Century Islam). Finally, we detail our initial work adopting the comparative approach of evolutionary biology to examine group differences within a single environment over a defined period of time (1200-1600 CE in the area of Europe, the Near East and the Mediterranean World). The groups are: Western Catholic societies, Eastern Christian societies, The Islamic world, Jewish societies and (After 1500) Protestant societies. We conclude by outlining our experimental work on HIV in modern Malawi and detail future experimental work in Europe and America were we examine the behavioral plasticity of disease-associated behaviors in the context of belief.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy03-i004-R*

Symposium 3
Evolution and human disease

Long-term balancing selection at the blood group-related gene B4galnt2 in the genus Mus (Rodentia; Muridae)

Linnenbrink M[1,2], Johnsen J[3], Montero I[4], Brzezinski C[3], Harr B[4], Baines JF[1,4]
[1]Christian Albrechts University of Kiel, Institute for Experimental Medicine, Kiel, Germany, [2]Ludwig-Maximilians-University, Evolutionary and Functional Genomics, Munich, Germany, [3]University of Washington, Research Division, Puget Sound Blood Center and Department of Internal Medicine, Seattle, United States, [4]Max Planck Institute for Evolutionary Biology, Plön, Germany

Summary statement:

A survey of the B4galnt2 gene region reveals long-term balancing selection associated with the maintenance of tissue-specific expression patterns in house mice and their relatives.

Abstract:

Recent surveys of the human genome have highlighted the significance of balancing selection in relation to understanding the evolutionary origins of disease-associated variation. Cis-regulatory variation at the blood group-related glycosyltransferase B4galnt2 is associated with a phenotype in mice that closely resembles a common human bleeding disorder, von Willebrand disease. In this study, we have performed a survey of the 5’ flanking region of the B4galnt2 gene in several Mus musculus subspecies and M. spretus. Our results reveal a clear pattern of trans-species polymorphism and indicate that allele classes conferring alternative tissue-specific expression patterns have been maintained for >2 million years in the genus Mus. Furthermore, analysis of B4galnt2 expression patterns revealed the presence of an additional functional class of alleles, which indicates that the alteration of a gastrointestinal phenotype likely plays a role in the long-term maintenance of expression variation at this gene.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy03-i005-R*

Symposium 3
Evolution and human disease

Does sexual antagonism cause disease?

Morrow EH[1]
[1]Uppsala University, Ecology and Genetics, Uppsala, Sweden

Summary statement:

Sexual antagonism is apparently common in organisms with separate sexes. I discuss why it may underlie many common human diseases and present the first test of this hypothesis.

Abstract:

The new science of Darwinian medicine seeks to provide ultimate explanations for the existence of the diseases and conditions that afflict modern humans, thereby generating a deeper understanding of, and new strategies for, both medical research and patient care. Its success relies on the principle that we, like every other living organism, are the product of evolutionary processes. To date, investigators studying the genetics of human disease have been working from the assumption that purifying selection is the major force that balances the deleterious effects of mutation. But evolutionary biologists now realize that selection can take some unexpected forms and not all mutations are always deleterious; context is everything. For example, a gene may be favoured by selection in one sex but disfavoured by selection in the opposite sex. This kind of genomic intralocus sexual conflict is known to be an important component of fitness variation but its potential role in causing human disease has yet to be fully explored. As well as presenting the first empirical test of this hypothesis, I discuss why there are good reasons to believe that sexually antagonistic selection may be an important factor underlying many common human diseases, and why the hunt for genes associated with elevated disease risk, using approaches such as GWAS, needs to be adjusted to the reality that males and females frequently experience conflicting selection pressures.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy03-i006-R*

Symposium 3
Evolution and human disease

Parasite virulence and persistence under various host conditions

Murall CL[1], Bauch C[1], McCann KS[1]
[1]University of Guelph, Guelph, Canada

Summary statement:

We use a framework that combines life history trade-offs and community ecology to explore outcomes of in-host dynamics across a gradient of different host environments.

Abstract:

A number of host-specific factors, such as smoking and HLA type, have been identified as being important to in-host dynamics of pathogens. Yet we still cannot predict when any given person will clear an infection, whether it will become chronic, or if resistance will evolve during treatment. The link between in-host environment, ecological processes and evolutionary responses is at the heart of these issues. Here we view in-host, life-history trade-offs within a community ecology framework consisting of community modules and interaction strengths as a way to help us complete the picture of how disease burden and outcomes, such as strain dominance, are context dependent. Using a simple model of viral dynamics, we show in both chronic and acute infections that by knowing the community structure of the infection and the in-host trade-offs that constrain the parasite-host system, one can help explain infection outcomes of in-host dynamics across a gradient of different host environments. As a specific example, we will discuss the replication/clearance trade-off and the cost of immune evasion in Human Papillomavirus and how the vaccine alters these natural conditions. We also show that under certain conditions co-infecting parasites can appear neutral to each other or even mutualistic when in fact they are still competing. Finally, we demonstrate how parasite traits (such as defense strategies and resource use) fit within the module framework and can lead to longer persistence within a host. Given the central role of trade-offs in ecological and evolutionary dynamics, this work emphasizes the importance of finding them inside hosts across a range of immunity types.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy03-i007-R*

Symposium 3
Evolution and human disease

Will dietary restriction extend life and health span in human beings? A phylogenetic meta-analysis

Nakagawa S[1], Lagisz M[1], Hector KL[1], Spencer HG[1]
[1]University of Otago, Department of Zoology, Dunedin, New Zealand

Summary statement:

Our meta-analytic results suggest that dietary restriction could extend life span of humans under ´certain´ circumstances.

Abstract:

Aging results in heightened risks of numerous diseases not only in humans but also in many other species. Dietary restriction (DR, reduced food intake without mal-nutrition) is claimed to be the most robust intervention to aging, decreasing risks of age-related diseases. Such a claim originates from the fact that DR has extended lifespan of taxonomically diverse species, and also DR has generally ameliorated many age-related diseases in laboratory mammals. However, the effect of DR for human longevity and health is still controversial. To obtain a holistic picture of available evidence, we conducted the first phylogenetic meta-analysis to investigate the relationship between DR and longevity, using 145 studies covering 36 species. The results suggested DR could prolong the lifespan of all species given that several factors were set ‘correctly’. We will reveal these important parameters for DR to improve longevity and discuss how our results can be interpreted for us, humans. We propose a new graphical model where we point out that there may be neglected pathways, which may reduce lifespan via DR, opposing to nutrient-signaling pathways, which have been found responsible for extending lifespans of many laboratory species. This model may guide future DR-related aging research and the associated endeavors to intervene aging via DR and DR mimetics.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy03-i002-E*

Symposium 3
Evolution and human disease

Preventing cancer by requiring altruistic signals

Oña L[1], Lachmann M[1]
[1]Max Planck Institute for Evolutionary Anthropology, Evolutionary Genetics, Leipzig, Germany

Summary statement:

Growth Factors (GFs) stimulate the proliferation of cells by a mechanism known as paracrine. Such mechanism reduce the rate of evolution, delaying the onset of cancer.

Abstract:

Developmental process and tumorigenesis have been long understood to be interrelated. In order to proliferate normal cells requires mitogenic growth signals (GS). Many oncogenes act by mimicking normal growth signalling. Growth Factors (GFs) use to stimulate the proliferation of another cells by a mechanism known as paracrine, this type of signalling is classified as heterotypic. In this work we will argue that such type of signalling works as a mechanism to reduce the rate of cancer evolution, delaying its onset. We investigate how the relationship between the cost of producing the signal and the area of benefit affecting cells can evolve to reduce the emergence of cancer. We find that there is a critical number of signalling cells from which selection favours cells generating such type of signal.

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MON 22 AUG at 1650 - Room N5
Oral presentation *B4-Sy03-1650-O*

Symposium 3
Evolution and human disease

Are old ages useless with respect to selection? A reconsideration of the common variants/common diseases hypothesis

Pavard S[1], Metcalf JC[2], Toupance B[1], Gagnon A[3], Evelyne H[1]
[1]National Museum of National History, Human Population Genetics, Paris, France, [2]Princeton University, Ecology and Evolutionary Biology, Princeton, United States, [3]University of Western Ontario, Department of Sociology, London, Canada

Summary statement:

Lecturer at the National Museum of Natural History, I study the evolution of humans' life-history and especially how social behaviours coevolved with survival and fertility.

Abstract:

Because few individuals survive at old ages and because no reproduction occurs after menopause, it is believed that alleles involved in late mortality are selectively neutral. However, most alleles associated with susceptibility to late onset diseases are at low frequency, which is characteristic of alleles under negative selection. Three phenomena may explain why these alleles may be negatively selected: (i) men often reproduce with younger women until old ages; (ii) parents enhance their offspring's fitness by caring for them during post-reproductive period; and (iii) variance in diseases' age of onset means that cases may occur during reproductive ages although the mean age at onset is long after. Here, we modelled (i) and (ii) for a large range of demographic behaviours and population dynamics. We also used literature on the 50 common late-onset diseases to determine (iii): the parameter space of their age of onset distribution. We incorporate these three phenomena into a population genetic framework to calculate selection coefficients corresponding to alleles associated with late-onset diseases. Results show that negative selection occurs for most of the parameter space encompassed by known late-onset genetic diseases. Moreover, estimated negative selection is capable of overcoming genetic drift for an effective population size Ne compatible with most human populations. For most common diseases (e.g., familial form of breast and ovarian cancer), variance in age of onset has the largest impact on selection coefficients' magnitude, followed by potential reproduction of older men and maternal care.

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MON 22 AUG at 1710 - Room N5
Oral presentation *B4-Sy03-1710-O*

Symposium 3
Evolution and human disease

Genetic determinants of lifespan: an evolutionary approach. A test of 120 candidate genes for early childhood survival and longevity in a cohort of 7000 Ghanaians

Pijpe J[1], Eriksson UK[2], Slagboom PE[3], De Knijff P[1], Metspalu A[4], Zwaan BJ[5,6], Westendorp RG[2]
[1]Leiden University Medical Center, Human Genetics, Leiden, Netherlands, [2]Leiden University Medical Center, Gerontology and Geriatrics, Leiden, Netherlands, [3]Leiden University Medical Center, Molecular Epidemiology, Leiden, Netherlands, [4]University of Tartu, Institute of Molecular Cell Biology, Tartu, Estonia, [5]Wageningen University, Laboratory of Genetics, Wageningen, Netherlands, [6]Leiden University, Institute of Biology, Leiden, Netherlands

Summary statement:

Variation in 120 candidate genes in immunity and endocrine signaling will be tested for association with survival during childhood and in old age, and with fertility.

Abstract:

The regulation of human lifespan is influenced by genetic factors. The conclusion from theoretical and experimental work in a range of organisms is that there is no selection for senescence, but rather a "side-effect" of selection for increased pre-adult survival and reproduction. The environments in which humans have lived for the past few thousand years were adverse. In contrast, most studies of genetic determinants of survival to old age in humans are solely based in affluent societies where there is little selective pressure on traits important for early survival due to sanitary and medical interventions. We investigate the association of genetic variation in candidate genes with human life history in rural northern Ghana, where the environment is highly adverse and infections diseases as malaria, typhoid fever, and diarrheal diseases are endemic.
We identify common allelic variation by high density tag SNP genotyping using a custom array in a selection of 120 candidate genes involved in immunity and endocrine signaling. We contrast allelic, genotypic, and haplotypic frequencies between three age categories:
1000 newborns that represent the standing genetic variation
3500 adults that survived until reproductive age, and for whom we associate genetic data with number and survival of offspring.
2500 individuals aged >60, that survived to old age.
We include socio-economic status and drinking source to investigate gene-by-environment interaction for each allele.
The first results of this project will be presented. In a second stage, we will test whether identified variants contribute to mortality and morbidity in cohorts from affluent societies.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy03-i008-R*

Symposium 3
Evolution and human disease

The role of blood group antigens in shaping diversity of the mammalian intestinal microbiota and susceptibility to disease

Rausch P[1], Baines JF[1,2]
[1]Max-Planck-Institute for Evolutionary Biology, Evolutionary Genomics, Plön, Germany, [2]Christian-Albrechts-University, Institute for Experimental Medicine, Kiel, Germany

Summary statement:

To study the role of fucosylated glycans on bacterial community structure in the gastrointestinal tract and host fitness, we are using a mouse Fut2 knockout model.

Abstract:

The microbial communities inhabiting the mammalian gastrointestinal tract play an important role in diverse aspects of host biology. However, little is known regarding the forces shaping variation in these communities and its influence on host fitness. Because blood group antigen genes are frequent targets of natural selection and influence the attachment and colonization of both pathogenic and commensal/symbiotic bacteria in the gastrointestinal tract, they represent good candidates for describing the evolutionary forces surrounding host-microbiota interactions. The FUT2 gene is responsible for the expression of ABO histo-blood group antigens on the gastrointestinal mucosa and in bodily secretions and is a target of balancing selection in human populations. Individuals lacking a functional copy of FUT2 are known as “nonsecretors” and display an array of differences in susceptibility to infection and disease. To determine whether altered host – microbiota interactions may in part mediate disease susceptibility, we are performing an analysis of bacterial colonization and community structure and composition under contrasting environmental conditions using a mouse Fut2 knockout model.

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MON 22 AUG at 1400 - Room N5
Invited talk *B3-Sy03-1400-I*

Symposium 3
Evolution and human disease

Unsolved problems in evolutionary medicine

Stearns S[1]
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Summary statement:

I will briefly sketch the reasons for a specific research agenda in evolutionary medicine.

Abstract:

What are the issues in evolutionary medicine that have important immediate implications for medical practice, and in which of these is additional research most badly needed? I will present and discuss a list of these high priority issues. They include evolution-proof antibacterial therapies, evolution-proof cancer therapies, the mechanisms that mediate auto-immune responses to hygiene, the mechanisms that mediate the hypothesized effects of parent-of-origin imprinting on mental function, the threat that leaky vaccines will select for increased virulence and how that virulence might be managed, and the issue of when it pays the host to tolerate rather than resist an infection.

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MON 22 AUG at 1500 - Room N5
Oral presentation *B3-Sy03-1500-O*

Symposium 3
Evolution and human disease

Intragenomic conflict in the social brain: Menopause

Ubeda F[1], Gardner A[2]
[1]University of Tennessee, Ecology and Evolutionary Biology, Knoxville, United States, [2]Oxford University, Zoology Department, Oxford, United Kingdom

Summary statement:

We present a series of models for the evolution of genomic imprinting in genes underpinning social behavior. We discuss their implications for the evolution of menopause in humans.

Abstract:

What are imprinted genes doing in the adult brain? Genomic imprinting is when a gene´s expression depends upon parent of origin. According to the prevailing view, the ‘kinship theory’ of genomic imprinting, this effect is driven by evolutionary conflicts between genes inherited via sperm versus egg. This theory emphasizes conflicts over the allocation of maternal resources, and focuses upon genes that are expressed in the placenta and infant brain. However, there is growing evidence that imprinted genes are also expressed in the juvenile and adult brain, after cessation of parental care. Here we advance the kinship theory by developing a series of evolutionary models of genomic imprinting for social behavior beyond the nuclear family. We consider the role of demography and mating system, emphasizing the importance of sex differences in dispersal, survival and variance in reproductive success. We discuss the implications for the evolution of menopause in human populations with different social structures.

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MON 22 AUG at 1550 - Room N5
Oral presentation *B4-Sy03-1550-O*

Symposium 3
Evolution and human disease

Deep re-sequencing reveals the abundance and geographic structure of rare variant diversity in humans

Wegmann D[1], Zawistowski MS[2], St. Jean PL[3], Zhang P[2], Kessner D[1], Gopalakrishnan S[2], Ehm MG[3], Li J[2], Li Y[4], Abecasis G[2], Whittaker JC[3], Chissoe SL[3], Mooser VE[3], Zöllner S[2], Nelson MR[3], Novembre J[1]
[1]University of California Los Angeles, Dept. of Ecology and Evolutionary Biology, Los Angeles, United States, [2]University of Michigan, Biostatistics, Ann Arbor, United States, [3]GlaxoSmithKline, Genetics, Research Triangle Park, United States, [4]University of North Carolina, Biostatistics, Chapel Hill, United States

Summary statement:

One of the deepest re-sequencing experiments to date provides insights into the exonic variation and patterns of selection at 202 genes encoding known or prospective drug targets.

Abstract:

The sample sizes used in re-sequencing studies to date have typically precluded the direct observation of rare variants (e.g. variants < 1% frequency), yet such variants are of exceptional interest to medical and population genetics. With the goal of discovering such variants and their phenotypic consequences, we re-sequenced at high depth (>25x) 202 genes encoding current or prospective drug targets in >14,000 individuals, including cases and controls for 12 common diseases. This sample provides a unique opportunity to study the geographic distribution of genetic variants as it includes >275 individuals from 4 globally distributed populations (African-American, East Asian, European, and South Asian). Within Europe, the sample contains >500 individuals from each of more than 6 geographically defined populations. The sequencing revealed variants at a rate much larger than expected from patterns of variation observed in smaller samples. We observed 38535 single nucleotide variants (SNVs) over nearly 800 kilobases of sequence in Europeans, corresponding to an average of one SNV every 21 bases. Over 9400 of these variants cause changes in the amino acid sequence and 5895 of them are predicted to affect protein function. These patterns arise because of recent demographic growth in humans and because many rare variants seem to be slightly deleterious variants that are not segregating at higher frequencies. We also find the rate of rare variant discovery differs among populations and rare variants are shared preferentially between geographically proximal populations. These results give insights to very recent demography and gene flow patterns in humans.

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Symposium 4

Cooperation and virulence

Talks: *Room N1*

***Essence posters**:* Upper floor lecture hall centre *HZ*

***Regular posters**:* Upper floor campus canteen *Mensa*

Invited Speakers:

Sam Brown, William Hughes

Organizers:

Rolf Kuemmerli, Adin Ross-Gillespie

Description:

In the struggle between pathogens and hosts, both sides have evolved complex cooperative behaviours. For example, microbial pathogens share virulence factors and toxins to facilitate infection, while hosts allogroom and share chemical prophylaxes to impede infection. Here, we gather researchers from opposite ends of the spectrum to share new insight on how social behaviour affects virulence.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy04-i001-R*

Symposium 4
Cooperation and virulence

Ecology and the evolution of public goods production in Microorganisms

Akos Dobay A[1], Rankin DJ[1]
[1]University of Zurich, Institute of Evolutionary Biology and Environmental Studies, Zurich, Switzerland

Summary statement:

Bacterial cooperation. Agent-based model. Public goods. Virulence. Ecology. Social biology.

Abstract:

Microorganisms display a wide range of cooperative behaviours. In particular, many microorganisms produce public goods, which can potentially be exploited by other organisms. While kin selection has been shown to be important in promoting microbial cooperation, many other factors remain unexplored. In particular, the influence of microbial ecology on virulence and sociality is only coming to light, and many factors, from density-dependence to interspecific interactions, are likely to be important in promoting, or inhibiting, cooperative behaviours. Here we build an explicit model of bacterial growth to look at the evolution of public goods production. We explicitly model public goods as individual, diffusing molecules, which allows us to alter the relative scale of cooperation and scale of competition. We explore how different aspects of the ecology, from density, interspecific interactions, durability and diffusion of public goods, and the scale of competition, affect the evolution of cooperation. We then look at the invisibility and stability of co-operators under these different ecological scenarios. Out results highlight the importance of ecology in the evolution of microbial sociality.

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TUE 23 AUG at 1440 - Room N1
Oral presentation *C3-Sy04-1440-O*

Symposium 4
Cooperation and virulence

Within-host parasite cooperation and the evolution of virulence

Alizon S[1], Lion S[2]
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Summary statement:

For parasite producing public goods, it is argued that co-infections select for less virulent strains. We show that this may not be the case because of epidemiological feedbacks.

Abstract:

Infections by multiple genotypes are common in nature and are known to select for higher levels of virulence for some parasites. When parasites produce public goods within the host, such co-infections have been predicted to select for lower levels of virulence. However, this prediction is based on frameworks that neglect potential epidemiological feedbacks on the multiplicity of infections. Here, we analyse the case of parasites producing a public good, for example siderophore-producing bacteria, using a nested model that ties together within-host and epidemiological processes. We find that the current prediction that co-infection should select for less virulent strains for public-goods producing parasites is only valid if both parasite transmission and virulence are linear functions of parasite density. If there is a trade-off relationship such that virulence increases more rapidly than transmission, or if virulence also depends on the total amount of public goods produced, then the opposite outcome can be reached (adding co-infections selects for more virulent strains). Our results reveal that theoretical or empirical studies that seek to determine optimal virulence within a single host may not be representative of the selection pressures faced by parasites at the population level. These results also underline the importance of taking epidemiological feedbacks into account when studying the evolution of infectious diseases.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy04-i002-R*

Symposium 4
Cooperation and virulence

Sick ants become unsociable

Bos N[1], Lefèvre T[2], Jensen AB[3], d'Ettorre P[1,4]
[1]University of Copenhagen, Centre for Social Evolution, Department of Biology, Copenhagen, Denmark, [2]Emory University, Department of Biology, Atlanta GA, United States, [3]University of Copenhagen, Department of Agriculture & Ecology, Copenhagen, Denmark, [4]University of Paris 13, Laboratoire d'Ethologie Expérimentale et Comparée, Villetaneuse, France

Summary statement:

Infected ants do not signal their physiological status to nestmates, but leave the nest by themselves, while becoming more aggressive against non-nestmates.

Abstract:

Parasites represent a severe threat to eusocial insects which form high density colonies of closely related individuals, and natural selection should therefore favour host traits that reduce infection risk. Here, using the ant Camponotus aethiops and the parasitic fungus Metarhizium anisopliae, we show that infected nestmates radically change their behaviour overtime in a way that decreases social contacts and hence potentially reduces the risk of colony infection. In particular, infected individuals (i) spent most of their time outside the nest from day 3 post-infection until death; (ii) did not interact with brood the days following infection and; (iii) performed significantly less trophallaxis and allo-grooming than their uninfected counterparts. Interestingly, infected individuals spent more time self-grooming and received more allo-grooming than uninfected nestmates only in the early days post-infection, possibly to ward off the freshly deposited infective spores. In dyadic encounter tests, infected ants displayed an increased aggressiveness toward non-nestmates. Finally, we found no significant differences in the cuticular chemical profile of infected and uninfected ants, suggesting that infected individuals do not signal their physiological status to nestmates. Our results provide evidence for the evolution of unsociability following parasite infection in a eusocial insect and confirm the role of inclusive fitness in driving such evolution.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy04-i001-E*

Symposium 4
Cooperation and virulence

The population genetics of AI-2 quorum sensing genes in Escherichia coli

Brito PH[1], Gordo I[1], Xavier K[1]
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Summary statement:

Genetic diversity and signals of selection on AI-2 QS genes (lsr operon and luxS) across all available genomes of E. coli.

Abstract:

Although single cell organisms, bacteria can express coordinated multicellular behaviors, such as virulence, biofilm formation, and quorum sensing (QS). Autoinducers-2 (AI-2) represent a nonspecies-specific signal produced to mediate both intra- and interspecies communication in bacterial QS. We analyzed the genetic diversity of AI-2 QS genes (lsr operon and luxS) across all available genomes of E. coli and found a level of polymorphism in gene content that cannot be explained by neutral evolution alone. Many strains do not hold a complete functional lsr operon, and the presence of genes does not correlate with phylogenetic history, pathogeneicity, or virotype. The loss of function occurred multiple independent times during the evolution of E. coli, and once initiated pseudogenization is fast and does not follow a fixed gene order. Analyses of selection show that two important genes are under balancing selection: the luxS (AI-2 synthase) and the lsrA the gene that codes for the ATPase enzyme that produces the energy necessary for the internalization of AI-2 into the cell. These signals of balancing selection at the nucleotide level may be the result of evolution on fluctuating environments or alternatively, the consequence of frequency-dependent selection acting on the efficiency of signal production and internalization. The later would support the hypothesis of AI-2 QS as a cooperative behavior vulnerable to the evolution of cheating. In P. aeruginosa social behaviors are routinely lost from isolates obtained from lung infections indicating a fitness advantage of cheating during infection. We hypothesize that a similar process also occurs with AI-2 system of E. coli.

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TUE 23 AUG at 1400 - Room N1
Invited talk *C3-Sy04-1400-I*

Symposium 4
Cooperation and virulence

Host-parasite sociality and virulence: bacteria as model hosts, parasites, cooperators and cheats

Brown SP[1]
[1]University of Edinburgh, Centre for Immunity, Infection and Evolution, Edinburgh, United Kingdom

Summary statement:

Social interactions among mobile genetic elements, bacteria and human hosts shape virulence.

Abstract:

Host-parasite interactions are inescapably social: the fitness of the host is influenced by the behaviour of the parasite, and vice-versa. When hosts are infected with multiple parasite genotypes, social interactions can also play out among cooperative and cheating parasites within the host. Here I review social interactions in microbial communities, with a focus on bacteria as both hosts (to phages and plasmids) and as parasites (within spatially-structured eukaryotic hosts). We show that plasmids can supply the genes and genetic structure to allow cooperation to establish, and that virulent phages can structure their bacterial host populations in ways that allow host cooperation to be maintained. We then explore the consequences of more complex (nested) eukaryotic host structures on the evolution of bacterial sociality and resulting virulence. The biomedical implications of socio-microbiology will be discussed.

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TUE 23 AUG at 1610 - Room N1
Oral presentation *C4-Sy04-1610-O*

Symposium 4
Cooperation and virulence

Longevity: A life history-based defense against parasites in a social insect

Buechel SD[1], Schmid-Hempel P[1]
[1]ETH Zürich, Environmental Sciences, Zürich, Switzerland

Summary statement:

Enhancing worker turnover reduces the spread of a bumblebee parasite. Short worker lifespan improves colony fitness and lifespan variation thus may pose a collective defense.

Abstract:

Colony "pace", as indicated by worker activity rate, timing of life history events, or worker turnover during the colony cycle, is an important but often overlooked element shaping social insect biology. In the bumblebee Bombus terrestris, and likely also in other social insects, some colonies seem to have rapid worker turnover. Workers die at young age but new workers are produced frequently and hence colony growth is sustained. For parasites however, rapid worker turnover should have consequences, too. We expect an infectious parasite such as Crithidia bombi (a common bumblebee parasite), to become highly infectious, more virulent and probably more specialized when workers are short lived. From the colony's perspective, rapid worker turnover might furthermore select for the most specialized parasite, reduce parasite strain diversity and ultimately lead to a lower infection probability for daughter queens. This is because infected workers might die before transmitting the disease, thereby reducing parasite spread in the colony. Here, we tested these assumptions in the laboratory by experimentally altering turnover rates in groups of workers. We investigated whether fewer workers get infected and whether Crithidia strain diversity is reduced in groups of Bombus terrestris workers with a rapid turnover rate. We found that rapid worker turnover indeed reduces the proportion of infected individuals in worker groups. As a short worker lifespan can improve colony fitness during infection, variation in worker lifespan might pose a collective defense against parasites in social insect colonies.

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TUE 23 AUG at 1500 - Room N1
Oral presentation *C3-Sy04-1500-O*

Symposium 4
Cooperation and virulence

Evolution of host life-history traits in a spatially structured host-parasite system

Debarre F[1], Lion S[2], van Baalen M[3], Gandon S[2]
[1]Universite Montpellier 2, Montpellier Cedex, France, [2]CNRS, Montpellier, France, [3]CNRS ENS UPMC, Paris, France

Summary statement:

Spatial structure allows for the evolution of altruistic host defense strategies like increased disease-induced mortality or reduced transmission.

Abstract:

Most models for the evolution of host defense against parasites assume that host populations are not spatially structured. Yet, local interactions and limited dispersal can strongly affect the evolutionary outcome, as they significantly alter epidemiological feedbacks and the spatial genetic structuring of the host population. In this presentation, we provide a general framework to study the evolution of various host life history traits in a spatially structured host population infected by a horizontally and locally transmitted parasite. Our analysis teases apart the selective pressures on hosts, and helps disentangle the direct fitness effect of mutations and their indirect effects via the influence of space on the genetic, demographic and epidemiological structure of the host population. We illustrate the evolutionary consequences of spatial structure by focusing on the evolution of two host defense strategies against parasitism: suicide upon infection (i.e. increase in disease-induced mortality, often referred to as parasite virulence, but here under the host's control) and reduced transmission. As they bring no direct fitness benefit, these strategies are counter-selected in a non-spatial setting, but we show that they can be selected for in a spatially structured environment. Our study thus sheds light upon the evolution of altruistic defense mechanisms that have been observed in various biological systems, and can account for the high levels of disease-induced mortality observed in nature.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy04-i003-R*

Symposium 4
Cooperation and virulence

Simulations and empirical data reveal the influence of population structure and the costs and benefits of defense on the evolution of host defenses in a social parasite system

Foitzik S[1], Pamminger T[1], Metzler D[2]
[1]Johannes Gutenberg Universität Mainz, Institut für Zoologie, Abteilung Evolutionsbiologie, Mainz, Germany, [2]Ludwig-Maximilians-Universität München, Department Biologie II, Planegg-Martinsried, Germany

Summary statement:

Population genetic data and simulations demonstrate that population structure and the costs / benefits of defense are crucial for the evolution of the defense trait slave rebellion

Abstract:

Geographic patterns of host resistance and parasite virulence depend on the fitness consequences of these traits and on the population structure. Socially parasitic slavemaking ants use allospecific workers to raise their young and slaves are stolen during raids. Parasite pressure led to the evolution of host defenses either to circumvent parasitism - e.g. defenses - or to mitigate its costs once workers have been enslaved such as the “slave rebellion” trait: enslaved Temnothorax workers were observed to kill pupae of the slavemaking ant Protomognathus americanus. The ensuing reduced growth of parasite nests lead to fewer and less destructive raids. We analyzed whether parasitic brood destruction increases the inclusive fitness of enslaved workers by reducing the raiding risk for related host colonies nearby. Genetic analyses detected weak population structure and host colonies that survived raids, which could directly profit from rebellion of their slave relatives. A simulation revealed the conditions under which the slave rebellion trait could spread. Beside host structure, the costs of resistance were found to be crucial. Costs could include the erroneous killing of own brood and indeed killing rates of parasite and host populations co-varied geographically. To avoid fitness costs in the absence of parasitism, defenses could evolve to be inducible and we demonstrated the first inducible defense trait in host-social parasite systems. Using a combination of empirical and theoretical methods we were able to explore under which conditions host defenses will evolve and spread in host populations.

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TUE 23 AUG at 1420 - Room N1
Invited talk *C3-Sy04-1420-I*

Symposium 4
Cooperation and virulence

Social immunity and virulence

Hughes W[1]
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Summary statement:

Highly social organisms, such as ants, cooperate to resist parasites and their ´social immunity´ may affect the virulence of parasites at multiple levels.

Abstract:

Social organisms are often characterised by cooperation between members of a group, with individuals in many of the more highly social taxa, such as the social insects, gaining fitness indirectly by helping relatives rather than directly via their own reproduction. The concept of parasite virulence in such social hosts is thus more complex than in solitary host species, and parasites can potentially be virulent at the individual-level but avirulent at the group-level, or vice versa. Host cooperation can extend to the resistance of parasites and this may result in groups exhibiting a form of ´social immunity´. In its broad-sense, social immunity consists of a variety of social interactions which help the group resist parasites and are analogous at the level of the group or ´superorganism´ to the physiological immune response of an individual. In its narrow-sense, social immunity entails the transfer between individuals of immunologically active compounds. Here I will describe work showing that social immunity in ants involves prophylactic and proactive measures, but can also be adaptive in a similar way to the physiological immune response. I will examine whether this social immunity is specific and consider if social immunity can affect the virulence that parasites express in hosts at the individual or group-levels.

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TUE 23 AUG at 1650 - Room N1
Oral presentation *C4-Sy04-1650-O*

Symposium 4
Cooperation and virulence

Spite and cooperation in Pseudomonas aeruginosa

Inglis RF[1], Brown S[2], Buckling A[3]
[1]Univeristy of Oxford, Zoology, Oxford, United Kingdom, [2]University of Edinburgh, Edinburgh, United Kingdom, [3]University of Exeter, Falmouth, United Kingdom

Summary statement:

Spite and cooperation are two important social traits in the evolution and virulence of bacteria. In this study we examine how they interact in Pseduomonas aeruginosa.

Abstract:

Social interactions have been shown to play an important role in bacterial evolution and virulence. However, the majority of empirical studies conducted have only considered social traits in isolation. This simplistic approach, although extremely useful in identifying conditions where individual traits can be favoured, may miss potentially important synergies or antagonisms between social traits that are expressed simultaneously. In this study we develop new theory and conduct experiments to elucidate how two social traits (spite and public goods cooperation) can interact in the bacterium Pseudomonas aeruginosa, and how this in turn can affect virulence. Consistent with our theoretical predictions, we find that spite and public goods cooperation work together in a synergistic manner, changing the ecological conditions where these two traits can be favoured. Specifically, spiteful genotypes are favoured at higher frequencies when competing against public good cheats. Furthermore, this interaction between traits predictably impacts bacterial virulence in our caterpillar model system. These results confirm the importance of considering multiple social traits simultaneously, especially under natural conditions where multiple traits can significantly contribute to bacterial fitness.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy04-i004-R*

Symposium 4
Cooperation and virulence

Colony level effects of multiple pathogen exposures in ant societies

Konrad M[1], Cremer S[1]
[1]Institute of Science and Technology Austria, Klosterneuburg, Austria

Summary statement:

We studied the colony level effects of simultaneous and sequential exposure to different fungal pathogens in the ant Lasius neglectus.

Abstract:

Similar to long-lived individual organisms, also long-lived societies face the problem of multiple infections with parasites and pathogens. Exposure to multiple parasites can occur simultaneously or sequentially, both within individuals and within colonies. Here we report on the colony level effects of simultaneous and sequential exposure to different fungal pathogens in the invasive garden ant, Lasius neglectus.

Insect societies have evolved sophisticated collective anti-parasite defences that combine the immune systems of all group members and their collective social hygienic behaviours. Nevertheless infections with single or multiple pathogens are highly likely to occur in nature. Spores of the studied entomopathogenic fungi are common in the soil surrounding ant nests, as well as in form of sporulating insect cadavers and thus spores of different fungi can be easily picked up by foragers of the colony.

We studied the susceptibility of ant workers to multiple pathogens in the nest in different populations of L. neglectus and found that colonies can pay an unexpectedly high cost of these multiple infections.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy04-i002-E*

Symposium 4
Cooperation and virulence

Cooperation and cheating can lead to the evolution of diversity in siderophore-producing bacteria

Lee W[1], Jansen VAA[1], van Baalen M[2]
[1]Royal Holloway University of London, Egham, United Kingdom, [2]Université Pierre et Marie Curie, UMR 7625 « Ecologie & Evolution », Paris, France

Summary statement:

This study provides an explanation for the maintenance of diversity in siderophore producing bacteria, through the interplay between cooperators and cheaters.

Abstract:

Genetical and phenotypical diversity in siderophore producing bacteria is high, but how such diversity has arisen and how it is maintained remains enigmatic. Siderophores are secreted into the extracellular environments to bind iron; then, they can be taken up by any organism that has the suitable receptor. In other words, organisms (strains, or clones) share their siderophores as a common good. Assuming that the production of siderophores is costly, this common good system may favour non producing siderophore users (cheaters). We suggest that diversity arises from the interplay between siderophore producing (cooperators) and non-producing (cheaters) individuals: when there are many cheaters exploiting a siderophore type it would be beneficial for a mutant to produce a siderophore that is incompatible with the dominant population.

Here we analyse a mathematical model of metapopulations to investigate the potential for the emergence of diversity. We found that diversity indeed collapses in the metapopulation when cheaters are absent. When present, cheaters act as a controlling agent, preventing any strains of cooperators from dominating the others: they counteract genetic drift by regulating the populations of cooperators. This frequency-dependent mechanism selects against any dominant siderophore producing strains and thus provides a mechanism for the maintenance of siderophore diversity in the population. However, cheaters are rare most of the time and only appear when one of the siderophore types becomes common.

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TUE 23 AUG at 1710 - Room N1
Oral presentation *C4-Sy04-1710-O*

Symposium 4
Cooperation and virulence

Multiple infection and evolution of interference in viral populations

Leggett HC[1], Benmayor R[1], West S[1], Buckling A[1]
[1]University of Oxford, Zoology, Oxford, United Kingdom

Summary statement:

We show for the first time that intraspecific interference evolves de novo, reducing viral population growth in multiple infections; with no apparent cost in single infections.

Abstract:

Infections of a single host with multiple parasite genotypes are common in natural populations, resulting in within-host parasite competition. Such within-host competition can select for a range of parasite strategies, including increased rates of host exploitation, exploitation of competitors' public goods (social cheating) and interference. Although these strategies can dramatically affect the severity of disease resulting from multiple compared to single genotype infections, empirical data is lacking and there is often no a priori reason to assume any one strategy (if any) is more or less likely to evolve. Here, using the bacterium Pseudomonas fluorescens SBW25 as a susceptible host, we experimentally evolved populations of a virus, lytic bacteriophage Φ2, in single and multiple infections, to determine the evolution, if any, of strategies resulting from within-host competition. We show for the first time that intraspecific interference evolves de novo, and results in reduced growth of the viral population under multiple infections; but has no apparent cost under conditions of single clone infections. These results suggest parasite interference strategies and the resultant reduction in growth of the total parasite population might be common responses to selection resulting from within-host competition in natural populations.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy04-i005-R*

Symposium 4
Cooperation and virulence

The Interplay between relatedness and horizontal gene transfer drives plasmid evolution and bacterial virulence

Mc Ginty SÉ[1,2], Lehmann L[3], Brown SP[4,5], Rankin DJ[1,2]
[1]University of Zurich, Institute of Evolutionary Biology and Environmental Studies, Zurich, Switzerland, [2]Swiss Institute of Bioinformatics, Lausanne, Switzerland, [3]University of Neuchatel, Institute of Biology, Neuchatel, Switzerland, [4]University of Oxford, Department of Zoology, Oxford, United Kingdom, [5]University of Edinburgh, Centre for Immunity, Infection & Evolution, Edinburgh, United Kingdom

Summary statement:

Using an explicit population genetic approach we highlight the importance of transmission and relatedness as factors driving the evolution of plasmid-borne cooperation.

Abstract:

Plasmids carry a wide range of genes which are often involved in bacterial social behaviour. The question of why such genes are frequently mobile remains unexplored. Here we use an explicit population genetic approach to model the evolution of plasmid-borne cooperation and virulence. Our findings highlight the importance of both transmission and relatedness as factors driving the evolution of plasmid-borne cooperation and virulence. Transmission promotes cooperation by converting neighbouring cells into cooperators. As relatedness is measured at the locus of interest, transmission also increases local relatedness between individuals via infectious plasmid transfer thus enhancing cooperation through kin selection. We find that cooperation is most successful when patches are founded by relatively few bacterial individuals and that the relationship between transmission and relatedness differs dramatically depending on the frequency of the plasmid in the population. We also examine the dynamics of resistance against plasmid carriage and how this is affected by the nature of the social traits they carry. Plasmids remain important vectors for the spread of genes involved in virulence and antibiotic resistance thus an understanding of their dynamics is highly relevant from a public health perspective.

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TUE 23 AUG at 1630 - Room N1
Oral presentation *C4-Sy04-1630-O*

Symposium 4
Cooperation and virulence

African Drosophila melanogaster appear more resistant to Type III secretion system cooperative virulence factors of Pseudomonas aeruginosa

McKean KA[1]
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Summary statement:

The type III secretion system is a cooperative virulence factor of Pseudomonas aeruginosa and host defense against this virulence factor is greater in African D. melanogaster.

Abstract:

The adaptive evolution of immune defense involves particular mechanisms of host defense interacting with specific pathogen virulence factors. The Type III secretion system (TTSS) is a virulence factor common to many Gram-negative pathogens. Virulence factors secreted by the TTSS are often involved in immunosuppression or immunomodulation. Because mutant cells lacking a TTSS (cheats) may benefit from the immunosuppression of their secreting neighbors, within-host evolution of mixed populations of secretors and cheats may reflect cooperative dynamics. Using infections of the ubiquitous Gram-negative pathogen, Pseudomonas aeruginosa, in Drosophila melanogaster, I show first that the TTSS is important in the expression of pathogen virulence. I then show that in mixed infections the relative fitness of non-secreting cheats is frequency dependent, consistent with the expectation of cooperative dynamics. Lastly I show that the relative fitness of the TTSS cheats varies across fly genotypes and in particular that flies from sub-Saharan Africa appear more resistant to TTSS virulence factors than 'cosmopolitan' flies from outside of Africa. The results have implications for understanding the specific factors promoting among-population divergence in patterns of immune defense as well how cooperative dynamics may affect the pathogen host interaction.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy04-i006-R*

Symposium 4
Cooperation and virulence

Stress increases disease susceptibility of ant colonies

Stock M[1,2], Heinze J[2], Cremer S[1,2]
[1]IST Austria (Institute of Science and Technology), Klosterneuburg, Austria, [2]University of Regensburg, Regensburg, Germany

Summary statement:

We demonstrate that colony-level investment into dispersal comes at a cost of decreased immune investment of group members and thus of higher disease susceptibility in ants.

Abstract:

It is well perceived that stress at the level of individual organisms can negatively affect immunocompetence. We here study social insects to analyse the effect of stress, imposed at the colony level, on the immunocompetence of individual group members. We use the ant Cardiocondyla obscurior as our study system, as this socially plastic species reacts to stressful conditions with the production of winged dispersal males in addition to the typical wingless males that are always found in the colony (Cremer & Heinze, 2003, Curr Biol). This colony-level investment into large and costly winged dispersal males is a successful strategy to create daughter colonies outside the area of deteriorating conditions, similar to stress-induced flowering in plants. However, this may come at a cost for the maternal colony in its ability to fight diseases. To test this, we compared the efficiency of workers, queens and wingless males from "stressed" as well as control colonies of C. obscurior to fight fungal infection with the entomopathogenic fungus Metarhizium anisopliae. We found that the immunocompetence of colony members was lower in stressed colonies that produced winged males than in our control colonies. This study provides first insights into a potential trade-off between investment into dispersal at colony level and immunocompetence at individual level of the remaining colony members, likely leading to a higher vulnerability of stressed colonies to epidemics.

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TUE 23 AUG at 1550 - Room N1
Oral presentation *C4-Sy04-1550-O*

Symposium 4
Cooperation and virulence

Pathogen detection in ant societies: the first step in cooperative disease defence

Ugelvig LV[1], Mitteregger B[1], Cremer S[1]
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Summary statement:

We investigate the nature of cues that are important for ants in detecting pathogens and eliciting cooperative antiseptic behaviours.

Abstract:

Where sociality has evolved among insect taxa, it has proven very successful. One drawback of this lifestyle is the elevated risk of pathogen transmission among colony members, due to their frequent and intimate interactions and high genetic relatedness. To counteract this constant threat a whole suite of cooperative disease defences have evolved. Such cooperative 'antiseptic behaviours' – including allogrooming of pathogen exposed colony members and brood, and removal of diseased brood from the nest – are thus found in termites, honey bees and ants.
For these behaviours to efficiently impede infection, rapid detection of pathogens and diseased individuals is indispensable. Studies confirm that healthy nestmates immediately detect pathogens on experimentally exposed nestmates and react with direct performance of antiseptic behaviours before an infection has been established. We recently showed, however, that inbred ant colonies lose their ability to quickly react to incoming pathogens (Ugelvig et al., 2010, Proc Roy Soc Lond B). This suggests that the ability to detect cues associated with pathogens and diseased brood is affected by the underlying genetics. Here we investigate which cues are important in detecting pathogens and eliciting cooperative antiseptic behaviours in ant societies. We focus our analysis on chemical cues produced by the pathogens themselves and on possible changes in ant's odour after pathogen exposure and infection.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy04-i003-E*

Symposium 4
Cooperation and virulence

The protein tyrosine phosphatase gene of the baculovirus AcMNPV induces hypermobile behavior in Spodoptera exigua larvae

van Houte S[1], Hoover K[2], Ros VI[1], van Oers MM[1]
[1]Wageningen University, Laboratory of Virology, Wageningen, Netherlands, [2]Pennsylvania State University, Laboratory of Entomology, University Park, PA, United States

Summary statement:

The protein tyrosine phosphatase gene of the baculovirus AcMNPV induces hypermobile behavior in Spodoptera exigua larvae.

Abstract:

‘Wipfelkrankheit’ or tree top disease is an evolutionary conserved phenomenon observed in lepidopteran insect larvae upon infection with a baculovirus. Infected host larvae show a behavioral change, characterized by enhanced mobility and climbing to the top of the plant. These behavioral changes are thought to be virus-induced, as they increase virus transmission. The genetic basis of this behavioral manipulation is, as yet, unknown. In our research we show the involvement of the baculovirus ptp gene, encoding a protein tyrosine phosphatase, in host hypermobility. Spodoptera exigua larvae show enhanced mobility three days after infection with Autographa californica (Ac) MNPV. In contrast, a mutant AcMNPV in which the ptp gene was deleted (Δptp), did not induce this enhanced mobility. With a repair virus, in which the ptp gene was placed back in the Δptp genome, the mobile phenotype was restored. Currently we are studying a virus that carries a ptp gene encoding a catalytically inactive enzyme to determine whether the phosphatase activity of the PTP protein is required for the induction of hypermobility. Substrate analysis of the AcMNPV PTP protein is currently being performed to get insight in downstream targets of PTP. In addition, PTP localization studies are performed in larval tissues, to get a better understanding of the mechanism behind ptp-induced insect mobility.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy04-i004-E*

Symposium 4
Cooperation and virulence

Quantitative real-time PCR detection of the fungal pathogens Metarhizium anisopliae and Beavaria bassiana in Lasius neglectus

Vyleta M[1], Klatt M[1], Cremer S[1]
[1]IST Austria, Evolutionary Biology, Klosterneuburg, Austria

Summary statement:

Determination of pathogen load by quantitative real-time PCR in fungus infected ants

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Abstract:

Transmission of parasites in social insect colonies depends on many factors, including pathogen virulence as well as behavioral, chemical and molecular defenses of the individual hosts. One important determinant of virulence is parasite load. In order to better understand the mechanisms underlying immune responses of the invasive garden ant Lasius neglectus to fungal pathogens, a real-time PCR assay was developed to detect and quantify two generalist fungal pathogens, Metarhizium anisopliae and Beauveria bassiana, within exposed individuals. By using species-specific primers to amplify the 18S rRNA gene, pathogen load was calculated by converting copy numbers of fungal DNA to spore counts based on standard curves of 18s rRNA copies amplified from known quantities of spores. When paired with analyses of host immune gene expression, this assay provides a sensitive, quantitative tool for investigating how parasite replication kinetics are linked with infection and immunity in Lasius neglectus.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy04-i007-R*

Symposium 4
Cooperation and virulence

The effect of individual experience on hygienic task performance

Westhus C[1,2], Doums C[2], Cremer S[1,3]
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Summary statement:

We analyze if repeated exposure to larvae treated with fungal spores (Metarhizium anisopliae) leads to changes in antiseptic behavior of individual Platythyrea punctata workers.

Abstract:

Pathogens strongly impact the survival of social insect colonies, where the transmission of disease is facilitated by the geographic and genetic proximity between nestmates. Social organisms evolved anti-pathogen defense mechanisms, hygienic tasks, to acquire resistance at the group level. We use the clonal ant Platythyrea punctata to examine whether the investment into a hygienic task varies as a function of individual experience. This parthenogenetically reproducing ant species offers the opportunity to study the effect of experience on task performance in absence of genetic diversity among workers. We analyze if repeated exposure to larvae treated with spores of the entomopathogenic fungus Metarhizium anisopliae leads to changes in antiseptic behavior of individual workers. Further, we investigate whether experienced workers are more efficient in task-performance and perform the task when being paired with a naïve worker.

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Symposium 5

Mutualism: Causes and consequences

Talks: *Room N3*

Essence posters*:* Upper floor lecture hall centre *HZ*

Regular posters*:* Upper floor campus canteen *Mensa*

Invited Speakers:

Nancy Moran, Ulrich Mueller

Organizers:

Christian Kost, Martin Kaltenpoth

Description:

In recent years, our understanding of mutualistic interactions has significantly advanced. Rigorous experimental studies have fostered new insights and enhanced mutualism theory. This symposium highlights the latest developments in the field by drawing together theoretical and empirical contributions thereby analysing the evolutionary ecology of mutualisms on all levels of biological organisation.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy05-i001-R*

Symposium 5
Mutualism: Causes and consequences

Parasitic attack on two mutualistic partners: The evolution of social parasite strategies and the coevolutionary consequences

Adams RMM[1,2], Shah K[3], Schultz TR[2], Brady SG[2], Mueller UG[4]
[1]University of Copenhagen, Centre for Social Evolution, Department of Biology, Copenhagen, Denmark, [2]Smithsonian Institution, Department of Entomology, Washington DC, United States, [3]University of Texas Health Science Center at San Antonio, San Antonio, United States, [4]University of Texas at Austin, Austin, United States

Summary statement:

We examine the fitness impact that a social parasitic ant species has on a mutualistic ant-fungus network in an evolutionary context using phylogenetics and experimentation.

Abstract:

In the entangled web of species associations, symbiotic interactions can range from mutualistic to parasitic. Parasites often take advantage of species interactions and attack mutualistic traits, exploiting the resources exchanged between partners. These complex relations are a fundamental innovation in evolution, shaping diversity and stabilizing species networks. The ant genus Megalomyrmex comprises 38 species and at least ten are social parasites of fungus-growing ants (Tribe: Attini) while the other species are free-living predators. There is a gradation of behavior that includes lestobiotic parasitism also described as raiding thief ants, agro-predatory associations, where the parasite usurps the nest and fungus garden, and the most derived, cohabiting xenobiotic parasitism. Megalomyrmex ants are chemical warriors, dispensing volatile venom alkaloids by waving their stings as they enter another ant species' nest as parasites or during competitive interactions. In the former case, if the host does not allow infiltration, then the parasite will attack and kill. Infiltration can be accomplished as just described (i.e. chemical weaponry) or through the alteration of cuticular hydrocarbons (i.e. surface chemistry) using chemical mimicry and/or insignificance. We examine the impact of Megalomyrmex adamsae ants on a mutualistic network where they exploit colony resources. This mutualism exploiter attacks both partners, consuming not only the fungus garden but also host larvae. Further, we consider the parasitic strategies used by the parasites in an evolutionary context with phylogenetic hypothesis testing, using a phylogeny constructed from five genes.

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SUN 21 AUG at 1550 - Room N3
Oral presentation *A4-Sy05-1550-O*

Symposium 5
Mutualism: Causes and consequences

Cooperation (without relatedness, assortment and iterations) in public goods games, from microbes to terrorists

Archetti M[1,2]
[1]University of Basel, Faculty of Business and Economics, Basel, Switzerland, [2]Harvard University, Department of Organismic and Evolutionary Biology, Cambridge, United States

Summary statement:

Cooperation. Beyond kin selection, assortment and iterations. Towards economics and the social sciences.

Abstract:

I will show that in generalised public goods games (not restricted to the N-person prisoner's dilemma) in which the public good is a non-linear function of the individual contributions (which is the case in most social species ranging from bacteria to humans) intermediate levels of cooperation can be stable in one-shot interactions without assortment, spatial structure, relatedness, punishment, fairness or other forces that are commonly believed to be necessary to maintain cooperation. This helps explain cases of cooperation in one-shot random interactions among non-kin, some apparently puzzling observations in microbes and the frequency of suicide terrorist attacks in recent conflicts. It also allows to go beyond the current debates on cooperation in evolutionary biology. A prescriptive approach to the study of cooperation is possible: we can devise practical ways to improve the production of public goods in social dilemmas without invoking assortment, relatedness, punishment or repeated interactions. This has implications in economics and in the social sciences.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy05-i001-E*

Symposium 5
Mutualism: Causes and consequences

Gut microbiota of the forest cockchafer (Melolontha hippocastani)

Arias Cordero E[1], Ping L[1], Delb H[2], Reichwald K[3], Platze M[3], Boland W[1]
[1]Max Planck Institute for Chemical Ecology, Bioorganic Chemistry, Jena, Germany, [2]Forstliche Versuchs- und Forschungsanstalt Baden-Württemberg, Freiburg, Germany, [3]Leibniz-Institut für Altersforschung - Fritz-Lipmann-Institut e.V., Jena, Germany

Summary statement:

This study allowed a deep insight of the microbiota inhabiting the gut of M. hippocastani; basis for a future identification of the bacterial species key for the insect fitness.

Abstract:

The forest cockchafer (Melolontha hippocastani) is a pest in European forests. Larvae live in soil and feed on plant roots and organic matter. Microbiota in gut help the insect to digest its food. To gain knowledge about the identity, function and transmission of the bacterial species present in different compartments of the insect alimentary canal, insects of different ages collected in the state of Baden-Württemberg were analyzed. Bacteria living in the mid- and hindgut of grubs and adults were cultivated, and in a culture-independent approach, metagenomic libraries were constructed. Among the species cultivated, five were isolated from the midgut, two from both mid- and hindgut, and one from the hindgut. In our metagenomic libraries, ~50% of the sequences represent low abundant species. 16 operational taxonomic units (OTUs) were found in different samples. The localization of 9 OTUs was further analyzed by fluorescence in situ hybridization (FISH) carried out on the guts of larvae and both female and male beetles. Some species, including Sediminibacterium, were present in the gut lumen, principally on food aggregates. Others such as Clostridiaceae and Desulfovibrionaceae were found on the gut epithelium. The bacterial community in the hindgut lobe was studied using scanning electron (SEM) and transmission electron (TEM) microscopy. The former showed bacteria in a sophisticated multilayered arrangement, whereas TEM showed bacteria tightly attaching to the surface. Interestingly, a pair of novel structures of unknown function was found at the end of the hindgut enlargement, TEM revealed bacteria present in the intercellular spaces in this tissue.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy05-i002-E*

Symposium 5
Mutualism: Causes and consequences

Expression of the glycosyltransferase B4galnt2 influences the intestinal microbiota in house mice

Baines JF[1,2], Staubach F[3], Bäckhed F[4], Johnsen JM[5]
[1]Institute for Experimental Medicine / Christian-Albrechts-University of Kiel, Evolutionary Genomics, Kiel, Germany, [2]Max Planck Institut for Evolutionary Biology, Plön, Germany, [3]Stanford University, Department of Biology, Stanford, United States, [4]University of Gothenburg, Department of Molecular and Clinical Medicine, Sahlgrenska Center for Cardiovascular and Metabolic Research/Wallenberg Laboratory, Gothenburg, Sweden, [5]Research Institute, Puget Sound Blood Center / University of Washington, Department of Medicine, Seattle, United States

Summary statement:

Bacterial metagenomic analysis reveals that the glycosyltransferase gene B4galnt2 significantly influences resident microbial communities in the gastrointestinal tract.

Abstract:

Glycans on mucosal surfaces play an important role in host-microbe interactions. The locus encoding the glycosyltransferase β-1,4-N-acetylgalactosaminyltransferase 2 (B4galnt2) is subject to strong selective forces in natural house mouse populations which contain a common allelic variant which specifically turns off gene expression in bowel. We reasoned that altered glycan-dependent intestinal host-microbe interactions may underlie these signatures of selection. To determine if B4galnt2 influences the intestinal microbial ecology, we profiled wild type and B4galnt2-deficient siblings throughout the GI tract using 16S rRNA gene pyrosequencing. This revealed both distinct communities at different anatomic sites and significant changes in composition with respect to genotype, indicating a role for B4galnt2 in host-microbial homeostasis. Interestingly, in contrast to other glycosyltransferases, B4galnt2 expression is not dependent on presence of the microbiota. Our data suggest that variation in B4galnt2 gastrointestinal expression affects fitness in natural populations, likely by altering susceptibility to gastrointestinal disease, such as infectious gastroenteritis.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy05-i003-E*

Symposium 5
Mutualism: Causes and consequences

Fungus agriculture and sociality in ambrosia beetles

Biedermann PHW[1], Taborsky M[1]
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Summary statement:

In the first study of ambrosia beetles fungiculture within their tunnel-systems we show that their sociality probably evolves in close association with the beetle-fungus symbiosis.

Abstract:

Fungiculture in insects is known from attine ants, macrotermitine termites and ambrosia beetles. The first two groups are eusocial and exhibit some of the most highly developed social organizations known among all organisms. In contrast, the social organization of ambrosia beetles is largely unknown. Adult female offspring in xyleborine ambrosia beetles delay dispersal from their natal nest, during which period they often engage in various brood care and fungus maintenance tasks. Dispersing females transmit spores of mutualistic ambrosia fungi (Ascomycetes) in special organs from the natal gallery to their new nest. These transmitted fungi usually dominate the microbial complex within the galleries. Our experiments show that adult females induce growth of the mutualistic fungus that is characterized by massive fruiting structures (sporodochia). These fruiting bodies seem to be an essential component of beetle nutrition. Our data suggest that an important function of delayed dispersal of adult females from their natal nest might be improved growth conditions of their ambrosia fungus creating potential for indirect fitness gains of philopatric females by an increase in sibling production.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy05-i004-E*

Symposium 5
Mutualism: Causes and consequences

Genome-wide pattern of polymorphism in the model legume Medicago truncatula and its associated rhizhobial symbionts

Branca A[1,2], Paape T[2], Zhou P[3], Briskine R[4], Farmer AD[5], Mudge J[5], Arvind BK[5], Gentzbittel L[6], Sadowsky MJ[7], Ronfort J[8], Bataillon T[9], Young ND[3], Tiffin P[2]

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Summary statement:

We studied genome-wide polymorphism of both partners in the mutualist interaction between the legume Medicago truncatula and nitrogen-fixator bacteria of genus Sinorhizobium.

Abstract:

Medicago truncatula is a model for investigating legume genetics, especially the genetics and evolution of legume-rhizobia symbiosis. Bacterial rhizobial symbionts have the capacity to fix the nitrogen from the atmosphere and provide it to the plant, within a specific structure of the root called nodule. In exchange, the plant provides essential nutrients to the bacteria. Genome evolution of both mutualistic partners is highly impacted through genotype-by-genotype interactions. First, we sequenced the whole genome of a diverse collection of 26 M. truncatula accessions to identify and characterize sequence polymorphisms and linkage disequilibrium. More than 3,000,000 SNPs were detected, of which approximately half are present in more than one accession. This polymorphism is a valuable resource and can be utilized genome-wide association study of genes responsible for phenotypic diversity in legumes, especially traits associated with symbiosis and nodulation. Among putative coding regions, members of four gene families harbour significantly higher diversity than the genome-wide average. Three of these families are known to be involved in resistance against pathogens. One of these, the Nodule-specific Cysteine Rich (NCR) gene family, is specific to the galegoid legumes and involved with control of rhizobia symbionts. Second, the complete genomes of Sinorhizobium symbionts, 12 strains of Sinorhizobium medicae and 24 strains of S. meliloti, were sequenced to identify genes under selection pressure related to symbiosis success. Our work provides new insights on the genome-wide effect of genotype-by-genotype interactions in legume-rhizobia symbiosis.

TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy05-i002-R*

Symposium 5
Mutualism: Causes and consequences

Costs of nucleotide synthesis, size and copy number of plasmids as model endosymbionts

Dietel A-K[1], Merker H[1], Kaltenpoth M[1], Kost C[1]
[1]Max Planck Institute for Chemical Ecology, Jena, Germany

Summary statement:

The interaction between bacteria and plasmids differing in their metabolic costs of nucleotide synthesis serve as model system to study the evolutionary ecology of endosymbionts.

Abstract:

The interaction between bacteria and their plasmids resembles the relation of endosymbionts and their hosts in many regards. Both plasmids and endosymbionts can confer benefits to their host, but may also incur a cost. Due to their experimental amenable plasmids are an ideal model to study the evolutionary ecology of endosymbionts. A common feature of endosymbiotic organisms is the reduction of genome size compared to their free-living relatives due to minor selection pressure on genes, which are dispensable in the intracellular environment.
In this project, the special genome features will be assigned on the plasmid-host system. Therefore, fitness experiments between plasmid containing Escherichia coli strains will be carried out. The strains will differ in plasmid copy number and plasmid size of the plasmid. By using specific fluorescently labeled probes for tagging the plasmid, qPCR and flow-cytometrical measurements enables us to measure the cost for plasmid replication on a single–cell level. The results of fitness experiments in which different cells are compared with respect to plasmids as model endosymbionts are discussed.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy05-i005-E*

Symposium 5
Mutualism: Causes and consequences

Are the Quaternary histories of mutualistic partners interrelated?

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Summary statement:

Based on the study of an obligate nursery pollination mutualism, we show that interactions not only drive ecological adaptations but can also shape the histories of its partners.

Abstract:

The coevolutionary theory predicts that interacting species should present similar histories, especially if interactions are specific and obligate. In spite of this, little is known about the effect of ecological interactions on the phylogeographic patterns of interacting organisms.
To investigate this, we use the mutualistic nursery pollination system formed by the Eurasian arctic-alpine species Trollius europaeus L. and its specific pollinators in the genus Chiastocheta Pokorny as a case study. Here, the plant is visited and pollinated exclusively by the flies, whose larvae feed specifically on the plant seeds. Because this system comprises a low number of interacting species, it is highly appropriate to test the effect of interactions in a simple comparative phylogeography framework.
Based on a large-scale sampling of both plants and pollinators, we first infer the phylogeographic history of the plant, and further compare it with that of each of its partners. By applying a comparative approach in a coalescent framework, we ask whether or not the phylogeographic patterns of the flies are significantly different of what would be expected under a scenario of plant-insect congruence.
Our results demonstrate that the plant presents four spatially structured genetic groups and that the phylogeographic pattern of the flies vary. While Chiastocheta lophota´s is largely explained by geography, the phylogeographic pattern of C. dentifera does not differ of what would be expected if it had evolved under a scenario guided by the plant.
Our results thus demonstrate that interacting species present not only ecological adaptations, but can also share historical traits.

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MON 22 AUG at 1440 - Room N3
Oral presentation *B3-Sy05-1440-O*

Symposium 5
Mutualism: Causes and consequences

The role of the innate immune system of the ant Camponotus floridanus in regulation and maintenance of its endosymbiont Blochmannia

Feldhaar H[1], Ratzka C[2], Gross R[2]
[1]University of Osnabrueck, Behavioural Biology, Osnabrueck, Germany, [2]University of Wuerzburg, Dep. of Microbiology, Wuerzburg, Germany

Summary statement:

The immune system of Camponotus ants plays a role in containing its endosymbiont Blochmannia within the midgut cells and may also play a role in regulating endosymbiont number.

Abstract:

Numerous insect species harbour mutualistic endosymbiontic bacteria. Insect hosts face the problem of having to maintain such mutualistic bacteria while staging an immune response towards pathogens upon infection. Camponotus floridanus ants harbour the obligate endosymbiont Blochmannia floridanus in specialized midgut cells and ovaries. During the holometabolous life cycle of the ant hosts the distribution of bacteriocytes and of Blochmannia endosymbionts is remarkably dynamic. The proportion of cells of the midgut harbouring Blochmannia increases strongly during host ontogeny and peaks in late pupal stages, where the entire midgut is transformed into a symbiotic organ. After eclosion of workers the symbiosis degenerates as bacterial numbers decreases with age of workers.

We identified genes transcriptionally induced in response to septic injury by suppression subtractive hybridization. Among these were genes involved in pathogen recognition, signal transduction, antimicrobial activity, or general stress response. A quantitative analysis of immune gene expression revealed different expression kinetics of individual factors and characteristic expression profiles after injection of gram-negative and gram-positive bacteria. B. floridanus injected into the hemocoel elicited a comparable immune response of its host C. floridanus. Furthermore, in untreated hosts some immune genes displayed distinct expression patterns according to developmental stage and tissue. Thus, the host´s immune system may prevent colonization of tissues other than the bacteriocytes by Blochmannia and may also play a role in the regulation of the number of bacteria present within bacteriocytes.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy05-i003-R*

Symposium 5
Mutualism: Causes and consequences

The mutualistic relationship between environmentally-acquired bacteria and three broad-headed bug species

Garcia JR[1], Trincot C[2], Gerardo NM[1]
[1]Emory University, Department of Biology, Atlanta, United States, [2]Indiana University, Bloomington, United States

Summary statement:

A bacterial gut symbiont provides positive fitness effects to three stinkbugs species.

Abstract:

Many insects have long-term associations with bacterial symbionts. Recently a number of taxonomically diverse stinkbugs have been found to harbor bacterial symbionts within their midguts. Although this stinkbug-symbiont association is widespread, the fitness effect of the association on the host has only begun to be explored. We screened three previously unstudied stinkbugs, Alydus eurinus, Alydus pilosulus, and a Megalotomus sp., for the presence of symbionts. We dissected the midguts from wild-caught bugs and found each species harbored symbionts identified as Burkholderia species closely related to other free-living and stinkbug-associated Burkholderia. We also found a colored bacteriome in each species that harbors an unidentified bacterial symbiont. In order to test the fitness effects and transmission route of the Burkholderia symbiont, we reared each host species in the laboratory either with soil collected from the bugs' natural habitat, with sterile soil, or without soil. We found that hosts raised with sterile soil or without soil do not harbor Burkholderia as adults while most raised with soil do. Stinkbugs without symbionts weighed less, were shorter and thinner, and had a shorter lifespan than their conspecifics that harbored Burkholderia symbionts. We conclude that the Burkholderia symbiont is a mutualistic symbiont of all three stinkbugs species and that host stinkbugs acquire these symbionts through the environment, likely shortly after hatching. We will also report on the effect of Burkholderia on host hatching rate, development rate, mating ability, and fecundity and the identity of the bacteriome-associated symbiont.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy05-i006-E*

Symposium 5
Mutualism: Causes and consequences

First record of the Acarinarium on bees of the family Andrenidae (Insecta; Hymenoptera)

Hajiqanbar H[1]
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Summary statement:

A kind of Acarinarium, structures for dispersal of mutualistic mites resulted from coevolutionary interactions, is recorded on bees of the family Andrenidae for the first time.

Abstract:

Interspecific interactions can exert the evolution of morphology and life history. Some groups of the insects (most frequently wasps and bees with social and subsocial behaviors) may have specialized pocket-like structures, Acarinaria, on their body in order to transferring the beneficial mites into nests. Such structures usually evolve as a result of two-sided coevolutionary interactions between mites and their hosts and are usually referred as evidence for mutualistic relationships. During study of the heterostigmatic mites (Acari; Prostigmata; Heterostigmatina) associated with insects in some regions of Iran, I found the mites of the genus Imparipes (Scutacaridae) phoretic and harbored in axillar acarinaria of its host bee, Andrena (Melandrena) morio Brulle (Hym.;Andrenidae). This is first record of the Acarinarium in bees of the family Andrenidae, and also first record of Acarinarium for being used to transfer mites of the family Scutacaridae.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy05-i004-R*

Symposium 5
Mutualism: Causes and consequences

Imprecise host sanctions in the fig tree – fig wasp mutualism enable free-riding of uncooperative pollinators

Jandér KC[1], Herre EA[2], Simms EL[3]
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Summary statement:

Mutualisms are vulnerable to cheating. Sanctions by Ficus nymphaefolia reduce the fitness of non-pollinating wasps, but are less effective when multiple wasps share a fig.

Abstract:

Mutualisms are of fundamental ecological importance. Most plants and animals are dependent on cooperative symbionts, yet it is poorly known how these symbionts can be prevented from turning into parasites. What prevents one partner from reaping the benefits of the interaction without paying the costs? Recent studies of several mutualistic systems have documented host sanctions that lower the fitness of uncooperative symbionts. But how precise are these sanctions? Can some cheating symbionts avoid host sanctions by free-riding on other symbionts' good behaviour, or have hosts evolved sanctions that are precise enough to target every symbiont individually?

In the mutualism between fig trees and their pollinating fig wasps, both partners are dependent on the other for reproductive success. In general, each species of fig has its own species of pollinating fig wasp. We have previously shown that fig trees can impose sanctions that reduce the fitness of non-pollinating wasps, and that these sanctions vary in strength across species. We have further shown that some wasp individuals in the supposedly mutualistic wasp species do not pollinate, and that these non-pollinating wasps are more common in fig species with weak sanctions. Using a combination of field experiments and molecular tools, we here investigate the level of precision of host sanctions: do sanctions operate on the level of individual flowers within a fig, or on the level of the entire fig fruit? Our data from Ficus nymphaefolia show that sanctions operate on the fig level, which enable non-pollinators to evade sanctions in figs shared by multiple wasps.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy05-i005-R*

Symposium 5
Mutualism: Causes and consequences

Beewolves´ bodyguards: Production dynamics and activity of symbiont-produced antibiotics on wasp cocoons

Koehler S[1], Kroiß J[1], Hertweck C[2], Kaltenpoth M[1]
[1]Max-Planck Institute for Chemical Ecology, Research Group Insect Symbiosis, Jena, Germany,
[2]Leibniz Institute for Natural Product Research and Infection Biology, (Hans-Knoell-Institute), Jena, Germany

Summary statement:

Dynamics and activity of symbiont-produces antibiotic substances in the defensive beewolf – Streptomyces symbiosis.

Abstract:

The European beewolf, Philanthus triangulum (Hymenoptera: Crabronidae), engages in a highly specific symbiosis with bacteria of the genus Streptomyces. Females cultivate endosymbiotic bacteria in specialized antennal gland reservoirs and secrete them into their brood cells prior to oviposition. Later, the symbionts are taken up by the larva and applied to the cocoon walls, where they serve as a protection against fungal infestation by producing at least nine different antibiotics.

To investigate the dynamics of antibiotic production during beewolf development, the number of Streptomyces cells and the amount of antibiotics was quantified for different time points after cocoon spinning using qPCR and HPLC-MS. The Streptomyces population size remained relatively constant over time. By contrast, the chemical analyses revealed a significant change in the amount of antibiotics, with a strong increase of antibiotics within the first week after cocoon-spinning, and a slow subsequent decrease.

We used agar-diffunsion bioassays to test several fungal and bacterial strains against the antibiotics provided by Streptomyces on the cocoon surface. The results show a strong inhibition for all tested microbes, suggesting that beewolf symbionts use a ´combination prophylaxis` against a wide spectrum of pathogens. Inhibition assays with different combinations of the three major antibiotic compounds will shed light on possible synergistic effects of the substances against various fungal strains. Such synergy might lead to a higher efficacy against specific pathogens and/or an efficient defense against a broader spectrum of microorganisms.

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MON 22 AUG at 1500 - Room N3
Oral presentation *B3-Sy05-1500-O*

Symposium 5
Mutualism: Causes and consequences

Attine ants: Farmers or livestock? New molecular insight into a complex ant-fungus mutualism

Kooij PW[1], Boomsma JJ[1], Schiøtt M[1]
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Summary statement:

Fungal symbionts use the leaf-cutting ants as a transportation device for providing substrate and for reallocation of enzymes in the fungus garden.

Abstract:

Research on the mutualism between fungus-growing ants and their symbionts normally views the ants as farmers and the fungi as crops. However, there is growing evidence suggesting that the fungus is actually using the ants as a live transportation device for providing substrate and transporting fungal enzymes to the new leaf material that the ants add to their fungus gardens. The ants manure gardens with their own fecal fluid, which is packed with fungal enzymes for the biodegradation of the leaf pulp that the ants deliver. Recent studies have shown that fungal pectinases in the fecal fluid serve complex adaptive functions in the symbiosis. The genes coding for these enzymes appear to be overexpressed in the gongylidia, the swollen hyphal tip structures on which the ants feed, which is consistent with a co-adaptation interpretation of these results. Here we show that also all endopeptidase activity in the fecal fluid of the leaf-cutting ant Acromyrmex echinatior has a fungal origin, and we were able to characterize the genes encoding these endopeptidases by using a partially sequenced genome of the fungal symbiont Leucocoprinus gongylophorus. Quantitative real time PCR showed that also these genes are overexpressed in the fungal gongylidia. Our results corroborate the idea that the ant-fungus symbiosis is an advanced mutualistic interaction in which partners have highly integrated complementary roles, including considerable manipulative control by the fungal symbiont.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy05-i006-R*

Symposium 5
Mutualism: Causes and consequences

Impact of symbionts on immunity in the pea aphid, Acyrthosiphon pisum

Laughton A[1], Gerardo N[1]
[1]Emory University, Biology Department, Atlanta, United States

Summary statement:

Pea aphids, which maintain symbionts, have a reduced immune response. Consequences of this on their ability to respond to varying ecological conditions are investigated.

Abstract:

The innate immune system of insects provides effective defence against a range of parasites and pathogens. The pea aphid, Acyrthosiphon pisum, is a novel study system for investigating host-parasite interactions due to its complex associations with both well-characterised bacterial symbionts and a diversity of pathogens and parasites. However, to date, little is known about the aphid's immune capacity, and how it is able to differentiate between beneficial symbiotic, versus harmful pathogenic bacteria.
Here we present recent work profiling the cellular immune responses in the pea aphid. Our findings indicate that pea aphids have a greatly reduced or altered immune system. One hypothesis for this reduction in immune capacity is to allow for the symbiotic relationships that exist between the aphid and bacteria to be established. Pea aphids maintain a vertically transmitted obligate symbiont, Buchnera aphidicola, but may acquire additional secondary bacterial symbionts via both vertical and horizontal transmission. We continue our work to show that these secondary symbionts exhibit a range of behaviours and population dynamics within their aphid hosts, and discuss the impact that secondary symbionts can have on host immunity under varying ecological conditions. Given the universal prevalence of host-symbiont relationships in nature, investigating the dynamics of the host immune system is a vital step towards understanding the delicate balance required to maintain such interactions.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy05-i007-R*

Symposium 5
Mutualism: Causes and consequences

Social parasites protect the nests of their social-wasp hosts from predators: Parasites or mutualists?

Lorenzi MC[1], Thompson JN[2]
[1]University of Turin, Dept. of Animal and Human Biology, Turin, Italy, [2]University of California at Santa Cruz, Dept. of Ecology and Evolutionary Biology, Santa Cruz, United States

Summary statement:

A longitudinal study in social wasps suggests that a mutualistic interaction can appear between two species linked by a host-parasite relationship under high predation pressure.

Abstract:

Social parasites are brood parasites of social insect colonies and integrate permanently into the colonies of their hosts. Host and parasites evolve reciprocal traits of virulence and resistance along population-specific trajectories. These trajectories may be shaped not only by differences in the physical environments in which the species are coevolving but also by geographic differences in interactions with other species. Here, we show that host and parasite interactions differ among populations depending on the reciprocal selection of hosts and obligate social parasites and by additional selection that predators place on host colonies. Longitudinal data on annual colonies of Polistes wasps from four geographically distinct host populations show that the fitness costs of parasitism to the host foundresses are very high. However, where predator pressure on host nests is high, parasite presence can increase nest survival relative to non-parasitized colonies. These results suggest that a mutualistic, or reduced antagonistic, interaction can occur between hosts and parasites where predation pressure is high.

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SUN 21 AUG at 1440 - Room N3
Oral presentation *A3-Sy05-1440-O*

Symposium 5
Mutualism: Causes and consequences

Horizontal transfer of facultative symbionts in aphids and the fitness consequences of infection in novel hosts

Lukasik P[1], Guo H[1,2], van Asch M[1], Ferrari J[1,3], Godfray C[1]
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Summary statement:

Facultative symbionts can be transferred between aphid clones and species. Novel symbionts in grain aphids do not generally incur fitness costs, and can provide important benefits.

Abstract:

Facultative endosymbionts of aphids can have important effects on the life history traits of their hosts. Phylogenetic and experimental studies have shown that the symbionts are capable of transferring to, and establishing successfully in, novel hosts, including those distantly related to their original hosts, and that the beneficial effects of infection can be expressed in novel hosts. However, there is limited understanding of symbiont specificity, of how the relatedness between the original and novel hosts affects the probability of successful symbiont transmission, and of the fitness consequences of novel infections.
We introduced eighteen strains of endosymbionts originating from five aphid species into two clonal genotypes of the grain aphid, Sitobion avenae. We measured the effects of the novel symbionts on aphid fecundity and resistance to natural enemies. Most novel symbiont strains formed stable infections, but strains originating from more distantly related donor aphids tended to establish less easily. Once established, most symbionts had no effect on aphid fecundity, regardless of their origin. Surprisingly, none of the strains protected grain aphids against parasitoids - an effect which is found commonly in pea aphid Hamiltonella - although some provided protection against a pathogenic fungus.
Our data indicate the presence of barriers to symbiont transmission, while suggesting that a strain which succeeds in establishing in a novel host may well persist and spread in a host population. These results support the view of aphid secondary symbionts as a eukaryote horizontal gene pool.

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Upper floor lecture hall centre *HZ*
Essence poster *E-Sy05-i007-E*

Symposium 5
Mutualism: Causes and consequences

Pollen flow mediated by different insect groups in generalized plant-pollinator system

Lysenkov SN[1]
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Summary statement:

Insect behavior influences pollen flow even in generalized plant-pollinator systems. Movement patterns of major insect pollinator groups were studied.

Abstract:

Patterns of behavior of different insect taxa, can influence pollen flow even in the generalized plant-pollinator systems. The temperate zone with little amount of specialized insect-pollinated plants and pollinators is a good place for studying these differences. So we investigated behavior of different groups of insects (hoverflies, Muscoid flies, beetles, butterflies and bees) foraging at generalist plants (mostly Asteraceae, Apiaceae and Geraniaceae) in Central Russia.

Even plant patches divided by several meters can have different pollinator set because most of insect species prefer visit denser plant patches but some others - sparser. These findings mean that the pool of pollen which can participate in pollination of different individuals of the same species depends on local density of the patch in which they grow.

Within one patch most of pollinators fly in the following manner: they visit blossoms within small area (usually near 4 mean distances between these object in the patch) and then move to another such area. Such behavior must put an additional constraint on pollen flow within a plant population. Beetles and butterflies don’t show such behavior. The former also significantly more often make very long flights between successive visits. But because of small pollen load butterflies hardly can be good long-distance pollen vectors in spite of small flight distance. On the contrary, social bees can also be good long-distance pollen vectors because of great pollen load in spite of small mean flight distances. The relative roles of different pollinator groups in pollen flow still need a further research.

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SUN 21 AUG at 1710 - Room N3
Oral presentation *A4-Sy05-1710-O*

Symposium 5
Mutualism: Causes and consequences

The importance of transmission mode in conflict resolution: insights from an ant-plant mutualism

Malé P-JG[1], Leroy C[2], Dejean A[2], Quilichini A[1,2], Orivel J[1,2]
[1]University Toulouse III, France, Lab EDB, Toulouse, France, [2]CNRS, UMR EcoFoG, Kourou, French Guiana

Summary statement:

The stability of an ant-plant mutualism is enhanced by partner fidelity feedback, which minimizes the negative consequences of parasitic castration exerted by the ant symbionts.

Abstract:

In theory, mutualisms are intrinsically unstable and every mutualist should become a cheater. However, mutualisms are ubiquitous and of major importance in ecosystems. This observation suggests the existence of “control mechanisms” that enhance the maintenance of such relationships. We focused on the highly specific and obligatory association between the neotropical plant Hirtella physophora and the ants Allomerus decemarticulatus. We demonstrated that H. physophora is subjected to a trade-off between its reproduction and its vegetative growth. Since the resources that the plant invests in its reproduction are supposed to be completely unavailable to the ants, theory predicts that ants should prevent their host plant to reproduce, thus getting more living space. Indeed, we demonstrated that ants manipulate the plant reproduction but contrary to what theory predicts, they do not destroy all of the floral buds.

This contradiction can be explained by the “local transmission” hypothesis, as the quantification of the dispersion distances of both the partners highlighted comparable population genetic structures. Such short and similar dispersion distances suggest that the reproduction of one partner depends on the reproduction of the other.

Altogether, these results demonstrate that the consequences of the conflict between A. decemarticulatus and H. physophora on the plant reproduction are partially contained by a control mechanism known as “partner fidelity feedback”. This control mechanism results in the interdependence of the partners’ reproductive successes and enhances the stability of the association.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy05-i008-R*

Symposium 5
Mutualism: Causes and consequences

On the origin of mutualism: interspecific cooperation favored by spatial structure?

Merker H[1], Pande S[1], Kost C[1]
[1]Max Planck Institute for Chemical Ecology, Department of Bioorganic Chemistry, Jena, Germany

Summary statement:

The influence of spatial structure on the origination of interspecific mutualism based on exchange of metabolites is validated in an experimental evolution approach.

Abstract:

Mutualisms are ubiquitous in all ecosystems and were profoundly influential in shaping ecosystems. Mutualism are cooperative interactions between two individuals to the benefit of both (+/+) and are found between individuals of the same species but also between individuals of different species (e.g. plant-pollinator-interaction). Since these benefits are often costly to the producer, evolutionary theory predicts that selection should favor strategies that reap the mutualistic benefits without providing commodities to the partner species (i.e. cheating). Solving this paradox, which is commonly referred to as the 'tragedy of the commons', is a pre-requisite for explaining the origin of mutualisms and a major challenge for evolutionary biology.

Several ecological factors have been suggested to assist the origin of cooperation as transmission mode of the partners, genetic diversity as well as spatial structure. In this study we tested if spatially structured environment facilitates the evolution of cooperation. For that purpose, we created a synthetic by-product mutualism between Escherichia coli and Pseudomonas fluorescence based on the exchange of essential, into the medium excreted metabolites. This was achieved by producing specific auxotrophic strains which were complemented in co-culture experiments by the respective partner. In a long term experimental evolution approach the partners were grown for several generations either under conditions with spatial structure (solid medium) or without (liquid medium). In a first step, we analyzed whether true cooperation evolved by measuring fitness of the bacteria and benefits and costs of the newly evolved interaction.

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SUN 21 AUG at 1630 - Room N3
Oral presentation *A4-Sy05-1630-O*

Symposium 5
Mutualism: Causes and consequences

The impact of mutualistic Wolbachia on manipulating Drosophila development, sexual behavior and infectious speciation

Miller W[1], Schneider D[1], Ehrman L[2]
[1]Medical University of Vienna, Center of Anatomy and Cell Biology, Vienna, Austria, [2]Purchase College, State University of New York, Division of Natural Sciences, Purchase, United States

Summary statement:

Wolbachia can switch easily from obligate mutualism to reproductive parasitism by affecting host fitness and sexual behavior and thereby fostering incipient host speciation.

Abstract:

The Drosophila paulistorum species complex serves a well-studied model system for evaluating the impact of symbiosis on host speciation since they evolve rapidly and comprise an ancestral, but highly dynamic, reservoir of microbial symbionts. Theory and some experimental evidence suggest that in evolutionary long-term host-symbiont interactions, reproductive parasites might evolve a more benign lifestyle towards mutualism, manipulate sexual mating behavior, and foster host speciation. However, it is an ongoing debate as to whether or not microbial symbionts are capable of driving host speciation in nature and if so, to what extent. Prime candidates are Wolbachia, inherited, endosymbiotic bacteria of many arthropods, presently attracting attention as potential biocontrol agents since they affect host reproductive biology.

Here we will document that all D. paulistorum semispecies harbor conspecific but distinctive Wolbachia strains that provide significant fitness benefits such as viability and fecundity to their natural hosts. In semispecies hybrids, however, these naturally obligate mutualists turn into pathogens, triggering embryonic lethality and male sterility. Besides their impact on post-mating isolation, we show that in their native D. paulistorum hosts Wolbachia manipulate sexual behavior by triggering pre-mating isolation via selective mate avoidance, i.e. avoiding mates harboring another, incompatible symbiont variant. Our study reveals that endosymbionts can co-evolve rapidly with their native hosts and play a significant role in host physiology, pheromone expression and sexual behavior, thereby they are capable of driving natural host speciation.

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SUN 21 AUG at 1400 - Room N3
Invited talk *A3-Sy05-1400-I*

Symposium 5
Mutualism: Causes and consequences

Consequences for hosts of symbiont population structure

Moran NA[1]
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Summary statement:

Insect symbioses with bacteria serve many beneficial functions, but have different long-term consequences for hosts, depending on the population structure of the bacteria.

Abstract:

Insects are diverse and use a great variety of terrestrial and fresh water niches, where they encounter many different challenges, including nutritional limitations, threats from various natural enemies, and extreme abiotic conditions. As a group, Bacteria possess many genes and pathways that can help insects to overcome environmental challenges. Thus, it is not so surprising that mutualistic associations between insects and bacteria are extremely widespread. Genomic approaches have revealed many details of these associations in sap-feeding insects such as aphids, revealing mechanisms by which bacterial symbionts assist with host nutrition or with defense against natural enemies. Sequence-based studies have also revealed that genomes of insect symbionts often exhibit signs of degradation and reduction. In fact, the most reduced of all known bacterial genomes are those of insect symbionts, and proteins encoded by the retained genes are predicted to be unstable. At the same time, some bacterial symbionts coevolve with insect hosts without undergoing genome reduction and degradation. These differences can be correlated to the mode of transmission of the symbiont and the imposition of strict clonality in some symbiont lineages and not others. In turn, differences in symbiont life cycles can have long-term consequences for the hosts that evolve dependence on symbiotic partners.

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MON 22 AUG at 1440 - Room N3
Invited talk *B3-Sy05-1400-I*

Symposium 5
Mutualism: Causes and consequences

Dos and Don’ts of elucidating evolution in host-microbe mutualisms

Mueller UG[1]
[1]University of Texas at Austin, Integrative Biology, Austin, United States

Summary statement:

I review strengths and limits of research tools to elucidate host-microbe evolution, drawing largely on examples from the attine ant-microbe symbiosis

Abstract:

Host-microbe research faces unique challenges when elucidating evolution and ecology. For example, the roles of symbiotic microbes are diverse and context-dependent, or the roles change rapidly over evolutionary time; strongly interacting host-microbe associations are sometimes difficult to distinguish from unimportant transient associations, and strong interaction can not readily be inferred from microbe abundance; strongly-interacting hosts and microbes often lack the footprints of evolutionary modification that would implicate co-evolutionary interplay; and in-vivo conditions are generally vastly different from the in-vitro conditions used to test microbial function. I review the strengths and limits of the available research tools used to elucidate host-microbe interactions, drawing largely on examples from the attine ant-microbe symbiosis that channeled that particular field into unproductive research directions. I will try to conclude with some guidelines to prevent overextension of the research tools, such as co-phylogenetic, functional, genomic, metagenomic, and 16S-amplicon 454-sequencing analyses.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy05-i009-R*

Symposium 5
Mutualism: Causes and consequences

Genome sequence of the defensive beewolf symbiont ´Ca. Streptomyces philanthi´

Nechitaylo T[1], Weiss RB[2], Dunn DM[3], Dale C, Kaltenpoth M[1]
[1]Max Planck Institute for Chemical Ecology, Research Group Insect Symbiosis, Jena, Germany, [2]University of Utah, Department of Human Genetics, Salt Lake City, United States, [3]University of Utah, Department of Biology, Salt Lake City, United States

Summary statement:

Genome sequencing of ´Ca. Streptomyces philanthi´ aims to access its genetic traits, evolutionary trajectory and to decipher pathways responsible for the production of antibiotics.

Abstract:

´Candidatus Streptomyces philanthi´ is so far the only known representative of the genus Streptomyces that is intimately associated with an insect host, the European beewolf Philanthus triangulum (Hymenoptera, Crabronidae). These bacteria populate specialized antennal gland reservoirs of female wasps and are transferred to the surface of the larval cocoon. There, the symbiont produces an antibiotic ´cocktail´ consisting of streptochlorin and eight piericidin derivatives and thereby protects the larva from fungal infection. Whole genome sequencing of ´Ca. Streptomyces philanthi´ is the method of choice to access genetic and biochemical traits that enable the symbiotic lifestyle of this bacterium, to estimate its evolutionary trajectory and to decipher biochemical pathways responsible for the production of known and (possibly) novel antibiotics. Genomic DNA was directly sequenced with three methods (Sanger, 454, Illumina) after isolation from beewolf antennal reservoirs. Since ´Ca. Streptomyces philanthi´ is yet uncultured, genome assembling was preceded by binning analysis to sort out contigs of contaminant origin (host or other bacteria). The draft genome of the beewolf symbiont has a total length of 6.5 Mbp with an average GC content of 71.4%. Among the 7000 predicted genes, multiple PKS and NRPS genes were identified that may be involved in the production of antibiotics on the beewolf cocoon. Furthermore, analysis of the whole set of genes may yield insights into nutritional requirements of ´Ca. Streptomyces philanthi´ and thereby allows to isolate it in pure culture.

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SUN 21 AUG at 1610 - Room N3
Oral presentation *A4-Sy05-1610-O*

Symposium 5
Mutualism: Causes and consequences

The carbon rhythm hypothesis: Reconciling the microbial loop and nutrient immobilization concepts

Ovadia O[1], Ben-Yosef U[1], Shemesh H[1]
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Summary statement:

Continuous rhizodeposition can support a constant microbial community that immobilizes nutrients. Intervallic emissions can cause community oscillations and nutrients liberation.

Abstract:

The release of carbonic compounds from plant roots has recently been shown to have diverse effects on soil nutrient cycling. On the one hand, carbon emission has been suggested to increase the amount of available nutrients via the "microbial loop", i.e., increased microbial mineralization followed by protozoa grazing and nutrient liberation. On the other hand, the exudation of carbonic substances from roots has also been suggested to limit nutrient availability for long periods of time due to microbial growth and mineral immobilization. We first present a conceptual model reconciling these two concepts based on the assumption that carbon exudation varies temporally. The model predicts that when carbon is emitted continuously it should support a relatively constant microbial community size, which in turn should immobilize nutrients, assisting slow growing plants to compete with fast growers. On the other hand, an intervallic emission should cause community oscillations, liberating nutrients during microbial community crashes, therefore assisting plants to increase their nutrient availability. We experimentally manipulated the soil carbon dynamics of wheat plants. We show that intervallic dynamics improve plant performance while continuous carbon additions reduce it. These results suggest that carbon dynamics, rather than the sheer amounts of carbon, play an important role in nutrient cycling in the soil and therefore plant performance.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy05-i010-R*

Symposium 5
Mutualism: Causes and consequences

Effect of spatial structure on the spread of cheaters in synthetically designed mutualistic interaction

Pande S[1], Merker H[1], Bohl K[2], Schröter A[2], Kost C[1]
[1]Max Planck for Chemical Ecology, Experimental Ecology and Evolution, Jena, Germany, [2]University of Jena, Department of Bio-Informatics, Jena, Germany

Summary statement:

The degree of spatial structure determines the spread of cheating types and population dynamics of interacting partners therefore affecting stability of mutualistic interactions.

Abstract:

Mutualisms are interspecific interactions, in which both partners derive a fitness benefit. Though mutualisms are ubiquitous their evolutionary stability is difficult to reconcile with natural selection: conflicts of interest are expected to arise whenever organisms direct benefits to non-relatives at their own cost. Such conflicts are predicted to lead to the evolution of cheating types that reap mutualistic benefits without bearing the costs for cooperation, which ultimately should collapse the interaction. Evolutionary theory predicts that spatial structure should limit the selective advantage for cheating and hence stabilize mutualistic interactions. To test this prediction, we designed and genetically engineered synthetic mutualistic interactions between two bacterial species, where both partner species benefit each other by reciprocally providing essential metabolites. In order to classify the interaction as mutualistic we tested and confirmed that
a) The engineered cooperative trait was costly for the acting individuals.
b) When grown together, the interacting partners have a higher growth advantage relative to the monoculture.
Since the arisal of cheating types is expected to be the main evolutionary force leading to instability by eroding the mutualistic interaction, we tested the evolutionary consequences of the introduction of cheaters arising in either a spatially structured (solid medium) or spatially unstructured (liquid medium) environment. By experimentally introducing cheaters in mutualistic populations that grow in either environment, we could identify that the cheaters affect growth dynamics of interacting partners differently in different environments.

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SUN 21 AUG at 1500 - Room N3
Oral presentation *A3-Sy05-1500-O*

Symposium 5
Mutualism: Causes and consequences

Adaptation of parasitoid wasps to protective endosymbionts in aphids under experimental evolution

Rouchet R[1], Vorburger C[1]
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Summary statement:

Parasitoids wasps were able to adapt to the the presence of facultative endosymbionts in their aphid hosts with a strong parasitoid genotype*endosymbiont genotype interaction.

Abstract:

Aphids are associated with several facultative bacterial endosymbionts that may influence their interactions with other organisms. One of this endosymbionts, Hamiltonella defensa, confers high level of resitance to Aphis fabae fabae, the black bean aphid, against its parasitoids. While the aphid-symbiont association is under intensive investigation, little is known about the role of parasitoids in the interaction. This study explores the potential of the main parasitoid of A. fabae fabae, Lysiphlebus fabarum, to adapt to endosymbiont-mediated defence in its host. We used an experimental evolution procedure in wich parasitoids were exposed to a same aphid clone harbouring different strains of H. defensa or H. defensa-free. Parasitoids exposed to H. defensa were able to adapt to its presence over time. Moreover, this adaption comes at costs and was specific to endosymbiont genotype, showing a strong parasitoid genotype*endosymbiont genotype interaction. This experiment emphasised the importance of considering the role of facultative endosymbiont in host-parasite coevolutionary systems.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy05-i011-R*

Symposium 5
Mutualism: Causes and consequences

Specificity and dynamics of the Coriobacterium-Pyrrhocoridae symbiosis

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[1]Max Planck Institute for Chemical Ecology, Insect Symbiosis Research Group, Jena, Germany,
[2]University of Regensburg, Department of Zoology, Regensburg, Germany

Summary statement:

Investigating the specificity of the Coriobacterium-Pyrrhocoridae nutritional symbiosis through a range of manipulation experiments that include symbiont exchange and elimination.

Abstract:

Nutritional symbioses between insects and bacteria are highly prevalent and widespread in nature. Many of these associations are described as mutualisms where the microbial partners improve the fitness of the host by supplying essential nutrients that are absent or at least limiting in the insect's natural diet. The red firebug (Pyrrhocoris apterus) and the African cotton stainer (Dysdercus fasciatus) of the Hemipteran family Pyrrhocoridae harbor actinomycete symbionts of the genus Coriobacterium within the M3 portion of their mid-gut. The bacteria are transmitted vertically via egg-smearing, but horizontal transmission through oral ingestion of feces from adult individuals can also result in infection. By surface sterilization of the eggs, we experimentally generated symbiont-free (aposymbiotic) individuals. These Coriobacterium-free Pyrrhocorids suffered reduced growth rates and higher mortality, indicating that the symbionts contribute significantly to the nutritional upgrading of their insect hosts. Re-application of the microbial community from mid-gut suspensions of conspecific individuals to the egg surface completely restored host fitness. However, when symbiont suspensions of heterospecific hosts were used for re-infection, the fitness of the resulting individuals was intermediate between untreated controls and aposymbiotic bugs. Such findings suggest that the Coriobacterium symbionts have a strong influence on host fitness and development, and that a high degree of specificity exists in this symbiotic association, because individuals infected with heterospecific symbionts show higher mortality and/or prolonged developmental time than those with native symbionts.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy05-i012-R*

Symposium 5
Mutualism: Causes and consequences

Molecular enzymatic adaptations to symbiotic life in leafcutter ants and their fungal symbionts

Schiøtt M[1], De Fine Licht HH[1], Boomsma JJ[1]
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Summary statement:

Recent studies of degradation enzymes using genomics and proteomics methods have given molecular insight into the mutualism between leafcutter ants and their fungal symbionts.

Abstract:

In contrast to the hunter-gatherer lifestyle of most ants, leafcutter ants have changed to a fungal diet derived from the mutualistic gardens that they maintain in their nests on a substrate of fresh plant material. The evolution of this symbiosis must have required significant changes in the physiology of both ants and fungal crops, but precise molecular documentation of such changes has hardly been available. Our research on fungal substrate-degradation enzymes has provided remarkable insights into some of these changes and their potentially adaptive significance for the symbiosis: 1) Enzyme production within fungus gardens resembles a multi-step process reminiscent of organic matter degradation in litter layer ecosystems performed by a series of microorganisms in distinct succession. 2) Whereas most fungal symbionts use metallo-endopeptidases to degrade the plant substrate, a single monophyletic clade of symbionts has shifted to using serine peptidases, perhaps to circumvent anti-herbivore protease inhibitors produced by plants. 3) Several different enzymes produced by the fungal symbiont pass unharmed through the gut of the ants, to end up in the fecal fluid that the ants mix with new plant substrate. The fecal fluid enzyme repertoire appears to resemble the enzyme spectrum used by phytopathogenic fungi for gaining access to live plant tissue, possibly representing a convergent adaptative syndrome for growing on fresh plant material in a fungal clade that otherwise consists of saprotrophic species. These results suggest that modern molecular techniques may be of great value to detect co-evolved adaptations that are difficult to validate with phenotypic studies.

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SUN 21 AUG at 1650 - Room N3
Oral presentation *A4-Sy05-1650-O*

Symposium 5
Mutualism: Causes and consequences

Mutualistic associations of ants: High interspecific tolerance and the evolution of chemical cues and signals

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Summary statement:

Evolutionary changes of cuticular chemistry reduces aggression between partner species in mutualistic ant associations.

Abstract:

Aggression between ant colonies is ubiquitos. However, there are exceptions to this rule - particular Crematogaster and Camponotus species tolerate each other to various degrees and some of these species even live together in mutualistic associations (parabiosis). In order to understand the proximate mechanisms for this unusual tolerance, we studied interspecific nestmate recognition in associated Camponotus and Crematogaster species in the rainforest of Borneo and French-Guyana and in the Mediterranean area. Individuals of the parabiotic ant species in the tropics did not discriminate individuals of their partner colony from individuals of foreign colonies. The cuticular hydrocarbon profile of all investigated parabiotic Camponotus species consists of unusual hydrocarbons with considerably higher molecular mass compared to non-parabiotic Camponotus. We conclude that parabiotic Camponotus species provide less recognition cues by shifting of the cuticular hydrocarbons towards higher chain-length, and thus permit unusual interspecific tolerance between parabiotic partners. Moreover, the parabiotic ant Crematogaster modiglianii from the Bornean rainforest produces high amounts of quite recently identified cuticular substances. In bioassays, these substances significantly reduced the aggressiveness of their partner Camponotus rufifemur. In summary, the high interspecific tolerance seems to be facilitated by the low volatility of long-chain cuticular hydrocarbons in combination with the C. modiglianii specific compounds that reduce aggression in Camponotus.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy05-i013-R*

Symposium 5
Mutualism: Causes and consequences

Selection on floral traits in a deceptive orchid: agents and targets of selection

Sletvold N[1], Ågren J[1]
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Summary statement:

Environmental and phenotypic manipulations reveal pollinator-mediated selection on traits influencing pollinator attraction and pollination efficiency in Dactylorhiza lapponica.

Abstract:

Current selection on floral morphology and phenology has been documented in numerous plant populations, but the agents and targets of selection have only rarely been identified experimentally. We examined the magnitude and mechanisms of selection on floral traits in the severely pollen limited deceptive orchid Dactylorhiza lapponica. We quantified pollinator-mediated selection (Δβpoll) on floral morphology and flowering start by subtracting estimates of selection gradients for plants receiving supplemental hand-pollination from estimates obtained for open-pollinated control plants. In addition, we experimentally manipulated number of flowers and spur length in a factorial design to determine whether these traits directly and independently affect female reproductive success. There was directional selection for taller plants with more flowers and longer spurs, but no statistically significant selection on corolla size or flowering start. Pollinator-mediated selection accounted for all observed selection on spur length (Δβpoll = 0.32), 76% of the selection on plant height (Δβpoll = 0.19), and 42% of the selection on number of flowers (Δβpoll = 0.30). Experimental manipulation demonstrated that number of flowers and spur length directly affect female reproductive success. We conclude that pollinators mediate selection on floral traits likely to influence both pollinator attraction and pollination efficiency. Our results are consistent with the hypothesis that deceptive species experience strong selection for increased display and mechanical fit between flower and pollinator.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy05-i014-R*

Symposium 5
Mutualism: Causes and consequences

Composition and evolutionary history of the bacterial community in the mid-gut of firebugs (Hemiptera, Pyrrhocoridae)

Sudakaran S[1], Kost C[2], Kaltenpoth M[1]
[1]Max Planck Institute of Chemical Ecology, Max Planck Research Group Insect Symbiosis, Jena, Germany, [2]Max Planck Institute of Chemical Ecology, VW Research Group Experimental Evolution, Jena, Germany

Summary statement:

Symbiotic microbiota of P. apterus is vital for its fitness and other Pyrrhocoridae species harbor similar microbiota suggesting that the microbiota has co-evolved with the hosts.

Abstract:

Symbiotic bacteria play a pivotal role in providing essential nutrients to insects and thereby allow them to exploit novel food sources and expand into otherwise inaccessible ecological niches. The Pyrrhocoridae are a family of land bugs that comprises about 300 species, which predominantly feed on the dry seeds of plants in the order Malvales. Previous studies on Pyrrhocoris apterus revealed the presence of a specific actinobacterial symbiont (Coriobacterium glomerans) in the mid-gut that is vertically transmitted and seems to be essential for growth and reproduction of the bugs. However, little is known about its whole symbiotic microbial community and the function of the symbionts. In this project, we characterized the microbiota of P. apterus from different geographical regions as well as that of several other Pyrrhocorid bug species using bacterial tag-encoded FLX 454 amplicon pyrosequencing (bTEFAP). The analyses revealed that the gut microbial community of P. apterus mainly consists of facultative and obligate anaerobes such as Clostridium, Coriobacterium, Eggerthella, Enterobacter and Lactococcus. Notably, members of the Coriobacteriaceae family are very unusual gut residents, and the co-occurrence of Eggerthella and Coriobacterium is unique among insects. The P. apterus microbiota is very stable across geographical locations, suggesting that it plays an important role for the fitness of the host. Furthermore, our results show that other species of the family Pyrrhocoridae harbor similar symbiotic microbial communities, suggesting that the complex microbiota has co-evolved with the hosts over millions of years.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy05-i015-R*

Symposium 5
Mutualism: Causes and consequences

Specificity, costs and benefits of symbiont-conferred resistance in aphids

Vorburger C[1], Gouskov A[2], Schmid M[3]
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Summary statement:

Genetic specificity characterises benefits (inreased resistance to parasitoids) and costs (reduced lifespan) of harbouring the bacterial endosymbiont Hamiltonella defensa in aphids

Abstract:

Maternally transmitted symbionts may spread in host populations if they provide a fitness benefit to their hosts. Hamiltonella defensa, a bacterial endosymbiont of aphids, protects hosts against parasitoids yet occurs only at moderate frequencies in aphid populations. This suggests that harbouring this symbiont is also associated with costs. Using experimentally infected lines with the same genetic background, we tested for the occurrence of such costs in the black bean aphid, Aphis fabae. We found that H. defensa had little effect on reproductive traits but strongly shortened the lifespan of its host, resulting in a significant reduction of lifetime reproduction. Interestingly, the magnitude of this cost was determined by genotype-by-genotype interactions between host and symbiont: different aphid genotypes were unequally affected by different isolates of H. defensa. In contrast, the benefits of harbouring H. defensa depended less on the host´s genetic background than on the genotypes of attacking parasitoids. Significant interactions between H. defensa isolates and parasitoid genotypes indicated a high specificity of symbiont-conferred resistance. Together, these findings imply a highly dynamical system of coevolutionary interactions between the interacting species, which may help explain the coexistence of aphids with and without H. defensa in natural populations.

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Symposium 6

Speciation by natural versus sexual selection

Talks: *Room N5*

***Essence posters**:* Ground floor lecture hall centre *HZ*

***Regular posters**:* Upper floor campus canteen *Mensa*

Invited Speakers:

Andrew Hendry, Maria Servedio, Martine Maan, Erik Svensson

Organizers:

Allan Debelle, Claudius Kerth

Description:

This symposium is organized on behalf of the ESF Frontiers of Speciation Research 'FroSpects' by the Marie Curie Initial Training Network 'SPECIATION'. We will examine the relative contribution of natural and sexual selection to the speciation process. We are particularly interested in addressing the question of whether the action of natural selection is pervasive in speciation involving sexual selection, or whether these two sources of selection can act independently to drive speciation.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy06-i001-R*

Symposium 6
Speciation by natural versus sexual selection

Incipient reproductive isolation between subspecies of Arabidopsis lyrata

Aalto EA[1], Virtanen A[1], Savolainen O[1]
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Summary statement:

We mapped four loci causing pollen sterility in hybrids between subspecies of A. lyrata diverged about 30 000 gen. ago. One of these loci is involved in cytoplasmic male sterility.

Abstract:

What are the genes involved in speciation and how do they evolve is a question without complete answer yet. We have studied post zygotic genic incompatibilities, for which to form a simple model was presented independently by Bateson, Dobzhansky and Muller in the beginning of the 20th century. Lyrate Rockcress (Arabidopsis lyrata) is an ideal model species to study how these BDM incompatibilities evolve in different time scales. In earlier studies (Leppälä 2011) incipient post zygotic reproductive isolation was observed between European and North American subspecies of A. lyrata, which have diverged about 30 000 generations ago. We crossed two populations from these different subspecies and grew over 2000 F2 plants in greenhouse in Oulu botanical gardens. The crosses were made reciprocally to see cytoplasmic effects. There was a striking difference between the reciprocal crosses. When the cytoplasm came from the European subspecies almost one fourth of the F2 plants did not produce any pollen, but this was not observed in their siblings containing cytoplasm from North American subspecies. We mapped the major locus causing the CMS to a 180 kb interval at the top of the chromosome 2 in a region containing a cluster of PPR genes. These genes are known to be involved in conflict between nuclear and mitochondrial genomes. In addition we found three other loci having highly significant effect on pollen fertility. We conclude that several different mechanisms causing incipient reproductive isolation have arisen during 30 000 generations of allopatric isolation. The role of drift and natural selection in the evolution of these genes remains to be studied.

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WED 24 AUG at 1140 - Room N5
Oral presentation *D2-Sy06-1140-O*

Symposium 6
Speciation by natural versus sexual selection

Landscape dynamics as a mechanism to explain radiations

Aguilée R[1], Claessen D[2], Lambert A[3]
[1]Université Montpellier II, CNRS UMR 5554, Montpellier, France, [2]Ecole Normale Supérieure, Laboratoire Ecologie et Evolution UMR 7625, Paris, France, [3]UPMC Univ Paris 6, Laboratoire Probabilités et Modèles Aléatoires, Paris, France

Summary statement:

We show with a model based on the cichlids of the African Lakes that allopatry-sympatry oscillations may promote speciation, leading to a radiation.

Abstract:

Species radiations have been explained assuming either a great diversity of habitats, or sympatric diversification under rather special conditions (e.g. few loci determining phenotypic traits). We propose a new scenario based on the biogeographic changes of the Great African Lakes. In our model, the landscape consists of a mosaic of three habitat types which may be separated by geographic barriers or not. We study the effect of the alternation of allopatry and sympatry, called "landscape dynamics", using a stochastic, individual-based model. We show that under disruptive selection, such landscape dynamics generate a radiation despite a small number of habitat types and despite inheritance rules impeding sympatric speciation. Diversity is generated by the joint action of allopatric, ecological divergence driven by natural selection, and of disruptive, sexual selection in sympatry, allowing for the coexistence of species following reinforcement or character displacement. Landscape dynamics provoke these and other evolutionary mechanisms (hybridization, evolutionary branching, and extinction) in different combinations, possibly increasing diversity at each landscape change. In this scenario, both natural and sexual selection are essential to successful, complete speciation. We find that diversity in each local site is significantly higher than the total number of differentiated habitats, and also higher than the level of diversity reached by sympatric diversification only. Time scales of the landscape dynamics are the main determinant of the features of the radiation (tempo of diversification, asymptotic level of local and total diversity).

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy06-i002-R*

Symposium 6
Speciation by natural versus sexual selection

MHC-independent olfactory cues and assortative mating in the three-spined stickleback

Andreou D[1], Milinski M[1]
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Summary statement:

Disentangling the potential role of the MHC and other olfactory signals in assortative mating using three-spined sticklebacks.

Abstract:

Female mate choice for sympatric males can accelerate population divergence and the process of speciation. Sympatric ecotypes of three-spined sticklebacks have been described from a wide range of geographical locations making this species a suitable model for investigating the role of sexual selection in speciation. In northern Germany, adjoining river and lake three-spined stickleback populations show population divergence in both neutral DNA markers and Major Histocompatibility Complex (MHC) loci. Previous work has demonstrated that female sticklebacks use self-reference and chose mates in order to optimise the number of MHC loci in their offspring. However, MHC ligand peptides need to be validated by an additional MHC-independent signal in order to be recognized and be used in mate choice. This validation signal is released by male sticklebacks in early spring before the MHC-signal is added. Assortative mating based on olfactory cues has been demonstrated in the northern Germany river-lake ecotypes suggesting the possible role of the pleiotropic MHC genes in sexual selection. However, in this work the full olfactory signal was used which at a minimum includes the validation factor and MHC ligands. In order to disentangle the potential role of the MHC and other olfactory signals in assortative mating and preference for sympatric males we investigated the role of the validation signal in female mate choice.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy06-i003-R*

Symposium 6
Speciation by natural versus sexual selection

Origin and maintenance of Dobzhansky-Muller incompatibilities in the presence of gene flow

Bank C[1,2], Bürger R[3], Hermisson J[2,3]
[1]Vetmeduni Vienna, Institut für Populationsgenetik, Vienna, Austria, [2]Max F. Perutz Laboratories, Mathematics and BioSciences Group, Vienna, Austria, [3]University of Vienna, Department of Mathematics, Vienna, Austria

Summary statement:

Using migration-selection models, we derive the limiting rates of gene flow allowing for ecological and mutation-order speciation via evolution of adaptive incompatibilities.

Abstract:

Recently, there has been put forward a classification of speciation by natural selection. According to Schluter (Science, 2009), “ecological speciation” happens when a heterogeneous environment drives the evolution of postzygotic isolation irrespective of the evolutionary history, while “mutation-order speciation” occurs when different globally adaptive substitutions spread in diverging subpopulations due to the spatial-temporal pattern. Here, we use a classical two-locus migration-selection model in order to analyze the conditions in which a Dobzhansky-Muller incompatibility (DMI) can emerge according to these scenarios. We obtain analytical and numerical results for the limiting effective rates of gene flow that allow for origin and maintenance of a DMI in haploid and diploid populations on an island that receives migrants from a continent, depending on the strength of adaptation, epistasis, recombination, and the evolutionary history. Our results demonstrate that ecological speciation is not restricted to the accumulation of locally adapted substitutions. We claim that the distinction between ecological and mutation-order speciation cannot be based exclusively on the shape of the fitness landscape, but is crucially dependent on the amount of gene flow between the diverging populations, and the linkage between the incompatibility loci. For the diploid model, we predict that the relevance of ecological versus mutation-order speciation is particularly dependent on the architecture of epistasis. In general, the limiting rate of gene flow does never exceed the order of the selective advantage of the substitution.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy06-i004-R*

Symposium 6
Speciation by natural versus sexual selection

What drives speciation: strong sexual selection, divergent sexual selection, or natural selection?

Boughman JW[1], Head ML[2]
[1]Michigan State University, Zoology, East Lansing, United States, [2]University of Exeter, BioSciences, Cornwall, United Kingdom

Summary statement:

Comparative methods are used to test whether sexual selection is responsible for speciation in diverse taxa, comparing forms of sexual selection and natural selection.

Abstract:

Elegant case studies tell us that sexual selection can cause speciation. Yet, these studies cannot tell us whether sexual selection is a primary process generating new species across taxa; only that it can do so in some cases. We use a comparative approach to circumvent this problem, amassing data for hundreds of pairs of taxa. We estimate the strength of sexual selection within species and the extent to which it differs between species, considering mating traits from different modalities. We also estimate the extent of divergence in naturally selected traits to compare to the sexually selected traits. We then ask whether the strength of sexual selection or the extent to which it diverges between species best predicts the strength of reproductive isolation. We also consider whether male competition contributes to isolation in addition to female choice, and the relative importance of sexual and natural selection. Our methods allow us to separate the effects of sexual and natural selection, and to control the effects of time. We show that sexual selection is a powerful driver of speciation across taxa. A key finding is that species differences in sexual selection predict the extent of reproductive isolation better than the opportunity or strength of sexual selection within species. We also find that traits specifically involved in conspecific mate recognition are more strongly associated with reproductive isolation than dimorphism itself. Our results suggest that the presence of sexual selection may not be enough to cause reproductive isolation, even if it is strong. Sexual selection needs to be divergent to cause new species to form.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy06-i005-R*

Symposium 6
Speciation by natural versus sexual selection

Polyandry decreases the potential role of sexual selection in speciation

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Summary statement:

This study reveals that polyandry decreases the potential for sexual selection to drive speciation.

Abstract:

Polyandry –female mating with multiple males- is a ubiquitous feature of sex that prolongs sexual selection after copulation. However, consequences of polyandry on sexual selection and speciation remain unclear. Polyandry can simultaneously (i) create male alternative strategies, thus driving reproductive isolation and (ii) increase the number of males in the effective population, lowering sexual selection and its role in speciation. We address these fundamental issues by combining detailed observations of mating behaviour with parentage data in replicate populations of red junglefowl, Gallus gallus. We show experimentally that polyandry had a drastic impact on male sexual selection. While the intensity of postcopulatory sexual selection was unaffected by the degree of polyandry of a population, precopulatory sexual selection was weaker in more polyandrous groups. Therefore, polyandry reduced the overall intensity of sexual selection while increasing the relative importance of postcopulatory sexual selection. Importantly, more polyandry across populations resulted in an overall weaker selection for male social status, a trait that mediates access to mating, through alternative mechanisms. When polyandry was low, status was selected mainly because dominant males had more mates, while in more polyandrous populations, sexual selection for status was largely limited to after copulation, as dominants would mate multiply with the same females and defend better their paternity. Taken together, these results reveal the previously unappreciated complex relationship between polyandry and sexual selection that leads to a lower potential for sexual selection to drive speciation.

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TUE 23 AUG at 1630 - Room N5
Oral presentation *C4-Sy06-1630-O*

Symposium 6
Speciation by natural versus sexual selection

Does sexual selection helps to maintain hybridizing large white-headed gull species distinct? A comparison between traits and markers

Crochet P-A[1], Lenormand T[1], Bell DA[2], Neubauer G[3], Zagalska-Neubauer M[3], Pons J-M[4], Gay L[1,5]
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Summary statement:

Natural and sexual selection were involved in speciation in gulls, but mate choice traits contributed most to reproductive isolation, indicating the importance of sexual selection.

Abstract:

The action of selection is difficult to measure directly on long-lived, large bodied species. An alternative to direct approaches is to infer the past action of selection by comparing patterns of differentiation between phenotypic traits and neutral markers.

Even if earlier claims of ring speciation have been rejected by recent studies, large white-headed gulls remain a classical example of recent avian speciation that is further characterized by a high incidence of hybridization.

We took advantage of this situation to examine the effects of selection on speciation at two evolutionary time scales. Firstly, we tested whether phenotypic traits were more divergent than neutral markers between species, thus investigating the past contribution of selection to phenotypic divergence. Secondly, we tested which traits were involved in reproductive isolation by comparing phenotypic variances in hybrid zones. We used two independent hybrid zones to increase the generality of our findings.

In both hybrid zones and in both species pairs, selection shaped phenotypic divergence and currently helps to keep the species distinct. It was more difficult to disentangle the actions of sexual and natural selection. However, based on previously published results, traits can be separated between those a priori involved in mate choice and sexual selection, and those a priori shaped by natural selection. Both types of traits showed the action of past selection, but traits linked to mate choice were more strongly involved in reproductive isolation in hybrid zones, adding to a growing number of studies pointing at the importance of sexual selection in avian speciation.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy06-i006-R*

Symposium 6
Speciation by natural versus sexual selection

The role of sexual selection in the evolution of reproductive isolation in Drosophila pseudoobscura

Debelle A[1], Hoikkala A[2], Ritchie MG[3], Snook RR[1]
[1]University of Sheffield, APS, Sheffield, United Kingdom, [2]University of jyväskylä, Jyvaskyla, United Kingdom, [3]University of St Andrews, School of Biology, St Andrews, United Kingdom

Summary statement:

The role of sexual selection in the evolution of reproductive isolation in Drosophila pseudoobscura.

Abstract:

Sexual selection has the potential to be a speciation driver due to population divergence in male signals and female preferences, but we are still lacking conclusive direct evidence for its importance in the speciation process. A promising approach to directly estimate the action of sexual selection on population divergence and the emergence of reproductive barriers is experimental evolution. We subjected populations of Drosophila pseudoobscura, a naturally promiscuous species, to two treatments: enforced monogamy (M) and elevated promiscuity (E). After more than 100 generations of experimental sexual selection, we tested for assortative mating between the treatments using a female choice design. The results showed that E males have a higher likelihood of mating with both E and M females compared to M males. We also found that M males had to court E females for a longer time to elicit copulation than E males. Modifying the level of sexual selection also significantly changed a male signal: aspects of courtship song showed rapid divergence between the treatments. In the future, we will investigate whether the higher mating success of E males is due to a change in male sexual signals and their impact on female preference.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy06-i001-E*

Symposium 6
Speciation by natural versus sexual selection

Variation in potential prezygotic isolating traits in Nasonia parasitoid wasps

Diao W[1], Schmitt T[2], Ritchie M[3], van de Zande L[1], Beukeboom L[1]
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[2]Univesity of Freiburg, Department of Evolutionary Biology and Animal Ecology, Freiburg, Germany,
[3]University of St. Andrews, School of Biology, St. Andrews, Scotland, United Kingdom

Summary statement:

My project focus on genetics and genomics of prezygotic isolation in Nasonia aiming to uncover genetic architecture of reproductive isolation.

Abstract:

Mate discrimination is one of the most important forms of prezygotic isolation. Divergence of male courtship behaviour and associated female preference are the most studied mechanisms of premating prezygotic isolation between closely related species in sympatric populations. Variation in male courtship behavior within a species may enable females to identify and choose the fittest mate, whereas variation in courtship behavior between species may help females to identify conspecific males and prevent costly interspecific matings. In the Nasonia species complex differences in mating behaviour and pheromones, including cuticular hydrocarbons (CHCs), and male song (wing vibration) appear to be most important in causing prezygotic isolation between species. We show the within and between species variation in these traits as well as approaches to unravel the genetic architecture of these traits.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy06-i007-R*

Symposium 6
Speciation by natural versus sexual selection

Speciation insights from a candidate gene approach: Chemosensory genes in the pea aphid

Duvaux L[1], Smadja C[2], Ferrari J[3], Zhou J-J[4], Butlin R[1]
[1]University of Sheffield, Animal and Plant Sciences, Sheffield, United Kingdom, [2]Université de Montpellier 2, Institut des Sciences de l'Evolution, Montpellier, France, [3]University of York, Department of Biology, York, United Kingdom, [4]Rothamsted Research, Harpenden, United Kingdom

Summary statement:

We analysed 200 pea aphid chemosensory genes to determine the role of natural selection and detect loci associated with the initiation of reproductive isolation between races.

Abstract:

The process of speciation involves the progressive evolution of reproductive isolation between divergent populations. When this process happens in the face of gene flow, differentiation is expected to be variable across the genome reflecting the direct operation of natural selection and the barrier created for regions surrounding selected loci. Although population genomics and QTL mapping approaches have recently contributed to detecting regions under selection and associated islands of differentiation, we argue that a candidate gene approach can advance this field even further. Since many insects use chemical cues to recognise host plants and because divergence in host plant recognition is an essential step in host race formation, chemosensory genes are good candidates to play a key role in prezygotic isolation. To address this prediction, the pea aphid system is unique in having multiple races at different levels of divergence, excellent background information and a sequenced genome. Here, we used Nimblegen capture arrays and Solexa sequencing to study sequence divergence for more than 200 chemosensory genes and 20 control genes in 8 host races of the pea aphid. Finally, we used an Approximate Bayesian Computation (ABC) framework and various selection tests to detect loci i) with significantly less gene flow between races than the mean of the genome and so probably implicated in isolation between races for some time, and/or ii) having likely evolved under positive selection which might be related to the high degree of ecological specialisation of this species.

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WED 24 AUG at 1120 - Room N5
Oral presentation *D2-Sy06-1120-O*

Symposium 6
Speciation by natural versus sexual selection

Mode of evolution of parallel phenotypes in monomorphic African cichlid species

Gante H[1], De Maddalena J[1], Salzburger W[1]
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Summary statement:

Analysis of sexually- and ecologically-relevant phenotypes across closely-related African cichlids to understand the mechanisms responsible for species divergence.

Abstract:

Analysis of sexually- and ecologically-relevant phenotypes across closely-related animal species can provide insight into the mechanisms responsible for species divergence. We use a comparative approach to elucidate the importance of coloration (a likely target for selection during mate choice and species recognition) and body shape (a correlate of ecological adaptation and niche partitioning) in the evolution of a group of monomorphic cichlid species from Lake Tanganyika, East Africa, the tribe Lamprologini. We place special emphasis in the Neolamprologus brichardi/pulcher species complex, from which robust phylogenies based on multiple nuclear genes were generated. Contrary to previous expectations of drivers of speciation in species lacking sexual dimorphism, we find multiple cases of repeated (parallel) evolution of several coloration phenotypes. We discuss these results in light of theoretical expectations and which source of selection is most likely driving speciation in these organisms.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy06-i002-E*

Symposium 6
Speciation by natural versus sexual selection

Genetics of reproductive behaviour in Nasonia

Giesbers M[1], Pannebakker BA[1], van de Zande L[1], Beukeboom LW[1]
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Summary statement:

Using artificial selection and quantitative genetics we aim to identify the genetic architecture of two reproductive behavioural traits in the Nasonia complex.

Abstract:

Mating behaviour is an important prezygotic isolating factor but its genetic basis is still poorly known. We use the Nasonia genus of parasitoid wasps to study the genetic architecture of prezygotic isolation. In this study we focus on three Nasonia species that occur in micro-sympatry in Eastern North America: N. vitripennis is a cosmopolitan species that parasitizes several fly species. N. giraulti and N. oneida occur in Eastern North America and specialize on pupae of blowflies (Protocalliphora) commonly found in bird nests. These species are reproductively isolated due to infection with species-specific strains of Wolbachia that cause cystoplasmic incompatibility. In the area of sympatry pre-zygotic isolation mechanisms might have evolved through reinforcement to prevent costly hybridization in nature. Indeed, the species differ in male courtship behaviour but this may not be sufficient to prevent interspecific matings. N. vitripennis and N. oneida females show high mate discrimination against heterospecific males, but N. giraulti females do not. N. giraulti typically shows within-host mating whereas the other two species mate after emergence. Within host mating may have evolved to prevent interspecific hybridization. We analysed the genetic architecture of interspecific mate discrimination and within host mating using hybridization experiments, artificial selection and quantitative genetics in order to identify the genes responsible of for these traits.

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WED 24 AUG at 1010 - Room N5
Oral presentation *D1-Sy06-1010-O*

Symposium 6
Speciation by natural versus sexual selection

Influence of natural and sexual selection on phenotypic divergence during the Tanganyikan cichlid radiation

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[1]Estación Biológica de Doñana, Integrative Ecology, Sevilla, Spain, [2]Kyoto University, Faculty of Agriculture, Kyoto, Japan, [3]Uppsala University, EBC, Population Biology, Uppsala, Sweden, [4]Uppsala University, EBC, Animal Ecology, Uppsala, Sweden

Summary statement:

Ecological characters and sexual traits presented different patterns of evolution; results suggest divergence late in the radiation is more strongly influenced by sexual selection.

Abstract:

Theory suggests sexual traits evolve faster than ecological characters. However, characteristics of a species niche may also influence evolution of sexual traits. Hence, a pending question is whether ecological characters and sexual traits present similar temporal dynamics of evolution during periods of rapid ecological divergence, such as adaptive radiation. We first analyzed whether characteristics of a species niche were associated with the evolution of sexual dimorphism in size, colour and shape. We then analyzed the rate of phenotypic evolution and historical pattern of phenotypic divergence for ecological characters and sexual traits. Our results indicate that different ecological characteristics influence the evolution of sexual dimorphism. Furthermore, although correlated, ecological characters and sexual traits present different patterns of evolution. Closely related species presented higher disparity in sexual traits than ecological characters and sexual traits were under stronger selection than ecological characters. Our results indicate that disparity in ecological characters was concentrated early in the radiation, in line with speciation linked to ecological specialization. While disparity in sexual traits remained high throughout the radiation, suggesting divergence late in the radiation is possibly more strongly influenced by sexual selection.

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TUE 23 AUG at 1710 - Room N5
Oral presentation *C4-Sy06-1710-O*

Symposium 6
Speciation by natural versus sexual selection

Natural versus sexual selection in moth sexual attraction

Groot AT[1,2], Barthel A[1], Karpinski A[1], Blanco C[3], Heckel DG[1], Vogel H[1]
[1]Max Planck Institute for Chemical Ecology, Entomology, Jena, Germany, [2]University of Amsterdam, IBED, Amsterdam, Netherlands, [3]USDA-APHIS, Biotechnology Regulatory Services, Riverdale, United States

Summary statement:

Speciation, Lepidoptera, Noctuidae, co-evolution

Abstract:

In moths, sexual attraction is a strong and well-defined prezygotic isolation barrier: females produce a species-specific sex pheromone that attracts males from a distance. Since in moths female signals and male response are governed by independently assorting genes, it is still a mystery of how moth signal and response may co-evolve. Our research focuses on the intraspecific variation of the female sex pheromones and the causes and consequences that this variation may have on the sexual attraction in males. One hypothesis is that environmental factors (interfering species, stress) may affect signal and response in the same direction. So far we have found that host plants may indirectly affect the sex pheromone composition, and with that sexual attraction of females, not because plant compounds are pheromone precursors but more likely because some plants may cause more stress in the larval stage than others. Stress factors may include low nutritional quality, (toxic) secondary plant metabolites and pathogens. Different moth populations may become differentially adapted to these stress factors, thus undergoing natural selection. Preliminary experiments indicate that genes involved in the pheromone biosynthetic pathway are differentially affected by some stress factors. If male response genes are affected in a similar way, sexual selection in moths may be affected by natural selection.

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TUE 23 AUG at 1440 - Room N5
Oral presentation *C3-Sy06-1440-O*

Symposium 6
Speciation by natural versus sexual selection

Pollinator-driven speciation in heterostylous plants: an individual-based model incorporating floral morphology, pollinator traits, and spatial effects

Haller BC[1], de Vos J[2], Keller B[2], Conti E[2]
[1]McGill University, Redpath Museum, Montreal, Canada, [2]University of Zürich, Institute of Systematic Botany, Zürich, Switzerland

Summary statement:

Using a spatial individual-based model, we explore the consequences of heterostyly, a floral morphological trait, for reproductive isolation, ecological divergence, and speciation.

Abstract:

The remarkable diversity of the angiosperms has often been attributed, at least in part, to their coevolution with pollinators. We model the interesting floral polymorphism “heterostyly,” which involves reciprocal inter-morph reproductive organ positioning coupled with intra-morph genetic incompatibility. This trait might promote speciation through pollinator-mediated mechanisms entailing both natural and sexual selection. Evidence for this assertion comes from the observation that some heterostylous clades (e.g. Primulaceae, Turneraceae) are more speciose than their non-heterostylous sister clades. We test whether this difference might be due to the opportunity provided by heterostyly for reproductive isolation between diverging lineages with differing reproductive organ positions (sexual selection), in combination with divergent selection on reproductive organ position caused by pollinator traits (natural selection). We hypothesize that heterostyly can be viewed as a “magic trait” governing both fitness and reproductive isolation, and further, that its degree of “magicness” (i.e. the balance between natural selection and sexual selection) may vary depending on both pollinator and floral traits. We investigate this interplay between natural and sexual selection using an individual-based evolutionary model of heterostylous plants in a mixed pollinator milieu. Effects due to space are considered and the dynamics of the model are contrasted between spatial contexts, with reference to reinforcement theory, character displacement, and ecological speciation.

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WED 24 AUG at 0930 - Room N5
Oral presentation *D1-Sy06-0930-O*

Symposium 6
Speciation by natural versus sexual selection

Ecological adaptation and life history divergence lead to changes in female-choice based sexual selection between allopatric populations of Drosophila mojavensis

Havens JA[1]
[1]University of Arkansas, Biological Sciences, Fayetteville, United States

Summary statement:

Host plant adaptation leads to divergence in life history traits and within-population mate communication systems in allopatric populations of Drosophila mojavensis.

Abstract:

Ecological adaptation has influenced life history divergence between allopatric populations of cactophilic Drosophila mojavensis, leading to premating isolation. Life history traits are genetically correlated with courtship signals that display G x E interactions caused by different cactus-rearing environments. Phenotypic plasticity of courtship traits has led to divergence in male-female communication systems, influencing the outcome of 'good-genes' sexual selection within populations. Cuticular hydrocarbons (CHCs), contact pheromones that mediate courtship within and between allopatric populations, are genetically correlated with egg-to-adult development time. Female discrimination of males leads to decreased offspring egg-to-adult development time in derived populations, particularly when reared on the host cactus that has been implicated in causing longer development times in nature. Thus, natural and sexual selection act antagonistically on this life-history trait. Different CHC components determined male mating success within each population, and there was a greater influence of host cactus on CHC mediated female discrimination in the derived population. Therefore, host cactus use causes changes in both CHC mediated courtship and the consequences of sexual selection between populations. Differences in sexual selection and divergence in life history traits due to host plant adaptation indicate that both sexual and natural selection interact to drive the formation of reproductive isolation. Further studies should examine the genetic basis of female preference as well as other male sexual traits to assess how G x Es influence coevolution between the two.

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TUE 23 AUG at 1550 - Room N5
Invited talk *C4-Sy06-1550-I*

Symposium 6
Speciation by natural versus sexual selection

The interplay between natural selection, sexual selection, and geography in the evolution of mating isolation in guppies

Hendry A[1]
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Summary statement:

Trinidadian guppies provide a good example of how natural selection, sexual selection, and geography all interact to influence progress toward ecological speciation.

Abstract:

Divergent natural selection is expected to promote the evolution of mating isolation: i.e., ecological speciation. In some natural systems, however, this process may be constrained by conserved sexual selection to an extent that depends on the geographic context. I will discuss the results of theoretical models, as well as laboratory and field experiments with Trinidadian guppies, that disentangle these interactions. We find that divergent natural selection favors the divergence of male mating signals. Sexual selection based on female choice is, however, conserved to some extent among environments, which implies that adaptive divergence might not promote symmetric mating isolation. However, we also find that mate choice evolves such that females disfavor immigrant males from parapatric populations of the opposite predation regime but not allopatric populations of the opposite predation regime. Thus, divergent selection promotes ecological speciation and sexual selection constrains it - except when the geographic context leads to direct selection against mating with the opposite type. In short, natural selection, sexual selection, and the geographic context all interact to determin progress toward ecological speciation.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy06-i003-E*

Symposium 6
Speciation by natural versus sexual selection

Ecological and life history consequences of shifts in polyandry across diverse dance fly mating systems

Herridge EJ[1]
[1]University of Stirling, School of Natural Sciences, Stirling, United Kingdom

Summary statement:

Ecological and life history consequences of shifts in polyandry across diverse dance fly mating systems.

Abstract:

Sexual selection in females is fairly common but female-specific ornamentation is rare. Sexually selected traits are thought to represent a diversion of resources away from other life history traits, and it has been suggested that if ornamentation in a female comes at a cost to fecundity it would undermine the benefits of male mate choice. Females in many species of dance flies have lost the ability to hunt and receive all their dietary protein through the procurement of nuptial gifts. In some lineages, competition for male donations has caused sex-role reversal, and females have developed elaborate ornaments to improve their attractiveness to choosy males. The development and maintenance of ornaments is known to increase predation risk in at least one species and may also come at a cost to female fecundity. To investigate the role of sexual selection in demography, and in particular the demographic consequences of shifts in polyandry across diverse dance fly mating systems, we assessed the covariance between measures of sexual dimorphism in dance flies and demographic parameters that could be associated with local extinction risk.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy06-i004-E*

Symposium 6
Speciation by natural versus sexual selection

Exploration of commensal (Mus musculus domesticus) and aboriginal (Mus spretus) mice

Hiadlovská Z[1,2], Vošlajerová Bímová B[1,3], Macholán M[1,2]
[1]IAPG AS CR v.v.i, Laboratory of Mammalian Evolutionary Genetics, Brno, Czech Republic, [2]Masaryk University, Faculty of Science, Brno, Czech Republic, [3]IVB AS CR v.v.i., Department of Population Biology, Brno, Czech Republic

Summary statement:

Exploration strategy in commensal (Mus musculus domesticus) and aboriginal (Mus spretus) mice as an adaptation to enclosed vs. open habitats.

Abstract:

Exploration includes investigation of unknown areas, where it is vital to accurately assess potential danger. Consequently, exploration should be under a direct influence of selection. Given their different ecologies, commensal Mus musculus and wild living ('aboriginal') Mus spretus should differ in their life styles and hence in various behavioral characteristics. This study compares exploratory behaviour of two wild-derived inbred strains representing both species and test whether observed differences reflect their ecological adaptations. Altogether, 30 males, 15 of each strain (STRA, representing M. m. domesticus, and SMON, representing M. spretus), were tested using a standard Open field test. Our results reveal differences in explorative strategies between the two species with M. spretus males being more prone to enter the open field arena where they display more self-confident explorative behaviour than M. m. domesticus males. We conclude that the observed phenotype is probably a part of their adaptation to open natural habitats.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy06-i005-E*

Symposium 6
Speciation by natural versus sexual selection

Contrasting patterns of molecular evolution of the Z chromosome and autosomes in flycatchers: Differential introgression or the faster-Z effect?

Hogner S[1,2], Sæther SA[2], Borge T[2], Bruvik T[2], Johnsen A[1], Sætre G-P[2]
[1]University of Oslo, Natural History Museum, Oslo, Norway, [2]University of Oslo, Centre for Ecological and Evolutionary Synthesis, Oslo, Norway

Summary statement:

We show that contrasting patterns of molecular evolution of the Z chromosome and autosomes are best explained by faster adaptive evolution on the Z chromosome in Ficedula species.

Abstract:

Recent multi-locus studies in congeneric birds have shown a pattern of elevated interspecific divergence on the Z chromosome compared to the autosomes. In contrast, pairs of species exhibit less polymorphism (and less shared polymorphism) on the Z chromosome relative to the autosomes. Under neutrality, the ratio of effective population size between Z-linked and autosomal loci, and hence the degree of nucleotide variation, is expected to be 3:4. However, several studies have found significantly lower ratios. This may be explained by faster adaptive evolution on Z, because recessive beneficial mutations are not masked by dominance in the heterogametic sex. Likewise, recessive deleterious mutations would be more effectively purged on the Z due to hemizygous exposure. Associated selective sweeps on the Z chromosome would contribute to further reduce intraspecific polymorphism. Alternatively, accumulation of incompatibilities on the Z chromosome (Haldane's rule) may reduce the rate of introgression of Z-linked compared to autosomal genes and produce the same pattern as predicted by the faster-Z hypothesis. Here, we show that the four black-and-white Ficedula flycatchers show greater divergence on the Z chromosome than on the autosomes, and that their Z:A ratios are below 75%. Furthermore, we found more fixed substitutions and fewer shared polymorphisms on the Z chromosome than on the autosomes. Finally, using isolation with migration models, we estimated gene flow and divergence times among the four closely related flycatchers. Our results are best explained by the faster-Z hypothesis since the estimated migration parameters were close to zero in most pairwise comparisons.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy06-i006-E*

Symposium 6
Speciation by natural versus sexual selection

What's wrong with grasshopper sex? Hybrid Sterility in the meadow grasshopper Chorthippus parallelus.

Hutchison JD[1], Butlin RK[1]
[1]University of Sheffield, Animal Plant Sciences, Sheffield, United Kingdom

Summary statement:

Utilising behavioural and genetic techniques to gain insight into barriers to gene flow between two sub species.

Abstract:

Identifying the loci involved in hybrid incompatibilities is a broad goal of speciation research. By identifying the functional classes of genes and the specific forces driving their divergence across species, we can come to understand their contribution to the evolution of new species.
Two sub-species of the meadow grasshopper Chorthippus parallelus come into contact and hybridise in the Pyrenees Mountains. Crosses between sub-species produce fertile F1 females and sterile F1 Hybrid males with dysfunctional testes. This incompatibility is widely thought to result from negative epistatic interactions (Dobzhansky-Muller model).
Within the hybrid zone grasshoppers display intermediate phenotypes. Clines in morphological and behavioural characteristics have been observed spanning the hybrid zone. By using back-crossing experiments, clines for sterility have also been mapped (Shuker et al. 2005).
Using a range of techniques including mating studies, expression analysis, sequence comparisons and genomic cline mapping I aim to gain insight into the underlying genetics which are maintaining the barrier to gene flow between the sub species.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy06-i008-R*

Symposium 6
Speciation by natural versus sexual selection

The magnitude and potential mechanisms of reproductive isolation among geographically isolated populations of a boreal insect, Drosophila montana

Jennings JH[1]
[1]University of Jyväskylä, Department of Biological and Environmental Science, Jyväskylä, Finland

Summary statement:

I discuss reproductive isolation in Drosophila montana with respect to natural and sexual selection, which both may potentially contribute to divergence and ultimately, speciation.

Abstract:

Widely distributed species that exhibit strong sexual selection and have populations adapted to different environmental conditions can provide valuable opportunities for tracing the onset of reproductive incompatibilities, their causes and their relative roles in the speciation process. Recently diverged populations of the boreal malt fly, Drosophila montana, provide an excellent model system for such studies, as much is known about selective pressures acting in nature. D. montana is a cold adapted, diapausing D. virilis group species found in high latitude forests in Nearctic and Palearctic regions around the globe. Previous studies have shown variation in wing and genital morphology, male courtship song and female song preference among Canadian, American and Finnish populations, and that these differences do not coincide with putatively neutral mtDNA divergence. I measured both pre- and postmating barriers to reproduction among flies representing these three populations and assessed cuticular hydrocarbon (CHC) variation, incorporating a test for the role of CHCs in mate choice. I show that flies from these populations exhibit significant assortative mating (i.e, sexual isolation) and a significant one-way reduction in interpopulation progeny production, affecting both male and female offspring equally in particular crosses. Data on postmating barriers suggest postcopulatory-prezygotic mechanisms. Thus, D. montana populations seem to be evolving multiple barriers to gene flow in allopatry. I discuss the potential mechanisms of these barriers with respect to natural and sexual selection.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy06-i009-R*

Symposium 6
Speciation by natural versus sexual selection

Rapid sperm evolution in the bluethroat subspecies complex

Johnsen A[1], Hogner S[1], Laskemoen T[1], Pavel V[2], Chutný B[2], Garcia Fernández J[3], Suárez Seoane S[4], Eybert M-C[5], Lifjeld JT[1]
[1]University of Oslo, Natural History Museum, Oslo, Norway, [2]Palacký University, Laboratory of Ornithology, Olomouc, Czech Republic, [3]Grupo Ibérico de Anillamiento, León, Spain, [4]University of León, León, Spain, [5]University of Rennes 1, Rennes, France

Summary statement:

We document high intraspecific divergence in sperm morphology between bluethroat subspecies, suggesting rapid evolution of sperm traits in this subspecies complex.

Abstract:

Sperm cells are the most variable animal cell types and much research is currently directed towards explaining inter- and intraspecific variation in sperm morphology and motility. Recent studies have found associations between levels of sperm competition and sperm length and/or sperm velocity, across passerine birds. Sperm competition thus acts as a potent selective force shaping sperm traits, and may potentially influence the evolution of reproductive barriers and the rate of speciation. However, the speed of evolutionary changes in sperm morphology is largely unknown, and studies of intraspecific sperm variation are needed in order to examine these processes at the finest levels. The bluethroat comprises several morphologically distinct subspecies that show small, but consistent genetic divergences according to neutral markers. Analyses of mtDNA suggest very recent divergence among the subspecies. We analysed variation in sperm morphology among four genetically distinct and geographically isolated bluethroat subspecies, in order to investigate the speed and direction of sperm evolution at the intraspecific level. We found highly significant variation in total sperm length, and its components (head, midpiece and tail), among the subspecies. High divergence in sperm morphology combined with low genetic divergence reveal rapid evolution of sperm traits in this system. We address the relative role of selection (e.g. sperm competition) and genetic drift for sperm divergence, and suggest that sperm divergence may play an important role in the early stages of the speciation process.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy06-i010-R*

Symposium 6
Speciation by natural versus sexual selection

Phylogeography of the hybrid origin of a swordtail fish in Mexico

Jones JC[1,2], Perez-Sato J-A[3], Meyer A[1]
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Summary statement:

We search for signs of recent hybridisation and introgression in a swordtail fish with a putative hybrid origin.

Abstract:

Studying hybridisation is important for an increased understanding of its role in speciation and evolution. Hybrid speciation may contribute significantly to generating biodiversity, but only a few well-documented examples exist so far that do not involve polyploidization as a mechanism. The swordtail fish, Xiphophorus clemenciae, and its putative parental species, the southern swordtail, X. helleri, and the platyfish, X. maculatus, provide an ideal system for investigating ongoing mechanisms of gene flow between hybrid and parental species. These fish overlap in their current geographic distribution and X. clemenciae shows several hall-marks of a hybrid origin. Here we use microsatellite and mitochondrial markers to investigate the population structure of this group of swordtails and search for signs of recent hybridisation. Individuals were sampled from 21 localities across the described range of X. clemenciae - the Isthmus of Tehuantepec (IT) Mexico, and several environmental parameters that might represent barriers to dispersal were recorded. Four main insights derived from our data. First, the hybridisation event that gave rise to X. clemenciae appears to be relatively ancient, a single origin is likely and there are no signs of contemporary introgression. Second, population structure within species shows an isolation-by-distance pattern and genetic differentiation between most populations is significant and high. Third we infer that tectonic evolution in the IT has greatly restricted gene flow between the southern and central populations of X clemenciae and X. helleri. Fourth, we provide preliminary information to aid in the conservation management of X. clemenciae.

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TUE 23 AUG at 1650 - Room N5
Oral presentation *C4-Sy06-1650-O*

Symposium 6
Speciation by natural versus sexual selection

On the origin of species by means of post-copulatory sexual selection: Ecotype-specific sperm and cryptic female choice in sticklebacks

Kaufmann J[1], Lenz TL[1], Milinski M[1], Eizaguirre C[1,2]
[1]Max Planck Institut for Evolutionary Biology, Evolutionary Ecology, Ploen, Germany, [2]Leibniz Institute for Marine Sciences (IFM-GEOMAR), Evolutionary Ecology of Marine Fishes, Kiel, Germany

Summary statement:

The role of post copulatory sexual selection in the process of ecological speciation is tested by a full-factorial fertilization experiment between stickleback ecotypes.

Abstract:

Ecology plays a major role in species diversification. Furthermore, sexual selection is increasingly being recognized as important process accelerating population divergence. In the three-spined stickleback, gene flow between connected lake and stream populations is repeatedly reduced, creating distinct ecotypes. In northern Germany, these ecotypes differ in parasite load as well as in diversity at the major histocompatibility complex (MHC). Recent experimental studies showed pre-copulatory female preference for sympatric males based on olfactory cues, suggesting a role of the pleiotropic MHC genes in maintaining reproductive isolation. However, mechanisms of post-copulatory sexual selection may also have evolved to limit gene flow between ecotypes, such as cryptic female choice to counteract the occasional matings with males from another habitat type and/or males' sneaking behavior. We therefore tested the role of assortative gamete preference on the maintenance of reproductive barriers between ecologically divergent populations in controlled in vitro experiments. We additionally focused on the important MHC genes to test for genetic incompatibility between fish ecotypes. Here, we report ecotype specific sperm characteristics and results of a full-factorial fertilization experiment with two lake/stream population pairs.

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TUE 23 AUG at 1500 - Room N5
Oral presentation *C3-Sy06-1500-O*

Symposium 6
Speciation by natural versus sexual selection

Sequential mate choice and reproductive isolation in threespine stickleback species

Kozak GM[1], Lackey ACR[2], Head ML[3], Boughman JW[4]
[1]University of Illinois, Animal Biology, Champaign, United States, [2]Michigan State University, Zoology, East Lansing, United States, [3]University of Exeter, Centre for Ecology and Conservation, Penryn, United Kingdom, [4]Michigan State University, Zoology; BEACON; Ecology, Evolutionary Biology & Behavior Program, East Lansing, United States

Summary statement:

In sympatric stickleback species, females learn to avoid heterospecifics during courtship but do not use sequential mate choice strategies between species.

Abstract:

Both natural and sexual selection can lead to sexual isolation between sympatric species. Fitness costs associated with hybridization can create selection to avoid heterospecific mates. Alternatively, heterospecific mates may be perceived as unattractive due to sexually selected preferences. Here, we ask if females use sequential mate choice strategies to avoid heterospecific males during mating in two threespine stickleback species (benthics and limnetics: Gasterosteus spp.). Previous work on sticklebacks found that females gauge male attractiveness relative to previously encountered males within species. If sexual isolation resulted from an extension of within species decision rules, we predicted that
1) females who have been courted by heterospecific males would subsequently find conspecific males more attractive than females without such experience,
2) females who experience conspecific males would find heterospecifics less attractive than naïve females, and
3) females who see two heterospecific males sequentially should find them equally attractive.
However, if females courted by heterospecifics subsequently find heterospecifics less attractive, it would suggest females are learning to avoid heterospecifics due to the costs of hybrid matings. We found that preferences for conspecific males did not change after experience with heterospecifics. In contrast, females did find heterospecifics less attractive after experience with either conspecific or heterospecific males. Thus, mating experience enhances sexual isolation in sticklebacks, but these effects are more likely to be the result of natural selection to avoid hybridization than sequential mate choice strategies.

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WED 24 AUG at 0910 - Room N5
Invited talk *D1-Sy06-0910-I*

Symposium 6
Speciation by natural versus sexual selection

Colours of speciation in fish and frogs

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[1]University of Groningen, Groningen, Netherlands, [2]University of Bern, Bern, Switzerland, [3]Eawag, Kastanienbaum, Switzerland

Summary statement:

Poison frogs and cichlid fish illustrate how interactions between natural and sexual selection may contribute to population divergence.

Abstract:

There is both theoretical and empirical support for various diversifying interactions between natural and sexual selection. For example, good-genes sexual selection may accelerate divergent adaptation, and divergence in sensory systems may pleiotropically cause divergence in mate preferences. To evaluate the macro-evolutionary consequences of these mechanisms, we need to identify how and when they operate in natural systems. In my contribution to this symposium, I will present some ongoing work on colour divergence in poison frogs and cichlid fish. These examples show how interactions between ecology and sexual selection may contribute to population divergence. They also illustrate, however, the difficulties of distinguishing alternative scenarios, and of determining their relative importance and temporal sequence.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy06-i012-R*

Symposium 6
Speciation by natural versus sexual selection

Evolutionary change in courtship behaviour is related to cladogenesis in a group of viviparous fish

Macias Garcia CJ[1], Ritchie MG[2], Mendez-Janovitz M[1]
[1]Universidad Anacional Autonoma de Mexico, Instituto de Ecologia, Mexico City, Mexico, [2]University of St. Andrews, School of Biology, St. Andrews, United Kingdom

Summary statement:

We looked for a link between sexual conflict and speciation in the viviparous Goodeine fish using courtship behaviour as a proxy measure of sexual selection. Clade formation was positively and significantly correlated with the number of courtship elements gained or lost along an ultrametric phylogenetic tree, lending support to the idea that there is a link between sexual selection and speciation in this group.

Abstract:

Speciation is expected to occur more quickly in clades where females can control the outcome of sexual conflict over matings. We tested this using the Mexican Goodeinae, a group of viviparous fish where insemination requires female cooperation. We used courtship evolution and complexity as proxies for intensity of sexual conflict, and described the courtship behaviour of 28 species. We then quantified the number of courtship elements and reconstructed the history of each element along an ultrametric phylogenetic tree. Courtship elaboration was calculated as the total number of courtship elements displayed by males of each species, and ancestral estates were computed for each node. Using all the ingroup nodes, we found a negative but non-significant trend between courtship elaboration and time to speciate. We then divided the ultrametric tree into five periods of 3.36 my each, and found a significant positive association between number of changes (gains/losses) of courtship elements and the number of lineages produced within each period ($R2 = 0.96$, $F(1,3) = 76.37$, $p = 0.0032$). Thus the occurrence of changes in courtship elements, which may constitute pre-mating requirements, is associated with the formation of new species in this clade with effective female control over matings.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy06-i013-R*

Symposium 6
Speciation by natural versus sexual selection

Niche expansion through ecological release in Neotropical crater lake cichlids. Do all species have the same potential?

Magalhaes IS[1], Hudson AG[1], Barluenga M[1]
[1]Museo Nacional de Ciencias Naturales, Dept. Biodiversity and Evolutionary Biology, Madrid, Spain

Summary statement:

The role of competition and niche availability in eco-morphological divergence in cichlid fish from Nicaraguan crater lakes.

Abstract:

Ecological adaptive radiation theory predicts a concomitant increase in eco-morphological and species diversification following the invasion of novel environmental niches. Whether species have the potential to respond to ecological opportunities, within a given time period, will depend on lineage-specific levels of genetic variation, genomic architecture of adaptive traits, phenotypic plasticity and strength of ecological trade-offs between niches. Due to their enormous diversity in morphology and colouration, fishes of the Family Cichlidae are among the best model systems for the study of biological diversification and ecological opportunity. Neotropical cichlids represent small-scale adaptive radiations relative to the more famous African Great Lake radiations, but are emerging as model systems for the study of early stages of adaptation and speciation in the absence of geographic isolation. In Nicaragua, several cichlid species inhabit geologically young crater lakes that differ in their geographic areas, niche availability and faunal composition. We investigated the niche width and ecological specialization of several cichlid fish species in different Nicaraguan lakes and test whether all species responded similarly to similar levels of ecological opportunity. Combining morphological and ecological analyses we evaluated levels of niche expansion and adaptability for each species. This approach provide information on how natural selection generated by inter-specific competition and niche and resources availability can affect their capacity of these fish to adapt to new environments, diversify and even speciate.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy06-i014-R*

Symposium 6
Speciation by natural versus sexual selection

Detecting niche divergence in an allopatric hybrid species complex of Pinus densata, P. tabuliformis and P. yunnanensis

Mao J-F[1,2], Wang X-R[2,3]
[1]Max Planck Institute for Developmental Biology, Tuebingen, Germany, [2]Institute of Botany, CAS, State Key Laboratory of Systematic and Evolutionary Botany, Beijing, China, [3]Umeå University, Department of Ecology and Environmental Science, Umeå, Sweden

Summary statement:

Ecological divergence and selection for novel adaptations have played main roles in homoploid hybrid speciation of Pinus densata on the Tibetan Plateau

Abstract:

Ecological divergence and selection for novel adaptations to new habitats have been theoretically proposed to play important roles in promoting homoploid hybrid speciation (HHS). To understand this process, the identification and characterization of ecological niches unique to hybrids may facilitate elucidation of the genetic basis of novel adaptations and species divergence. The successful establishment of Pinus densata on the Tibetan Plateau is one of the few known examples of HHS. In this study, we carried out extensive field expeditions to obtain representative coverage of occurrence sites of P. densata and its two putative parents. We then applied a series of GIS-based analyses to define the patterns of environmental variation within and among the three pine species, to remove potentially confounding effects of spatial autocorrelation in the environmental data due to allopatric ranges, and to build species distribution models. All results consistently indicated that the ecological preferences of P. densata and its parental species have diverged, and identified candidate ecological factors associated with habitat-specific adaptation. Our findings provide evidence of a distinct niche shift in P. densata, and support the hypothesis that ecological selection-induced local adaptation and geographic isolation help maintain and reinforce between-species differences and reproductive isolation in the species complex. Furthermore, these findings are valuable for understanding the origin of biodiversity in the Tibetan vegetation, and for predicting the evolutionary responses of the high plateau plants to global environmental changes.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy06-i007-E*

Symposium 6
Speciation by natural versus sexual selection

Size, ecotype and male courtship behavior in the stream-resident-anadromous stickleback species complex

McKinnon JS[1], Hamele N[2], Frey N[2]
[1]East Carolina University, Biology, Greenville, United States, [2]University of Wisconsin-Whitewater, Biological Sciences, Whitewater, United States

Summary statement:

We used size-manipulation to investigate male courtship preferences in anadromous and stream-resident sticklebacks. Our results suggest stronger responses to similar sized females.

Abstract:

We investigated the potential role of male behavior in reproductive isolation between divergent anadromous and stream-resident populations of threespine stickleback, Gasterosteus aculeatus, using size-manipulated females of both ecotypes. Specifically, we asked if male courtship preferences are present, and if they are based on ecotype, relative body size, or other traits. Mating trials were 'no choice' tests involving one male and one female paired in a 96-liter aquarium. To minimize the influence of female behavior on male courtship data, male behavior was scored only from the first five minutes of each trial. Because most male behaviors were strongly and significantly correlated with each other, we conducted a principal components analysis on the correlations and also ran analyses on the principal components. The two male ecotypes differed in overall behavioral frequencies, with stream-resident males exhibiting consistently more vigorous and clearly positive courtship than anadromous males. Analysis of PC1 indicated more vigorous courtship toward smaller females by (relatively small) stream-resident males and the reverse pattern for (relatively large) anadromous males. We found little evidence of males responding preferentially to females of their own ecotype independent of body size.

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TUE 23 AUG at 1420 - Room N5
Oral presentation *C3-Sy06-1420-O*

Symposium 6
Speciation by natural versus sexual selection

It's a kind of magic: Divergent ecological selection on a mating trait

Merrill RM[1], Wallbank R[1], Stevens M[1], Jiggins CD[1]
[1]University of Cambridge, Cambridge, United Kingdom

Summary statement:

Using models designed with respect to avian vision, we show that wing colour patterns in Heliconius, which are used during mate recognition, are under disruptive natural selection.

Abstract:

Traits under disruptive ecological selection that also influence non-random mating can facilitate speciation in the face of gene flow. However, the existence of such 'magic traits' in nature has been considered unlikely. Mimicry in tropical butterflies has long been championed as an example of adaption driving speciation. In the Neotropical genus Heliconius pairs of unpalatable species converge on the same bright warning-pattern to more efficiently advertise their distastefulness to predators. Closely related taxa often belong to different mimicry rings, and experiments have shown that males use colour pattern during mate recognition. Hybrids display intermediate warning patterns that are unlikely to be recognized as distasteful. The sister species, Heliconius melpomene and H. cydno are sympatric across much of Central and northern South America. Using model butterflies we reveal selection against non-mimetic hybrid colour patterns between these two species. To our knowledge, these data provide the first explicit experimental evidence of disruptive ecological selection acting on a trait that is also used during mate recognition. In addition, by testing mate preferences in hybrid males we demonstrate a genetic association between male mate preference and wing colour pattern. In particular, male preference for red patterns is associated with the locus responsible for the red forewing band. Thus we demonstrate disruptive selection acting on a mating trait that is genetically associated with the corresponding mate preference.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy06-i015-R*

Symposium 6
Speciation by natural versus sexual selection

Potential roles of natural and sexual selection in two avian radiations: The North American bird genus Junco and the gray white-eye of Reunion Island

Mila B[1], Bertrand J[2], Thebaud C[2]
[1]National Museum of Natural Sciences, Madrid, Spain, [2]Universite Paul Sabatier, Toulouse, France

Summary statement:

Phylogeographic and ecomorphological analyses suggest the combined roles of selection and drift in driving divergence in radiations of the avian genera Junco and Zosterops.

Abstract:

Assessing the relative importance of selection and drift is essential to understanding the processes of divergence and speciation. Phylogeographic analysis of mtDNA sequences and AFLP loci revealed that the radiation of the genus Junco of North America includes both recently diversified taxa of postglacial origin and old allopatric lineages in Central America and Guadalupe Island. At least six parapatric morphotypes of the Junco hyemalis complex diversified as a result of a recent postglacial expansion and show marked plumage color differences against a similar ecomorphological design, suggesting the role of sexual selection in their divergence. In contrast, J. insularis of Guadalupe Island off Baja California shows marked divergence in mtDNA and ecomorphological evidence of adaptive divergence. In turn, both neutral and selective factors appear to be involved in the intra-island diversification of the gray white-eye (Zosterops borbonicus) of Reunion Island in the South Indian Ocean, where four distinct plumage forms are found in either parapatry or sympatry in different parts of the island. AFLP and microsatellite data have revealed genetic clusters related to elevation, and cryptic contact zones along steep ecological gradients suggest low dispersal and the role of strong selection in maintaining genetic discontinuities at very small spatial scales. Both natural systems (Junco and Zosterops) provide ideal scenarios in which to test the relative roles of drift, natural selection and sexual selection in speciation, and we are currently investigating divergence mechanisms with the use of candidate genes and SNP libraries from next-generation-sequencing genome scans.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy06-i016-R*

Symposium 6
Speciation by natural versus sexual selection

Sperm morphology and reproductive isolation in Ficedula flycatchers

Podevin M[1], Immler S[2], Qvarnström A[1]
[1]Uppsala University, EBC, Animal Ecology, Uppsala, Sweden, [2]Uppsala University, EBC, Evolutionary Biology, Uppsala, Sweden

Summary statement:

Comparison of sperm morphology in two flycatcher species and their hybrids, link to fitness and phenotypic traits and discussion on altered spermatogenesis in the hybrids.

Abstract:

Understanding the mechanisms leading to the evolution of reproductive isolation is central in speciation research. Despite its important role in reproductive isolation, postmating, prezygotic isolation remains under-represented among the empirical studies of speciation. This is mainly because of the practical difficulties to study the events happening after mating but before fertilization. Low fertilization success in interspecific matings can occur due to (i) poor sperm transfer and/or storage, (ii) divergence in gamete recognition proteins or (iii) low sperm competitive ability. The latter is particularly important where females mate with both conspecific and heterospecific males, which may lead to interspecific sperm competition. Morphological (e.g. midpiece length, flagellum length) and functional (e.g. viability, longevity, swimming velocity and motility) sperm traits play a crucial role for fertilization success. Here we compared sperm morphology in two hybridizing species of flycatchers (Ficedula albicollis and F. hypoleuca) from a well-studied hybrid zone population on the island of Öland (Sweden), in the Baltic Sea. We analyzed samples from over fifty males of the two species, as well as some hybrid individuals. We present the association between male phenotypic traits, sperm morphology, fertilization success, extra-pair paternity and fertilization status of unhatched eggs. We are also discussing the role of reduced sperm production and spermatogenesis dysfunction in explaining reduced fitness of hybrid males.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy06-i017-R*

Symposium 6
Speciation by natural versus sexual selection

Rapid divergence of internal female genitalia between recently diverged sister taxa, as revealed by a comparative study of 41 sepsid species (Sepsidae: Diptera)

Puniamoorthy N[1,2], Meier R[2]
[1]University of Zurich, Institute of Evolutionary Biology and Environmental Studies, Zurich, Switzerland, [2]National University of Singapore, Department of Biological Sciences, Singapore, Singapore

Summary statement:

We show that the internal female genitalia are diverse in sepsid flies and we identify two fast-evolving structures that are likely involved in post-copulatory sexual selection.

Abstract:

Numerous studies suggest sexual selection as the driving force behind the morphological diversity and species-specificity of male genitalia in insects. In sharp contrast, the internal female genitalia often remain poorly studied. Here, we present a comparative study of the internal female reproductive system of sepsid flies across 41 species, representing 21 of the 37 described genera and we test the species-specificity of the female genitalia by comparing recently diverged sister taxa. We define 19 morphological characters and using a well-resolved molecular phylogeny based on 10 genes, we reconstruct the evolution of the female structures across the family. We also compare rate of change in female characters with fast-evolving molecular characters (i.e. non-constant third positions of the COI barcoding gene). We identify two structures, in particular, that evolve faster than the rest: (1) the ventral receptacle, a secondary sperm storage organ, that accounts for more than half of all the evolutionary changes observed; and (2) the dorsal sclerite, which is associated with the opening of the spermathecal ducts and is distinct even among sister species. Overall, we find the internal female genitalia are diverse in Sepsidae and fast-evolving structures like the ventral receptacle and dorsal sclerite are likely involved in post- copulatory sexual selection.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy06-i008-E*

Symposium 6
Speciation by natural versus sexual selection

The role of selection and drift in shaping quantitative genetic variation in male genital morphology in Drosophila melanogaster

Schäfer MA[1], Orozco-terWengel P[2], Blanckenhorn WU[1], Schlötterer C[2]
[1]University of Zurich, Institute of Evolutionary Biology and Environmental Studies, Zurich, Switzerland, [2]Veterinary Medicine University of Vienna, Institute for Population Genetics, Vienna, Austria

Summary statement:

Our population genetics approach reveals contrasting phylogenetic signals in genital size and shape indicating distinct processes causing evolutionary change.

Abstract:

Male insect genitalia show strikingly rapid and divergent evolution in shape and complexity. Directional or diversifying sexual selection rather than neutrality has been invoked to explain the pattern. However, the comparative evidence for this hypothesis is still limited and remains largely restricted to inter-species analyses focussing on long-term evolutionary changes. Here, we assessed the relative importance of drift versus selection operating on genital shape and size by comparing multiple natural populations of Drosophila melanogaster. Although populations were found to harbour substantial standing genetic variation in genital shape, indicating a great potential for rapid morphological change, shape differences between populations were much smaller than expected under neutrality and corresponded to that of other morphological traits such as wing vein positioning. Genital size, on the other hand, revealed a strong phylogenetic component with cosmopolitan, European and Asian populations developing larger genitalia compared to the ancestral, sub-Saharan populations. Our results not only implicate that shape and size variation of the genital arch might be affected by distinct evolutionary processes, but also that rates of morphological change are quite distinct within and between species belonging to the D. melanogaster lineage.

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TUE 23 AUG at 1400 - Room N5
Invited talk *C3-Sy06-1400-I*

Symposium 6
Speciation by natural versus sexual selection

Divergent selection, sexual selection, and magic traits

Servedio MR[1], Van Doorn GS[2], Kopp M[3], Frame AM[1], Nosil P[4]
[1]University of North Carolina, Department of Biology, Chapel Hill, United States, [2]University of Bern, Institute of Ecology and Evolution, Hinterkappelen, Switzerland, [3]University of Vienna, Mathematics and Biosciences Group, Max F. Perutz Laboratories and Faculty of Mathematics, Vienna, Austria, [4]University of Colorado, Department of Ecology and Evolutionary Biology, Boulder, United States

Summary statement:

The concept of magic traits is used to develop a framework that may help to determine the extent of the importance of sexual selection in speciation.

Abstract:

The evolution of assortative mating generally, but not universally, involves sexual selection. In order to ultimately understand the role of sexual selection during speciation it is of interest to determine not only how often sexual selection is involved in the speciation process, but how effective it is when it is involved. One type of trait that is though to be particularly effective in driving speciation is a “magic trait” – a trait that is both under divergent selection and through pleiotropy leads to assortative mating. A more thorough examination of the concept of magic traits, including how often they may occur, how effective they may be, and how often they involve sexual selection, introduces a framework for categorizing traits that may ultimately be useful in determining the extent of the importance of sexual selection in speciation.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy06-i009-E*

Symposium 6
Speciation by natural versus sexual selection

Speciation Genomics: Molecular evolution of asymmetric gene misregulation in hybrids between Drosophila simulans and D. sechellia

Singh RS[1], Haerty W[1], Loomer M[1]
[1]McMaster University, Department of Biology, Hamilton, Canada

Summary statement:

These results provide support for the "Fast Sex-X-Male" hypothesis of Haldane´s Rule and speciation.

Abstract:

According to the Dobzhansky-Muller model hybrid sterility and inviability are consequence of disruption of gene interactions due to accumulation of different allelic combinations between diverging populations. Several studies previously reported strong variation in gene misregulation patterns in interspecific hybrids of Drosophila simulans, D. mauritiana and D. sechellia across development and crosses. Most analyses so far have focused on the comparison of hybrids from different species pairs, and even though morphological variations in spermatogenesis were found between reciprocal hybrids, no analysis have been conducted at the molecular level comparing hybrids that differ only by the origin of their sex chromosomes and mitochondria. Here we report results of extensive difference in gene expression between reciprocal hybrids of D. simulans and D. sechellia using both microarray and real time quantitative PCR analyses. These results strongly support the importance of sex-chromosome /autosomes interactions in the evolution of hybrid incompatibilities.

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TUE 23 AUG at 1610 - Room N5
Oral presentation *C4-Sy06-1610-O*

Symposium 6
Speciation by natural versus sexual selection

Pleiotropic effect of chemosensory genes in speciation

Smadja C[1]
[1]CNRS, Institut des Sciences de l'Evolution, Montpellier, France

Summary statement:

Coupled action of natural and sexual selection: the case of chemosensory genes

Abstract:

During the course of a speciation process, natural selection usually initiates divergence by driving the evolution of postzygotic isolation, while sexual selection can accelerate the final stages of speciation by promoting the evolution of non-random mating. However, the completion of speciation in the face of gene flow depends on the efficacy at which these different components of reproductive isolation get coupled together. Here I will present a series of multi-gene families which, due to their function in olfactory and gustatory processes, can be involved in both habitat specialisation, habitat choice and mate choice in phytophagous insects, and thus are susceptible to evolve under the coupled action of natural and sexual selection. This context predicts a rapid divergence at these genes and therefore a very favourable scenario for speciation-with-gene-flow. I will review potential cases in nature where natural and sexual selection could jointly act on this type of genes, and I will present current work in aphids addressing the adaptive evolution of these genes among different host races specialised on different host plants.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy06-i018-R*

Symposium 6
Speciation by natural versus sexual selection

Amphibian hybrid zones: Patterns of introgression at autosomal and sex-linked DNA-markers in relation to divergence time and ecological niche

Stöck M[1], Bonato L[2], Colliard C[1], Dufresnes C[1], Novarini N[3], Pio D[1], Sicilia A[4], Turrisi GF[5], Perrin N[1]
[1]University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland, [2]University of Padova, Department of Biology, Padua, Italy, [3]Museo di Storia Naturale di Venezia, Venice, Italy, [4]University of Palermo, Departement of Animal Biology, Palermo, Italy, [5]University of Catania, CUTGANA, Section of Nature Reserve Management, Catania, Italy

Summary statement:

Empirical speciation research, hybridization, reproductive isolation, autosomal and sex-linked microsatellites, introgression, divergence time, ecological niche, Haldane´s rule.

Abstract:

Speciation research in amphibians can rarely examine secondary contacts of differently diverged lineages of the same radiation. We study three lineages of green toads (Bufo viridis subgroup) in Italy, diverged during different Plio-Pleistocene periods. Using mitochondrial, and nuclear DNA, we examine divergence times, and interactions with autosomal and sex-linked microsatellites. Sicilian endemic B. siculus and Italian mainland-origin B. balearicus (divergence 2.7 Mya) form a narrow (40 km) hybrid zone in NE-Sicily with limited bidirectional mtDNA introgression. Nuclear genomes barely admix, and hybrid breakdown occurs in backcrosses. Selection against hybrids likely has intrinsic genomic causes, possibly reinforced by adaptation to climate, as ecological niches overlap just 38%. Thus, B. siculus and B. balearicus have evolved almost complete reproductive isolation. In contrast, Italian B. balearicus and SE-European B. viridis, diverged only 1.9 Mya, display a wider (120 km) zone of mtDNA introgression and considerable nuclear admixture (40 km) in the Po valley. While patterns document successful backcrosses, transects reveal narrow clines, supporting selection against hybridization. However, genetic clines also coincide with large rivers as dispersal barriers. Bufo balearicus and B. viridis exhibit 27% of niche overlap, suggesting ecological adaptation might play a greater role in the climatic transition zone of the Po valley. Newly established sex-linked microsatellites will allow testing whether differential introgression of autosomal and sex-chromosomal markers in these hybrid zones occurs, and if predictions from Haldane´s rule apply to the observed patterns.

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WED 24 AUG at 1100 - Room N5
Invited talk ***D2-Sy06-1100-I***

Symposium 6
Speciation by natural versus sexual selection

The roles of natural selection, sexual selection, climatic niche divergence and learned mate preferences in speciation processes of odonates: a challenge to ecological speciation?

Svensson E[1]
[1]Lund University, Biology, Lund, Sweden

Summary statement:

I will discuss the the role of natural and sexual selection in speciation processes in odonates and some findings that challenge predictions from ecological speciation theory

Abstract:

During the past decade, ecological speciation has emerged as a major paradigm in speciation research, with an emphasis on divergent selection, adaption to ecological niches and reproductive isolation that is a direct or indirect result of ecology. It is now widely acknowledged that natural selection to exploit different trophic resources and adaption to different ecological environments play an important role in several taxa, such as seed eating birds, phytophagous insects and certain freshwater fishes. Recently, the ubiquity of ecological speciation has been challenged, however, and several workers have pointed out that not all speciation proceeds by ecological means. Alternative non-ecological and non-adaptive speciation mechanisms include various forms of reproductive interactions, sexual selection, sexual conflict and learned mate preferences. Moreover, ecology might play a more conservative role than has been assumed and ecological factors might sometimes constrain divergence and are therefore unlikely to always lead to divergent selection (e. g. niche conservatism). In this talk, I will discuss how natural and sexual selection, climatic niche divergence and learned mate preferences interact in speciation processes of odonates (dragonflies and damselflies). I will show that odonates are characterized by
(i) weak divergent natural selection,
(ii) strong sexual selection,
(iii) pronounced sexual isolation between species,
(iv) limited climatic niche divergence and
(v) an important role for learned mate preferences.
These findings challenge predictions from ecological speciation theory and call for a more pluralistic perspective on speciation mechanisms.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy06-i011-E*

Symposium 6
Speciation by natural versus sexual selection

Are you sexual? Asexual genomic signatures

Tang C[1], Barraclough T[1], Fontaneto D[1]
[1]Imperial College London, Life Sciences, Ascot, United Kingdom

Summary statement:

Are you sexual? Sex is widespread in nature, while putative and ancient asexual lineages are rare. Here we test an indirect genomic signature to identify asexuality in rotifers.

Abstract:

Sex is a widespread phenomenon in life. Yet, there are few putative ‘ancient asexuals’ that defy the generality of sex. In order to indirectly test for the reality of the asexuality of these organisms, we can look for the genetic expectations of lack of sexual recombination. Some of them have already been tested, e.g. accumulation of deleterious mutation, intra-nuclear divergence and adaptations to resist parasites. In this study we investigate whether asexual reproduction results in congruent evolutionary trajectories for different genetic regions.

Complete lack of sexual reproduction and genetic recombination should result in a complete linkage of all the genome in asexual organisms. Thus, topologies of phylogenetic trees from different loci should be congruent, or at least more congruent than in sexual organisms.

Bdelloid rotifers are the most notorious ancient asexuals and provide a unique model system to test for the effect of sexuality, as comparative tests can be performed using their sister clade, monogonont rotifers, cyclical parthenogens.

We test for congruence between tree topologies using different markers from different genomic regions (cox1 mtDNA, 16S mtDNA, 18S rRNA, 28S rRNA, ITS1 rRNA, ITS2 rRNA, and histone 3) in bdelloids and monogononts.

For the younger branches in the trees, representing those within members of coherent populations, we expect higher congruence between different loci in bdelloids than in monogononts.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy06-i012-E*

Symposium 6
Speciation by natural versus sexual selection

The function of eggspots in the haplochromine cichlid fish Astatotilapia burtoni

Theis A[1], Salzburger W[1], Egger B[1]
[1]University of Basel, Zoological Institute, Basel, Switzerland

Summary statement:

Behavioural experiments with a haplochromine cichlid show that eggspots do not serve as sexual advertisement to attract females, but rather play a role in intrasexual interactions.

Abstract:

The perciform family Cichlidae represents the most species-rich family of vertebrates. The majority of African cichlid species are members of a single tribe, the Haplochromini. The cichlid’s special mouthbrooding behaviour evolved several times during evolution, but only haplochromines show a characteristic polygynous or polygynandrous maternal mouthbrooding system with males carrying eggspots on the anal fin. These eggspots are ovoid markings and are considered to be one of the key innovations that could be responsible for the diversification of haplochromine cichlids. The function of eggspots has been under experimental investigation and various hypotheses have been formulated: eggspots could serve as egg-dummies to attract females, trigger egg laying, maximize fertilization rates and/or work as a species recognition signal. All these hypotheses assume eggspots to be a sexually selected trait mediated by female mate preference. Several studies, however, have shown that secondary sexual traits are targets of inter- and/or intra-sexual selection. The aim of this study was to uncover the function of eggspots in the species Astatotilapia burtoni on the levels of inter- and intra-sexual selection. Our behavioural experiments show that A. burtoni females chose randomly between males with many or few eggspots and even tended to prefer males without eggspots. Preliminary results of ongoing male-male competition experiments indicate an important function of eggspots in intrasexual interactions. Our results are in contrast to findings of previous studies and suggest that eggspots have multiple functions in haplochromine cichlids.

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WED 24 AUG at 1200 - Room N5
Oral presentation *D2-Sy06-1200-O*

Symposium 6
Speciation by natural versus sexual selection

A potential role for sexual selection in the divergence of Tropical Pacific honeyeaters (Myzomela)

Thomassen HA[1,2], Dekker RWRJ[3], Smith TB[2]
[1]University of Tübingen, Tübingen, Germany, [2]University of California, Los Angeles, Center for Tropical Research, Los Angeles, United States, [3]National Museum of Natural History, Naturalis, Leiden, Netherlands

Summary statement:

Landscape genetics of Pacific island honeyeaters (Myzomela) implicate sexual selection, not natural selection or drift as key in population divergence.

Abstract:

The relative roles of neutral and selective processes in divergence are of key interest in evolutionary biology. Due to the many large and small islands, the Indopacific area constitutes an ideal natural laboratory to study the different modes of diversification. It is a biotically extremely rich region, and as a result is designated as several distinct biodiversity hotspots. It was suggested that the islands of the Pacific are a likely source of biodiversity, rather than a sink of species that originated on the mainland, as has long been the established hypothesis. We use landscape genetic approaches to study the potential roles of drift, natural selection, and sexual selection to study the divergence among island and mainland species of sexually dimorphic honeyeaters, Myzomela sp. We found that males exhibit distinct differences between islands in plumage coloration and song, but not in other, fitness-related morphological traits. Females did not show divergence in any morphological traits between islands. Neither environmental heterogeneity nor oceanic barriers explained the observed divergence in plumage coloration and song. These results suggest that sexual selection is a potential factor in maintaining and deepening population differentiation. Sequence and microsatellite data indicate that these populations either very recently diverged or experience ongoing gene flow, and planned coalescence-based analyses will be useful in distinguishing these two hypotheses. The role of sexual selection in population divergence will be further evaluated using mate choice experiments.

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WED 24 AUG at 0950 - Room N5
Oral presentation *D1-Sy06-0950-O*

Symposium 6
Speciation by natural versus sexual selection

Latitudinal variation in wing colour in the green-veined white butterfly: Opposing natural and sexual selection?

Tuomaala M[1], Kaitala A[1], Rutowski RL[2]
[1]University of Oulu, Department of Biology, Oulu, Finland, [2]Arizona State University, School of Life Sciences, Tempe, United States

Summary statement:

Opposing natural and sexual selection may have caused sex dependent latitudinal colour variation in the green-veined white butterfly (Pieris napi).

Abstract:

In butterflies, wing colour has a significant role in reproductive isolation and speciation because mate location and mate choice are very often based on visual cues. In addition to being an intraspecific signal, butterfly wing colour may play a role in thermoregulation. Wing colour can therefore be simultaneously affected by natural and sexual selection. We investigated the roles of sexual and natural selection in producing the latitudinal wing colour variation in the green-veined white butterfly (Pieris napi) by studying: 1) wing surface reflectances at wavelengths from 300 to 700nm and 2) the degree of melanisation. We expect the reflectance traits to show a pattern of variation that suggests colour is a sexually selected trait and melanisation because of its role in heat absorption to increase with increasing latitude. Females of P. napi were collected from locations spanning a 960 km latitudinal range across Finland and their progeny raised from eggs they laid to determine typical wing reflectances and melanisation for each collecting locale. Sexual dimorphism was evident: compared to males, females reflected more incident light in short wavelengths (< 400nm) and less in the long wavelengths (>450nm) than males, and they were more melanised than males. Among females short wavelength reflectance and melanisation increased towards north. Among males, latitudinal variation was found only in the ventral hindwing melanisation. From these results we conclude that the colouration of male dorsal wing surface may be used for sexual signalling and that selection in the context of thermoregulation only affects ventral wing surface properties.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy06-i019-R*

Symposium 6
Speciation by natural versus sexual selection

Anticipate and adapt to a seasonal change: a latitudinal cline in Drosophila montana

Tyukmaeva VI[1]
[1]University of Jyväskylä, Biological and Environmental Science, Jyväskylä, Finland

Summary statement:

Is local adaptation, being an important step in early stage of speciation, possible in presence of unlimited gene flow? An examination of Drosophila montana latitudinal cline.

Abstract:

In the ecological speciation hypothesis reproductive isolation is suggested to be ultimately a consequence of divergent natural selection on traits between environments, i.e. local adaptation. Several scenarios for sympatric/parapatric speciation suggest that local adaptation plays an important role in early stages of population divergence. One way to study the interplay of natural selection in gradually changing environments and a diluting effect of gene flow is to trace phenotypic and genetic divergence of overlapping populations from latitudinal clines.

One of the most critical challenges for insects living in temperate zones is to survive the cold winter period when many species undergo diapause in which they adjust their metabolic processes in order to survive unfavourable conditions. The correct timing of diapause represents an important factor in evolutionary adaptation and ecological trade-offs between survival and reproduction which has been examined in Drosophila montana, where females are able to survive through the severe winter conditions by entering adult reproductive diapause.

I examine variation in diapause incidence in different D. montana populations along a latitudinal cline in Finland and estimate the importance of gene flow in the formation of a clinal diapause response. Although the results suggest a strong latitudinal cline in reproductive diapause in presence of high gene flow, it seems that certain ecologically important genomic regions become especially adapted, even with a effect of gene flow over the rest genome.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy06-i020-R*

Symposium 6
Speciation by natural versus sexual selection

Learning and character displacement in damselflies

Verzijden MN[1], Svensson EI[1]
[1]Lund University, Biology, Lund, Sweden

Summary statement:

Female damselflies learn to discriminate between conspecifics and others, based on male wing spots size. This can contribute to character displacement in male wing coloration.

Abstract:

Learned mate preferences are increasingly recognized as an important study subject in sexual selection and speciation. A well-known phenomenon in psychology, peak shift, predicts that generalisation from learning to discriminate between two phenotypes produces preferences for exaggerated traits. This phenomenon has recently been implicated in sexual selection, due to it's abilities to generate directional selection on sexual traits. Sexual selection is also key to explaining the evolution of species' specific traits and preferences, mediating reproductive isolation. Theoretical models show that learning could greatly facilitates the evolution of reproductive isolation. Ongoing evolution of species isolation in damselflies of the genus Calopteryx, provides an exciting opportunity to test these novel ideas in the field. Calopteryx damselflies have melanised wing spots, which show species' specificity, and are a classic example of character displacement. I will present results of a field study of whether, and how, Calopteryx females learn both within-species preferences and between-species preferences based on these wing spots. I will relate this to how female preferences may contribute to the selection gradient on male wing spots in these species.

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Symposium 7

Fossils and evolutionary biology

Talks: *Room N0*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Upper floor campus canteen *Mensa*

Invited Speakers:

Walter G Joyce, Krister T Smith

Organizers:

Hervé Bocherens

Description:

Evolutionary studies that utilize extant data sources routinely make retrodictions that can only be evaluated directly using evidence from fossils. This symposium features diverse examples of the importance of fossils to evolutionary biology drawn from ongoing studies in the fields of biogeography, ecology, ontogeny, and systematics.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

WED 24 AUG at 1100 - Room N0
Oral presentation *D2-Sy07-1100-O*

Symposium 7
Fossils and evolutionary biology

Isotopic tracking of fossil mammal palaeoecology: implications for evolutionary biology

Bocherens H[1], Drucker DG[1]
[1]Universität Tübingen, Geowissenschaften, Tübingen, Germany

Summary statement:

Isotopic tracking of fossil mammal palaeoecology: implications for evolutionary biology

Abstract:

Carbon and nitrogen isotopic signatures preserved in fossil bones and teeth are linked to the ecology of the animals while they were alive, even for specimens several dozens of thousand years old. Using such isotopic signatures, it is possible to reconstruct the ecological niches of ancient populations of extant species. Examples taken from herbivores (Saiga antelope Saiga tatarica, Asian Serow Capricornis sumatraensis) or carnivores (brown bear Ursus arctos, lion Panthera leo) show that, during the Pleistocene, these species exhibited habitat and/or dietary preferences clearly different from those extrapolated from the modern representatives of these taxa. Such differences may be due to differing abiotic factors, such as climate, or to biotic factors, such as available dietary resources, competition and anthropogenic impact. Adequate knowledge of the spectrum of ecological preferences for a given taxon is essential to understand the relationships between ecology and evolution. We therefore recommend extended use of isotopic tracking in ancient populations of extant mammals to evaluate properly their ecological preferences.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy07-i001-R*

Symposium 7
Fossils and evolutionary biology

Life-history of the giant sauropod dinosaur Mamenchisaurus inferred from bone histology

Griebeler EM[1], Sander PM[2], Wings O[3,4], Fowler DW[5], Henderson DM[6]
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Summary statement:

We present the first well-constrained growth curve for a sauropod individual and derive reliable estimates of its maximum growth rate, longevity and age of sexual maturity.

Abstract:

Sauropods were the largest terrestrial animals ever. In order to understand the evolution of these giants it is very intriguing to reconstruct their life-history. Growth patterns in dinosaurs have been assessed by bone histology. Growth-lines are counted in long bones and are used to estimate longevity. Growth rates have been difficult to quantify in sauropods, because histologic growth-lines are rare and at best appear late in ontogeny. The age at sexual maturity is estimated as the inflexion point of the growth curve. Beside recording lines, fitting series of growth-lines to mathematical growth models is also applied to assess these life-history characteristics. Fitting is very problematic, because (1) the number of growth marks is mostly low, and (2) growth marks in the inner part of the bone are often lost due to the expansion of the medullary cavity.
Here, we present the first well-constrained growth curve for a sauropod, a very large individual (ca. 25 t) of the basal eusauropod cf. Mamenchisaurus from the Shishugou Formation, Junggur Basin, China having preserved in its ulna 33 growth-lines and an unknown number in the inner part of the bone. We establish growth curves by counting growth-lines and estimating the number of lost lines and by applying non-linear regression analysis to estimate the maximum growth rate, longevity and age of sexual maturity of the individual. The estimates derived from both methods are very similar. Longevity is 40 to 50 years, age at sexual maturity is reached in the first third of life and the maximal growth rate is similar to the rate observed in extant birds and mammals.

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WED 24 AUG at 1140 - Room N0
Oral presentation *D2-Sy07-1140-O*

Symposium 7
Fossils and evolutionary biology

Estimating divergence times Using fossil calibrations and the birth-death process

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Summary statement:

We show how and when information from the fossil record can be used in addition to molecular sequence data to accurately estimate divergence times.

Abstract:

Divergence times are frequently estimated from molecular sequence alignments. However, without exact knowledge of the substitution rate per time (clock rate) and the molecular clock model, being either strict or relaxed, estimates of divergence times require additional information. One way to obtain precise estimates uses fossil calibrations.

In this project we consider two types of information from the fossil record. First, if the fossil has extant descendants, then a fossil represents a time and the group of descending taxa. Second, if the fossil has no extant lineage, then the fossil gives a time and ancient DNA. The second case might be considered as serially sampled data, e.g. sequences with different ages. We base our model for speciation and extinction on the linear birth-death process and sequences evolution under the strict molecular clock. Extending the ordinary linear birth-death process by integrating the fossil record, we show that it is then possible to infer accurate estimates of divergence times under perfect conditions. Furthermore, we demonstrate under which conditions such estimates are valid or misleading. Conditions include uncertainty in fossil times, single and multiple fossil calibrations, model violations, number of extant taxa and sequence length.

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WED 24 AUG at 0950 - Room N0
Invited talk *D1-Sy07-0950-I*

Symposium 7
Fossils and evolutionary biology

The importance of fossils to systematic biology

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Summary statement:

A number of examples will be presented from various aspects of systematic biology that demonstrate the lasting value of fossils to this field of research.

Abstract:

Systematic biology is a highly dynamic field that has changed dramatically over the course of the last 30 years, particularly through the addition of molecular data. Indeed, molecular methods have become so refined at this point and molecular data so abundant that some have declared the use of morphology in general and fossil in particular to be of no relevance to the field.
For this contribution I will summarize a number of examples from my own research and from that of others that highlight the lasting importance of fossils to the field of systematic biology. Examples will include the impact of fossils to phylogenetic analyses, the value of fossils in establishing primary homology, the utility of fossils in establishing rates of evolution, and the unique ability of fossils to correctly establish ancestral morphologies. As diverse as these issues are, most can be classified as pertaining to sampling: although ever-refined techniques allow neontologists to collect ever increasing amounts of data from extant organisms, only fossils have the potential to document unique character state combinations that do not exist today. Fossils should generally not been seen as a distracting source of conflict with molecular data, but rather as a sounding board that allows testing neontologically derived hypotheses against the only true source of historical data.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy07-i002-R*

Symposium 7
Fossils and evolutionary biology

Phylogeny and evolution of the Macaronesian endemic moss genus Echinodium (Echinodiaceae)

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Summary statement:

Molecular data are used to infer origin and relations of the Macaronesian paleoendemic moss family Echinodiaceae and genetic differentiation of the extant Echinodium species.

Abstract:

Echinodiaceae, with the single genus Echinodium, is the only endemic moss family in Europe. It is restricted to the laurel forests (Laurisilva) of the Macaronesian archipelagos (Azores, Madeira and Canary Islands) and considered to be a paleoendemic relict from the Tertiary period. Echinodium comprises three extant species, E. setigerum (Madeira Island), E. spinosum (Madeira and Canary Islands), and E. renauldii (Azores), all with a similar morphology. Fossil records of Echinodiaceae (E. savicziae) are known from Continental Europe (Caucasus and Poland). Circumscriptions and relationships of the extant Echinodium species remain unclear, and no closest relatives of Echinodiaceae among the species-rich crown group of mosses, the pleurocarpous Hypnales, are known yet. Based on molecular phylogenetic analyses using markers from all three plant genomes and AFLP fingerprinting analyses, this study aims to address the following questions: (i) are there closely related taxa within extant Hypnales that would allow inferences about the evolutionary origin of Echinodiaceae, (ii) to what extent do the extant Echinodium species differ at the molecular level, and (iii) does the molecular differentiation support the hypothesis that they are paleoendemics and allow biogeographic inferences on the colonization history and dispersal capability between the Macaronesian archipelagos.

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WED 24 AUG at 1120 - Room N0
Oral presentation *D2-Sy07-1120-O*

Symposium 7
Fossils and evolutionary biology

Fossil-constrained molecular dating of adaptive radiations

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Summary statement:

Time-constrained molecular phylogenies shed light on triggers, dispersal mode, and phylogeography in the large adaptive radiations of cichlids and icefishes.

Abstract:

Adaptive radiation - the evolution of ecological and phenotypic diversity within rapidly multiplying lineages - is often though to be responsible for a great part of life on Earth. Prominent examples of adaptive radiation, such as Darwin finches on Galapagos, and Anolis lizards of the Caribbean, are well-investigated, yet open questions remain, e.g. why some clades radiate, and others do not. Particularly species-rich adaptive radiations occur in fishes, where, for example the colourful family of cichlids has diversified into over 1500 species in the Great Lakes of East Africa alone, supported by adaptations in mouth morphology, body shape, brooding behaviour, and colouration. In the marine realm the largest species flock can be found in Antarctic waters, where fishes of the perciform suborder Notothenioidei (icefishes) have radiated into over 130 species along with adaptations in buoyancy and freezing resistance. Here, we investigate the evolution of the largest lacustrine and marine species flocks using massive molecular datasets (>100 taxa, and on a genomic scale) and multiple cross-validated fossil constraints to resolve questions concerning the triggers of the radiation, modes of dispersal, and their phylogeography. In particular, we find strong support for transatlantic dispersal of cichlids, and that the evolution of antifreeze glycoproteins acted as a key innovation for the radiation of ice fishes in Antarctica.

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WED 24 AUG at 1200 - Room N0
Oral presentation *D2-Sy07-1200-O*

Symposium 7
Fossils and evolutionary biology

Rates of morphological evolution in seeds: Fossils and phylogeny

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Summary statement:

Phylogeny-based estimates of morphological rates of seed size evolution capture only part of the temporal variation documented by paleontological analyses.

Abstract:

Quantifying the evolution of morphological novelty is key to understanding relationships between environmental change and ecophenotypic variation on geologic time scales. Seed size evolution is an intriguing system because of the trait's correlates with biotic (e.g., dispersal vector, growth form) and abiotic (e.g., latitude, climate) factors. The fossil record shows that basal seed plants had small seeds (median = 68.7 mm3) but the maximum size of extant seed plants was reached by the Mississippian (ca. 330 million years ago). Although lower in species richness, the Paleozoic seed size distribution was not significantly different from extant gymnosperms. However, the extremely small seeds evolved in multiple angiosperm lineages appear to be unique to flowering plants.
I compare rates of morphological evolution (measured as change in variance of seed size among species over time in millions of years) estimated from (1) molecular phylogenies of extant taxa; and (2) stratigraphic ranges of Paleozoic taxa. Morphological variance is a useful metric because it is unitless and the variance of one lineage is 0. Results from the two methods are strikingly different. Although phylogeny-based rate estimates may be comparable to each other, results presented here demonstrate that they do not capture a significant portion of the true temporal variation. Specifically, phylogeny-based metrics capture only positive net change whereas paleontological results demonstrate that morphological variance has increased and decreased repeatedly over geologic time.

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WED 24 AUG at 0910 - Room N0
Invited talk *D1-Sy07-0910-I*

Symposium 7
Fossils and evolutionary biology

Cenozoic climate change, biogeography and diversity patterns: a diachronic perspective

Smith KT[1]
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Summary statement:

A time-series of mid-latitude Cenozoic fossil localities bracketing major climatic events implies significant range changes and a concentration of diversity into the tropics.

Abstract:

Climate shifted profoundly over the course of the Cenozoic. This era is commonly divided into an early "greenhouse" period of warm and equable temperatures, and an "icehouse" which saw the development large-scale glaciation on Antarctica. The Eocene in particular is bracketed by dramatic climatic events, beginning with the Paleocene-Eocene thermal maximum and concluding with global cooling which ushered in the icehouse climate of today.

In order to explore the influence of Cenozoic climate change on biogeography, I studied the squamates (lizards and relatives) from a time-series of mid-latitude fossil localities that bracket the Paleocene-Eocene and Eocene-Oligocene boundaries. The early Eocene witnesses the first occurrence of numerous squamates lineages, particularly anguids and iguanids, whose living relatives are largely confined to the Neotropics. These lineages evolved over the course of the Eocene and disappear from the record around the early Oligocene deterioration.

These results support the proposition that large-scale climate change caused significant meridional range shifts among squamates. This conclusion, in turn, implies that post-Eocene global cooling may have influenced the latitudinal diversity gradient not only by the extirpation of warm-adapted extratropical forms. Rather, diversity may have been concentrated into the tropics. Some taxa presently endemic to the tropics may have had extratropical origins.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy07-i003-R*

Symposium 7
Fossils and evolutionary biology

Reproductive investment in moa: a K-selected life history strategy?

Werner J[1], Griebeler EM[1]
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Summary statement:

Combining biological and paleontological knowledge enables us to reconstruct species traits which are only insufficiently or not preserved in the fossil record.

Abstract:

The exaggerated K-selected life history strategy of moa has been suggested as an important factor causing their rapid extinction observed soon after the arrival of Polynesian colonists in New Zealand. Classically a K-selected life history strategy is characterized by few, large offspring and low fecundity rates. We tested i) if eggs of moa were larger than the average of similar sized birds, ii) if all moa species had a clutch size between one and two eggs as suggested by the (sub-)fossil record and iii) we estimated annual number of broods. Therefore, we established allometries on body mass and different reproductive traits (egg mass, clutch mass, annual clutch mass) for extant close relatives of moa. These were applied to moa for which information on body mass, egg mass and clutch mass exists. Body mass and reproductive traits were highly correlated in extant close relatives. In contrast to our expectation (i), moa had egg to body mass relations as "average" extant birds. We were unable to rule out (expectation ii) whether they had extremely low clutch sizes (1-2 eggs, fossil record) or rather moderate sizes (4.5 to 7.4 eggs), predicted by the allometry. Depending on clutch size assumed, one or several (3-5) clutches per year and female are realistic for moa. The discovery of further fossil clutches will clarify which of these two alternatives is more realistic or if both reproduction strategies had existed in different moa species.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy07-i002-E*

Symposium 7
Fossils and evolutionary biology

Dating the models: robust temporal estimates of arthropod macroevolutionary events and divergences, with a focus on model genomic species

Wheat C[1], Wahlberg N[2]
[1]University of Helsinki, Bioscience, Helsinki, Finland, [2]University of Turku, Biology, Turku, Finland

Summary statement:

Phylogenomic analysis of arthropod divergences provides temporal insights into key macroevolutionary events and robust divergence estimates among the model genomic species.

Abstract:

Understanding the evolutionary history of the Arthropoda is central to understanding the tempo and mode of evolution on Earth, as it is the largest and most diverse animal phylum. While advances in phylogenomics have begun to clarify relationships among arthropods, parallel advances in relaxed clock molecular dating have yet to be applied to these large phylogenomic datasets. Such analyses are needed to investigate the Cambrian origins of arthropods and assess the subsequent macroevolutionary events such as the colonization of land, the evolution of flight and complete metamorphosis. Additionally, the 25 arthropod genomes currently available have yet to be integrated into a large phylogenomic study, leaving what is arguably the largest fraction of the research community without a robust phylogenetic and temporal foundation. Here, incorporating the current and emerging model genomic systems into a large scale phylogenomic study (122 taxa, 62 genes), we used a Bayesian relaxed molecular clock to simultaneously reconstruct robust phylogenetic relationships and the absolute times of divergences among the arthropods, with a focus on the model genomic species. We also conducted simulations to assess whether our analysis could detect a Cambrian explosion scenario had it occurred. Our analysis and simulations indicate a Precambrian origin of the arthropods following the last ‘snowball earth’ glaciation event of the Ediacaran (635 Mya), and significantly alter the generally accepted divergence times among important model genomic species. These findings provide an essential, empirically based foundation for macroevolutionary and comparative genomic study of the Arthropoda.

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Symposium 8

Predicting macroevolution from microevolution

Talks: *Room N0*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Upper floor campus canteen *Mensa*

Invited Speakers:

Emma Goldberg, Oliver Pybus

Organizers:

Gavin Thomas, Rob Freckleton

Description:

Most current quantitative macroevolutionary models are divorced from the ecological and microevolutionary processes that underpin broad-scale evolutionary trends. This symposium will explore how theory, empirical data and methodological approaches from diverse fields including community ecology and evolutionary genetics can reveal the processes that underpin macroevolutionary patterns.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy08-i001-R*

Symposium 8
Predicting macroevolution from microevolution

Getting from one host to the next: selection, genetic variation, and macroevolutionary pattern in complex parasite life cycles

Benesh D[1]
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Summary statement:

Concordance between optimality models, microevolutionary responses, and macroevolutionary patterns in the life cycle evolution of a model tapeworm.

Abstract:

Many parasites have complex life cycles in which they infect multiple hosts before reproducing. Transmission from one host to the next is a critical life history transition in these parasites, and the optimal size and age at transmission is thought to be shaped by growth and mortality rates experienced in the different hosts. I provide one of the few estimates of these rates for a parasite species, the trophically-transmitted tapeworm Schistocephalus solidus, and explore their consequences at both micro- and macroevolutionary levels. I focused on the transmission of the worm from its copepod first host to its stickleback second host. The parasite experiences far higher growth rates and far lower mortality rates in fish, suggesting any growth in the first host is wasted time. Artificial selection for rapid development in the first host produced no response, indicating that there is little potential in this species for evolutionary change in the predicted direction. Such constraints on change seem quite persistent, as other parasite species with comparable life cycles exhibit very similar growth and developmental rates. Even parasite taxa that have independently evolved a copepod-fish life cycle converge on this life history strategy. Thus, using inferences from optimality models, quantitative genetics, and macroevolutionary patterns, I conclude that particular life history strategies are universally associated with certain life cycles, which implies highly conserved selection pressures and/or functional constraints.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy08-i001-E*

Symposium 8
Predicting macroevolution from microevolution

Determinants of the evolution of weediness in the Capsella genus: niche breadth and variation of life-history traits

Caullet C[1], Reboud X[1], Le Corre V[1]
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Summary statement:

Determinants of the evolution of weediness are studied for two related plant species, by examining niche breadth and variation of life-history traits.

Abstract:

Identifying determinants of invasiveness and weediness –adaptation to man-made habitats- is a major goal in plant ecology. At the macro-evolutionary scale, weediness has redundantly evolved in numerous plant taxa. At the micro-evolutionary scale, weediness and invasiveness have been frequently connected to habitat shifts, to particular combination of traits' values, and/or to a higher level of intra-specific trait variation. We present empirical data for a pair of phylogenetically close annual species belonging to the genus Capsella (Brassicaceae), C. rubella and C. bursa-pastoris. These two species have dissimilar geographical ranges. C. rubella grows mainly in southern Europe and around the Mediterranean Sea, whereas C. bursa pastoris is an invasive that grows all over the world except in the tropics. C. rubella is a diploid, whereas C. bursa-pastoris is a tetraploid. The two species are otherwise very similar, having a nearly identical morphology and a similar reproductive system (high selfing).
First, the niche breadth of the two species was studied in an agricultural landscape located in their native range of sympatry (Fénay, France). C. bursa pastoris was more frequent and occurred in both cultivated and uncultivated habitats, whereas C. rubella was found only in the less disturbed habitats. Second, variation of life-history traits in the two species was measured in a common garden experiment. Results showed phenotypic divergence for several traits, as well as a higher genetic variation and higher level of plasticity in C. bursa pastoris as compared to C. rubella. Our study contributes to the understanding of the evolution of weediness in plants.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy08-i003-R*

Symposium 8
Predicting macroevolution from microevolution

Rapid body shape differentiation in the invasive cichlid Oreochromis mossambicus

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Summary statement:

Body shape differentiation in a global invasive cichlid species results both from historical and functional constraints.

Abstract:

Populations having recently invaded remote islands provide fruitful case studies to investigate the earliest stages of differentiation and speciation. In this context, identifying the respective implications of population relatedness, founder events and selective pressures is a key step to detect and understand incipient bursts of phenotypic diversity. We focus on the African cichlid fish Oreochromis mossambicus transplanted worldwide during the 20th century. We first used mtDNA and AFLP data to establish a genetic framework among 15 populations originated from native and invaded ranges. We then concentrate on a geometric morphometric approach to study body shape differentiation. We aim at (1) quantifying the constraints of population histories in shaping differentiation and (2) identifying environment-morphotype correlations possibly influencing differentiation. Genetic analyses indicate that invasive populations stem from a common genetic source and, as expected, exhibit a low genetic diversity. Surprisingly, shape differentiation primarily occurs at a macrogeographic scale and with no detected correlation with local ecological variation indicating that the phylogeographic background would mainly structure shape variation. In addition, a major axis of the shape space characterizing both macrogeographic and inter-population divergence is significantly related to morpho-functional traits. These traits could refer to different swimming abilities and to a release of predation pressure in novel habitats. Overall, our results illustrate the relevance of invasive species as models to investigate the effects of historical and functional constraints on phenotypic divergence.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy08-i004-R*

Symposium 8
Predicting macroevolution from microevolution

Plasticity and macroevolution: how temperature affects wing diversity

Gidaszewski NA[1], Debat V[2]
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Summary statement:

We explore the role of a microevolutionary process (phenotypic plasticity to temperature of the Drosophila wing) in the divergence of the species of the melanogaster subgroup.

Abstract:

Temperature is a major ecological factor, which has led to the evolution of the ability for organisms to produce different phenotypes when temperature changes (phenotypic plasticity). Plasticity to temperature is an extremely widespread phenomenon, known to evolve substantially. Yet, it was mostly studied as a microevolutionary process, whose role in macroevolution was little explored. The Drosophilids are a fascinating example of macroevolutionary diversity, with cosmopolitan and specialised species, which adapted to temperature. Wing plasticity has been extensively studied, revealing substantial evolution along latitudinal clines and among species, suggesting an adaptive plasticity. Yet, its physiological mechanism still remains unclear and the role of plasticity in species divergence has not been explored.
Here we explored the macroevolution of plasticity to temperature of wing morphology among the nine species of the Drosophila melanogaster subgroup, including two subpopulations of the ubiquitous species (D. simulans and D. melanogaster). Each species was raised at 3 different temperatures (14°C, 21°C and 28°C), allowing us to explore shape plasticity at 2 different temperature shifts. A morphospace was built using geometric morphometrics, to determine the shape changes observed among temperature shifts and species and directly compare them to those observed among species. By exploring the patterns of plasticity and macroevolution, this study contributed to enhance the role of phenotypic plasticity as a major macroevolutionary process and hence identifying the processes involved in the adaptation to climate change at both micro and macro-evolutionary scales.

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SUN 21 AUG at 1400 - Room N0
Invited talk *A3-Sy08-1400-I*

Symposium 8
Predicting macroevolution from microevolution

Selection on breeding system through multiple levels and modes

Goldberg EE[1]
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Summary statement:

The irreversible loss of self-incompatibility, its interactions with other traits, and its effects on lineage diversification inform and are informed by phylogenetic modeling.

Abstract:

Selection may operate simultaneously at multiple levels of evolutionary hierarchy, causing interactions between micro- and macroevolutionary processes. We illustrate the power of synthesizing data and methods from different scales in the study of self-incompatibility (SI)---the ability of a plant to recognize and reject its own pollen---in the nightshade family Solanaceae. Molecular and population genetic work indicates that after SI breakdown, fixation of self-compatibility (SC) in a population is rapid and irreversible. SI species in this family are consequently connected by a continuous history of functioning SI, and this knowledge strongly influences macroevolutionary inferences regarding breeding system. Despite irreversible loss in this family, phylogenetic analyses show that SI is maintained by selection at a different level: SC is associated with higher speciation but even higher extinction rates, so SI confers a greater rate of net diversification. Loss of SI can occur through two macroevolutionary modes. Within a lineage, SC mutants may increase in frequency until the parental species is replaced, or, in association with speciation events, rapid evolution of other traits in conjunction with SC may yield swift reproductive isolation. New phylogenetic methods are designed to quantify the contributions of these two modes of character change. Additional traits may also affect the evolution of SI and lineage diversification. Polyploidy directly causes breakdown of SI, and it provides a tractable example of how macroevolutionary inference can be customized to and benefit from study of character interactions and diversification.

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MON 22 AUG at 1420 - Room N0
Oral presentation *B3-Sy08-1420-O*

Symposium 8
Predicting macroevolution from microevolution

Diversification and the rate of molecular evolution in mammals

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Summary statement:

Using phylogenetically independent contrasts of mammalian sister clades, we do not find evidence of a link between clade size and rates of molecular evolution.

Abstract:

Recent research has indicated a positive association between rates of molecular evolution and diversification in a number of taxa. However debate continues concerning the universality and cause of this relationship. Here, we present the first systematic investigation of this relationship within the mammals. We used phylogenetically independent sister-pair comparisons to test for a relationship between substitution rates and clade size at a number of taxonomic levels. Total, non-synonymous and synonymous substitution rates were estimated from mitochondrial and nuclear DNA sequences. We found no evidence for an association between clade size and substitution rates in mammals, for either the nuclear or the mitochondrial sequences. We found significant associations between body size and substitution rates, as previously reported. Our results present a contrast to previous research, which has reported significant positive associations between substitution rates and diversification for birds, angiosperms and reptiles. There are three possible reasons for the differences between the observed results in mammals versus other clades. First, there may be no link between substitution rates and diversification in mammals. Second, this link may exist, but may be much weaker in mammals than in other clades. Third, the link between substitution rates and diversification may exist in mammals, but may be confounded by other variables.

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SUN 21 AUG at 1550 - Room N0
Oral presentation *A4-Sy08-1550-O*

Symposium 8
Predicting macroevolution from microevolution

From micro- to macroevolution: What do we need to explain and how do we do it?

Hansen TF[1]
[1]University of Oslo, CEES, Department of Biology, Oslo, Norway

Summary statement:

From microevolution to macroevolution

Abstract:

I will review and present some novel statistical patterns of macroevolution based on fossil time series and phylogenetic comparative data. I will then review what we know about important microevolutionary parameters such as evolvability and strengths and patterns of selection. I will use these patterns to evaluate some microevolutionary models and hypotheses for explaining macroevolutionary change.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy08-i005-R*

Symposium 8
Predicting macroevolution from microevolution

The phylogenetic distribution of extinctions in Early Jurassic ammonite assemblages

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Summary statement:

We explored new statistical methods for analyzing the role of phylogenetic relationships in the susceptibility to extinction among Jurassic ammonites.

Abstract:

We investigate the phylogenetic distribution of past extinctions by testing them for phylogenetic clustering (ie, species in a same clades are more extinction-prone than expected by chance). Our study focuses on ammonites (fossil cephalopods) from the Early Pliensbachian (Early Jurassic) in western Tethys. That part of the fossil record is suitable because it has been recently revised at the species level and it is now associated to a phylogenetic hypothesis that includes 214 species.
Phylogenetic clustering of extinctions can be measured either (1) by computing the correlation between two binary variables (extinction state vs. a single level of phylogenetic inclusiveness), or (2) between a binary variable (extinction state) and a continuous node-based phylogenetic distance, thus taking into account the entire phylogeny. For case (1), we computed the Pearson Phi correlation coefficient for various levels of the phylogenetic hierarchy. For case (2), we computed two indices with overall phylogenetic distances among species (Fritz and Purvis' D (2010) and a new index based on multidimensional scaling of a distance matrix), thus yielding a single value for the entire phylogeny. In both cases, confidence intervals were computed by randomizing the extinction state across species.
Results show that ammonite extinctions were significantly clustered, suggesting a strong signal from extinction-prone clades during the Early Pliensbachian. Indices do not seem to be significantly affected by tree balance or extinction rate. This ongoing work shall provide new insights on the evolution of ancient marine biodiversity from a phylogenetic perspective.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy08-i006-R*

Symposium 8
Predicting macroevolution from microevolution

Additive genetic variance of fitness-related traits – estimation based on Bayesian animal models and Integrated Nested Laplace Approximations (INLA)

Holand AM[1], Steinsland I[2], Martino S[2], Jensen H[1]
[1]Centre for Conservation Biology, Norwegian University of Science and Technology, Department of Biology, Trondheim, Norway, [2]Norwegian University of Science and Technology, Department of Mathematical Sciences, Trondheim, Norway

Summary statement:

The additive genetic variance of fitness-related traits was shown to be low using a new and fast method for inference for Bayesian animal models.

Abstract:

Estimates of the additive genetic variance of fitness-related traits (heritability) are vital in evolutionary biology as they give insight into the potential for evolutionary change and enable us to predict evolutionary response to selection. The animal model is a general linear mixed model (GLMM) that enables us to identify the genetic part of quantitative traits. To do inference for Bayesian animal models we use the recently introduced Integrated Nested Laplace Approximation (INLA) methodology. We demonstrate that the INLA methodology can be used for many versions of a Bayesian animal model using both simulated data and real data from natural house sparrow (Passer domesticus) populations. Additive genetic variances of Gaussian, Binomial and Poisson likelihoods / traits were estimated, showing low heritability of traits closely related to fitness. These results were compared with results using MCMC (Markov Chain Monte Carlo) methods. The two methods for inference gave similar results, but inference using INLA was significantly faster. We also introduce an R package, AnimalINLA, which will enable evolutionary biologists and animal breeders to easily do fast inference for Bayesian Animal models using INLA. We expect that this will aid our understanding of evolutionary processes in natural populations and in animal breeding.

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MON 22 AUG at 1400 - Room N0
Oral presentation *B3-Sy08-1400-O*

Symposium 8
Predicting macroevolution from microevolution

Evolution of significant units of diversity above the species

Humphreys AM[1], Barraclough TG[1]
[1]Division of Biology, Imperial College London, Ascot, United Kingdom

Summary statement:

We use simulations and analyses of empirical data to investigate the presence of significant, evolutionary entities above the level of the species.

Abstract:

Integration of evolutionary processes into the delimitation of species has seen major advances in recent years. For instance, development of algorithms for inferring the most likely species tree from a number of gene trees has allowed identification of putative species in the presence of hybridisation or incomplete lineage sorting. Likewise, analyses of branching patterns have been drawn upon to delimit significant, evolutionary clusters ('species') from time calibrated gene trees. Clusters are inferred at the point where coalescence shifts to speciation, thus making species delimitation explicitly process based. Identification of significant clusters in asexual organisms demonstrated that processes beyond reproductive isolation, e.g. divergent selection and geographic isolation, can cause significant clustering. This opens the possibility that the same processes can cause clustering above the level of reproductively isolated species as well. Delimitation of higher taxa (genera, families, etc.) is currently largely arbitrary, with no consideration of processes beyond shared ancestry (at best). This means that the reliability of higher taxa as meaningful units of diversity is questionable. In this talk we use simulations and analyses of empirical data to test the idea that the processes that cause clustering at the level of the species may cause clustering at broader scales as well. We use individual-based simulations to show under what conditions clustering above the species is expected and what conditions preclude cluster formation. Analyses of densely sampled time calibrated trees, for cowries (Cypraeidae) and Lepidoptera, are used to test these expectations.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy08-i007-R*

Symposium 8
Predicting macroevolution from microevolution

Natural variation of vulva development among different Pristionchus pacificus isolates

Kienle S[1], Sommer RJ[1]
[1]Max Planck Institute for Developmental Biology, Dept. for Evolutionary Biology, Tübingen, Germany

Summary statement:

Gonad ablation experiments revealed natural variation of vulva development among Pristionchus pacificus isolates. A candidate gene was mapped and is currently being tested.

Abstract:

The nematode Pristionchus pacificus has been established as a model system in evolutionary developmental biology and evolutionary ecology. Previous studies focused on macroevolutionary differences between the reference strains of P. pacificus (PS312) and Caenorhabditis elegans (N2). To add a microevolutionary perspective to the evo-devo studies in P. pacificus, we isolated more than 150 different strains of the species from around the world and examined natural variation. These strains showed high diversity, both at the molecular and the phenotypic level. One of the observed variations involves development of the vulva specifically due to induction by the gonad. The vulva (the egg laying organ of nematodes) develops from three vulva precursor cells (VPCs). In PS312 differentiation of the VPCs depends on a continuous and redundant Wnt signal from the somatic gonad and the posterior of the animal. However in some of the P. pacificus strains, VPCs were still able to differentiate after ablation of the gonad. To identify the involved loci we crossed the two isolates showing the most extreme phenotypes. We obtained recombinant inbred lines (RILs) by selfing individual F2 and near isogenic lines (NILs) by continuously backcrossing the RILs to PS312 animals. Gonad ablation experiments and genotyping of more than 200 RILs revealed a 430kb region on Chromosome I associated with the VPC differentiation trait. Currently we are testing a candidate gene in this interval by transgenesis experiments. Together, the microevolutionary perspective of P. pacificus vulva development is an effort to integrate evo-devo studies in evolutionary theory.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy08-i008-R*

Symposium 8
Predicting macroevolution from microevolution

Origin and diversification of the Neotropical butterflies “Taygetis” (Nymphalidae: Satyrinae)

Matos Maravi P[1], Wahlberg N[1]
[1]University of Turku, Department of Biology, Turku, Finland

Summary statement:

Diversification quantitative models reveal that the often-invoked geological events into the Neotropical biodiversity debate had no significant effect on “Taygetis” diversification

Abstract:

It has been proposed that the enormous species richness in the Neotropics is due to a complex interaction of factors including geological rearrangements, ecological dynamics and climate change during the past million of years. Moreover, recent works based on molecular phylogenetics have proposed the origin of diversity and major diversification processes to be dated mostly before the drastic climatic oscillations during the Quaternary but often ignoring diversification rate estimates. Based on a four gene dataset and a dated phylogenetic tree of a group of ten butterfly genera, the so-called “Taygetis-clade” (Nymphalidae, Satyrinae, Euptychiina), we argue that although the visual inspection through the phylogeny and Lineage Through Time (LTT) plots suggest the existence of periods of time of major changes in lineage origination which roughly coincide with the times of major uplift of the Andes cordillera and the termination of the long-lived Lake Pebas, two of the most-invoked geological events into the origin of Neotropical biodiversity debate, a quantitative macroevolutionary model reveal that actually there were no significant diversification rate shifts across the phylogeny. We hypothesize that the origin of “Taygetis” diversity in the Neotropics might be related to the expansion of ecological limits and the increase of limiting diversity capacity by the availability of new potential habitats rather than drastic change in diversification patterns caused by palaeogeographic events. Finally, we propose several systematic arrangements based on the inferred phylogenetic relationships in the poorly understood and taxonomically chaotic “Taygetis-clade”.

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SUN 21 AUG at 1650 - Room N0
Oral presentation *A4-Sy08-1650-O*

Symposium 8
Predicting macroevolution from microevolution

How diversification rates and diversity limits combine to create large-scale species-area relationships (SARs)

McInnes L[1], Kisel Y[1], Orme D[1]
[1]Imperial College London, Biology, Ascot, United Kingdom

Summary statement:

We present new analyses using data on the distributions, ages and traits of mammals to illustrate an integrated perspective on the evolutionary processes shaping SARs.

Abstract:

Species-area relationships have mostly been treated from an ecological perspective, focusing on immigration, local extinction, and resource-based limits to species coexistence. However, a full understanding across large regions is impossible without also considering speciation and global extinction. Rates of both speciation and extinction are known to be strongly affected by area and thus should contribute to spatial patterns of diversity. Here, we explore how variation in diversification rates and ecologically-mediated diversity limits among regions of different sizes can result in the formation of species-area relationships. We explain how this area-related variation in diversification can be caused by either the direct effects of area or the effects of factors that are highly correlated with area, such as habitat diversity and population size. We also review environmental, clade-specific, and historical factors that affect diversification and diversity limits but are not highly correlated with region area, and thus are likely to cause scatter in observed species-area relationships. We present new analyses using data on the distributions, ages and traits of mammalian species to illustrate these mechanisms; in doing so we provide an integrated perspective on the evolutionary processes shaping species-area relationships.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy08-i009-R*

Symposium 8
Predicting macroevolution from microevolution

Convergence is the natural outcome of processes driving adaptive radiation

Muschick M[1], Salzburger W[1]
[1]University of Basel, Zoological Institute, Basel, Switzerland

Summary statement:

Convergence in body and pharyngeal jaw shape in Lake Tanganyika´s cichlid fishes show that adaptive radiations produce convergences notwithstanding geographical settings.

Abstract:

Instances of convergence are known from replicate adaptive radiations, e.g. the recurrent ecomorphs of Anolis lizards on Caribbean islands. Intuitively, this would not be expected from radiations within a single continuous environment where similar species would co-occur and compete for resources. This competitive exclusion principle, however, attracted criticism from empirical studies and theoretical considerations and might be much less important than initially thought. Here, we present evidence for extensive convergence in an adaptive radiation, the cichlid fishes of Lake Tanganyika, that has taken place in a single lacustrine environment. We used a new, well supported molecular phylogeny for 71 Tanganyikan cichlid species in conjunction with a large set of morphological and ecological data as well as coloration patterns to detect cases of convergence. The observed instances of convergence include naturally and sexually selected traits, which differ in their relative importance throughout the history of the radiation. The pharyngeal jaws of these cichlids - an important trophic trait hypothesized to be a key-innovation - show a trajectory of shape evolution distinct from that of body shape or coloration. Possibly, these differences reflect discernible stages of an adaptive radiation. We argue that adaptive radiations driven by ecological speciation processes should be expected to produce convergences in general, regardless of the geographical settings.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy08-i010-R*

Symposium 8
Predicting macroevolution from microevolution

Sexually selected traits in butterflies : Canalization in the expression of a pleiotropic mutation

Nieberding CM[1], San Martin G[1], Saenko S[2], Brakefield PM[3]
[1]Université catholique de Louvain, Biodiversity Research Institute, Louvain-la-Neuve, Belgium, [2]Leiden University, Evolutionary Biology, Leiden, Netherlands, [3]Cambridge University, University Museum of Zoology, Department of Zoology,, Cambridge, United Kingdom

Summary statement:

A mutation modified pleiotropically two adaptive traits and epistatic interactions with the genetic background likely restored the wild-type phenotype by means of sexual selection.

Abstract:

Two major adaptive traits in the tropical polyphenic butterfly Bicyclus anynana are the production of male sex pheromone and the shape of the forewing eyespots, as these traits determine male mating success and are under sexual selection by females. The comet mutant originally displayed modified eyespots and sex pheromone production at all rearing temperatures, compared to wild-type males. Here we characterized the morphological (size of the androconia, the structures producing the pheromones, and eyespot shape), physiological (production of male sex pheromone), and behavioural (mating success) effects induced by the comet mutation across 5 larval rearing temperatures covering the natural range of the species (19°C to 28°C). Results reveal that a single recessive mutational event affects largely and pleiotropically the two adaptive traits. During the course of the experiments (across successive lab-generations), the comet phenotype reversed to wild type at higher, but not at lower, rearing temperature. Epistatic interactions between the comet mutation and the genetic polymorphism of wild type individuals was likely responsible for the rapid canalization of the mutation at higher temperature. Epistatic interactions also disentangled the effect of the mutation on the two adaptive traits, producing a range of individuals with varying degree of phenotypic change. Sexual selection exerted by females likely drove the canalization of the comet phenotypic effects back to normal at high, but not at lower, temperature.

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SUN 21 AUG at 1710 - Room N0
Oral presentation *A4-Sy08-1710-O*

Symposium 8
Predicting macroevolution from microevolution

Major processes and phylogenetic patterns of metacommunity evolution

Pontarp M[1]
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Summary statement:

We investigate the link between eco-evolutionary processes and macro-evolutionary patterns.

Abstract:

We develop a theory of competitive metacommunity evolution and identify three major processes responsible for the local diversification, coexistence and phylogenetic relatedness of species assemblages. Our model community consist of a set of separate habitat patches, or island, connected by random nearest-neighbor dispersal. Each habitat is characterized by a resource distribution along an abstract trait axis and we use an adaptive dynamics approach to model population dynamics, adaptation, and diversification, keeping track of the populations´ ancestry through the adaptive radiation process. Resulting communities of competitors can show varying levels of phylogenetic clustering, i.e., the degree to which the members of a local community are closer or more distantly related to each other than expected by chance. We show that the local rate of radiation, the rate of invasion of existing local communities, and the rate of colonization of empty habitats together determine whether a local community is phylogenetically overdispersed or clustered. Those three major processes are in turn dictated by the relative strength of local and regional habitat heterogeneity of the resource distributions. We show that high levels of phylogenetic clustering ("habitat filtering") are expected when both local habitat and regional heterogeneities are large. Low levels of clustering ("phylogenetic "overdispersion") are expected when local and regional resource heterogeneities are low. We also show how metacommunity properties such as species richness patterns and phylogenetic relatedness emerge from the interplay among the three major processes.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy08-i011-R*

Symposium 8
Predicting macroevolution from microevolution

Local adaptation in an evolutionary radiation: the role of population differentiation in speciation of the white proteas

Prunier R[1], Holsinger KE[2], Carlson JE[2]
[1]Michigan State University, Kellogg Biological Station, Hickory Corners, United States, [2]University of Connecticut, Ecology and Evolutionary Biology, Storrs, United States

Summary statement:

Differentiation in response to environmental gradients differs at the population and species levels in a young evolutionary radiation.

Abstract:

Adaptive radiations are responsible for much of the world's biotic diversity and, as such, much work has focused on understanding associations between species and their environments. However, in order to understand the mechanisms responsible for radiations, it is important to understand how trait-environment correlations within species are related to those among species because among-species differences ultimately arise from among-population differences. Here we investigate a young radiation, the white proteas (Protea section Exsertae, Proteaceae L.), to determine the degree to which trait-environment associations at the local population level mirror those at the species level and to assess the extent to which differences among species are an extrapolation of differences between populations or are the result of different processes. Using a structural equation model, we investigate the associations among seed, leaf, shoot, and root traits and the environment in greenhouse-grown seedlings from seeds collected across the ranges of the white protea species. We found that differentiation along a winter temperature gradient occurs primarily between species, while differentiation along gradients of summer drought and rainfall seasonality occurs both among populations within species and among species. In addition, species and population level trait-environment associations were usually in opposite directions, suggesting that speciation is not a simple extrapolation of the evolutionary processes leading to among-population differences.

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SUN 21 AUG at 1440 - Room N0
Invited talk *A3-Sy08-1440-I*

Symposium 8
Predicting macroevolution from microevolution

The evolutionary dynamics of RNA virus at different biological scales

Pybus OG[1]
[1]University of Oxford, Department of Zoology, Oxford, Turkey

Summary statement:

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Abstract:

The incredibly rapid evolution of many RNA viruses and retroviruses makes it possible to study viral genomic change though time. This enables the micro- and marco-evolution of natural viral populations to be observed directly, helping to understand the contribution of evolution to properties such as transmission and virulence. Further, for some viruses, a "fossil record" is available in the form of endogenous viral elements that integrated into host genomes millions of years ago. In this talk I will introduce new methods for measuring the rate of adaptive evolution in pathogen populations and illustrate these with data from influenza viruses, retroviruses and the hepatitis C virus. I will consider how the nature of viral evolution varies across short and long time-scales, and how it differs between the within-host and among-host biological scales.

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MON 22 AUG at 1440 - Room N0
Oral presentation *B3-Sy08-1440-O*

Symposium 8
Predicting macroevolution from microevolution

Evolution of floral variation mediated by pollinators in Narcissus: is there congruence between macro and microevolutionary levels?

Santos Gally R[1], Simon V[2], Perez Barrales R[3], Arroyo J[2]
[1]Universidad de Sevilla, Biologia Vegetal y Ecologia, Sevilla, Spain, [2]Universidad de Sevilla, Departamento de Biologia Vegetal y Ecologia, Sevilla, Spain, [3]Universidad de Sevilla, Sevilla, Spain

Summary statement:

Evolution of floral variation mediated by pollinators in Narcissus: is there congruence between macro and microevolutionary levels?

Abstract:

Darwin´s early work on the functional and evolutionary significance of plant sexual polymorphism has generated much interest in understanding how precise interactions between ecological and genetic mechanisms act on the evolution and maintenance of floral diversity. Heterostyly, the reciprocal position of the sexual organs, was considered by Darwin as a mechanism to promote cross pollination; where the precise deposition of pollen on the pollinator´s body is crucial to promote dissasortative mating. Because heterostyly is a convergent trait amongst at least 28 angiosperms families, reconstruction of the evolutionary pathways including floral conditions and their relationships to pollinator guilds could shed much light on underlying evolutionary mechanism of this polymorphism. In this sense, work on Narcissus has been very relevant, since the genus presents a variety of floral polymorphisms which may represent the ancestral and intermediate stages for the evolution of heterostyly and concomitant changes in flower form. Here we present results of a microevolutionary study on a style dimorphic species of Narcissus showing that ecological changes in the pollinator's fauna can lead to monomorphic populations. We then tested whether these processes are congruent at a macroevolutionary level in the whole genus. Phylogenetic comparative methods allowed us to explore the evolutionary association between pollinators, sex polymorphisms and perianth form, and test whether pollinator guilds drive evolutionary transitions in floral polymorphisms in Narcissus.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy08-i002-E*

Symposium 8
Predicting macroevolution from microevolution

Evolutionary ecology of Colonization: Adaptive potential of inbred founder populations

Swillen I[1], Vanoverbeke J[1], De Meester L[1]
[1]K.U.Leuven, Leuven, Belgium

Summary statement:

Using an experimental evolution approach, we quantify inbreeding depression and evolutionary potential of inbred offspring of Daphnia magna in comparison to outbred offspring.

Abstract:

In cyclical parthenogens, alternating phases of clonal and sexual reproduction, a population can in principle be founded by one individual and its clonal descendants. Although produced in large numbers, the sexual offspring of this founder clone are,by definition the product of genetic selfing. The combined effect of reduced genetic variation and inbreeding depression may limit evolutionay potential and viability of the population. Yet, purging among the massively produced offspring may in theory allow sufficient flexibility to respond to selection pressures. In this study we quantify the potential of a single colonist of the cladoceran, Daphnia, to establish a population that harbours sufficient genetic variation to monopolize resources in a newly colonized habitat through adaptive evolution and thus hamper the establishment success of secondary, outbred immigrants. By exposing laboratory populations to different selection pressures (predation, pesticides and parasites), we quantify inbreeding depression and evolutionary potential of offspring of single clones in comparison to outbred offspring. As such we want to assess whether large numbers of locally produced (but inbred) offspring can harbour comparable evolutionary potential as a limited number of outbred immigrants.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy08-i003-E*

Symposium 8
Predicting macroevolution from microevolution

Evolution of generation-biased gene expression and the origin of the embryophyte sporophyte

Szovenyi P[1], Rensing SA[1], Lang D[1], Wray GA[2], Shaw JA[2]
[1]University of Freiburg, Freiburg, Germany, [2]Duke University, Durham, United States

Summary statement:

Gene expression, land plants, bryophytes, alternation of generations.

Abstract:

The origin of plant alternation of generations and that of land plants are tightly coupled, and for this reason, elucidating the genomic mechanisms associated with the origin of the multicellular sporophyte are of fundamental importance. Toward this end we analyze gene expression differences associated with the alternation of isogenic sporophyte and gametophyte generations in bryophytes, extant representatives of early land plants, using a moss model system (Funaria hygrometrica) and high-throughput next-generation expression profiling. We find that differentiation in gene expression between the sporophyte and gametophyte generations is weaker in the bryophyte model system than in Arabidopsis thaliana. This is in line with the basal phylogenetic position of bryophytes and with the origin of alternating generations from a purely haplontic life-cycle. Comparative analysis of bryophyte and Arabidopsis gene expression data shows that there is limited conservation of generation-biased gene expression across land plants. However, genes showing shared sporophyte-biased expression in both Funaria and Arabidopsis appear to be enriched for biological pathways representing critical molecular adaptations to terrestrial life. Comparative analyses of Funaria and Arabidopsis transcription factor/regulator gene expression suggest that conserved regulatory networks are involved in growth and reproductive tissue development of the angiosperm and bryophyte sporophyte generations despite their morphological divergence.

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SUN 21 AUG at 1610 - Room N0
Oral presentation *A4-Sy08-1610-O*

Symposium 8
Predicting macroevolution from microevolution

Modelling character displacement on phylogenies

Thomas GH[1]
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Summary statement:

How does competition affect trait evolution on phylogenies? Using models of character displacement I reveal distinct signals of competition driven trait evolution.

Abstract:

How do competitive interactions between related species influence trait evolution on phylogenies? I apply previous models of two-species character displacement to the evolution of traits among multiple interacting species on phyloegentic trees. The dynamics of trait evolution are governed by the interplay between the intensity of species interactions, constraints and the effects of evolutionary history (phylogeny). I show that competition can leave distinct signals in the distribution of traits that may be detected even with data from only the phylogeny and contemporary trait values.

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MON 22 AUG at 1500 - Room N0
Oral presentation *B3-Sy08-1500-O*

Symposium 8
Predicting macroevolution from microevolution

Community assembly, evolution and geographic scaling: From ponds to islands

Vanoverbeke J[1], De Meester L[1], Urban MC[2]
[1]K.U.Leuven, Biology, Laboratory of Aquatic Ecology and Evolutionary Biology, Leuven, Belgium,
[2]University of Connecticut, Department of Ecology and Evolutionary Biology, Storrs, United States

Summary statement:

We model colonization success of multiple, competing species and compare results ranging from local interactions to adaptive radiation on islands.

Abstract:

Depending on the spatial scale of interest, theories of community assembly differ in how much they incorporate joint evolutionary and ecological dynamics. At regional scales, community ecologists often overlook adaptive evolutionary dynamics and instead assume that evolution occurs at a much lower rate than ecological dynamics. In contrast, biogeographic theories incorporate evolutionary dynamics, but generally neglect interactions between species. Here we explore the relative roles of ecological species sorting and evolution in multi-patch systems. Specifically, we model community assembly when multiple competing species colonize and potentially adapt to multiple niches. By evaluating results along a gradient in dispersal, we can evaluate the importance of evolutionary responses along a continuum from local adaptation in adjacent habitat patches to adaptive radiation on isolated islands. Our results indicate that the importance of adaptive evolution in determining community assembly within patches is increasing with reduced dispersal among patches. Where at the lowest levels of dispersal, adaptive radiation dominates our results, at intermediate levels of dispersal our results are reminiscent of some classical examples of colonization on islands, with each island having a distinct composition of pre-adapted species and species adaptively evolved to novel niches. By including evolution of assortative mating, we also explore to what extent reduced gene flow among differently adapted populations might facilitate the occurrence of reproductive isolation and speciation in newly colonized habitats.

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SUN 21 AUG at 1630 - Room N0
Oral presentation *A4-Sy08-1630-O*

Symposium 8
Predicting macroevolution from microevolution

Slow evolution of static allometries in stalk-eyed flies

Voje KL[1], Hansen TF[2]
[1]University of Oslo, Department of Biology, OSLO, Norway, [2]University of Oslo, Department of Biology, Oslo, Norway

Summary statement:

The static allometric slope of eye span in male stalk-eyed flies evolves slowly, indicating that the allometric slope is a potential constraining factor in adaptive evolution.

Abstract:

Proportional changes in traits following a power relationship, known as allometry, are widely recognized and much used in explaining both micro- and macroevolutionary trends. Whether the allometric slope is a constraining factor in adaptive evolution has been debated, but studies of the evolvability of the slope coefficient on an evolutionary time scale are missing. We use a phylogenetic comparative approach to disentangle the relative effects of adaptation and phylogenetic inertia (resistance to adaptation) in the evolution of the static allometric slope of eye span in the fly family Diopsidae. Despite a strong selection pressure, it takes approximately 3.5 million years (about 20 million generations) for the allometric slope in male flies to move half the distance from the ancestral state to the optimum defined by the strength of sexual selection in each lineage. Our results therefore tend to disagree with a high evolutionary flexibility of static allometric slopes.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy08-i012-R*

Symposium 8
Predicting macroevolution from microevolution

Phylogeographic structure of Pinus densata revealed an ancient colonization history on the Tibetan Plateau

Wang B[1], Mao J-F[2], Gao J[2], Zhao W[2], Wang X-R[1]
[1]Umeå University, Department of Ecology and Environmental Science, Umeå, Sweden, [2]Institute of Botany, CAS, State Key Laboratory of Systematic and Evolutionary Botany, Beijing, China

Summary statement:

Mitochondrial and chloroplast phylogeography of Pinus densata

Abstract:

Pinus densata is a successful homoploid hybrid species that occupies a habitat from which both of its parental species are absent. Its colonization of vast areas of the southeastern Tibetan Plateau is fascinating but not well defined. To shed light on how it colonized and became established on the plateau, we surveyed paternally inherited chloroplast (cp) and maternally inherited mitochondrial (mt) DNA variation within and among 54 populations of P. densata and its putative parental species throughout their distribution. Strong spatial genetic structures of both cp and mtDNA were detected in P. densata. A putative ancestral hybrid zone in the northeastern periphery of P. densata was identified, and from there it is proposed that the species migrated westwards to colonize the plateau. Along the route of colonization, consecutive bottlenecks and surfing of rare alleles caused significant reduction of gene diversity and strong population differentiation. The direction and intensity of introgression from parental species varied among geographic regions. The western range of the species seems to have been isolated from seed and pollen flow for a long time. The observed spatial distribution of gene diversity in P. densata reflects the persistence of the species on the plateau during the last glaciation. Both ancient and contemporary population dynamics contributed to the spatial distribution of genetic diversity in P. densata, which in turn characterizes its evolutionary history.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy08-i004-E*

Symposium 8
Predicting macroevolution from microevolution

Silica - a secondary plant compound affecting population dynamics of the root vole, Microtus oeconomus

Wieczorek M[1], Zub K[1], Szafrańska P[1], Konarzewski M[1,2]
[1]Mammal Research Institute Polish Academy of Sciences, Bialowieza, Poland, [2]Institute of Biology University of Bialystok, Bialystok, Poland

Summary statement:

Silica in plants as a potential selection factor driving population dynamics of the root vole, Microtus oeconomus.

Abstract:

It has been hypothesized that secondary plant compounds may drive dynamics of rodent populations. To test it we analyzed the relationship between concentration of silica in the fibrous tussock sedge (Carex appropinquata) and density of the root vole population (Microtus oeconomus), enclosed in natural habitat. Our results showed that there was a delayed-density dependence of silica concentration in plants. Intense grazing during peak densities of voles induced high rates of silica deposition in sedges. Conversely, low intensity of grazing resulted in a low levels of silica in plants. Correspondingly, there was a delayed-density dependence in body mass- corrected resting metabolic rate (RMR) of voles. We hypothesize that this was driven by changes in metabolic costs of maintenance of voles' guts, and reflects metabolic costs of repair of guts' damage and reduction of nutrient absorption incurred by abrasive properties of silica.
Considering a potentially adaptive role of physiological mechanism, we also evaluated the genetic component of variation in RMR. The highest narrow sense heritability of RMR was found when past high abundance of voles induced high levels of silica in plant food. Our results suggest that silica may act as a selection factor driving population dynamics of voles.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy08-i005-E*

Symposium 8
Predicting macroevolution from microevolution

Unequal evolutionary lability between abdominal and caudal vertebral numbers in a fish Oryzias latipes

Yamahira K[1]
[1]University of the Ryukyus, Tropical Biosphere Research Center, Okinawa, Japan

Summary statement:

Field collections and lab experiments suggested that unequal evolutionary lability between abdominal and caudal regions may have restricted morphological diversification of a fish.

Abstract:

Because body axes of fish consist of two anatomically distinct vertebrae: abdominal and caudal, one type may be more variable in number than the other and thus contribute more to morphological diversification. Vertebral observations of wild populations of the medaka (Oryzias latipes) revealed that the number of abdominal vertebrae increases with increasing latitudes, whereas caudal vertebrae do not vary systematically across latitudes. Laboratory experiments revealed that this latitudinal cline in abdominal vertebral number persists in a range of common environments, suggesting local adaptation of abdominal vertebral numbers. Offspring-midparent regressions demonstrated substantial heritability of abdominal vertebral numbers in each of two latitudinally extreme populations, whereas the heritability of caudal vertebral numbers was not significant. Moreover, the genetic correlation between abdominal and caudal vertebral numbers was very weak. These results indicate that abdominal and caudal vertebrae are controlled by separate developmental modules, and that they can evolve independently. The weak heritability of caudal vertebrae suggests that the evolution of caudal vertebrae may be restricted, causing unequal evolutionary lability between abdominal and caudal regions. This genetic constraint may have restricted morphological diversification of not only this fish but also the order Beloniformes as a whole.

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Symposium 9

Polyploid ecological genomics

Talks: *Room N0*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Upper floor campus canteen *Mensa*

Invited Speakers:

Brian Husband, Jonathan Wendel

Organizers:

Christian Parisod, Malika L Ainouche

Description:

Much progress was accomplished toward understanding the mechanisms driving evolution of polyploid genomes and the biological consequences of polyploidy in the wild. However, the genomics and ecology of polyploid lineages remain to be integrated. This symposium offers an opportunity for molecular and ecology people to explore concepts and tools that could unify research in ecological genomics.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

TUE 23 AUG at 1630 - Room N0
Oral presentation *C4-Sy09-1630-O*

Symposium 9
Polyploid ecological genomics

Ecological genomics of the recent Spartina hybrids and allopolyploid invading salt-marshes

Ainouche ML[1], Chelaifa H[1,2], Ferreira de Carvalho J[1], Bellot S[1,3], Salmon A[1]
[1]University of Rennes 1, Rennes, France, [2]URGV, Evry, France, [3]University of Munich (LMU), Munich, Germany

Summary statement:

Spartina, hybridization, polyploidy, transcriptome evolution, ecological genomics, microarrays, next-generation sequencing.

Abstract:

Hybridization and polyploidy represent recurrent and ongoing processes in natural populations of genus Spartina (Poaceae, Chloridoideae). This genus offers then an excellent opportunity to explore the genomic consequences of reticulate evolution and genome duplication at various evolutionary time scales. In the last years, various lines of data were gathered on the genetic context of the hybrid and allopolyploid formation in natural populations, phylogenetic relationships among polyploid lineages and genome evolutionary dynamics of recent European hybrids S. x neyrautii and S. x townsendii and its allopolyploid derivative S. anglica. Genome expression evolution resulting from hybridisation and polyploidy was investigated in controlled environmental conditions using heterologous Oryza sativa microarray, which revealed various non-additive parental expression patterns, including maternal expression dominance and transgressively expressed genes that include stress- and growth-related genes. We are now exploring utility of next-generation sequencing to develop Spartina-specific genome analysis tools, in order to (i) identify homeologous gene copies from the different duplication events in the hexaploid parental species and their allo-dodecaploid derivative (ii) explore the deepest history of polyploid Spartina lineages (iii) to investigate repetitive genomic components of the genome which are most likely target to epigenetic regulation following allopolyploidy and (iiii) develop genome expression analyses targeting ecologically relevant genes suspected to be involved the adaptive success of the invasive Spartina anglica that has colonised a vacant niche on the salt-march.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy09-i001-R*

Symposium 9
Polyploid ecological genomics

The association between polyploidy and clonality in Chamerion angustifolium

Baldwin SJ[1], Husband BC[1]
[1]University of Guelph, Integrative Biology, Guelph, Canada

Summary statement:

This study involves a fine-scale comparison of the abundance, genetic divergence, and spatial organization of diploid and tetraploid clones of the plant, Chamerion angustifolium

Abstract:

Since the beginning of the 20th century Evolutionary Biologists have observed a strong association between polyploidy and asexuality. Although repeatedly confirmed with vegetation surveys, the reason for this association is unknown. The most common hypothesis is that populations with asexual reproduction are more likely to produce polyploid populations since asexuality circumvents many barriers to establishment (i.e. mate limitation and between-ploidy mating). It is also possible for polyploidy to increase asexuality directly through genome duplication or indirectly through selection. In this study we examine the size and diversity of clones in the mixed-ploidy, clonal species Chamerion angustifolium by addressing the following three questions. First, is asexuality through clonality greater in tetraploids than in diploids? If genome duplication promotes asexuality we expect fewer clones and less genetic similarity between clones in tetraploids than in diploids. Second, is the spatial organization of clones different between ploidies? If there is selection against between-ploidy mating during polyploid establishment, we expect more clumping in tetraploid clones than in diploid clones. Third, is genetic variation larger in tetraploids than in diploids? We expect greater genetic diversity in tetraploids because of increased Ne. From each of nine sites in the Canadian Rockies (three diploid, three tetraploid and three mixed-ploidy) we collected approximately 100 ramets along 10m2 grids. AFLP genotypes and ploidy were then determined. This will be the first study to empirically test the degree and nature of clonality between ploidies in a natural population.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy09-i001-E*

Symposium 9
Polyploid ecological genomics

Genome size variation along the altitudinal gradient in Mercurialis perennis L.

Cvetkovic D[1], Jovanovic V[2], Blagojevic J[2]
[1]Faculty of Biology, University of Belgrade, Belgrade, Serbia, [2]Institute for Biological Research, University of Belgrade, Belgrade, Serbia

Summary statement:

Genome size was positively correlated with altitude in Mercurialis perennis L. (Euphorbiaceae) populations representing the largest part of its altitudinal range (190-1730m asl).

Abstract:

Background and aim: Intraspecific genome size variation in plants has been subject to considerable research interest. Correlations of genome size with various ecological and geographical variables, and specifically with altitude, were analysed in numerous plant taxa, but the results were often contradictory. The aim of present study was to examine intraspecific genome size variation in Mercurialis perennis L. (Euphorbiaceae) along the altitudinal gradient. Mercurialis perennis is a dioecious perennial with wide geographic and altitudinal distribution in Europe. It is known as the example of cytogenetic diversity; more than 40 cytotypes were described, with 2n = 42 – 112.
Methods: We analyzed samples from 11 populations from Serbia, representing altitudinal range from 190 to 1730m a.s.l. Genome size was estimated using flow cytometry on fresh leaf material. Chromosome counts were done on material obtained from root tips.
Results: Mercurialis perennis has shown remarkable intraspecific variation in genome size along the analysed gradient; the mean DNA content differed up to 1.3-fold. Genome size showed significant positive correlation with altitude; higher values were found in montane populations compared to lowland ones. Considering ploidy-level variation, our results reveal that octoploids are most represented. Chromosome numbers varied in populations at all altitudes (total range 51-74); although higher numbers were found in montane populations, this difference was not significant.
Conclusion: genome size was positively correlated with altitude in Mercurialis perennis populations representing the largest part of its altitudinal range (190-1730m a.s.l.).

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TUE 23 AUG at 1500 - Room N0
Oral presentation *C3-Sy09-1500-O*

Symposium 9
Polyploid ecological genomics

Overcoming the multiple gene copy problem in polyploid genomics with next-generation sequencing of barcoded amplicon mixtures

Griffin PC[1,2], Robin C[1], Hoffmann AA[1,3]
[1]University of Melbourne, Department of Genetics, Parkville, Australia, [2]University of Neuchâtel, Institute of Biology, Neuchâtel, Switzerland, [3]University of Melbourne, Department of Zoology, Parkville, Australia

Summary statement:

We present a simple method for obtaining all alleles from multiple-copy genes in multiple taxa using 454 sequencing, demonstrated in 60 individuals from 11 polyploid Poa species.

Abstract:

Molecular phylogenetic and population genetic studies of polyploid organisms have been limited in the past. Sequencing multiple-copy nuclear genes by Sanger sequencing has usually required expensive and low-throughput bacterial cloning. We demonstrate that next-generation sequencing of a simple barcoded amplicon mixture can reliably sample all alleles of homeologous loci in multiple individuals of multiple polyploid taxa. This next-generation sequencing method is more affordable than and at least as reliable as bacterial cloning. It could be applied to any experiment involving sequencing of amplicon mixtures.

Using 64 3-bp barcodes, we successfully sequenced three chloroplast and four nuclear gene regions (each of which contained two gene copies with up to two alleles per individual) in a total of 60 individuals across 11 species of sympatric Australian alpine Poa grasses. This method had high replicability, a low sequencing error rate (after appropriate quality control) and a low rate of missing data. Our results support a common allotetraploid ancestor for all Australian alpine Poa species. Extensive allele sharing is evident among species and so we recommend that the current taxonomy be re-examined, but co-estimation of gene and species trees with the *BEAST software revealed some species and geographic structure. We also detected hypermutation in the trnH-psbA chloroplast marker, suggesting it should not be used as a land plant barcode region.

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TUE 23 AUG at 1400 - Room N0
Invited talk *C3-Sy09-1400-I*

Symposium 9
Polyploid ecological genomics

Evolutionary dynamics of polyploidy: Insights from synthesized polyploids

Husband BC[1]
[1]University of Guelph, Integrative Biology, Guelph, Canada

Summary statement:

Experiments involving synthetic polyploids have provided new insights into the evolutionary dynamics and ecological attributes of polyploids in natural plant populations.

Abstract:

Polyploidy, or whole genome duplication, has occurred repeatedly throughout the diversification of plants and animals and is widely viewed as a rapid mechanism of speciation and adaptation. However, the population processes by which polyploids arise and establish, and the role of genome duplication versus selection in driving ecological divergence and reproductive isolation, are poorly understood. Here, I describe an ongoing research program into polyploid evolution in the perennial plant, fireweed (Chamerion angustifolium, Onagraceae). Using synthesized polyploids along with field experiments and genetic markers, a dynamic picture is emerging in which polyploids arise at high frequencies within diploid populations, and their establishment is facilitated by assortative mating, mediated by reproductive and ecological divergence. Surprisingly, experimental research using synthesized polyploids reveals that divergence in reproductive and ecological traits is not fully established through the genome duplication. Rather, selection after genome duplication may be just as important and may occur at altered rates in polyploids. Our results suggest that the common portrayal of polyploid speciation is perhaps an oversimplification and underestimates the importance of the interaction between selection and genome duplication in guiding the evolution of species divergence.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy09-i002-R*

Symposium 9
Polyploid ecological genomics

Population genetic study of an asexual bdelloid rotifer species and its gene expression pattern in response to desiccation and radiation

Li X[1], Hespeels B[1], Flot J-F[1], Van Doninck K[1]
[1]University of Namur (FUNDP), Biology, Namur, Belgium

Summary statement:

Population genetic study of the asexual bdelloid rotifer Adineta vaga and its gene expression pattern after rounds of desiccation and radiation.

Abstract:

Rotifers of the class Bdelloidea are abundant micro-invertebrates well known for their remarkable ability to survive desiccation at any stage in their life cycle and their long-term persistence as obligate asexuals. Moreover, they are extraordinarily resistant to ionizing radiation, being able to resume reproduction after a dose of radiation that causes hundreds of DNA double strand breaks (DSBs). Sequencing of selected genomic regions has demonstrated that bdelloid rotifers are degenerate tetraploids, and the two colinear chromosome pairs have been proposed to act reciprocally as templates for the repair of DNA double-strand breaks that may occur after desiccation (see Poster Hespeels et al.). Desiccation is a phenomenon that bdelloid species experience frequently in the semi-terrestrial environments they inhabit. It has also been postulated that desiccation and improper DNA repair may create genetic variability.
However, population genetic studies are still lacking for natural bdelloid rotifer populations. Therefore, we used mitochondrial cytochrome c oxidase subunit I (COI) gene and microsatellites developed by 454 sequencing to study the genetic diversity and population genetic structure of bdelloid rotifer species Adineta vaga in various natural mosses and lichens.
Furthermore, we took advantage of the ongoing de novo sequencing of the complete genome of A. vaga to investigate which genes are expressed by bdelloids in response to desiccation and radiation.

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TUE 23 AUG at 1440 - Room N0
Oral presentation *C3-Sy09-1440-O*

Symposium 9
Polyploid ecological genomics

Genome duplication in amphibians and fish: An extended synthesis

Mable BK[1], Alexandrou MA[2], Tayolor MI[2]
[1]University of Glasgow, Institute of Biodiversity, Animal Health & Comparative Medicine, Glasgow, United Kingdom, [2]Bangor University, Environment Centre Wales, Molecular Ecology and Fisheries Genetics Laboratory, Bangor, United Kingdom

Summary statement:

Geographic, ecological, and phylogenetic distributions of sexually reproducing polyploid fish and amphibians are reviewed to assess what drives their formation and establishment.

Abstract:

Whole genome duplication (WGD) is widely accepted as an important evolutionary force in plants, but is less recognised as a driver of animal diversification. We review the current geographic, ecological, and phylogenetic distributions of sexually reproducing polyploid fish and amphibians (the vertebrates for which polyploidy is most common) and question what factors drive their formation and establishment. We find that although polyploidy is phylogenetically restricted in both taxonomic groups, difficulty of detection could mean that it is more frequent than documented. The diploid ancestors of polyploids in both groups are characterized by external reproduction in freshwater environments, where variation in temperature during the breeding season would be common. Since polyploidy can be experimentally induced through unreduced gamete formation by temperature or pressure shock, this could enhance the rate of polyploid formation. In addition, the production of large numbers of gametes and group breeding in relatively confined areas could increase the probability of compatible gamete combinations. Although the relative rates of autopolyploidy and allopolyploidy are unknown, both groups have a propensity to form reproductively successful hybrids and to retain duplicate genes following WGD. Unlike plants, we find no clear association of sexually reproducing polyploids with range expansion, harsh environments, pathogen responses, physiological adaptations, or risk of extinction, which could suggest that stronger correlations in plants may be driven by shifts in mating system more than ploidy. However, insufficient data currently exist to test this hypothesis.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy09-i003-R*

Symposium 9
Polyploid ecological genomics

Genomic assessment of sequence divergence and expression levels in sexual vs asexual lineages of a New Zealand snail

Neiman M[1]
[1]University of Iowa, Biology, Iowa City, United States

Summary statement:

Comparisons of sequence divergence and expression levels among EST libraries from 2 sexual and 2 asexual lineages of a New Zealand snail reveal few initial major differences.

Abstract:

While sexual reproduction has been the subject of substantial inquiry in evolutionary biology, how sex affects genomic evolution and expression remains largely unstudied, especially in closely-related sexual and asexual non-model systems. Here, we used high-throughput next-generation sequencing of cDNA libraries generated from 2 sexual and 2 asexual lineages of Potamopyrgus antipodarum, a New Zealand freshwater snail that has become a natural model for the study of sex, to perform an initial assessment of how sex affects sequence evolution and gene expression. After de novo assembly of 20066 contigs and sequence-similarity-based annotation of 3190 contigs, we compared contig expression between sexual and asexual populations in order to identify genes putatively underlying the difference in reproductive mode. We found that 239 contigs were differentially expressed between sexuals and asexuals, with overexpression documented in 169 contigs in sexuals and in 70 contigs in asexuals. An analysis of gene ontology enrichment amongst the differentially expressed genes showed that genes involved in protein catalysis were relatively overrepresented, but that there was no difference in the extent of overexpression between sexual and asexual transcriptomes. We also did not detect any relationships between across-lineage sequence divergence and differentiation of expression levels, suggesting that changes in gene regulation – if any- have occurred independently of changes in DNA sequence.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy09-i002-E*

Symposium 9
Polyploid ecological genomics

Exploring Bayesian segregation analysis with simulated data: SSR inheritance patterns in the tetraploid plant Bromelia antiacantha (Bromeliaceae)

Pinheiro FG[1], Zanella CM[2], Goetze M[2], Buttow MV[2], Janke A[2], Bered F[2]
[1]Universidade Federal do Rio Grande do Sul, Estatística, Porto Alegre, Brazil, [2]Universidade Federal do Rio Grande do Sul, Genética, Porto Alegre, Brazil

Summary statement:

We explore Bayesian allelic segregation analysis through virtual progenies intending to discriminate loci inheritance patterns and infer polyploid origin of Bromelia antiacantha.

Abstract:

Polyploidy is an important phenomenon for evolution in plants. The investigation of inheritance patterns of molecular markers through allelic segregation analysis is a reliable alternative to discriminate between tetrasomic and disomic inheritance, which indicates autopolyploid or allopolyploid origins respectively. Bayesian procedures are an appropriate way to access inheritance patterns since the results obtained are not biased. However, its limitations remain poorly explored, e.g. how a specific allelic combination between parents, which represents a crossing type, can affect the method performance. The aim of this study was to find, through virtual progenies, the crossing types between tetraploid parents that can be correctly identified by Bayesian segregation analysis, as well to determine the appropriate number of individuals in their progenies. Also we intend to infer the polyploidy origin of a tetraploid B. antiacantha by analyzing the allelic segregation of microsatellite markers in progenies of controlled crossings. The meiotic behavior and pollen viability will be analyzed in order to support the segregation data. The results from simulations showed that the accuracy of Bayesian segregation analysis is affected proportionally by the number of exclusive alleles in parents. Moreover, the number of plants required is inversely proportional to the test accuracy. Until the moment, 24 individuals from a single cross and their parents were genotyped with two SSR loci and each marker points significantly to an opposite inheritance pattern. The mean pollen viability was 97.72 ± 0.2% which suggest an apparent regular meiosis to be confirmed with the meiotic analysis.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy09-i003-E*

Symposium 9
Polyploid ecological genomics

Cytogenetic diversity and ploidy variation in diploid and polyploid Limonium species

Róis A[1], Espírito-Santo D[1], Sharbel TF[2], Caperta AD[1]
[1]Instituto Superior de Agronomia, Technical University of Lisbon, Secção de Genética, Centro de Botânica Aplicada à Agricultura, Lisbon, Portugal, [2]Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Apomixis Research Group, Dept of Cytogenetics and Genome analysis, Gatersleben, Germany

Summary statement:

Chromosome diversity and ploidy variation within populations is demonstrated for diploid and polyploidy Limonium species revealing high diversification within these complex groups.

Abstract:

The genus Limonium Miller, a taxonomically intricate group, is the most species-rich in the Plumbaginaceae comprising sexual and apomictic herbs and subshrubs. Individuals from the L. ovalifolium complex have been described as sexual, whereas those from the L.multiflorum were reported as apomictic. Previous studies have shown that polyploid apomictic species present karyological polymorphisms that were used to infer their ploidy levels. We conducted a detailed characterization of 9 Portuguese populations from sexual and apomictic species through cytogenetic analysis and flow-cytometry screens in leaves and seeds. Our studies revealed a surprisingly intra- and inter-population diversity in terms of chromosome morphology, number, and ploidy variation, both in sexual as in apomictic accessions. Chromosome peculiarities such as variable numbers of small chromosomes or presence of chromosomes with a "rod-like" morphology were detected in both species complexes. Fluorescence in situ hybridization revealed correlations between ploidy levels and numbers of rDNA loci in sexual and apomictic taxa. Although most L.ovalifolium individuals are found to be diploids, we unexpectedly detected some aneuploids and triploids. Also in L.multiflorum, usually described as an apomictic and polyploid species, we observed intra- and inter-population variation concerning ploidy level. The most striking observation was the identification of diploid individuals in some L. multiflorum accessions. The coexistence of different cytotypes and intraspecific variation concerning ploidy level reveal high diversification in these complex groups.

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TUE 23 AUG at 1710 - Room N0
Oral presentation *C4-Sy09-1710-O*

Symposium 9
Polyploid ecological genomics

Transposable elements in allopolyploid wild wheats and potential genomic conflicts at hybridization

Senerchia N[1], Parisod C[1], Felber F[1]
[1]University of Neuchatel, Neuchâtel, Switzerland

Summary statement:

Artificial crosses and TE fraction analysis in allopolyploid wild wheats characterize potential genomic conflicts at hybridization.

Abstract:

Allopolyploidy is a fascinating model that associates interspecific gene flow and genome reorganization. Transposable elements (TE) are highly mutagenic, repressed by various epigenetic mechanisms, and are postulated to induce genomic conflicts at hybridization. TE activation can trigger structural and epigenetic modifications, thus playing a central role in fuelling genome reorganization and reproductive isolation during polyploid speciation. Using Aegilops allotetraploid species, we intend to evaluate how TE-induced genome reorganization influences hybrid viability and stability. Reciprocal and spontaneous crosses between pairs of species in experimental sympatry were done. In the same time, TE genome fraction has been characterized for Ae. cylindrica and Ae. geniculata using 454 massive sequencing of shotguned DNA. We then developed specific bioinformatic tools to analyze short sequences (~1’300’000 reads of ca 380bp) corresponding to known TEs. Reciprocal crosses revealed asymmetrical hybridization rates supporting the genome conflict hypothesis. TE-fraction analysis detected specific differences in TE content. The most abundant TEs are considered as having influenced recent genome evolution and those TEs showing dissimilar distribution between a species are postulated to be major candidates for inducing genome conflicts at hybridization. Future work will assess genome reorganization in artificial hybrids and introgression between wild populations in order to better understand the impact of TEs on interspecific gene flow.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy09-i005-R*

Symposium 9
Polyploid ecological genomics

Polyploidization induced genomic and epigenetic restyling in the wheat-rye system

Tomás D[1], Bento M[1], Gustafson JP[2], Viegas W[1], Silva M[1]
[1]CBAA, Instituto Superior Agronomia, Technical University of Lisbon, Tapada da Ajuda, Lisboa, Portugal, [2]Curtis Hall, University of Missouri, Columbia, United States

Summary statement:

Genomic restructuring of retrotransposon and microsatellite sequences and epigenetic remodeling of rDNA in triticale and wheat-rye addition lines.

Abstract:

Polyploidization is a major evolutionary process where two or more genomes are joined into the same nucleus. Sharing of the same nuclear environment leads to genetic and epigenetic modifications that are involved in polyploids higher geographic dispersion.
The synthetic intergeneric allopolyploid triticale results from the hybridization of wheat (Triticum ssp.) and rye (Secale cereale L.) and is used as the starting point to the production of wheat lines with the addition of rye chromosomes. The maintenance and stability of rye chromatin in the wheat background is correlated with the amount of heterochromatin introgressed.
We used PCR-based methodologies to assess genetic rearrangements in triticale and wheat-rye addition lines involving repetitive genome fractions, namely retrotransposon, microsatellite and rDNA. Comparative analysis of the banding profiles disclosed higher levels of sequence elimination in the addition lines comparatively to triticale, involving preferential elimination of rye-origin bands. rDNA sequences presented however a distinct dynamics since wheat-origin rDNA spacer sequences seem to be lost in the presence of rye rDNA loci. rDNA transcription levels were also evaluated through Real Time quantitative PCR revealing distinct levels of wheat- rDNA transcription between wheat lines with different rye chromosomes. The results obtained emphasize the role of genome rearrangements and epigenetic remodeling in polyploid evolutionary success and in the ability of hybrid genotypes to colonize new environmental niches.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy09-i006-R*

Symposium 9
Polyploid ecological genomics

Simultaneous Mendelian and clonal genome transmission in an all-triploid vertebrate

Ustinova J[1], Stöck M[2], Colliard C[2], Schartl M[3], Moritz C[4], Perrin N[2]
[1]Karlsruhe Institute of Technology (KIT), Zoologisches Institut I, Lehrstuhl für Zell- und Neurobiologie, Karlsruhe, Germany, [2]University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland, [3]University of Würzburg, Lehrstuhl für Physiologische Chemie I, Theodor-Boveri-Institut, Biozentrum, Würzburg, Germany, [4]University of California, Berkeley, Museum of Vertebrate Zoology, Berkeley, United States

Summary statement:

Polyploid speciation, vertebrates, hybridization, triploidy, reproductive modes, extreme environment, selection

Abstract:

Meiosis in triploids faces the seemingly insuperable difficulty of dividing an odd number of chromosomes by two. Triploid vertebrates usually circumvent this problem either through asexuality, forms of hybridogenesis, or meiotic hybridogenesis, which involves a reproductive community of different ploidy levels and genome composition. Batura toads (Bufo baturae), however, present an all-triploid sexual reproduction and a new reproductive mode in vertebrates ("pre-equalizing hybrid meiosis"). This hybrid species has two genome copies carrying a nucleolus-organizing region (NOR+) on chromosome 6, and a third copy without it (NOR-). Males only produce haploid NOR+ sperm, while ova are diploid, containing one NOR+ and one NOR- set (Stöck et al. 2002). Here we conduct sibship analyses with co-dominant microsatellite markers (i) to confirm the purely clonal and maternal transmission of the NOR- set, and (ii) to demonstrate Mendelian segregation and recombination of the NOR+ sets in both sexes. The coexistence of two genomes with respectively Mendelian and clonal inheritance might conjugate the benefits of sexuality (preventing Muller's ratchet) and asexuality (preserving beneficial epistatic interactions), and thereby be favored in the harsh conditions inhabited by Batura toads (high mountain deserts), where selection stems mostly from the abiotic environment.
First and second author: equaly contribution

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TUE 23 AUG at 1650 - Room N0
Oral presentation *C4-Sy09-1650-O*

Symposium 9
Polyploid ecological genomics

The success story of invasive androgenetic, poplyploid Corbicula clams

Van Doninck K[1], Pigneur L-M[2], Etoundi E[2], Marescaux J[2], Descy J-P[2]
[1]University of Namur (FUNDP), Biology, Namur, Belgium, [2]University of Namur (FUNDP), Biology (URBO), Namur, Belgium

Summary statement:

Androgenesis in invasive Corbicula clams can induce cytoplasmic-nuclear phylogenetic discordance and egg parasitism.

Abstract:

Clams of the genus Corbicula are native to Africa, Australia, Asia and the Middle East but they are also successful aquatic invaders in America and Europe. The genus Corbicula includes sexually reproducing species as well as hermaphrodites reproducing by androgenesis, a peculiar "all-male" asexual mode of reproduction. In androgenetic Corbicula clams, an unreduced sperm fertilizes the oocyte and maternal chromosomes are extruded as two polar bodies. As a consequence, the whole nuclear genome of the descendant is inherited from the father.
We investigated the phylogenetic relationships of Asian, American and European Corbicula populations combining morphometrics, mitochondrial gene sequencing, microsatellite analysis and reproductive data. Due to androgenesis, mitochondrial-nuclear mismatches were found. They may result from "egg parasitism" when a spermatozoon from one lineage fertilizes the egg of another lineage. The maternal chromosomes of that second lineage are expelled but the mitochondria and other organelles are retained, resulting in discrepancies between nuclear and mitochondrial phylogenies. This phenomenon challenges species delimitation and can be misleading for phylogenetic relationships. Furthermore, we emphasize the role of androgenesis and ploidy in their invasion ability, regarding that androgenetic Corbicula taxa are widespread while their sexual relatives seem restricted to their native areas. Our latest results, part of it accepted recently for publication in BMC evolutionary biology, will be presented here.

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TUE 23 AUG at 1550 - Room N0
Invited talk *C4-Sy09-1550-I*

Symposium 9
Polyploid ecological genomics

Genes, jeans, and genomes: exploring the mysteries of polyploidy in cotton

Wendel JF[1]
[1]Iowa State University, Ecology, Evolution, and Organismal Biology, Ames, United States

Summary statement:

Allopolyploidy sets in motion novel evolutionary trajectories enabled by a combinatorially more complex regulation of a suddenly doubled complement of genes.

Abstract:

Gossypium includes allopolyploids arising from a reunion1-2 MYA of diploids from different hemispheres. This merger generated a spectrum of genomic responses, including gene silencing, intergenomic gene conversion, and genome-wide disruption and reconciliation of ancestral gene expression patterns. Allopolyploid formation induces massive alteration in gene expression and complex transcriptomic responses, including genomic dominance and novel (transgressive) expression patterns. Expression alteration of duplicated genes (homoeologs) is temporally partitioned into immediate and longer term effects, e.g., neofunctionalization and subfunctionalization. Expression is biased toward the paternal D-genome, demonstrating unequal contribution of two genomes to the transcriptome. We are exploring gene expression during cotton fiber development and evolution, taking advantage of a phylogenetic framework and the opportunity offered by multiple, parallel domestications of different wild progenitors by aboriginal peoples in both Africa-Asia and Mesoamerica. The fiber transcriptome is extraordinarily complex, with homoeolog expression varying widely even at the level of development and maturation of a single cell. Most homoeolog expression bias reflects polyploidy rather than domestication, but domestication has increased expression bias in fibers towards the D-genome. We are exploring the functional consequences of gene duplication in cotton and the possibility of novel gene recruitment following genome doubling. This work provides insights into the genetic architecture underlying the evolution of morphology, as well as the potential evolutionary significance of genome doubling.

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Symposium 10

Causes of epistasis

Talks: *Room N4*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Upper floor campus canteen *Mensa*

Invited Speakers:

Roy Kishony, Dan Weinreich

Organizers:

Arjan GM de Visser, Santiago F Elena

Description:

Epistasis fundamentally affects all evolutionary processes, including speciation, the rate and direction of adaptation and the origin and maintenance of sex. Studies of epistasis have long had an exclusive focus on its consequences. This is changing now, since recent studies both from theoreticians and experimentalists have begun to address also the causes of epistasis.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

WED 24 AUG at 1100 - Room N4
Oral presentation *D2-Sy10-1100-O*

Symposium 10
Causes of epistasis

Effect of genetic quality on deleterious mutation rate in Drosophila melanogaster

Agrawal AF[1], Sharp NP[1]
[1]University of Toronto, Toronto, Canada

Summary statement:

We report on experiments indicating that the rates of mutational decline appear to be greatest in genetic backgrounds of low quality.

Abstract:

The rate of deleterious mutation is a key property in many evolutionary theories. While estimates of the rate are improving, little is known about within-species variation. We examine the possibility that mutation rate is related to the genetic quality of an individual. To do so, we performed a mutation accumulation (MA) experiment on 10 different genetic backgrounds. We accumulated mutations on chromosome 2 in backgrounds that varied with respect to chromosome 3. Backgrounds varied in whether chromosome 3 carried zero, one, or two known deleterious alleles of large effect. After accumulation, we extracted chromosome 2 from each background and placed them all on a common background to assay fitness (i.e., compare fitness after removing the initial large effect alleles). Lines that had accumulated mutations in the presence of deleterious alleles appear to decline in fitness at a higher rate, implying higher mutation rates for genotypes of lower genetic quality. This is expected to result in a positive feedback loop whereby genotypes that initially carry an excess of deleterious alleles will tend to have a higher mutation rate and have descendants with an even greater excess of deleterious alleles. Such a relationship would likely have important implications for mutation load as well as a wide variety of theories based on deleterious mutations. This result also provides an alternative explanation for some observations that have previously been interpreted as evidence for synergistic epistasis.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy10-i001-E*

Symposium 10
Causes of epistasis

Bateson-Dobzhansky-Muller incompatibilities and line-cross analyses

Bolstad GH[1], Griffin DV[2], Pélabon C[1], Hansen TF[3]
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Summary statement:

We have developed models to analyse Bateson-Dobzhansky-Muller incompatibilities in line crosses and used published data to investigate epistasis in postzygotic isolation.

Abstract:

The Bateson-Dobzhansky-Muller model of postzygotic isolation relies on epistasis. However, the classical method of measuring epistasis in line-cross analyses as additive by additive, additive by dominance and dominance by dominance epistasis is not well connected to the theory on epistasis in the context of postzygotic isolation. We have developed a new set of models to study epistasis in line-cross analyses that can measure the strength of genetic incompatibilities due to epistasis either between parental and/or hybrid genotypes, or between parental alleles. Using model selection, the statistical support for the different models describing different forms of epistasis can be compared. We have used these models on published data to investigate the evolution and form of Bateson-Dobzhansky-Muller incompatibilities.

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WED 24 AUG at 1140 - Room N4
Oral presentation *D2-Sy10-1140-O*

Symposium 10
Causes of epistasis

Sign epistasis – Stabilizing selection reverses fitness effects of adaptive mutations

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Summary statement:

The concave fitness landscape set by stabilizing selection preferentially causes antagonistic epistasis and sign epistasis among adaptive mutations acting on the same phenotype.

Abstract:

Stabilizing selection that favors intermediate phenotypes plays an eminent role in shaping the magnitude of gene expression and many organismal traits. Despite our success of revealing these evolutionary consequences, it remains unclear how stabilizing selection affects the dynamics of adaptation and interactions among adaptive mutations acting on the same phenotype. To this end, we investigated epistasis among mutations arising from our prior evolution experiment to optimize the performance of a metabolic pathway. Enzymes of this pathway are essential to bacterial growth, but overproducing them incurs substantial fitness costs. Evolving from an excessive level, replicate populations acquired mutations that reduced gene expression through distinct mechanisms. Here we experimentally combined two classes of mutations that cut down expression by reducing the gene dosage and its mRNA stability, respectively. Moreover, we developed a simple model that accurately predicted fitness values of double mutants based on parameters estimated from single mutants and a strain with an inducible promoter that explored a wide range of expression levels. Consistent with Fisher's geometric model, mutations conferring higher benefits exhibited stronger diminishing returns epistasis with other mutations. Notably, introducing any second adaptive mutations into the most competitive single mutant significantly reduced its fitness value (i.e. sign epistasis) due to overshooting the phenotypic optimum. Results indicate that this concave fitness landscape preferentially causes antagonistic epistasis and may even lead to hybrid inferiority when mixing adaptive mutations fixed in separate populations.

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WED 24 AUG at 1200 - Room N4
Oral presentation *D2-Sy10-1200-O*

Symposium 10
Causes of epistasis

Invertebrate resistance to a parasite is based on two linked loci with strong epistasis

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Summary statement:

Experiments show that resistance of Daphnia to a bacterial parasite is caused by two closely linked loci with strong epistasis. These finding supports the Red Queen model for sex.

Abstract:

The Red Queen hypothesis for the maintenance of sex requires strong genetic interactions among host and parasite genes, including strong epistasis, as for example proposed in the matching-allele-model. Evidence for this is so far based on phenotypic patterns, with the genetic basis not being understood. We investigated the genetics behind patterns of resistance of Daphnia magna to its parasite Pasteuria ramosa. We crossed inbred host clones to obtain F1s, which were selfed to produce F2 clones and then backcrosses. 637 recombinants were scored for resistance against P. ramosa clones C1 and C19. Segregation for resistance against each of the two parasites was found to be consistent with Mendelian segregation, each at one locus with 2 alleles. Resistance is dominant. However, double resistant hosts were totally absent and single resistance hosts over represented. By selfing of the backcrossed hosts, we tested for and confirmed epistasis. Epistasis had the strongest value possible. In addition, these crosses indicated that the two resistance loci are very closely linked and a QTL analysis revealed that all genetic variation for resistance is explained by a single small genomic region. Genomic and mechanistic studies suggest that collagen-like proteins on the surface of the parasite interact with the cuticular of the host to cause variation in the attachment process to the host. Their role in shaping epistasis is currently investigated. The genetic system uncovered here, can lead to coevolution by negative frequency dependent selection, which is believed to be important for the maintenance of genetic diversity and sexual reproduction.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy10-i001-R*

Symposium 10
Causes of epistasis

The causes of epistasis in genetic networks

Elena SF[1,2], Macía J[3], Solé RV[2,3]
[1]CSIC, Instituto de Biología Molecular y Celular de Plantas, Valencia, Spain, [2]The Santa Fe Institute, Santa Fe, United States, [3]Universitat Pompeu Fabra, Complex Systems Laboratory, Barcelona, Spain

Summary statement:

In a simualtion study, epistasis was positive for small networks but negative for large robust ones. Negative epistasis results from the existence of redundant elements.

Abstract:

Epistasis stands for the non-additive interactions between genes in determining phenotypes. Considerable efforts have shown that for a given organisms, epistasis vary both in intensity and sign. Recent comparative studies suggested that the overall sign of epistasis switches from positive to negative as the complexity of organisms increases, and it has been hypothesized that this change shall be a consequence of the underlying gene network properties. Why should this be the case? What characteristics of genetic networks determine the sign of epistasis? Here we show, by evolving genetic networks that differ in their complexity and robustness against perturbations while still performing the same tasks, that robustness increased with complexity and that epistasis was positive for small non-robust networks but negative for large robust ones. Our results indicate that negative robustness and negative epistasis appear as a consequence of the existence of redundant elements in regulatory structures of genetic networks and that the correlation between complexity and epistasis seems to be a byproduct of such redundancy, allowing for a decoupling of epistasis from complexity.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy10-i002-R*

Symposium 10
Causes of epistasis

Sign epistasis and evolutionary accessibility

Franke J[1], de Visser JAGM[2], Krug J[1]
[1]Cologne University, Institute of Theoretical Physics, Cologne, Germany, [2]Wageningen University, Laboratory of Genetics, Wageningen, Netherlands

Summary statement:

Sign epistasis limits the order in which individually beneficial mutations can be incorporated in an organism. We study its consequences for genome-wide adaptation.

Abstract:

Epistasis between different mutations implies that individual fitness effects combine in a non-additive way to yield the fitness of the strain carrying all mutations. Cases where individually beneficial mutations are jointly deleterious or vice versa are said to display (reciprocal) sign epistasis. While the underlying biochemical mechanisms are largely unexplored, sign epistasis is known to have important implications for the adaptation of populations. Specifically, in the presence of sign epistasis a fraction of the mutational pathways leading from an initial genotype to the global fitness optimum are inaccessible, if adaptation is constrained to increase fitness in each step. Here we theoretically investigate accessibility of the global optimum for a wide variety of model landscapes. We find that accessibility is high, in the sense that at least one accessible pathway exists with a substantial probability that approaches unity as the dimensionality of the fitness landscape (set by the number of mutational loci) becomes large. At the same time the number of alternative accessible pathways grows without bound.
We verify the model predictions by comparison to an empirical 8-locus fitness landscape obtained for the filamentous fungus Aspergillus niger. Our results imply that the globally optimal configuration should be accessible to genome wide evolution, but the repeatability of evolutionary trajectories is limited owing to the presence of a large number of alternative mutational pathways.

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WED 24 AUG at 0950 - Room N4
Invited talk *D1-Sy10-0950-I*

Symposium 10
Causes of epistasis

Genomic evolutionary pathways to antibiotic resistance

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[1]Harvard Medical School, Systems Biology, Boston, United States, [2]Harvard University, Faculty of Arts and Sciences, Cambridge, United States, [3]Harvard University, Department of Organismic and Evolutionary Biology, Cambridge, United States

Summary statement:

The evolution of antibiotic resistance follows recurrent genotypic pathways.

Abstract:

Antibiotic resistance can evolve through sequential accumulation of multiple genetic changes. To study such gradual evolution in the laboratory, we developed a microbial selection device, the “morbidostat”, which dynamically adjusts drug concentrations to maintain a constant challenge on evolving bacterial populations. We analyzed evolutionary trajectories of Escherichia coli towards resistance to chloramphenicol, doxycycline, and trimethoprim. Resistance increased dramatically and consistently in replicate populations. Whole-genome sequencing revealed that some genetic changes were shared between drugs, and others were antibiotic-specific. Chloramphenicol and doxycycline resistance were acquired through different combinations of mutations in genes involved in translation, transcription, and membrane proteins. In contrast, trimethoprim resistance was acquired stepwise, through a limited pool of mutations restricted to the target enzyme (dihydrofolate reductase); parallel populations not only evolved similar mutations, but also acquired them in similar order. Uncovering such predictable genotypic pathways to strong antibiotic resistance may help slow down the evolution of resistance.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy10-i004-R*

Symposium 10
Causes of epistasis

The role of mutational history in the evolution of bistability in Pseudomonas fluorescens

Nestmann S[1], Rainey PB[2,3]
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Summary statement:

The influence of evolutionary history on the origin of a stochastic switcher was studied using reconstructed genotypes, fitness measurements and re-evolved populations.

Abstract:

In nature, organisms face perpetually changing environmental conditions. The challenge to survive drives the evolution of novel traits. It is unknown to what extent evolutionary history influences the process. Theory suggests that the history of mutations influence the outcome of evolution as a result of interactions between mutations that may either constrain or promote the evolution of a certain trait.

Here, we disentangle the role of evolutionary history in the evolution of a stochastic switching phenotype in the bacterium Pseudomonas fluorescens. The switching type, caused by a mutation in the carB gene, appeared after nine rounds of evolution set by distinctive selection treatments. In theory mutations are random and can occur after each round of evolution but will only be detectible if the fitness of the resulting type is higher than the fitness of the ancestor. We reconstructed the carB mutation into genotypes from previous rounds of evolution. Fitness experiments comparing the reconstructed carB type to the original genotypes showed that this mutation had an unequal likelihood of occurring during the course of evolution. The importance of history was confirmed by a re-evolution experiment where original genotypes act as starting points for the evolution of a switching phenotype.

We show that evolutionary – and therefore mutational – history affects the evolution of the derived switching phenotype. It is also likely that interactions with other newly evolved types influence the establishment of the switcher.

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WED 24 AUG at 1120 - Room N4
Oral presentation *D2-Sy10-1120-O*

Symposium 10
Causes of epistasis

Epistatic modules: Does size matter?

Østman B[1], Adami C[2]
[1]Michigan State University, BEACON Center for the Study of Evolution in Action, East Lansing, United States, [2]Keck Graduate Institute, Claremont, United States

Summary statement:

Larger modules make bigger contributions to fitness on average, because the synergistic epistasis between genes creates novel opportunities unavailable to modules with fewer genes.

Abstract:

In computational models of rugged fitness landscapes, high peaks are associated with epistatic loci that define modules. Landscapes that are more rugged give rise to higher peaks as well as modules with more epistatically interacting loci, because the increased number of interactions increases the fitness potential. As a consequence, adaptation in rugged landscapes is more effective, since the height of the global peak increases with ruggedness. Here, we address the question whether the scaling of the global peak height with the number of interacting loci is biologically plausible or an unrealistic artifact of the model. By comparing detailed statistics of the relationship between epistasis and knockout fitness defects (indicating peak height) in the model with single and double-knockouts fitness measurements in yeast, we argue that there is a biologically plausible relationship between the number of components in a module and module fitness. We contend that the increase in adaptive potential with increasing ruggedness is germane, because interacting loci can work synergistically to produce higher fitness compared to a set of non-interacting loci. The more genes that are involved in a function, the more complex and fine-tuned it can be. The fibrin blood-clotting cascade, for example, consists of twenty-six distinct proteins, ensuring a blood-clotting response at the right time and place under a variety of conditions. The hypothesis that larger modules make larger fitness contributions is difficult to test experimentally, since function has to be preserved while varying module size. We propose to test this hypothesis by engineering functional modules in yeast.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy10-i005-R*

Symposium 10
Causes of epistasis

Mutation accumulation in bacteria in the light of Fisher's geometrical model

Sousa A[1], Trindade S[1], Gordo I[1]
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Summary statement:

Study of the dynamics of fitness and variance between populations that undergo severe reductions in size under Fisher's framework.

Abstract:

In a mutation accumulation (MA) experiment genetic drift is intensified over natural selection, such that mutations accumulate at approximately neutral rates and mean fitness declines as the population evolves. Classical models to interpret these experiments assume that the rate (U) and effects of deleterious mutations (s) are constant and independent of the genetic background in which they arise. Evidence for epistasis between mutations has increased recently and novel models of analysis of the MA data are required. Fisher's geometrical model offers a framework to start doing just that.

Here we study the dynamics of fitness decline and increase in fitness variance between populations that undergo severe reductions in size under Fisher's framework.

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WED 24 AUG at 0910 - Room N4
Invited talk *D1-Sy10-0910-I*

Symposium 10
Causes of epistasis

Dissecting the mechanistic basis of epistasis in a drug resistance enzyme of bacteria suggests genetic constraints on adaptation may be common

Weinreich DM[1], Knies JL[1], Cai F[1]
[1]Brown University, Department of Ecology and Evolutionary Biology, Providence, United States

Summary statement:

Epistasis can sharply constrain adaptive evolution of organisms. We show that in the case of one enzyme, mechanistic tradeoffs are at least in part responsible.

Abstract:

We previously used reverse genetics to show that epistasis for fitness is widespread among a panel of beneficial mutations in the β-lactamase gene, which encodes a key antibiotic resistance enzyme in E. coli. We further found that this epistasis causes sharp constraints on the evolutionary trajectories accessible to this gene during natural selection. This finding raised the question of mechanism: Why does the same mutation affect drug resistance differently in different allelic backgrounds? We have now purified all the β-lactamase variants defined by the mutations in our previous study, and characterized the melting temperature and enzymatic kinetics of each. We find that mutations often perturb both traits, and that this feature explains much of the fitness epistasis observed. This appears to be a rather general property of protein evolution, implying that epistatic constraints on adaptation may be widespread.

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Symposium 11

Non-genetic inheritance and evolution

Talks: *Room N2*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Upper floor campus canteen *Mensa*

Invited Speakers:

Troy Day, Alex Badyaev

Organizers:

Tobias Uller, Heikki Helanterä

Description:

There is more to transgenerational inheritance than vertical genetic transmission, including epigenetic, behavioural and cultural mechanisms. Yet, the evolutionary implications of non-genetic inheritance remain poorly understood. This symposium creates a forum for exchange of ideas and facilitates development of a conceptual framework for the evolutionary implications of extended inheritance.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

SUN 21 AUG at 1400 - Room N2
Invited talk *A3-Sy11-1400-I*

Symposium 11
Non-genetic inheritance and evolution

Origin of the fittest: cycles of developmental emergence and genetic determination in evolution

Badyaev AV[1]
[1]University of Arizona, Ecology and Evolutionary Biology, Tucson, United States

Summary statement:

How does inheritance become associated with emergent developmental processes to produce evolutionary change?

Abstract:

Our sense of organismal functionality and adaptability comes from emergent features of development and homeostasis. Yet, it is not known how these processes become associated with inheritance to produce evolutionary change. I will review empirical evidence for a scenario under which initially emergent biological processes integrate into functional and genetic systems, spread through a population, and become stabilized in developmental sequences under natural selection. Such a scenario is expected to produce short spurts of exploratory evolution followed by adaptive diversification and specialization of lineages in the range of environments with the greatest fit.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy11-i001-R*

Symposium 11
Non-genetic inheritance and evolution

Social transmission of oviposition site preference in Drosophila melanogaster

Battesti M[1], Joly D[1], Mery F[1]
[1]CNRS, Legs, Gif sur Yvette, France

Summary statement:

Oviposition site preference can be socially transmitted in groups of Drosophila melanogaster by using a transmission chain method.

Abstract:

The understanding of the diversity and complexity of behaviors and their transmission from one generation to the next has always been a central question in evolutionary biology and psychology. By comparison with individual learning which requires process of trial and errors every generation, social learning can be potentially transmitted from one generation to the next and generate the emergence and maintenance of new behaviors. Despite the potential importance of cultural transmission on animal behavior relatively little is known about the processes which may facilitates or prevent this transmission, their genetic bases and their potential fitness impacts. In the present study we show for the first time social transmission of oviposition preference in a non-social insect, Drosophila melanogaster, using a “transmission chain” approach. Such studies simulate natural traditions by training a population of founders to perform a task, and gradually replacing these experienced individuals (demonstrators) with naive animals (observers). This will allow to test whether the original behavior remains in the population in spite of this change in personal. Using this protocol, we can investigate whether a preference for a specific oviposition site can be transmitted in an environment where observers can not only observe demonstrators but also interact with them and other observers. This type of experiments allows appreciating how individuals weight social information compared to personal information. Results open new perspectives on the study of the evolution of sociality, its impact on behavioral evolution and its genetic bases.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy11-i002-R*

Symposium 11
Non-genetic inheritance and evolution

Grandmaternal age as a determinant of grandoffspring quality and reproduction

Bleu J[1], Meylan S[1,2], Clobert J[3], Massot M[1]
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Summary statement:

We assessed in a natural population of lizards the effects of grandmaternal age on grandoffspring morphology at birth, on survival and on reproduction.

Abstract:

Maternal effects are increasingly studied in evolutionary biology. In particular, maternal age is known to influence offspring fitness due to reproductive senescence and maturation processes. Maternal age may affect not only their direct offspring, but also the offspring of the next generation, leading to grandmaternal effects. The effect of grandmaternal age has been studied on animals in laboratory experiments, as well as on humans in medical studies. However, to our knowledge, it has never been studied in wild populations. In this study, we investigated the effects of grandmaternal age in the common lizard, Zootoca vivipara. This natural population has been surveyed annually for 18 years. Each year, pregnant females were kept several weeks in the laboratory, until parturition. We thereby obtained data on maternal lineages, female reproductive performances (litter size and litter success) and offspring morphology at birth (body size and corpulence). We assessed the influence of grandmaternal age on morphology at birth, on survival of grandoffspring and on reproductive performances of female grandoffspring. We showed that grandmaternal age influences grandoffspring morphology, both in males and females, and also influences granddaughters reproduction, with effects on both litter size and litter success. These results emphasize the importance of age in shaping life history traits up to three generations.

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SUN 21 AUG at 1610 - Room N2
Oral presentation *A4-Sy11-1610-O*

Symposium 11
Non-genetic inheritance and evolution

Déjà vu? The re-emergence of the inheritance debate and what's different this time

Bonduriansky R[1]
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Summary statement:

The current iteration of the inheritance debate is conceptually different from past iterations, and lingering confusion flows from ambiguity over the definitions of key terms.

Abstract:

The establishment of Mendelian-genetic inheritance as the sole mechanism of heredity is portrayed in every textbook as an iconic success-story of scientific progress, whereby a century-long debate grounded in copious theoretical and empirical research finally led to the triumph of truth over fallacy. Yet, we are now witnessing a dramatic re-emergence of debate over the nature of inheritance. What's going on? In this talk, I will outline the history of the inheritance debate, and attempt to clarify the key ideas at stake. I will argue that the current iteration of the inheritance debate is conceptually different from past iterations, and that much of the lingering confusion flows from ambiguity over the definitions of key terms. I will suggest that recent advances in understanding of cell biology and development are driving an on-going re-conceptualization of the nature of inheritance, which promises to have interesting implications for evolutionary biology.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy11-i003-R*

Symposium 11
Non-genetic inheritance and evolution

Non-genetic inheritance of male condition: there's more to paternal effects than 'like father like son'

Crean AJ[1], Bonduriansky R[1]
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Summary statement:

The scope and consistency of the effect of paternal diet on offspring traits is examined in the neriid fly Telostylinus angusticollis.

Abstract:

Recent advances in our understanding of inheritance reveals that offspring variability cannot be explained solely by the transmission of genes from parents to offspring. Commonly referred to as 'Lamarckian' or non-genetic inheritance, mounting empirical evidence shows that the parental environment can influence offspring phenotype and generate heritable variation for a broad array of traits. However, while the ecological and evolutionary importance of maternal effects are well studied, corresponding paternal effects are still largely considered to be rare or insignificant. Previous work in our laboratory showed that in the neriid fly, Telostylinus angusticollis (a species without paternal care), fathers transmit their environmentally-acquired condition to offspring: large fathers that were reared on a high-quality larval diet produced larger offspring. To explore the scope and consistency of this paternal effect, we conducted a series of follow-up experiments manipulating the timing of copulation with respect to female age and maturation, and the time from copulation to fertilization. In addition, we measured a variety of offspring traits at different life history stages. Initial findings suggest the effects of paternal diet on offspring phenotype are more complex than previously observed, further complicating interpretation of the evolutionary implications of such effects.

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SUN 21 AUG at 1440 - Room N2
Invited talk *A3-Sy11-1440-I*

Symposium 11
Non-genetic inheritance and evolution

A unified approach to the evolutionary consequences of multiple inheritance systems

Day T[1], Bonduriansky R[2]
[1]Queen's University, Kingston, Canada, [2]University of New South Wales, Biology, Sydney, Australia

Summary statement:

I present some work that develops a unified theoretical framework for modeling evolution under the combined effects of genetic and nongenetic inheritance.

Abstract:

There has been widespread interest in recent years in inheritance mechanisms that exist alongside genetic inheritance, and the role that these might play in evolution. I will present some work (joint with Dr. Russell Bonduriansky) that develops a unified theoretical framework for modeling evolution under the combined effects of genetic and nongenetic inheritance. Despite the considerable diversity of proximate mechanisms of nongenetic inheritance, I will show how they can all be integrated within a relatively simple theory. The approach will be illustrated by examining a variety of scenarios, including non-transmissible environmental ‘noise’, maternal effects, indirect genetic effects, transgenerational epigenetic inheritance, RNA-mediated inheritance, and cultural inheritance. Our results demonstrate that the incorporation of nongenetic inheritance within evolutionary models leads to novel predictions and patterns of evolution that would otherwise be unexpected.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy11-i004-R*

Symposium 11
Non-genetic inheritance and evolution

Trans-generational immune priming in the red flour beetle, Tribolium castaneum

Diddens-de Buhr MF[1], Eggert H[1], Kurtz J[1]
[1]Institute for Evolution and Biodiversity / Westfälische Wilhelms-Universität Münster, Animal Evolutionary Ecology, Münster, Germany

Summary statement:

Trans-generational immunity in the red flour beetle, Tribolium castaneum, is transferred via mothers and fathers. In our study we investigate potential mechanisms of this transfer.

Abstract:

All living organisms have to cope with one extraordinary force – parasites. Parasites and hosts impose strong selection pressure on each other, and may thus find themselves in an arms race involving rapid genetic and phenotypic changes. These dynamics may underpin the evolution of efficient host immune systems for host defence.

Since parasites and pathogens impact the survival and performance of individuals, it might be beneficial to directly invest into protection of the offspring. This process has been described as trans-generational immune priming, where parents provide their offspring with enhanced immunological protection. However, the mechanisms of transmission of this parental information still remain largely obscure.

In T. castaneum trans-generational immune priming occurs via mothers and fathers. Roth et al. (2009) showed that, whereas mothers transfer specific resistance, fathers seem to prime their offspring in a more general way and suggested an allocation of tasks in immune protection between parents. In the current project, we aim to investigate the mechanisms of maternally and especially paternally derived immune priming as well as its potential fitness consequences.

As the immune response in insects is far more plastic and specific than previously believed, results of this study are potentially relevant also for current theories of host-parasite coevolution.

Roth, O., Joop, G., Eggert, H., Hilbert, J., Daniel, J., Schmid-Hempel, P. and Kurtz, J. (2010), Paternally derived immune priming for offspring in the red flour beetle, Tribolium castaneum. Journal of Animal Ecology, 79: 403–413

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy11-i005-R*

Symposium 11
Non-genetic inheritance and evolution

Additive transgenerational effects in a butterfly evidenced through artificial selection

Ducatez S[1], Fréville H[2,3], Stevens VM[1,4], Baguette M[1,5]
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Summary statement:

Flight performance tests induce transgenerational cumulative costs on physiological and life history traits (eg flight performance, lifespan and fecundity decrease) in a butterfly.

Abstract:

Habitat fragmentation in our changing environments is a strong selective pressure which can induce the apparition of residency versus dispersal strategies. Dispersal costs have been demonstrated to be determinant in the evolution of dispersal related traits, and were evidenced to impact the offspring generation. However transgenerational effects of dispersal costs have rarely been considered in models of dispersal evolution, although parental effects are known to strongly influence evolutionary processes.

Such effects are hard to detect in the field, but experiments of artificial selection in laboratory might be the key to understand the importance of transgenerational effects in the evolution of dispersal, as they permit to disentangle parental and genetic effects. Here we artificially selected butterflies according to their flight performance and measured their life history traits over 4 generations. Results showed that flight performance had a genetic basis, and highlighted an additive transgenerationnal cost of the flight performance test during our artificial selection experiment, causing flight performance to decrease across generations due to cumulative costs of flight tests, counteracting the artificial selection pressure that aimed at increasing flight performance over time. Flight test costs also decreased individuals’ fecundity, and decreased males’ lifespan. This provides one of the first evidence of additive transgenerational effects on physiological and demographic traits. It underlines the potential counterintuitive effects of non-genetic inheritance on the evolution of dispersal and more generally on populations’ adaptation to environmental changes.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy11-i006-R*

Symposium 11
Non-genetic inheritance and evolution

Maternal effects may alter the course of evolutionary change

Ezard TH[1], Johnstone R[2], Townley S[3]
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Summary statement:

We show that non-Mendelian maternal inheritance can (1) enlarge the range of achievable phenotypes and (2) in some cases even change its course.

Abstract:

The clear adaptive benefits of an ability to respond rapidly to ecological change has prompted an explosion of interest in evolvability in general and alternative inheritance mechanisms in particular, including phenotypic plasticity, epigenetic inheritance and parental effects. Lande and Kirkpatrick used Quantitative Genetic models to explore how non-Mendelian maternal inheritance (hereafter, maternal effects) can cause evolutionary transients or momentum: the phenotype continues to change even when selection is turned off. Recasting the same quantitative genetic models in a control engineering context, we provide `proof of concept’ that the evolutionary consequences of maternal effects are more far reaching. We show that maternal effects can (1) enlarge the range of achievable phenotype and (2) in some cases even change its course.
Without maternal effects, according to the multivariate breeders equation, phenotypes will evolve along paths of least genetic resistance. These paths of evolution can be visualized by plotting ellipsoids in phenotype space. When maternal effects are included we find that these ellipsoids can warp, increasing in volume as the maternal effect is strengthened suggesting an enhancement of phenotypic diversity. Furthermore, we find that the direction of evolution in the presence of maternal effects can be orthogonal to the direction of evolution under Mendelian inheritance alone. In this sense, maternal effects may alter the course of evolution.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy11-i001-E*

Symposium 11
Non-genetic inheritance and evolution

The better to eat you with (or eat with you): the evolution of stealing vs. arachnophagy in Argyrodes spiders

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Summary statement:

A look into the evolution of different foraging behaviors in two closely related arachnids: Argyrodes trigonum and Argyrodes argyrodes using empirical and theoretical methods.

Abstract:

The genus Argyrodes (Theridiidae) contains approximately 200 species, with diverse behavioral backgrounds. These spiders have drawn the curiosity of many researchers because of their exploitation of other arachnids, primarily arachnophagy (eating of other spiders) and kleptoparasitism (stealing food or web material from other spiders). These species have been separated into six species groups via behavioral and morphological characteristics, though a firm phylogeny has not yet been formed. I focus on two species, each from a different species group: A. trigonum and A. argyrodes. Though closely related, these two species have contrasting foraging strategies: A. trigonum is a generalist forager, using both arachnophagy and kleptoparasitism, whereas A. argyrodes appears to specialize in kleptoparasitism. Using a combination of field studies and simple behavioral models, I have explored the mechanisms behind the evolution of different foraging strategies in these two closely related species.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy11-i002-E*

Symposium 11
Non-genetic inheritance and evolution

Transcriptional effects of parental age in the Drosophila melanogaster brain: Linking a non-genetically transmitted effect to its genetic targets

Foucaud J[1], Burns JG[2], Mery F[1]
[1]CNRS, Gif/Yvette, France, [2]University of Toronto, Mississauga, Canada

Summary statement:

We investigated the transcriptional profile of a non-genetically transmitted memory impairment due to parental age and its specific rescue by oxidative stress resistance selection.

Abstract:

Genetic effects on learning and memory performance have been documented since decades in various species, from humans to invertebrates. In the Drosophila melanogaster model species, numerous genes have been showed to play a role in learning aversive olfactory stimuli (e.g. dunce, rutabaga). Beyond traditional genetic effects, a recent study demonstrated that parental age influenced memory performance in D. melanogaster offspring and grand-offspring. Indeed, the (young) offspring of old parents showed a decreased short-term memory performance relative to offspring of young parents, despite similar olfactory sensitivity and locomotor activity. Interestingly, this transgenerational effect of ageing on memory could be rescued by imposing a selection on oxidative stress resistance, a major regulator of ageing and neurodegeneration. Therefore, genetic variation exists for this non-genetic effect on phenotype, and is expected to participate in the evolution of senescence and behavioral plasticity in natural populations. In this study, we seek to evaluate the transcriptomic effects of parental age and oxidative stress resistance in the adult D. melanogaster brain. This work enables us to better understand how the non-genetic effect of parental age influences the expression of individual genetic variation on behavioral plasticity.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy11-i007-R*

Symposium 11
Non-genetic inheritance and evolution

Kin selection under blending inheritance

Gardner A[1]
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Summary statement:

I determine whether it is possible to develop a quantitative theory of kin selection upon the assumption of blending inheritance.

Abstract:

Why did Darwin fail to develop his insights on kin selection into a proper theory of social adaptation? A possible answer is that his inadequate understanding of heredity kept the problem out of focus. Here, I determine whether it is possible to develop a quantitative theory of kin selection upon the assumption of blending inheritance. I find that, whilst Hamilton's rule can readily be derived under the assumption of blending, this mechanism complicates the computation of relatedness coefficients, and can even cause them to fluctuate over generations. Nevertheless, I show that the ultimate criterion for selection to favour any social trait remains the same as under Mendelian inheritance. By eliminating the gene from the theory of kin selection, I clarify the role that it plays in the theory of social adaptation.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy11-i003-E*

Symposium 11
Non-genetic inheritance and evolution

Signaling territoriality. Male wing red pigmentation affects survival via intraspecific competition in American rubyspot (Zygoptera)

González Santoyo I[1], González Tokman DM[1], Munguía Steyer RE[1], Córdoba Aguilar A[1]
[1]Universidad Nacional Autónoma de México, Ecología Evolutiva, Mexico City, Mexico

Summary statement:

Red wing pigmentation is used by males of American rubyspot to signaling territoriality status.

Abstract:

Adult males of American rubyspot (Hetaerina americana) damselflies contend for territories that females visit to mate. Territorial residents accrue a significantly higher mating success compared with nonterritorials. Males bear a red pigmentation spot in the basis of each wing whose average size is positively correlated with their ability to obtain territories. The function of the wing spot color in natural selection and intraspecific competition is poorly known. Using only territorial males of the same age, an experiment was conducted to evaluate the relationship of the red wing spot color with male survival and their ability to obtain and defend territories. In a first group the red wing spot was replaced by a blue artificial pigment. Survival in the field and reproductive behavior were compared with two control groups. Behavior was evaluated following the next parameters: number of total fights, number of won fights and effective fighting time. The results showed that blue-manipulated animals survived less than controls. In addition, this group had less fights earning too. These results show that the red color is important for natural and sexual selection on males of this species.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy11-i008-R*

Symposium 11
Non-genetic inheritance and evolution

Clonal variation and maternal effects on probabilistic maturation reaction norms (PMRNs)

Harney ED[1], Van Dooren TJM[2], Paterson S[1], Plaistow SJ[1]
[1]University of Liverpool, Institute of Integrative Biology, Liverpool, United Kingdom, [2]Ecole Normale Supérieure-CNRS, Ecologie & Evolution, Paris, France

Summary statement:

Maturation rate models were used to compare PMRN variation in two species of Daphnia and determine whether mothers can alter the PMRN's of their offspring.

Abstract:

Age and size at maturity are key life history traits influencing an organism's fitness. Understanding how reaction norms for age and size at maturity evolve requires an appreciation of the developmental traits that underpin them and how these traits, and the interactions between them, change in spatially and temporally heterogeneous environments. It has been suggested that determinants of maturation play a key role in shaping age and size at maturity. Maturation thresholds represent a minimum state that an organism must achieve before the onset of maturity. These thresholds have been documented in many taxa, suggesting that they are highly conserved. However we still have little idea of why these traits have evolved, whether they are fixed or plastic, or which states (size, age, condition etc) influence maturation probability.
PMRNs provide estimates of age and size at maturity that incorporate stochasticity and are not biased by the average growth and mortality of the population. We used maturation rate models, a type of PMRN, to determine whether maturation in 7 Daphnia magna and 7 D. pulex clones was triggered by changes in size, age, or size and age. Our results confirm that maturation is triggered by a size threshold and demonstrated substantial variation in maturation processes for both species. In a second experiment we used the same approach to test whether maternal environment influenced the maturation reaction norms for offspring. Mixed results were observed, suggesting that mothers may be able to influence maturation processes in their offspring, but that this effect varies between clones.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy11-i004-E*

Symposium 11
Non-genetic inheritance and evolution

The evolutionary history of the Uralic languages

Honkola T[1], Korhonen K[2], Lehtinen J[3], Syrjänen KJ[4], Vesakoski O[5], Wahlberg N[5]
[1]University of Turku, Biology, Turku, Finland, [2]University of Helsinki, Helsinki, Finland, [3]KOTUS, Helsinki, Finland, [4]University of Tampere, Tampere, Finland, [5]University of Turku, Turku, Finland

Summary statement:

The divergence times of the Uralic languages obtained by computational analyses coincided with climatic and cultural fluctuation suggesting close connections between these factors.

Abstract:

Quantitative phylogenetic methods have been used to illustrate the evolutionary relationships and divergence times of biological species. During the last decade these methods have been applied also to linguistic material to explain evolutionary emergence of language families. We studied the quantitatively yet unexplored Uralic language family which is of special interest as it is a compact and well-studied group providing references from the linguistic studies. Furthermore, as the written history of Uralic speakers is limited, the Uralistic studies likely gain advantage from quantitative approach as it can possibly provide light to earlier discrepancies. In our study we first estimated the divergence times of Uralic languages by computational timing analysis and then compared our results to climatic, historical and archaeological evidence. Our aim was to get a more complete picture of the history of the Uralic languages by considering whether the divergence of Uralic languages we see today can be explained through the changes in abiotic and biotic factors in the past. The divergence times obtained from the analysis corresponded with the ones suggested earlier by traditional linguistic studies verifying our approach. They also coincided with the climatic and cultural fluctuation suggesting that divergence events of languages may be caused by language-external factors. Thus, we conclude that computational timing analysis is an applicable method for the study of the Uralic languages and point out the importance of language-external factors in the attempt to achieve a better understanding of evolutionary histories of language groups.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy11-i009-R*

Symposium 11
Non-genetic inheritance and evolution

Effects of maternal inheritance in adapting to a novel environment

Hoyle RB[1], Ezard TH[1]
[1]University of Surrey, Department of Mathematics, Guildford, United Kingdom

Summary statement:

We show how maternal inheritance speeds up adjustment to a novel environment, but can destabilise the system.

Abstract:

The clear benefits of the ability to adapt rapidly to a novel environment has prompted an explosion of interest in evolvability, with particular focus on alternative inheritance mechanisms that facilitate adaptation. Here, we begin with Lande´s reaction norm model of the evolution of phenotypic plasticity and extend it to incorporate maternal (non-Mendelian) inheritance. We show that positive maternal inheritance speeds up adjustment to the new environment regardless of whether plasticity is evolving, is constant or absent. As a cautionary note, strong positive maternal inheritance can lead to oscillatory dynamics that overshoot the optimal phenotype and can lead to extinction. Weakly negative maternal inheritance might not hit the target phenotype as quickly as possible, but nonetheless stabilise the system and in doing so maximise fitness in stochastic environments.

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SUN 21 AUG at 1710 - Room N2
Oral presentation *A4-Sy11-1710-O*

Symposium 11
Non-genetic inheritance and evolution

Prenatal and postnatal parental antibodies: A new insight into the interaction between parental effects at different time scales

Jacquin L[1], Blottière L[1], Haussy C[1], Perret S[2], Gasparini J[1]
[1]Université Pierre et Marie Curie- CNRS, Laboratoire Ecologie et Evolution, Paris, France, [2]Ecole Normale Supérieure-CNRS, Station biologique de Foljuif CEREEP, Saint-Pierre-les-Nemours, France

Summary statement:

We show that prenatal and postnatal antibodies act in interaction on offspring traits, opening the interesting possibility of combined parental effects at fine time scales.

Abstract:

Parental transmission of antibodies can have profound effects on offspring phenotype and has been demonstrated to affect the evolution of host-parasite interactions in nature. However, little is known about the relative influence of prenatal antibodies (transmitted before the birth of the young) versus postnatal antibodies (transmitted after the birth) on offspring traits, because suitable models to disentangle their effects are very rare. Columbidae such as pigeons and doves can feed their young with a lipid-rich substance produced in their crop, named crop milk, which contains antibodies. Such birds are thus unique models to disentangle the role of prenatal antibodies (transmitted through the egg yolk) and postnatal antibodies (transmitted through the crop milk). In this study, we created experimental groups of chicks receiving maternal antibodies before and/or after hatching by cross-fostering eggs, and examined the short- and long-term specific humoral response, growth and survival of nestlings. We show for the first time that pre- and postnatal antibodies act in interaction on the immune response and growth of their young at different time scales. This study thus opens the exciting possibility that parents could be able to shape the phenotype of their offspring by a combination of prenatal and postnatal adjustments of antibody transmission and calls for further investigations on the potential adaptive role of such combined parental effects.

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SUN 21 AUG at 1630 - Room N2
Oral presentation *A4-Sy11-1630-O*

Symposium 11
Non-genetic inheritance and evolution

Phenotypic plasticity favors the evolution of heritable parental effects

Kuijper B[1], Johnstone RA[1]
[1]University of Cambridge, Behaviour & Evolution Group, Department of Zoology, Cambridge, United Kingdom

Summary statement:

Phenotypes of plastic individuals provide more reliable information on the environment than those of non-plastic individuals, enhancing the evolution of parental effects.

Abstract:

Despite growing evidence for nongenetic inheritance in many taxa, the ecological conditions that favor heritable parental or grandparental effects remain poorly understood. We systematically assess when selection favors the evolution of heritable parental effects, as opposed to strategies such as bet-hedging or the production of a single phenotype only. We show that heritable parental effects prevail when environmental fluctuations are relatively infrequent and different environments are encountered with frequencies that are not too dissimilar. Where one environment is more common than another, asymmetric inheritance is favored, corresponding to scenarios such as bacterial persistence. Interestingly, heritable parental effects can evolve over a wider range of conditions when individuals exhibit a certain degree of phenotypic plasticity. Organisms that can adjust their phenotype to the current environment provide a more reliable source of information to their offspring than non-plastic individuals, challenging the conventional view that plasticity and parental effects are alternative means to the same outcome. However, we also show that direct transmission of environmental information to offspring, which is not mediated by the parental phenotype, diminishes the scope for heritable parental effects.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy11-i005-E*

Symposium 11
Non-genetic inheritance and evolution

Mating preference and egg laying sequence influence female egg investment in bird species: a comparative overview on the non- hormonal maternal effects

Malacarne G[1], Grenna M[1], Pellegrino I[1], Cucco M[1]
[1]Piemonte Orientale, DISAV, Alessandria, Italy

Summary statement:

We present an overview of studies on the effects of male attractiveness on egg characteristics and allocation of substances like carotenoids and antibacterial molecules.

Abstract:

In oviparous species, the eggs represent a strong maternal allocation of resources.
Females can differentially allocate substances in their eggs as a response to the environment experienced during the laying period, including the quality of their mate. This field of maternal effects has been primed by Schwabl's finding (1993) that females of some passerine bird species deposit testosterone in their eggs and that if mated with more attractive males lay eggs with higher androgen levels (reviewed in Kingma 2009). These studies on endocrine-mediated maternal effects have been spread considering also yolk deposition of other steroids as oestradiol and corticosterone but with more contradictory results. Since the eggs contains a huge variety of non-endocrine substances that can influence chick prospects of survival, the interest has also been directed to micro-nutrients as carotenoids, antioxidants and antibacterial substances (lysozyme, avidin etc). On the basis of our studies on egg allocation after mate choice in two partridges (Alectoris rufa and Perdix perdix) we present here an up-dated overview of the results on egg mass, yolk mass, vitamins, innate and acquired immunity allocation in birds. We discuss these data in the light of Different Allocation Hypothesis (DHA) or Compensatory Hypothesis (CH). Furthermore we show comparative data on how the substances are allocated across a clutch with respect to laying order.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy11-i010-R*

Symposium 11
Non-genetic inheritance and evolution

Can maternal effects facilitate adaptation to a novel food source in a host-specific phytophagous insect?

Newcombe D[1], Moore PJ[1], Moore AJ[1]
[1]University of Exeter, College of Life and Environmental Sciences, Penryn, United Kingdom

Summary statement:

We investigated the effects of maternal host diet on offspring performance in a specialist insect herbivore to test if maternal effects could facilitate adaptation to a novel host.

Abstract:

Our aim was to investigate if maternal effects facilitate adaptation to a novel host in a specialist insect, the large milkweed bug Oncopeltus fasciatus (Hempitera: Lygaeidae).
We used two different populations of O. fasciatus for this experiment. One population was artificially selected to feed on sunflower seeds (Helianthus annus) for over 45 years while the other was naturally adapted to toxic milkweed seeds (Asclepias syriaca). We used a nested full-sib, split brood design to test if manipulation of maternal diet had an effect on offspring life history traits.
We found population differences in diet-based maternal effects on egg mass and clutch fertility. There were strong differences between populations and effects of offspring diet on offspring performance, but no significant effect of maternal diet, and a weak but statistically significant population by maternal diet effect on nymph development time. A reintroduction of the toxic ancestral diet to the sunflower-adapted population did not detrimentally affect offspring growth or development to adulthood. In both populations, offspring fed milkweed developed faster and grew into larger adults than offspring fed sunflower. Survivorship depended on population and offspring diet, and their interaction, but was unaffected by maternal diet or other interactions. Survivorship was higher for sunflower-adapted bugs and for individuals fed milkweed, with evidence of a strong population by offspring diet interaction reflecting poor survivorship of milkweed-adapted bugs fed sunflower.
Our results indicate that for this species maternal effects may have limited influence in adapting to novel hosts.

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SUN 21 AUG at 1650 - Room N2
Oral presentation *A4-Sy11-1650-O*

Symposium 11
Non-genetic inheritance and evolution

The biological clock ticks for female house sparrows – a Lansing effect in a wild bird population

Schroeder J[1], Nakagawa S[1,2], Burke T[1]
[1]University of Sheffield, Animal and Plant Sciences, Sheffield, United Kingdom, [2]University of Otago, Departement of Zoology, New Zealand

Summary statement:

Age-dependent maternal epigenetic effects can limit the evolvability of reproductive fitness and longevity in a wild, closed and pedigreed bird population.

Abstract:

Within-individual consistency in fitness correlates can arise through environmentally induced heterogeneity between individuals, through epigenetic effects or have a genetic basis. Age is often used to describe the inherent quality of an individual in avian systems, because older individuals often have higher fitness. We studied phenotypic and genetic correlations, repeatability, narrow-sense heritability, maternal and early environment effects of variation in longevity, annual and life-time reproductive output, with the help of bayesian animal models. We used long-term data from a closed pedigreed island population of house sparrows. Low dispersal rates, together with a high re-sighting rate, resulted in unusually reliable fitness estimates, both for longevity and recruitment. We found that individual annual reproductive success was repeatable within individuals and increased with age. As expected for traits closely related to fitness, heritability was low, as was heritability of longevity. We found no significant additive genetic covariances between longevity and annual reproductive fitness. Therefore, epigenetic and environmental rather than genetic factors are responsible for maintaining within-individual consistency in reproductive success. Surprisingly, we found a strong transgenerational effect: sparrows born to older mothers had shorter lives than those born to younger mothers. Being born to older mothers consequently translated into a reduction in lifetime fitness. Thus, age-dependent epigenetic maternal effects can limit the evolvability of reproductive fitness and, more fundamentally, the evolution of longevity.

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SUN 21 AUG at 1550 - Room N2
Oral presentation *A4-Sy11-1550-O*

Symposium 11
Non-genetic inheritance and evolution

Evolutionary Implications of Trans-generational Epigenetic Effects

Uller T[1]
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Summary statement:

Analysing how epigenetic mechanisms transmit information clarifies their role in inheritance and evolution

Abstract:

One of the most exciting aspects of epigenetic mechanisms is their involvement in the inheritance of phenotypes across generations. However, it remains unclear what the evolutionary implications of epigenetic inheritance are. Taking a developmental perspective, I show that epigenetic mechanisms, such as DNA methylation, can serve two fundamentally different adaptive functions in trans-generational inheritance; as transmission of environmental information from one organism to its immediate offspring, or as information generated by natural selection on variants stably transmitted down a lineage of organisms. Only the latter forms an inheritance system on a par with genetic inheritance. However, the former – which may give rise to trans-generational plasticity – has more important roles for phenotypic evolution than previously appreciated, for example, by contributing to the generation and retention of novel phenotypic variation. Analysing the potential for epigenetic effects to act as channels of information clarifies the extent to which epigenetic mechanisms can form the basis of an inheritance system analogous to DNA and provides a formal framework for addressing the adaptive evolution of epigenetically-based trans-generational plasticity.

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Symposium 12

Plant epigenetics

Talks: *Room N0*

***Essence posters**:* Ground floor lecture hall centre *HZ*

***Regular posters**:* Upper floor campus canteen *Mensa*

Invited Speakers:

Vincent Colot, Koen Verhoeven

Organizers:

Joop Ouborg, Oliver Bossdorf

Description:

Epigenetic processes such as DNA methylation may play a greater role in phenotypic evolution than previously acknowledged. Particularly in plants, there is now increasing evidence of epigenetic inheritance, natural epigenetic variation, and environmentally-induced heritable epigenetic changes. This symposium will give an insight into some of the questions and novel findings in this new field.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

Ground floor lecture hall centre *HZ*
Essence poster *E-Sy12-i001-E*

Symposium 12
Plant epigenetics

High temperature stress affects nuclear topology and transcription status of repetitive sequences in rye seedlings

Brazão J[1], Tomás D[1], Carvalho L[1], Viegas W[1], Silva M[1]
[1]Technical University of Lisbon, Centro de Botânica Aplicada à Agricultura, Secção de Genética, Instituto Superior de Agronomia, Lisboa, Portugal

Summary statement:

High temperature induces descondensation of rDNA and subtelomeric sequences, nucleoli area increase and enhanced rDNA transcription level in rye

Abstract:

All organisms are exposed to environmental stimuli that can induce stress situations and plants sessile life style renders impossible the ability to avoid environment negative impacts. Heat stress (HS) induces the switch on of heat shock proteins and transcription factors, affecting gene expression patterns. However, little is known about HS effects on physical organization and transcription patterns of repetitive sequences. To address this question we characterized chromatin topology and transcription levels of 45S rDNA and repetitive pSc200 sequences in rye seedlings subjected to high temperature treatment (4hours 40oC) using fluorescence in situ hybridization (FISH) in interphase nuclei and Real Time quantitative PCR, respectively. Additionally, we used imunocytochemestry with fibrillarine antibody to evaluate nucleoli morphology and dynamics.

The results obtained clearly demonstrated that high temperature induces decondensation of both repetitive sequences analyzed, as well as an increase in nucleolar area. 45S rDNA expression level is increased by high temperature stress, whereas transcription level of subtelomeric non-coding sequences (pSc200) is not affected. rDNA chromatin organization and nucleoli dimension changes seem to result from an higher requirement of ribosome synthesis need to accompany the increase in protein synthesis after HS, although we cannot rule out the hypothesis of cell cycle arrest. Our work unravels the role of repetitive coding and non-coding sequences nuclear topology and transcription modulation in the epigenetic control of plant pathways involved in stress response.

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MON 22 AUG at 1550 - Room N0
Invited talk *B4-Sy12-1550-I*

Symposium 12
Plant epigenetics

Epigenetic variation across generations

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Summary statement:

Genome-wide epigenetic perturbation can rapidly generate heritable variation for complex traits.

Abstract:

The heritable basis of phenotypes has long been assumed to depend on the transmission of DNA sequence alleles from parents to offspring. However, this view is being increasingly challenged by the observation that changes in chromatin states, which are central to the control of genome activity, can in some instances be inherited through multiple sexual generations independently of any DNA sequence change. This so-called epigenetic inheritance of chromatin states concerns primarily transposable elements and other repeats. Although it is best documented in plants and often involves differential DNA cytosine methylation, we still know very little about what causes transgenerational epigenetic variation or how stable and prevalent it is. I will describe our efforts at answering these questions using epigenetic recombinant inbred lines (epiRILs) that were obtained by crossing two parents with near identical genomes but contrasted DNA methylomes. I will show how these epiRILs are enabling us to assess genome-wide the stability of DNA methylation variants as well as their impact on phenotypes and the physical integrity of the genome.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy12-i001-R*

Symposium 12
Plant epigenetics

Epigenetic processes in Scabiosa columbaria, the first steps into studying the role of epigenetic variation in an ecological evolutionary perspective

Groot MP[1], Vergeer P[1], Ouborg NJ[1]
[1]Radboud University Nijmegen, Molecular Ecology, Nijmegen, Netherlands

Summary statement:

Epigenetic processes in Scabiosa columbaria, the first steps into studying the role of epigenetic variation in an ecological evolutionary perspective.

Abstract:

There is increasing evidence that epigenetic variation and processes play a more important role in phenotypic variation and microevolution than previously thought. Several studies with plants have shown that there is natural epigenetic variation, and that this variation is responsible for heritable variation in phenotypic traits. Moreover, previous research shows that exposure to different environmental factors may alter epigenetic processes such as DNA methylation. There are four main questions that require an answer to find out how important epigenetic variation is in ecological evolutionary processes; what is the extent and distribution of epigenetic variation? What is the effect of environmental change on epigenetic variation? What are the phenotypic consequences of epigenetic variation? And are these epigenetic effects heritable?
To answer these questions we will use a new model species for ecological genomics, namely Scabiosa columbaria. By choosing a plant with different ecology and life-history than the general genetic model plant, Arabidopsis thaliana, we are also testing for the generality of results that are already obtained from Arabidopsis. We will present our first results towards answering our questions.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy12-i002-R*

Symposium 12
Plant epigenetics

Large-scale screening of natural epigenetic variation in a broad European collection of A. thaliana

Lampei C[1], Schmid K[1]
[1]University Hohenheim, Institute of Plant Breeding, Seed Science and Population Genetics (350), Stuttgart, Germany

Summary statement:

First results and design of a two generations transplanting experiment, to evaluate the relative contribution of genetic and epigenetic variation to adaptive phenotypic variation.

Abstract:

Recent epigenomic studies in A. thaliana repeatedly showed that epigenetic variation is responsible for phenotypic variation in potentially adaptive traits. Furthermore, it was suggested that some of this variation may be heritable over several generations. These findings offer the possibility that environmentally induced epigenetic changes may accelerate adaptation to changing climatic conditions. However, most studies are conducted in highly controlled environments what makes it difficult to judge the fitness relevance of epigenetic variation under natural conditions. To investigate the relative importance of epigenomic variation and the possibility of accelerated adaptation we conduct a transplanting experiment along an environmental gradient in southern Germany. Mother plants, originating from a wide geographic range, are raised in a full-factorial experimental design in three sites which differ strongly in winter minimal and all year average temperature. The offspring will than be transplanted among the sites in the following year. In addition to phenotyping of adaptive traits, we will re-sequence both, the genome and the methylome, which will enable us to quantify the relative contribution of both to variation in the phenotype using techniques of genome-wide association mapping. First results show strong differences among ecotypes in winter survival in the coldest side, suggesting differential frost tolerance.
Here we present results of phenotyping of the first years experiment and the design of the complete project.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy12-i003-R*

Symposium 12
Plant epigenetics

Epigenetic variation causes heritable variation in induced plant defenses and pathogen resistance

Latzel V[1], Zhang Y[1], Moritz KK[1], Slaughter A[2], Mauch-Mani B[2], Fischer M[1], Bossdorf O[1]
[1]University Bern, Institute of Plant Sciences, Bern, Switzerland, [2]University of Neuchatel, Laboratory of Cell and Molecular Biology, Neuchatel, Switzerland

Summary statement:

Epigenetic variation causes variation in induced defences and consequently in resistance to pathogen in Arabidopsis thaliana.

Abstract:

There is currently much speculation about the potential role of epigenetic variation as an additional, hitherto overlooked, determinant of heritable variation in important plant traits. However, we still know very little about the phenotypic consequences of epigenetic variation, in particular with regard to more complex traits related to the ecological interactions between plants and other species. Here, we explored to what extent heritable variation in DNA methylation affects plant responses to jasmonic acid (JA) and salicylic acid (SA), two important hormones involved in the induction of plant defences against herbivores and pathogens, respectively, as well as the actual plant resistance to the bacterial pathogen Pseudomonas syringae. In order to be able to unambiguously ascribe phenotypic differences to epigenetic variation, we used epigenetic recombinant inbred lines (epiRILs) of Arabidopsis thaliana – lines that are genetically very similar but variable at the level of DNA methylation. Plant resistance P. syringae was quantified both through the growth responses of plants as well as through real-time PCR assays of pathogen abundances. We found that the epiRILs not only differed in their mean phenotype, but that there were also significant differences in the degree to which they responded to treatment with JA or SA, and in their resistance to P. syringae. Our study thus demonstrates that epigenetic variation alone can cause heritable variation and thus potentially microevolution of plant defences. It is possible that part of the variation and adaptation of plant defences observed in natural populations is due to underlying epigenetic rather than genetic variation.

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MON 22 AUG at 1710 - Room N0
Oral presentation *B4-Sy12-1710-O*

Symposium 12
Plant epigenetics

The interaction between genetic, epigenetic and environmental variation: Effects of inbreeding

Vergeer P[1], Wagemakers N[1], Ouborg J[1]
[1]Radboud University Nijmegen, Molecular Ecology, Nijmegen, Netherlands

Summary statement:

Substantial differences in epigenetic variation was observed in response to different environmental factors and these differences increased with increased levels of inbreeding.

Abstract:

One of the most intriguing current puzzles of evolutionary plant biology is to understand the role of epigenetic processes in ecology and evolution: How do plants respond to environmental changes and what is the role of epigenetic processes in these evolutionary processes? Theory predicts that genetically eroded populations, such as inbred populations, have a poor ability to adapt to environmental changes due to a lack of genetic variation. However, epigenetic variation may provide populations, independently of genetic variation, with the plasticity needed to cope with environmental changes.
We studied phenotypic and epigenetic variation of Scabiosa columbaria in response to different environmental factors, such as nitrogen, drought, salinity and herbivory. Substantial differences in phenotypic as well as epigenetic variation were observed in response to different environmental factors. In an experiment, with over 20 families selected from populations from the UK, the Netherlands and France, epigenetic variation, scored as the percentage of methylation using MSAP markers, increased significantly in inbred individuals compared to outbred individuals. Environmental stressors resulted in lower methylation levels in inbred individuals, whereas no such patterns were observed in outbred individuals. The ecological consequences of the differences in epigenetic variation between inbred and outbred plants will be discussed.

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MON 22 AUG at 1630 - Room N0
Invited talk *B4-Sy12-1630-I*

Symposium 12
Plant epigenetics

Epigenetic inheritance in apomictic dandelions

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Summary statement:

In dandelions, exposure to environmental stress leads to epigenetic changes that are passed on to offspring. The consequences for offspring are explored.

Abstract:

Environmental factors can trigger epigenetic modifications and epigenetic information can in some instances be transmitted between generations. These observations have fueled speculation about the contribution of ´soft inheritance´ to heritable trait variation and adaptation. However, this contribution remains largely undemonstrated. Using apomictic dandelions as a model system we explored natural causes of heritable DNA methylation variation, including ploidy level change (which occurs naturally when new triploid apomicts arise in crosses between diploid mothers and polyploid pollen donors) and environmental stress. Exposure to various biotic and abiotic stresses triggered genome-wide DNA methylation changes, as detected by methylation-sensitive AFLP markers. Most of the induced changes were faithfully transmitted to offspring. In order to demonstrate transgenerational epigenetic inheritance that is relevant to ecology and evolution, it needs to be established that the stress-induced epigenetic modifications cause heritable effects on transcriptomes and traits, and that they persist for more than one offspring generation. I will discuss ongoing work that addresses these aspects in the dandelion system.

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MON 22 AUG at 1650 - Room N0
Oral presentation *B4-Sy12-1650-O*

Symposium 12
Plant epigenetics

Epigenetic variation can cause heritable variation in complex traits and phenotypic plasticity

Zhang Y[1], Fischer M[1], Bossdorf O[1]
[1]University of Bern, Institute of Plant Sciences, Bern, Switzerland

Summary statement:

The experiments with epiRILs suggests that DNA methylation variation alone can cause variation and microevolution.

Abstract:

We now know that heritable phenotypic variation within species can not only be caused by underlying genetic variation, but also by heritable variation in epigenetic modifications of the genome, such as DNA methylation. However, in most systems it is impossible to disentangle genetic and epigenetic effects, and to unambiguously demonstrate the phenotypic consequences of epigenetic variation. A rare exception are epigenetic recombinant inbred lines (epiRILs) of Arabidopsis thaliana, which are genetically identical but significantly different at the level of DNA methylation. We used these epiRILs to thoroughly test for the effects of epigenetic variation on complex plant traits and the plasticity of plants to different environmental changes. We planted replicates of 134 epiRILs as well as several control lines into three different environments (control, drought, nutrient addition), and examined the heritability of phenotypic traits (flowering time, root: shoot ratio, biomass, reproductive allocation, fitness), as well as their plasticity across environments. We found significant heritability in all of these traits, and we also found significant variation in plasticity among the epiRILs, which suggests that DNA methylation variation alone can cause variation, and thus presumably also microevolution, in such important plant traits. While there was a positive correlation between the drought tolerance and nutrient plasticity of epiRILs, variation was uncorrelated for several of the other measured traits, such as growth and flowering time, which suggests that these traits have a different epigenetic basis.

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Symposium 13

Evolution outside of the nucleus

Talks: *Room N4*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Upper floor campus canteen *Mensa*

Invited Speakers:

Ron Burton, David McCauley

Organizers:

Maurine Neiman, Dan Sloan, Doug Taylor

Description:

The primary defining feature of eukaryotes is the existence of intracellular organelles containing genomes that have very different modes of inheritance. Our goal is to use this symposium to explore what these various cytoplasmic genomes have in common, how they differ, and how the peculiarities of their biology can be used to generate fundamental insights into key questions in evolutionary biology, from the maintenance of sex and recombination to sexual conflict and speciation to the evolution of genome architecture.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy13-i001-R*

Symposium 13
Evolution outside of the nucleus

Within species patterns of reproductive isolation and the role of cyto-nuclear interactions

Barnard-Kubow KB[1], Galloway LF[1]
[1]University of Virginia, Department of Biology, Charlottesville, United States

Summary statement:

Cytonuclear interactions contribute to substantial intraspecific reproductive isolation in a plant species. Chloroplast divergence partially explained observed hybrid inferiority.

Abstract:

Genetic incompatibilities are one of the primary causes of reproductive isolation associated with the formation of new species. Most studies of genetic incompatibilities have focused on interactions between nuclear genes. However, given the role the organelles play in both respiration and photosynthesis, co-adaptation of the nucleus and cytoplasm within populations and cytonuclear incompatibilities between populations are both likely to occur and may play a significant role in the speciation process. We studied the role of cytonuclear interactions in reproductive isolation in the plant species Campanulastrum americanum. Populations from across the species range were crossed and the F1 hybrids were examined for the presence of hybrid breakdown. In addition, chloroplast loci were sequenced to construct a phylogeny and determine chloroplast divergence between populations. F1 hybrid breakdown was observed in crosses between Appalachian populations and other populations, with up to an 84% reduction in viability relative to the parents. Other crosses showed no hybrid breakdown. Asymmetrical breakdown between reciprocal F1 hybrids was common, indicating the role of cytonuclear incompatibilities. Cytonuclear incompatibilities were further supported by leaf variegation in the F1. Chloroplast genetic distance was correlated with degree of hybrid breakdown, but did not fully explain the observed patterns of reproductive isolation. Our results indicate the importance of cytonuclear incompatibilities in intraspecific reproductive isolation, and suggest that such incompatibilities may contribute significantly to the speciation process.

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MON 22 AUG at 1610 - Room N4
Oral presentation *B4-Sy13-1610-O*

Symposium 13
Evolution outside of the nucleus

Novel protein genes in animal mtDNA: a new sex determination system in freshwater mussels (Bivalvia: Unionoida)?

Breton S[1]
[1]Kent State University, Biological Sciences, Kent, United States

Summary statement:

This study demonstrates that the genetic and functional repertoire of animal mtDNA is considerably greater than typically acknowledged.

Abstract:

Mitochondrial function depends critically on optimal interactions between components encoded by mitochondrial and nuclear DNAs. Strict maternal mtDNA inheritance (SMI) is thought to have evolved in animal species to maintain mito-nuclear complementarity by preventing the spread of selfish mitochondrial elements thus typically rendering mtDNA heteroplasmy evolutionarily ephemeral. Here we show that mtDNA intra-organismal heteroplasmy can persist for hundreds of millions of years. We demonstrate that the only exception to SMI in the animal kingdom, i.e., the doubly uniparental mtDNA inheritance system in bivalves, with its three-way interactions among egg mt-, sperm mt- and nucleus-encoded gene products, is tightly associated with the maintenance of separate male and female sexes (dioecy) in freshwater mussels. Specifically, this mother-through-daughter and father-through-son mtDNA inheritance system, containing highly differentiated mt genomes, is found in all dioecious freshwater mussel species. Conversely, all hermaphroditic species lack the paternally transmitted mtDNA (= possess SMI) and have heterogeneous macromutations in the recently discovered, novel protein-coding gene (F-orf) in their maternally transmitted mt genomes. Our results support the hypothesis that proteins coded by the highly divergent maternally and paternally transmitted mt genomes could be directly involved in sex determination in freshwater mussels. Concomitantly, our study demonstrates novel features for animal mitochondrial genomes: the existence of additional mtDNA-encoded proteins with functional significance and the involvement of mtDNA-encoded proteins in extra-mitochondrial functions.

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MON 22 AUG at 1400 - Room N4
Invited talk *B3-Sy13-1400-I*

Symposium 13
Evolution outside of the nucleus

The causes and consequences of of nuclear-mitochondrial incompatibilities in hybrid breakdown between allopatric populations

Burton RS[1]
[1]Scripps Institution of Oceanography, Marine Biology Research Division, La Jolla, United States

Summary statement:

Mitonuclear interactions sensitive to hybrid breakdown include not only the synthesis of ATP energy, but also the replication and transcription of the mitochondrial genome itself.

Abstract:

Despite widespread use of mtDNA as a powerful marker for evolutionary analyses, the complexity of selective forces acting on the mitochondrial genome remains under-appreciated. Animal cells rely the mitochondrial electron transport system (ETS) for ATP production; four of the five ETS complexes are composed of subunits encoded in both the mtDNA and nuclear genomes. The maintenance of functional interactions among nuclear and mtDNA encoded ETS subunits is the most widely cited driver of intergenomic coadaptation. However, mitonuclear coadaptation extends far beyond structural interactions among ETS subunits. The two genomes experience different mutation, repair and inheritance, and they are separately replicated, transcribed, and translated. It is not surprising, then, that then as populations diverge in allopatry, a diversity of mitonuclear incompatibilities may arise.
Allopatric populations of the copepod Tigriopus californicus readily interbreed in the lab, producing hybrids that consistently show F1 hybrid vigor but F2 hybrid breakdown. Several lines of evidence suggest that mitonuclear interactions underlie much of the loss in fitness in F2 and later hybrids. In addition to disruption of interactions among proteins involved in the ETS, transcription of the entire mtDNA genome may be impacted by changes in non-coding regions of the mtDNA that function in the initiation of transcription by the nuclear-encoded RNA polymerase and associated transcription factors. Hypotheses regarding the importance of these interactions in generating hybrid breakdown can now be directly tested using tools such as RNA interference and high throughput transcriptome sequencing.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy13-i002-R*

Symposium 13
Evolution outside of the nucleus

Mitogenomics of European Mytilus mussels

Burzynski AS[1], Śmietanka B[1], Zbawicka M[1], Sańko T[1], Wenne R[1]
[1]Institute of Oceanology Polish Academy of Sciences, Genetics and Marine Biotechnology, Sopot, Poland

Summary statement:

The data set consisting of several dozen complete mitochondrial sequences from animals having two divergent mitochondrial genomes reveals the complexities of cytoplasmic evolution.

Abstract:

The unusual mitochondrial inheritance system known as Doubly Uniparental Inheritance (DUI) first discovered in marine bivalves from the genus Mytilus gives the unique opportunity to study evolution of two divergent mitochondrial genomes within the same species. Under DUI, in addition to the usual, maternally inherited genomes present in both sexes (maternal lineage) some mitochondrial genomes, present exclusively in males, are inherited paternally forming the second, paternal lineage. The two lineages diverged before the speciation occurred within the three-species Mytilus edulis species complex (consisting of M. edulis, M. galloprovincialis and M. trossulus) and so the two mitochondrial genomes of a single individual may differ, on average by 20%. Several interesting features of mitochondrial evolution have been described within this system: variable evolutionary rate (the paternal lineage evolves faster), inter-species introgression in the context of cross-species hybridisation, inter-lineage recombination, and possible involvement of positive selection acting on the mitochondrial genome. To better understand the forces governing the evolution of mitochondrial DNA in this complex system we have sequenced a sample set of several dozen complete mitochondrial genomes, representative for the European populations of all three species. The detailed analysis of this mitogenomic data set allowed us to precisely date the major evolutionary events and evaluate the role of drift, selection and recombination in shaping the observed pattern of polymorphisms in extant Mytilus mitochondrial genomes. These may have big implications for the evolution of mitochondrial genomes in general.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy13-i001-E*

Symposium 13
Evolution outside of the nucleus

Changes in mitochondrial DNA molecule conformations: The case of the atypical mtDNA of terrestrial isopods (Metazoa; Crustacea)

Doublet V[1,2], Helleu Q[2], Souty-Grosset C[2], Marcadé I[2]
[1]Martin-Luther-Universität Halle-Wittenberg, Institut für Biologie, Halle (Saale), Germany, [2]Université de Poitiers, Laboratoire Ecologie Evolution Symbiose, Poitiers, France

Summary statement:

Atypical mtDNA of terrestrial isopods is composed of two uncommom molecules that are supposed to have been generated via the formation of haiprin structures in the control region.

Abstract:

Coexistence of multiple molecular forms in mitochondrial DNA (mtDNA) is common in plant or protist mitochondria but not in metazoan. The atypical mtDNA of terrestrial isopods present two uncommon molecular forms: ~14kb linear monomers associated to ~28kb head-to-head circular dimers. Previous sequencing of the terrestrial isopod Armadillidium vulgare mtDNA failed to obtain the control region sequence, tought to be present at the extremities of linear molecules and at the junction zones of the circular dimers. Recently, we succeed in this sequencing for several individuals, thus completing the mitochondrial genome sequence. These sequences obtained with primers designed from linear monomers extremities indicate that standard circular monomeric molecules might also be present in the atypical mtDNA of A. vulgare. Their alignment shows a particular section showing inverted repeats that appear in reverse orientations according to the sampled populations. Moreover, this specific section, that putatively fold in a hairpin structure, has been found in both orientations in a single individual, generating a heteroplasmy that testify the dynamical behavior of this sequence. Such inverted repeats folding in hairpin structures have already been observed in yeasts mtDNA where they are responsible of molecular conformation changes (i.e. from circular monomers to circular dimers via linear monomers). Interestingly, the hairpin structure observed in A. vulgare mtDNA control region is localised where linearization and dimerization of the atypical mtDNA should take place, thus confirming that different molecular shapes in terrestrial isopods might be generated from one to another.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy13-i003-R*

Symposium 13
Evolution outside of the nucleus

Could selection for mitonuclear co-adaptation explain the evolution of two sexes?

Hadjivasiliou Z[1], Pomiankowski A[2], Seymour RM[3], Lane N[2]
[1]UCL, CoMPLEX, London, United Kingdom, [2]UCL, GEE, London, United Kingdom, [3]UCL, Mathematics, London, United Kingdom

Summary statement:

Could selection for mitonuclear coadaptation explain the evolution of uniparenatal inheritance of mtDNA and the existence of two sexes? We explore this using a mathematical model.

Abstract:

Mitochondria are descended from free-living bacteria that were engulfed by another cell some 2 billion years ago. A major redistribution of DNA led to genetic information being mainly maintained by a large central genome in the nucleus supported by a smaller genome held by the mitochondria. Oxidative phosphorylation, the most vital function of mitochondria, is carried out by proteins encoded by both nuclear and mitochondrial genes. ATP synthesis therefore depends on the functional compatibility of proteins encoded by distinct genomes that can have radically different tempi and modes of evolution. It has been postulated that the existence, or maintenance, of two sexes may be explained by the requirement for mitonuclear coadaptation. This hypothesis suggests that the major features of mitochondrial inheritance, notably uniparental inheritance and bottlenecking act to enhance the coadaptation of mitochondrial and nuclear genes. We explore this possibility using a mathematical model. This allows us to specify the conditions under which selection for mitonuclear coadaptation could favour the evolution of uniparental inheritance of mitochondria and so the existence of two sexes.

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MON 22 AUG at 1710 - Room N4
Oral presentation *B4-Sy13-1710-O*

Symposium 13
Evolution outside of the nucleus

Sex and selfishness: Experimental evolution of parasite virulence

Harrison E[1], MacLean RC[2], Koufopanou V[3], Burt A[3]
[1]University of Liverpool, Institute of Integrative Biology, Liverpool, United Kingdom, [2]University of Oxford, Dept. of Zoology, Oxford, United Kingdom, [3]Imperial College London, Silwood Park Campus, Ascot, United Kingdom

Summary statement:

Using an experimental evolution approach, we demonstrate that sexual reproduction selects for increasing virulence in two extra-chromosomal elements of Saccharomyces cerevisiae.

Abstract:

Genetic elements that are transmitted in a non-Mendelian manner can be subject to within-individual selection as well as the more conventional between-individual selection. The magnitude of this within-individual selection depends on the breeding system, being larger in outcrossed species and smaller in inbred or asexual species. We have studied the effect of varying the magnitude of the within-individual component of selection by analyzing the evolution of two extra-chromosomal elements in experimental sexual and asexual populations of Saccharomyces cerevisiae. The 2 micron plasmid is a biparentally transmitted, multicopy element which appears to be entirely parasitic. In contrast, mitochondria are established endosymbionts in the cell, which in S. cerevisiae are also biparentally inherited. In asexual populations, the fitness of extra-chromosomal elements is entirely linked to that of the host, and selection to minimize harm is strong. However, in sexual populations, elements which do not adhere to Mendelian inheritance are able to spread, and host imposed selection is reduced. As predicted, we find that sexually reproducing populations are subject to that sexual populations are subject to both an increase in plasmid burden, and the invasion of non-functional 'selfish' mitochondrial mutants. To our knowledge, this is the first experimental demonstration of parasite virulence evolving in response to the host sexual system.

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MON 22 AUG at 1630 - Room N4
Oral presentation *B4-Sy13-1630-O*

Symposium 13
Evolution outside of the nucleus

Experimental evidence for a sex-specific selective sieve in mitochondrial genome evolution

Innocenti P[1], Morrow EH[1], Dowling DK[2]
[1]Uppsala University, Uppsala, Sweden, [2]Monash University, School of Biological Science, Melbourne, Australia

Summary statement:

Different mtDNA strains have major effects on male, but not female, nuclear gene expression in D. melanogaster, suggesting sex-specific mutation accumulation.

Abstract:

Mitochondria are maternally transmitted, hence their genome can only make a direct and adaptive response to selection through females, while males represent an evolutionary dead-end. In theory, this creates a sex-specific selective sieve, enabling deleterious mutations to accumulate in mitochondrial genomes if they exert male-specific effects. We tested this hypothesis, expressing five mitochondrial variants alongside a standard nuclear genome in Drosophila melanogaster, and found striking sexual asymmetry in patterns of nuclear gene expression. Mitochondrial polymorphism had few effects on nuclear gene expression in females but major effects in males, modifying nearly 10% of transcripts. These were mostly male-biased in expression, with enrichment hotspots in the testes and accessory glands. Our results suggest an evolutionary mechanism that results in mitochondrial genomes harboring male-specific mutation loads.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy13-i005-R*

Symposium 13
Evolution outside of the nucleus

Mitochondrial genome evolution and body size in the Nematoda

Lagisz M[1], Poulin R[1], Nakagawa S[1]
[1]University of Otago, Department of Zoology, Dunedin, New Zealand

Summary statement:

Exploring mitochondrial genomes of the Nematoda

Abstract:

The rate of molecular evolution varies greatly among species and has been linked to various factors such as body size, longevity and generation time. To obtain an insight into the evolution of mitochondrial genomes within the Nematoda, we analysed the mtDNA genomic sequences of 46 species. We looked at the genome size, gene order, genomic rearrangements, nucleotide composition and rates of sequence evolution. We uncovered extensive mitochondrial genomic diversity within the Nematoda; in other words, genomes vary considerably in their size, gene content, gene order, amount of non-coding regions, nucleotide composition, and the rates of sequence evolution. Furthermore, we examined associations between the aforementioned traits and nematode body size, used as a proxy for longevity and generation time, in order to test the mitochondrial theory of aging. Additionally, we look at the effects of the lifestyle, host type and host size to understand the patterns of mitochondrial genome evolution.

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MON 22 AUG at 1440 - Room N4
Invited talk *B3-Sy13-1440-I*

Symposium 13
Evolution outside of the nucleus

Paternal leakage and heteroplasmy of the mitochondrial genome in the plant Silene vulgaris

McCauley DE[1]
[1]Vanderbilt University, Biological Sciences, Nashville, United States

Summary statement:

Mitochondrial paternal leakage and heteroplasmy in the plant Silene vulgaris will be described, along with evolutionary consequences for its breeding system and genome.

Abstract:

In plants it is usually the case that the mitochondrial genome is maternally inherited. However, recent studies have questioned this in the gynodioecious plant Silene vulgaris. Results of experimental crosses will be presented documenting a low frequency of paternal leakage of mitochondrial gene markers. Most often this leakage results in a degree of bi-parental inheritance and heteroplasmy, though very rare cases of pure paternal inheritance also occur. When heteroplasmy is already in the maternal lineage it can be transmitted to the next generation, or lost, according to the rules of vegetative sorting. Heteroplasmy has also been observed in a small percentage individuals sampled from natural populations of S. vulgaris, and paternal leakage has been inferred from the genetic composition of open pollinated progeny arrays derived from homoplasmic individuals. Consequences of this leakage and resulting heteroplasmy will be discussed, including the potential impact of leakage on the evolution on gynodioecious systems with cyto-nuclear sex determination, and the impact of heteroplasmy on the outcome of recombination between mitochondrial genomes. An apparent discordance between the rate of leakage seen in the crosses and the level of heteroplasmy seen in natural populations will also be discussed.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy13-i002-E*

Symposium 13
Evolution outside of the nucleus

Comparative study of the evolution of mitochondrial and chloroplast genomes respect to the tree of life

Mer AS[1], Reynaud EG[2], Andrade MA[1]
[1]Max-Delbrueck-Centrum fuer Molekulare Medizin (MDC), Computational Biology and Data Mining Group, Berlin, Germany, [2]University College Dublin, School of Biology and Environmental Science, Dublin, Ireland

Summary statement:

We are analysing organelle (mitochondrial and chloroplast) genomes evolution with respect to the tree of life.

Abstract:

The evolution of organelle genomes (e.g. mitochondria and chloroplast) goes in the direction of moving genes to the nuclear genome to produce a reduced genome. However, in different branches of the tree of life this process has occurred on different genes. The recent increase in the number of complete organelle genomes sequenced (currently around 6300 mitochondrial and 213 chloroplast are available from [GOBASE: an organelle genome database, NAR, 2009]) allows to study this process in detail. We are exploring how organelle genomes are similar to each other in terms of orthologous genes in order to identify ancient events of organelle genome evolution. We discuss the correlation of these events to the structure of the tree of life.

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MON 22 AUG at 1650 - Room N4
Oral presentation *B4-Sy13-1650-O*

Symposium 13
Evolution outside of the nucleus

Epistasis and the evolution of the mitochondrial DNA in Drosophila

Montooth KL[1], Meiklejohn CD[2], Rand DM[3]
[1]Indiana University, Biology, Bloomington, United States, [2]University of Rochester, Biology, Rochester, United States, [3]Brown University, Ecology and Evolutionary Biology, Providence, United States

Summary statement:

Mitochondrial-nuclear incompatibilities do not fix between Drosophila species, despite the potential for strong epistasis that compromises metabolic fitness.

Abstract:

Mitochondrial and nuclear genomes are posited to diverge coordinately under positive selection to enable adaptation to new physiologies, ecologies and life histories, and/or as the consequence of compensatory evolution. A prediction of this co-evolutionary model is that more divergent lineages should accumulate more incompatibilities between mitochondrial and nuclear genomes. Using strains that precisely combine mitochondrial and nuclear genomes from different species, we show that this is not the case in the D. melanogaster subgroup. mtDNAs from D. simulans and D. mauritiana are largely compatible with the D. melanogaster nuclear genome. This pattern contrasts with other invertebrates, such as the parasitic wasp Nasonia and the marine copepod Tigriopus. These taxonomic differences likely arise from differences in the rates of substitution in the mtDNA due to differences in population structure, the presence of cytoplasmic driving elements, and the mutational process. The mtDNA of Drosophila appears to maintain function not through compensation of deleterious substitutions by the nuclear genome, but through a largely effective mutation-selection balance. Nevertheless, this happens in the face of the potential for strong epistasis for fitness that can arise between mitochondrial and nuclear variants that segregate within species. We have currently mapped one particular mitochondrial-nuclear incompatibility to the causal nucleotides. I will discuss the consequences of this epistatic interaction, which putatively impacts mitochondrial protein synthesis, for the fate of nucleotide variants in mitochondrial genomes.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy13-i004-R*

Symposium 13
Evolution outside of the nucleus

Recombination in Control Region precedes masculinization of Mytilus mitochondrial DNA

Sańko TJ[1], Filipowicz M[1], Burzyński A[1]
[1]Institute of Oceanology Polish Academy of Science, Genetics and Marine Biotechnology Department, Sopot, Poland

Summary statement:

Recombination in Control Region of Mytilus mitochondrial DNA may be just the first step in masculinization of the female mitochondrial genome.

Abstract:

The Mytilus mitochondrial (mt) genome is structurally similar to mitochondrial DNA (mtDNA) of other animals but it features quite unique genetics. Contrary to other animals, Mytilus mtDNA is inherited through two separate lineages (Doubly Uniparental Inheritance): males are heteropalsmic, having mtDNA both from their fathers (in germ cells) and from their mothers (in somatic cells) whereas females are homoplasmic, having only mtDNA from their mothers. The male mt genome (M genome) is evolving at much higher rate and under lower selective pressure than the female genome (F genome).

The F genome is known to occasionally invade the paternal lineage of inheritance in the process called role-reversal or masculinization. There have been several reports on masculinization in Mytilus. It has been postulated that mosaic Control Region (CR) sequences are indicative of the genome masculinization. We have sequenced and compared CR and coding fragments of the recently masculinized genome from one male specimen from Baltic M. trossuslus with its closest but not masculinized relative - the genome isolated from a female M. galloprovincialis. In both genomes the CRs had similar recombinant M-F structures, but only the Baltic genome showed the signature of masculinization: faster evolutionary rate and relaxed selection.

This is consistent with the hypothesis that CR recombination may precede masculinization. However, the mosaic CR structure by itself should not be taken as a proof of the genome masculinization.

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MON 22 AUG at 1550 - Room N4
Oral presentation *B4-Sy13-1550-O*

Symposium 13
Evolution outside of the nucleus

Rapid evolution of mitochondrial genome size and structure in lineages with accelerated mutation

Taylor DR[1], Sloan DB[1]
[1]University of Virginia, Department of Biology, Charlottesville, United States

Summary statement:

Accelerated rates of mitochondrial mutation in the genus Silene are associated with rapid and profound changes in genome architecture and complexity.

Abstract:

Comparisons across nuclear and organelle genomes from diverse eukaryotes have suggested that increased mutational pressure selects for reduced genome complexity. In the angiosperm genus Silene, a recent ~100-fold acceleration in the mitochondrial mutation rate presents a unique opportunity to explore this hypothesis. We sequenced the mitochondrial genomes of four Silene species with highly divergent mutation rates. Contrary to expectations, high mutation rate genomes exhibited a dramatic proliferation of non-coding content to the extent that they are by far the largest known mitochondrial genomes, surpassing even the genome size of free-living bacteria that share the most recent common ancestor with the mitochondrion. Genomes with low mutation rates occupy the lower end of the angiosperm size range, thus ~98% of the known range of organelle genome size is captured in this single genus. These immense genomes have also undergone rapid changes in many aspects of genome architecture and recombinational activity, including novel multi-circular structures. Thus, the evolution of many elements of eukaryotic genome diversity can be studied in this experimental system.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy13-i006-R*

Symposium 13
Evolution outside of the nucleus

Reproductive parasitism and gene flow modification

Telschow A[1], Kobayashi Y[2], Flor M[3], Werren JH[4], Hammerstein P[3]
[1]Westfalian Wilhelms University Muenster, Institute for Evolution and Biodiversity, Muenster, Germany, [2]University of Tokyo, Tokyo, Japan, [3]Humboldt-University of Berlin, Berlin, Germany, [4]University of Rochester, Rochester, United States

Summary statement:

Reproductive parasites like Wolbachia modify host gene flow and convert infected populations into population genetic sinks if populations differ in the degree of infection.

Abstract:

The term reproductive parasitism is commonly used to describe infective agents that manipulate the reproductive system of their host to their own advantage. Among the reproductive manipulations are feminization, male killing, and cytoplasmic incompatibility. Well studied reproductive parasites belong to the bacterial groups Wolbachia, Rickettsia, Cardinia, Arsenophonus, and Spiroplasma. The wide distribution of these bacterial groups among arthropods makes the study of reproductive parasitism an important topic in evolution. The present (theoretical) study is motivated by the (experimental) findings that different host populations often differ with respect to their infection state, i.e. some populations are infected while others are not or with a different strain. Based on these findings we constructed several population genetic models in order to investigate how such infection polymorphism affect the gene flow between populations. To measure gene flow we make use of the concept of effective migration rate. Our analysis revealed that, generally, infection with reproductive parasites modify host gene flow. Interestingly, populations with highest degree of infection are thereby converted into population genetic sinks. This is true for all forms of reproductive parasitism. These results give general insights to the evolution of selfish genetic elements. We discuss the implications with respect to host evolution and host-parasite coevolution, especially speciation and local adaptation.

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Symposium 14

Family interactions

Talks: *Room N3*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Upper floor campus canteen *Mensa*

Invited Speakers:

Allen Moore, Mathias Kölliker

Organizers:

Reinmar Hager, Per T Smiseth

Description:

Family interactions are ubiquitous in mammals, birds and other species where one or both parents provide food or other forms of care for offspring after hatching or birth. Such interactions include sibling competition over resource share, parent-offspring conflict and interactions among caring parents. The evolution of family interactions is a major area of research in behavioural ecology and quantitative genetics.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

TUE 23 AUG at 1500 - Room N3
Oral presentation *C3-Sy14-1500-O*

Symposium 14
Family interactions

Evolution of elaborate parental care: genetic architecture of complex suites of parental & offspring behaviours

Andrews C[1], Smiseth PT[1], Kruuk LEB[1]
[1]University of Edinburgh, Institute of Evolutionary Biology, Edinburgh, United Kingdom

Summary statement:

To better understand the evolution of elaborate parental care, we examine the genetic architecture of suites of parental & offspring traits involved using an insect model system.

Abstract:

Parental care commonly involves complex suites of parental & offspring behaviours, such as investment in eggs, preparation & provisioning of food, & offspring begging. Yet previous studies have often focused on only a limited set of traits. Here, we further our understanding of the evolution of elaborate parental care by analysing patterns of additive genetic variance for, & co-variance between, multiple parental & offspring behaviours, & between these traits & components of offspring fitness, using the burying beetle Nicrophorus vespilloides as model system. Using a full-sib, paternal half-sib mating design, we estimate the effects of additive genetic variation, common environmental effects, & the direction of genetic & environmental correlations between parental & offspring traits. We first test the prediction that life-history trade-offs will give rise to negative genetic covariances between traits. We next examine the extent to which genotype-by-environment interactions affect parental & offspring behaviours, testing the prediction of higher additive genetic variances & co-variances under conditions of greater resource availability. Finally, we test whether combined effects of parental & offspring behaviours on offspring fitness favour co-adaptation, resulting in genetic correlations between parental & offspring traits. Our study provides insights into how the evolution of elaborate parental care is shaped by genetic architecture, including genetic constraints, & by selection pressures acting on elaborate parental & offspring strategies.

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TUE 23 AUG at 1440 - Room N3
Oral presentation *C3-Sy14-1440-O*

Symposium 14
Family interactions

Indirect parental care using secreted antimicrobials increases offspring fitness in the burying beetle Nicrophorus vespilloides.

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Summary statement:

Nicrophorus vespiloides parents can dramatically increase the fitness of their offspring through the application of antimicrobial secretions directly to a breeding resource .

Abstract:

Parental care represents the suite of behaviours parents use to tend dependent offspring before and after their birth. While care is often viewed in terms of behaviours directed towards offspring, it can also be characterized by indirect parental behaviours that modify, and thus improve, the offspring developmental environment. Direct parental care in the form of larval provisioning is well known in the burying beetle, Nicrophorus vespilloides. However, indirect care is likely to be of equal importance, because larvae are reared on decomposing carrion facing intense competition from harmful bacteria. Here we investigate the role and mechanistic basis of antibacterial secretions applied to carcasses by N. vespilloides as a form of indirect parental care. We first confirm that parental anal secretions are directly bactericidal, with effects specific to certain gram positive bacteria. Next, we identify that the cause of bacterial lysis is due to an insect lysozyme, and show that the concentration of lysozyme is developmentally regulated. Finally, using a novel in situ developmental assay, we show that lysozyme is essential for larval survival and maximizing the rate of larval growth. These results expand the repertoire of indirect parental care behaviours utilised by insects to protect dependent offspring from microbial threats.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy14-i001-R*

Symposium 14
Family interactions

What's a few kilobases between family? Investigating telomere dynamics in the cooperatively breeding Seychelles warbler

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Summary statement:

We investigate whether telomere dynamics can be used as a bioindicator of the costs incurred by differing forms of social behaviour in a wild population of Seychelles warbler

Abstract:

Understanding what shapes life-history evolution in cooperative breeding species is complex as the costs and benefits of reproduction are spread among reproductive and non-reproductive group members. While the benefits of cooperative breeding are measured in terms of direct and inclusive fitness, costs prove difficult to measure. Telomere dynamics have gained considerable recent attention as a potential biomarker of individual quality. Telomeres are repetitive DNA sequences that act as a physical buffer to protect coding DNA. Telomeres can shorten with age due to processes including oxidative stress; consequently telomeres may chronicle an individual's life costs. Here, we investigate whether telomere dynamics can be used to measure the costs of differential social behaviour in a wild cooperative breeding species. In the Seychelles warbler (Acrocephalus sechellensis) ecological constraints restrict independent breeding and consequently many individuals become subordinates in an established group, often on their natal territory, where they 1) remain as non helping subordinates, 2) become helpers or 3) become co-breeders. These alternative strategies create a range of familial situations with dominant breeders that are either helped or not, subordinate co-breeders that are helped, and non-breeding subordinates that do or do not help. We investigate the prediction that reproductive costs are spread between dominant and subordinate helpers, and that this can be measured in terms of telomere rate of change. Ultimately, we assess whether telomeres can measure the costs associated with the fitness benefits of cooperative breeding.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy14-i002-R*

Symposium 14
Family interactions

Genetic influences on parental care in a beetle, Nicrophorus vespilloides

Bird C[1]
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Summary statement:

We have demonstrated that the gene foraging plays an important role in controlling parental care behaviour in a sub-social beetle, Nicrophorus vespilloides.

Abstract:

The burying beetle Nicrophorus vespilloides has highly developed parental care. Burying beetles reproduce on vertebrate carcasses that the parents prepare and feed their offspring. Thus, parents provide both indirect care in the form of protection, preparation, and maintenance of the carcass. They also provide direct care by feeding their offspring regurgitated and pre-digested food. This level of care is rare outside of eusocial species. Adults switch to caring after discovering a suitable carcass for reproduction, and revert to non-caring state once the larvae disperse. Quantitative genetic studies show that the amount of direct care given is genetically influenced and heritable. Studies in other insects suggest that the gene foraging has an influence on behaviour in social insects, particularly related to food acquisition. We hypothesise that changes in the level of expression of foraging influence the initiation and cessation of parental care and the feeding behaviour associated with it. We analysed foraging expression using QRT-PCR. We compared relative expression levels in virgins, caring parents and parents that had completed their parenting. We found that in both male and female the burying beetle homologue of foraging was more highly expressed during parental care, returning to the lower level once care was completed. Pharmacological investigations show that this is more than a correlation; caring parents treated with cGMP increased the intensity of direct parental care, and prolonged the duration to the extent that the parents were willing to accept and care for a second, unrelated brood. Levels of indirect care were not affected.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy14-i003-R*

Symposium 14
Family interactions

Sibling interactions in the least killifish (Heterandria formosa): do outbred offspring save their inbred siblings in mixed-paternity broods or is it ‘each fish for itself’?

Blyth JE[1], Lindström K[1]
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Summary statement:

Sibling interactions in the least killifish (Heterandria formosa): do outbred offspring save their inbred siblings in mixed-paternity broods or is it ‘each fish for itself’?

Abstract:

The least killifish (Heterandria formosa) is a live-bearing poeciliid found throughout the south eastern USA. Females provision foetuses after fertilisation (matrotrophy) through a placenta-like structure and are able to carry several broods at different stages of development at the same time (superfetation). In this species there is a complex network of interactions and conflicts between relatives due to differences between the optimal levels of maternal provisioning for maximising fitness. This complexity is compounded by polyandry which results in females provisioning mixed paternity broods simultaneously. We used a series of mating experiments and paternity analysis to establish whether outbred offspring from mixed paternity broods can ‘save’ their inbred half-siblings when sharing communal resources i.e. do inbred offspring that develop with outbred siblings have greater fitness and survival than offspring from entirely inbred broods? We determined parent size, number of live/dead offspring born to each female, size of offspring at birth, offspring paternity, birth-order and offspring gestation for the purpose of answering this question. We hypothesise that inbred offspring in mixed broods may be ‘saved’ because their outbred siblings bring in enough communal nutrients from the mother to sustain the whole brood. However, this may be at the expense of the outbred offspring being unable to gain enough resources for optimal fitness. This is important because it would suggest that female least killifish can increase their overall reproductive success by using polyandry to counteract the costs of inbreeding, but that it comes with a fitness cost for outbred offspring.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy14-i004-R*

Symposium 14
Family interactions

Maternal perception of the larval environment affects offspring performance but not paternity

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Summary statement:

Maternal perceptions of larval competition have strong effects on offspring performance, but this does not include adaptive paternity manipulation (i.e., cryptic choice).

Abstract:

The developmental performance of a genotype can vary substantially depending on the conditions in which it finds itself immersed, and mothers are consequently expected to exercise strong choice concerning oviposition sites. The extent to which females can also adaptively adjust the provisioning or paternity of offspring for local conditions remains unclear. To determine how offspring fitness depends on larval competitive environment, female perceptions of the larval environment, and sire paternity, we mated female yellow dung flies (Scathophaga stercoraria) with two different males each. We manipulated female perceptions of larval competition levels, and subsequently split clutches across high and low competition conditions. We found that females lay more eggs in the perceived absence of competition, especially when large in size. The effect of competition on offspring survival and size but not development time depended on maternal perceptions, but offspring performance was not better when the larval environment corresponded with maternal perception of it. Finally the effects of competition on paternity did not depend on maternal perceptions of larval environment, as would be expected if females were exercising adaptive cryptic choice. In our experiment we fail to support adaptive sperm choice, but nevertheless suggest surprising plasticity in maternal allocation that may function to improve direct fitness.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy14-i018-R*

Symposium 14
Family interactions

Parent-offspring conflict in humans and psychological disorders later in life: Evidence from the Danish Health Registries

Byars SG[1], Boomsma JJ[1]
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Summary statement:

Using health data contained in the Danish Health Registries we present initial findings from analyses that test the recently developed imprinted brain theory of psychois and autism.

Abstract:

Parent-offspring conflict is a well-developed branch of kin selection theory, which has recently been extended by genetic imprinting concepts that have helped to unravel intra-genomic social conflicts over shared resources. While kin selection theory has been fruitfully applied to almost all aspects of social evolution, its application for understanding conflicts in human reproduction is still in its infancy. This is remarkable as pregnancy (e.g. preeclampsia) and psychological (e.g. autism) disorders remain a major source of human suffering and recent research suggests that these disorders could be partly associated with genetic conflicts between the parents that occur during early development (i.e. embryo, fetus). Using the large scale medical and social information contained in the Danish Health Registries, we investigated whether the perinatal incidence of phenotypic markers of genetic parent-offspring conflict correlate with the risk of developing psychological disorders later in life, providing the first large-scale test of Badcock and Crespi's genomic imprinted brain theory of psychosis and autism. We present initial findings from these analyses.

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TUE 23 AUG at 1550 - Room N3
Oral presentation *C4-Sy14-1550-O*

Symposium 14
Family interactions

Experimental suppression of reproduction in a wild cooperative mammal

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Summary statement:

This large-scale field experiment on a mammalian cooperative breeder shows that the outcome of reproductive conflict is a costly compromise, and is not optimum for any party.

Abstract:

Animal societies vary enormously in the evenness with which reproduction is distributed among group members, or the degree of reproductive skew. Evolutionary models proposed to explain this variation differ in whether they assume that observed skew is optimum from the perspective of one or more group members; or whether it represents a compromise resolution. The best way to distinguish the models is to manipulate the degree of skew experimentally, but this experiment has yet to be carried out in any species. Here we report the results of a five-year experiment in which we experimentally manipulated reproductive skew among female banded mongooses (Mungos mungo) using short-acting contraceptives. In this species multiple dominant and subordinate females breed together and give birth on the same day. In separate experiments we suppressed (i) dominant females; and (ii) subordinate females, and measured the consequences for pup survival and growth, female aggression, and helping effort. We show that both dominant and subordinate females stand to gain a positive inclusive fitness payoff from the suppression of co-breeders. Suppressed females were less aggressive around the time of birth, and invested less in helping compared to breeding attempts in which they reproduced. No females dispersed in response to suppression. Our results show that the distribution of reproduction in this species is not optimal for any one party but instead represents a compromise between the interests of dominant and subordinate breeders. Behavioural strategies employed in conflict are shaped by self-interest and persist despite large costs to group productivity.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy14-i001-E*

Symposium 14
Family interactions

Facultative polygyny and queen recruitment in the ant Formica fusca

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Summary statement:

Monogyne and polygyne colonies of facultatively polygyne black ant Formica fusca did not differ in their propensity to accept additional queens and retained the resident queens.

Abstract:

Presence of multiple queens in a colony is associated with enhanced colony productivity, colony longevity and increased genetic diversity. However, it can also be costly as reproduction is divided between several individuals and workers face reduced inclusive fitness returns. The costs can be mitigated if queens in a colony are related, which in turn requires precise recognition system in order to reject unrelated intruders. Here we compared adoption and over-wintering survival of young queens of the facultatively polygyne black ant Formica fusca. We show that resident queens were preferentially retained in both monogyne and polygyne colonies. Contrary to our expectations related daughter queens were not more eligible for adoption than unrelated queens. Monogyne and polygyne colonies did not differ in the tendency to adopt additional queens, but the queens were more likely to be culled than to die in monogyne than in polygyne colonies. This provides a possibility for even unrelated queens to be granted adoption in polygyne colonies if they manage to survive not being taken care of.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy14-i002-E*

Symposium 14
Family interactions

Breeding system evolution and sex-biased offspring mortality

dos Remedios N[1,2], Küpper C[3], Kosztolányi A[4], Burke T[2], Lee P[5], Székely T[1]
[1]University of Bath, Department of Biology & Biochemistry, Bath, United Kingdom, [2]University of Sheffield, NERC Biomolecular Analysis Facility, Department of Animal and Plant Sciences, Sheffield, United Kingdom, [3]Harvard University, Museum of Comparative Zoology, Department of Organismic and Evolutionary Biology, Cambridge, United States, [4]Eötvös Loránd University, Department of Ethology, Budapest, Hungary, [5]Swansea University, Department of Biosciences, Institute of Environmental Sustainability, Swansea, United Kingdom

Summary statement:

We report for the first time that offspring sex ratios vary with breeding system across populations of small plovers, Charadrius spp., as predicted by recent theoretical models.

Abstract:

Does sex ratio influence mating systems and parental care? Theoretical models strongly suggest that breeding systems and sex ratios are tightly linked, although the empirical evidence for these links is scanty in wild populations. Biased offspring sex ratios may produce a biased adult sex ratio, and hence biased mating opportunities for males and females within a population. We investigated primary and secondary offspring sex ratios and their association with breeding systems across four populations of small plovers (Charadrius alexandrinus and C. nivosus) that exhibit different breeding systems (polyandry and monogamy). We determined the sex of newly hatched chicks using CHD gene markers (in total 1,253 chicks from 507 broods), and monitored the survival of the chicks until fledging (in total 365 broods). Offspring sex ratio at hatching in each population did not differ from unity. However, after hatching, mortality of female chicks was higher in the polyandrous populations but not in the monogamous one. We also show that the sex differences in juvenile survival are likely to be related to seasonal differences in resource availability, since male chicks tended to hatch at times of higher resource availability whereas female chicks tended to hatch when resources were low. In conclusion, our results provide support for a key prediction of recent theoretical models by showing that differential chick survival may lead to biased mating opportunities, and that this pattern appears to be governed by ecological factors. Biased mating opportunities, in turn, induce variation in mating system and patterns of parental care.

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MON 22 AUG at 1710 - Room N3
Oral presentation *B4-Sy14-1710-O*

Symposium 14
Family interactions

Does chronic sibling bullying prejudice adult development?

Drummond H[1], Carmona C[1], Nuñez A[1], Oro D[2], Rodríguez C[1], Sanchez O[1]
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Summary statement:

Growing up as subordinate or dominant sibling througout the nestling period did not prejudice perfomance of blue-footed boobies during adulthood.

Abstract:

Infant vertebrates often spend their most formative developmental period competing with their siblings, and disadvantaged individuals can suffer chronic food deprivation and routine aggression as well as endocrine alterations. Potentially these experiences could generate individual differences in adult behavioral phenotypes (e.g. deficits, personality differences) and individual variation in life histories and, ultimately, reproductive value. Although we know that disadvantaged infant siblings often die before independence, we know very little about how survivors fare in adult life. We studied effects of sibling oppression on lifetime viability in a species (the blue-footed booby) where the younger broodmate suffers violent aggressive subordination (involving “trained losing”) food deprivation, poor growth (followed by compensatory growth), and elevated circulating corticosterone. Although we analysed large samples of fledglings from several cohorts and looked at numerous variables (e.g. body size, immune response, natal dispersal, recruitment, age of recruitment, aggressiveness, age-related reproductive success, lifetime RS), the broad conclusion seems to be that (1) adversity in infancy leaves booby fledglings unscathed and (2) privileged development as a dominant confers no long-term benefit. There is even evidence that females benefit from adversity!

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy14-i003-E*

Symposium 14
Family interactions

Determinants and fitness consequences of infidelity in the cooperatively breeding Seychelles warbler

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Summary statement:

Infidelity is widespread yet its evolutionary basis remains elusive due to low power to assign paternity; we apply powerful techniques to unravel this.

Abstract:

Female infidelity is widely reported in the literature, yet the causes and fitness consequences of extra-pair parentage remain elusive mainly due to low power to assign paternity and difficulties in monitoring fitness accurately. The low power results from the presence of unsampled candidate fathers, especially in open populations, and the presence of closely related candidate fathers, which is particularly problematic in group-living species with limited dispersal. The latter problem can be overcome by using large numbers of polymorphic microsatellites and applying a powerful Bayesian technique that uses these genotypic data to assign parentage, while incorporating informative phenotypic data, such as paternity distance. Furthermore, closed wild systems represent a rare opportunity to measure fitness accurately. The Seychelles warbler Acrocephalus sechellensis is such a system; warblers almost never leave their resident island, so through annual monitoring and genetic sampling we can accurately measure survival and fecundity of the whole population. We use the Bayesian pedigree construction method on a 15-year dataset (30 microsatellite loci and paternity distance) to assess the effect of age and social status on paternity. Paternity success was predicted by age and dominance status. Males, but not females, displayed individual variation in extra-group parentage; however, extra-group paternity did not significantly increase a male’s annual breeding success. We combine our findings to improve our understanding of the adaptive basis of reproductive decisions and trade-offs between helping, breeding and extra-group parentage in the cooperatively breeding Seychelles warbler.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy14-i005-R*

Symposium 14
Family interactions

On the co-adaptation of offspring begging and parental provisioning in canaries

Estramil N[1], Eens M[1], Müller W[1]
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Summary statement:

This study provides evidence of the (genetic) co-variation between parental provisioning and offspring begging and shows how it is stabilized by associated fitness costs.

Abstract:

Parental care includes complex parent-offspring interactions and its evolution, therefore, depends on the evolution of two traits, parental provisioning (PP) and offspring begging (OB). Both behaviours should ultimately become (genetically) correlated. Such parent-offspring co-adaptation is thought to be stabilized by fitness costs to parents and/or offspring, which will become apparent when the correlation between parental and offspring behaviours is disrupted. However, few empirical studies have tested these predictions. Using a cross-fostering design we tested in canaries: (1) whether there is co-variation between OB and PP and (2) whether changes in begging intensity between genetic and foster offspring chicks do have fitness consequences for the parents. OB was scored in a standard begging test and PP was measured by using (a) the growth rate of the foster chicks (day 1-13) as a proxy for parental behaviour and (b) the actual feeding rate during a 2h observation. All females were re-mated twice with the same partner to establish potential fitness costs based on their investment in subsequent clutches. We indeed found co-variation between OB and PP, confirming previous evidence. However, this was only true when using the growth rate as a proxy for PP, but not when using the actual feeding rate, which may be due to timeframe differences. Our data also suggest the existence of fitness costs, since females tend to lay lighter eggs when they raised foster chicks with a higher begging intensity than their own chicks. However, this last data set is as yet not completed.

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TUE 23 AUG at 1630 - Room N3
Oral presentation *C4-Sy14-1630-O*

Symposium 14
Family interactions

Monogamy and haplodiploidy act in synergy to promote the evolution of eusociality

Fromhage L[1], Kokko H[2]
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Summary statement:

We present a theoretical model showing that monogamy and haplodiploidy act in synergy to promote the evolution of eusociality.

Abstract:

The evolution of eusociality requires explaining why some individuals sacrifice their own reproduction for the benefit of others. This transition has occurred repeatedly during the course of evolution, but its underlying causes remain a subject of debate. The transition may have been facilitated by ancestral species having a monogamous mating system (the monogamy hypothesis) or a haplodiploid genetic system (the haplodiploidy hypothesis), or it may have been entirely driven by other (ecological) factors. Here we evaluate these claims using a mathematical model that describes the dynamics of insect colony foundation, growth, and death. We show that monogamy and haplodiploidy facilitate the evolution of eusociality in a novel, mutually reinforcing way. Whereas monogamy has an effect via kin selection, the more subtle effect of haplodiploidy arises because its associated relatedness structure strengthens the extent of positive assortment between rare phenotypes, thus creating synergies that favour the evolution of cooperation. Our findings strongly support the recently questioned importance of relatedness for the evolution of eusociality, and simultaneously highlight the importance of explicitly accounting for the ecological rules of colony foundation, growth, and death in models of social evolution.

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TUE 23 AUG at 1400 - Room N3
Oral presentation *C3-Sy14-1400-O*

Symposium 14
Family interactions

A study of the genetic basis for maternal provisioning and offspring solicitation, and their implications for parent offspring conflict, using recombinant inbred mouse strains

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Summary statement:

Genetic architecture and candidate genes of maternal provisioning support maternal but not offspring influence on parent offspring conflict resolution

Abstract:

The resolution of parent offspring conflict over maternal resource allocation can either be influenced by parents, offspring or both. These different assumptions have formed the basis of conflict resolution models but empirical tests have been somewhat lagging behind theoretical work, especially in mammalian systems. Here, mothers are known to significantly affect their offspring's phenotype through maternal effects. In order to separate offspring from maternal effects, cross-fostering of young is necessary, which breaks the maternal offspring correlation. Both theoretical and empirical work suggests an important role for offspring and maternal genotype mutually influencing each other's phenotype, acting either as direct or indirect genetic effects. The extent to which variation in offspring and maternal phenotype is affected by such effects, however, has not been ascertained. Separating these effects is important for our understanding of the underlying sources of variation observed in offspring and maternal phenotypes without which a clear assignment of effects of offspring versus maternal genotype is not possible.

We investigated direct and indirect genetic effects on maternal behavioural traits, offspring development and parent-offspring conflict resolution over maternal resource allocation in recombinant inbred mice using QTL and system genetics analyses. We demonstrate that offspring development is affected by genetic variation in mothers but, surprisingly, not by offspring genotype and identify several QTL that underlie this effect. We further found no evidence for genetic coadaptation between BXD mothers and their pups, in contrast to model predictions.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy14-i006-R*

Symposium 14
Family interactions

Changes in nestling flange reflectance reflect honest signalling

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Summary statement:

Changes in nestling reflectance signals varied with body condition. We discuss physiological trade-offs underlying this honest signalling in the context of the handicap principle.

Abstract:

When begging, nestlings exhibit coloured traits that are used by parents in their allocation decisions, and that have been hypothesized to convey honest information about nestling need or condition. However, experimental support for such honesty of begging signals is still sparse. By experimentally exposing nestlings to a three hours food shortage we examined whether nestling flange and/or skin reflectance components changed within this short period of time. As nestling skin reflectance has been found to convey information about hunger level in other species, we predicted that skin reflectance should increase with food deprivation. We found that overall mean change in nestling reflectance is not significant, showing that these components do not convey information about hunger level in this species. According to the “handicap principle” hypothesis, we predicted that the change in nestling reflectance components should depend on nestling condition. Our results revealed short-term changes in both flange “carotenoïd-based” and ultraviolet (UV) reflectance. As predicted, nestlings in low body condition showed a decrease in these reflectance components whereas nestlings in good condition showed an increase. Nestling flange reflectance changed in different directions according to nestling phenotypic condition. Our results suggest that nestlings of different condition faced different trade-offs when mounting signals. We discuss the potential physiological trade-offs underlying this honest signal expression and their relevance for the handicap principle.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy14-i007-R*

Symposium 14
Family interactions

Female competition makes females picky

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Summary statement:

Competition among females for paternal care affects female choice. Female gobies prefer males with large and empty nests. Male size only matters under female competition.

Abstract:

Competition among females for access to mating opportunities and its effect on sexual selection are poorly studied so far. Under natural conditions, the operational sex-ratio fluctuates seasonally. Female common gobies (Pomatoschistus microps) compete for access to mates when availability of nests and paternal care is limited under female-biased conditions. Female-female competition can be expected to affect female decisions on mate choice and reproductive effort. I studied the effect of a female-competitive social environment on female mating decisions for male and nest quality. Female choice for male size, nest size and male mating status were tested either in presence or absence of competitive females. Females prefer males with larger and empty nests regardless of the social environment. Preferences for male size, however, highly depend on the social context.

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TUE 23 AUG at 1610 - Room N3
Oral presentation *C4-Sy14-1610-O*

Symposium 14
Family interactions

Multiple begging signals and independent indexes of nestling condition in European starlings

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Summary statement:

We show that begging signals include multiple independent components conveying information about two indexes of nestling condition that parents could use for allocation decisions.

Abstract:

Parental food allocation decisions are based on information about nestling condition conveyed by begging signals. It is expected that parents should have evolved the ability to obtain detailed information about their nestlings´ condition through multiple independent signals, thus allowing them to use optimal food allocation strategies depending on resource availability. In this study, we explore (i) which components of acoustic and visual begging signals produced by European starling nestlings (Sturnus vulgaris) vary independently from each other, and consequently have the potential to evolve as separate signals, and (ii) whether they conveyed multiple or redundant information about nestlings. We measured nestling stature and lipid reserves, two independent indexes of nestling phenotypic quality that have been suggested to be used in parental food allocation decisions. In multivariate analyses we show that (i) acoustic and visual begging signals consist of several components that vary independently from each other, and that (ii) begging components correlated with nestling lipid reserves were different from those correlated with stature. Our results show that nestling begging signals include multiple independent components that can provide parents with information about two independent indexes of nestling condition that could be used in flexible allocation strategies.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy14-i004-E*

Symposium 14
Family interactions

Parental care and the evolution of (non-)migration

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Summary statement:

Changing migration shortened parental care in barnacle geese. Shorter parental care makes offspring more exploratory, thereby establishing new populations and population admixture.

Abstract:

Geese are well known for their long duration of parental care, which is suggested to play an important role in the cultural transmission of migratory behaviour. A recent delay in onset of spring migration and the emergence of a non-migratory population of barnacle geese suggest changes in this mechanism of cultural transmission of migration. We studied 1) whether a delay in migration resulted in an delay of termination of parental care, 2) whether the non-migratory life-style of the new non-migratory barnacle geese led to shorter parental care and 3) what the population genetic consequences are of these migratory changes.

Therefore, we studied the parental care behaviour of migratory and non-migratory barnacle geese throughout the season in the field, and we studied the population genetics of the entire population of barnacle geese using a 384 SNP set.

We show that migratory barnacle geese have shortened parental care with one month, and now terminate parental care two months before the onset of spring migration. Additionally, non-migratory barnacle geese have shortened parental care with three months, compared to the currently migratory barnacle geese. Our population genetic analysis shows linkage disequilibrium in all populations, suggesting recent population admixture.

We conclude that a delay in migration may have caused unsuccessful cultural transmission of migration, leading to the emergence of a non-migratory population. Consequently, this non-migratory population may have a larger proportion of exploratory young individuals, thereby increasing exchange between this non-migratory and other populations, previously separated by cultural conservatism of migration.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy14-i005-E*

Symposium 14
Family interactions

Ecological constraints leading to a cooperative breeding system within a South American parrot species

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Summary statement:

Ecological constraints leading to a cooperative breeding system within a South American parrot species.

Abstract:

Cooperative breeding systems are thought to develop through ecological constraints limiting the possibility to breed for an individual. Individuals therefore join breeders to profit of direct or indirect benefit gained by helping. Our study species the El Oro Parakeet (Pyrrhura orcesi) is an endemic parakeet species of Southern Ecuador. During my first field season, we demonstrated that this parakeet breeds cooperatively, a behavior thought to be atypical in parrots. We carried out behavioral observations with nest cameras installed at artificial nest boxes as well as genetic analyses with microsatellite markers. Groups consist of up to eight individuals with males and females helping in provisioning the offspring. The relatedness within flocks is variable due to changing flock composition between breeding seasons. Offspring produced by helpers within breeders nests indicate that these individuals can gain direct benefit. Furthermore manipulating nest site availability suggests that nest sites per se are not a limiting ecological factor leading to cooperative breeding. Instead, the development of cooperative behavior in this species may also be explicable by a lack of available territories maybe due to the enormous habitat fragmentation.

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MON 22 AUG at 1550 - Room N3
Invited talk ***B4-Sy14-1550-I***

Symposium 14
Family interactions

Parent-offspring coadaptation

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Summary statement:

Parent-offspring coadaptation: The evolutionary genetic process and outcome of reciprocal adaptation of offspring to parents, and of parents to offspring.

Abstract:

Parent-offspring coadaptation describes the process and outcome of reciprocal adaptation of offspring to parents, and of parents to offspring, from an evolutionary genetic perspective. Viewing parental care as a heritable and evolving component of the family environment affecting offspring development and behaviour is more than as yet another way of defining parental care. It allows us to ask questions about phenotypic expression, inter-individual variation and genetic bases of parent-offspring interaction. And it reveals that the traits expressed in families can have a "socially complex" genetic basis. Interacting parent and offspring traits cannot be attributed unambiguously to a genotype or individual, challenging the common assumption that the evolution of behavioural phenotypes can be studied as if they represented simple haploid genotypes (i.e., the "phenotypic gambit" assumption of behavioural ecology). In this talk, I will discuss why and how the explicit consideration of the socially complex genetic architecture of parent-offspring interaction matters for the evolution of family interactions. I will present models of parent-offspring coadaptation and the growing experimental evidence supporting predictions of these models. Finally, I will make a brief excursion on how I see the relationship between parent-offspring coadaptation and conflict resolution.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy14-i009-R*

Symposium 14
Family interactions

Reproductive conflict between generations in humans

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Summary statement:

The fitness costs of reproductive conflict and the inclusive fitness gains of grandmothering together select for reproductive termination at menopausal age in women.

Abstract:

Menopause in human females is unexpected from an evolutionary viewpoint because there should be no selection for living beyond one's reproductive capacity. Fitness calculations considering the direct benefits of rearing own offspring to independence and the indirect fitness of helping to rear grand-offspring typically yield values insufficient to offset the costs of lost reproduction that results from menopause. Recently, it has been suggested that the costs of overlapping generations of reproductively capable individuals might provide a key part of the puzzle but empirical tests are lacking.

We investigate by using pre-industrial Finns as a model system the degree to which mothers and offspring overlap in their reproductive lives, the costs for each party of reproducing at the same time and whether there is evidence that mothers cease reproduction early when offspring are of breeding age.

We found that only 5% of mothers and offspring breed at the same time. Moreover, breeding at the same time was associated with an up to 44% decline in survival among grand-offspring and 38% among offspring. Also, mothers ceased reproduction a year earlier when in reproductive competition with offspring. Finally, we show by using a quantitative modelling approach that the reproductive conflict between generations could be central in setting the menopause around age of 50 years. Our study provides the first evidence that extreme reproductive conflict occurs between generations in humans and gives support for the Reproductive Conflict Hypothesis for the evolution of menopause.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy14-i010-R*

Symposium 14
Family interactions

Consequences and mechanism of male-male competition in a mammalian cooperative breeder

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Summary statement:

Living in family group implies to live with potential competitors, which has strong consequences on the dominant male´s capacity to secure its paternities and its social status.

Abstract:

In social species, reproduction is generally monopolized by a few number of dominant individuals while other members of the family group fail to reproduce. In such a system, on the one hand, the reproductive success of a dominant male depends on its capacity to maintain dominance over time and to prevent access of other males to the receptive female. On another hand, subordinate males are expected to maximize their reproductive success by seeking for extra-dominance paternities and/or by trying to reach dominance themselves. Dominant males are then faced to potential competitors in the family group, and male-male competition is therefore expected to have consequences on their ability to secure paternity and on dominance tenure.
Using a long term study of a natural population of Alpine marmots (Marmota marmota), a mammalian cooperative breeder, we investigated both consequences and underlying mechanisms of male-male competition within family group on dominance tenure and on the occurrence of extra-dominance paternity. Our results showed that the presence of more than one sexually mature male subordinate decreased the dominant body mass, used as a proxy of the competitive abilities, and that both paternity monopolization and dominance tenure decreased as the number of competitors in the group increased. Moreover, we also found that males unable to prevent extra-dominance paternity are also unable to maintain their dominance status. This suggests that the occurrence of extra-dominance paternity is the first symptom of the loss of control loss over its group by the dominant male. We discuss the implications of these results for the test of reproductive skew hypotheses.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy14-i011-R*

Symposium 14
Family interactions

Socially complex phenotypes: Epigenetic basis of parental investment in earwigs

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Summary statement:

Social epistasis between paternal genes expressed in offspring and genes expressed in tending mothers influenced future reproduction of female earwigs.

Abstract:

Conflict and coadaptation drive the evolution of family life and are expected to influence the socially complex genetic bases of offspring demand and parental investment. In this study, we investigated whether reciprocal interactions between origins of offspring and tending mothers influenced future female reproduction in the European earwig, Forficula auricularia, a species where females tend young nymphs and produce either one or two clutches in their lifetime. A total of 190 males and females originating from mothers with small or large investment into second clutches were mated in a fully crossed mating design. Females and eggs were then cross-fostered to obtain all possible combinations of maternal and paternal origins of offspring, and origin of tending mothers. The likelihood of second clutch production by tending mothers was affected by a significant interaction between their own origin and the paternal origin of nymphs they cared for. Mismatches resulted in a lower likelihood than matches. Furthermore, the size of the second clutch depended on a triple interaction between the paternal origin of nymphs, the origin of tending mother and the number of eggs produced in the first clutch. Sizes of first and second clutches were positively correlated when paternal origins of nymphs and origin of tending females were mismatched, but not when origins were matched. These findings demonstrate that mother offspring coadaptation influences future reproduction of caregivers, possibly through social epistasis between genes expressed in mothers and, in accordance with the kinship theory of genomic imprinting, paternally inherited genes expressed in offspring.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy14-i006-E*

Symposium 14
Family interactions

Partner choice and population divergence – Hints for paternal imprinting and population specific signals influencing mate choice

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Summary statement:

Partner choice experiments with recently separated house mouse populations indicate the influence of population specific signals and paternal imprinting on mate choice.

Abstract:

Partner choice can play an important role in the divergence of lineages. Two recently separated populations of the Western European house mouse Mus musculus domesticus, which are known to be genetically distinct, were investigated for assortative mating patterns and occurrence and consequences of hybridization.
We conducted long-term experiments, in which individually tagged mice of both populations were held in a semi-natural enclosure. Paternities were used as measures for mate choice and reproductive success and the frequent examination of individuals allowed the assessment of their physical condition. The results suggest that (1) hybrids have no significant fitness disadvantages, (2) familiarity with signals characterizing the own population are important for assortative mating and (3) mating patterns of animals born in the enclosure gave hints for parental imprinting of mate preferences. As a follow up project, we are currently searching for imprinted genes that could be involved in differential signalling and recognition.
We consider also the influence of molecular genetic parameters, such as the t-haplotype, a selfish genetic element, and MHC alleles on partner choice. For the latter, sequence polymorphism of several exons within the MHC class I and II regions was assessed by 454 technology.

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MON 22 AUG at 1630 - Room N3
Invited talk *B4-Sy14-1630-I*

Symposium 14
Family interactions

The genetics and evolution of biparental care

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Summary statement:

Research into quantitative and molecular genetic influences help explain the diversity and complexity of parental care roles in a burying beetle.

Abstract:

Parental care, especially elaborate parental care, is unusual. Where parental care is found, it is typically the female that cares. Sexual conflict theory predicts that the resolution of parental care depends on selection arising from costs, benefits, and the nature of selection. However, like all traits, parental care is highly variable even within species. In the burying beetle, Nicrophorus vespilloides, females (uniparental female care), males (uniparental male care) and both sexes (biparental care) are seen. Why hasn't sexual conflict been resolved in N. vespilloides? We use quantitative and molecular genetic studies to examine how genetic variation among individuals influence the evolution of parental care. Genetic architecture, examined using quantitative genetic studies, suggests that variation in both males and females reflects genetic differences among individuals. Furthermore, males tend to specialise in indirect care (maintenance and defence of the food) while females specialise in direct care (regurgitating food to the offspring). Thus, evolutionary lines of least resistance allow any form of care including division of labour and biparental care. Molecular genetic studies show that one gene, a cGMP-dependent protein kinase ("for") involved in food-related behaviours in other species, influences direct care. Pharmacological manipulations support a direct role for expression of this gene, and show that it influences the level of direct but not indirect care in both males and females. Genetic studies, therefore, complement optimality approaches and help explain how behavioural diversity and complexity evolves despite a strong theoretical prediction for a simple outcome.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy14-i012-R*

Symposium 14
Family interactions

Are elder siblings helpers or competitors? Long-term fitness effects of sibling interactions in a historical human population

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Summary statement:

Are elder siblings helpers or competitors? Long-term fitness effects of sibling interactions in a historical human population.

Abstract:

Determining the fitness consequences of sibling interactions is pivotal for understanding the evolution of family living in species with altricial young, such as humans. Theory suggests that both competition and cooperation with other siblings could lead to maximization of individual fitness, but the benefits of each strategy may depend on several factors such as family size, age or sex. Although these two types of interactions imply opposite effects on fitness, studies investigating both hypotheses simultaneously over the whole lifespan of individuals are lacking. We used a large demographic dataset on preindustrial humans from Finland to study both the positive and negative effects of elder siblings on key life-history traits of younger siblings across different ages. We found that the presence of both elder sisters and brothers improved the relative survival to sexual maturity of their younger siblings. These results suggest that despite global competition for resources during childhood, elder siblings may cooperate with their younger siblings. However, for both men and women, the presence of same-sexed elder siblings was associated with reduced reproductive success (probability of reproducing, number of offspring and proportion of offspring raised to adulthood). These latter results indicate competition among same-sexed siblings for resources such as mating opportunities once individuals have reached sexual maturity. This study is one of the first showing opposing effects of siblings interactions depending on the life-history stage, and highlights the need for using long-term measures of fitness to understand the selection pressures on sibling interactions.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy14-i013-R*

Symposium 14
Family interactions

Experimental assessment of mating time in Kittlitz's Plover

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Summary statement:

An experimental test was carried out to measure the time spent by males and females finding a new mate in the social monogamous Kittlitz's plover.

Abstract:

Recent theory suggests that mating systems, parental care and adult sex ratios have complex relationships, although it is not yet known how these relationships evolve in natural populations. In a polygamous species, the Kentish plover that has male-biased parental care, theory predicts male-biased care should emerge when the adult sex ratio is male-biased. Consistently with theory, an experimental test of the latter proposition found that male Kentish plovers spent more time finding a new mate than the female plovers. In 2010 we repeated the experiment in a common African wader, the Kittlitz´s plover, a socially monogamous species, to assess their mating time. We predicted that male and female Kittlitz's plovers will spend more time finding a new mate than the polygamous Kentish plover, and importantly, we expected no difference in mating times of males and females. By experimentally creating unmated male and female Kittlitz's plovers in SW Madagascar, we found that: (i) mating times in Kittlitz's plovers are comparable to that of the Kentish plovers, and (ii) males spend less time finding a new mate than females. The sex-biased mating time in Kittlitz's plover suggests that either the adult population is female-biased, or that more females are engaged in care provisioning than males. Testing these alternative hypotheses will be needed to identify the causes and implications of the mating system, mating opportunity bias and adult sex ratio.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy14-i014-R*

Symposium 14
Family interactions

Multiple mating increased number of children, but not number of grandchildren in a historical monogamous human population

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Summary statement:

Our results highlight the need to investigate also offspring quality in addition to their quantity when assessing the benefits of multiple mating in species with bi-parental care.

Abstract:

How mating system affects strength of sexual selection in humans is not clear. Fitness of men is often, but not necessary always, predicted to benefit from multiple partners whereas for women the benefit is not as clear. By using life-history pedigree data from 18th and 19th century Finland, we investigated the consequences of remarriage in men and women for their offspring quality-quantity tradeoff. Our study population precedes time before demographic transition and fertility and child mortality were thus both high. In historical Lutheran Finland, remarriage was possible only after death of the spouse. In our study population men were more likely to remarry than women, and they were also likely to remarry woman of pre-menopausal age. Remarried men gained more offspring compared to men with only one lifetime spouse, whereas remarried women did not have more offspring than once married women. However, because of the important role of mother on the survival and reproductive success of offspring, quality of children of twice married men was compromised. Consequently, the long-term fitness (number of grandchildren) of remarried men did not differ from that of once married men. These results highlight the need to investigate also offspring quality in addition to their quantity when assessing the benefits of multiple mating in species with bi-parental care, and suggest that in human societies where multiple mating is only possible with succeeding partners (enforced monogamy) and long-term parental care is essential for offspring success, the overall fitness benefits of multiple mating may not differ radically between the sexes.

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TUE 23 AUG at 1650 - Room N3
Oral presentation *C4-Sy14-1650-O*

Symposium 14
Family interactions

Evolutionary genetics of maternal effects

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Summary statement:

Population genetic models show that the influence of family member on fitness has to be considered to make accurate evolutionary prediction.

Abstract:

Though it has long been recognized that genes expressed by family members, particularly mothers, can have can have important phenotypic consequences, we do not fully understand how trait evolution in one genome is altered by gene expression in another. Here we consider the evolutionary genetic consequences of maternal genetic effects and other family interactions. We show that though both direct and indirect epistasis contribute in the same way to the fitness landscape, indirect epistasis generates non-heritable additive genetic variation and encodes substantial environmental variation. Using Wright´s concept of the adaptive fitness landscape as a graphical tool, we find that indirect epistasis can have diabolic consequences for our standard evolutionary genetic models. We find that the indirect influence of distant relatives on fitness generates substantial environmental variation in outbred populations, but not in inbred populations. These results imply that we need to understand more about the mechanisms of trait inheritance and family structure to accurately predict trait evolution.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy14-i015-R*

Symposium 14
Family interactions

Resource heterogeneity and the evolution of helping behaviour

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Summary statement:

We examine the impact of spatial and temporal heterogeneity in resource availability on the evolution of unconditional and conditional helping in viscous populations.

Abstract:

There has been much interest in understanding how demographic factors can mediate helping behaviour among relatives in viscous populations. Spatial and temporal heterogeneity have been suggested as important factors mediating the evolution of helping among relatives, e.g., the evolution of cooperative breeding in birds and the evolution of eusociality in insects. Here we examine the impact of heterogeneity in resource availability on the evolution of helping. We find that, owing to a cancellation of relatedness and kin competition effects, the evolution of helping is neither promoted nor inhibited in viscous populations characterized by spatial or temporal heterogeneity in resource availability. However, helping may be promoted or inhibited when there is both spatial and temporal heterogeneity in resource availability. In particular, facultative helping that is expressed only under high resource availability is favoured when such high availability of resources is rare, and facultative helping that is expressed only under low resource availability is favoured when such low availability of resources is rare. In general, the factors favouring facultative helping under high resource availability are those that disfavour facultative helping under low resource availability, such that obligate helping that is not adjusted facultatively according to resource availability is unaffected by spatial and temporal heterogeneity in resource availability.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy14-i007-E*

Symposium 14
Family interactions

Cannibalism and conflict in Formica ants

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Summary statement:

Ant larvae may engage in egg cannibalism as a means of selfishly influencing their caste fate. We study the effects of relatedness in mediating this conflict in the genus Formica.

Abstract:

The polyphenic development into reproductive queens and sterile workers is a fundamental property of social insect colonies. In such systems, conflict over caste determination can arise because individuals gain direct fitness benefits by developing into queens. Selection would therefore favor larvae with selfish traits that increase their chances of turning into queens. Egg cannibalism is an example of such a selfish trait. In ants, brood is reared in batches and larvae commonly feed on eggs, which represent a high-quality food source. As caste fate is influenced by nutrition, cannibalistic larvae can increase their chances of developing into queens, while at the same time removing competitors. In mediating this conflict, the relatedness between colony members is crucial because closely-related individuals would suffer severe indirect fitness losses from cannibalizing kin. The level of competition between larvae is therefore predicted to be intense in colonies headed by multiple queens and decrease in single queen colonies. Ecology, behavior and genetics thus all play a role in determining cannibalistic tendencies of larvae.

We investigate larval egg cannibalism in the genus Formica, an ideal system for studying the effects of relatedness on selfishness, since queen number, and consequently predicted levels of selfishness, vary widely between species. In particular, we study the use of recognition cues underlying cannibalistic behavior by comparing intensity of cannibalism in broods with experimentally manipulated levels of genetic diversity.

With this study, we aim to provide a better understanding of how cooperation is maintained in the presence of selfish behavior.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy14-i016-R*

Symposium 14
Family interactions

Patriline distributions across the gametic and somatic life stages of a leafcutter ant

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Summary statement:

Novel molecular tools reveal that sperm number predicts fertilization success and genetics affect worker caste determination in leafcutter ants.

Abstract:

The co-occurrence of multiple ejaculates within the reproductive tract or sperm storage organ of females can lead to sperm competition where males continue intrasexual competition to affect fertilization rates after copulation. Mating system idiosyncrasies should predict whether such sperm rivalry takes place or is counteracted by the female, as it might compromise her reproductive success, but sperm competition is difficult to monitor directly. We studied the level of sperm competition in the leaf cutter ant Atta colombica at an unprecedented level of detail. These ants are particular, because females (queens) mate multiply upon leaving their natal nest, but never mate again over their decades-long life. We developed a method to isolate newly laid egg batches from individual queens and to determine their paternity with microsatellite markers with high success rate. We also used a novel "competitive PCR" method to quantify the relative contributions of males to stored sperm inside naturally mated queens, and compared this to the proportion of eggs and adult workers sired by each male.We show that sperm is not spatially structured within the sperm storage organ, that sperm is utilized in accordance with prevalence in storage, and that sperm use is consistent over time. We also found strong evidence for worker size polymorphism in A. colombica having a genetic component, as was previously shown to also be the case in the Acromyrmex sister clade. This study sheds new light on previously inaccessible details of ant mating systems, and validates a new molecular method that is easily portable to other organisms with minimal genetic resources.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy14-i017-R*

Symposium 14
Family interactions

Family fortunes and individual investments in the ant Formica fusca

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Summary statement:

Reproductive competition among mother queens, worker-queen interactions, and worker interventions shape both reproductive partitioning and worker inclusive fitness.

Abstract:

Sociality entails benefits through shared work load in defense and brood rearing, but also costs through competition for resources and, for some, reduced personal reproduction. When multiple reproductives come to share the resources held by a society, conflicts are bound to arise among them over reproductive shares and among non-reproductives over who should reproduce. Here we analyse the factors that shape the reproductive output of queens and the inclusive fitness returns gained by workers in the ant Formica fusca. We use behavioural assays on brood rearing and field data, combined with genetic marker data to tackle these questions:
do old queens gain a reproductive head start after hibernation,
does early reproduction indeed translate into a greater share of reproduction,
can queens affect brood composition by signaling their presence, and
what effects does reproductive competition among queens have on inclusive fitness returns gained by workers?
The results show that old queens gain a reproductive head start, and that this translates into greater output of sexual brood, but not worker brood. Secondly we show that queens signal their presence and can influence their reproductive share even without physical contact with the workers raising the brood. Finally, we show that this process leads to enhanced inclusive fitness returns for workers. Thus reproductive partitioning in multi-queen ant colonies highlights complex interactions between queen demography, worker-queen interactions, and worker interventions during brood rearing with a net gain in inclusive fitness returns for workers.

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TUE 23 AUG at 1420 - Room N3
Oral presentation *C3-Sy14-1420-O*

Symposium 14
Family interactions

Family life of birds: Conflict and cooperation

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Summary statement:

Here we overview the results of key studies we carried out to tease apart the influence of conflict and cooperation on breeding system of two avian model systems.

Abstract:

Family affairs often emerge as a careful balance between cooperation and conflict. We will use two ecological model species, the Eurasian penduline tit and the Kentish plover, to investigate how these antagonistic forces shape breeding systems. Both species exhibit highly variable mating systems (that include monogamy, polygyny and polyandry), and diverse parental care patterns. Our team has tested a range of hypotheses underlying this variation using molecular ecology, experiments and observations in the wild, and phylogenetic comparative methods. Our research illustrates two key points. Firstly, within-family relationships may rapidly switch between conflict and cooperation depending on the environment. Secondly, ecological and social traits may have counter-intuitive influences on breeding system. We propose that the antagonistic forces, and the conflicts and cooperation may lead to rapid evolution and diversification. To further dissect family life, we need to understand the direction and intensity of selection acting on the underlying traits, to work out how communication and role division between partners may stabilise (or destabilise) families, and to unravel the neural-genetic bases of mating systems, pair bonds and parental behaviour.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy14-i008-E*

Symposium 14
Family interactions

The role of male-male relatedness in intrasexual competition in Drosophila melanogaster

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Summary statement:

We examined the interplay between kin selection and male-male competition in D. melanogaster to understand how relatedness affects intra-sexual interactions.

Abstract:

Kin selection theory predicts that social behaviours, which reduce the fitness of an actor, can evolve when direct costs are compensated by the inclusive fitness benefits derived by a related recipient. However, theoretical models have suggested that local competition between kin can counteract and even completely remove kin selection for altruism. By manipulating the relatedness between males relative to the average relatedness in a three-male one-female group, we examined the direct interplay between male-male relatedness and competition in Drosophila melanogaster. Unmated males related to males that had previously mated with a female displayed a significant reduction in courtship toward the female. In addition, we examined the paternity gained by the related males versus unrelated individuals. Results suggest that related males adopt a strategy to avoid sperm competition with each other.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy14-i010-E*

Symposium 14
Family interactions

Mothers know best? Inbreeding avoidance in a parasitic wasp

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Summary statement:

We discuss whether single-sex broods could have evolved as a means of inbreeding avoidance in the gregarious parasitoid Bracon variator.

Abstract:

In many species of Hymenoptera (ants, bees, wasps) we find a genetic sex determination system (CSD) that absolutely counteracts the usual inbreeding tolerance found in haplo-diploid species and strongly selects for the avoidance of sib-mating. With CSD, infertile, diploid males arise if the same CSD allele is inherited from both parents and their presence can drive populations into an extinction vortex very easily.

Bracon variator (Hymenoptera: Braconidae) is a gregarious parasitoid, i.e. one female lays a clutch of approximately 6-7 eggs per host larva. If brothers and sisters hatch in such close proximity, they may be especially prone to sib-mating. But B. variator seems to have found an interesting way to enjoy the advantages of gregarious broods together with efficient inbreeding avoidance: they lay clutches that are either all-male or all-female, thereby separating the sexes. We show experimental evidence supporting this idea.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy14-i019-R*

Symposium 14
Family interactions

Behavioral control over food intake and dispersal in the European earwig

Wong JWY[1], Kölliker M[1]
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Summary statement:

We show that dispersal is independent of female nutritional condition and that the female controls the duration of food provisioning in Forficula auricularia.

Abstract:

Parental care enhances offspring survival, but it can lead to disagreement about the duration and amount of care provided. In the subsocial earwig species Forficula auricularia post-hatching maternal care is beneficial, but not obligate. Female condition is expected to be a critical factor mediating the decision of females or nymphs for disperal. A female in good condition is expected to care longer than a female in low condition because of lower evolutionary costs of care. We tested, if females or nymphs of F. auricularia control the time of dispersal from the nest and the duration of food provisioning, and if the period of care is dependent on the nutritional condition of the female. We used two different experimental set-ups. In the first set-up, nymphs controlled dispersal and food intake via self-foraging, as the female was confined to the nest. In the second set-up, females controlled nymph food intake via food provisioning, and dispersal was under the control of both, nymphs and female. In both setups, a low food and high food treatment on females was used to manipulate their nutritional condition. Nymphs or females dispersed in only a minority of cases. Self-foraging of nymphs was independent of female condition. However, low food females provided food to significantly fewer nymphs and for a shorter period than high food females. Overall nymph feeding was higher under nymph than under female control. We show that dispersal is independent of female nutritional condition and that the female controls the duration of food provisioning in F. auricularia

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy14-i009-E*

Symposium 14
Family interactions

Kinship and pay-to-stay affect reproductive investment and brood care of female helpers

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Summary statement:

This experiment investigating reproduction and brood care in a cooperative breeder highlights that pay-to-stay theory and kin selection explain differences in cooperative behaviour.

Abstract:

Evolutionary models predict that kin selection is important for group stability, reproductive skew and helping behaviour in cooperative breeders. However, studies in vertebrates are usually limited to an observational approach because kinship is difficult to vary experimentally. We manipulated female kinship in groups of three cichlids (a pair and one female subordinate), where the females were either kin ($r = 0.5$), or non-kin ($r = 0.0$). We tested for effects of kinship on reproduction and brood care in the cichlid fish Neolamprologus pulcher. Kinship increased subordinate females' investment in reproduction due to a rise in egg mass, while clutch size and clutch number remained unaffected. Dominant females' reproduction was independent of the treatment. Subordinate females provided more alloparental and maternal brood care in the non-kin treatment, which was not reciprocated by the dominant females. As female reproductive success was independent of treatment, this suggests that unrelated subordinate females need to pay more for continued group membership, which supports theoretical models of the pay-to-stay hypothesis. Importantly, dominant females' reproductive performance as well as their brood care were not influenced by relatedness to the subordinate female, which confirms predictions from pay-to-stay theory stating that subordinates should only compensate for the costs inflicted to dominants. Our results stress the importance of interactions between different evolutionary hypotheses aiming to explain cooperative breeding. Despite having a large impact, mechanisms can be obscured unless they are distinguished from each other by controlled experiments.

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Symposium 15

Division of labour

Talks: *Room N5*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Upper floor campus canteen *Mensa*

Invited Speakers:

Richard Michod

Organizers:

Claus Rueffler, Sergey Gavrilets

Description:

Division of labour exists between colony members as well as between iterated units of already highly integrated organisms. By bringing together researchers working on a wide variety of systems we wish to identify underlying commonalities and systems specific differences in order to understand its role in major transitions of evolution and in the evolution of organismal complexity.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy15-i002-R*

Symposium 15
Division of labour

Variation in fungal enzyme spectra may affect mutualistic division of labour between ants and fungus gardens

De Fine Licht HH[1,2], Boomsma JJ[2]
[1]Lund University, Department of Biology, Lund, Sweden, [2]University of Copenhagen, Department of Biology, Copenhagen, Denmark

Summary statement:

Symbiotic division of labour is influenced by consistent variation in enzyme metabolism among cultivar strains of fungus-growing ants.

Abstract:

Partners in obligate mutualisms often contribute complementary elements to joint pathways for synthesizing or degrading metabolites. Their committed cooperation can make new niches accessible, with evolutionary diversification and speciation as possible consequences. However, when individual partners vary in metabolic performance, division of labour may not always be optimized and co-evolutionary trajectories become less predictable. The higher fungus-growing (attine) ants consist of the leafcutter ants (Acromyrmex and Atta), which rear a single fungal species throughout their Latin American range, and a paraphyletic assembly of Trachymyrmex and Sericomyrmex species that cultivate more genetically diverse fungal symbionts. Leaf-decomposition productivity of colonies depends on the combined efforts of ant foragers collecting and macerating plant material and fungal enzymes excreted directly or indirectly via ant fecal fluid. We determined the interaction specificity between ant species and fungal strains across sympatric populations of six Trachymyrmex and Sericomyrmex species in Panama, and established that these ants jointly reared eight fungal haplotype groups that differed significantly in garden enzyme activity independent of ant species association. This illustrates that the mosaic of coevolutionary interactions in Trachymyrmex and Sericomyrmex fungus-growers may be fundamentally different from the interactions in Acromyrmex and, particularly, Atta leaf-cutting ants. The former appear to be analogous to a diverse array of subsistence farming practices at the mercy of local conditions, whereas the latter resemble large-scale, low-diversity “industrial” farming.

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SUN 21 AUG at 1630 - Room N5
Oral presentation *A4-Sy15-1630-O*

Symposium 15
Division of labour

Evolution of self-organized division of labor

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Summary statement:

Individual-based models show that self-organized division of labor can evolve if switching tasks is costly. The implementation of decision rules affects the evolutionary outcome.

Abstract:

Division of labor, a prominent feature of social insects, is considered key to their ecological success. Theoretical work on division of labor tends to fall in two categories. Evolutionary models provide adaptive (ultimate) explanations, often neglecting underlying mechanisms. Self-organization models provide mechanistic (proximate) explanations without discussing how mechanisms are shaped by adaptive evolution. Here we discuss two models that integrate the evolutionary and the self-organization perspective in a common framework. In our models, the behaviour of individual agents is governed by genetically encoded decision rules. Colony fitness depends on the efficiency of division of labor, which emerges from the interaction of agents and, hence, reflects the agents' decision rules. We consider two implementations of the decision rules ("behavioural architectures"); a response-threshold model and a neural network model. In both models, self-organized division of labor can evolve from initially undifferentiated populations. However, the course and outcome of evolution strongly depend on the behavioural architecture. In the threshold model, worker specialization evolves through evolutionary branching of thresholds, but only under restrictive genetic assumptions and when the costs of task switching are high. By contrast, in the neural network model, worker specialization evolves under less restrictive conditions. Additionally, the distribution of workers over tasks is constrained to be symmetric under the threshold model while it tends to be asymmetric in the neural network model. We discuss future avenues of research, such as implementing more mechanistic fitness measures.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy15-i002-E*

Symposium 15
Division of labour

Temporal patterns of specialization: leaf traits and light environment in Olea europaea L.

Escribano AG[1], Ventre-Lespiaucq AB[1], Granado-Yela C[1], Carrillo K[1], Delgado JA[2], López-Pintor A[2], Dorado G[3], Balaguer L[4]
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Summary statement:

Light environment, crown concert, phenotipic plasticity, modularity, division of labour.

Abstract:

All trees share high modularity and phenotypic plasticity. These qualities enable structural and functional responses to the immediate environmental variation across tree crown. It has been argued that, besides those responses, there must be coordination mechanisms that optimize plant performance, such as those described in clonal plants and in colonial and social animals. The aim of the present study is to search for temporal patterns of specialization within crown subunits. Specifically we test the following hypothesis; complementary module's spatial layout patterns are linked to photosynthetic exploitation of segregated time windows: morning/afternoon/winter (outer-canopy layers) vs. midday/summer (inner-canopy layers). We analyzed data from 150 fully expanded leaves per crown position, 2 crown positions (exposed vs. sheltered) per tree in three adult reproductive trees of wild olive. We created a model which allows us to forecast the silhouette leaf area at different time scales, providing conspicuous information related to light interception. The elucidated patterns contribute to a better understanding of the role of phenotypic plasticity of vegetative traits on the fitness, as well as it provides insight into daily photosynthate allocation. The study is one of the subsidiary goals in the frame of our search for temporal patterns of specialization among tree canopy modules and spatial division of labour among tree crown subunits.

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SUN 21 AUG at 1710 - Room N5
Oral presentation *A4-Sy15-1710-O*

Symposium 15
Division of labour

Division of labor via evolution of developmental plasticity

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[1]University of Tennesee, Knoxville, United States, [2]National Institute for Mathematical and Biological Synthesis, Knoxville, United States

Summary statement:

Rapid division of labor can be achieved via evolution of developmental plasticity driven by individual selection for reduced fitness trade-offs.

Abstract:

A crucial step in several major evolutionary transitions is the division of labor between components of the emerging higher-level evolutionary unit. Examples include the separation of germ and soma in simple multicellular organisms, appearance of multiple cell types and organs in more complex organisms, and emergence of casts in eusocial insects. How the division of labor was achieved in the face of selfishness of lower-level units is controversial. I present a simple mathematical model describing the evolutionary emergence of the division of labor via developmental plasticity starting with a colony of undifferentiated cells and ending with completely differentiated multicellular organisms. I explore how the plausibility and the dynamics of the division of labor depend on its fitness advantage, mutation rate, costs of developmental plasticity, and the colony size. The model shows that the transition to differentiated multicellularity, which has happened many times in the history of life, can be achieved relatively easily. My approach is expandable in a number of directions including the emergence of multiple cell types, complex organs, or casts of eusocial insects.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy15-i001-R*

Symposium 15
Division of labour

Spatio-temporal division of labour within the crown of the wild olive tree (Olea europaea L.)

Granado-Yela C[1], García-Verdugo C[1,2], Carrillo K[1], Rubio de Casas R[3], Kleczkowski LA[4], Balaguer L[1]
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Summary statement:

The differential leaf arrangement at contrasting locations within the tree crown (sun and shade exposures) enables the exploitation of complementary time-windows for photosynthesis

Abstract:

Plants have been traditionally viewed as colonies of repeated modules. Nevertheless, division of labour in vascular plants has been characterized only in clonal angiosperms. Trees exhibit large size, high modularity and great phenotypic plasticity. Thus, if increased module population plus the ability to express alternative phenotypes (i.e., phenotypic plasticity) brings about a further increase in the potential relationships among modules, the synergy between modular demography and modular plasticity appears to be particularly relevant in the case of trees. It has long been known that trees adjust their within-crown morphophysiology in response to within-crown light gradients, but whether this variation represents a strategy for optimizing light absorption at the whole-plant level has not been formally tested.

We investigated the photosynthetic performance of interconnected populations of leaves within a wild olive tree crown that experience heterogeneous light environments under field conditions (sun and shade exposures). Then we compare it with that of populations of leaves from experimentally disconnected modules (i.e. cuttings) that experience homogeneous light environments at two contrasted levels (sun and shade treatments) in a greenhouse experiment.

Diurnal patterns of light interception, carbon assimilation and carbohydrates export were complementary between sun and shade leaves within the crown: sun leaves fixed and exported carbon mainly during the morning and the afternoon, while shade leaves mainly at midday. In contrast, and as consequence of the non-integrated condition, patterns for the sun and shade leaves in cuttings were not complementary in time.

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SUN 21 AUG at 1500 - Room N5
Oral presentation ***A3-Sy15-1500-O***

Symposium 15
Division of labour

Life cycles, levels of selection and the evolution of individuality

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Summary statement:

A possible origin of the soma/germ line distinction is explored in experimental populations of Pseudomonas fluorescens.

Abstract:

The mechanism whereby selection transitions from individual cells to groups of cells (multicellularity) is unknown. Recent theory suggests that emergence of a life cycle is the critical event. Life cycles decouple fitness of higher (group) levels from lower (individual cell) levels; they allow groups to leave group-offspring – they transition individuality.
Here we describe experiments that explore the role of life cycles in the evolutionary transition from single cells to groups of cells. We use experimental populations of Pseudomonas fluorescens that form simple undifferentiated groups in spatially structured environments. The groups are susceptible to destruction by cheating types. The cheats, while the nemesis of the group, are also its saviour – acting as propagules for the foundation of new groups. Thus, from nothing other than the tension among levels of selection arises a simple life cycle whereby Darwinian individuality is conferred upon the higher level "as if by magic".
In a specially designed experiment in which groups were subject to selection at the level of both group viability and fecundity we show an adaptive response at the group level that was dependent upon expression of the life cycle and between group selection. We will discuss our results with particular focus on the division of labour and a possible origin of the soma/germ line distinction.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy15-i003-R*

Symposium 15
Division of labour

Two roads to two sexes

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Summary statement:

Anisogamy (male and female gametes) evolves when there are either very many gametes competing for each opposite-sex gamete or when there are very few.

Abstract:

Why does sexual reproduction so often lead to two sexes, males and females? This is perhaps the most primitive form of division of labour since one sex evolves to 'parasitize' the parental investment of the other. The definition of the two sexes indeed rests on anisogamy, the fact that one sex produces far smaller gametes than the other. Previous explanations have not taken into account that gamete success is heavily influenced by the evolving numerical imbalance: not all gametes of the more numerous sex can ever hope to find an opposite-sex gamete. Also, under broadcast spawning, low density of gametes can mean difficulties for both sexes to find each other. A unified model of gamete dynamics predicts that two apparently distinct routes to anisogamy (gamete competition and gamete limitation) can be understood in the same framework, that there is a link between uncertain paternity, sperm size evolution and parental investment theory, and that there are results in the literature from 80 years ago that have been dismissed as group selectionist but that are still valid under certain assumptions.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy15-i004-R*

Symposium 15
Division of labour

Worker castes of leaf-cutting ants show differences in nestmate recognition

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Summary statement:

We show that worker castes in leaf-cutting ants exhibit differences in nestmate recognition. This is due to differences in the perception component, and not the action component.

Abstract:

Some of the reasons why social insect colonies are so successful are the division of labor that allows colony members to specialize on certain tasks and nest defense which relies on a sensitive nestmate recognition system. We hypothesized that the colony would benefit if some workers would specialize on such an important task, and test this assumption using the leaf-cutting ants Acromyrmex echinatior. In this study we investigate the nestmate-recognition ability of three morphologically distinct worker castes. We demonstrate that major workers (which are generally involved in foraging and nest defense) are better than minors in discriminating nestmates from non-nestmates. They can detect smaller differences between their own recognition label and that of encountered ants. The fact that larger individuals are more sensitive than smaller ones in recognition seems to be a common phenomenon, which in the case of worker castes is likely to be caused by differences in the perception component and not the action component in the recognition system.
Keywords: Acromyrmex echinatior, caste differentiation, cuticular hydrocarbons, division of labor, leaf-cutting ants, nestmate recognition

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy15-i005-R*

Symposium 15
Division of labour

Complex genetic influences on division of labor in social insects

Libbrecht R[1], Keller L[1]
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Summary statement:

We report complex genetic influences on worker nursing abilities. Such influences are likely to play an important role in the division of labor in social insects

Abstract:

One of the hallmarks of insect societies is the division of labor. Several studies reported that increased genetic diversity (through multiple queens per colony and/or multiple mating per queen) facilitate the division of labor among workers. However none of these studies focused on the influences of the paternal and maternal genetic backgrounds and the genetic compatibility effects between parental genomes. In this study we investigate such genetic influences on two nursing tasks: feeding and gathering brood. We conducted controlled crosses in the Argentine ant Linepithema humile and established single-queen colonies to investigate the influences of both parents on worker nursing abilities. The time to gather pupae was affected by the maternal genotype while the ability to feed larvae was influenced by the interaction between parental genomes. First these results reveal that different worker nursing abilities can be differently influenced by the parental genotypes. Second they suggest complex effects of the genetic architecture on ant behavior. Such effects are likely to play an important role in the division of labor among workers in insect societies.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy15-i006-R*

Symposium 15
Division of labour

Physiological integration increases stress tolerance in Iris pumila

Manitašević Jovanović S[1], Vuleta A[1], Tucić B[1]
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Summary statement:

Physiological integration within I. pumila clones can buffer against environmental stress in heterogeneous natural habitats they commonly encounter.

Abstract:

Interconnected ramets of clonal plants may reciprocally exchange essential resources, such as water, nutrients and assimilate, when encounter spatially heterogeneous environments. We tested the hypothesis that resource sharing between the source and sink ramets increases stress tolerance of the whole clone growing in a patchy environment. Our experiment was conducted in a sun-exposed population of Iris pumila growing in the wild. In early spring, circle-shaped clone (genotypes) were cut in two parts with different integration status: one, with intact (I) and the other with disconnected rhizomes (D). One-half of each clone was then shaded with a neutral screen (which transmitted 50% of ambient) so that both I part and D part consisted of a fully illuminated and a shaded quarter. In summer, the leaf samples were collected from each of clone quarters and analyzed for the relative concentration of stress proteins (Hsp70 and two isoforms of Hsp90: Hsp90a and Hsp90b), the specific activity of antioxidative enzymes (SOD, CAT, POD), and the extent of lipid peroxidation (MDA content). Whereas the activity of SOD, CAT and POD enzymes decreased with irradiance, the content of Hsp90a and MDA increased, regardless of their integration status. Conversely, the amount of Hsp70 and Hsp90b markedly elevated, but exclusively in an exposed quarter that was interconnected with the shaded one. Our results indicate that the physiological integration in I. pumila plants provides fitness benefit by enhancing the tolerance to environmental stress that commonly occurs within their spatially varying natural habitats.

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SUN 21 AUG at 1400 - Room N5
Invited talk *A3-Sy15-1400-I*

Symposium 15
Division of labour

Cooperation and conflict during evolutionary transitions in individuality

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Summary statement:

Concepts and principles from population genetics and evolutionary ecology explain the major transition in individuality from unicellular to multicellular life.

Abstract:

The evolution of multicellular organisms is the premier example of the integration of lower-level individuals (cells) into a new higher-level individual (the cell group or multicellular organism). How and why does a cell group evolve into a multicellular individual? Evolutionary transitions in individuality require the reorganization of fitness, by which we mean the transfer of fitness from the old lower-level individual to the new higher level, and the specialization of lower-level units in fitness components of the new higher-level individual. Our hypothesis is that fitness tradeoffs drive the transition of a cell group into a multicellular individual through the evolution of cells specialized at reproductive and vegetative functions of the group. We have modeled this hypothesis and have tested our models in the volvocine green algae in two ways. We have studied the origin of the genetic basis for soma and reproductive altruism in the multicellular Volvox carteri by showing how an altruistic gene may have originated through co-option of a life-history tradeoff gene present in a unicellular ancestor. Second, we ask why reproductive altruism and individuality arise only in the larger members of the volvocine group (recognizing that high levels of kinship are present in all volvocine algae groups). Our answer is that the selective pressures leading to reproductive altruism stem from the increasing cost of reproduction with increasing group size. Concepts from population genetics and evolutionary ecology appear to be sufficient to explain this major evolutionary transition in individuality.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy15-i007-R*

Symposium 15
Division of labour

Behavioural thresholds for colony defence: flexible in virgin queens, but hard-wired in workers

Nehring V[1], Larsen J[1], d'Ettorre P[2]
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Summary statement:

Our study of nestmate recognition shows that behavioural thresholds can be realised at two different levels of the recognition system: the perception and the action component.

Abstract:

One of the key tasks for maintaining the integrity of social insect colonies is nest defence, which should rely on an efficient nestmate recognition system. We tested the assumption that some workers could specialize in colony defence using one of the most derived and complex insect societies, the leaf-cutting ants. We investigated the nestmate recognition ability of three morphologically distinct worker castes of the leaf-cutting ant Acromyrmex echinatior, and demonstrate that major workers are more likely than minors to attack non-nestmates. We furthermore describe a hitherto unknown behavioural flexibility of young unmated queens (gynes), which upon wing loss begin to assume worker tasks, including nest defence. The gynes´ propensity to attack non-nestmates increased when dealate, but following a different mechanism than workers. While major workers are simply better than minors in discriminating nestmates from non-nestmates, alate and dealate queens do not differ in their recognition abilities, but in their motivation to attack instead of flee upon presentation of non-nestmate stimuli. Our data demonstrate that selection in favour of varying behavioural thresholds can lead to the evolution of adaptations at two different levels of the recognition system: the perception component, as it is the case for workers, which have a hard-wired sensitivity to the stimulus; and the action component, as for queens, which perceive the stimulus always in the same way, but vary their response to it.

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SUN 21 AUG at 1610 - Room N5
Oral presentation *A4-Sy15-1610-O*

Symposium 15
Division of labour

The evolution of a division of labour in the production of public goods

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Summary statement:

We model the division of labour in the production of two possible public goods. We show that both relatedness and accelerating returns are essential for a division of labour.

Abstract:

All multicellular organisms display some form of a division of labour. Most research on the division of labour has generally focused on the division between germ and soma cell, or between queen and workers, in the case of social insects. However, the division of labour applies to a much broader variety of behaviours, from parental care or the specialization in vigilance or foraging tasks, to the production of multiple public goods in bacteria. Few models have looked at the evolution of a division of labour in the absence of reproductive asymmetries, where individuals specializing in either task can also reproduce. Here we build a kin selection model looking at the specialization in the production of one of two possible public goods. We show that genetic relatedness between individuals is required for public good production, but that the division of labour in the production of both goods is dependent on accelerating returns in the benefit the goods bring. Our model illustrates a simple, but general, mechanism for the evolution of a division of labour, and we further identify key issues which need to be addressed to unify the currently disparate use of division of labour in the biological literature.

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SUN 21 AUG at 1440 - Room N5
Oral presentation *A3-Sy15-1440-O*

Symposium 15
Division of labour

Experimental evolution of cellular division of labor during the transition to multicellularity

Ratcliff WC[1], Denison RF[1], Borrello M[1], Travisano M[1]
[1]University of Minnesota, Ecology, Evolution and Behavior, St. Paul, United States

Summary statement:

We evolved simple multicellularity in the unicellular yeast Saccharomyces cerevisiae. This precipitated the evolution of among-cell division of labor.

Abstract:

The evolution of multicellularity was one of the most significant innovations in the history of life. Its initial evolution, however, remains poorly understood largely because all known transitions are ancient. Using experimental evolution, we demonstrate that key steps in the transition to multicellularity, including among-cell division of labor, evolve far more easily than previously thought. We subjected the unicellular yeast Saccharomyces cerevisiae to an environment in which we expected multicellularity to be adaptive. We observed the rapid evolution of clustering genotypes that display a novel multicellular life-history characterized by reproduction via multicellular propagules, a juvenile phase, and determinate growth. Subsequent evolution resulted in the de novo evolution of among-cell division of labor. The first multicellular yeast to evolve in our experiments consist of cells that are all similar. After several hundred additional generations, however, we observed the evolution of programmed cell death (apoptosis) among cells within multicellular clusters. Cellular suicide, while costly to the cells that express this behavior, is nevertheless adaptive, benefiting viable cells within the multicellular cluster by regulating propagule size. Multicellular clusters are composed of clonally related cells, not chimeras of separate lineages, thereby minimizing potential conflicts of interest over which cells should apoptose. These results demonstrate that key aspects of multicellular complexity can readily evolve from unicellular eukaryotes, and provide unique insight into the ultimate evolutionary causes of cellular division of labor.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy15-i008-R*

Symposium 15
Division of labour

Experimental evolution in a multi-level selection framework

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[1]New Zealand Institute for Advanced Study and Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, Albany, New Zealand, [2]Department of Biology, University of Washington, Seattle, Washington, United States, [3]Max Planck Institute for Evolutionary Biology, Plön, Germany

Summary statement:

The evolutionary transition to multicellularity via a soma-germ distinction is investigated with experimental populations of the bacterium Pseudomonas fluorescens.

Abstract:

The transition from single-celled to multi-celled organisms requires individual cells to relinquish their ability to reproduce as independent units and instead reproduce and evolve only as members of a collective whole. This shift in the hierarchical level of selection necessitates competition between groups which, by definition, must already have the capacity to reproduce themselves. We propose that the evolution of multicellularity therefore requires the almost simultaneous emergence of division of labour and development from a single germ-cell, enabling natural selection to act on replicating groups.

Very particular ecological conditions are necessary to enable division of labour, development and between-group competition to occur simultaneously. We use multilevel selection (MLS) theory to guide an experimental design that recreates these specific conditions with populations of the bacterium Pseudomonas fluorescens. MLS2 conditions are imposed (in which a group's fitness is the number of group offspring it produces) and contrasted with MLS1, in which group fitness is defined as the average cell fitness. The experimental evolution regime imposes division of labour, single-cell bottlenecks, and both between-group and between-cell competition during different stages of a lifecycle. Cooperative "somatic" groups compete to produce germ cells, and germ cells compete to produce groups that occupy limited niche space.

Here we present results from this evolution experiment in a multi-level selection framework and discuss the emergence of several intriguing derived types.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy15-i009-R*

Symposium 15
Division of labour

Phenotypic plasticity can lead to division of labour in tree canopies

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Summary statement:

We present a conceptual model of division of labour in tree canopies based on differential light use and photosynthetic performance among canopy modules.

Abstract:

Trees are modular organisms that adjust the shape and physiology of their leaves in response to environmental inputs and developmental constraints. The phenotype of any given leaf depends on its position within the tree crown. This phenomenon is known as intracanopy plasticity and has complex functional and evolutionary implications that remain to be thoroughly assessed. Here we propose that one major consequence of canopy plasticity is the emergence of division of labour between sun and shade modules of the crown. Our results indicate that leaves in various positions of the canopy can use different types of solar radiation and operate at different time windows. Additionally, light availability inside the canopy is conditioned by the shape of external leaves. In light of these results, we present a conceptual model of spatio - temporal segregation of resource use and productivity in tree canopies. Sun leaves would use direct solar radiation and be more active when the sun is close to the horizon while shade leaves specialize in the capture of diffuse radiation and would be more active when the sun is higher. Additionally, outer canopy leaves might play a niche constructing role by creating a beneficial environment for the inner canopy.

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SUN 21 AUG at 1650 - Room N5
Oral presentation *A4-Sy15-1650-O*

Symposium 15
Division of labour

A general model identifying necessary conditions for the evolution of division of labor

Rueffler C[1], Wagner GP[2]
[1]University of Vienna, Department of Mathematics, Vienna, Austria, [2]Yale University, Department of Ecology and Evolutionary Biology, New Haven, United States

Summary statement:

Division of labour occurs at all levels of biological organisation. I present a simple and general model identifying necessary conditions for evolution of labour to evolve.

Abstract:

Division of labour evolves when units of an organism (or individuals in a group) that were ancestrally involved in more than one task undergo evolutionary modifications such that in derived taxa different units (or individuals) are specialized on different tasks. Division of labour underlies several major evolutionary transitions and is a phenomenon occurring at all levels of biological organization in both animals and plants. Well known examples include the evolution of specialized enzymes with high substrate specificity from ancestors with low substrate specificity after a gene duplication, the evolution of specialized cell types (e.g. germ and soma), limb diversification in arthropods, certain instances of left-right asymmetry where the left and right copy of a unit are specialized on different tasks and the evolution of specialized colony members in many taxa of marine invertebrates where individuals are comprised of genetically identical zooids and of castes in social insects.

With few exceptions, the evolution of division of labour has been investigated, both empirically and theoretically, with a focus on specific taxa. In my talk I will present a simple and general model that allows to identify necessary conditions for division of labour to be favored by selection in terms of maps that link organismal traits to performances.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy15-i003-E*

Symposium 15
Division of labour

The evolution of colony size in cavity-dwelling ants: the interplay between colony size and different life-history traits

Scharf I[1], Kramer B[2], Foitzik S[1]
[1]University of Mainz, Institute of Zoology, Mainz, Germany, [2]Max Planck Institute for Demographic Research, Laboratory of Evolutionary Biodemography, Rostock, Germany

Summary statement:

Colony size interacts with various demographic and life-history traits in cavity-dwelling ants. Such traits can also explain why these ant colonies are usually small.

Abstract:

Evolution led to typical life-history traits, such as age and size at first reproduction. In social insects, group size is also under selection. Larger colonies show increased survival, reproduction and competitive abilities. However, many social insect species show small colonies, so other factors must restrict colony growth. We focus here on cavity-dwelling Myrmicine ants and study eight species from ten populations. These ants reside in woody material in the leaf litter of temperate forests, and have small colonies (average of 30-100 workers). We show that these ants are restricted to small colonies due to different factors. Worker production increases with colony size but levels-off quickly, pointing to an early end of the ergonomic phase. The common size distribution is right-skewed, with many small colonies and few large ones. This suggests a low colony survival and a high reproduction rate. In accordance with the "Michener´s paradox", per-capita productivity sharply decreases with colony size. We can show that polydomy, the usage of several nest sites by a single colony, can moderate this effect. In these solitarily foraging ants, polydomy should lower the costs of central-place foraging by decreasing the travel time. Colony size is also linked to the social structure. Only larger colonies are polygynous, having several reproducing queens. We uncover these general patterns in most ant populations and provide universal ecological explanations for why cavity-dwelling ants live in small societies. Colony size probably depends on the foraging mode of these ants, their patterns of productivity, nest structure and social organization.

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SUN 21 AUG at 1550 - Room N5
Oral presentation *A4-Sy15-1550-O*

Symposium 15
Division of labour

Cooperative defense by post-reproductive adults and young nymphs in a social aphid

Uematsu K[1], Shimada M[1], Shibao H[1]
[1]University of Tokyo, Department of General Systems Studies, Tokyo, Japan

Summary statement:

The oldest and the youngest individuals altruistically defend their colony against predators in a social aphid.

Abstract:

A colony of social insects functions as a highly integrated unit, which is often referred to as superorganism. Since aphids reproduce by parthenogenesis, there is no kin-selected conflict over reproduction within the clones, thus they have provided many examples of altruistic behavior. Here we show a novel defense system in a social aphid. The aphid Quadrartus yoshinomiyai forms closed galls on its host plant. After galls open, two types of defenders perform altruistic colony defense. First-instar nymphs of this species attack intruding predators with their stylets. In addition, post-reproductive wingless adults defend the colony by sticking themselves to intruding predators with waxy secretion, which is accumulated in their body with aging. Both types of defenders were preferentially located around the gall entrance vulnerable to invasion of predators, whereas reproductive individuals away from the gall entrance. Our results suggest that cooperative defense as well as reproductive division of labor in this system is attained through the spatial organization of each colony member with different task preference based on its residual reproductive value.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy15-i004-E*

Symposium 15
Division of labour

Characterization of the light environment across wild olive (Olea europaea L.) crowns: considering light distribution conditions required for niche construction

Ventre-Lespiaucq AB[1], Escribano AG[1], Granado-Yela C[1], García-Verdugo C[1,2], Carrillo K[1], Serrano JM[3], Jiménez-Escobar MD[3], Balaguer L[1]
[1]Complutense University of Madrid, Vegetal Biology I, Madrid, Spain, [2]Rancho Santa Ana Botanic Garden, Claremont, United States, [3]Complutense University of Madrid, Ecology, Madrid, Spain

Summary statement:

Light environment, hemispheric photography, phenotipic plasticity, niche construction.

Abstract:

Crown development changes the environment experienced by the tree. This environment modification, suspected to be a niche construction process, is expected to involve consequences that are not restricted to ecology, but can affect evolution by modifying sources of natural selection in their environments. To assess whether across-crown light distribution pattern is driven by a niche construction process, it is necessary to confirm that: 1) Light distribution across the crown is heterogeneous, and 2) Light extinction through the crown follows a non-gradual pattern. We have characterized light variation across wild olive crown using hemispheric photography and remote sensing. As expected, light distribution along the crown was not homogeneous. Light interception by outer crown leaves resulted in an abrupt reduction that gave rise to a more homogeneous shade environment. Thus, light variation from outer to inner layers displayed a threshold like pattern. Light variation in relation to phenotypic plasticity and modular tree structure is discussed in order to set the basis for further experiments to assess the effect of niche construction on fitness at both the individual and module levels.

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Symposium 16

Viviparity, placentation and conflict

Talks: *Room N2*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Upper floor campus canteen *Mensa*

Invited Speakers:

Derek Wildman, David Reznick

Organizers:

Isabella Capellini, Robert Barton

Description:

The placenta evolved multiple times and it exhibits striking and still unexplained morphological variation. We welcome contributions on how and why viviparity and placental diversity evolved, covering evolution in molecular, morphological and physiological traits, the role of sexual conflict and environmental pressures in driving these changes and the implications for macroevolutionary patterns.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

WED 24 AUG at 1120 - Room N2
Oral presentation *D2-Sy16-1120-O*

Symposium 16
Viviparity, placentation and conflict

Could parent-offspring conflict explain the costs of polyandry in a placental poeciliid fish, Heterandria formosa?

Ala-Honkola O[1], Friman E[2], Lindström K[3]
[1]Syracuse University, Syracuse, United States, [2]University of Helsinki, Helsinki, Finland, [3]Åbo Akademi University, Turku, Finland

Summary statement:

Parent-offspring conflict may reduce the benefits of polyandry in viviparous species.

Abstract:

Polyandry (female mating with multiple males) has been shown to increase female reproductive success in many species. We performed two experiments to study the effects of polyandry (number of mates) and brood relatedness on offspring growth in a placental poeciliid fish, Heterandria formosa. Polyandry was beneficial as it increased the probability of pregnancy. However, polyandry also brought upon costs in terms of offspring quality. Females mated to four males produced offspring that had a longer maturation time than those of monandrous females. In the second experiment, we manipulated within brood genetic relatedness by mating females to three males that were either highly related to each other (brothers) or unrelated. We found that the newborn offspring became smaller with time when within brood relatedness was low, while highly related broods produced offspring of constant size throughout the experiment. These results are in accordance with Haig's 1996 model of placental hormone production; when within brood relatedness is low, offspring become less cooperative and demand less resources from their mother, because resource extraction is an altruistic act. Possibly polyandrous females produced less cooperative offspring, which led to impaired development during gestation, and therefore to longer maturation time. Parent-offspring conflict may thus reduce the benefits of polyandry especially in viviparous species.

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WED 24 AUG at 1140 - Room N2
Oral presentation *D2-Sy16-1140-O*

Symposium 16
Viviparity, placentation and conflict

Placentation, maternal investment and parasites

Capellini I[1,2], Venditti C[3], Barton R[2]
[1]Queen's University of Belfast, School of Biological Sciences, Belfast, United Kingdom, [2]Durham University, Anthropology, Durham, United Kingdom, [3]University of Hull, Department of Biological Sciences, Hull, United Kingdom

Summary statement:

Greater placental interdigitation is associated with shorter gestation and higher foetal growth rate while higher invasiveness might be constrained by parasite pressure.

Abstract:

Despite undertaking the same function in all mammals, the placenta is structurally very diverse. Why such variation evolved and how it impacts maternal investment and offspring development, however, is unclear. Direct contact between foetal tissues and maternal blood supply (invasiveness) is believed to facilitate nutrient transfer and enhance foetal growth rate, particularly of the brain. The extent of interdigitation between maternal and foetal tissues might also be crucial because higher interdigitation is associated with greater surface area of exchange. We show that higher interdigitation is associated with shorter gestation, but there is no difference in neonatal brain or body mass across type of interdigitation. Thus, higher interdigitation leads to greater foetal growth rate, which is however traded-off against shorter gestation time. After accounting for the effects of interdigitation, invasiveness is unrelated to any of our foetal growth variables. While these results reveal a crucial role of interdigitation in maternal investment and offspring growth, possibly suggesting an arms race between offspring and mothers over allocation of resources, the evolution of placental invasiveness remains mysterious. We suggest that parasite pressure might have been a constraint on the evolution of highly invasive placentation if direct contact between maternal blood and foetal tissues facilitates vertical transmission.

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WED 24 AUG at 1200 - Room N2
Oral presentation *D2-Sy16-1200-O*

Symposium 16
Viviparity, placentation and conflict

Oviparous or viviparous?

Kühnel S[1], Kupfer A[1,2]
[1]Friedrich-Schiller-Universität Jena, Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Jena, Germany, [2]University of Siegen, Department of Biology, Section Integrative Zoology and Biodiversity, Siegen, Germany

Summary statement:

We try to find evidence for an oviparity-viviparity continuum in anamniote vertebrates, i. e. caecilian amphibians.

Abstract:

A crucial point of reproduction is the mechanism of sperm transfer leading to external or internal fertilization. The exclusive advantage of internal fertilization is the decoupling of fertilization and oviposition, a pre-requisite for viviparity. In modern amphibians, not only viviparity has evolved independently from oviparity, but also various transitions towards a terrestrialisation of reproduction have been realised. Exceptional among amphibians, caecilians (Gymnophiona) all practice internal fertilization with the aid of a true copulatory organ. Reproductive modes include oviparity with aquatic larvae or direct development and viviparity. In the latter reproductive mode, fertilized eggs are retained in the female oviduct and although lacking placental structures embryos are nourished by alternative matrotrophic mechanisms. In oviparous species eggs are not deposited directly after copulation as well, offering potentials for embryogenesis prior to oviposition, however evidence for this is little.
Our examination of female oviducts in two oviparous caecilian species representing different reproductive modes yielded embryos of advanced developmental stages. We evidence a rare example of an oviparity-viviparity continuum in anamniotes aiding the understanding of the evolution of viviparity in vertebrates.

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WED 24 AUG at 1100 - Room N2
Oral presentation *D2-Sy16-1100-O*

Symposium 16
Viviparity, placentation and conflict

The marsupial yolk-sac placenta expresses MHC class I-a homologues

Leinweber I[1], Drews B[1], Renfree MB[2], Hildebrandt TB[1], Menzies BR[1]
[1]Leibniz Institute for Zoo and Wildlife Research, Reproduction Management, Berlin, Germany, [2]The University of Melbourne, Department of Zoology, Melbourne, Australia

Summary statement:

Silencing of MHC class I may not be required as the fetus would be delivered prior to any maternal immune challenge.

Abstract:

Mammalian pregnancy requires that two immunologically different tissues grow in apposition to one another. In well characterised Eutherian mammal species, where pregnancy is relatively longer and more invasive than the vast majority of Marsupial mammals, there is differential regulation of classical class I MHC molecules (transplantation antigens) presumably to avoid self/non-self confusion and maternal/fetal incompatibility at the site of nutrient and gaseous exchange. However, this specific regulation of class I molecules may not be necessary in the Marsupialia where the conceptus is enclosed in a protective shell coat for up to 80% of gestation, and the period of placental/uterine interaction is relatively short. To better understand this process in marsupials we have characterised mRNA and protein expression of the recently described MHC class I loci of the tammar wallaby (Macropus eugenii) from the period of shell coat rupture (day 19) through to the last days (25/26) of pregnancy. We found prevalent expression of class I-a molecules in both tri- and bi-laminar yolk sac tissues throughout the attachment phase of pregnancy in the tammar wallaby. These loci showed similar nucleotide identity and allelic diversity to those previously described for non-reproductive nucleated tissue types in the tammar. These data suggest that the short-lived placenta of marsupials expresses the same complement of class I MHC molecules as normal nucleated cells such as kidney, liver and skin and that the fetus does not hide its immunological identity from the mother.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy16-i001-R*

Symposium 16
Viviparity, placentation and conflict

Detection of imprinted porcine genes through high-throughput cDNA-sequencing (RNA-seq)

Madsen O[1], Crooijmans R[1], Rund L[2], Schook L[2], Groenen M[1]
[1]Wageningen University, Animal Breeding and Genomics Centre, Wageningen, Netherlands,
[2]University of Illinois, Department of Animal Sciences, Urbana, United States

Summary statement:

Genomic imprinting, porcine, mammals, comparative analyses, RNA-seq.

Abstract:

Genomic imprinting is an epigenetic phenomenon in which the levels of allelic expression are dependent upon parental origin. In mammals >100 genes have been shown to be imprinted, mainly through studies in humans and mice. Studies in other mammals for imprinted genes are relatively sparse and have generally been limited to either an ad hoc single gene analysis or analyses on "unnatural" systems such as uniparental embryos. Imprinted genes play important roles in many stages of development, and dysregulation can result in diseases such as cancer and neurological disorders. Since the pig is one of the most widely used model organism for human diseases and biomedical research, a comprehensive investigation of imprinted genes in pigs contributes to a detailed understanding of the evolution of imprinted genes in relation to their key role in development and reproduction.

RNA-seq is a powerful tool to analyze allele specific expression and therefore provides an excellent opportunity for detecting imprinted genes, by comparing the genetic variation present in a genome with the variation in allelic expression. By combining this information with the variation present in the genome of the parents, it will be possible to detect imprinted genes.

This study aims to detect the whole range of imprinted genes (the imprintome) in pigs. This will be done by whole genome sequencing of two family trios (father, mother and offspring) plus RNA-seq of tissues from the two offspring (starting out with placenta, brain and liver). Results from these analyses will be presented and related to the imprintome of other eutherian mammals.

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WED 24 AUG at 0910 - Room N2
Invited talk *D1-Sy16-0910-I*

Symposium 16
Viviparity, placentation and conflict

The evolution of placentas in the fish family poeciliidae

Reznick DN[1]
[1]University of California, Biology, Riverside, United States

Summary statement:

The recent and repeated evolution of placentas in this fish family enables us to study evolution in a way that is not possible in mammals.

Abstract:

Most of what we know about placentas pertains to the mammalian placenta. Nature has much more to offer since the equivalent of the mammalian placenta has evolved many times in other organisms. If our goal is to study the evolution of the placenta, then some of these other organisms have far more to offer than mammals. The mammalian placenta evolved once in a common ancestor that lived over 100 myr ago, so the causes of its evolution are lost to history. I will show that placentation has evolved at least six times in this fish family, and that some origins are quite recent. This combination of multiple, independent origins with recency creates research opportunities unattainable in mammals. I can address the biological consequences of evolving a placenta by comparing close relatives that do or do not have a placenta and can evaluate the generality of my conclusions by making multiple such comparisons, each representing an independent origin of the placenta. It is also possible to ask whether the placenta evolves to facilitate the evolution of other components of the life history, whether or not it causes an acceleration in the formation of new species or to address a diversity of other questions that lie outside the realm of what can be done with mammals.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy16-i001-E*

Symposium 16
Viviparity, placentation and conflict

Mate choice, mating competition and sexual signals in syngnathidae

Rosenqvist G[1], Berglund A[2]
[1]Norwegian University of Science and Technoloyg (NTNU), Department of Biology, Trondheim, Norway, [2]Uppsala University, Dept. of Ecology and Genetics/Animal Ecology, Uppsala, Sweden

Summary statement:

The connection between mating patterns, strength of sexual selection, sex roles and ornament expression is far from simple and straight-forward.

Abstract:

The male pregnancy in the family Syngnathidae (pipefishes, seahorses and seadragons) predisposes males to limit female reproductive success: if male brooding space is insufficient to take care of the eggs produced by females, females will compete for access to males, i.e., sexual selection will operate strongly on females and female sexual signals may evolve (“sex role reversal”). This is indeed the case in many syngnathids, but this is not the complete picture: in several species also males evolve ornaments, females are choosy in addition to being competitive, and males compete as well as chose partners. Thus, sex roles form a continuum, spanning from conventional to reversed within this group of fishes. We here present cases suggesting that stronger sexual selection on females, and hence sex role reversal, may be most extreme in species showing classical polyandry (such as many trunk brooders), intermediate in polygynandrous species (as in many tail brooders), and least extreme, even going over to conventional sex roles, in monogamous species (as in many seahorses and tropical pipefish). At the same time caution is needed before unanimously establishing this pattern: first, the connection between mating patterns, strength of sexual selection, sex roles and ornament expression is far from simple and straight-forward, and second, our knowledge of the actual morphology, ecology and behavior of most syngnathid species is scanty. We do know, however, that this group of fish exhibits a remarkable variation in sex roles and ornamentation, making them an ideal group for the study of these questions.

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WED 24 AUG at 0950 - Room N2
Invited talk *D1-Sy16-0950-I*

Symposium 16
Viviparity, placentation and conflict

The mammalian placenta: From anatomical to transcriptomic variation

Wildman D[1]
[1]Wayne State University, Center for Molecular Medicine and Genetics, Detroit, United States

Summary statement:

This talk describes phylogenetic and phylogenomic analyses of the evolution of placenta anatomy and patterns of gene expression, especially in the immune system.

Abstract:

During development the placenta performs functions analogous to those of the lung, kindney, liver, intestine, pituitary, ovary, and hypothalamus. In extant eutherian mammals (i.e. Placentalia) the placenta can be considered the most anatomically variable organ. Using phylogenetic techniques we have been able to trace the evolution of key characters of placenta anatomy, and we have inferred that the last common ancestor of placental mammals possessed a hemochorial interface, a labyrinthine interdigitation, and a discoid shape. The hemochorial form of placentation represents the most intimate type of interface, and fetal tissue comes in direct contact with maternal blood. It has been proposed that the maternal immune system needs to be suppressed at the fetal-maternal interface in order to avoid immune-mediated rejection of the semi-allograft feto-placental unit. The hemochorial form is present in members of many placental orders. Despite its wide conservation, in some cases the hemochorial placenta appears to have evolved independently. Other lineages of mammals have a lesser degree of invasiveness, and it has remained unclear whether relaxed pressures on immune function have accompanied anatomical modification to the placenta. To study this phenomenon we examined the patterns of gene expression in the term placentas of four mammalian species representing a wide range of phylogenetic diversity and placental anatomy. We found evidence of wide variation in placenta gene expression across mammals. The most enriched clusters of human-specific placenta expressed genes are signal/glycoprotein and immunoglobulin, which may relate to the deeply invasive human hemochorial placenta.

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Symposium 17

Novel techniques in behavioural ecology

Talks: *Room N3*

***Essence posters**: Ground floor lecture hall centre HZ*

***Regular posters**: Upper floor campus canteen Mensa*

Invited Speakers:

Tracey Chapman, Michal Polak

Organizers:

Amanda Bretman, Thomas Price

Description:

Novel techniques create exciting new ways to investigate evolutionary behavioural ecology. This symposium will be dedicated to presenting novel techniques and their application. Talks will focus on the novelty and usefulness of methods used, and speakers will be encouraged to discuss the practicalities and pitfalls of the techniques, as well as the results of their experiments.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy17-i001-R*

Symposium 17
Novel techniques in behavioural ecology

High-throughput expression analysis of gonad-specific genes in Macrostomum lignano using RNAseq, in situ hybridization and RNA-interference

Arbore R[1], Sekii K[1], Beisel C[2], Berezikov E[3], Schärer L[1]
[1]University of Basel, Evolutionary Biology, Zoological Institute, Basel, Switzerland, [2]ETH Zürich, D-BSSE, Basel, Switzerland, [3]Hubrecht Institute, Utrecht, Netherlands

Summary statement:

Analysis of gene expression and function provide new opportunities to test sexual selection and sex allocation theory in this hermaphroditic flatworm.

Abstract:

The free-living flatworm Macrostomum lignano is a powerful model organism for the study of sexual selection and sex allocation theory in simultaneous hermaphrodites. Established tools for gene expression and function analysis (i.e., in situ hybridization and RNA-interference), combined with recent genome and transcriptome data, are providing new opportunities to experimentally test important assumptions and predictions of this theory. For instance, a phenotypic engineering approach through the direct manipulation of a testis-specific target gene has already allowed the production of different sperm production phenotypes, which we used for experimental tests of sex allocation theory in our model organism. A further aim is to completely prevent the development of the testis and to measure the resulting resource reallocation to the ovaries and vice versa. So far a literature-based approach has been used to select candidate genes for this purpose. To overcome inherent limitations of this approach we have performed a whole-transcriptome deep sequencing analysis (RNAseq) and determined the levels of expression in different anatomical locations (head, testis, ovary and tail) of more than 65.000 transcripts. Our analysis reveals the presence of a great number of genes with organ-specific expression and the overwhelming majority of them appear to be testis-specific. A subset of these transcripts is currently being screened using in situ hybridization to analyze in more detail their expression patterns and to generate list of candidate genes for functional tests. We report the results of this expression screening and the corresponding RNAi phenotypes obtained so far.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy17-i002-R*

Symposium 17
Novel techniques in behavioural ecology

An integrative approach to study the causes and consequences of reproduction in a wild population of eastern chipmunks

Bergeron P[1], Réale D[2], Humphries MM[3], Garant D[1]
[1]Université de Sherbrooke, Sherbrooke, Canada, [2]UQAM, Montréal, Canada, [3]McGill University, Ste-Anne de Bellevue, Canada

Summary statement:

An integrative approach, using molecular, physiological and demographic tools, to study the causes and consequences of reproduction in a wild population of eastern chipmunks.

Abstract:

Understanding the determinants of reproduction is a central aspect of evolutionary behavioral ecology studies. As molecular and physiological laboratory techniques improve, a contemporary challenge is now to integrate such techniques to study reproduction and its demographic consequences in wild populations. Here, we studied the determinants of reproduction, from various perspectives, and the demography of a wild population of eastern chipmunks. We used molecular tools to determine patterns of parentage. We found multiple paternity in 100% of the litters across three summer breeding seasons and one spring breeding season. Males that were more closely related to their partners sired fewer offspring, suggesting selection for inbreeding avoidance despite promiscuous matings. Data on litter size were then contrasted with measures of daily energy expenditure (DEE) and oxidative damage to evaluate the physiological costs of reproduction at the individual level. We found that both female DEE and oxidative damage increased with litter size. Finally, we measured food availability and used Mark-Recapture methods to investigate the effects of reproductive events on survival at the population level. We found that adult chipmunks survival was unaffected by environmental variation, probably due to their ability to adjust their reproductive activities with food availability. In conclusion, molecular tools revealed patterns of selection that would have been impossible to detect from behavioral observations alone, physiological analyses revealed costs of reproduction at the individual level, but reproductive events did not translate into lower survival at the population level.

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WED 24 AUG at 1140 - Room N3
Oral presentation *D2-Sy17-1140-O*

Symposium 17
Novel techniques in behavioural ecology

The use of robotic fiddler crabs to manipulate male group composition during female choice

Callander S[1], Jennions MD[1], Backwell PRY[1]
[1]The Australian National University, Evolution, Ecology & Genetics, Canberra, Australia

Summary statement:

We used robotic male fiddler crabs to test whether female choice for identical focal males varied depending on the identity of their neighbours over short and long distances.

Abstract:

In fiddler crabs mate searching females always approach males that are visible from a distance. This could generate a potential conflict of interest for males if having more attractive neighbours increases the likelihood that a female will approach a group of males, while simultaneously decreasing the chances that a focal male will be chosen from the males within the group. These effects might vary, however, if male attractiveness changes with the distance at which a female first locates and then approaches groups of males. Determining what factors affect female choice from groups of males is difficult using observational data because group composition is rarely random, and composition can change male's investment in courtship. We used custom-built robotic fiddler crabs to test experimentally whether female choice for focal males of standardised attractiveness varied depending on the identity of their neighbours (either more or less attractive) over both short and long distances. This novel technique allowed us to control and manipulate two traits known to be imperative to female choice; male claw size and wave rate. We found that neighbour attractiveness did not affect the likelihood that a female approached a group of males from a distance. However, female preferences did differ depending on the identity of the focal male's two closest neighbours during her final mate choice decision. Our findings help to explain the formation of defence coalitions in which residents assist their smaller neighbours in fighting off intruders.

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WED 24 AUG at 0910 - Room N3
Invited talk *D1-Sy17-0910-I*

Symposium 17
Novel techniques in behavioural ecology

Genomics and sexual selection

Chapman T[1]
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Summary statement:

Genomics provides (i) unprecedented insights into mechanisms of sexual selection and conflict, and (ii) novel opportunities to discover how much, and which parts, of genomes are modified by sexual interactions.

Abstract:

Molecular genetic, genomic and proteomic techniques are being developed at an ever-increasing rate, allowing unprecedented insights into the mechanisms that mediate sexual selection and sexual conflict.
For example, genome wide profiles into mating interactions allow novel research questions to be addressed, such as how much, and which parts, of the genomes in males versus females are modified by sexual interactions. In addition, what proportion of these changes can be viewed as co-operative versus antagonistic.
In addition, identifying full genomic profiles can allow us to test the relative importance and fitness benefits of controlling responses to reproduction at both transcriptional and post-transcriptional levels. These questions are also becoming more focussed as the widespread role of small RNA molecules such as microRNAs is emerging.
These issues will be discussed with reference to the interactions between males and females in the Drosophila melanogaster model system. The pitfalls both from a conceptual, practical and analytical perspective will also be discussed.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy17-i001-E*

Symposium 17
Novel techniques in behavioural ecology

Game theory, game practice: costs and benefits of cooperation in humans

Harrison F[1], Sciberras J[1], El Mouden C[1], James R[2]
[1]University of Oxford, Department of Zoology, Oxford, United Kingdom, [2]University of Bath, Department of Physics, Bath, United Kingdom

Summary statement:

Simple modifications to traditional protocols can increase the ecological validity of economic games, thus advancing the study of human social behaviour.

Abstract:

Aims: Experiments derived from economic game theory are commonly used to explore cooperative or pro-social behaviour in humans. These have almost without exception relied on recruiting groups of participants who are strangers to one another and giving them monetary tokens, which they may choose to invest in a cooperative venture, or retain. While this methodology has spawned a vast and interesting literature, suprisingly little attempt has been made to assess its ecological validity. Specifically, we aim to address two issues. Firstly, it is not clear how well token-based games capture the costs inherent in real-life social behaviour and how this impacts on their usefulness: are decisions to invest or retain money provided by an experimenter actually correlated with decisions to use one’s own resources to aid others in a social world? Secondly, anonymous economic games likely fail to capture certain direct (selfish) benefits that accrue from cooperative acts ´in the wild,´ where social ties link individuals together in structured networks.
Methods: We present empirical data which test the validity of token-based games by comparing individual behaviour in such games with behaviour in analogous games where monetary endowments must be earned through labour or physical discomfort. We then use an experiment with high ecological validity to present a novel study of pro-social behaviour in a real-world social network.
Results & conclusions: Our work demonstrates how simple modifications to traditional protocols can be used to increase the realism of experimental games and extend the toolkit available to students of human social behaviour.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy17-i003-R*

Symposium 17
Novel techniques in behavioural ecology

Behavioural QTL and brain eQTL mapping in an intercross of wild and domestic chickens

Johnsson M[1], Andersson L[2], Jensen P[1], Wright D[1]
[1]Linköping University, IFM Biologi, Linköping, Sweden, [2]Uppsala University, IMBIM, Uppsala, Sweden

Summary statement:

QTL mapping of behaviour and gene expression traits is used to search for candidate genes for fear-related behaviours in a red junglefowl x White Leghorn advanced intercross.

Abstract:

Domestication can serve as a model of evolution. Because of its compact genome and high recombination rate, the chicken is an appropriate animal for genetic mapping of traits related to domestication. We have performed quantitative trait locus (QTL) mapping of fear-related behaviour in an F8 advanced intercross of White Leghorn, a domestic layer line, and the red junglefowl, the main progenitor of domestic chicken breeds. In an advanced intercross, recombinations accumulate over generations of interbreeding, increasing map resolution. 575 chickens were genotyped at 650 SNP markers, and phenotyped for fear-related behaviours. We detected eight QTL for behaviour in a social reinstatement test, with an average LOD score of 6 and an average confidence interval size of 4 Mb. For tonic immobility, we detected two QTL with LOD scores 7 and 5, respectively, and interval sizes of 3 and 2 Mb. We have also isolated hypothalamus RNA from a subset of 130 chickens, and are running them on Nimblegen gene expression microarrays, to be used for expression QTL (eQTL) mapping. DNA samples from the founder individuals of the intercross have been resequenced using SOLiD paired-end sequencing, to identify sequence variations segregating in the cross. Domestication can potentially give rise to selective sweeps. Putative selective sweeps in the chicken genome have previously been identified. By overlaying QTL, eQTL, resequencing, and selective sweep data we will be able to identify putative candidate genes responsible for the genetic difference in fearfulness between wild and domestic chickens.

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WED 24 AUG at 0950 - Room N3
Oral presentation *D1-Sy17-0950-O*

Symposium 17
Novel techniques in behavioural ecology

A natural history of sperm: shedding light on sperm behavioral ecology within the female reproductive tract

Manier MK[1], Belote J[1], Wong M[1], Pitnick S[1]
[1]Syracuse University, Biology, Syracuse, United States

Summary statement:

We introduce a new field of sperm behavioral ecology that examines what sperm do in the female reproductive tract within the evolutionary context of sperm-female interactions.

Abstract:

The role of sperm-female interactions in sperm performance and function is critical to reproductive success, yet we understand little about what sperm do within their natural selective environment, the female reproductive tract. Transgenic lines with red or green fluorescent sperm heads have recently allowed unprecedented access to sperm dynamics and behavior within the female reproductive tract. In particular, we can now distinguish between sperm from two different males in situ and thus gain a nuanced understanding of patterns of sperm transfer, sperm storage, sperm use, and cryptic female choice during sperm competition. An unexpected development with this novel technique is the observation that sperm are highly motile in storage and exhibit complex behaviors. Some sperm behaviors including rapid bending of the sperm head to reverse direction in the absence of any obvious physical obstruction, reverse motility to swim backward, and emergent properties of the entire sperm mass, including vortices. Sperm behaviors are heritable, density-dependent and may be adaptive within the context of ejaculate-ejaculate and ejaculate-female interactions.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy17-i002-E*

Symposium 17
Novel techniques in behavioural ecology

Effect of larval density on the behavioural development and life-history in a field cricket

Niemelä PT[1], Vainikka A[1], Lahdenperä S[1], Kortet R[2]
[1]University of Oulu, Department of Biology, Oulu, Finland, [2]University of Eastern Finland, Joensuu, Finland

Summary statement:

To our knowledge, the present work is among the first ones to examine if population density during ontogeny would have an impact on personality-associated behaviours at adult stage

Abstract:

Animal personalities (consistent, individually characteristic behaviours) and their evolution are currently a topic of wide interest among ecologists. However, despite of broad theoretical background of animal personalities and environmental factors affecting the emergence of them, a very few studies have concentrated on how environmental factors such as population density affect their development during individuals ontogeny. We use a novel and integrative approach and simultaneously study the effect of density during larval development on animal personality, immune defence, developmental time and adult body mass using field cricket, Gryllus integer. The results will be discussed.

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WED 24 AUG at 1100 - Room N3
Invited talk *D2-Sy17-1100-I*

Symposium 17
Novel techniques in behavioural ecology

A new laser surgical application for the experimental study of micron-scale morphological traits

Polak M[1]
[1]University of Cincinnati, Biological Sciences, Cincinnati, United States

Summary statement:

A laser surgical technique is described for the ablation of micron-scale morphological traits, opening up for experimental study a rich diversity of previously inaccessible traits.

Abstract:

An important challenge in some areas of behavioural ecology research is the microscopic size and difficult-to-access placement of morphological traits, whose functions may be of great interest but which remain unresolved because of the practical impasses that limit trait manipulation. We have developed a laser surgical technique permitting the experimental manipulation of traits previously inaccessible with standard mechanical cutting tools. With the present system, laser ablation of morphological structures is conducted with micron-scale, and even submicron-scale, precision, with little or no collateral damage to adjacent structures. The technique is described in detail, and several examples of its application are presented, including the manipulation and functional analysis of genital traits of insects, and the sex combs of Drosophila species, among other traits. The advantages and limitations of the technique are discussed.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy17-i005-R*

Symposium 17
Novel techniques in behavioural ecology

Estimating indirect selection on female extra-pair reproduction in the wild: a quantitative genetic approach to behavioural ecology

Reid JM[1], Arcese P[2], Sardell RJ[1], Keller LF[3]
[1]University of Aberdeen, Institute of Biological & Environmental Sciences, Aberdeen, United Kingdom, [2]University of British Columbia, Centre for Applied Conservation Research, Vancouver, Canada, [3]University of Zurich, Institute of Evolutionary Biology & Environmental Studies, Zurich, Switzerland

Summary statement:

Explicit quantitative genetic analyses revealed little indirect selection on female extra-pair reproduction in wild birds, contradicting key a hypothesis in behavioural ecology.

Abstract:

The forces driving the evolution of extra-pair reproduction (EPR) by socially monogamous females remain a major enigma in behavioural ecology. One key hypothesis is that female EPR is under indirect selection, reflecting increased genetic value of offspring sired by extra-pair males. Most explicitly, if extra-pair males sired offspring of higher additive genetic value than a female's social mate, and there was additive genetic variation in female propensity for EPR, then genes underlying female EPR could become correlated with genes underlying high paternal fitness. Female EPR could then evolve through indirect selection. This hypothesis is explicitly genetic and has proved extremely difficult to test using traditional behavioural ecological approaches that measure phenotypic associations in the wild. We therefore applied state-of-the-art quantitative genetic analyses to 16 years of complete genetic paternity data from free-living song sparrows (Melospiza melodia) to explicitly estimate key genetic parameters and estimate the magnitude of indirect selection on female EPR. Female EPR showed significant additive genetic variance and was heritable. However, offspring sired by extra-pair males tended to have lower rather than higher breeding values for recruitment than offspring sired by social mates. The genetic correlation between female EPR and male fitness was small, suggesting that there is currently little indirect selection on female EPR. This work illustrates major advantages and practical and theoretical challenges inherent in using explicit quantitative genetic approaches to answer key behavioural ecological questions in wild populations.

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WED 24 AUG at 1010 - Room N3
Oral presentation *D1-Sy17-1010-O*

Symposium 17
Novel techniques in behavioural ecology

Sperm metabolism: laser technology meets sexual selection, or does it?

Reinhardt K[1], Ribou A-C[2], Breunig HG[3], Koenig K[4]
[1]University Tuebingen, Tuebingen, Germany, [2]University Perpignan, Perpignan, France, [3]jenlab GmbH, Saarbruecken, Germany, [4]University Saarland, Saarbruecken, Germany

Summary statement:

Female manipulation of sperm metabolism reduces the power of paternity predictions based on traits of sperm collected from the male.

Abstract:

Variation in sperm traits can translate into variation in male reproductive success but it is not clear how. Borrowing laser technology - fluorescence-lifetime fluorimetry and multi-photon imaging - from cancer research we studied two aspects of sperm physiology that appear relevant to sexual selection: the metabolic rate of sperm cells as well as the production of reactive oxygen species (ROS). Using the results from two model organisms, crickets and bedbugs, we discuss the benefits of these methods and show that females reduce intracellular in situ ROS production in spermatozoa strongly (25-40%), rapidly (within 2 h) and for extended periods (at least 30 days). We provide support for the notion that ROS production was positively correlated with sperm metabolic rate but show that this was only the case in females. However, ROS production of sperm collected from males did predict ROS production of sperm stored in females - challenging a key assumption in sexual selection and reproductive medicine. We provide preliminary data for a hypothetical mechanism of female ROS suppression using cellular autofluorescence analysis. Finally, we provide support for the idea of sperm ageing by showing that the onset of infertility correlates with the time of an increased ROS production.

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WED 24 AUG at 1200 - Room N3
Oral presentation *D2-Sy17-1200-O*

Symposium 17
Novel techniques in behavioural ecology

A framework for modelling growth, aging, and plasticity

Robinson MR[1], Beckerman AP[1]
[1]University of Sheffield, Department of Animal and Plant Science, Sheffield, United Kingdom

Summary statement:

We present a novel analytical framework which estimates the influence of age, the environment, and social factors on morphological, behavioural, and life-history traits.

Abstract:

To understand adaptation in natural populations it is vital that we are able to reliably estimate the influence of age, the environment, and social factors on variation that we observe in morphological, behavioural, and life-history traits. Here, we present a novel analytical framework which combines Bayesian Monte Carlo Markov Chain multi-response mixed models and eigenvector analysis, to examine the influence of any factor on the relationships between traits at the phenotypic, genetic, and environmental level. By analysing a series of simulated datasets that are representative of the types of data gained from behavioural ecology studies of laboratory and wild populations, we demonstrate the effectiveness of the methods that we propose for examining genotype-age and genotype-environment interactions. We discuss potential advantages of this simple and general framework over existing methods and its potential applications.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy17-i006-R*

Symposium 17
Novel techniques in behavioural ecology

Parasitic manipulation: Baculovirus-induced changes in insect host behaviour

Ros VID[1], van Houte S[1], van Oers MM[1]
[1]Wageningen University, Laboratory of Virology, Wageningen, Netherlands

Summary statement:

Comparative analysis of lepidopteran insect hosts infected with wildtype and mutated baculovirus strains to reveal potential genes and pathways involved in insect behaviour.

Abstract:

Parasitic modification of host behaviour is a widely adopted strategy of parasites to enhance their own transmission. The molecular mechanisms leading to these behavioural changes are poorly understood. A typical case of behavioural manipulation is found in insects infected with baculoviruses. Infected caterpillars show enhanced mobility and start climbing to the top of plants or the forest canopy. As a consequence, the virus is spread over a larger area, thereby increasing the chance to infect a new caterpillar.

The baculovirus-insect system provides an excellent platform to study parasitic manipulation of insect host behaviour. Intriguing questions are which viral genes modify host behaviour and which behavioural pathways in the host transduce the parasite-induced signal into altered host behaviour. The baculovirus-insect system allows the comparative analysis between wildtype viruses enhancing locomotion (‘movers’) and single gene knock-out mutants (‘sitters’). Selected host candidate genes (those genes known to determine behaviour in other organisms) are compared for expression patterns and encoded protein activity levels between hosts infected with ‘mover’ and ‘sitter’ viruses. A strong candidate is the pkg gene, encoding cGMP-dependent protein kinase. We show data on pkg in Spodoptera exigua, and its relation to other insect pkg homologues. Additional host candidate genes will also be discussed.

Our approach yields novel and unique insights in the mechanism of parasitic host manipulation, and will contribute to a more general understanding of the regulation of (insect) behaviour.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy17-i003-E*

Symposium 17
Novel techniques in behavioural ecology

Pollutants, behaviour and climate change in a seabird of the Gulf of Mexico

Vallarino A[1], Gonzalez-Zuarth C[2], Vazquez-Botello A[3]
[1]Universidad Nacional Autonoma de Mexico, Instituto de Ciencias del Mar y Limnologia, Cd Del Carmen, Mexico, [2]Universidad Nacional Autonoma de Mexico, Cd del Carmen, Mexico, [3]Universidad Nacional Autonoma de Mexico, Mexico City, Mexico

Summary statement:

This is original research carried out by the authors.

Abstract:

The consequences of climate change in natural populations have to be widely studied. For example, its effect on the distribution of pollutants in tropical species. Several metabolic routes will be affected by climate change increasing the severity of pollutants on the organism. More affected individuals are those on the higher position of the trophic chain like seabirds. It is unknown how pollutants accumulate and affect seabirds nesting on the tropics and their effects on incubation behaviour and overall fitness. Persistent organic pollutants and heavy metals were measured in eggs and chick´s blood of two species of terns nesting in the Gulf of Mexico with very different antropogenic influence. Moreover, experimental enlarged clutches (3 eggs) of were created and incubation behaviour and nest temperature measured and compared with that from clutches of average size (2 eggs) in both species. Enlarged clutches showed lower temperatures and less nest unattendance than average size ones, suggesting that it is expensive to maintain optime temperatures in larger clutches and a hot environment is not necessarily detrimental for seabirds nesting in the tropics. However, how contaminants concentrations affect incubation behaviour different in the two species has to be tested in order to establish a direct link between contaminant concentrations and reproductive success.

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Symposium 18

Perceptual manipulation and mimicry

Talks: *Room N1*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Upper floor campus canteen *Mensa*

Invited Speakers:

Rebecca Fuller, Steve Johnson

Organizers:

Martin H Schaefer, Florian Schiestl

Description:

In the last two decades, the exploitation of innate biases has become a core model of the evolution of communication in mate choice. Exploitation relies on receiver biases arising in the sensory or perceptual system, which are widespread in communication systems. Here, we compare exploitation to mimicry in different visual and olfactory communication systems and examine the mechanisms underlying each model of signal evolution.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy18-i001-R*

Symposium 18
Perceptual manipulation and mimicry

Evolutionary evidence of sensory exploitation in the Tanganyikan cichlids

Amcoff M[1], Gonzalez Voyer A[2], Kolm N[1]
[1]Uppsala University, Department of Ecology and Genetics /Animal Ecology, Uppsala, Sweden,
[2]Doñana Biological Station (CSIC), Seville, Spain

Summary statement:

Phylogenetic evidence that the egg-spot ornament of Tanganyikan cichlids has evolved as a sensory exploitation signal that functions as an egg-mimic.

Abstract:

Sexual selection has been shown repeatedly to be an important evolutionary force driving variation in animals. Despite this, our understanding of the evolutionary origin of mate choice for sexual signals is limited. One attractive mechanism is that of sensory exploitation where males exploit pre-existing sensory biases in females. The cichlids of the great lakes of East Africa offer an interesting study system not least because they have gone through one of the most impressive adaptive radiations with hundreds of species forming in relatively recent evolutionary time.

Females of haplochromine species are often mouth brooders and the males carry bright, spot-like ornaments on the anal fin. These ornaments have been proposed to act as egg-mimics as the female is often seen to be snapping at the male anal fin while collecting the eggs for mouth brooding. The egg-spots may serve to increase male fertilization rate and have been proposed to have promoted the rapid speciation in this species group. Although it has been proposed that this ornament has evolved through sensory exploitation it has never been formally tested.

Here we constructed the, to date, largest phylogeny over the Tanganyikan cichlids containing over 160 species. We also collected detailed information from literature and photographs regarding egg spot morphology and whether the species were mouth brooding or not. We combined this information in a phylogenetic comparative analysis to investigate how egg spot morphology have evolved over the phylogeny and provide formal evidence for egg-spots having preceded the evolution of female mouthbrooding in support of sensory exploitation driving this trait.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy18-i001-E*

Symposium 18
Perceptual manipulation and mimicry

Feature saltation and the evolution of mimicry

Balogh ACV[1,2], Gamberale-Stille G[2], Tullberg BS[2], Leimar O[2,3]
[1]Environmental & Marine Biology, Åbo Akademi University, Turku, Finland, [2]Stockholm University, Department of Zoology, Stockholm, Sweden, [3]Wissenschaftskolleg zu Berlin, Berlin, Germany

Summary statement:

Based on a novel approach to predator cognition, we construct scenarios for important examples of Batesian mimicry evolution, backed up by theoretical evolutionary simulations.

Abstract:

In Batesian mimicry, harmless prey species imitate the warning colouration of unpalatable species to avoid predation. It is, however, unresolved how this adaptation originates. Using theoretical evolutionary simulations and reconstruction of examples of mimicry evolution, we show that the evolution of Batesian mimicry can be initiated by a mutation that causes prey to acquire a trait that is used by predators as a feature to categorize potential prey as unsuitable. The theory that species gain entry to mimicry through feature saltation allows us to formulate hypotheses about the sequence of events during mimicry evolution and to reconstruct an initial mimetic appearance. Our work illustrates how evolution can bring a complex phenotype across a fitness valley and to a new fitness peak.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy18-i002-R*

Symposium 18
Perceptual manipulation and mimicry

A new system to study aposematic colouration; Conspicuousness and toxicity in marine opisthobranchs

Cortesi F[1,2], Cheney KL[2]
[1]University of Basel, Zoological Institute, Basel, Switzerland, [2]The University of Queensland, School of Biological Sciences, Brisbane, Australia

Summary statement:

Aposematism, a long recognised biological phenomenon but how do aposematic species evolve and persist in an environment coined by visually hunting predators?

Abstract:

Poison-dart frogs, blue ringed octopus, and coral snakes are just a few examples of animals that use conspicuous signals to advertise their noxiousness towards predators. Although this strategy, referred to as aposematims, has been known for over a century, the evolution and persistence of aposematic species remains ambiguous. The general view is that aposematic species evolve from ancestral cryptic but already defended prey species, which increase their conspicuousness to enhance protection against predation. Theoretical and empirical studies have shown that once aposematism is established, resources can be allocated in to being either more conspicuous, more noxious, or a combination of both. Here, we investigated the evolution of conspicuous signals in the aquatic environment by determining the relationship between conspicuousness and toxicity in marine opisthobranchs. We used spectral reflectance measurements and theoretical vision models to determine the conspicuousness of colour signals displayed by opisthobranchs from the perspective of potential reef fish signal receivers. We then assessed the toxicity of chemicals extracted from each species using brine shrimp toxicity assays. A significant correlation between conspicuousness and toxicity using a phylogenetic comparative analysis was found, indicating that warning signals appear to act as an honest signal when signifying level of defence. This provides evidence that some species of opisthobranchs are aposematic. Over time, opisthobranchs appear to have allocated resources into becoming both more conspicuousness and toxic, which may suggest that both strategies are needed to protect against predation.

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WED 24 AUG at 0950 - Room N1
Oral presentation *D1-Sy18-0950-O*

Symposium 18
Perceptual manipulation and mimicry

A pre-existing bias for egg-spots in cichlid fishes

Egger B[1], Klaefiger Y[1], Theis A[1], Salzburger W[1]
[1]University of Basel, Zoological Institute, Basel, Switzerland

Summary statement:

Behavioural experiments with haplochromine cichlids uncovered a female bias for orange or red egg-like structures, suggesting that egg spots evolved through sensory exploitation.

Abstract:

Anal fin egg-spots are a key characteristic of the most species-rich group of cichlid fishes, the haplochromines. Males of about 1500 mouth-breeding species utilize conspicuous egg-spots during courtship – apparently to attract females and to maximize fertilization success. Typically, a gravid female lays a batch of eggs and immediately takes them up into her mouth; the male instantly presents his egg-spots, to which the female responds by snatching, thereby positioning the mouth close to the males' genital papilla that discharges sperm. Egg-spots are believed to mimic the eggs of a species as they resemble real eggs. We were interested whether egg-spot-evolution was triggered by a pre-existing bias for eggs or egg-like colouration. To this end, we performed mate-choice experiments in the basal haplochromine Pseudocrenilabrus multicolor, which manifests the plesiomorphic character-state of an egg-spot-less anal fin. Monitor trials indeed revealed that females prefer images of males with virtual ('in-silico') egg-spots over images showing unaltered males. In addition, we tested for colour preferences in a phylogenetically representative set of East African cichlids under laboratory conditions and in their natural environment. We uncovered a strong preference for orange to reddish spots in all haplochromines tested and, importantly, also in most other species representing more basal lines, suggesting that egg spots evolved through sensory exploitation.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy18-i003-R*

Symposium 18
Perceptual manipulation and mimicry

Mimicry and divergence by host-shift in orchids and beyond

Ellis TJ[1], Barton NH[1]
[1]IST Austria, Klosterneuburg, Austria

Summary statement:

A theoretical model is presented for speciation by host-shift in an orchid mimic incorporating sensory preference and Batesian mimicry.

Abstract:

Olfactory mimicry is often highly specific, but where related species respond to similar signals from the existing host there is the potential for mimetic divergence by host switch. Orchids of the genus Ophrys achieve pollination via Batesian mimicry of the female insect’s smell, which attracts sexually-excited males. Mimicry is highly specific to a target insect species, and so the mechanism is under strong sexual selection and may be considered a “magic trait”. Several studies have suggested that pollinator switch may be a major driver of speciation in this group. Here, we apply Lande´s framework for sexual selection to examine the factors affecting mimetic divergence in the presence of a novel host, incorporating host preferences and the dynamics of Batesian mimicry, whereby host response to a mimic depends both on its own innate preferences and on the relative abundance of models and mimics. Divergence occurs in allopatry, but divergence in sympatry was found to be unlikely owing to the paucity of extreme phenotypes. This model is applied not only to orchids, but may be extended to apply to any system where mimicry also mediates reproductive isolation.

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WED 24 AUG at 1100 - Room N1
Invited talk *D2-Sy18-1100-I*

Symposium 18
Perceptual manipulation and mimicry

Testing the sensory bias hypothesis: measuring variation in opsin expression, mating and foraging preferences, and male color patterns in a colorful killifish

Fuller RC[1]
[1]University of Illinois, Department of Animal Biology, Champaign, United States

Summary statement:

Lighting environments have complex effects on vision, preferences, and color patterns, but there are no genetic constraints among these traits.

Abstract:

The terms “sensory exploitation” and “sensory bias” are used in a variety of ways. On the one hand, sensory bias/exploitation describes a model for the evolution of female mating preferences where preferences evolve as a by-product of natural selection on non-mating behaviors mediated through the sensory system. The critical assumption is that pleiotropy creates genetic constraints between mating and non-mating behaviors that share a common sensory system. On the other hand, sensory bias/exploitation is used as a hypothesis concerning which types of secondary sex traits males should evolve. Sensory bias/exploitation predicts that males evolve traits that maximally stimulate the female sensory system. In this talk, I describe a series of experiments that address these two hypotheses in the bluefin killifish.

Bluefin killifish are small, colorful fish that occur in Florida. The salient feature of this system is that lighting environments are variable among populations which also vary in visual system properties and male coloration. I created crosses within and between a spring and a swamp population, raised the offspring under clear and tea-stained water, and measured a number of traits in the offspring (opsin expression, foraging and mating preferences, and male color pattern). While there were strong treatment effects on all traits, there was no evidence for genetic correlations indicative of pleiotropy. Hence, lighting environments are critically important in the development of (a) the visual system, (b) visually based preferences, and (c) color patterns, but the fact that these traits rely on a common sensory system does not result in genetic constraints among them.

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WED 24 AUG at 0910 - Room N1
Invited talk *D1-Sy18-0910-I*

Symposium 18
Perceptual manipulation and mimicry

The evolution of Batesian floral mimicry in food-deceptive plants

Johnson SD[1]
[1]University of KwaZulu-Natal, Biological and Conservation Sciences, Pietermaritzburg, South Africa

Summary statement:

Floral mimicry in food-deceptive plants evolves when morphotypes that match the colour and shape of rewarding models attract more pollinators. This process can drive speciation.

Abstract:

Plants that lack floral rewards may nevertheless be attractive to pollinators if their flowers resemble those of co-occurring rewarding species. Floral Batesian mimicry has evolved in several orchid lineages and is strongly associated with specialized pollination systems. Experiments show that attraction of pollinators to mimics is determined largely by the degree to which spectral properties of reflectance and transmittance of their flowers match those of the models. In well-developed mimicry systems, pollinators are unable to distinguish between flowers of mimics and their models. As a result, mimics achieve high rates of pollination when intermingled with models, and are generally ecologically dependent on them. Selection in food-deceptive plants for floral phenotypes that match those of rewarding plants results in population diversification when model phenotypes vary, and can ultimately result in speciation when mimics shift between pollinators of different models.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy18-i004-R*

Symposium 18
Perceptual manipulation and mimicry

Sex, drugs and aposematism: tritrophic interactions between anemones, beetles and birds

Keasar T[1], Shmida A[2,3], Koplovich A[1], Katzir G[1]
[1]University of Haifa - Oranim, Biology, Tivon, Israel, [2]Hebrew University, Ecology, Evolution and Behavior, Jerusalem, Israel, [3]Hebrew University, Center for Rationality, Jerusalem, Israel

Summary statement:

The combined results suggest an important role for the visual signals of the host plant in mediating the beetles' interactions with both potential mates and predators.

Abstract:

Insect herbivores can utilize signals obtained from their food plants to communicate with predators and mates. Such communication is often chemical, i.e., utilizing plant secondary metabolites. Yet, visual plant-produced cues can also advertise herbivores living on the plant. Here we test the roles of chemical and visual plant-derived signals for pollen-feeding beetles (Fam. Glaphyridae), which specialize on the red morph flowers of Anemone coronaria. The chemical communication hypothesis predicts that beetles that feed on A. coronaria would be less attractive to predators, but more attractive to mates, than beetles exposed to other food sources. The visual communication hypothesis predicts that beetles on red backgrounds would enjoy these advantages, compared with beetles on other backgrounds. We offered yellow-vented bulbuls, Pycnonotus xanthopygus, common omnivorous songbirds, dead beetles that had fed on either anemones or cat-food, and were placed on either red or green backgrounds. The birds picked up and manipulated a larger proportion of anemone-fed beetles from green backgrounds than from red ones. Latency to approaching and picking up anemone-fed beetles was shorter for green backgrounds than for red backgrounds. Latency to consuming cat-food-fed beetles was shorter than for anemone-fed beetles. The total number of beetles consumed was not affected by their diet or background color. Beetles oriented to large red displays of A. coronaria, where their prospects of finding mates are higher, and to large red plastic models. Contrary to the chemical communication hypothesis, glaphyrid females preferred cat-food-fed males to anemone-fed males in choice tests.

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WED 24 AUG at 1140 - Room N1
Oral presentation *D2-Sy18-1140-O*

Symposium 18
Perceptual manipulation and mimicry

Predator perception and the evolution of mimicry

Kikuchi DW[1], Pfennig DW[1]
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Summary statement:

Predator perceptual biases and proximate mechanisms of phenotype production impinge strongly on the evolution of mimicry. I describe experiments designed to elucidate their effect.

Abstract:

In Batesian mimicry, a harmless organism evolves to resemble a defended one and thereby co-opts protection from predators. Although this topic has long been studied, few have considered the ways that predator perception can dictate if and how mimicry evolves. However, different levels of analysis of predator behavior can impinge on predictions about the evolution of mimicry. Optimality models have successfully described some dynamics of mimicry evolution, but deviations from these models can be explained by proximate limitations in predator perception.

Mimicry has been analyzed at the ultimate level using signal detection theory (SDT). It predicts that mimicry is broadly favored over phenotypic space when models are abundant, but that only the best mimics are favored when models are rare. In a field experiment, I show that SDT accurately predicts changes in predator behavior over a natural gradient in model abundance, and that the different extremes of predator-mediated selection yield alternate scenarios for the evolution of mimicry from cryptic prey.

SDT also predicts that high costs of attacking models may allow imperfect mimics to persist once mimicry has evolved. This prediction holds for some aspects of mimetic phenotype – mimics are more variable where models are abundant, but under selection for precise resemblance where models are rare. However, I show that other dimensions of mimetic phenotype can render mimics 100% discriminable from models, yet not contribute to increased predation risk. Thus predators do not pay attention to all aspects of their prey, and a holistic understanding of mimicry must include biases in predator perception.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy18-i005-R*

Symposium 18
Perceptual manipulation and mimicry

Prey community structure affects how predators select for Müllerian mimicry

Mappes J[1], Ihalainen E[2], Rowland H[3], Ruxton G[3], Speed M[4]
[1]University of Jyväskylä, Jyväskylä, Finland, [2]Univeristy of Jyväskylä, Jyväskylä, Finland, [3]University of Glasgow, Glasgow, United Kingdom, [4]University of Liverpool, Liverpool, United Kingdom

Summary statement:

Our data provide a concrete synthesis on how community structure and predator behaviour are linked and facilitate the evolution of mimicry in concert .

Abstract:

Müllerian mimicry describes the close resemblance between aposematic prey species (defended and warning signaling), and is thought to be beneficial because sharing a warning signal decreases per capita mortality caused by sampling by inexperienced predators learning to avoid the signal. Despite being one of the celebrated examples of natural selection, the evolutionary pathways to mimicry are still unclear. It has been hypothesized that selection for mimicry is strongest in complex, multi-species prey communities where predators are more prone to misidentify the prey than in simple communities. Contrary to this expectation, we show that accurate signal mimicry is more likely to evolve in simple prey communities even though predator avoidance learning is slower in complex communities. Wild great tits (Parus major) foraged from an artificial prey community that was either simple (few prey appearances) or complex (several prey appearances) but always contained a specific model prey. Due to slower learning the model suffered higher mortality in complex communities when the birds were inexperienced. In a subsequent generalization test on potential mimics of the model prey (a continuum of signal accuracy) only birds that had foraged from simple communities selected against inaccurate mimics. Because the effective prey community where mimicry evolves consists of the predators' diet, specialist predators can create 'pockets of simplicity' and select for accurate Müllerian mimicry in the most diverse environments.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy18-i006-R*

Symposium 18
Perceptual manipulation and mimicry

Predicting and quantifying the role of sensory exploitation with more than a single receiver

Renoult JP[1], Schaefer HM[1]
[1]University of Biology I, Schaefer Lab, Freiburg, Germany

Summary statement:

We present a model that predicts and quantifies the role of sensory exploitation in signal evolution when several receivers with different perceptual abilities are involved.

Abstract:

The exploitation of receiver biases arising in the sensory system is increasingly recognized to play a major role in the evolution of many communication systems. However, current approaches used to study the role of sensory exploitation in communication do not allow to account for the complexity of communication processes occurring beyond simple, binary sender-receiver interactions. To resolve this limitation, we developed a novel framework, the stimulation landscape, which is rooted in the evolutionary concept of the adaptive landscape. The stimulation landscape is a model which merges the physical-chemical space describing signal characteristics of the sender with the perceptual spaces describing the sensory system of one or multiple animals. A growing number of studies has evidenced that increasing receiver stimulation directly translates into the fitness of the sender. A stimulation landscape has therefore the same properties as an adaptive landscape and can thus be used to predict signal evolution. Using this model, we show that a private communication channel in bird plumage limits the visual stimulation of avian predators. We further show the role of sensory exploitation in the generalists vs. specialists strategies of flowers. Specifically, we show how small changes in the coloration of specialist flowers can lead to generalists that are well perceived by pollinators with distinct sensory abilities. By analyzing trait evolution within multiple perceptual spaces simultaneously, the stimulation landscape is the first generalist model that quantifies the importance of sensory exploitation in virtually all communication systems and communities.

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WED 24 AUG at 1200 - Room N1
Oral presentation *D2-Sy18-1200-O*

Symposium 18
Perceptual manipulation and mimicry

Seeing red – exploitation of receiver biases in the facial colouration of humans

Wehrle FT[1], Schaefer HM[2]
[1]University Paris 1 Pantheon-Sorbonne, PRISM-Sorbonne - EA 4101, Paris, France, [2]University of Freiburg, Evolutionary Biology and Animal Ecology, Freiburg, Germany

Summary statement:

We present first experimental evidence that skin colouration of humans may exploit receiver biases for the colour red in the context of mating and other social interactions.

Abstract:

Catarrhine primates (old world monkeys, apes and humans) communicate intensely via colourful stimuli. Primates respond to a variety of colour stimuli that are associated with distinct food qualities during foraging. The trichromatic colour vision of catarrhines allows them to perceive red colouration, and red stimuli are assumed to be very effective in capturing the attention of catarrhines. It is a long-standing hypothesis that individuals may exploit the receiver bias of an innate attraction to reddish colours in the mating context through pelage and skin colouration. This hypothesis is difficult to experimentally disentangle from the hypothesis that red colour signals evolved because skin colouration indicates the hormonal status of individuals. To this end, we presented colour stimuli on computer screens to humans. We first experimentally assessed their colour preferences for social, sexual, and food-related stimuli. Second, we tested the prediction unique to the exploitation hypothesis that colour stimuli from one context (e.g., fruit colour related to food intake) can influence the reactions of humans to colour stimuli in a distinct context (e.g., skin colouration). Indeed, when previously viewing a red apple, males and females prefer more reddish skin compared to viewing a green apple. Based on our results we discuss the applicability of the receiver bias model to the evolution of human skin colour signals as well as its limitations.

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WED 24 AUG at 1010 - Room N1
Oral presentation *D1-Sy18-1010-O*

Symposium 18
Perceptual manipulation and mimicry

The mating habits of Australian sexually-deceptive orchids

Whitehead MR[1], Peakall R[1]
[1]The Australian National University, Research School of Biology, Canberra, Australia

Summary statement:

First mating system analysis for sexually-deceptive orchids finds multiple paternity and extreme outcrossing despite self-compatibility and clonality.

Abstract:

The terrestrial orchid genus Chiloglottis secures pollination by sexual deception whereby male wasps are attracted to the plant by mimicry of specific sexual signals. Remarkably, sexual deception has evolved independently on at least four continents, with a wide range of insects known to be exploited. The “outcrossing hypothesis” posits that by hijacking the sexual behaviour of their pollinator, sexually-deceptive orchids ensure their pollen is transported far enough away from the parent plant to promote outcrossing. Furthermore, divergent floral volatile chemistry linked to different pollinator species´ sex pheromones is predicted to act as a strong pre-zygotic reproductive barrier, thereby limiting hybridization in sympatric species.

Investigating pollen mediated gene flow within and between taxa is the aim of mating system analysis, yet these studies are rare for orchid species. This is because of the unique challenges posed by miniscule orchid seed which requires infection by a specific mychorrizal partner for germination. This study addresses these challenges through symbiotic germination of orchid seed collected from naturally pollinated orchids. Outcrossing measures are obtained by microsatellite genotyping of orchid offspring and show that Chiloglottis orchids occupy an extreme position on the spectrum of plant outcrossing rates. Along with data from pollinator field experiments and the partitioning of neutral genetic variation, the results indicate that sexual deception is finely adapted to maximise outcrossing despite clonality and that divergent floral odour is capable of maintaining strict pre-zygotic reproductive isolation in sympatric taxa.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy18-i002-E*

Symposium 18
Perceptual manipulation and mimicry

The way in is the way out – alternative intrusion strategies affect an arms race

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Summary statement:

Alternative intrusion strategies and their impact on the adjustment of the cuticular chemistry of brood parasites to their hosts’ profile

Abstract:

Brood parasites invade their host’s nest to oviposit whereby their brood is reared by the host. The host’s brood is killed or impaired by loss of provisioned resources. Parasite and host have conflicting interests to either successfully parasitise a nest or to detect the parasite. This situation sets the board for an evolutionary arms race between both parties. The parasites need to avoid detection by the host in order to neither be attacked while in the nest nor risk the nest to be abandoned by the host afterwards. While visual recognition can be avoided by entering in the host’s absence, detection of a past intrusion (e.g. in insects, chemical cues from cuticular hydrocarbons (CHC) adsorbed to nest material) may be harder to avert. Avoidance of olfactory detection could be achieved by mimicking the host’s CHC profile or by an alternative intrusion strategy. In this study, a solitary Vespid host and its specific Chrysidid parasitoids serve as a model to evaluate a possible scenario of the evolution of chemical mimicry. We compare the CHC profiles and predict that a parasitoid whose intrusion is detectable by the host should develop chemical mimicry (i.e. should resemble the host’s CHC) while a parasitoid that can avoid detection by developing a new intrusion strategy does not participate in this coevolutionary arms race and may display a more distinct CHC pattern. The comparison of two populations of hosts and parasites reveals a strong effect on the CHC profile of both the host and the parasite.

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Symposium 19

Evolution of chirality

Talks: *Room N9*

Regular posters*:* Upper floor campus canteen *Mensa*

Invited Speakers:

Spencer Barrett, Rich Palmer

Organizers:

Menno Schilthuizen, Barbara Gravendeel

Description:

Asymmetric shapes in animals and plants can come in two mirror-image forms. However, such chiral dimorphism is found in some structures but not in others. This makes chirality one of the very few developmental traits that can be studied consistently across all multicellular organisms, offering a goldmine of research questions in evo-devo, evolutionary ecology, and macro-evolution.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

MON 22 AUG at 1550 - Room N9
Invited talk *B4-Sy19-1550-I*

Symposium 19
Evolution of chirality

What we know and don’t know about mirror-image flowers

Barrett SC[1]
[1]Toronto, Ecology and Evolutionary Biology, Toronto, Canada

Summary statement:

Mirror-image flowers promote cross-pollination in bee-pollinated plants. Their occurrence in two distinct forms raises intriguing questions about their evolutionary origins.

Abstract:

Although mirror-image flowers (enantiostyly) have been recognized for over a century, their biology has been investigated only recently and our understanding of their origins and adaptive significance are rudimentary. The condition is a form of directional asymmetry in which the style (female sex organ) is deflected away from the main axis of the flower to either the right or left side. Enantiostyly is commonly associated with bee-pollinated, non-tubular, heterantherous, nectarless flowers and is reported from at least 10 angiosperm families. Unlike other stylar polymorphisms in plants, it comes in several forms complicating functional interpretation. The commonest involves plants with both right- and left-styled flowers (monomorphic enantiostyly); more rarely populations are polymorphic for right- and left-styled plants (dimorphic enantiostyly). Genetic analysis and studies of morph frequencies in polymorphic populations indicate that dimorphic enantiostyly is governed by a single diallelic locus with dominance. Experimental studies using genetic markers have provided evidence that enantiostyly functions to increase the precision of bee-mediated cross-pollination and reduce sexual interference resulting from self-pollination, both within and between flowers on a plant. These functional benefits are more evident for dimorphic than monomorphic enantiostyly because of the segregation of alternate floral forms on different plants. Yet the latter condition is much more common suggesting that there are strong constraints on the origin of dimorphic from monomorphic enantiostyly. Some suggestions are made on what these constraints may be.

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MON 22 AUG at 1710 - Room N9
Oral presentation *B4-Sy19-1710-O*

Symposium 19
Evolution of chirality

Evolution and development of orchid flower chirality

Gravendeel B[1], Davin N[1], Klinge R[2], van Vugt R[3], Welch C[4], Palmer R[5]
[1]NHN Leiden University, NCB Naturalis, Leiden, Netherlands, [2]Klinge Orchideeën, Nederhorst den Berg, Netherlands, [3]Leiden University, Hortus Botanicus, Leiden, Netherlands, [4]Merck and Co. Inc., Rahway, United States, [5]Alberta University, Biological Sciences, Alberta, Canada

Summary statement:

Slipper orchid flowers are chiral when both inner tepals coil to the same side. Slipper orchids do not offer rewards. Chirality might play a role in pollinator deception.

Abstract:

Although some drivers for the evolution of plant chirality were recently discovered, nothing is known yet about chiral orchid flowers. In slipper orchids, the two inner tepals of a single flower either coil both to the left, both to the right, one to the left and one to the right or not at all. The first two cases make the flower chiral (non-superimposable onto its mirror image). Morph mapping suggests tepal chirality is phylogenetically conserved which suggests selection. Time lapse studies revealed that chirality develops at very late stages of development. PIN-gene knockouts of Arabidopsis thaliana show altered floral chirality. PIN- and other candidates retrieved from the genome of the emergent orchid model Erycina pusilla currently serve as a basis for gene expression and functional studies. The possible rol of tepal chirality in pollinator deception is studied in behavioural experiments. Slipper orchids do not offer rewards. Pollinators learn less quickly to avoid deceptive flowers when these show high intraspecific variation. Choice experiments are set up using Y-mazes to test the importance of chirality in pollinator attraction by deceptive orchids.

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MON 22 AUG at 1650 - Room N9
Oral presentation *B4-Sy19-1650-O*

Symposium 19
Evolution of chirality

A speciation gene for left-right reversal in snails results in anti-predator adaptation

Hoso M[1], Kameda Y[2], Wu S-P[3]
[1]Tohoku University, Sendai, Japan, [2]Kyoto University, Kyoto, Japan, [3]Taipei Municipal University of Education, Taipei, Taiwan, Republic of China

Summary statement:

Snake specialization for the predation of commoner dextral snails drives the speciation of sinistral snails by offsetting the mating disadvantage of left-right reversal.

Abstract:

How speciation genes can spread in a population is poorly understood. In land snails, a single gene for left–right reversal could be responsible for instant speciation, because dextral and sinistral snails have difficulty in mating. However, the traditional two-locus speciation model predicts that a mating disadvantage for the reversal should counteract this speciation. In this study, we show that specialized snake predation of the dextral majority drives prey speciation by reversal. Our experiments demonstrate that sinistral Satsuma snails (Stylommatophora: Camaenidae) survive predation by Pareas iwasakii (Colubroidea: Pareatidae). Worldwide biogeography reveals that stylommatophoran snail speciation by reversal has been accelerated in the range of pareatid snakes, especially in snails that gain stronger anti-snake defense and reproductive isolation from dextrals by sinistrality. Molecular phylogeny of Satsuma snails further provides intriguing evidence of repetitive speciation under snake predation. Our study demonstrates that a speciation gene can be fixed in populations by positive pleiotropic effects on survival.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy19-i001-R*

Symposium 19
Evolution of chirality

Possible functions of Dpp in gastropod shell formation and shell coiling

Keisuke S[1], Isao S[2], Hiroyuki K[3], Kazuyoshi E[2]
[1]University of Tsukuba, Master's Program in Science Education, Tsukuba, Japan, [2]The University of Tokyo, Department of Earth & Planetary Science, Hongo, Japan, [3]The University of Tokyo, Geochemical Research Center, Hongo, Japan

Summary statement:

Dpp gene shows asymmetric expression in the shell gland and in the mantle tissues. Treatment of later embryos with a Dpp inhibitor results in uncoiling of otherwise coiled shell.

Abstract:

Shell is one of the features of molluscs and has become greatly diversified in morphology. However, the molecular mechanism of shell formation has not been revealed yet. We examined dpp expression patterns in the pulmonate snail Lymnaea stagnalis, and analyzed the functions of dpp using the Dpp signal inhibitor dorsomorphin in order to understand developmental mechanisms and evolution of shell formation in gastropods. The dpp gene is expressed in the right half of the circular area around the shell gland at the trochophore stage and at the right-hand side of the mantle at the veliger stage in the dextral snails. Two types of shell malformations were observed when the Dpp signals were inhibited by dorsomorphin. When the embryos were treated with dorsomorphin at the 2-cell and blastula stages before the shell gland is formed, the juvenile shells grew imperfectly and were not mineralized. On the other hand, when treated at the trochophore and veliger stage after the shell gland formation, juvenile shells grew to show a cone-like form rather than a normal coiled form. These results indicated that dpp plays important roles in the formation and coiling of the shell in this gastropod species.

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MON 22 AUG at 1630 - Room N9
Oral presentation *B4-Sy19-1630-O*

Symposium 19
Evolution of chirality

Ditectional asymmetry: A ubiquitous feature of bilaterian animals?

Klingenberg C[1]
[1]University of Manchester, Faculty of Life Sciences, Machester, United Kingdom

Summary statement:

Directional asymmetry is widely found in the shapes of external structures in many phyla and may result from regulatory "leakage" from setting up the chirality of internal organs.

Abstract:

Since studies of morphological asymmetry started using the methods of geometric morphometrics in the 1990s, directional asymmetry has been found in almost all studies that used sufficient sample sizes and accurate measurement methods. It therefore appears that directional asymmetry is almost ubiquitous across phyla and even in structures that are expected to be under selection for precise symmetry, such as wings.

I present an overview of several quantitative genetic analyses of the asymmetry of shape in insects and mammals. It appears that genetic variation for directional asymmetry is widely present, although it is subtle, so that directional asymmetry has a clear evolutionary potential and should respond to selection if it is sufficiently strong. In particular, selection against directional asymmetry ought to be able to eliminate it.

Comparisons of directional asymmetry among related species show that it does evolve, but there are consistent features of directional asymmetry that are shared among species. Accordingly, it appears to be a feature that is conserved to some extent.

As a possible explanation for the presence of apparently maladaptive directional asymmetry of external features, I hypothesize that it might result from regulatory "leakage" from developmental signalling systems that are involved both in setting up the chirality of internal organs and in the development of external structure.

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MON 22 AUG at 1610 - Room N9
Invited talk *B4-Sy19-1610-I*

Symposium 19
Evolution of chirality

Genes as leaders or followers in evolution: Evidence from animal asymmetries (with a digression on the enigma of gastropod coiling direction)

Palmer AR[1]
[1]University of Alberta, Biological Sciences, Edmonton, Canada

Summary statement:

Surveys of animal asymmetries shed light on the prevalence of genes as leaders or followers in evolution and help explain a major chirality enigma: predominance of dextral snails

Abstract:

Natural selection eliminates variation from populations, generation after generation. So where does the new variation come from? Are mutation and recombination the primary sources of new variation (genes as leaders) or does the remarkable capacity of organisms to produce new forms as developmentally plastic responses to new environments -- at least initially -- also contribute (genes as followers)? A wide-ranging survey of asymmetry variation within and among species of animals and plants offers some of the strongest evidence to date that a ´genes as followers´ mode of evolution may be much more common than previously thought. A more detailed survey of asymmetry variation in gastropods reveals some valuable clues about a persistent enigma in studies of animal chirality: why are gastropods so overwhelmingly dextral? It also reveals a surprising example where an evolutionary loss of genetic determination of a trait (direction of shell coiling) yields increased phenotypic variation.

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MON 22 AUG at 1720 - Room N9
Oral presentation *B4-Sy19-1720-O*

Symposium 19
Evolution of chirality

The evolution of balanced chiral dimorphism in Amphidromus snails

Schilthuizen M[1,2], Haase M[3], Nakadera Y[4], Hendrikse S[1,4], Koene J[1,4]
[1]Netherlands Centre for Biodiversity 'Naturalis', Terrestrial Zoology Dept., Leiden, Netherlands, [2]Leiden University, IBL, Leiden, Netherlands, [3]University of Greifswald, Greifswald, Germany, [4]VU University, Amsterdam, Netherlands

Summary statement:

New data on the impact of chiral dimorphism on development, reproduction, and ecology of the chirally dimorphic snail species Amphidromus inversus

Abstract:

Chirality (the non-superimposability of asymmetric, three-dimensional mirror-image forms) is a widespread phenomenon in nature and one of the few developmental traits that can be studied in a meaningfully comparative fashion across almost all organisms. Gastropods are among the animal groups in which chirality is most obviously displayed by the existence of clockwise- and anticlockwise-coiled snails.

In most snail species, asymmetry is directional: direction of coiling is genetically determined and only one chiral form is found in a species, with directionality maintained by strong frequency dependent selection against reversals. There are a few groups of snails, however, most notably the Asian subgenus Amphidromus, in which chiral dimorphism exists with often equal proportions of dextrals and sinistrals within a population. We study the Malaysian species A. inversus to elucidate the evolutionary processes involved in the maintenance of chiral dimorphism. We report new data on the impact of chirality on ontogeny, sperm morphology, and ecology.

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Symposium 20

Chemical communication

Talks: *Room N1*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Upper floor campus canteen *Mensa*

Invited Speakers:

Mark Blows, Jane Hurst

Organizers:

Ally Harari, Tamar Keasar

Description:

Sex pheromones may have evolved under natural selection, as a means of species recognition, and/or by sexual selection, allowing mate choice. Natural selection is expected to be stabilizing, favoring low variation in pheromone characteristics. Sexual selection may result in variance in pheromone traits, and in costly signal production. These seemingly contrasting predictions will be discussed.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

Ground floor lecture hall centre *HZ*
Essence poster *E-Sy20-i001-E*

Symposium 20
Chemical communication

Evolution of male sex pheromone and diversification of the butterfly genus Bicyclus

Bacquet P[1], Brattström O[2], Wang H-L[3], Löfstedt C[3], Brakefield PM[2], Nieberding C[4]
[1]Université catholique de Louvain, ELIB - Evolutionary Ecology and Genetics, Louvain-la-Neuve, Belgium, [2]Cambridge University, University Museum of Zoology, Department of Zoology, Cambridge, United Kingdom, [3]Lund University, Chemical Ecology and Ecotoxicology, Department of Ecology, Lund, Sweden, [4]Université Catholique de Louvain, ELIB - Evolutionary Ecology and Genetics, Louvain-la-Neuve, Belgium

Summary statement:

We use the comparative method to understand if sexual selection on the male sex pheromones in the Bicyclus genus could have been a diversifying factor.

Abstract:

The importance of olfactory communication in generating reproductive isolation remains poorly understood. The pioneering work of M. R. E. Symonds and collaborators on Ips (Coleoptera), Drosophila and Bactrocera (Diptera) revealed that a saltational or gradual mode of evolution (by large or slight modifications) of chemical signals was consistent with their behavioural role, for example to avoid closely related species.

In the species-rich genus Bicyclus Kirby, 1871 (Nymphalidae) the male wing structures producing MSP, the androconia, are key characters to discriminate among species. Moreover, the MSP of the model species B. anynana (Butler, 1879), was shown to play a role in mate choice and to be under sexual selection. Therefore, we expect that reproductive isolation between species was achieved through pheromone evolution under sexual selection in this butterfly group.

Potential MSP of 33 Bicyclus species sampled in Western and Eastern Africa (Cameroon, Liberia, Nigeria and Uganda) were analysed in regards to their sympatric or allopatric distribution ranges and to their phylogenetic relatedness. If this trait is actually under sexual selection across the genus, we expect the rapid shifts of female preference to induce a pattern of saltational evolution and potentially a loss of phylogenetic signal. Additionally, in case the changes in pheromone composition participated to reproductive isolation in a reinforcement process, we expect larger differences in pheromone composition between sympatric than allopatric species, and that this pattern inflates for younger compared to older pairs of species.

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MON 22 AUG at 1400 - Room N1
Invited talk *B3-Sy20-1400-I*

Symposium 20
Chemical communication

Selection and the evolution of genetic variance in the Drosophila serrata chemical communication system.

Blows M[1]
[1]University of Queensland, Brisbane, Australia

Summary statement:

Pleiotropy between sexually selected traits, and other traits under natural selection, plays a vital role in the maintenance of genetic variance in chemical communication.

Abstract:

Determining how the genetic variance evolves under selection in the presence of widespread pleiotropy is a fundamental issue that is ultimately related to the question of how genetic variance is maintained in populations. The study of sexually-selected traits is particularly useful here as male sexually-selected traits are often relatively easy to identify and selection generated by mate choice can be readily quantified. At the same time, sexually-selected traits are often postulated to be subject to natural selection, either through pleiotropic associations with condition and other fitness components, or as a consequence of selection on mate recognition generated by the presence of other species. In a series of experiments using the chemical communication system of D. serrata as a model, we have investigated the relationship between selection and genetic variance in a multivariate set of contact pheromones. While directional sexual selection is associated with very low levels of genetic variance in natural populations of this species, the genetic variance in these traits can rapidly evolve, increasing dramatically as males are selected for higher attractiveness. However, it is the pleiotropic associations between the sexually-selected traits and other (unmeasured) traits under natural selection that have been revealed to play the key role in limiting the response to sexual selection, and the maintenance of multivariate genetic variance in traits under sexual selection.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy20-i001-R*

Symposium 20
Chemical communication

Diversity of androconial structures in Bicyclus butterflies and their role in pheromone communication

Brattstrom O[1], Bacquet P[2], Wang H-L[3], Brakefield PM[1], Löfstedt C[3], Nieberding CM[2]
[1]University Museum of Zoology, Department of Zoology, Cambridge, United Kingdom, [2]Université Catholique de Louvain, Biodiversity Research Centre, Louvain-la-Neuve, Belgium, [3]Lund University, Department of Ecology, Lund, Sweden

Summary statement:

The diverse androconial structures of Bicyclus butterflies were analysed within a phylogentic context and their role in pheromone communication studied in a comparative way.

Abstract:

Males of many butterfly species have androconias; clearly defined and often complex secondary sexual characters consisting of dense hair bushes and patches of scales different to the normal wing scales. Being conspicuous and showing limited variation between conspecifics these structures are of major importance in taxonomy. Traditionally androconias have been considered producers of male sex pheromones, often referred to as scent scales, but empirical tests of this claim are remarkably few.

The butterflies of the genus Bicyclus (Nymphalidae) display an extraordinary diversity of androconias. Behavioural experiments using the model species B. anynana suggested that androconias per se were not necessary for mating success as long as the pheromone compounds were still present. This study suggested that they have no, or a very limited, role outside chemical communication between the sexes.

Given the high diversity of wing surface based androconias within the genus, and B. anynana being the subject of much previous research, they provide a suitable model system for comparative studies. We analysed the position and structure of androconias in a phylogenetic context across several species groups of Bicyclus, and also investigated male specific chemical compounds in relation to the androconias. It is remarkable that many androconias were found to be producing no such chemicals suggesting they have other functions, perhaps including being involved in visual signalling during courtship or acting as pheromone dispersers. Since the structures are highly elaborate and conserved within each species, it is unlikely they that they have lost their function but still remain intact.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy20-i002-R*

Symposium 20
Chemical communication

The smell is not enough: Complex cues for plastic male mating strategies.

Bretman A[1], Westmancoat J[1], Gage MJ[1], Chapman T[1]
[1]University of East Anglia, School of Biological Sciences, Norwich, United Kingdom

Summary statement:

Chemical communication is part of the system by which males assess rivals, but is not used in isolation, highlighting the importance of investigating multiple signals concurrently.

Abstract:

Within sexual selection, pheromones can be involved in female choice and male-male competition, with potentially differing selection pressures on the same compounds. We have investigated the cues males use to assess the presence of rivals and mount a behavioural response to competition in the fruit fly Drosophila melanogaster. We find that chemical communication is important, but not in isolation: males require a combination of sound, smell and touch cues from rivals, but any combination of two of these three signals. This suggests that making an inappropriate response is extremely costly to males. One possibility for the evolution of this complex system is that different components signal different aspects of such as sex, species or the persistence of competition. What is clear is that chemical communication is involved in both male-female and male-male interactions, and that different forms of communication should not be considered in isolation.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy20-i003-R*

Symposium 20
Chemical communication

Dissecting behavioral isolation in nature: Evolution of mate choice in the closely related species Drosophila subquinaria and D. recens

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Summary statement:

Male cuticular hydrocarbons are important signals that females use to choose among conspecific mates and to discriminate against males of the opposite species.

Abstract:

The divergence among populations in male signal traits and female preferences may be an important source of behavioral isolation during the speciation process. Here we investigate the traits involved during mate choice within, and behavioral isolation between, the closely related species D. subquinaria and D. recens. In sympatric populations, D. subquinaria females discriminate strongly against both D. recens males as well as allopatric conspecific D. subquinaria males, consistent with a pattern of reinforcing selection to avoid mating with D. recens. Our long-term goal is to understand the mechanism(s) by which the male signal traits and female preferences diverge in nature to cause these changes in mate discrimination and ultimately reproductive isolation. To this end, we will present evidence that chemical forms of communication, namely male contact pheromones that consist of cuticular hydrocarbons (CHCs), are an important form of communication in these species, and likely form the basis upon which females choose among conspecific mates and discriminate against males of the opposite species. We will present the results of

1) manipulative experiments that infer which sensory modalities are most important during mate choice for males and females of each species,
2) mate choice experiments that specifically examine the importance of male CHCs in female preference within each species, and
3) a geographic survey across allopatric and sympatric populations of each species to investigate whether CHCs themselves show a pattern of reproductive character displacement, as would be expected if this trait is the target trait of reinforcing selection.

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MON 22 AUG at 1650 - Room N1
Oral presentation *B4-Sy20-1650-O*

Symposium 20
Chemical communication

Context-dependent communication in a non-social insect

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[1]University of Amsterdam, IBED - Population Biology, Amsterdam, Netherlands

Summary statement:

Pheromones are typically assumed to convey context-independent information, but we show that thrips larvae vary their alarm pheromone composition in response to various predators.

Abstract:

Communication is the basis of social interactions. It involves sending and receiving signals and a decision of the receiver as to which action to undertake. Signals may be sent in a fixed form (e.g. sex-pheromones) or in a form that varies in relation to the context (e.g. signals conveying information on the quality of a food source). Because danger may come from a variety of sources and these sources vary in the risk they impose, it is hypothesized that alarm signals are context-dependent. Indeed, the literature on vocal alarm in vertebrates lends support for this hypothesis, but the literature on chemical alarm signals, largely pertaining to invertebrates, lacks a critical test and seems to suggest that alarm pheromones do not vary within species. We have tested for context-dependence of an alarm pheromone of the Western Flower Thrips, Frankliniella occidentalis. In the presence of danger, thrips larvae excrete anal droplets containing an alarm pheromone that consists of decyl acetate and dodecyl acetate. Our experiments provide evidence that signal-sending thrips larvae modify the ratio of these two alarm chemicals depending on whether they face the risk of being eaten by a predatory mite (low risk) or by a predatory bug (high risk) and that the alarm pheromone induces a response in the signal-receiving thrips larvae that depends on the context perceived by the sender. In future tests we hope to assess whether thrips larvae communicate the nature of danger to kin and non-kin larvae.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy20-i004-R*

Symposium 20
Chemical communication

Always trust the queen: Costs and constraints conspire to produce honest signalling

Holman L[1]
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Summary statement:

I will present a simple model and some experiments with ant queen pheromones, illustrating the dual role of costs and constraints in honest signalling.

Abstract:

The handicap principle is the most well-known mechanism enforcing honest signalling, but some honest signals have little or no obvious cost. The index hypothesis proposes that some signals are cost-free but are constrained to be honest by unevolvable, causative relationships with the trait being advertised. Researchers have tried to classify signals as either handicaps or indices based on their apparent costs and constraints, although many signals have characteristics of both types. I will present a simple model that illustrates how costs and constraints work together to produce honest signalling, and explains why some signals are costly and others are cheap. I illustrate the new conceptual framework with an experimental study on the only known ant queen pheromone, which keeps workers sterile and honestly signals the queen's fertility. The data suggest that both costs and constraints keep the queen's signal honest. Pheromone production has endocrine-mediated costs, but the nature and severity of these costs is shaped by constraints such as resource trade-offs and antagonistic pleiotropy.

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MON 22 AUG at 1440 - Room N1
Invited talk ***B3-Sy20-1440-I***

Symposium 20
Chemical communication

Scent signals underlying female mate choice in rodents

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Summary statement:

Scent signals play an integral role in mediating reproductive interactions, allowing animals to locate individuals of the opposite sex and to assess their attractiveness as mates.

Abstract:

Scents play an integral role in mediating reproductive interactions in many species, allowing animals to recognize and locate individual conspecifics of the opposite sex and to assess the attractiveness of potential mates. Most rodents communicate through numerous urinary scent marks that contain species, sex and individual-specific volatile odorants together with a high concentration of lipocalin proteins that are detected on contact with scent. By far the best-studied urinary lipocalins are the major urinary proteins (MUPs) of the house mouse (Mus musculus domesticus), encoded by a gene cluster that has undergone recent rapid expansion in this species. Highly polymorphic MUP patterns provide an individual genetic identity signature that is used by females to recognize and assess individual males from their competitive territorial scent marks. MUP type is also used to recognize and avoid inbreeding with close kin, and to assess male genetic heterozygosity. An atypical male-specific MUP named darcin acts as a sex pheromone, eliciting the innate sexual attraction of females to male urine scent. Contact with darcin stimulates strong and rapid associative learning of volatiles in an individual male's scent, such that subsequently females are attracted to the airborne urinary odor of that particular male but not to airborne odours of other males. The airborne odour that females learn is determined by volatiles that bind to the individual-specific pattern of MUPs expressed in a male's urine and are slowly released from scent marks. Thus, darcin combined with an individual scent signature allows female sexual attraction to be innate but also selective towards individual males.

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MON 22 AUG at 1550 - Room N1
Oral presentation *B4-Sy20-1550-O*

Symposium 20
Chemical communication

Extensive and variable positive selection in the vomeronasal-1 receptor (V1R) gene repertoire of mouse lemurs (Microcebus)

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[1]University of Veterinary Medicine Hannover, Institute of Zoology, Hannover, Germany, [2]University of Cambridge, Department of Zoology, Cambridge, United Kingdom

Summary statement:

V1R diversity in mouse lemurs reflects their adaptive evolution and is likely related to the importance of olfactory communication in these primates.

Abstract:

Most mammals possess a vomeronasal organ which is specialized for pheromone detection. However, data on the possible evolutionary role of pheromones in primates are limited. Mouse lemurs (Microcebus) are small nocturnal strepsirrhines and an ideal model system to study pheromonal communication in primates. They heavily rely on pheromonal communication and possess a huge repertoire (~200) of class 1 vomeronasal receptors (V1Rs). Here we investigated patterns of positive selection among the identified V1R loci in the gray mouse lemur as well as individual V1R loci across multiple mouse lemur species. From phylogenetic reconstructions of published sequences we identified ~9 major clusters of V1Rs in mouse lemurs. Selection analysis using PAML showed that the majority of clusters evolved under significant positive selection. Interestingly, most codons identified as being under positive selection are located in the extracellular domains of the receptors and hence may be involved in pheromone binding. Positive selection is also detected in single V1R loci sequenced from a range of mouse lemur species, indicating ongoing selection within the genus, which is potentially related to sexual selection. The diversity of V1R loci in mouse lemurs reflects their adaptive evolution and is likely related to the importance of olfactory communication in these primates.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy20-i005-R*

Symposium 20
Chemical communication

Behavioural and genetic aspects of peptide courtship pheromone differentiation in hybridization between two Lissotriton newts species

Osikowski A[1], Babik W[2], Stuglik M[2], Szymura JM[1]
[1]Jagiellonian University, Department of Comparative Anatomy, Institute of Zoology, Kraków, Poland,
[2]Jagiellonian University, Institute of Environmental Sciences, Kraków, Poland

Summary statement:

Asymmetric female preferences for pheromone producing glands extracts and characterization of the pheromone encoding gene family in Lissotriton vulgaris and L. montandoni.

Abstract:

Sexual signals play a crucial role in the emergence of prezygotic reproductive barriers which may further lead to speciation. Proteinaceous pheromones are amongst the most important stimuli in the tailed amphibians acting during their complex and prolonged courtship. In salamandrids courtship pheromones influence species recognition in closely related species. The smooth (Lissotriton vulgaris) and the Montandon's (L. montandoni) newts (Salamandridae) are two morphologically and ecologically distinct species which hybridize in nature producing viable offspring. There is substantial prezygotic isolation between these species. Comparative studies involving morphological, genetic and ecological data suggest that sexual behaviour may be the major force limiting gene flow. Our laboratory experiment showed that females of the Montandon's newt prefer the pheromone producing glands extracts of their own males whereas the females of the smooth newt did not exhibit such preference. This supports previous observations suggesting that reproductive isolation between this species pair is asymmetric. To indentify olfactory cues involved in mate preferences we analysed the transcriptomes of male pheromone producing glands of the smooth and the Montandon's newt using next generation sequencing techniques. The peptide pheromones are encoded by a large gene family composed of both nearly similar and highly divergent genes. Phylogenetic analysis of the gene family showed that the newt species does not form distinct clades. This result indicates that the smooth and the Montandon's newts have not diverged in isolation.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy20-i006-R*

Symposium 20
Chemical communication

Odour maps in the brain of butterflies with divergent host-plant preferences

Schäpers A[1], Carlsson MA[1], Bisch-Knaden S[2], Mozuraitis R[3], Hansson BS[2], Janz N[1]
[1]Stockholm University, Department of Zoology, Stockholm, Sweden, [2]Max Planck Institute for Chemical Ecology, Department of Evolutionary Neuroethology, Jena, Germany, [3]The Royal Institute of Technology, Department of Organic Chemistry, Stockholm, Sweden

Summary statement:

Odour-evoked activity in the antennal lobes of nymphalid butterflies is species-specific and can be related to host-plant preferences.

Abstract:

Butterflies are generally considered to be mainly visual animals. However, their olfactory system is well developed and morphologically similar to moths. Host plant range is highly variable within the butterfly family Nymphalidae, with extreme specialists and wide generalists found even among closely related species. Here we measured odour evoked Ca2+ activity in the antennal lobes of two nymphalid species, Aglais urticae and Polygonia c-album, with diverging host plant preferences. The butterflies responded with stimulus specific combinations of activated glomeruli. We also found that both species responded to a number of extracts of host and non-host plants. In general, responses were similar across the species but we also found differences that may to some extent explain their respective host plant range. The more specialised of the species, A. urticae, responded more specifically to its preferred host plant. We also found a difference in sensitivity to two common green leaf volatiles.

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MON 22 AUG at 1610 - Room N1
Oral presentation *B4-Sy20-1610-O*

Symposium 20
Chemical communication

Impacts of endosymbiotic Wolbachia on chemical communication in Drosophila paulistorum

Schneider D[1], Ehrman L[2], Daeuble W[1], Kubiak M[2], Chao T[2], Miller WJ[1]
[1]Medical University of VIenna, Cell and Developmental Biology, Vienna, Austria, [2]State University of New York, Division of Natural and Social Sciences, Purchase, United States

Summary statement:

Wolbachia of D. paulistorum can modulate pheromone patterns adaptively and so they have the potential to contribute to host speciation by mediating impacts on mate recognition.

Abstract:

Mate recognition, a pivotal mechanism in sexual isolation, is an essential parameter in speciation. In Drosophila, some cuticular hydrocarbons (CHCs) are sex pheromones, playing a crucial role in conspecific communication. CHC composition, i.e., the pheromonal profile of an individual is characteristic and it has recently been proposed that quantitative alterations in these profiles contribute significantly to sexual isolation in Drosophila and Lepidoptera.
All members of the neotropical D. paulistorum, a natural speciating system complex in statu nascendi, are infected with maternally inherited endoymbiotic bacteria, Wolbachia. Obligate mutualistic Wolbachia of D. paulistorum manipulate sexual behavior by influencing mate choice. In this model system, we have analyzed, via gas chromatography/mass spectrometry, CHC profiles of all six semispecies, which differ significantly in compound quantities but not in composition. In a pilot proportion screen, we have evaluated potential influences of Wolbachia on pheromonal signatures. Preliminary results show massive changes in CHC profiles between naturally Wolbachia-infected and artificially-depleted flies, suggesting strong influences exerted by this bacteria on D. paulistorum CHC signatures. Studies in D. melanogaster and related sibling species have indicated that desaturase genes are essential for sex pheromone production, and that they are the most rapidly evolving genes. Hence, we have determined the divergence of desat genes among the D. paulistorum semispecies of plus their expression levels in naturally-infected and artificially-depleted flies since Wolbachia might manipulate expression of desat genes.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy20-i002-E*

Symposium 20
Chemical communication

Variation in sex pheromone receptor genes affects male mating behaviour – a possible driver of speciation in moths?

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[1]School of Biological Sciences, University of Auckland, Auckland, New Zealand, [2]The New Zealand Institute of Plant & Food Research Limited, Auckland, New Zealand, [3]The Allan Wilson Centre for Molecular Ecology and Evolution, Auckland, New Zealand

Summary statement:

In this study I will evaluate how evolution at the mol. level facilitates the rapid evolution of sex pheromone systems at the species level in New Zealand native leafroller moths.

Abstract:

The major feature of mate recognition in moths is the ability of the male to recognise the female's sex pheromones. As evolution of new species requires changes in both female sex pheromone composition and male pheromone reception systems, the exact mechanism of speciation is still unclear. Although considerable information is known concerning sex pheromones and how they are produced by female moths, the male's ability to recognise new compositions of the female's sex pheromone blends remains a mystery in many species, especially on the molecular level. The major hypothesis that addresses how males evolve to recognise novel female-produced pheromone blends is the 'asymmetric tracking hypothesis', but there is no hypothesis that explains changes on the molecular level. In this study I will focus my PhD research on sibling species pairs within the New Zealand endemic leafroller genera Ctenopseustis and Planotortrix to evaluate how evolution at the molecular level facilitates rapid evolution of olfactory systems at the species level. For this I will isolate pheromone receptor genes and will investigate sequence and expression differences between the species. The functional characterisation of receptors will be tested by standard cell-based assays. Co-segregation analysis between behaviour toward different pheromone blends and genetic variation within pheromone receptor genes will be used to determine whether differences in male response to pheromones are encoded by pheromone receptor genes. After evaluating associations between molecular differences in pheromone receptors and the behavioural phenotype, tests on wild populations will be undertaken.

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MON 22 AUG at 1710 - Room N1
Oral presentation *B4-Sy20-1710-O*

Symposium 20
Chemical communication

Floral scent mediating reproductive isolation in deceptive and rewarding orchid-pollination systems

Sun M[1], Schiestl FP[1]
[1]Institute of Systematic Botany, University of Zürich, Zürich, Switzerland

Summary statement:

Floral scent plays a significant role in reproductive isolation in orchid-pollination systems.

Abstract:

Pollinators have an important function for maintaining species reproductive barriers and mediating speciation in plants. Plant traits, such as floral scent, are associated with pollinator attraction. These traits are under both sexual selection and natural selection. The remarkable diversity of pollination systems and species number in orchids provide an ideal study system for investigating these processes in detail. We studied the role of floral scent as a reproductive isolation (RI) mechanism in two sexually-deceptive species of Ophrys and two food-rewarding species of Gymnadenia. The floral scent of Ophrys mimics the sex pheromone of female solitary bees, inducing copulatory behaviour from male bees and thereby mediating pollination. We aimed to reduce the difference between the scent bouquets of O. sphegodes and O. exaltata through the addition of EAD active scent compounds of the major alkene group of one species to the other. In the genus Gymnadenia, the same principle was employed to manipulate the scent bouquet of G. conopsea by the addition of benzenoids compounds present in G. odoratissima but not in G. conopsea. Massulae transfer was tracked to determine the (1) establishment of RI, and (2) the breakdown of RI. For both Ophrys and Gymnadenia species, there are indications that scent manipulation induced the establishment and breakdown of RI. This study demonstrates potential pollinator shifts through the manipulation of a few volatile compounds in a scent bouquet, indicating the principal role of these compounds as an effective barrier to gene flow. This highlights the significance of chemical communication in reproductive isolation and speciation in plants.

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MON 22 AUG at 1630 - Room N1
Oral presentation *B4-Sy20-1630-O*

Symposium 20
Chemical communication

Modelling bistability in trisporic acid synthesis in Mucorales fungi and the advantages of exchanging intermediates

Werner S[1], Schroeter A[1], Schimek C[2], Woestemeyer J[2], Schuster S[1]
[1]Friedrich Schiller University Jena, Department of Bioinformatics, Jena, Germany, [2]Friedrich Schiller University Jena, Institute of General Microbiology and Microbial Genetics, Jena, Germany

Summary statement:

We present an ODE model of the synthesis of trisporic acid in Mucorales which includes an exchange of intermediates and shows bistable behaviour.

Abstract:

Mucorales are the largest order of Zygomycete fungi. An important substance in the signaling between individuals of Mucorales fungi is trisporic acid (TSA). This serves as a pheromone in the mating between (+)- and (-)-mating types. The synthesis pathway of trisporic acid in Mucorales is very interesting because one mating type alone can produce TSA only very slowly or not at all. The pathway includes an exchange of intermediates between the two mating-types.
Trisporic acid enhances its own synthesis rate by a positiv feedback loop.
Since systems with positive feedback loops often tend to show bistability, we want to demonstrate that there is bistable behaviour in our model of the trisporic acid production.
For simulation we reduce the whole synthesis pathway to a mathematical model of 11 species. By this model, we analyse the number of stable steady states and tackle the question which physiological advantage is provided by the exchange of intermediates.
Therefore we develop a second model that only includes an exchange of the end product and no exchange of intermediates.
By solving the system of equations, which describes our model, we obtain three steady states two of which are asymptotically stable.
Furthermore we identify differences in the bistable behaviour of the model with and without exchange of the intermediates.

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Symposium 21

Evolutionary ecological genomics

Talks: *Room N6*

***Essence posters**:* Ground floor lecture hall centre *HZ*

***Regular posters**:* Upper floor campus canteen *Mensa*

Invited Speakers:

Michael Pfrender, Ilkka Hanski

Organizers:

Luisa Orsini, Christophe Eizaguirre

Description:

Progress in ecological genomics is hindered by limited genome information in non-model species and the lack of an ecological context in genetic model species. This symposium will focus on integrating cutting edge molecular biology in model and non model organisms within an evolutionary context. Our aim is to understand adaptive responses in multidimensional selection regimes in the wild.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i001-R*

Symposium 21
Evolutionary ecological genomics

Genetic diversity and differentiation among populations of the yellow necked mouse, Apodemus flavicollis, harbouring B chromosomes in different frequencies

Adnadjevic T[1], Bugarski-Stanojević V[1], Stamenković G[1], Blagojević J[1], Vujošević M[1]
[1]Institut for Biological Research 'Siniša Stanković', Department of genetic research, Belgrade, Serbia

Summary statement:

Potential contribution of B chromosomes to the genetic structure of four populations of A. flavicollis differing in frequency of Bs and settled in ecologically different habitats.

Abstract:

Two alternative models are used to explain maintenance of polymorphism of supernumerary chromosomes named B chromosomes (Bs) in populations of a great number of species. The parasitic model suggests deleterious effects of Bs on fitness of carriers, so their continuous presence in a population results from accumulation processes. The heterotic model assumes that, in the absence of accumulation, equilibrium is produced by beneficial effects of Bs at low numbers. Bs are found in almost all studied populations of Apodemus flavicollis in a wide range of frequencies.

In order to determine the potential contribution of Bs to the genetic structure and diversity of four populations of A. flavicollis differing in frequency of Bs (from 0.23 to 0.38) and settled in ecologically different habitats, we used 471 AFLP loci amplified with 14 primer combinations in 166 specimens. We found that one population had different diversity level then other three (0.24 vs. 0.12, 0.12, 0.13). The SAMOVA revealed two distinct groups which coincide with frequency of Bs. The greatest diversity was found in the population settled in optimal conditions for this species while the frequency of animals with Bs was the lowest. At the same time AMOVA revealed that the presence of Bs does not affect population structuring.

Smaller genetic diversity in 3 populations suggests habitat related higher selection pressure followed by higher frequency of B carriers, pointing to adaptive significance of Bs presence. This is in accordance with the heterotic model of Bs maintenance.

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SUN 21 AUG at 1710 - Room N6
Oral presentation *A4-Sy21-1710-O*

Symposium 21
Evolutionary ecological genomics

Eco-genomics of inbreeding depression in the non-model plant species Scabiosa columbaria L.

Angeloni F[1], Ouborg JN[1]
[1]Radboud University Nijmegen, Molecular Ecology, Nijmegen, Netherlands

Summary statement:

Eco-genomics of inbreeding depression in the non-model plant species Scabiosa columbaria L.

Abstract:

Inbreeding, the mating between individuals that are more genetically similar than individuals drawn at random from the population, is known to reduce reproduction and survival of the offspring (i.e., inbreeding depression). In plants, inbreeding depression is an important phenomenon which has extensively been studied in relation to the evolution of mating systems, plant breeding, habitat fragmentation and the management of endangered species.

Understanding what determines the magnitude of inbreeding depression and its relationship with population size is, therefore, of fundamental importance. Extant theoretical and empirical studies suggest that values of inbreeding depression at family level may be as relevant as population values to mating system evolution and population genetics. Thus, we examined the extent of family-level variation in inbreeding depression in several different-sized populations of the perennial herb Scabiosa columbaria. Among other interesting results, we found that, for a number of fitness traits, family-level variation was inversely correlated to population size. In addition, since little is known about the effect of inbreeding at the transcriptome level, we compared the change in gene expression level of several different families of inbred and outbred individuals of S. columbaria, using a combination of next-generation sequencing techniques. This approach allowed us to estimate how many genes are associated with inbreeding depression and which functional classes of genes are responsible for the decrease of fitness associated with inbreeding.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i002-R*

Symposium 21
Evolutionary ecological genomics

Inter- and intraspecific polymorphism in passerine Toll-like receptor 4

Bainova H[1], Bryjova A[2], Promerova M[2], Bryja J[2], Johnsen A[3], Lifjeld JT[3], Albrecht T[1,2], Vinkler M[1,2]
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Summary statement:

We described Toll-like receptor 4 in selected passerines. We found high variability intra- and interspecies in this receptor. This can be evidence for parasite-host co-evolution.

Abstract:

Toll-like receptors (TLRs) belong to the first innate immunity molecules to detect the pathogen infection in vertebrates. Their optimal function is essential for successful defence against various parasites, acting either by direct triggering of effector immunological mechanisms or by co-stimulation of adaptive immunity. It may therefore be predicted that parasites evolve to impair this type of detection while hosts evolve to improve it. This co-evolutionary arms-race might be tracked in the TLR structure. As different hosts harbour distinct sets of parasites, comparative research in TLRs may provide some basis for understanding of the evolution of host-parasite interactions. Contrary to the number of fish and mammalian TLRs described, avian inter- and intraspecific TLR-variability is only very insufficiently explored. This is especially true for passerine birds. In this study we therefore aimed at characterising variability in one receptor from TLRs family (TLR4) among selected passerine species (Great reed warbler Acrocephalus arundinaceus, Common rosefinch Carpodacus erythrinus, Collored flycatcher Ficedula albicollis, Barn swallow Hirundo rustica, Bluethroat Luscinia svecica, Great tit Parus major, House sparrow Passer domesticus) and map potential evolutionarily important sites. For two species, the Great tit and the Bluethroat, we also present data for the intraspecific polymorphism. Our results indicate remarkable structural variability in TLR4, both on interspecific and intraspecific level which might arise at least partially from adaptive evolution.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i003-R*

Symposium 21
Evolutionary ecological genomics

Allelic variability in Toll-like receptor 1, 2, 4 and 6 in wild-derived mice (Mus musculus)

Bainová Z[1,2], Fornůsková A[2], Čížková D[2], Bryja J[2], Piálek J[2], Vinkler M[2,3]
[1]Faculty of Science, Charles University in Prague, Department of Cell Biology, Praha, Czech Republic, [2]Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, v.v.i., Brno, Czech Republic, [3]Faculty of Science, Charles University in Prague, Department of Zoology, Praha, Czech Republic

Summary statement:

Broad functional polymorphism has been found in several TLR genes in free-living mice. Distinct allele variability has been revealed in different subspecies.

Abstract:

Permanent contest between hosts and their parasites is supposed to be one of the major driving forces in evolution of most organisms. As many parasites are potent to cause substantial harm to their hosts, all organisms require some defence mechanisms to fight the infection. Although more sophisticated immunological mechanisms have evolved in various taxa, the first line of defence is in all multicellular animals formed by so called innate immunity. Its receptor apparatus ("pattern recognition receptors" - PRRs) is responsible for the earliest detection of potential danger by recognition of pathogen-associated molecular patterns (PAMPs) or danger-associated molecular patterns (DAMPs). Several protein families belong to PRRs among which Toll-like receptors are most well known. Although their ligands are considerably conserved in structure, PRRs seem to be highly polymorphic both on interspecific and intraspecific level. Association of the intraspecific polymorphism with increased resistance or susceptibility to infectious or autoimmune diseases has been reported in humans as well as in laboratory animals. There is, however, deficiency of similar studies in other (especially free-living) animals. In our research we therefore focused on characterization of allelic variability in four members of Toll-like receptor family (Tlr1, 2, 4 and 6) in several murine wild-derived inbred strains and in a sample of free-living individuals from allopatric populations. Our data show remarkable differences in Tlr polymorphism among distinct house mouse populations. This might be indicative of evolutionary differences in host-parasite interactions in distinct populations of free-living mice.

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SUN 21 AUG at 1500 - Room N6
Oral presentation *A3-Sy21-1500-O*

Symposium 21
Evolutionary ecological genomics

Transposable elements in sexual and asexual oribatid mites

Bast J[1], Schaefer I[1], Maraun M[1], Scheu S[1], Kraaijeveld K[2]
[1]Georg-August-University Goettingen, J.F. Blumenbach Institute of Zoology and Anthropology, Goettingen, Germany, [2]Leiden University Medical Center, Department of Human Genetics, Leiden, Netherlands

Summary statement:

Transposable elements are purged in parthenogenetic oribatid mites compared to sexuals, potentially explaining the long-term persistence of asexual taxa.

Abstract:

Transposable elements (TEs) are deleterious DNA fragments with the ability of self-replication and random insertion. Sexual reproduction promotes the spread of TEs whereas in parthenogenetic lineages TE proliferation is restricted to vertical transmission. Therefore, TEs are expected to be stuck in parthenogenetic lineages and to decline over time. Loss of TEs may help to explain the long-term persistence of parthenogenetic species, termed “ancient asexuals”, which include several taxa of oribatid mites (Oribatida, Acari). As oribatid mites also include species-rich sexual taxa they offer the unique opportunity to investigate the fate of TEs in long-term asexual lineages. We compared the abundance of TEs in a sexual (Steganacarus magnus) and a parthenogenetic (Platynothrus peltifer) oribatid mite species by using new generation sequencing and current bioinformatic tools. We hypothesized that the parthenogenetic species has a smaller TE load compared with the sexual species. Based on full genome information, our data show that DNA transposons and LTR retroelements are less abundant in parthenogenetic lineages, suggesting that TEs either degenerate or diminish during evolution. Only one group of TEs, non-LTR elements, was slightly more abundant in the parthenogenetic species P. peltifer. Non-LTR elements may evade selection by jumping to genomic „safe sites”, by domestication or the inability to be excised from genomes. Overall, our data indicate that TE load may be reduced in the long-term in parthenogenetic lineages. This may help to explain the long-term persistence of parthenogenetic species, since the loss of TEs presumably is a slow process.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i004-R*

Symposium 21
Evolutionary ecological genomics

The riddle of African Pygmies' stature: Results from an interdisciplinary approach

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Summary statement:

We show here that Pygmies' stature is due to genetic factors among which GHR and IGF1 and that sexual selection do not play a role in this phenotype.

Abstract:

The « riddle » of African Pygmy stature has interested anthropologists, endocrinologists, ethno-ecologists and geneticists for years. Still the causes and evolution of the stature of the shortest human populations remain unknown. Through the comparison of stature and non-Pygmy admixture in 213 individuals, we have shown that the difference in height between Pygmies and non-Pygmies nowadays is probably due to genetic factors. In search for these genetic factors, we developed a candidate gene approach that revealed that polymorphisms in the Growth Hormone Receptor and Insulin-like Growth Factor 1 genes play a role in this phenotype and explain 15.8% of the variation in stature in a sample of 60 Pygmies and 30 non-Pygmies. Our study therefore confirms that the difference in height observed between Pygmies and non-Pygmies is not due to phenotypic plasticity in response to differences in the environment but is likely the result of long term selective pressures. Several evolutionary hypotheses have been put forward to explain the pygmy phenotype. One known key factor regarding the evolution of human height is mate choice. We studied mating patterns concerning stature in 72 Cameroonese Baka Pygmy couples and found significant assortative mating and male taller norm in this Pygmy population as well as in 27 neighboring Nzimé non-Pygmy couples and in many other human populations. In the Pygmy population, shorter individuals were not chosen as mate more often and did not have a higher reproductive success than taller individuals. Therefore, sexual selection does not seem to play a role in Pygmies' short stature. The evolution of the Pygmy phenotype remains thus to be explained.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i002-E*

Symposium 21
Evolutionary ecological genomics

Patterns of genetic diversity of endemic species of Ortgiesia (Aechmea, Bromeliaceae) in the Southern Brazilian Atlantic Rainforest

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Summary statement:

Aechmea winkleri shows high genetic diversity despite its restricted geographical distribution. This is in agreement with the hypothesis of refugia in this area during Pleistocene.

Abstract:

Ortgiesia, one of the eight subgenera of Aechmea (Bromeliaceae), occurs in Brazilian Atlantic Rainforest where the Southern area is hypothesized as the diversity center of this group. These species are morphologically very similar, leading to taxonomic delimitation problems. Eight Ortgiesia species endemic to Southern Brazil were used to evaluate aspects as speciation, hybridization, intra and inter-specific gene flow, and genetic diversity based on a combined data set of nuclear and chloroplast microsatellites markers. We are interested in investigating whether these eight species are distinct evolutionary units; how is the distribution of genetic diversity in the natural populations; and whether there was a potential refuge area of the Pleistocene in Southern Brazil. Partial results of this study revealed that A. winkleri shows high genetic diversity despite its restricted geographical distribution. Moderate levels of genetic structure was detected (FST = 0.082) with a number of migrants ranging from 1.654 to 4.933 individuals per generation. A. winkleri is an outcrossing species with high proportional asexual reproduction with moderate connectivity among the four subpopulations studied. The high genetic diversity showed in the four subpopulations of A. winkleri indicates also that this population is stable and old in this area. One hypothesis is that this region could be refugia during the Pleistocene. Recent studies indicated a migratory route from the coastal region in Southern Brazil to inland during the Pleistocene. The complete investigation including the others seven species are in progress.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i005-R*

Symposium 21
Evolutionary ecological genomics

Adaptive genetic variation, individual fitness and pathogen infection in house sparrows explored using next generation sequencing

Borg ÅA[1], Jensen H[1], Westerdahl H[2], Holand H[1], Ringsby TH[1], Sæther B-E[1]
[1]CCB, Department of Biology, NTNU, Trondheim, Norway, [2]Department of Biology, Lund University, Lund, Sweden

Summary statement:

Next generation sequencing with individually tagged primers was used to examine the relationship between MHC-variation and individual fitness in a house sparrow metapopulation.

Abstract:

There is variation between individuals in pathogen resistance, which affects infection rates. This variation is also crucial in understanding the genetic processes that may affect population viability. Such understanding may be especially important when a population is exposed to novel pathogens. Using next generation genomics techniques we explore the importance of adaptive genetic variation in immune system alleles for individual fitness. We assess genetic variation at functional loci that are known to be under strong balancing selection, i.e. genes of the Major Histocompatibility Complex (MHC), as well as at neutral loci (non-coding microsatellite DNA markers). We compare the genetic diversity of individuals at both types of loci, and relate this to individual fitness. Furthermore, by relating genetic pathogen resistance to individual fitness parameters, we evaluate the adaptive consequences of genetic variation. To examine these questions we use a well studied natural house sparrow metapopulation in northern Norway. MHC genotyping of 1600 individuals was performed using the 454 amplicon sequencing technique and individually tagged primers. We relate individual genotypes at MHC class I and II loci to survival, reproduction and occurrence of pathogens, for example bird malaria and the macroparasite Syngamus trachea. We discuss how information on individual MHC variation and pathogen resistance increase the understanding of population viability and disease transmission within and between natural populations.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i006-R*

Symposium 21
Evolutionary ecological genomics

Gene expression and evolutionary responses to environmental stress in the pond snail Lymnaea stagnalis exposed to pesticides

Bouetard A[1], Coutellec M-A[1], Lagadic L[1]
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Summary statement:

Differential molecular stress responses in Lymnaea stagnalis exposed to pesticides. An innovating way to investigate of evolutionary processes induced by environmental pollutants.

Abstract:

In natural populations, environmental stress due to pollutants may trigger evolutionary processes, which can occur rapidly. Potential genetic changes due to these human-induced alterations may involve random genetic drift and inbreeding (e.g., when pollutants induce repeated demographic bottlenecks), as well as selection (fitness reduction, adaptive processes). We investigate this question in a freshwater snail which populations are often exposed to pesticides used in agriculture. First, to study the evolutionary potential of molecular responses to stress, a nested paternal half-sib design was used to estimate the heritability of gene expression, for a set of candidate genes involved in oxidative stress and more general stress. Families are experimentally exposed to two herbicides known to generate oxidative stress. Second, to improve the ability to detect adaptive genetic changes in a set of natural populations, we used pyrosequencing to develop genomic resources from the transcriptome of various tissues. These resources will serve as reference for further quantitative analysis of the transcriptome (RNAseq). The hypothesis of population adaptive divergence due to historical exposure to pesticides will be tested at the transcriptomic level, using Qst-Fst approaches. Preliminary results on gene expression (QRT-PCR) and on transcriptome sequencing will be presented in the framework of this project.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i045-R*

Symposium 21
Evolutionary ecological genomics

Reproduction and fertility in Aechmea winkleri (Bromeliaceae), an endemic endangered species of Southern Brazil

Büttow MV[1], Goetze M[1], Paggi GM[2], Zanella CM[1], Pinheiro FG[1], Janke A[1], Bered F[1]
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Summary statement:

We explore the ecological and genetic factors influencing the success of reproduction and persistence of Aechmea winkleri (Bromeliaceae) in nature.

Abstract:

Patterns of population fertility and mating system and their consequences for the evolution of mating systems in non-model species are poorly understood. Aechmea winkleri is a preferential terrestrial or saxicolous bromeliad species endemic of a small region in the Southern Brazil. Subpopulations of this species suffer from habitat fragmentation resulted from conversion of forests in urban and agricultural areas, which may be threatening to its survival and evolution. We explore the ecological and genetic factors influencing the success of reproduction and persistence of this species in nature. Our data showed that this species is self-incompatible, dependent of bees and birds for pollination and fruit set. We observed high flower, fruit and seed production, and high proportion of seed viability, without differences among subpopulations. The experiment of pollen supplementation using manual cross- and open-pollination showed a similar value for number of seeds per fruit, showing no pollen discounting. Two years of demographic surveys revealed a high investment in vegetative reproduction. On average, there are fourteen ramets for each adult genet. For the mating system analysis we sampled 61 mother plants with 15 seedlings for each, totalizing 915 individuals from the four subpopulations. We will evaluate the outcrossing rate, the genetic structure of pollen pool and the genetic variability parameters within mother-plants populations through microssatelite markers. Regarding the rapid ongoing fragmentation of habitat, the results achieved will help to elucidate the directions of evolution and conservation in this species.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i004-E*

Symposium 21
Evolutionary ecological genomics

Effect of recombination on the expression of chemical defense traits in forest tree species with porous genomes

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Summary statement:

We discuss the evolutionary genetics of chemical defence traits in two ecologically divergent members of the model forest tree Populus

Abstract:

Evolutionary ecological genomics is expected to benefit greatly from the use of model systems with genome information and well defined ecology, as is the case for forest trees of the genus Populus. Sessile organisms such as plants cannot move to escape environmental challenges such as herbivores, so defense can have a direct impact on their fitness. Localities in which two or more related plant species interact genetically (also known as hybrid zones) are invaluable arenas for evolutionary genomic studies. Hybrid zones often exhibit a greater abundance and diversity of herbivores, but interspecific recombination also opens the opportunity to combine multiple defense mechanisms from each participating species. We studied patterns of expression of key secondary metabolites involved in defense (salicylic acid derivatives, flavonoids, and quinic acids) in a large natural hybrid zone of two ecologically divergent European Populus species. We obtained metabolomic profiles for genotypes previously characterized for 80 DNA microsatellites and picked 30 chemical traits for further work. We show that recombinant hybrids are differentiated from their parental species for many functionally important compounds and present novel combinations of traits. A correlation between chemotype and genotype indicates the heritability of many of the studied traits. We will discuss first results on the genomic architecture of these defense traits and their possible role in introgressive evolution.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i005-E*

Symposium 21
Evolutionary ecological genomics

Gene order in two species of sculpins (Cottus) and the conservation of synteny with fish model species

Cheng J[1], Czypionka T[1], Nolte A[1]
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Summary statement:

This study constructs two independent genetic linkage maps of two Cottus species that permit to assess map variation and conserved synteny within Cottus and with fish model species

Abstract:

The possibility to transfer genomic information between model organisms and other species can permit to generalize knowledge about the genetics of model organisms and to study new evolutionary phenomena in unexplored species. This study focuses on sculpins of the genus Cottus that we study to learn about the genetics of adaptation and as an example for hybrid speciation. We have screened sequences obtained by 454 transcriptome sequencing to identify SNP markers that are diagnostic between the species Cottus rhenanus and Cottus perifretum. Of these, we chose 384 gene linked markers that could be BLAST mapped to the Stickleback genome in which they were evenly spaced. F2 intercrosses among four independent populations representing the two Cottus species were genotyped to construct two independent genetic linkage maps that permit to assess map variation. A conservative algorithm was used that identifies conserved synteny regions within Cottus and with more distantly related model fishes. The Cottus genome has been rearranged between the two species of Cottus. However, at the same time Cottus show an almost complete conservation of synteny with the stickleback, with 1:1 orthologs present on a single chromosome in one species also found on a single chromosome in the other. Moreover, orthologs tend to remain in the same region of the chromosome. As a consequence, the genome of the stickleback serves as an excellent reference for evolutionary studies in Cottus. This high utility is unmatched by other reference organisms.

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SUN 21 AUG at 1440 - Room N6
Oral presentation *A3-Sy21-1440-O*

Symposium 21
Evolutionary ecological genomics

Genomic analysis of the sex-determining region of the brown alga Ectocarpus

Coelho SM[1], Ahmed S[1], Robouchon M[1], Luthringer R[1], Dittami S[1], Bothwell JH[2], Marais G[3], Roze D[1], Cock JM[1]
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Summary statement:

We report the mapping and genomic analysis of the male and female sex determining regions in the dioecious brown algae Ectocarpus, elucidating its evolution and regulation.

Abstract:

The genetic determination of sex requires either non-recombining chromosome regions or complete sex chromosomes, both of which have evolved independently and repeatedly across different species. Comparative analyses of sexual systems found in land plants and animals and other eukaryotes have played a key role in understanding how such sexual systems evolve. In this context, the brown algae represent a highly interesting group not only because of their evolutionary distance from other eukaryotic lineages but also because they exhibit a broad range of levels of gamete dimorphism, ranging from isogamy to oogamy; furthermore, sex is expressed in the haploid phase, which should affect the evolution of sex chromosomes. Here, we report the mapping and genomic analysis of the male and female sex determining regions in the dioecious brown algae Ectocarpus, elucidating its evolution and regulation. By exploiting resources generated as part of the Ectocarpus genome project (Cock et al., Nature 2010), we have identified a sex determining region of 1 Mbp on the male genome, where recombination is totally suppressed. We are exploring the differences between male and female sequences in this region to retrace their evolutionary history. In parallel, deep transcriptome analysis is unraveling the transcriptional network involved in Ectocarpus sex determination and differentiation. We will discuss how the elucidation of sex determination in this third major eukaryotic lineage will help to test existing theories of the evolutionary dynamics of sex determining regions.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i006-E*

Symposium 21
Evolutionary ecological genomics

SNP marker diversity in common bean (Phaseolus vulgaris L.)

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[1]Uppsala University, Uppsala, Sweden, [2]International Center for Tropical Agriculture, Cali, Colombia, [3]Universidad de los Andes, Bogota, Colombia

Summary statement:

I graduated with honors from Biology and the Master in Biology at Universidad de los Andes (Colombia). I am a PhD student at Uppsala University in the area of ecological genetics.

Abstract:

Single nucleotide polymorphism (SNP) markers have become a genetic technology of choice because of their automation and high precision of allele calls. In this study our goal was to develop 94 SNPs and test them across well-chosen wild and cultivated common bean (Phaseolus vulgaris L.) germplasm. We validated and accessed SNP diversity at 84 gene-based and 10 non-genic loci using KASPar technology in a panel of 70 genotypes that have been used as parents of mapping populations and have been previously evaluated for SSRs. SNPs exhibited high levels of genetic diversity, an excess of middle frequency polymorphism, and a within-genepool mismatch distribution as expected for populations affected by sudden demographic expansions after domestication bottlenecks. This set of markers was useful for distinguishing Andean and Mesoamerican genotypes but less useful for distinguishing within each gene pool. In summary, slightly greater polymorphism and race structure was found within the Andean gene pool than within the Mesoamerican gene pool and polymorphism rate between genotypes was consistent with genepool and race identity. Our survey results represent a baseline for the choice of SNP markers for future applications because gene-associated SNPs could themselves be causative SNPs for traits. Finally, we discuss that the ideal genetic marker combination with which to carry out diversity, mapping and association studies in common bean should consider a mix of both SNP and SSR markers. The domestication of common bean offers a good scenario to understand the adaptive responses in multidimensional selection regimes in a diploid non-model species.

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Ground floor lecture hall centre ***HZ***
Essence poster *E-Sy21-i007-E*

Symposium 21
Evolutionary ecological genomics

Benefits of using genome-wide data versus genealogical data in the management of populations in conservation programmes

de Cara MAR[1], Fernández J[1], Toro MA[2], Villanueva B[1]
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Summary statement:

Using genome-wide data maintains a higher diversity than using genealogical data in the management of populations in conservation programmes.

Abstract:

We will present the results of using genome-wide versus genealogical data in population management for conservation purposes. We thoroughly re-examine the effect of using these sources of information (molecular information vs. pedigree data), for different population and genome sizes, and compare different management strategies according to the group of individuals where we take decisions (parents or offspring).

We also study the consequences of using estimated genealogical coancestries from markers as opposed to using genealogical coancestry or molecular coancestry. Using genome-wide data performed consistently better than using pedigree data for maintaining gene diversity. Similarly, when we could make our decisions based on the potential offspring, a larger gene diversity was maintained than when we based our decisions on the potential parents.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i007-R*

Symposium 21
Evolutionary ecological genomics

Development of a linkage map of the great tit Parus major: new insights into genomic structure and recombination in passerine birds

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[2]University of Oxford, Department of Zoology, Oxford, United Kingdom

Summary statement:

Construction a linkage map by examining the co-segregation of markers through a pedigree of 2880 birds genotyped for 9193 single nucleotide polymorphisms (SNPs).

Abstract:

The construction of genetic linkage maps in natural populations is a promising tool to study the genetic basis of fitness differences among individuals, as well as the mechanisms of adaptation in complex and variable environments. We took advantage of the ecological data generated by a long-term study of the great tit, Parus major, an important model for studies of life-history evolution and quantitative genetics, to construct a linkage map by examining the co-segregation of markers through a pedigree of 2880 birds genotyped for 9193 single nucleotide polymorphisms (SNPs). This map represents an advance in the dissection of the genetic diversity in the wild and provides the foundation for QTL analyses in the study population.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i008-R*

Symposium 21
Evolutionary ecological genomics

Linking genetic variation to life history and thermal performance in wild populations of the Glanville fritillary butterfly (Melitaea cinxia)

de Jong MA[1], Saastamoinen MAK[1], Hanski I[1]
[1]University of Helsinki, Department of Biosciences, Helsinki, Finland

Summary statement:

We studied genetic variation in candidate genes in relation to variation in life history and thermal performance under both semi-natural and laboratory conditions.

Abstract:

Understanding how variation in the genome underlies the phenotypic variation that enables wild populations to cope with and adapt to divergent environmental conditions lies at the heart of ecology and evolutionary biology. We studied wild populations of the Glanville fritillary butterfly (Melitaea cinxia) under both semi-natural and laboratory conditions, aiming to link variation in life history and thermal performance to coding variation in a set of candidate genes associated with the studied traits. We performed and analysed experiments carried out in large outdoor cages where we studied various life history traits, including dispersal- and reproduction-related traits, of 200+ butterflies throughout their adult life. Identical experiments were carried out in subsequent years, which allowed us to estimate narrow sense heritabilities of the studied traits using animal models. Detailed climatic data was recorded during the experiments and taken into account during the analysis to assess thermal performance of the butterflies. Furthermore, we investigated larval and adult thermal acclimation under controlled laboratory conditions, showing both larval and adult thermal acclimation in response to ambient temperature. Butterflies of both experiments are genotyped for a set of ~30 candidate genes associated with life history variation and thermal adaptation, including the metabolic gene Pgi.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i009-R*

Symposium 21
Evolutionary ecological genomics

The genetic basis and ecological significance of flowering time in populations of Arabidopsis thaliana

Dittmar EL[1], Ågren J[2], Schemske DW[1]
[1]Michigan State University, Plant Biology, East Lansing, United States, [2]Uppsala University, Uppsala, Sweden

Summary statement:

Natural populations of Arabidopsis thaliana from divergent habitats were used in a mapping experiment that identified QTL contributing to flowering time and fitness in the field.

Abstract:

Biodiversity is explained by local adaptation to divergent habitats. Understanding the genetics of adaptation can give insight into the speed and ease of the adaptive process. Whether adaptive traits are caused by many genes, each of small effect as Fisher proposed, or few genes of large effect as in Orr’s model, could change the degree of constraint involved in the climb to an adaptive peak.
This study examines the genetic basis of flowering time in the model plant Arabidopsis thaliana. Study populations were taken from natural populations in Sweden and Italy, two habitats that differ greatly in temperature and photoperiod. Reciprocal transplant experiments showed differential flowering time between these populations and higher fitness of the local population.
Recombinant Inbred Lines (N>400) created from these populations were grown at both field sites in 2010 and 2011 and in growth chambers simulating local field conditions to characterize flowering time. All lines were genotyped using >350 SNP markers. A modest number of QTL were identified (< 10), some with large effects. For plants grown in Italy in 2010, nine QTL were found, explaining from 1-16% of the variance in flowering time. In all experiments, the largest QTL maps near the candidate gene FLC. In contrast, no QTL were located near FRI, a major flowering time gene found in many other studies. QTL contributing to fitness in the field were evaluated and several showed an overlap with flowering time QTL, indicating that flowering time is an adaptive trait in these populations. Further experiments will dissect these QTL to determine the number and effect sizes of individual genes within these genomic regions.

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MON 22 AUG at 1550 - Room N6
Oral presentation *B4-Sy21-1550-O*

Symposium 21
Evolutionary ecological genomics

Origin and strength of selection acting on adaptive pigmentation alleles in beach mice

Domingues VS[1], Peterson BK[1], Poh Y-P[2], Jensen JD[2], Hoekstra HE[1]
[1]Harvard University, OEB, Cambridge, United States, [2]University of Massachusetts Medical School, Program in Bioinformatics and Integrative Biology, Worcester, United States

Summary statement:

We are using phylogenetics and population-genomics to determine the source, timing and strength of selection acting on beneficial mutations in nature.

Abstract:

With our ability to identify alleles contributing to adaptive variation, we are now in a position to understand their evolutionary histories.We want to know the primary source of beneficial mutations (i.e. pre-existing or de novo mutations), if those mutations have evolved repeatedly, and the timing and strength of selection acting on them.We are studying natural populations of mice, Peromyscus polionotus, which occurs throughout the southeastern US, where they have dark coats, and the coastal dunes of Florida, where they have evolved pale coats for camouflage.Using QTL mapping, we previously identified three pigmentation genes, which explain most of the variation in adaptive color.In the case of one gene, Mc1r, we identified and functionally characterized a single derived amino acid change that plays a role in producing pale coat color.To determine the origin and selection strength acting on this mutation, we designed a capture array and resequenced a 150-kb genomic region surrounding Mc1r as well as 3000 1.5kb non-coding regions scattered throughout the genome in both beach and mainland populations.We first used a genome-wide phylogenetic approach to estimate the number of independent origins of the derived Mc1r allele. Second, we focused on one beach mouse population to employ a population-genomic approach to estimate demography.Then, controlling for demographic effects, we tested if patterns of nucleotide variation are consistent with a hard vs. soft selective sweeps and estimated the strength and timing of selection acting on the Mc1r mutation.This study provides a model in which to study the molecular basis and evolutionary history of adaptation in wild populations.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i010-R*

Symposium 21
Evolutionary ecological genomics

Lifespan and food responses are regulated through a trade-off between reproduction- and stress-related gene expression in Drosophila

Doroszuk A[1], Jonker MJ[2,3], Pul N[1], Breit TM[2,3], Zwaan BJ[1,4]
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Summary statement:

First evidence of the trade-off between expression of reproduction- and stress-related genes in a multicellular eukaryote.

Abstract:

According to the most inclusive evolutionary theory of ageing, the disposable soma theory, the trade-off between reproduction and stress/body maintenance plays a core role in shaping lifespan and ageing rate. Our previous study of Drosophila genome-wide expression patterns suggested that this trade-off is present at the level of transcription. Here, we test this hypothesis directly.

The analysis of 46 microarrays carrying samples of middle-aged and old female Drosophila kept under three nutritional environments (malnutrition, optimal food and overfeeding) indicated a strong negative correlation between expression of reproduction- and stress-related genes. We show that higher food levels are associated with higher expression of reproduction- and lower expression of stress- related genes, following general predictions of life-history theory. Also, old flies (regardless diet) displayed higher expression levels of stress-related genes and a lower expression of reproduction-associated genes. This indicates a key role of the detected trade-off in age- and food-related responses and shows that transcription signatures are constrained to follow the trade-off's axis. Moreover, the observed gene expression patterns follow the predictions of life-history and the disposable soma theories.

Our study provides the first evidence of the coordinated regulation of the stress- and reproduction-related transcription at the whole organism level in a multicellular eukaryote. It confirms the strong association between nutrition and ageing known from dietary interventions and provides a novel link between the disposable soma theory of ageing and the mechanisms operating at molecular level.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i011-R*

Symposium 21
Evolutionary ecological genomics

Application of salmon SNP microarray for studies of genetic polymorphism of the related non-model fish species

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Summary statement:

SNP microarray analysis of three salmonid species demonstrated the usefulness of this tool for the non-model related species. A lot of highly polymorphic loci were identified.

Abstract:

Salmonid family includes many ecologically and economically important fish species such as atlantic salmon Salmo salar, sea trout Salmo trutta and rainbow trout Oncorhynchus mykiss. S. salar is a farmed fish which is used as a model species in genetic mechanisms of growth and development, reproduction and immune response. Most of the basic information on the atlantic salmon genome is known. O. mykiss have been also widely utilized in research and is so well characterized as salmon. S. trutta trutta is an anadromous form of brown trout Salmo trutta L. with, as many others non-model species, has limited information about the genome. It is important to develop genetic markers that provide polymorphism analysis of non-model fish species, farmed and living in the wild specimens, which the structure of the genome is not known. Single nucleotide polymorphisms (SNPs), with are the most common type of DNA variation in vertebrates, seem to be very useful markers in this case. The use of microarrays allows simultaneous analysis of thousands SNPs from the whole genome, which makes these markers very useful in species genotyping. In the present study the Illumina´s SNP microarray designed in Centre for Integrative Genetics in Norway based on the known sequence from the Norwegian salmon was used. 42 individuals belonging to these three related fish species were genotyping. Polymorphism was analyzed at the interspecies level and within two salmon populations from Norway and Southern Baltic Sea. This method allowed to extract of highly discriminatory loci between species and populations.

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MON 22 AUG at 1440 - Room N6
Oral presentation *B3-Sy21-1440-O*

Symposium 21
Evolutionary ecological genomics

The genetic basis of behavior in an ecological specialist, Drosophila sechellia

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Summary statement:

Using next-gen genome sequencing combined with ecological and behavioral assays, we uncover the genetic basis of a complex ecological adaptation in Drosophila sechellia.

Abstract:

Since the Modern Synthesis, evolutionary biologists have sought to link ecological phenotypes with underlying genotypes. We have been successful in uncovering some of the genes leading to so-called “simple” Mendelian traits. For example, adaptive pigment evolution in a diversity of species is caused by changes at one locus, melanocortin receptor 1. Despite these successes, we still know relatively little about genes underlying complex adaptations. Still less is known about the genetics underlying adaptive behavior, potentially the most complex set of phenotypes yet arguably the most interesting. By combining next-gen whole genome sequencing with ecological and behavioral assays, we seek to find causative genetic changes accompanying a behavioral adaptation. Drosophila sechellia is a hyperspecialist on the tropical fruit of Morinda citrifolia. Sister species, including Drosophila melanogaster, are repulsed by Morinda fruit and its volatile organic acids. By coupling a candidate gene search with a modified genome-wide bulk segregant analysis we link changes at key chemoreceptor genes with gain and loss of preference toward Morinda. Interestingly, a broken chemoreceptor in D. sechellia appears to be critical in the transition from an ancestral generalist diet to a derived specialism of Morinda.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i012-R*

Symposium 21
Evolutionary ecological genomics

Altitudinal patterns of life history variation among Drosophila melanogaster populations from sub-Saharan Africa

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Summary statement:

Here we report the first study of altitudinal life history variation in Drosophila melanogaster populations from sub-Saharan Africa.

Abstract:

Although life history traits are important determinants of fitness, the genomic basis of life history adaptations in natural populations is poorly understood. For example, several recent studies have begun to unravel the genetic and genomic basis of life history adaptations to latitudinal climate gradients, but whether similar mechanisms underlie patterns of altitudinal clines remains unknown. Adaptations to life at high altitudes have been well-documented in plants (e.g., Mount Kenya Lobelias) and animals (e.g., Sierra Nevada grasshoppers), but with the exception of hypoxia responses in mammals (e.g., Rocky Mountain deer mice, Tibetan humans) little is known about the genetic underpinnings of altitudinal adaptation. In our project we are using whole-genome sequenced isofemale lines from populations of sub-Saharan Drosophila melanogaster collected at different elevations to identify population genomic signatures of altitudinal life history adaptation. Here we report preliminary data on altitudinal patterns of life history variation by comparing three low-elevation (295m to 350m) populations from Gabon, Nigeria and South Africa and three high-elevation (1927m to 2492m) populations from Rwanda, Cameroon and Ethiopia. To this end, we have tested for altitudinal differentiation by measuring developmental time, dry weight at eclosion, viability, lifetime fecundity, lifespan, and the incidence of reproductive diapause. These phenotypic data will be used in candidate gene and genome-wide association studies to identify genes associated with altitudinal adaptation in life history traits.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i008-E*

Symposium 21
Evolutionary ecological genomics

Short read Illumina data for the de novo assembly of a non-model snail species transcriptome (Radix balthica, Basommatophora, Pulmonata), and a comparison of assembler performance

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Summary statement:

The results of de novo assembled Illumina-transcriptome reads strongly depend on assembly method. A meta-assembly of contigs sets is recommended to increase contig quality.

Abstract:

Until recently, read lengths on the Solexa/Illumina system were too short to reliably assemble transcriptomes without a reference sequence, especially for non-model organisms. However, with read lengths up to 100 nucleotides available in the current version, an assembly without reference genome should be possible. For this study we created an EST data set for the common pond snail Radix balthica by Illumina sequencing of a normalized transcriptome. Performance of three different short read assemblers (Velvet, Oases, and SeqMan NGen) was compared with respect to: the number of contigs, their length, depth of coverage, their quality in various Blast searches and the alignment to mitochondrial genes.
We discuss the results for each assembly separately and show that de novo transcriptome assembly yields contigs useful for downstream applications, in particular if a meta-assembly of contig sets is used to increase contig quality.

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SUN 21 AUG at 1610 - Room N6
Oral presentation *A4-Sy21-1610-O*

Symposium 21
Evolutionary ecological genomics

Genome evolution and adaptation in parapatric lake-stream populations of the three-spined stickleback Gasterosteus aculeatus

Feulner PGD[1], Chain FJJ[2], Panchal M[2], Mundry M[1], Bornberg-Bauer E[1], Reusch T[3], Milinski M[2]
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Summary statement:

Evaluating structural variation of the genome within and between parapatric lake-stream populations of sticklebacks using whole genome short-read sequencing data.

Abstract:

The tree-spined stickleback has recently been established as a super model for evolutionary ecological genomics. However, despite extensive amounts of ecological and genomic data that are currently available, genome-wide variation data from natural populations remain scarce. Here we present whole genome data sampled from a broad geographic range of parapatric three-spined stickleback ecotypes – lake-stream population pairs. For each population, the sequencing of six individuals per population allows an in-depth evaluation of genome-wide polymorphism. Population diversity is contrasted between parapatric and geographically distant (allopatric) population pairs undergoing parallel ecological adaptation. Our sequencing approach combining different insert-sizes was designed to analyse the structural variation between genomes. Large structural variations such as deletions, insertions, copy number variations, inversions, and translocation are accessed exploiting different signatures apparent in short-read sequencing data. Utilizing paired-end mapping, depth of coverage, and split read analysis, we are constructing a structural variation discovery set for the three-spined stickleback. In a preliminary analysis on a small subset of the data, we identified population specific structural variations, most of which interfere with know protein coding regions. Evaluating structural variation of the three-spined stickleback genome within and between natural populations will contribute towards a better understanding of the evolution of genomes. Due to our nested experimental setup we will gain insights about the importance of structural variations for an adaptive response in the wild.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i013-R*

Symposium 21
Evolutionary ecological genomics

Genomic consequences of long-term asexuality in the bdelloid rotifer Adineta vaga

Flot J-F[1], Van Doninck K[1]
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Summary statement:

The sequencing of the complete nuclear genome of the bdelloid rotifer Adineta vaga reveals the apparent absence of Meselson effect in this species despite it long-term asexuality.

Abstract:

Bdelloid rotifers are considered as “something of an evolutionary scandal” because of their apparent persistence for more than 40 million years without sex, which contradicts the common assumption that strict asexual reproduction represents an evolutionary “dead end” for metazoans. Indeed, bdelloid rotifers not only appear to have survived without sex for a very long time, but have even diversified into more than 460 currently recognized species. Moreover, bdelloids are extremely resistant to radiations and desiccation, which allows them to survive in semi-terrestrial environments that dry out frequently.

To investigate the genomic consequences of a long-term absence of meiosis, 454 shotgun sequencing of the genome of the bdelloid Adineta vaga (a degenerate tetraploid) was performed using three different libraries with insert sizes of 3kb, 8kb and 20kb, respectively. Assembly proved very challenging due to the moderate heterozygosity of this organism, which was at the same time too high for allelic regions to be fused together and too low for them to be assembled separately. This was unexpected, as theory predicts that allelic regions of ameiotic organisms should become more and more divergent with time (the so-called ‘Meselson effect’). The apparent absence of Meselson effect in Adineta vaga may be explained by the occurrence of mitotic recombination.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i014-R*

Symposium 21
Evolutionary ecological genomics

Genomic adaptation of deep-sea hydrothermal vent alvinellid polychaetes from mesophilic to highly thermophilic environments

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Summary statement:

Genomic scan for thermophily in hydrothermal polychaetes.

Abstract:

Adaptation to extreme environments and specially to high temperatures may represent a very challenging model in the long way to understand how genomes and their associated proteomes are shaped by selective processes at various scales/levels of the organismal evolution. Temperature is indeed expected to affect both the codon usage and the protein composition over the whole genome in order to increase the stability of the transcriptional/translational machinery and the subsequent produced proteins that are necessary to survive and reproduce at high temperatures. The alvinellidae familly represents an excellent opportunity to explore hypotheses about the emergence of the thermophilic trait in poikilothermic metazoans as this clade includes a series of closely related species that evolves in highly contrasted thermal conditions over a very long period of time (fossil evidence from the Devonian period). We performed a preliminary genomic scan on a dataset of 227 putative orthologous loci from three Alvinellidae species including two "hot" species, Alvinella pompejana and Paralvinella sulfincola (50-60°C) and one "cold" species, Paralvinella grasslei (2-20°C) to explore amino acid composition, codon usage, divergence, orientation of residue changes and the evolution of dN/dS ratio along branches and sites using codon models. This work allowed us to determine whether adaptation to ´high´ temperatures is a recently-derived trait in the two "hot" species (adaptive convergence) or has been ancestrally inherited during the colonization of this peculiar habitat with subsequent losses in the ´cold´ lineages (selective relaxation).

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i015-R*

Symposium 21
Evolutionary ecological genomics

Whole-genome inference of speciation and domestication mechanisms in pig and related species

Frantz LAF[1], Madsen O[1], Menges HJ[1], Crooijmans R[1], Groenen M[1]
[1]Wageningen University, Animal Breeding and Genetics, Wageningen, Netherlands

Summary statement:

Adaptative and phylogeographic history of the Sus genus (pigs and related species) from Asia and Europe using whole-genome resequencing data from over 40 individuals.

Abstract:

The Genus Sus (Suidae, Cetartiodactyla) have diverged from a common ancestor with Phacochoerus, in Asia, probably during the Miocene/Pliocene boundary (7-5 Mya). Island Southeast Asia (ISEA) harbors the largest pig diversity in the world with some 7 species of Sus and many more subspecies. This diversity can be explained by the influence of repeated vicariant events which have isolated and reconnected ISEA islands since the early Pliocene (5.3 Mya) creating a perfect environment for allopatric speciation. However, the phylogeny and phylogeographic patterns of those species still remains unclear. Besides their attractiveness to infer speciation mechanisms, the Sus genus is also of particular interest to study the process of domestication. Previous studies suggest that pigs have been domesticated independently at least once in Europe and Asia from the widely-spread wild boar: Sus scrofa. However, these studies mainly used small genomic and mitochondrial fragments. Here, using whole genome re-sequencing of 6 species of Sus (~ 40 samples) and one outgroup (Phacochoerus) we investigated the coalescence patterns of large genomic orthologous regions. We aim to identify lineages that have undergone episodic positive selection in order to find evidence of adaptation and domestication. Inferring these genome-wide patterns will help to resolve the phylogeographic history of Sus. Moreover, we expect this analysis to reveal precious observations on the influence of adaption due to speciation and artificial selection, on mammalian genomes. Finally, we aim to infer accurate estimates of origin and timing of domestication of the pig, and subsequent breed formation in China and Europe.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i016-R*

Symposium 21
Evolutionary ecological genomics

An evolutionary genomics approach reveals a novel gene underlying interpopulation variation in ethanol resistance in Drosophila melanogaster

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Summary statement:

A novel use of genome-wide expression data implicates a neurotransmitter receptor in natural variation in ethanol resistance in Drosophila melanogaster

Abstract:

Ethanol occurs naturally in decaying fruit, the breeding substrate of wild Drosophila melanogaster. Resistance to ethanol, as measured by the dose required to kill or sedate flies, is markedly higher in strains collected from Europe than in strains collected from tropical Africa. The powerful genomic resources and genetic tools available for D. melanogaster make this an excellent system for elucidating the genetic basis of a trait with both ecological and biomedical relevance. Previous work has focused exclusively on polymorphisms in Alcohol dehydrogenase and other enzyme genes, but these polymorphisms explain at most half of the resistance variation. To find other genes contributing to the variation, we used microarrays to identify genes that are differentially expressed between larvae from a European and African population, AND whose expression responded to artificial selection for ethanol resistance in an independent experiment. One such gene is a neurotransmitter receptor that showed lower expression in European than African larvae, and in selected than control larvae, suggesting that downregulation of the receptor increases ethanol resistance. Confirming this prediction, a mutant lacking the receptor shows a marked increase in ethanol resistance compared to genetically matched wild-type strains. We are currently investigating whether the downregulation of the receptor is due to cis-regulatory evolution. We are also using RNAi to knock down other genes that showed expression variation consistent with a role in ethanol resistance, and using QTL mapping and DNA sequence variation data to identify other genes that may contribute to ethanol resistance variation.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i009-E*

Symposium 21
Evolutionary ecological genomics

The effect of band sampling on accuracy of AFLP phylogeny estimation

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[1]Universidad de Vigo, Departamento de Bioquímica, Genética e Inmunología, Vigo, Spain

Summary statement:

Determining how many characters are required to eventually recover an accurate and well supported phylogeny is a key issue in modern molecular phylogenetics.

Abstract:

We examined the effect of increasing the number of sampled Amplified Fragment Length Polymorphism (AFLP) bands to reconstruct an accurate and well-supported AFLP-based phylogeny. In silico AFLP was performed using simulated DNA sequences evolving along balanced and unbalanced trees with recent, uniform and ancient radiations, and average branch lengths (from the most internal node to the tip) ranging from 0.02 to 0.05 substitutions per site. Trees were estimated by minimum evolution and maximum parsimony methods from both DNA sequences and virtual AFLP fingerprints. The comparison of the true tree to the estimated AFLP trees suggests that moderate numbers of AFLP bands are necessary to recover the correct topology with high bootstrap support values (i.e > 70%). This effect was most marked for shorter trees. However, branch length estimation was rather unreliable and did not improve substantially after a certain number of bands were sampled. These results hold for different levels of genome coverage and number of taxa analyzed. In silico AFLP using bacterial genomic DNA sequences recovered an accurate and well supported tree topology that mirrored an empirical phylogeny based on a set of 31 orthologous gene sequences when as few as 300 AFLP bands were scored. These results suggest that AFLPs may be in some circumstances an efficient alternative to traditional DNA sequencing for accurate phylogenetic reconstruction.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i018-R*

Symposium 21
Evolutionary ecological genomics

Identifying drivers of European wild boar disease prevalence, a genetic approach

Goedbloed DJ[1], Lutz W[2], Megens H-J[3], van Hooft P[1], van Wieren SE[1], Ydenberg RC[1], Prins HHT[1]
[1]Wageningen University, Resource Ecology Group, Wageningen, Netherlands, [2]Wildlife Research Institute, Bonn, Germany, [3]Wageningen University, Animal Breeding Genomics Centre, Wageningen, Netherlands

Summary statement:

We aim to identify key host population characteristics that influence European wild boar disease prevalence using genome-wide SNP assessment.

Abstract:

Wildlife diseases are considered a major risk factor for public health and livestock safety. Strikingly little is known about the spatial distribution and dynamics of diseases in natural populations. In this study we combine population genetic and antibody data from European wild boar (Sus scrofa scrofa) to identify population parameters that influence disease prevalence. We collected blood samples from disease monitoring programs in the Netherlands and two districts in Germany (Northrhine-westphalia and Rhineland-palatinate). Population genetic analysis was performed using a genome-wide 384 Single Nucleotide Polymorphism (SNP) assay based on the illumina 60k porcine SNP chip. In addition, we screened the samples for two host-specific respiratory diseases: Porcine Circovirus 2 (viral) and Mycoplasma hyopneumoniae (bacterial) using ELISA antibody tests. With these analyses we will try to correlate disease occurrence with effective population size, baseline genetic diversity and gene-flow. We hope to contribute towards a better understanding of wildlife disease dynamics and risk assessment.

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MON 22 AUG at 1630 - Room N6
Oral presentation *B4-Sy21-1630-O*

Symposium 21
Evolutionary ecological genomics

Comparative population genomics of the great ape male ejaculate

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Summary statement:

We collected targeted population genomic data from four great ape species to examine the selective forces driving the evolution of the male ejaculate.

Abstract:

The rapid evolution of reproductive genes is pervasive across many animals yet the selective forces driving this divergence remain poorly understood. Different species of great apes show divergent mating ecologies, providing a powerful system to investigate the influence of sperm competition on the evolution of reproductive genes. We have used custom microarrays to capture and Illumina sequence the majority of genes expressed in the male ejaculate of gorillas, chimpanzees, humans, and bonobos (20 individuals per species). To facilitate efficient population level sampling, we bar-coded individual samples to facilitate highly parallel sample multiplexing. Using this approach, we have generated high average sequencing coverage (>30X per individual) of over 1,000,000 target base pairs, spanning 385 genes. Our analysis of these population genomic data indicate high levels of evolutionary constraint across much of the ejaculate combined with pervasive positive selection on certain functional components. In particular, genes involved in immune defense and proteolysis appear to be recurrent targets of positive selection. We did not find strong evidence for more positive selection in bonobos and chimpanzees, as would be predicted given more intense sperm competition in these species. Rather, we found that the intensity of positive selection depends more strongly on species effective population size, as predicted by basic population genetic theory. These surprising results indicate that overall patterns of male reproductive protein evolution are not strongly dependent on inferred differences in the intensity of sperm competition between ape species.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i019-R*

Symposium 21
Evolutionary ecological genomics

The Arabidopsis lyrata genome sequence and the basis of rapid genome size change

Guo Y-L[1], Hu TT[2], Pattyn P[3,4], Bakker EG[5,6,7], Cao J[1], Cheng J-F[8], Clark RM[1], Fahlgren N[6,9], Fawcett JA[3,4], Grimwood J[8,10], Gundlach H[11], Haberer G[11], Hollister JD[12], Ossowski S[1], Ottilar RP[8], Salamov AA[8], Schneeberger K[1], Spannagl M[11], Wang X[11], Yang L[12], Nasrallah ME[13], Bergelson J[5], Carrington JC[6,9], Gaut BS[12], Schmutz J[8,10], Mayer KFX[11], Van de Peer Y[3,4], Grigoriev IV[8], Nordborg M[2,14], Weigel D[1]

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Summary statement:

The high-quality reference genome sequence for Arabidopsis lyrata will be a valuable resource for functional, evolutionary and ecological studies in the genus Arabidopsis.

Abstract:

We present the 207 Mb genome sequence of the outcrosser Arabidopsis lyrata, which diverged from the self-fertilizing species A. thaliana about 10 million years ago. It is generally assumed that the much smaller A. thaliana genome, which is only 125 Mb, constitutes the derived state for the family. Apparent genome reduction in this genus can be partially attributed to the loss of DNA from large-scale rearrangements, but the main cause lies in the hundreds of thousands of small deletions found throughout the genome. These occurred primarily in non-coding DNA and transposons, but protein-coding multi-gene families are smaller in A. thaliana as well. Analysis of deletions and insertions still segregating in A. thaliana indicates that the process of DNA loss is ongoing, suggesting pervasive selection for a smaller genome.

Tina T. Hu and Pedro Pattyn contributed equally to this work.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i020-R*

Symposium 21
Evolutionary ecological genomics

How specific is innate immunity? - Assessing genome wide gene expression under controlled parasite challenge in three-spined sticklebacks

Haase D[1], Rieger J[1], Eizaguirre C[1], Sietmann A[2], Bornberg-Bauer E[3], Stoll M[2], Kalbe M[4], Reusch T[1]
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Summary statement:

We investigated transcriptome patterns of trematode infected three-spined sticklebacks to understand differences and specificity of vertebrate adaptive and innate immunity.

Abstract:

Host-parasite interactions are regarded as being one of the major driving forces in evolution. Species are constantly confronted with attacks of numerous pathogen species. In response to these selective pressures host populations developed genetically encoded immune responses that in turn need to be overcome by parasite counter-adaptations, an ongoing evolutionary arms race. Adaptive MHC based immunity is a highly specific system to counteract parasite attacks, but its initiation is rather slow. Hence, most parasite attacks are cleared by the phylogenetically older innate immune defence, which may be more specific than previously thought. We investigated genome wide gene expression patterns of naive lab-bred three-spined sticklebacks (Gasterosteus aculeatus) experimentally challenged with a parasitic trematode (Diplostomum pseudospathacaeum), using deep coverage Illumina RNA sequencing. These unique data allow us to disentangle differences between expression profiles of single and multiple infections, gaining insight into gene expression patterns of innate and adaptive immunity. In addition we tested for specificity of gene expression in innate immunity using monoclonal parasite lines in single infection treatments in comparison to heterologous repeated infections.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i010-E*

Symposium 21
Evolutionary ecological genomics

Variation in female reproductive condition in wild Drosophila melanogaster populations

Haddrill P[1]
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Summary statement:

Linking population genetics to variation in reproductive condition of wild female D. melanogaster from Europe, North America and Africa.

Abstract:

D. melanogaster is one of the most important model organisms in evolutionary biology both in terms of the level of understanding we have of its genome and the ease with which it can be used in the laboratory. In particular, the abundance of genetic data both within and between species make D. melanogaster and its close relatives an ideal system in which to test the predictions of population genetics theory. One notable area in which we know very little about D. melanogaster, however, is in the ecology of its natural populations. An understanding of features such as the mating system and reproductive biology of wild populations would make this species a powerful tool for linking population genetics theory to the reality of a natural species. One important aspect of the mating system is the reproductive condition of females in the wild, since this will have significant implications not only for the reproductive output and remating behaviour of individual females, but also in terms of the effective population size of females relative to males in the population. Female D. melanogaster can control egg maturation in response to nutritional status, so reproductive condition might be predicted to vary between populations depending on the resources available to females and how well adapted they are to different habitats. I am using dissection to determine the vitellogenic status of maturing oocytes in the reproductive tract of female D. melanogaster from Europe, North America and Africa, in order to assess variation in reproductive condition within and between populations and the impact of this on the predictions of population genetics models.

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MON 22 AUG at 1400 - Room N6
Invited talk *B3-Sy21-1400-I*

Symposium 21
Evolutionary ecological genomics

Ecological genomics and eco-evolutionary dynamics in the Glanville fritillary butterfly

Hanski I[1]
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Summary statement:

This talk illustrates the opportunities to combine ecological and genomic research and how mathematical modeling can be employed to address eco-evolutionary dynamics.

Abstract:

The Glanville fritillary butterfly has become an ecological model system for the study of the ecological, genetic and evolutionary consequences of spatially fragmented population structures. A large-scale genomic project has been initiated involving transcriptome and genome sequencing and studies of genetic variation in natural populations. In this talk, I will highlight some of the research questions especially with work on one gene, phosphoglucose isomerase (Pgi). This example illustrates the opportunities to combine ecological and genomic research in the context of long-term observational studies of natural populations and how mathematical modeling can be employed to address eco-evolutionary dynamics.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i021-R*

Symposium 21
Evolutionary ecological genomics

Evidence of a neo-sex chromosome in birds

Hansson B[1], Pala I[1], Naurin S[1], Stervander M[1], Hasselquist D[1], Bensch S[1]
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Summary statement:

Evidence of a neo-sex chromosome in birds offers an exciting starting point for studying the role of sexually antagonistic selection on genome evolution in this lineage.

Abstract:

Neo-sex chromosomes often originate from sex chromosome–autosome fusions and constitute an important basis for the study of gene degeneration and expression in a sex chromosomal context. Neo-sex chromosomes are known from many animal and plant lineages, but have not been reported in birds, a group in which genome organization seems particularly stable. Following indications of sex linkage and unexpected sex-biased gene expression in warblers (Sylvioidea; Passeriformes), we have conducted an extensive marker analysis targeting 31 orthologues of loci on zebra finch chromosome 4a in five passerine species, representative independent branches of Passerida. We identified a region of sex linkage in three Sylvioidea passerine species, covering approximately the first half (10 Mb) of chromosome 4a. The sex-specific sequence patterns suggest an association of the markers to both Z and W. For the same species, markers located between 10 and 21 Mb of chromosome 4a showed no signs of sex linkage, suggesting that only half of the chromosome was involved in this transition. No sex linkage was observed in non-Sylvioidea passerines, indicating that the neo-sex chromosome arose at the base of the Sylvioidea branch of the avian phylogeny, at 47.2–37.4 MYA, substantially later than the ancestral sex chromosomes (150 MYA). We hypothesize that the gene content of chromosome 4a might be relevant in its transition to a sex chromosome, based on the presence of genes (e.g. the androgen receptor) that could offer a selective advantage when associated to Z-linked sex determination loci.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i011-E*

Symposium 21
Evolutionary ecological genomics

Is the genome integrity of Bdelloid rotifers preserved following desiccation?

Hespeels B[1], Li X[1], Flot J-F[1], Koszul R[2], Van Doninck K[1]
[1]Unit of Research in Organism Biology (URBO), University of Namur (FUNDP), Namur, Belgium, [2]2 Team of “spatial regulation of genomes”, Institut Pasteur, Paris, France

Summary statement:

Pulsed Field Gel Electrophoresis (PFGE) method investigates the genome integrity of ancient asexual bdelloid rotifers Adineta vaga after desiccation

Abstract:

Bdelloid rotifers are of particular interest to evolutionary biologists. Their unique clonal mode of reproduction, together with their ready accessibility to laboratory experimentation, make this group an unusual, attractive model to study the consequences of long-term asexual evolution. In addition to their famous ancient asexuality, bdelloid rotifers have the capacity to desiccate at any stage in their life cycle and therefore can inhabit semi-terrestrial habitats.

Desiccation is prone to induce DNA DSBs, this has been demonstrated in Deinoccoccus radiodurans, but never in bdelloid rotifers. We apply the Pulsed Field Gel Electrophoresis (PFGE) method to investigate the genome integrity of bdelloid rotifers after desiccation. First, the bdelloid species Adineta vaga is experiencing desiccation for different lengths of time following the “kinetic” applied for D. radiodurans: 1, 4, 8, 14, 28 and 42 days. Survival and DNA integrity is checked after each period. This experiment investigates whether DNA double strand breaks appear after desiccation and when. Second, the kinetics of DNA double strand break repair will be investigated.

In parallel, we develop AFLP and microsatellite markers. These markers will be used to study the clonal diversity found in natural bdelloid rotifer populations (see Poster X. Li et al.). Moreover, we will investigate the evolution of genetic diversity in bdelloid clones experiencing rounds of desiccation.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i013-E*

Symposium 21
Evolutionary ecological genomics

Resistance of D. melanogaster against parasitation by A. tabida in artificially selected populations

Jalvingh K[1], Werheim B[1], Nuzhdin S[2], Bijlsma K[3]
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Summary statement:

Using Drosophila melanogaster lines artificially selected for increased parasitoid resistance against Asobara tabida we associate genetic variation to the differential phenotype.

Abstract:

We study the evolutionary consequences of a rapid selection response for increased parasitoid resistance in Drosophila melanogaster. In this parasitoid-host system larvae from the Drosophila genus are parasitized by Asobara parasitoid wasps. Through an evolved innate immune response, in some cases the fly larva is able to sequester and kill the parasitoid egg. There is considerable genetic variation in the strength of the immune response both within and between Drosophila populations. We aim to elucidate the genetic basis of this adaptive variation in parasitoid resistance, by HT sequencing of lines selected for increased parasitoid resistance. While differences in gene expression associated with parasitoid defense are being characterized, the genetic basis of parasitoid resistance is poorly understood. By combining artificial selection techniques and next generation sequencing, we look for candidate positions involved in the selection response for increased parasitoid resistance.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i014-E*

Symposium 21
Evolutionary ecological genomics

Lack of linkage disequilibria between chromosomal arrangements and mtDNA haplotypes in Drosophila subobscura population from the Sicevo Gorge (Serbia)

Jelic M[1], Castro JA[2], Kurbalija Novicic Z[3], Kenig B[3], Dimitrijevic D[3], Savic Veselinovic M[1], Jovanovic M[1], Milovanovic D[4], Stamenkovic-Radak M[1,3], Andjelkovic M[1,3,5]

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Summary statement:

Our results mostly go in favor to the hypothesis of transience of cytonuclear linkage disequilibria in natural populations of Drosophila subobscura.

Abstract:

Aims: The aim of our study was to shed more light on the role of cytonuclear interactions in shaping the variability of mtDNA haplotypes in natural populations of Drosophila subobscura.
Methods: D. subobscura flies were collected from the Sicevo Gorge, which is exceptionally interesting from the geo-botanical point of view as refugia during the Ice Age. Compared to surrounding region, it represents more stable habitat where temperature fluctuations are buffered. The population was analyzed with respect to mtDNA haplotypes and chromosomal arrangements. Population was tested for the presence of Wolbachia. Analysis of nuclear microsatellite variability was also conducted to investigate possibility of recent bottleneck.
Results: The presence of Wolbachia was not detected. Recent bottleneck for nuclear microsatellite loci was also discarded. Two main haplotypes (I and II) were found, as well as a series of less common ones. One of the haplotypes harbored large duplication (2.7kb) in the A+T rich region. The Tajima's D value was negative, but not significant. We did not detect any significant linkage disequilibrium between two most frequent mtDNA haplotypes and any of the chromosomal arrangements.
Conclusions: Lack of linkage disequilibria in the analyzed population, with its habitat distinctiveness, mostly go in favor to the hypothesis of transience of cytonuclear linkage disequilibria in natural populations of D. subobscura.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i022-R*

Symposium 21
Evolutionary ecological genomics

Genome-wide association mapping reveals selection, heterozygote superiority and evolutionary dynamics at the Horns locus in Soay sheep

Johnston SE[1,2], Pickering NK[3], McEwan JC[3], Gratten J[4], Kijas JW[5], Beraldi D[6], Pemberton JM[6], Slate J[1]
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Summary statement:

Genetic mapping using ~36,000 SNPs identifies a candidate gene for Horns, and indicates that increased fitness in heterozygous sheep maintains genetic variation in horn morphology.

Abstract:

Revealing genes and genomic regions contributing to trait variation in wild populations creates the opportunity to understand why genetic variation is often maintained despite apparent directional selection. This is particularly true in cases where different genotypes can cause similar phenotypes with unequal fitnesses. Soay sheep have an inherited polymorphism for horn type in both sexes, which is likely to be controlled by a single locus, Horns. Males present either large, normal horns or small, deformed horns (scurs), and females are either normal-horned, scurred or without horns (polled). Scurred males and polled females have reduced fitness, and so it is counterintuitive that they persist within in the population. A genome-wide association study using ~36,000 single nucleotide polymorphisms (SNPs) mapped Horns to a single candidate gene, Relaxin-like receptor 2 (RXFP2) on chromosome 10. Further investigation revealed that Horns has two alleles, Ho+ and HoP, with differences in dominance between the sexes and for the first time, sheep with the same horn phenotype but different underlying genotypes can be identified. We found that despite its association with reduced fitness phenotypes, the HoP allele has been increasing in frequency at a greater rate than expected through drift alone. By examining the relationship between fitness and Horns genotype, we show that the presence of the HoP allele (and therefore the horn type polymorphism) is likely to be maintained by heterozygote superiority in this population.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i023-R*

Symposium 21
Evolutionary ecological genomics

Hybridisation promotes adaptation in the Faroe house mouse

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Summary statement:

From genome-wide SNPs ,we show that the Faroe house mouse is the result of a M. m. musculus introgression into a largely domesticus background, which may have promoted adaptation.

Abstract:

Island biology has a special place in evolutionary biology, with islands acting as natural laboratories in which theories about evolution, ecological turnover, speciation and adaptation can be formulated and tested. Here we investigate the role of hybridisation on adaptation and differentiation in the context of the Faroe house mouse. Originally described as a distinct subspecies, Mus musculus faeroensis, the Faroe house mouse has long attracted attention as being unusually large and possessing unique morphological characters. Using high-density genotyping, we identified >73,000 ancestry informative SNP markers and show that the Faroese house mice arose through a M. m. musculus introgression into a largely M. m. domesticus background. Having identified areas of M. m. musculus introgression within the genome, we estimated a likely demographic scenario of this hybridization. Our molecular data supports multiple selective sweeps arising from these introgressions. A geometric morphometric analysis revealed that the Faroe house mice exhibit greatly divergent skull morphology compared to continental populations, as was described in the early literature, and show similarities to F1 hybrid morphology generated in laboratory crosses between M. m. musculus and M. m. domesticus strains. Taken together, our results suggest that the Faroe house mouse genome has undergone extensive hybridisation and the molecular data support an adaptive trajectory. Therefore, despite founder effects and small effective population sizes, rapid adaptation is clearly possible among island populations, and we hypothesise that hybridisation may promote such adaptation.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i024-R*

Symposium 21
Evolutionary ecological genomics

Chromosomal rearrangements and the genomics of polymorphic mimicry in butterflies

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Summary statement:

Genomic rearrangements explain the maintenance of highly divergent alleles controlling the coexistence of multiple mimetic forms in a tropical butterflly.

Abstract:

Heliconius butterflies are emerging models to understand the genomics of major morphological adaptations, such as wing-pattern mimicry. Heliconius are very diverse for their colourful wing-patterns used to advertise predators of their unpalatability. Geographic variation in mimicry is generally controlled by multiple, large-effect loci scattered around the genome. In one species though, Heliconius numata, multiple mimetic forms fly together in sympatry, under balancing selection for mimicry of multiple models (Melinaea butterflies), and the polymorphism is controlled by one single "supergene" locus (P). This supergene is homologous to one cluster of loci known from the other species. To understand how the supergene has evolved in H. numata from a scattered multilocus "toolbox", we investigated the role of rearrangements in maintaining co-adapted gene complexes, and explored the effects of the ancestral multilocus architecture in controlling phenotype. Using BAC-walk approach and 454-based gene annotation, we detected multiple genetic rearrangements coexisting in wild polymorphic populations. Those rearrangements are strictly associated with colour-pattern polymorphism at P, and with striking patterns of long-range linkage disequilibrium, in contrast with control loci around the genome. We show that genomic rearrangements explain the maintenance of divergent alleles controlling the coexistence of multiple mimetic forms in this butterfly. Analysis of Illumina sequences covering the entire length of this region (Agilent sequence capture) and comparison to the reference Heliconius genome will be discussed, to explore the role of structural variants in adaptive evolution.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i025-R*

Symposium 21
Evolutionary ecological genomics

Evolution of gene expression variation in Capsella grandiflora

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Summary statement:

Using next-generation DNA and RNA sequence data to evaluate variation in gene expression and investigate selection on variably expressed genes.

Abstract:

Genetic and phenotypic variation is widespread in natural populations; however, it is unknown whether this variation is most commonly maintained by selective or neutral forces. By examining patterns of variation in genotype and phenotype, in this case gene expression levels, it is possible to better understand the role that selection may play in maintaining variation. Capsella grandiflora is a useful model system for this endeavor, as previous studies have found high levels of polymorphism in coding regions. Here we use genome-wide next generation DNA and RNA sequence data from individuals collected across C. grandiflora's range to determine both the extent of variation in gene expression levels and whether selection acts differently on genes with high and low expression levels and on genes that are more or less variably expressed.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i026-R*

Symposium 21
Evolutionary ecological genomics

Genetic variation in mitochondrial and immunological genes between two resource morphs of Arctic charr (Salvelinus alpinus) in Lake Thingvallavatn, Iceland

Kapralova KH[1], Reynisdottir S[1], Vilmundarson RO[1], Santos CB[1,2], Guðbrandsson J[1], Maier V[1], Snorrason SS[1], Palsson A[1]
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Summary statement:

Genetic differentiation between two resource morphs of Arctic charr from Thingvallavatn based on sequence variation in the mitochondrial control region and immune system genes.

Abstract:

Lake Thingvallavatn (Iceland) harbors four closely related morphs of Arctic charr (Salvelinus alpinus): two limnetic (planktivore and piscivore) and two benthic (large and small benthivorous charr). Although the two smaller morphs, the planktivorous (PL) and small benthivorous (SB) charr show a complete reproductive overlap in time and space, they are quite distinct in morphology and ecology. These morphs exhibit distinctive patterns in parasite load and prevalence: SB charr had high parasite load and prevalence of the eye fluke Diplostomum sp whereas PL were highly infected with Diphyllobothrium spp. (Frandsen and al. 1989). The different infection patterns between the two morphs are consistent with differences in food partitioning and habitat usage. Moreover previous study using 10 neutral microsatellite markers has shown a small but significant genetic differentiation between small benthivorous and planctivorous charr, consistent with a strong reproductive isolation between the morphs throughout the Holocene (Kapralova et al. 2011). Here we report on a study of sequence variation in the mitochondrial control region and immune system genes (cathelecidin, hepcidin, MHC2-alfa) and assess the degree of differentiation between small benthivorous and planctivorous charr at these loci. Second, we will test for association between immunological genes and ecological attributes such as parasite load and prevalence in 250 freshly caught small benthic and planctivorous charr.

References:

Frendsen F, Malmquist HJ, Snorrason SS (1989). J. Fish Biol. 34, 281-297
Kapralova KH, Morrissey MB, Kristjansson BK, Olafsdottir GA, Snorrason SS, Ferguson MM (2011).Heredity 106, 472-487

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i027-R*

Symposium 21
Evolutionary ecological genomics

Genome scanning reveals habitat dependent selection and an intermediate optimal heterozygosity level in a marine angiosperm

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Summary statement:

In the clonal plant Zostera marina, we detected habitat dependent selection and an intermediate optimal outcrossing at the molecular genetic level.

Abstract:

Seagrasses are important ecosystem-engineers in coastal soft sediments worldwide that are studied in widely diverging habitats. Eelgrass (Zostera marina L.) has recently become a genetic semi-model species with growing genetic resources such as EST databases and ~100 genetic markers (microsatellites and SNP). We aimed to detect divergent selection and putative habitat adaptation at the molecular genetic level. To this end, we compared replicated habitat pairs of permanently submerged versus intertidal eelgrass populations using genome scans, a powerful tool to detect natural selection in natural populations among a larger sample of marker loci. Three different statistical approaches for outlier identification revealed divergent selection at 6 loci that are linked to genes involved in osmoregulation and water balance, suggesting different osmotic stress, and reproductive processes (seed maturation), pointing to different life history strategies.
Using a larger collection of markers, we also assessed whether intermediate heterozygosity and hence, intermediate outcrossing levels are correlated with maximal fitness among seagrass clones. As clone size is an appropriate proxy for fitness in a clonal plant such as Z. marina, we correlated the spatial extension of 168 clones with multi-locus heterozygosity values. For the first time in a clonal plant, we show that intermediate heterozygosity is associated with the largest clone sizes, confirming the hypothesis that not only inbreeding but also outbreeding depression contributes to fitness components in a long living clonal organism.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i028-R*

Symposium 21
Evolutionary ecological genomics

Patterns of neutral and potentially adaptive genetic divergence between trout and bullhead populations along altitudinal gradients in the Swiss Alps

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Summary statement:

The extent of adaptive genetic divergence between Alpine trout and bullhead populations is assessed with genome scans and related to gene flow.

Abstract:

The ability of species to respond to environmental change depends critically on the amount and distribution of adaptive genetic diversity within and between populations. We compare these spatial patterns between two key fish taxa in pre-alpine and alpine streams, the European trout species complex (Salmo spp) and the bullhead (Cottus gobio). Both taxa have a very wide altitudinal distribution but the levels of natural and human-mediated dispersal are expected to be markedly higher in trouts than bullheads. If local adaptation is primarily constrained by gene flow, these differences predict stronger divergent adaptation in bullheads than in trouts.Samples were collected along altitudinal transects replicated in three major drainage systems in the Swiss Alps and genotyped at microsatellite and amplified fragment length polymorphism (AFLP) markers. In both taxa, we detected distinct genetic clusters corresponding to different European drainages. While some neutral genetic differentiation and evidence of isolation by distance within drainages was observed also in trout, local population differentiation was more pronounced in the less mobile bullheads. The extent of potentially adaptive divergence at different spatial scales is quantified as the proportion of markers showing evidence of divergent selection in outlier scans. We then investigate if potentially adaptive divergence is i) consistently higher in bullheads than in trouts and ii) increases with geographical distance between populations of the same species as would be predicted if local adaptation is indeed constrained by gene flow

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SUN 21 AUG at 1650 - Room N6
Oral presentation *A4-Sy21-1650-O*

Symposium 21
Evolutionary ecological genomics

Black or red: Identification of a polymorphic pigmentation gene associated with genetic incompatibility in the Gouldian finch (Erythrura gouldiae)

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Summary statement:

A sex-linked polymorphic gene that determines melanin / carotenoid pigmentation was identified in the Gouldian finch (Erythrura gouldiae).

Abstract:

The Gouldian finch (Erythrura gouldiae) has three genetically determined colour morphs in the wild: red, black and yellow. The colour polymorphism is known to be under the control of two Mendelian loci. The sex-linked Red locus that determines melanin (black, Zr) / carotenoid (red, ZR) pigmentation is linked to many physiological and behavioural differences between morphs. In particular, previous studies have shown assortative mating and genetic incompatibility among the morphs in a captive population and it is possible that these morphs represent incipient species. While the colour polymorphism is the key identifiable trait, the molecular genetic basis of the polymorphism has not been determined.

The Gouldian finch is a close relative of the zebra finch (Taeniopygia guttata), the genome of which is now available; there is strong synteny between these avian genomes. We have constructed a genetic marker linkage map of the Gouldian finch Z chromosome and identified the location of the Red locus to a 6.2-Mbp region of the zebra finch Z chromosome. To pinpoint the gene itself, we constructed and sequenced restriction site associated DNA (RAD) libraries by next-generation sequencing and typed >3000 Z markers in black and red morphs. We identified a locus with perfect association with the colour polymorphism that also fell in the target region found by linkage mapping; the locus is located in the potential regulatory region of a gene that may act as a regulator of melanin production. This study has potential to illuminate our understanding of incipient speciation as well as providing new insights into the mechanism of pigmentation and the wider action of the underlying gene.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i029-R*

Symposium 21
Evolutionary ecological genomics

Contrasting whole-genome sequence diversity in the selfer Arabidopsis thaliana and the outcrosser A. lyrata

Kim S-T[1], Mao J-F[1], Hagmann J[1], Lanz C[1], Cao J[1], Guo Y-L[1], Schneeberger K[1,2], Weigel D[1]
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Summary statement:

Whole-genome sequences of 80 A. thaliana and 32 A. lyrata individuals provide insight into effects of life history on genomic diversity in two closely related species.

Abstract:

Arabidposis lyrata is a close relative of model plant, A. thaliana, but the two species differ in many important life history and other traits: Outcrossing versus selfing, annual versus perennial life style, genome size and chromosome numbers. As part of the 1001 Genomes project for A. thaliana (http://1001genomes.org), we have recently sequenced 80 inbred strains of this species. Because A. lyrata is an outcrosser, resequencing natural strains is problematic, because phasing information is difficult to recover. We have therefore developed a new strategy, the sequencing of F1 hybrids between natural strains and the inbred reference strain MN47. In 32 individuals, we have identified between 0.6 and 1.3 million SNPs, which compares with an average of 0.6 million SNPs in each of the A. thaliana strains. There is a distinct genome-wide pattern of genetic differentiation between North American and European accessions. We will present inferences about how the different life histories have shaped sequence diversity in A. thaliana and A. lyrata.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i030-R*

Symposium 21
Evolutionary ecological genomics

Population genomic analysis of speciation and radiation in Capsella rubella

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Summary statement:

Investigation of the genetic and phenotypic effects of speciation and radiation after an extreme and very recent bottleneck.

Abstract:

Despite the importance of speciation as a biological phenomenon, speciation as a process remains poorly understood. To amend this situation, we are investigating the genomic footprints of the recent speciation of the plant Capsella rubella. C. rubella is thought to have diverged from C. grandiflora via a single individual in the north of Greece under 25,000 years ago. After this massive bottleneck, C. rubella successfully colonized the majority of Western Europe where it was required to adapt to new environmental conditions. It is unclear how such adaptation might occur given the short time frame and extremely limited genetic diversity at the birth of this species. To initiate our study of this phenomenon, we have generated whole genome sequences from 24 C. rubella individuals collected from throughout Europe. From this sequence data we can reconstruct the process of radiation, and identify regions of the genome that have been under recent selection. The pattern of diversity in these lines is strikingly dissimilar to that previously shown in the related plant, A. thaliana, and may make C. rubella a more tractable system to link phenotypic variation to causal genotypic differences. In parallel, we have initiated studies of phenotypic divergence and its genetic basis in C. rubella. Our work provides a snapshot of speciation and radiation in process and insight into the rapid evolution of new phenotypes.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i016-E*

Symposium 21
Evolutionary ecological genomics

Ecological significance of microsatellite variation in Central Balkan populations of Drosophila subobscura

Kurbalija Novicic Z[1], Jelic M[2], Jovanovic M[2], Dimitrijevic D[2], Savic Veselinovic M[2], Stamenkovic-Radak M[2,3], Andjelkovic M[4,5,6]

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Summary statement:

The microsatellites variability in five Central Balkan populations are shaped by distinct ecological and micro-habitat conditions.

Abstract:

The Balkan Peninsula acted as one of the main European refugia during the last two million years of glacial-interglacial climatic oscillations. In the present study we performed screening of population genetic structure of five Drosophila subobscura natural populations settled on geographically and ecologically different habitats of Central Balkan region, using 11 microsatellite loci. Two populations (B and O) are two closely situated but are within very distinct microhabitats; other two (T and S) were collected in highly stable ecosystems where temperature fluctuations are buffered; the fifth one (BG) was collected from habitat with very specific microclimate and surrounded by high anthropogenic activity. The aim was to assess the level of genetic diversity and population differentiation in the context of different ecological background.

The highest level of genetic diversity was detected in population collected in habitat with very specific microclimate (BG). The statistically significant differences in allelic size range and expected heterozygosity were found between populations situated in ecologically distinct microhabitats, irrespective of their geographical distance. The locus by locus AMOVA showed slight between population differentiation (FST=0.00996, p>0.05).

Our results strongly suggest adaptive population divergence and indicate local adaptations at the DNA level (probably between inversions and microsatellite loci) in a background of high levels of gene flow. Furthermore, this study highlights the contribution of the analysis of microsatellite loci for demonstrating local selection.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i031-R*

Symposium 21
Evolutionary ecological genomics

Inheritance of gene expression in threespine stickleback

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Summary statement:

In order to investigate the importance of specific genes on the response to thermal stress and sex, we examined genome-wide heritability in 60 families of threespine stickleback.

Abstract:

Studies from the wild suggest that the amount of genetic variation expressed in phenotypic traits relate inversely to traits' importance to fitness. However, whether the lower heritability of the fitness related traits is caused by lower levels of additive genetic variance or increased levels of environmental variance remains unclear. Likewise, whether expression of genetic variation – and hence evolutionary potential – is generally increased or reduced by environmental stress remains an open question. In attempt to address these issues, we went directly to the gene level to estimate heritability across the genome, specifically focusing on the response to thermal stress as well as sex-specific heritabilities. Using an Aligent custom oligonucleotide microarray designed for threespine stickleback (Gasterosteus aculeatus), we determined mRNA expression of 10899 genes for 570 individuals originating from a half-sib design in which individuals from 60 full-sib families were subject one of two temperature treatments. Patterns of inheritance with respect to sex, treatment, chromosomal location and functional gene category were determined. Overall the power to detect heritability was high, and most genes had heritabilities significantly above zero, with approximately 10% of genes having heritabilities over 0.5. Many genes exhibited higher heritabilities in a stressed environment than in ambient conditions. Additionally, certain gene categories seemed overrepresented among genes with high heritabilities, which may impact fitness.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i017-E*

Symposium 21
Evolutionary ecological genomics

Ecological vs. phylogenetic determinants of trophic associations in a plant-leafminer-parasitoid food web

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Summary statement:

We investigated the evolutionary assembly and current structure of the tritrophic food web involving plants, leaf-mining sawflies, and parasitoids.

Abstract:

Plants, insect herbivores, and parasitoids form extremely complex and species-rich food webs. Specialist parasitoids can theoretically spur herbivore speciation if parasitoid–herbivore associations are influenced by the herbivores' host-plant use; in such cases, parasitoid pressure could push herbivores onto "enemy-free space" provided by novel hosts. The purpose of this study was to investigate the evolutionary assembly and current structure of the tritrophic food web involving northern plants, tenthredinid leaf-mining sawflies in the tribe Fenusini, and the numerous parasitoids that attack fenusines. We reconstructed the phylogenies of focal plants and sawflies on the basis of DNA sequence data, and combined the information with a classification-based parasitoid phylogeny and a matrix of parasitoid–leafminer associations. Thereafter, we used the phylogenetic bipartite linear model (pblm) in R to estimate the effects of plant and leafminer phylogenies on parasitoid–leafminer associations. Our results show that: (1) leaf-mining sawflies have radiated well after their host plants, and there have been frequent convergent shifts among a handful of plant taxa; (2) parasitoid–leafminer associations are only weakly influenced by the phylogenetic relationships among leaf-mining sawflies; and (3) by contrast, phylogenetic relationships among the leafminers' host plants have a clear effect on how parasitoids attack different leafminer species. The strong effect of leafminer ecology on parasitoid attack patterns indicates that host-plant shifts may provide leafminers with a refuge from parasitoids, meaning that natural enemies can accelerate speciation in herbivorous insects.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i032-R*

Symposium 21
Evolutionary ecological genomics

Selection patterns on hybrid genomes provide new insights into mechanisms of reproductive isolation in Populus

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[1]University of Fribourg, Biology, Ecology & Evolution, Fribourg, Switzerland, [2]University of Wyoming, Wyoming, United States, [3]Royal Botanic Gardens Kew, Kew, United Kingdom

Summary statement:

Genomic admixture analysis in ecologically divergent, hybridizing Populus spp. indicates unexpected patterns of selection.

Abstract:

The study of hybrid zones offers great opportunities for evolutionary ecological genomics because (1) reproductive isolation is not yet complete, thus the formation of species barriers can be caught in action, and (2) introgression of genes from one species into another due to porous species barriers can be a shortcut to adaptation to rapidly changing environments. Postzygotic reproductive isolation is often attributed to selection against heterozygotes, but few studies exist that explicitly examined the distribution of heterospecific genotypes across loci. We used individual-based methods to study the degree of interspecific heterozygosity across the genome of natural hybrids from three replicate hybrid zones of Populus alba and P. tremula, two ecologically divergent forest trees, to get insight into the patterns of selection acting on hybrid genomes. We show that (1) marked genotypic gaps exist between recombinant hybrids and each of their parental species, consistent with strong reproductive isolation both between the two species and between hybrids and parents, (2) the genomes of admixed individuals show signatures of both, selection for and against heterospecific genotypes, depending on each locus, and (3) most of these patterns are consistent across individuals and replicate hybrid zones, indicating strong genome-wide processes of selection. We will discuss how the complex selection patterns might contribute to the maintenance of reproductive isolation while at the same time retaining the potential for adaptive introgression of ecologically important phenotypic traits, which might be an important feature in rapidly changing environments.

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MON 22 AUG at 1650 - Room N6
Oral presentation *B4-Sy21-1650-O*

Symposium 21
Evolutionary ecological genomics

Finding genes under selection by integrating high-throughput sequencing into AFLP genome scans of non-model organisms

Lischer HE[1], Excoffier L[1], Heckel G[1]
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Summary statement:

Next-generation sequencing was used to identify candidate loci in amplified fragment length polymorphism genome scans of Microtus arvalis populations.

Abstract:

Genome scans provide means to identify the genetic basis of adaptations without previous knowledge about the selectively advantageous genetic variants or the particular traits under selection. For non-model species, amplified fragment length polymorphisms (AFLP) provide access to very large numbers of markers which can be used to identify outlier loci relative to the neutral genomic background. However, AFLP genome scans provide no information on where the markers of interest are located in the genome and e.g. whether they consist of coding or non-coding sequences. Here we used next-generation sequencing to remove this issue of anonymous genome scans and connect allele frequency-based inferences from natural populations with information on genomic location and functionality of candidate loci. We applied this development to two case studies where we scanned the genomes from population samples of a small rodent (Microtus arvalis) for outlier AFLP loci associated with adaptation to high altitude or balancing selection across Europe. We sequenced the AFLP fragments from 15 individuals with Roche 454 Titanium technology. Mapping of the de novo assembled reads showed that our analyses covered AFLP markers randomly distributed along all chromosomes with a strong correlation between marker number and chromosome length. Using information about the length of the AFLP markers and presence/absence in individuals, we were able to identify candidate sequences, which we used to determine the genomic location of markers identified as under selection in the genome scan. This approach allowed us to identify promising candidate genes involved in adaptation in natural rodent populations.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i033-R*

Symposium 21
Evolutionary ecological genomics

Using Affymetrix Mouse Genome Diversity Array for whole genome SNP analysis in wild mice populations

Lorenc A[1], Staubach F[2], Tautz D[1]
[1]MPI Evolutionary Biology, Evolutionary Genetics, Plön, Germany, [2]Stanford University, Palo Alto, United States

Summary statement:

We demonstrate issues with using whole-genome SNP Affymetrix Mouse Genome Diversity Array with wild mice and present a way to improve the data quality.

Abstract:

Assessment of genome wide variation in wild mice with genotyping arrays is confounded by unforeseen SNPs or indels. Those additional polymorphisms flanking the polymorphism that is supposed to be genotyped can hamper binding to the probes and lead to false genotype calls.
By application of the Affymetrix Mouse Genome Diversity Array, which was based on the genomic sequence of mainly laboratory mice of Mus musculus domesticus origin, we found that many SNP probes are not complementary to wild mice genome, as their target regions contain additional polymorphisms. SNP calling algorithms do not cope well with this problem and create artificial heterozygous calls, making the data hard to interpret in population genetics analyses.
We developed a filtering method, to be used after the standard calling algorithm, that efficiently removes false heterozygous calls. We show that this method and specific calling parameters do improve SNP data and make it more reliable.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i018-E*

Symposium 21
Evolutionary ecological genomics

Contrasting genetic architecture of reproductive isolation and differential adaptation in a marine hybrid zone: The bivalve Macoma balthica

Luttikhuizen PC[1,2], Drent J[1], Peijnenburg KT[3], van der Veer HW[1], Johannesson K[2]
[1]NIOZ Royal Netherlands Institute for Sea Research, Marine Ecology, Den Burg, Netherlands,
[2]University of Gothenburg, Strömstad, Sweden, [3]University of Amsterdam, Amsterdam, Netherlands

Summary statement:

From AFLP genome scans across a marine hybrid zone, we conclude that genomic clines analysis is a useful statistical tool for genome analysis in non-model taxa.

Abstract:

Genetic architecture of reproductive isolation and differential adaptation is studied in a secondary contact zone where extensive admixture occurs. In a non-model marine bivalve (Macoma balthica) we apply both Fst outlier analysis and genomic clines analysis to AFLP genome scans of samples spanning the contact zone in the Skagerak-Kattegat-Baltic (SKB) region. The genomic clines analysis shows that large portions of the genome are involved in reproductive isolation inside the hybrid zone. As much as 38% of the AFLP markers do not conform to a neutral mixing model of hybrid genotypes. Differential adaptation is detected in the form of 19% of markers that are significant Fst outliers. Interestingly, the loci involved in reproductive isolation and those in differential adaptation show only limited overlap. This suggests that some genomic regions are differentiated but behave neutrally in hybrids, while, at the same time, other regions behave non-neutrally within hybrid genomes but are not differentiated between genetic lineages. We conclude that genomic clines analysis is a useful statistical tool for genome analysis in non-model taxa.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i019-E*

Symposium 21
Evolutionary ecological genomics

Genomic consequences of a genetic rescue in a small population of bighorn sheep (Ovis canadensis)

Miller JM[1], Poissant J[1], Hogg JT[2], Coltman DW[1]
[1]University of Alberta, Biological Sciences, Edmonton, Canada, [2]Montana Conservation Science Institute, Missoula, United States

Summary statement:

Following a genetic rescue alleles were inherited non-neutrally, and at different rates. In addition, longevity and reproductive success were correlated with genomic ancestry.

Abstract:

Genetic rescue is a management intervention whereby a small population is supplemented with individuals from other populations in an attempt to reverse the effects of inbreeding and increased genetic load. One such rescue was carried out in the population of bighorn sheep (Ovis canadensis) within the National Bison Range wildlife refuge (Montana, USA). We examined the genomic consequences of the rescue using a newly developed genome-wide set of 169 microsatellite loci. We found that the rate of introgression varied among loci, and that 89 loci, 53% of those examined, deviated from patterns of neutral inheritance. The most common deviation was an excess of homozygous genotypes relative to neutral expectations, indicative of directional selection. Individual ancestry was found to be associated with several life history traits, such that individuals who were expected to carry more introduced alleles had higher lifetime reproductive success and longevity. In addition, we found 32 loci, spread throughout the genome, which seem to have individual effects on these life history traits. Though the potential for outbreeding depression is a major concern when translocating individuals between populations, we saw no evidence of such an occurrence in this population.

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MON 22 AUG at 1420 - Room N6
Oral presentation *B3-Sy21-1420-O*

Symposium 21
Evolutionary ecological genomics

Genomic evolutionary hotspots of mimicry and divergence in the Heliconius butterflies, characterised using targeted high-throughput sequencing

Nadeau NJ[1], Whibley A[2], Davey J[3], Dasmahapatra KK[4], Baxter SW[1], Joron M[2], Blaxter M[3], Mallet J[4], Jiggins CD[1]
[1]University of Cambridge, Zoology, Cambridge, United Kingdom, [2]Muséum National d'Histoire Naturelle, Département Systématique et Evolution, Paris, France, [3]University of Edinburgh, Institute of Evolutionary Biology, Edinburgh, United Kingdom, [4]University College London, The Galton Laboratory,, London, United Kingdom

Summary statement:

We show how new genetic techniques can be used to address questions about adaptive evolution, divergence and mimicry at the genome level in a typically “non-model” system.

Abstract:

The Heliconius butterflies are a system that has fascinated biologists since the early days of evolutionary biology because of their close mimicry between species and striking divergence within species in colour pattern. We now have a relatively good understanding of the ecological factors driving the evolution of these traits and also their relatively simple Mendelian genetic control. Several loci that control wing pattern phenotypes have been mapped and we have high quality genomic sequence for regions containing two of the major loci. Here we use targeted next-generation sequence capture to survey patterns of divergence across these entire regions in divergent geographic races and species of Heliconius. This reveals peaks of high divergence between races, allowing us to narrow down the genomic regions under divergent selection. These data also allow us to draw inferences about the evolutionary history of the colour patterns between divergent and convergent races and species.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i034-R*

Symposium 21
Evolutionary ecological genomics

Genomics of thermal adaptation in redband trout

Narum S[1], Campbell N[1]
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Summary statement:

This study utilizes genome scan methods to identify regions associated with thermal tolerance in redband trout (Oncorhynchus mykiss).

Abstract:

Previous work has demonstrated local adaptation in populations of redband (Oncorhynchus mykiss) trout occupying desert and montane habitats. To further elucidate the genetic mechanisms of thermal adaptation, gametes were collected from a single representative wild population adapted to each of warm and cool climates. Gametes were fertilized to produce progeny of a pure warm adapted line, pure cool adapted line, and their F1 crosses. Fish from each of these lines were reared in constant conditions at the Hagerman Fish Culture Experiment Station until they reached an average of 5 grams, and then were divided into treatment and control groups. Fish in treatment tanks experienced diel temperature cycles that reached a maximum of 28.5°C in the afternoon and a minimum of 17.0°C at night. Control tanks were held at a constant temperature of 15°C (spring water). Mortality was measured throughout the duration of the experiment (6 weeks) from three replicate tanks for each line. Tissue samples were collected throughout the experiment, with fin clips collected from all survivors and mortalities in the treatment tanks, and liver and gill tissue from both control and treatment tanks at various time periods (24 hours, 72 hours, 7 days, 30 days). DNA was extracted from fin clips of individuals that survived or died in treatment tanks and were screened with numerous SNP markers throughout the genome. Results of this genome scan are being used to identify the gene regions involved in thermal adaptation in this species. Gene expression data is also being collected from liver and gill samples.

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SUN 21 AUG at 1420 - Room N6
Oral presentation *A3-Sy21-1420-O*

Symposium 21
Evolutionary ecological genomics

Genomic signature of selection in a geographic mosaic of environmental stressors

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Summary statement:

By combining genomics, evolutionary biology and resurrection ecology, we identify repeatable genomic signatures of selection along complex environmental gradients in the wild.

Abstract:

Natural populations are confronted with multiple selection pressures resulting in a mosaic of environmental stressors at landscape level. Identifying the genetic underpinning adaptation to these complex selection environments is challenging. Capitalizing on the strengths of an ecological model system, the water flea Daphnia, with its well-documented ecology, the possibility to analyze subfossil dormant egg banks, and the short generation time allowing an experimental evolution approach, we here link candidate genome regions to three selection pressures, known to induce micro-evolutionary responses in Daphnia: fish predation, parasitism, and land-use. Using a multisciplinary approach that combines genomics in space and time (paleogenomics) with detailed ecological characterization of environmental variation and experimental evolution, we provide solid evidence of selection at genome level under well-characterized environmental gradients in the wild. Our study shows the potential of the genome scan approach to identify ecologically relevant genes in an unbiased way, and reveals strong, repeatable signals of local adaptation at the genome level in Daphnia. Our contribution is innovative, as we demonstrate how limited genomics tools associated with a well-known ecological context in non-classical genetic model species promote the unbiased identification of ecologically relevant genes. Most importantly, we show that the use of a realistic ecological context in non-model species is of crucial importance in association with the fast growing field of genomics to quantify adaptive responses of wild populations to environmental stress, both natural and human induced.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i035-R*

Symposium 21
Evolutionary ecological genomics

Evaluating the relative contribution of life history of genes involved in gamete recognition

Patino SA[1], Hart MW[1]
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Summary statement:

We explore the pattern of bindin sequence variation among sea stars species with respect to the life history, in particular the modes of fertilization.

Abstract:

Our work explores the co-evolution of life history traits and gamete recognition proteins, especially the sperm acrosomal vesicle protein bindin, which is exposed by the acrosomal reaction and interacts with the egg bindin receptor. The compatibility between bindin and the egg receptor affects fertilization success within and between species. We successfully sequenced the bindin locus from 10 sea star species, including closely related species within two distantly related orders. Some features of the gene structure are similar among species and orders, including:
a) a highly conserved core region similar to sea urchins,
b) a collagen-like region, which varies in sizes and copy number,
c) a single intron, and
d) several short tandemly repeated amino acid sequences.
Other features of sea star bindin are extremely variable between species. This variation includes the length of the coding sequences, principally because of the accumulation or loss of several different amino acid repeats, the nucleotide composition, and the size of the intron. The amino acid sequences of the tandem repeats vary among species, although the repetitive structure appears to be highly conserved in some comparisons, and this pattern suggests a complex history of insertions, deletions, and concerted evolution – in addition to nucleotide substitutions – shape sea star bindin evolution and its functional properties in fertilization.

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SUN 21 AUG at 1550 - Room N6
Oral presentation *A4-Sy21-1550-O*

Symposium 21
Evolutionary ecological genomics

Genetics of adaptation and ecological speciation in sticklebacks

Peichel K[1]
[1]Fred Hutchinson Cancer Research Center, Human Biology, Seattle, United States

Summary statement:

Genetics of phenotypic traits that contribute to adaptation to divergent environments and to the evolution of reproductive isolation between divergent stickleback populations.

Abstract:

What is the genetic basis of phenotypic variation between species? How do these differences lead to the formation of new species? In order to address these questions, my laboratory studies the threespine stickleback (Gasterosteus aculeatus). This small fish has long been a model system in behavior, ecology, and evolution. More recently, a number of genetic and genomic tools have been developed for the stickleback. Thus, sticklebacks have become an ideal system to identify the genetic changes that contribute to adaptation to new environments. In particular, marine threespine sticklebacks have adapted to freshwater habitats within the past 10,000 years. In this time, they have evolved an incredible diversity of morphological, physiological, life history, and behavioral traits. We have the ability to cross any two diverse populations of sticklebacks using artificial fertilization in the lab. Therefore, we can use genetic and genomic approaches to determine the number of genetic changes that underlie phenotypes important for adaptation, to map the location of these changes, and to ultimately find the DNA sequence changes responsible for the evolution of phenotypic diversity. Recent work in my laboratory has focused on the genetic basis of phenotypic traits that contribute to adaptation to divergent environments and to the evolution of reproductive isolation between these divergent populations. Thus, our work is also providing insight into the genetic mechanisms that underlie the process of ecological speciation.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i036-R*

Symposium 21
Evolutionary ecological genomics

Niche segregation among cryptic sister species of non-biting midges is rather driven by positive selection than neutral evolution

Pfenninger M[1], Schmidt H[1], Feldmeyer B[1], Hankeln T[2]
[1]Biodiversity & Climate Research Centre, Molecular Ecology Group, Frankfurt, Germany, [2]Universität Mainz, Institut for Molecular Genetics, Mainz, Germany

Summary statement:

Comparative evolutionary analysis of the transcriptome is a useful tool to detect the genomic basis of ecological niche segregation among closely related species.

Abstract:

The cryptic sister species of non-biting midges Chironomus riparius and C. piger co-occur in the same area but occupy different ecological niches. Evolutionary analysis of their larval transcriptomes by next generation sequencing has shown that the divergence of the species is mainly driven by either positive (mean $\omega = 1.44$) or negative selection (mean $\omega = -0.367$). Strictly neutral protein evolution as independent process could not be detected, contrary to the expectation of Neutral Theory of Molecular Evolution. Enrichment analyses of the 405 genes with $\omega > 1$ revealed that in particular genes responsible for energy metabolism (OXPHOS pathway) and ATP production were differentially selected in concordance with the observed niche differences concerning habitat temperature and oxygen availability.

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SUN 21 AUG at 1400 - Room N6
Invited talk *A3-Sy21-1400-I*

Symposium 21
Evolutionary ecological genomics

Genome structure, functional diversification, and adaptation in an ecoresponsive organism: Daphnia

Pfrender ME[1]
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Summary statement:

An extensive history of ecological investigation along with recent advances in genomics make Daphnia a model system for evolutionary ecological genomic research.

Abstract:

The availability of genome sequences for a growing number of traditionally non-model organisms is opening new avenues of investigation into the interactions between organism and their environment. A particularly useful organism for this investigation is the freshwater crustacean Daphnia. Long used as a model for ecological studies in freshwater systems, and for examining rapid evolutionary responses to changing environments, Daphnia is now equipped with a range of functional genomic tools and genome sequences. I will discuss our emerging understanding of the genome structure of Daphnia and present functional genomic data on gene expression patterns in response to multiple environmental stressors. Functional genomic approaches examining adaptive divergence in natural populations set the stage for a greater understanding of genome X environment interactions, and the relationship between short-term transcriptional responses and genetic adaptation to accommodate environmental challenges.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i020-E*

Symposium 21
Evolutionary ecological genomics

Opsin gene expression variation in an adaptive radiation: Sailfin silverside fishes in the Malili Lakes (Sulawesi)

Pierotti ME[1], Scemama J-L[1], Tantu FY[2], Loew ER[3], McKinnon JS[1]
[1]East Carolina University, Department of Biology, Greenville, United States, [2]Tadulako University, Faculty of Agriculture, Palu, Indonesia, [3]Cornell University, Department of Biomedical Sciences, Ithaca, United States

Summary statement:

Opsin expression variation is assessed from retinas of sailfin silverside (Telmatherinidae) species and intraspecific color morphs and correlated with ecological parameters.

Abstract:

The adaptive radiation of sailfin silverside fish (Telmatherinidae) in the Malili Lakes system in Indonesia ('Wallace's Dreampond') provides an extraordinary opportunity to test fundamental questions regarding the origin and maintenance of color polymorphism, the role of natural and sexual selection in ecological speciation and in particular whether environment-driven selection on the sensory system is responsible for repeated patterns of phenotypic diversity across lakes. We collected retinal RNA samples from a set of diverging species as well as color morphs within and between lakes and tested for correlations of differential gene expression with known ecological parameters, microhabitat light conditions, with the spectra of fish nuptial coloration and the amount of within-species phenotypic variation in color patterns. We discuss our findings in the context of the ecological diversification of the sailfin silversides and compare patterns with other model fish adaptive radiations.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i037-R*

Symposium 21
Evolutionary ecological genomics

Fungus-farming microbiomes: Metagenome analyses suggests bacterial contributions to biomass breakdown in fungus-growing termites

Poulsen M[1,2,3], Suen G[2,3], Aylward FO[2,3], Moeller JA[2,3], Adams SM[2,3], Tringe SG[4], Barry KW[4], Malfatti S[4], Goodwin LA[4], Aanen DK[5], Currie CR[2,3]

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Summary statement:

Community metagenomes and CAZy analyses of fungus-growing termite guts and fungus comb reveal the presence of bacteria with properties suggesting involvement in biomass degradation.

Abstract:

Fungus-growing termites (Macrotermitinae) evolved in Africa approximately 35 mya and have subsequently diverged into more than 330 termite species, all dependent on farming fungi for food. The success of termite fungiculture is arguably their close association with fungi that aid in the breakdown of plant material, but the role of additional microbes in the symbiosis has remained largely unexplored. To gain insight into bacterial contributions to biomass breakdown, we sequenced 16S pyrotag libraries and community metagenomes of worker guts and fungus comb (a specialized structure housing the mutualistic fungus) from the South African termite Macrotermes natalensis. 16S rRNA analysis revealed that both guts and fungus comb are dominated by Gamma-proteobacteria, and phylogenetic binning analyses of the associated community metagenomes showed that the majority of these are in the family Enterobacteriaceae. Carbohydrate-active enzyme (CAZymes) analyses revealed that the bacterial communities harbor a large amount of enzymes that hydrolyze hemicelluloses, starch, and pectin, suggesting bacterial contribution to the plant cell wall polysaccharide deconstruction, particularly in the termite gut. Comparisons to other plant-biomass degrading microbiomes revealed that they were more similar to other fungus-farming insects with respect to bacterial diversity, overall gene content, metabolism, and CAZymes, than to other plant-biomass degrading microbiomes. This suggests convergent evolution of the bacterial communities associated with fungus farming insects, likely due to the shared similarity of associations with insect-fungus symbioses for plant biomass breakdown.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i021-E*

Symposium 21
Evolutionary ecological genomics

Methuselah-like variability explains lifespan differences in divergent insect species

Reis M[1], Araújo AR[1], Aguiar B[1], Rocha H[1], Vieira CP[1], Vieira J[1]
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Summary statement:

Molecular variation at methuselah-like genes is associated with longevity differences in divergent Drosophila species.

Abstract:

The study of traditional model species only makes sense if the findings can be generalized to distantly related species. However when a candidate gene belongs to a gene family it is conceivable that only paralogous copies of the candidate gene can be found in more divergent species. Thus it is unclear whether other distant members of a gene family should be considered candidate genes as well. This is the case of the Drosophila melanogaster methuselah (mth) gene. Molecular variation at mth has been previously associated with lifespan differences. This gene is a member of a gene family comprising 16 genes and encodes a putative G protein-coupled receptor (GPCR) required in the presynaptic motor neuron to acutely upregulate neurotransmitter exocytosis. In this work, we show that mth is present only in the melanogaster subgroup of species and therefore it has an estimated age of 10 million years. So we were interested in determining if variation at mth paralogous genes (mth-like) could explain lifespan differences in a species (Drosophila americana) that has been diverging from D. melanogaster for 40 million years. It is here shown that molecular variation at mth-like genes encoding proteins that share less than 50% amino acid identities with the D. melanogaster Mth protein explain a considerable amount of the lifespan differences observed in a F2 association experiment. Furthermore, only mth-like genes that encode proteins showing a recognizable Mth ectodomain with the 10 typical cysteine residues, as well as a seven transmembrane domain (7tm) have variation associated with lifespan differences.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i038-R*

Symposium 21
Evolutionary ecological genomics

Patterns of immune gene expression in the water flea, Daphnia magna, during infection with its parasite, Pasteuria ramosa.

Riddell CE[1], McTaggart S[1], Little T[1]
[1]University of Edinburgh, Edinburgh, United Kingdom

Summary statement:

To begin examining immunity in a natural host-parasite system, we present evidence of immune gene expression in Daphnia magna during infection with the parasite, Pasteuria ramosa.

Abstract:

The molecular basis of the invertebrate innate immune response is being characterised in ever-increasing detail in model organisms such as Drosophila and Anopheles. However, genomic analyses show that some of these immune gene families are entirely absent or much larger in other invertebrate taxa suggesting that additional, alternative immunological mechanisms are utilised by some species. In addition, ecological studies of natural, co-evolved host-parasite systems demonstrate that there is substantial genetic variation and specificity in the invertebrate immune response, yet the mechanisms generating susceptible/resistant phenotypes are not well described and require further investigation. The water flea, Daphnia magna, shows evidence for co-evolution with its endobacterial parasite and susceptibility for infection shows strong genotypehost x genotypeparasite interactions. Currently, we are testing whether a similar degree of specificity is present in the interaction between D. magna immune gene expression and specific P.ramosa strains. We have also characterised both temporal and spatial expression of immune gene candidates during the first 24 hours after exposure to an infective strain of P. ramosa. These findings are being used to develop a clearer understanding of how D. magna gene expression is structured after initial P.ramosa infection and how these changes correlate with the infection stage and also the cellular response that is known to be rapidly activated once P.ramosa invades the haemolymph from the gut.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i039-R*

Symposium 21
Evolutionary ecological genomics

Adaptive processes in an invasive marine invertebrate: insights from a genome scan study of the mollusk Crepidula fornicata

Riquet F[1], Viard F[1]
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Summary statement:

Adaptation from standing genetic variation could occur in invasive species. A genome scan approach was used to examine this hypothesis in the marine invader, Crepidula fornicata.

Abstract:

Explaining non-indigenous species (NIS) success in a novel environment, where they have been introduced, is a puzzling issue in evolutionary biology. Besides the role played by ecological and physiological factors, the successful establishment of NIS outside their native range may be due to adaptive evolution in the newly colonized habitats. In addition to evolution from new mutations, adaptation may arise from standing genetic variation (i.e. pre-existing polymorphism in the native range of the NIS). The likelihood of such a process is increased when genetic polymorphism in the introduced range is enhanced by recurrent introductions from genetically diversified sources, a pattern often observed in aquatic NIS.

We used a genome scan approach to examine the hypothesis of adaptation from standing genetic variation and to determine the nature of the selection process by studying invasive and native populations of the slipper limpet Crepidula fornicata. This emblematic marine invader had been introduced repeatedly since the end of the 19th century from the North-Western coasts of Atlantic into Europe. We analyzed 506 individuals from 17 locations (6 in the native range, 11 in the European introduced range) over a large number of loci, 20 SSRs and 249 AFLPs, aiming to (1) document the polymorphism of introduced and native populations, (2) distinguish selective and demographic effects and (3) test for the presence of outliers (i.e. loci showing unusual patterns of variation). Based on the comparison of the native and introduced populations, the results are discussed to examine the likelihood of the evolution of adaptation following introduction events in a novel environment.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i040-R*

Symposium 21
Evolutionary ecological genomics

Genomic divergence during incipient speciation in stickleback

Roesti M[1], Salzburger W[1], Hendry AP[2], Berner D[1]
[1]University of Basel, Zoological Institute, Basel, Switzerland, [2]McGill University, Redapth Museum and Department of Biology, Québec, Canada

Summary statement:

We compare the signature of genome-wide divergence among multiple lake and stream stickleback population pairs with a high genetic marker density.

Abstract:

During the early stages of speciation, genomic regions under divergent ecological selection are thought to be more resistant to gene flow while the remainder of the genome can still be homogenized. This should result in heterogeneous genomic differentiation between populations occupying distinct selective environments. Important aspects of this process, however, remain controversial, such as the number and physical extent of genomic regions under divergent selection. We seek to address these questions by performing genome scans on multiple stickleback population pairs occupying lake and stream habitats in Canada and Europe. These population pairs differ in the extent of genetic and phenotypic differentiation due to differences in age and in the magnitude of gene flow between the habitats. Our genome scans are based on polymorphism identified by Illumina-sequenced restriction-site associated DNA (RAD).

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i041-R*

Symposium 21
Evolutionary ecological genomics

Contrasting patterns of parasite resistance in Daphnia magna

Routtu J[1], Ebert D[1]
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Summary statement:

The genetic basis of host-parasite interaction was tested in a D.magna F2 panel against microsporidium Hamiltosporidium tvaerminnensis and gram-positive bacteria Pasteuria ramosa.

Abstract:

Genetic basis of parasite resistance determines which model like matching alleles or gene-for-gene best describes the coevolutionary potential of host-parasite interaction. Two different parasite species, microsporidium Hamiltosporidium tvaerminnensis and gram-positive bacteria Pasteuria ramosa, were used to infect a D. magna F2 panel. Parental populations of the D.magna F2 panel show very similar pattern of resistance and susceptibility against the parasites. However, the pattern of resistance and susceptibility is radically different in the D.magna F2 panel. P. ramosa resistance is clearly dominant trait controlled by one or closely linked loci in a single position of the genome. H.tvaerminnensis resistance is more like a quantitave trait with resistance based on many loci scattered in different linkage groups and epistatic interactions. The genetic basis of resistance against these two parasites will lead to coevolutionary dynamics that are profoundly different.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i042-R*

Symposium 21
Evolutionary ecological genomics

The genetic basis of heterozygosity-fitness correlations

Schielzeth H[1], Wolf JBW[1], Kempenaers B[2], Forstmeier W[2], Ellegren H[1]
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Summary statement:

We explore the prevalence of directional dominance vs. overdominance as the causal agent behind heterozygosity fitness correlations and inbreeding.

Abstract:

Heterozygostity fitness correlations (HFC) are commonly found in animal and plant populations, but their molecular genetic basis is not fully understood. We studied HFC in a captive population of zebra finches, which was maintained at low levels of inbreeding. Here we focus on 11 traits that include morphological traits, sexual traits and reproductive success in a competitive environment. We measured heterozygosity using almost 1,400 SNP markers. All traits showed positive HFC, but effect sizes varied between different categories of traits. We then applied a marker-by-marker analysis to address the largely unanswered question if HFC arise primarily from directional dominance or from overdominance. We found that several traits showed patterns of overdominance. Such pattern of overdominance at marker loci could be produced by true overdominance at causal loci or by pseudooverdominance caused by recessive deleterious mutations in repulsion disequilibrium. While our approach lacks resolution to distinguish between these alternatives at the very fines scale, it goes far beyond the local versus global effects discussion that dominates the literature on HFC. With the decreasing cost for genotyping large numbers of markers in outbred population, our approach holds great promises to better understand the genetic basis of HFC in natural populations.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i043-R*

Symposium 21
Evolutionary ecological genomics

Characterisation of barrier genes underlying pollinator-mediated reproductive isolation in sexually deceptive orchids

Schlüter PM[1,2], Xu S[1,3], Gagliardini V[2], Whittle EJ[4], Shanklin J[4], Grossniklaus U[2], Schiestl FP[1]
[1]University of Zurich, Institute of Systematic Botany, Zurich, Switzerland, [2]University of Zurich, Institute of Plant Biology, Zurich, Switzerland, [3]Swiss Federal Institute of Technology Zurich, Institute of Integrative Biology, Zurich, Switzerland, [4]Brookhaven National Laboratory, Department of Biology, Upton, United States

Summary statement:

Differences in stearoyl-ACP desaturase expression and enzyme function contribute to differential pollinator attraction and reproductive isolation in sexually deceptive orchids.

Abstract:

Sexually deceptive orchids of the genus Ophrys are reproductively isolated from each other by the attraction of different specific pollinators. Field experiments showed no evidence of inter-species pollen transfer among the two orchid species O. sphegodes and O. exaltata. Specific pollinator attraction by these orchids relies on the chemical mimicry of the pollinators' sex pheromones, specifically alkenes with different double-bond positions. Stearoyl-acyl-carrier-protein desaturase (SAD) homologues are candidate enzymes controlling this difference in alkene biosynthesis. We identified genes encoding these enzymes in Ophrys orchids, and found alkene production to be associated with SAD gene expression. Some SAD copies showed evidence of positive selection after gene duplication, and encode functional desaturase proteins that can catalyse the enzymatic reactions necessary for production of the correct alkenes. By contributing to the production of species-specific alkene bouquets, these SAD genes contribute to differential pollinator attraction and reproductive isolation among the orchid species. These barrier genes may thus represent genic targets of pollinator-mediated selection of large phenotypic effect.

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SUN 21 AUG at 1630 - Room N6
Oral presentation *A4-Sy21-1630-O*

Symposium 21
Evolutionary ecological genomics

Divergent transcriptomic and physiological responses to heat stress in garter snake life-history ecotypes

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Summary statement:

We identify nodes in molecular stress networks at which snake ecotypes respond in parallel (cort. & HSP) and other nodes at which they have diverged (aspects of oxidative stress).

Abstract:

For a species to persist in a changing environment, individuals need to respond appropriately to physiological/environmental stress, and the molecular networks underlying these responses need to evolve at the population level. Evidence from laboratory model systems suggest that molecular networks regulating stress response share nodes with networks underlying life-history traits. To understand how these molecular networks are functioning in natural populations, we compare stress responses, at both the transcriptome and physiological levels, between naturally evolved populations of garter snake ecotypes. These two ecotypes lie on opposite ends of a pace-of-life-history continuum with the fast-living ecotype having faster growth, higher reproductive output, and shorter lifespan relative to the slow-living ecotype. In a common garden experiment, we used heat stress as an activator of general stress and metabolic response. We measured whole genome quantitative transcription using RNA-seq and aspects of organismal oxidative stress using live cell physiology. We identify nodes in the molecular stress networks at which the ecotypes respond in parallel (corticosterone, HSP transcription) and other nodes at which the ecotypes have diverged. The ecotypes respond differently to heat stress in their levels of circulating free radicals, likely due to differences in both the production of free radicals by mitochondria, and in their degradation via antioxidants. The ecotypes also varied in the accumulation of DNA damage in blood cells. These similarities and differences in stress response are particularly interesting in the context of the ecotypes' evolved differences in life-history.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i044-R*

Symposium 21
Evolutionary ecological genomics

Microevolution in Daphnia in response to dietary protease inhibitors?

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Summary statement:

With the release of the Daphnia genome, adaptive responses which putatively underly microevolution of this ecological model organism can be investigated on a molecular level.

Abstract:

Since long Daphnia is a model organism in limnic ecological systems. Only recently has the Daphnia genome been published and a fusion between ecological and genetic studies is now possible. Daphnia are the main grazers of phytoplankton and cyanobacteria in ponds and lakes. However, cyanobacteria have been shown to produce harmful grazer toxins of which the most frequently occurring are protease inhibitors. These inhibitors directly affect their targets - proteases of Daphnia - in situ. However, one clone of Daphnia magna has been demonstrated to respond to digestive protease inhibitors by increasing its protease gene-expression. Also high plasticity in the clone's gene-expression has been revealed after exposure to different types of protease inhibitors. Here we compare D. magna clones from different populations which differ in the strength of their response to the same protease inhibitors. Such an intraspecific variation might have developed due to microevolution of the D. magna populations with or without cyanobacteria.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i022-E*

Symposium 21
Evolutionary ecological genomics

Habitat selection predicts genetic relatedness in an alpine ungulate

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Summary statement:

Landscape resistance surfaces based on patterns of habitat selection are better predictors of genetic relatedness compared to traditional landscape genetics models.

Abstract:

Landscape heterogeneity plays an integral role in shaping ecological and evolutionary processes. Despite obvious links between the two disciplines, ecologists and population geneticists have taken different approaches to evaluating the effects of landscape features on processes such as habitat selection, animal movement, and gene flow. Commonly, ecologists use statistical models such as resource selection functions (RSFs) to identify habitat variables disproportionately selected by animals. Population genetic approaches, on the other hand, attempt to model patterns of genetic differentiation according to the distribution of habitat variables. Here for the first time we combine ecological and genetic approaches by using RSFs and step selection functions (SSFs) to predict genetic relatedness across a heterogeneous landscape. We constructed resistance surfaces based on RSFs and SSFs estimated using data from 102 GPS radiocollared mountain goats (Oreamnos americanus) in southeast Alaska. All individuals were genotyped at 22 microsatellite loci, which we used to estimate genetic relatedness. Resistance surfaces derived from summer RSFs were the best predictors of genetic relatedness, and winter models the poorest. The traditional models of isolation-by-distance and isolation-by-barrier marginally outperformed the winter models. Moreover, summer resistance surfaces were shown to account for both the influence of distance and barriers. Our study represents the first merger of GPS and genetic data that can be used to validate and parameterize landscape genetics models, and should further elucidate the relationship between landscape heterogeneity and genetic differentiation.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i023-E*

Symposium 21
Evolutionary ecological genomics

Transcriptome of Poecilia reticulata and comparative analysis for identification of sex-linked loci associated with evolution of the guppy sex chromosomes

Sharma E[1], Zipperich G[1], Henz S[1], Dreyer C[1], Weigel D[1]
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Summary statement:

De novo transcriptome assembly from Illumina reads and analysis of male and female transcriptomes to gain molecular insights into the evolution of adaptive traits in guppies.

Abstract:

Poecilia reticulata (the guppy) has long been used as a model in evolutionary biology and ecology. While poecilids display many diverse sex-determining mechanisms, the guppy in particular displays male heterogamety and overt sexual dimorphism, which reflects some of its adaptations as a livebearer, for example, larger size and camouflage in females in contrast to the highly variable ornamental traits in smaller males. Variation and habitat-specific adaptation of male patterns are thought to evolve in the wild by interplay of sexual selection by mates and natural selection by predators. These polymorphic traits set a paradigm for inheritance of male advantageous genes that may have played important roles in sex chromosome evolution.

Previously our laboratory has generated a dense linkage map of the guppy; however, no molecular markers are available for the highly heterochromatic male-specific region of the Y chromosome, as yet. To circumvent some problems of highly repetitive sequence for genomic walks or genome assembly using short NGS reads, we first perform sex-specific deep transcriptome sequencing with embryos and adults. We compare efficiency and fidelity of de novo assembly by Velvet, Multiple-k, STM and Oases and scrutinize the resulting transcriptomes for male-specific transcripts. These sex-specific expression profiles in complement to ongoing WGS experiments will facilitate identification of Y-linked ornamental genes and the Sex Determining Locus on the Y-chromosome. A comprehensive knowledge of the guppy exome is also useful for predicting gene models, and markers linked to expressed genes will enhance knowledge of regions under selection pressure in the wild.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i046-R*

Symposium 21
Evolutionary ecological genomics

Addressing the genetic response of Bornean elephants to habitat loss and fragmentation

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Summary statement:

This study is focused on studying the effect of habitat fragmentation on the genetic diversity of Bornean pygmy elephants (Elephas maximus borneensis).

Abstract:

Biodiversity loss due to habitat destruction and habitat degradation poses a major threat to the rainforests of Borneo. The abundance and distribution of various species have been affected in these forests due to anthropogenic factors. Forest fragmentation can have a dramatic effect on landscape connectivity and the dispersal of animals, potentially reducing gene flow between populations, which could lead to significant inbreeding and loss of genetic diversity within fragments. We are studying the effect of habitat fragmentation on the genetic diversity of Bornean pygmy elephants (Elephas maximus borneensis). The Bornean elephants are critically endangered; smaller than other mainland Asian elephants and are found only in the north of Borneo, in the State of Sabah, Malaysia, and across the border of Sabah and Kalimantan, Indonesia. We developed de novo genomic markers for this species using next generation sequencing platforms. We found around 1000 SNPs as potential candidates for genotyping assay using plexes. We are currently optimizing and genotyping these plexes on elephant blood and dung samples collected from different geographical regions by using Sequenom Mass Array technology. SNP markers are increasingly becoming popular as an addition to the existing molecular ecology tools in non model organisms, but their efficient use still remains challenging. To our knowledge, this is a first study where attempt has been made to genotype SNPs on DNA from dung samples. I will present the results including details of the methodology used, together with a discussion on the limitations of the chosen approach on non invasive samples.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i047-R*

Symposium 21
Evolutionary ecological genomics

Did the pathogenic fungus Colletotrichum kahawae emerged through a very recent host-jump speciation event?

Silva DN[1,2], Talinhas P[2], Cai L[3], Várzea V[2], Paulo OS[1], Batista D[2]
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Summary statement:

Pathological, molecular and biogeographical data suggest that host specialization may have been the main route leading to C. kahawae speciation following a host-jump event.

Abstract:

Ecological speciation remains a contentious subject in evolutionary biology, especially when it occurs in sympatry due to its difficult demonstration. However, despite the substantial build up of theoretical constraints for most taxa, fungi possess several remarkable features that may promote ecological speciation in sympatry. These features can be particularly evident when addressing emergent infectious diseases, since their recent origin provides a unique opportunity to study, in first hand, the mechanisms underlying speciation. Here, we made use of a range of pathological, molecular and geographic data to present evidence that host-jump speciation, a particular case of ecological speciation, underlies the emergence of the fungal pathogen Colletotrichum kahawae, with several lines of evidence suggesting that it might have occurred in sympatry. C. kahawae emerged causing Coffee Berry Disease, due to its unique adaptation of infecting green coffee berries. We posit that this adaptation could have been instrumental in driving speciation considering that it would pleitropically affect local adaptation (exploitation of an unoccupied niche) and mating patterns (immigration inviability), since in Colletotrichum spp., mating only occurs between individuals able to grow on the same host. Using *BEAST, we estimate that C. kahawae emerged at < 1400 yrs leaving a very short time frame since the divergence from its sibling lineage (~4600 yrs), during which a severe drop in C. kahawae´s population size was detected, further supporting a recent introduction and subsequent adaptation. This suggests that host specialization can be an important route of ecological speciation in sympatry.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i048-R*

Symposium 21
Evolutionary ecological genomics

Using next generation RNA sequencing to uncover targets of natural and sexual selection on the transcriptome of Drosophila mojavensis

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Summary statement:

We used next generation sequencing to uncover the targets of natural and sexual selection during incipient speciation using the transcriptome of Drosophila mojavensis.

Abstract:

Natural and sexual selection both play a role in evolutionary change during speciation. Identification of the genetic targets of selection has been largely limited to genomic regions. However, it is now obvious that targets of selection are likely to be factors influencing gene expression variation as well as coding regions. There is much evidence that selection acts on the transcriptome and especially so for traits linked to sex and reproduction and this may be of importance for adaptation to novel environments. It is therefore likely that adaptive divergence between incipient species is under complicated genetic or even epigenetic control. Thus, a transcriptomic approach for identifying targets of selection may be an efficient method for identifying so-called ‘speciation genes’. We aimed to identify the targets of natural and sexual selection across the transcriptome of a cactophilic fruit fly, Drosophila mojavensis. Mexican populations of D. mojavensis live on different species of host cactus, exhibiting significant levels of behavioural isolation. Using RNA sequencing on the ABI SOLiD3 platform we reared male flies on two different species of cactus to identify targets of natural selection. We then utilised mate choice experiments to discover differentially expressed targets of sexual selection between mated and unmated males. From this framework we identify the genetic targets of natural selection and mating success as well as the interaction between the two. Examining this link between natural and sexual selection will aid in the understanding of the interplay of these forces during speciation.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i049-R*

Symposium 21
Evolutionary ecological genomics

The genetic basis of the solitary-eusocial transition in the socially polymorphic sweat bee Halictus rubicundus

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Summary statement:

Characterisation of SNPs differentiating the transcriptomes of solitary and eusocial populations of a socially polymorphic sweat bee.

Abstract:

Eusociality has evolved few times in the bees. Interestingly, some sweat bee species straddle this major evolutionary transition; they are socially polymorphic, exhibiting both solitary and eusocial behaviour. We tested whether there is a genetic underpinning of this transition in the socially polymorphic sweat bee Halictus rubicundus, which across its Holarctic range exhibits solitary behaviour in cooler regions and eusociality in warmer ones. Mt-DNA data suggest eusocial, low-elevation populations are genetically differentiated from solitary, high-elevation populations in North America. Our microsatellite data from European populations show subtle genetic differentiation among populations, yet differentiation between social and solitary populations is no greater than expected by geography alone (isolation by distance), suggesting lack of reproductive isolation between solitary and social populations in Europe. Common garden experiments, in which we cross-foster social H. rubicundus into a solitary environment and vice versa, indicate plasticity in social behaviour in Europe. If differences in social behaviour are encoded by the same sets of genes in North American and European lineages of H. rubicundus, then they may be constitutively expressed in North America yet conditionally expressed in Europe. Here we explain an integrative computational and wet-lab genomics approach aimed at the identification of key genes underpinning the solitary-eusocial transition, involving the characterisation of SNPs differentiating the transcriptomes of solitary and eusocial populations. Such loci could be genes responsible for the altruistic behaviour of workers in eusocial populations.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i050-R*

Symposium 21
Evolutionary ecological genomics

Identification of candidate genes for adaptive responses to environmental stress in Daphnia magna

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Summary statement:

We identify candidate genes for adaptation to environmental gradients in the waterflea Daphnia magna building on genome scan data and through next generation sequencing.

Abstract:

Understanding the genetic underpinning of adaptation of organisms to their natural environment is a key objective in the rapidly developing field of ecological and environmental genomics. However, assessing specific causes of natural selection in the wild is challenging because it is nearly impossible to unambiguously determine selective forces in a multidimensional natural context.
Capitalising on the fast development of genomic tools, the genome sequence and the rich ecological background available for Daphnia magna, we identify candidate genes underlying adaptive responses to key selection pressures in the wild.
A previous genome scan analysis was able to link genome regions to three selection pressures known to induce micro-evolutionary responses in D. magna. We here build on these findings and identify all genes located within those regions by in silico genome walk. Part of those genes show homology to genes with known function in other organisms, whereas for the rest there is no functional annotation. We target the latter genes for prioritisation using integrated information from parallel experiments (microarray and proteome studies). We use Next Generation Sequencing to sequence the prioritised genes and their promoter regions in natural and experimental populations. This provides us with insights into the type of selection (directional or balancing) that affects the genes under consideration.
This study will advance our understanding of the link between fitness and gene variants and is therefore a valuable contribution to ecological genomics.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i051-R*

Symposium 21
Evolutionary ecological genomics

The genome sequence of Atlantic cod reveals a unique immune system

Star B[1], Nederbragt AJ[1], Jentoft S[1], Grimholt U[1], Malmstrøm M[1], Gregers TF[2], Rounge TB[1], Sharma A[3], Wetten OF[4], Andersen Ø[5], Lagesen K[1], Solbakken MH[1], Jonassen I[3], Omholt SW[1,6], Stenseth NC[1], Jakobsen KS[1]
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Summary statement:

The annotated genome sequence of Atlantic cod, a major marine resource, shows evidence for unconventional rewiring of its immune architecture.

Abstract:

Atlantic cod (Gadus morhua) is a large, cold-adapted teleost in the Northern Atlantic Ocean that sustains long-standing commercial fisheries and incipient aquaculture. We assembled the genome sequence of Atlantic cod, showing evidence for unconventional rewiring of its immune machinery relative to other sequenced vertebrates. The genome assembly was obtained exclusively by 454 sequencing of shotgun and paired-end libraries, and automated annotation identified 22,154 genes. The major histocompatibility complex (MHC) II is a conserved feature of the adaptive immune system of jawed vertebrates, but we show that Atlantic cod has lost the genes for MHCII, CD4 and Ii that are essential for the function of this pathway. Concordant with the fact that Atlantic cod is not unusually susceptible to disease under natural conditions, we find a highly expanded number of MHCI genes and the highest number of toll-like receptor (TLR) genes in a teleost so far. This suggests how the Atlantic cod immune system has evolved compensatory mechanisms within both adaptive and innate immunity in the absence of MHCII. The observations affect fundamental assumptions about the evolution of the adaptive immune system and its components in vertebrates.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i052-R*

Symposium 21
Evolutionary ecological genomics

Genome-wide scan for single nucleotide polymorphisms (SNPs) reveals patterns and causes of allele sharing between ecologically divergent species

Stölting KN[1], Nipper R[2], Lindtke D[3], Barbara T[3], Caseys C[3], Waeber S[3], Castiglione S[4], Lexer C[1]
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Summary statement:

RAD based high density SNP mapping reveals the architecture of genomic isolation and genomic exchange in ecologically divergent species

Abstract:

Hybridization between closely related species reshuffles blocks of genomic material, the size of which decreases with repeated hybridization events. Periods of independent divergence of species prior to hybridization lead to genomic differentiation, thus permitting the detection of the origin of blocks of genomic elements from either parental species in hybrids. Genomic studies of hybrid zones thus allow identification of genomic elements conferring species identity, as well as those chromosomal regions particularly susceptible to invasion by foreign genomic material. Here we used Restriction site Associated DNA (RAD) sequencing to interrogate 34,821 SNPs across the genomes of the ecologically divergent species Populus alba and P. tremula for regions of increased interspecific divergence, potentially indicative of loci involved in reproductive isolation, and regions of unusually low divergence. The autocorrelation signature of RAD-SNPs varied widely among chromosomes. Contrary to expectations, we identified extensive allele sharing on the proximal end of chromosome XIX, the incipient sex chromosome of Populus. We corroborate the RAD sequencing results by a detailed analysis of mapped microsatellite loci sampling >400 individuals of two independent Populus hybrid zones. We infer the likely causes of allele sharing in genomic regions exhibiting low genomic divergence such as the incipient sex chromosome, and identify the relative roles of shared ancestral polymorphism versus recurrent gene flow between these ecologically divergent, hybridizing species.

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i053-R*

Symposium 21
Evolutionary ecological genomics

Major Histocompatibility Complex class I and II diversity and mate choice in a subantarctic bird, the Blue petrel, Halobaena caerulea

Strandh M[1], Westerdahl H[2], Bonadonna F[1]
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Summary statement:

MHC class I and II genotype similarity among breeding pairs of a sea bird using a 454-amplicon sequencing approach.

Abstract:

The great polymorphism observed in the Major Histocompatibility Complex (MHC) genes is thought to be maintained by pathogen-mediated selection. Female disassortative mate choice on MHC to maximize offspring MHC-heterozygosity and thereby fitness, has also been shown to play a role in several vertebrates. However, among birds, evidence of MHC-disassortative mating is still scarce. We characterized MHC class I and II in the blue petrel; a bird that is long-lived, mates monogamously for life, and that recognizes its partner by olfaction. An accurate mate choice process should therefore be particularly important in this species and an olfactory MHC-based choice possible. The blue petrel MHC was found to be highly polymorphic, showed classical MHC characteristics and harbored at least eight MHC class I and two MHC class IIB loci. We used ’next generation’ 454-amplicon sequencing to determine MHC genotypes of 80 blue petrel pairs and then evaluated MHC class I and II similarity between breeding and random pairs.

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MON 22 AUG at 1610 - Room N6
Oral presentation *B4-Sy21-1610-O*

Symposium 21
Evolutionary ecological genomics

Introgression and recent local selection: Source of adaptations in wild populations of two Mus musculus subspecies

Tautz D[1], Staubach F[1,2], Lorenc A[1], Messer PW[2], Tang K[3], Petrov D[2]
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Summary statement:

In a genome-wide SNP screen in mouse wild populations we found evidence of potentially adaptive genomic introgression after an initial subspecies split.

Abstract:

Introgression from closely related species has emerged as a new way of acquiring adaptations, not only in plants, but also in animals. To shed light on the extent and significance of introgression events in natural mouse populations we took advantage of a unique set of a total of four geographically isolated populations from two Mus musculus subspecies (M. m. domesticus and M. m. musculus) with well known history. We used the Affymetrix Mouse Genome Diversity Array to perform a systematic search for signals of introgression. We also implemented a composite of several statistics to screen the mouse genome for recent local adaptations including a search for soft sweeps. Several genomic regions which most likely introgressed from one subspecies into the other show complex recombination patterns with genomic regions of the resident mouse subspecies, suggesting the presence of past introgression events after an initial split of the subspecies. High frequency of introgressed genomic regions points towards their potential adaptive value.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i024-E*

Symposium 21
Evolutionary ecological genomics

Historical sampling reveals dramatic demographic changes in western gorilla populations

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Summary statement:

Prolonged gene flow after population divergence is characteristic of gorillas and a population decrease of the Cross River gorillas occurred very recently.

Abstract:

Demographic modelling using genetic data can estimate changes in long-term population sizes while temporal sampling provides a way to directly compare genetic variation present today with that sampled in the past. In order to better understand the dynamics associated with the divergences of great ape populations, these analytical approaches were applied to western gorillas (Gorilla gorilla) and in particular to the isolated and Critically Endangered Cross River gorilla subspecies (G. g. diehli). We used microsatellite genotypes from museum specimens and contemporary samples to infer both long-term and recent population history. We find that Cross River gorillas diverged from the ancestral western gorilla population ~17,800 years ago. However, gene flow ceased only ~420 years ago, followed by a bottleneck beginning ~320 years ago that caused a 60-fold decrease in the effective population size of Cross River gorillas. Direct comparison of heterozygosity estimates from museum and contemporary samples suggests a loss of genetic variation over the last 100 years. The composite history of western gorillas could plausibly be explained by climatic oscillations inducing environmental changes in western equatorial Africa that would have allowed gorilla populations to expand over time but ultimately isolate the Cross River gorillas, which thereafter exhibited a dramatic population size reduction. The recent decrease in the Cross River population is most likely attributable to increasing anthropogenic pressure over the last several hundred years.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i054-R*

Symposium 21
Evolutionary ecological genomics

Genes that affect salmon growth in wild don't matter in captivity: insights from QTL mapping in multiple environments

Vasemägi A[1], Primmer C[2]
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Summary statement:

QTL mapping in the wild and controlled hatchery environments revealed a non-overlapping set of QTLs affecting growth in Atlantic salmon.

Abstract:

Over the last two decades quantitative locus (QTL) mapping methods have been widely used for describing the genetic basis of continuous variation in experimental crosses and controlled environments. More recently QTL approaches have been applied to wild populations in their natural environment. However, very few studies in animals have evaluated whether the same genes affect phenotypic traits in both natural and controlled environments. Here, I will describe the results from comparative QTL mapping of growth in Atlantic salmon (Salmo salar L.) measured both in hatchery conditions and the natural environment. We found strong evidence for multiple growth related QTLs but none of the identified genomic regions showed significant associations in both environments. We also evaluated the evidence for contemporary natural selection on the identified growth QTLs. Our results suggest that environment plays an important role in the expression of complex traits, such as growth, and genotype-phenotype relationships observed in laboratory conditions do not necessarily hold in the wild.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i025-E*

Symposium 21
Evolutionary ecological genomics

From genes to macrobentic communities in lagoonal ecosystems

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[1]University of Patras, Department of Biology, Patra, Greece, [2]HCMR, Institute of Marine Biology and Genetics, Heraklion, Greece, [3]HCMR, Oceanography, Anavyssos, Greece

Summary statement:

The present work is an attempt to compare the patterns from macrobenthic communities to those deriving from genetic data.

Abstract:

Genetic data are only recently used in scientific research to answer ecological questions. The present study attempts to compare the patterns from lagoonal macrobenthic communities to those deriving from molecular data. For this purpose, mtDNA of the most abundant polychaetes from five Greek lagoons were used. Lagoons are a tempting field for the study of genetic adaptations and community behavior. Lagoonal species diversity is low as a result of a relatively small number of species to respond to severely fluctuating abiotic conditions. Polychaetes are one of the most abundant taxa in the lagoons of Amvrakikos Gulf (NW Greece) and they have been found to provide a good assessment of the benthic community showing comparable trends to those produced by the total macrobenthic fauna. Multivariate analyses are used to depict species and genetic diversity patterns (non-metric multidimensional scale (MDS)) as well as for the comparison of the aforementioned patterns (2nd stage MDS).

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MON 22 AUG at 1500 - Room N6
Oral presentation *B3-Sy21-1500-O*

Symposium 21
Evolutionary ecological genomics

QTLs for courtship song and cuticular hydrocarbons in natural populations of Drosophila montana

Veltsos P[1], Morrissey B[2], Gregson E[2], Wicker-Thomas C[3], Butlin RK[2], Slate J[2], Hoikkala A[4], Ritchie MG[1]
[1]University of St Andrews, School of Biology, St Andrews, United Kingdom, [2]University of Sheffield, Animal & Plant Sciences, Sheffield, United Kingdom, [3]CNRS, Laboratoire Evolution, Génomes et Spéciation (LEGS), Gif sur Yvette Cedex, France, [4]University of Jyvãskylã, Department of Biological and Environmental Science, Jyvãskylã, Finland

Summary statement:

QTLs on candidate (sexual selection) and non-candidate genes developed from 454 sequencing of the transcriptomes of two populations.

Abstract:

Drosophila melanogaster is the model system for genetic studies par excellence. However, relatively little work has been done on genetic variability in natural populations of this or other Drosophila species. We have studied QTLs for important behavioral traits in two natural populations of the non-model Drosophilid D. montana. The populations represent different phylogeographic clades that split 0.5 Myr ago. We have collected individuals from the field and set-up laboratory pedigrees to detect QTLs for cuticular hydrocarbons, potentially associated with adaptation and mating success, and for a sexually selected male trait, male song. We developed 384 SNPs from candidate genes and 454 transcriptomes from both populations. Here we will present heritabilites, QTL surveys and comparisons of the regions detected with laboratory crosses.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i055-R*

Symposium 21
Evolutionary ecological genomics

A fine-scale genetic map of the chimpanzee genome reveals concordance of rates at the megabase scale

Venn O[1], Fledel-Alon A[2], Auton A[1], Melton C[2], Pfeifer S[3], Leffler E[2], Segurel L[2], Hernandez R[4], Bowden R[3], Bontrop R[5], Iqbal Z[1], Turner I[3], Maller J[3], Lunter G[1], Broxholme J[1], Humburg P[1], Myers S[1,3], Donnelly P[1,3], Przeworski M[2], McVean G[1,3]
[1]University of Oxford, Wellcome Trust Centre for Human Genetics, Oxford, United Kingdom, [2]University of Chicago, Dept. of Human Genetics, Chicago, United States, [3]University of Oxford, Dept. of Statistics, Oxford, United Kingdom, [4]University of California, San Francisco, Dept. of Bioengineering and Therapeutic Sciences, San Francisco, United States, [5]Biomedical Primate Research Centre, Rijswijk, Netherlands

Summary statement:

We describe features of a fine-scale genetic map of the chimpanzee genome estimated from variation data we obtained from sequencing 10 Western chimpanzees

Abstract:

Statistical analysis of human linkage disequilibrium data enabled the construction of a fine-scale genome-wide map of recombination rates. This effort revealed a landscape dominated by recombination hotspots, led to the discovery of a 13-bp motif associated with the specification of human hotspots and to the identification of a rapidly evolving zinc-finger protein that binds this motif. Despite this progress, we know little about how recombination rates evolve; in particular, whether there exist classes of hotspot that are conserved between primate species, and whether recombination rates are conserved at broader scales. To address these questions, we have sequenced 10 Western chimpanzees (Pan troglodytes verus) to ~8X coverage. This resource, which will be publicly released, is the first to document genome-wide sequence variation in the chimpanzee. From these data, we constructed a high-resolution, genome-wide recombination map for chimpanzee. We find that the chimpanzee recombination landscape is dominated by hotspots in a manner similar to humans, with recombination rates peaking outside of coding regions. Interestingly, while there is no evidence of hotspot sharing between humans and chimpanzees, recombination rates between the two species are largely concordant at the scale of megabases. The human-specific fusion of chromosome 2 is an interesting exception. We discuss the implications for our understanding of recombination factors at different scales.
(Last three authors contributed equally).

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TUE 23 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *C5-Sy21-i056-R*

Symposium 21
Evolutionary ecological genomics

A large scale gene expression scan in white spruce reveals differentially expressed genes in trees resistant to the white pine weevil

Verne S[1], White R[2], Jaquish B[3], Ritland C[1], Ritland K[1]
[1]University of British Columbia, Forest Sciences, Vancouver, Canada, [2]University of British Columbia, Department of Statistics, Vancouver, Canada, [3]British Columbia Ministry of Forests and Range, Kalamalka Research Station, Vernon, Canada

Summary statement:

Constitutive expression of genes with unexpected functions involved in the resistance to weevils in spruce.
Results suggest resistance to weevils is a complex trait in spruce.

Abstract:

White pine weevil is a major pest of conifers in North America. Constitutive defenses are important in understanding defense mechanisms because they constitute the first barrier to the attacks of the weevils and other pests. Resistant and susceptible trees exhibit constitutive differences in spruce, such as resin ducts size and number, bark thickness and terpene content. To improve our knowledge of their genetic basis, we compared the constitutive expression levels of 17825 genes between 20 resistant and 20 susceptible trees in interior spruce, as previously identified in the spruce breeding program in British Columbia. We identified 54 up-regulated and 137 down-regulated genes in resistant phenotypes, relative to susceptible phenotypes, with a maximum fold change of 2.24 and 3.91, respectively. It is puzzling that resistance is conferred by predominant down-regulation of genes, as one would think that procuring "armaments" is the best defense. Also, although terpenes and phenolic compounds play an important role in conifer defense, we found few of these genes to be differentially expressed. We found 15 small heat shock proteins (sHSP) and several other stress related proteins to be down-regulated in resistant trees. Down-regulated sHSP belong to several sHSP classes and represent 58% of all tested sHSP. sHSP are well known to be involved in plant response to various kinds of abiotic stress. Their role in constitutive resistance is not yet understood. The lack of correspondence between transcriptome profile clusters and phenotype classifications suggests that resistance in spruce to the weevil is a complex trait, with several types of resistant and susceptible phenotypes.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy21-i026-E*

Symposium 21
Evolutionary ecological genomics

First step toward ´-omic´ ecological immunology: 454 transcriptome sequencing of Black Grouse (Tetrao tetrix) for immune gene discovery

Wang B[1], Ekblom R[1], Pollock D[2], Bongcam-Rudloff E[3], Höglund J[1]
[1]Uppsala University, Population Biology EBC, Uppsala, Sweden, [2]University of Colorado School of Medicine, Biochemistry and Molecular Genetics, Denver, United States, [3]Uppsala University, Linnaeus Centre for Bioinformatics, Uppsala, Sweden

Summary statement:

We found 195 immune-related genes of Black Grouse by 454 transcriptome sequencing. The information will be used in the future ecological immunology studies.

Abstract:

Facing continuous threats of parasites, most organisms have evolved an effective immune system. In addition to affecting an organism´s fitness from parasitism, the system also plays important roles in many ecological mechanisms such as sex selection or population dynamics. In vertebrates, the major histocompatibility complex (MHC) is a large gene region which encodes molecules for the immune system. However, due to limited genomic resource, most ecological researches only rely on the genetic diversity of selected short antigen-presenting fragments of MHC. In this study, we employed 454 sequencing to discover more immune genes of Black Grouse for the future ecological studies. We ran ¼ plate of 454 titanium sequencing of spleen tissue. This generated 182179 reads with an average length of 321bp. The reads are assembled into 9035 contigs, 5472 of which could be annotated using the Chicken genomic database. After removing the duplicate information from the isoform contigs, we finally obtained 3978 unigenes. The Gene Ontology analysis showed that 195 unigenes are related to ´immune system process´. We also found 8 MHC-related genes which are located in Chromosome 16, including the Class I gene and the Class II gene. These findings will greatly facilitate the future ecological immunology study of this species.

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SUN 21 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *A5-Sy21-i057-R*

Symposium 21
Evolutionary ecological genomics

Transcriptome variation between natural African vs. French populations and natural vs. axenic food ressource in Drosophila

Wurmser F[1,2], Mary-Huard T[3,4], Daudin J-J[3,4], Joly D[1,2], Montchamp-Moreau C[1,2]
[1]CNRS, Evolution, Genomes and Speciation Lab, Gif-sur-Yvette, France, [2]University Paris-Sud XI, Orsay, France, [3]INRA, Genomes and Statistics, Paris, France, [4]AgroParisTech, Paris, France

Summary statement:

Adaptive and plastic response of gene expression to environmental difference.

Abstract:

Natural variation of population has been extensively studied at the DNA level, assessing population origin and history, the effect of adaptation and drift. Variation of expression in natural populations is however quite a new topic of interest, and if first studies focused on laboratory strains, we gradually come closer to the natural variation of expression.

In this study, we examined the role of expression in both adaptation and plasticity. To do so, we collected large samples of Drosophila simulans females from two different populations. The first one was from the ancestral range (Mayotte), while the second one was a derived population (Rhone Valley, France). Female collected were then individually raised either on artificial axenic medium or on natural medium (apple for France, banana for Mayotte). The expression of male offspring was examined using 3´ Digital Gene Expression, a RNA count high throughput technique (Illumina Genome Analyzer).

Our result show striking adaptive differences between populations in pesticide detoxification genes, notably Gluthatione transferases, and Cytochrome P450s. Main differences between medium reside in the downregulation of genes implicated in defense against bacteria and fungi in individuals raised on the axenic medium. Indeed this medium is much less subjected to microbian invasion than natural medium (fruits). We did not detect major responses in metabolism to the medium shift by itself (new sugar source,...). At the expression level, we therefore revealed both plastic response to nutritive medium (immune system) and adaptive response linked with variation of population exposure to pesticides.

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MON 22 AUG at 1730 - upper floor campus canteen *Mensa*
Regular poster *B5-Sy21-i058-R*

Symposium 21
Evolutionary ecological genomics

Gene flow, selection and speciation in two closely related pine species with overlapping distributions in southeast China

Zhou Y[1,2], Liu J[2], Savolainen O[1]
[1]University of Oulu, Department of Biology, Oulu, Finland, [2]Lanzhou University, Department of Life Sciences, Lanzhou, China

Summary statement:

Adaptation and demography were studied in two Chinese pine species, P. massoniana and P. hwangshanensis on cpDNA, mtDNA and 40 nuclear loci

Abstract:

The balance between gene flow and selection governs the potential for local adaptation and also is related to potential for speciation. Pairs of related species with sympatric distributions allow us to examine differentiation and local adaptation within species, and the relationship of this process to speciation. We studied two closely related pine species: Pinus massoniana and P. hwangshanensis. Both species occur in southeast China with overlapping distributions. We compared the variation of chloroplast and mitochondrial makers of these two species and found that the shared polymorphisms between them are mostly due to incomplete lineage sorting rather than introgression. To examine adaptive differentiation, we then sequenced 25 candidate genes and other 15 loci for reference and attempted to define the demographic histories of these two species and further to uncover the roles of selection in shaping genetic differentiation between them. We also compared the patterns of divergence in the two related species.

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Symposium 22

Environment, G matrices and adaptation

Talks: *Room N9*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Ground floor campus canteen *Mensa*

Invited Speakers:

Steve Chenoweth, Johanna Schmitt

Organizers:

Matthew Robinson, Andrew Beckerman

Description:

The environment influences the genetic basis of phenotype, but the consequences of this for adaptation are little understood. We will bring together a broad range of evolutionary biologists, to examine the consequences of environmental influence on G matrices for evolutionary dynamics, by connecting genetic architecture and patterns of gene expression to fitness, and the processes of adaptation.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy22-i001-R*

Symposium 22
Environment, G matrices and adaptation

Latitudinal variation in the genetic architecture of physiological traits

Bacigalupe LD[1], Gaitan JD[1], Nespolo RF[1]
[1]Instituto de Ecologia y Evolucion, Valdivia, Chile

Summary statement:

We evaluated if the genetic architecture of key physiological traits has changed among populations of a snail along a wide latitudinal gradient.

Abstract:

The genetic architecture or the G-matrix of additive genetic variances and covariances for a suite of traits shows the restrictions and potentialities of adaptive evolution and, together with natural selection determines the direction and rate of phenotypic evolution. Phenotypic variation among populations in a latitudinal gradient is thought to be genetically based and therefore to reflect differences among environments and (or) phenotypic plasticity. If local adaptation occurs, then, G may vary among widespread populations along the gradient. We tested one of the most prominent hypotheses in evolutionary ecophysiology related to energy allocation: the Latitudinal Compensation Hypothesis. This hypothesis states that at the same ambient temperature the metabolic rate of ectotherms from high latitude is higher than that of their counterparts from lower latitudes. The increase in metabolic rate is considered to be an adaptation to compensate for the short period of favorable environmental conditions for development, growth and reproduction. To address this problem, we chose the garden snail, Helix aspersa, as our study model. We captured animals from three populations along their latitudinal range in Chile from 30ºS to 39ºS. We carried out a half-sibs/full-sibs breeding design in the second generation, and estimated G for the following traits: standard metabolic rate, evaporative water loss and energy intake. Matrices were compared using Flury and the Jacknife-MANOVA method. We discuss the distribution of means and genetic (co)variances identifying the potentials and restrictions for adaptive evolution and differentiation of physiological traits in ectotherms.

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SUN 21 AUG at 1500 - Room N9
Oral presentation *A3-Sy22-1500-O*

Symposium 22
Environment, G matrices and adaptation

The role of phenotypic plasticity in local adaptation: a G-matrix perspective

Beckerman A[1]
[1]University of Sheffield, Department of Animal and Plant Sciences, Sheffield, United Kingdom

Summary statement:

Using new MCMC methods for estimating and comparing covariance matrices, I show that there is substantial differentiation between daphnid populations facing contrasting selection and that predator induced phenotypic plasticity is central to this local adaptation.

Abstract:

Phenotypic plasticity is an adaptation that allows organisms to adapt to variable environments. Plasticity can be described as a cross-environment genetic correlation. Here, I examine the role of multivariate plasticity in local adaptation of two sets of four populations of Daphnia facing contrasting selection pressure based around predation. Using new MCMC methods for estimating and comparing covariance matrices, I show that there is substantial differentiation between populations in each selection regime and that predator induced phenotypic plasticity is central to this local adaptation.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy22-i001-E*

Symposium 22
Environment, G matrices and adaptation

Flavonoid pathway adaptation in high and low altitude populations of Silene vulgaris (Caryophyllaceae)

Berardi AE[1], Taylor DR[1]
[1]University of Virginia, Dept of Biology, Charlottesville, United States

Summary statement:

Silene vulgaris populations vary in average calyx pigmentation and in other ecologically relevant flavonoids, allowing for analysis of selection and adaptation.

Abstract:

The plant flavonoid pathway is responsible for several important ecological functions of plants. Each branch of the pathway creates a sub-group of chemicals that are biologically active, including floral pigmentation, protection from UV radiation, deterring herbivores, antibiotics, antifungals, and antioxidants. Different environmental conditions call for different flavonoid chemicals, which allows for a priori expectations for changes in flavonoid production. Often plants at high altitudes experience more UV radiation than lowland populations, and therefore produce more sun-screening flavonols - what then happens to production of anthocyanin pigments or defensive flavones? Populations of Silene vulgaris (Bladder Campion, Caryophyllaceae) were collected from sites that varied in altitude, latitude, and longitude in Europe and grown in two common gardens to explore how production of the various flavonoid subgroups evolved to suit each population´s environmental needs and selective pressures.

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SUN 21 AUG at 1440 - Room N9
Oral presentation *A3-Sy22-1440-O*

Symposium 22
Environment, G matrices and adaptation

The biological interpretation of G's eigenvectors – a fundamental flaw in evolutionary quantitative genetics

Berner D[1]
[1]University of Basel, Zoological Institute, Basel, Switzerland

Summary statement:

I present a simulation study demonstrating that the eigenstructure of the G matrix does not reliably reflect the genetic architecture of the constituent traits.

Abstract:

A key goal of evolutionary quantitative genetics is to understand how patterns of genetic variance and covariance among multiple traits constrain the rate and direction of evolution. Such constraints are generally studied using geometric approaches, where vectors of multivariate selection or population divergence are related to the vectors of genetic trait (co)variance. The latter vectors are expressed as eigenvectors obtained by spectral decomposition of the additive genetic (co)variance matrix G. A fundamental assumption underlying this research approach is that the eigenvectors of G mirror the genetic architecture of the constituent traits, that is, their magnitude of variance and associations due to pleiotropy or linkage. I here use simulated populations with explicit genetic architecture to demonstrate that this assumption is incorrect. An interpretable relationship between eigenvectors of G and genetic architecture cannot be taken for granted. This finding represents a major challenge to geometric approaches in evolutionary quantitative genetics, and indicates that the research field should urgently reconsider its concepts and empirical toolkit.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy22-i002-R*

Symposium 22
Environment, G matrices and adaptation

Adaptation and natural selection on anti-predator reaction norm

Carter MJ[1], Dennis SR[1], Beckerman AP[1]
[1]University of Sheffield, Animal and Plant Sciences, Sheffield, United Kingdom

Summary statement:

We used quantitative genetic and selection analyses to detect impact of predation on induced defences. We found fine G-matrix differentiation and different patterns of selection.

Abstract:

Inducible anti-predator traits are strong plastic features allowing species to survive in heterogeneous predator environments. The evolutionary dynamics of anti-predators traits depends on their genetic background and the predation regime that populations have experienced. Opposite patterns of selection are expected in environments with predators differing in hunting strategy, which should leave marks on genetic architecture of induced defences. We examined the reaction norms of morphological defence in two waterflea (Daphnia pulex) populations differing in predation regime (Phantom midge versus Fish). Across an imposed gradient of risk by Chaoborus (Phantom midge) we describe the reaction norm of morphological defence in three parameters, which were considered as traits. We compared genetic (co) variance between populations, and showed that genetic (co) variance of morphological defences differed in magnitude and sensitivity between populations. Furthermore, we found evidence for different patterns of present and past selection on reaction norms of morphological defence in Daphnia pulex.

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SUN 21 AUG at 1400 - Room N9
Invited talk ***A3-Sy22-1400-I***

Symposium 22
Environment, G matrices and adaptation

Dissecting sexually-selected variation within and among populations of flies: from genetic (co)variances to pleiotropic variants

Chenoweth S[1]
[1]The University of Queensland, School of Biological Sciences, Brisbane, Australia

Summary statement:

I cover our recent efforts to connect molecular variants with the pattern of genetic covariance structure among functionally related traits in the fly, Drosophila serrata.

Abstract:

In this talk I share our recent efforts to connect patterns of phenotypic variation in sexually-selected cuticular hydrocarbons with naturally-segregating genomic variants in Drosophila serrata. First, in an association study where both multivariate sexual selection and genetic variance in sexual fitness was estimated, pleiotropic SNP associations at a desaturase locus suggested that natural and sexual selection may be aligned in their effects. We then performed a genome-wide experimental test of this hypothesis, resequencing an experimental evolution study where both natural and sexual selection were manipulated during adaptation to a novel environment. In the second part of my talk I will focus on patterns of sexually-selected trait divergence along a cline. Cuticular hydrocarbons in D. serrata exhibit strong clinal variation in both mean and G-matrix structure along the eastern Australian coastline. For some axes of trait variation there is a loose association between mean and genetic variance along the cline whereas for others the relationship is much tighter; suggesting fundamental differences in genetic architecture. We have detected a large–effect pleiotropic variant, confined to tropical populations, that underlies the major axis of phenotypic divergence, dmax. I discuss our recent progress combining pleiotropic QTL mapping and NGS bulk-segregant analyses to dissect this variant and understand its effects on G-matrix structure..

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy22-i002-E*

Symposium 22
Environment, G matrices and adaptation

Natural variation in the dauer larva development of wild-type nematodes of Caenorhabditis elegans

Diaz A[1], Harvey S[2], Viney ME[1]
[1]University of Bristol, School of Biological Sciences, Bristol, United Kingdom, [2]Canterbury Christ Church University, Department of Geographical and Life Sciences, Canterbury, United Kingdom

Summary statement:

Our ecological knowledge of C. elegans´ life history is very scant compared to its genomic information. We investigate the life history of worms recently isolated from the wild.

Abstract:

Organisms live in variable environments. It is widely recognised that natural selection favours the evolution of strategies which allow genotypes to cope with their environments. If conditions become harsh and surviving until reproduction is reduced, genotypes displaying strategies for surviving until maturation are expected to be favoured. Strategies such as hibernation, dormancy or developmental arrest are common in nature, however, our understanding of the genetic basis of these strategies is not complete. Despite having a full genome sequenced, the nematode Caenorhabditis elegans is not the exception. In C. elegans, if environmental conditions become harsh, a young larva will arrest its growth and develop into an alternate state called “dauer” larvae. Once conditions become favourable, developmental growth is reassumed and the larva matures into an adult. In the wild, C. elegans is mainly found as dauer larvae rather as adults, suggesting the importance of this strategy. Previous work has found that different laboratory strains of C. elegans differ in their dauer larvae formation and that changes in the environment affect genotypes differently. Furthermore, dauer larva formation was found to be negatively correlated with other fitness components (i.e. population growth rate), suggesting a potential trade-off within its life history. We investigate this relationship in wild-type worms recently isolated from nature. We explore possible local adaptations and the genetic basis of the dauer larva formation in wild-type worms. We expect our results can help to understand better the life history of one of the most intensively studies species.

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SUN 21 AUG at 1500 - Room N9
Oral presentation *A3-Sy22-1500-O*

Symposium 22
Environment, G matrices and adaptation

Genetic and environmental constraints on the evolution of sexual dimorphism

Dmitriew C[1], Blanckenhorn W[1]
[1]University of Zurich, Institute of Evolutionary Biology and Environmental Studies, Zurich, Switzerland

Summary statement:

We compared intersexual genetic correlations among populations to assess the roles of genetic and environmental constraints in the evolution of sexual dimorphism.

Abstract:

Sexual selection and sex-specific natural selection favour optimal trait values that differ between the sexes. In theory, the evolution of sexual dimorphism resolves the gender load associated with sexually antagonistic selection. However, the common genetic architecture of males and females may constrain the evolution of certain traits towards their respective fitness optima. This may have important consequences for evolutionary dynamics, acting to maintain genetic variation in fitness and potentially contributing to divergence among populations.

In the scavenger fly Sepsis punctum, the degree of sexual dimorphism in overall body size and in morphological traits under sexual selection differs markedly among populations and in response to variation in food availability and temperature. This suggests that forces such as genetic drift and local adaptation may contribute to the evolution of distinct male and female phenotypes.

G matrices were estimated for morphological traits in two representative populations of S. punctum (one highly and one weakly dimorphic) that were reared under benign or stressed conditions. Our experiment addresses two key questions. First, does the strength of intersexual genetic correlations correspond to the degree of sexual dimorphism expressed in a given trait? Second, are across-environment correlations sex-specific, reflecting different selective regimes in response to environmental variation? These data contribute to our understanding of the roles of genetic and environmental constraints on the evolution of sexual dimorphism.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy22-i003-R*

Symposium 22
Environment, G matrices and adaptation

Age-related depletion of genetic variance in immunocompetence and body mass in the blue tit (Cyanistes caeruleus)

Drobniak SM[1], Dubiec A[2], Cichoń M[1]
[1]Jagiellonian University, Institute of Environmental Sciences, Kraków, Poland, [2]Polish Academy of Sciences, Museum and Institute of Zoology, Warszawa, Poland

Summary statement:

Heritability of cell-mediated immune response and body mass in blue tits is lower in offspring of older mothers.

Abstract:

Strong selection is usually expected to deplete additive genetic variance due to selective removal of certain genotypes from the genetic pool. Thus, differences in heritabilities among groups of individuals may provide information on selection episodes. Here we aimed at testing whether heritability of some traits differ between offspring produced by young and old females. Such differences would be indicative of selective survival of some genotypes among adult birds. We estimated heritabilities of cell-mediated immune response (CMI), body mass and tarsus length in blue tit nestlings produced by young (1 year old) and old females (2 or more years old). To separate genetic and environmental sources of variation we partially cross-fostered hatchlings in pairs of nests containing one young-female nest and one old-female nest. All three traits showed significant heritabilities. More importantly, in agreement with our predictions, two traits – CMI and body mass – showed age related patterns of expression, with heritabilities being lower among nestlings of young females. Such pattern suggests that body mass and CMI are subjects to selection during the life of an individual, resulting in the depletion of genetic variance.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy22-i003-E*

Symposium 22
Environment, G matrices and adaptation

Complex selection on morphology and condition during mate search on males of a sexually highly dimorphic orb-web spider

Foellmer MW[1], Pereira D[2], Moya-Laraño J[3]
[1]Adelphi University, Biology, Garden City, United States, [2]Trent University, Department of Biology, Peterborough, Canada, [3]Estación Experimental de Zonas Áridas - CSIC, Functional and Evolutionary Ecology, Almería, Spain

Summary statement:

We demonstrate temporal and spatial variation in selection on morphology and condition during mate search as a function of season "quality" and habitat features.

Abstract:

The period of mate search has long been hypothesized to generate selection on morphology and performance in males, which is most often the mate-searching sex. For male web-building spiders, mate search involves a dramatic shift from being essentially sessile to actively roaming the habitat to find receptive females. Thus the period of mate search has been central to various hypotheses trying to explain the evolution and maintenance of sexual size dimorphism (SSD) in spiders, a taxon where males are of minute size compared to females in several genera. However, published patterns of selection on morphology, as well as results from experimental performance trials have been inconclusive. Here we report the results from an extensive field study that estimates selection on morphology and condition in male Argiope trifasciata over three years in habitat patches with manipulated vegetation densities. We found considerable temporal variation in patterns of selection, as well as habitat effects, although little effect of vegetation density. In a "good" year when males matured at a relatively large size, leg length and initial condition were positively related to mate search success. In a "poor" year when males matured at a smaller size, no significant effects of morphology or initial condition could be detected. We discuss these results in the context of body size and performance evolution. Importantly, these results highlight the shortcomings of studies that do not embrace temporal variation, which has in part contributed to our limited understanding of the evolutionary significance of mate search in web-building spiders.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy22-i004-R*

Symposium 22
Environment, G matrices and adaptation

How strongly do environmental covariances among relatives bias estimates of G in studies of natural populations?

Gienapp P[1]
[1]University of Helsinki, Dept. of Biosciences, Helsinki, Finland

Summary statement:

Using simulations I tested how strongly environmental covariances among relatives bias G and whether we are likely to get meaningful estimates from studies of natural populations.

Abstract:

Genetic correlations among traits under selections obviously affect evolutionary trajectories and are hence important for our understanding of evolution in natural populations. Hence, multi-trait approaches studying heritabilities, genetic correlations and selection have been encouraged and are increasingly applied. Quantitative genetic methods to estimate genetic (and other) variances and covariances rely on the phenotypic resemblance among relatives. In studies of natural populations pedigree information can be used to estimate the desired quantitative genetic parameters. One problem with this approach can be that relatives are more similar than expected from their shared genes because they live in more similar environments than unrelated individuals, e.g. due to limited dispersal. Advanced statistical methods that include all pedigree information, so-called 'animal models', are generally thought to be less affected by environmentally caused covariance among relatives than 'classical' approaches that include only two generations, as parent-offspring regression. It is however still unclear how much pedigree information is necessary to reliably environmental and genetic covariance among relatives. Pedigrees tend to be imperfect and shallow due to methodological limitations, e.g. only one parent could be captured. Using simulated data sets reflecting different life-histories and mating systems I will test how strongly environmental covariance among relatives can bias the estimated genetic variances and covariances and whether we are likely to get meaningful estimates of G from studies of natural populations.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy22-i004-E*

Symposium 22
Environment, G matrices and adaptation

Brazilian Passiflora foetida reveals that his strong seed dormancy detected in tissue culture can only be broken by scarified seeds in GA3 growth regulator

Gniech Karasawa MM[1], Vieira LR[2], Bendande MM[2], Oliveira JC[3]
[1]Federal University of Alfenas, Nature Science Institut, Alfenas, Brazil, [2]Federal University of Alfenas, Natural Science Institut, Alfenas, Brazil, [3]Sao Paulo State University, Jaboticabal, Brazil

Summary statement:

Non weedy Brazilian Passiflora foetida has shown evolutionary strong seed dormancy in tissue culture even after 2 years can only be broken by scarified seeds in GA3growth regulator

Abstract:

Passiflora foetida a South America native species belongs from genus Passiflora subgenus Dysosmia. This species considered a serious weed in Southeast Asia, Pacific region, West of Africa, Central America and Hawaii, but no weed behavior in Brazil. Most weeds are important and their distribution is influenced by environmental and biological factors. Seed dormancy is a primitive adaptive trait of wild species which prevents early germination and helps to preserve a soil seeds supply, an obvious selective advantage, especially in environments that undergo favorable/unfavorable seasons. Dormancy also enhance seedling survival avoiding climate risk distributing germination in time. In order to better understand factors that regulate seeds germination of Brazilian P. foetida we designed two in vitro experiments with seeds stored at room temperature since Oct 2008. First experiment started on Jan 2010 and was conducted on ½MS media with 5 repetitions and 2 seeds with coat per repetition. The second started on Dec 2010 and was conducted on ½ MS media with five GA3 levels (0, 125, 250 and 500 mg/L),3 repetitions and 2 scarified seeds per repetition. Complete randomized design was used. Analysis were performed by F test. No seed germination was verified in the first test even after a year, nor with scarified seeds without GA3. On the other hand, germination occured after six days using scarified seeds in ½ MS media supplemented with GA3. Roots were stimulated in all GA 3 levels but not tall and leaf. Also we detect that only 1 each 2 scarified seeds germinated. This let us infer that P. foetida may also present chemical allelopathy that prevents the germination of a second seed.

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MON 22 AUG at 1440 - Room N9
Oral presentation *B3-Sy22-1440-O*

Symposium 22
Environment, G matrices and adaptation

Evolution of genetic correlations and evolutionary potential in the invasive plant species Ulex europaeus

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Summary statement:

This study reveals that in an invasive species, enemy release can lead to weaker genetic correlations between traits, potentially facilitating local adaptation and niche expansion.

Abstract:

Biological invasions represent spectacular examples of species facing new environments. In many cases, a rapid evolution of traits was observed as well as local adaptation to the new conditions. Although genetic correlations can constrain local adaptation of linked traits, and thus impede further expansion of a species, the present work is the first to explore the evolution of genetic correlations after introduction of an invasive species, gorse Ulex europaeus. A first quantitative genetic experiment performed in the native range of the plant revealed a high genetic diversity of traits related to growth and reproduction. In addition, we found strong genetic correlations between these traits and resistance to the main natural enemy of gorse, the seed-eating weevil Exapion ulicis, revealing the coexistence of two strategies of seed-eating avoidance. In a second common garden experiment, we compared gorse individuals from the native and the invaded range. In invaded regions, where U. europaeus has initially been introduced without its enemies, genetic correlations between seed-eating avoidance and some life-history traits disappeared or were greatly weakened. This process could have enabled more independent evolution of these key traits and potentially facilitated local adaptation and niche expansion. Considering the evolution of genetic correlations during biological invasions may help understand the high evolutionary potential and the rapid spread of several introduced species. Reciprocally, biological invasions may offer interesting cases to study environmental influence on genetic architecture and adaptation.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy22-i005-R*

Symposium 22
Environment, G matrices and adaptation

The evolution of allocation strategies when condition is manipulated in the decorated cricket (Gryllodes sigitallus)

Houslay TM[1], Bussière LF[1]
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Summary statement:

Resource allocation trade-offs between sexual and life-history traits when condition is manipulated, using inbred lines of the decorated cricket.

Abstract:

Variation in male reproductive success depends on differences in characters such as intra-specific competitive ability and attractiveness. Typically, these ´performance indicators´ depend upon condition – the ability to acquire and convert resources to metabolically useful forms. Males that have higher condition should be able to allocate more resources to sexual signalling than low condition males. However, resource allocation trade-offs may occur between sexually selected structures and other life history traits, as energy used in the generation of any character is then unavailable for other competing functions. Resource acquisition was manipulated in inbred lines of decorated crickets (Gryllodes sigillatus) by varying diet quality. Measurements of condition-dependence in a number of sexually and naturally selected traits were taken in both sexes. We found striking differences in trait expression across diets for morphological features, and interactions across diets and genotypes for male advertisement mate-calling effort and adult longevity. These findings raise questions concerning the evolution of allocation strategies to competing life history functions. I shall discuss the relevance of my results in the context of mate choice theory for indirect benefits.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy22-i006-R*

Symposium 22
Environment, G matrices and adaptation

Evolution of reproductive systems in libellulid dragonflies (Odonata: Anisoptera)

Koch K[1], Karlsson M[2], Sahlén G[3], Ware J[4]
[1]Johannes Gutenberg-University Mainz, Department of Ecology, Mainz, Germany, [2]Lund University, Department of Animal Ecology, Lund, Sweden, [3]Halmstad University, Ecology and Environmental Sciences, Halmstad, Sweden, [4]American Museum of Natural History, Division of Invertebrate Zoology, NY, United States

Summary statement:

Evolution of egg-laying and mate-guarding behaviour of Libellulidae using Bayesian analyses, ancestral state reconstruction and phylogenies with various outgroups.

Abstract:

In Libellulidae, a continuous oocyte production has been assumed, with periods of egg-laying interspersed with periods of resting and eating. Recent work suggests that two types of egg-laying behavior are common in this taxon: either (a) continuous or (b) stepwise oocyte production; this is mirrored in the arrangement of the ovarioles in the abdomen. Likewise, two types of mate guarding behaviour exist in Libellulidae: (1) non-contact guarding, in which the male hovers above the female during oviposition and (2) tandem guarding where it is physically attached to her during oviposition. We examined the evolution of reproductive behaviors and morphology using Bayesian analyses and ancestral state reconstruction. With the program r8s we estimated divergence times for the nodes of Anisoptera. In addition, we recovered phylogenies of Libellulidae rooted with a range of anisopteran outgroups from Libelluloidea, Petaluridae, Gomphidae and Aeshnidae to examine the effect of outgroup selection on tree topology and divergence time estimates. Continuous egg production appeared to have evolved more than once in this taxon, as have the alternatives tandem and non-contact guarding. Here we explore how the evolution of different ovariole types and guarding behavior may have been influenced by habitat instability, dispersal, and crowded oviposition sites. It is possible that migratory behavior or habitat availability may have driven the evolution of different ovariole types.

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SUN 21 AUG at 1550 - Room N9
Oral presentation *A4-Sy22-1550-O*

Symposium 22
Environment, G matrices and adaptation

Genetic constraints on life history trait evolution in a wild red deer population

Kruuk LEB[1], Walling CA[1], Morrissey MB[1], Clutton-Brock TH[2], Pemberton JM[1]
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Summary statement:

We explore the extent to which the multivariate genetic relationship amongst life history traits may constrain adaptive evolution in a wild red deer population.

Abstract:

The extent to which the evolution of life histories is hampered by genetic constraints is a fundamental question for evolutionary biologists, but one which can be difficult to address for wild populations inhabiting natural environments. Here we use data from a long-term study of red deer in Scotland to investigate the evidence for constraints underlying a suite of life-history traits. Using a combination of multivariate quantitative genetic and demographic tools, we consider in particular the role of trade-offs between fecundity and survival and the presence of sexually-antagonistic genetic variation. We find evidence that the multivariate genetic relationship amongst traits may constrain adaptive evolution. Our analyses illustrate the importance of considering genetic, not just phenotypic, associations between traits when testing for evolutionary trade-offs.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy22-i007-R*

Symposium 22
Environment, G matrices and adaptation

Natural selection through male and female fitness: Floral traits of five milkweed (Asclepias) species over four years

La Rosa R[1], Conner J[1]
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Summary statement:

Milkweed floral traits are adaptive for both male and female fitness. Selection fluctuates between years and can act on a trait simultaneously through male and female fitness.

Abstract:

The milkweed sub-family Asclepiadoideae has unique floral structures that, although conserved across species, show a huge amount of diversity in shape and size. Even within the single genus Asclepias, the flowers can vary wildly. It is presumed that these floral traits are adaptations, but that has not been studied outside of Asclepias syriaca.
Milkweed flowers have a single structure (a gynostegium) that houses both male and female reproductive parts. Surrounding the gynostegium is a ring of five hood-like structures that form the corona and hold the nectar reward for pollinators. Pairs of pollinia (pollen packets) are attached by a gland that catches onto generalist pollinators as they brush against it. If a pollinium is then inserted through one of five slits in the wall of the gynostegium, it can pollinate the flower.
Are milkweed floral traits adaptive? We measured natural selection on six floral traits in five species of Asclepias, some over multiple years. Results of significant selection on all six floral traits shows that these traits are likely adaptations, not only for A. syriaca as shown by Morgan and Schoen (1997) and Caruso et al. (2005), but more generally for the genus.
Does selection on floral traits differ across years? We measured selection on A. incarnata over four consecutive years and found five of the six traits are likely adaptive. Selection fluctuated between years for one trait, which resulted in no net selection. Two other traits, which may act to attract pollinators, were under selection through both male and female fitness. Differences in the pollinator community may be responsible for differences in selection between years.

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SUN 21 AUG at 1630 - Room N9
Oral presentation *A4-Sy22-1630-O*

Symposium 22
Environment, G matrices and adaptation

The evolutionary quantitative genetics of continuous reaction norms: Dissecting the genetic architecture of standing and mutational variance in thermal performance curves

Latimer CAL[1], Wilson RS[1], Chenoweth SF[1]
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Summary statement:

A study of geographic divergence and distribution of the effects of genetic and mutation variance for genetic by environment interactions of performance response to temperature.

Abstract:

Thermal performance curves (TPCs) are functions that describe the relationship between individual performance and environmental temperature. TPCs provide a powerful framework for studying thermal adaptation and more broadly, the evolution of continuous reaction norms. Genetic variation in TPCs can be characterized by three modes of variation; 1) height, describing performance variance independent of temperature, 2) temperature optimum, describing variation of temperature for maximum performance, and 3) generalist-specialist, describing a tradeoff between maximum performance and range of temperatures for performance. Although TPC evolution has long been studied using comparative methods, microevolutionary quantitative genetic studies have been generally lacking. We developed a high throughput approach to TPC phenotyping in a Drosophila species that inhabits a broad range of thermal regimens and have applied quantitative genetic methods to dissect patterns of genetic covariance structure within and among natural populations. Here I discuss our recent efforts to characterize the distribution of genetic variance across these covariance functions due to both standing and mutational genetic variation. First, I show that TPCs have diverged genetically among geographical populations. Second, I estimated the mutational variance-covariance matrix, M, for TPCs using mutation accumulation lines. Finally, I performed a mapping experiment to characterize the distribution of QTL effects underlying genotypic divergence between two natural populations.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy22-i008-R*

Symposium 22
Environment, G matrices and adaptation

Genetic basis of local adaptation and phenotypic differentiation in diverged natural populations of a perennial plant Arabidopsis lyrata

Leinonen PH[1], Remington DL[2], Leppälä J[1], Savolainen O[1]
[1]University of Oulu, Department of Biology, Oulu, Finland, [2]University of North Carolina at Greensboro, Department of Biology, Greensboro, United States

Summary statement:

Genetic basis of local adaptation in two diverged Arabidopsis lyrata populations is governed by nuclear and cytoplasmic genes, and genetic changes resulting from adaptation.

Abstract:

We examined the genetic basis of local adaptation and phenotypic differentiation in diverged natural populations of a perennial model plant Arabidopsis lyrata. This study was enabled by the close relatedness to the annual Arabidopsis thaliana and availability of the genome sequence for A. lyrata. Our main goal was to examine the genetic architecture of previously documented local adaptation (fitness advantage of the local population in each environment) and phenotypic differentiation in two diverged allopatric populations. More specifically, we ask whether the differences are caused by adaptation or result from genetic drift. The genetic basis of local adaptation and phenotypic differentiation was examined using QTL mapping in reciprocal between-population F2 progeny planted in a reciprocal transplant field experiment in the original sites of the populations originating from Spiterstulen (Norway) and Mayodan (North Carolina, USA). Our prediction was that local QTL alleles would increase fitness if the genetic differences were due to local adaptation.
Using single nucleotide polymorphisms covering the genome at low density, we performed quantitative trait locus (QTL) mapping using R/qtl software. We found that local QTL alleles provided a fitness benefit in most cases, consistent with genetic differences due to local adaptation. The role of cytoplasmic factors was also examined, and we found evidence that QTL x cytoplasm interactions contribute local adaptation.

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SUN 21 AUG at 1650 - Room N9
Oral presentation *A4-Sy22-1650-O*

Symposium 22
Environment, G matrices and adaptation

Bioenergetic consequences of asexual specialization on the genetic architecture and life histories of an organism with mixed reproductive strategies

Nespolo RF[1], Simon JC[2], Carter M[3]
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Summary statement:

Funded by ECOS-Conicyt grant C08B02 to RN and JCS. RN thanks FONDECYT gran 1090423.

Abstract:

Organisms with co-existing sexual and asexual populations are ideal models for studying the consequences of either reproductive mode on the quantitative genetic architecture of life history traits. Here, we studied the energetics of the reproductive variation in the aphid Rhopalosiphum padi, which exhibits lineage specialization for sexual/asexual reproduction. Specifically, we estimated maintenance costs as Standard Metabolic Rate (SMR), together with life history traits and fitness (intrinsic rate of increase) in sexual and asexual lineages of this aphid. Our results show that asexual lineages exhibit higher SMR, higher production of wingless individuals, higher fecundity and fitness, compared with sexual lineages. Also, SMR and fitness exhibited significant heritabilities, only in asexual lineages. We found large and positive genetic correlations between SMR and several traits in asexual lineages, which were not present in sexual lineages. These results, together with Fst and Qst comparisons, suggest that asexual genotypes increased energetic costs as a correlated response of selection promoting high fecundity, low dispersal and reducing age at maturity. Hence, it appears that in asexual lineages, energy is fully allocated to maximize the rate of production of wingless parthenogenetic individuals, the simplest possible form of aphid repertoire of life histories strategies.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy22-i009-R*

Symposium 22
Environment, G matrices and adaptation

The effects of modular pleiotropy on the distribution of fitness effects of mutations and on adaptation

Polster R[1], Guillaume F[1]
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Summary statement:

How the distribution of pleiotropic effects of mutations influences the distribution of fitness effects of mutations and the rate of adaptation of a population.

Abstract:

It becomes more and more evident that the genotype-phenotype map is modular and that mutational effects do not have a universal impact on the phenotype. Thus, in many previous theoretical models on evolvability and adaptation of populations, key assumptions on the extent of pleiotropic effects do not hold.
By integrating modular pleiotropy into a computational evolutionary framework it is possible to answer questions like: How important is modularity for evolvability and adaptation to changing environments? Is there a difference in evolvability between organisms/populations with different genetic architectures?
The framework is a stochastic model in which the empirical distribution of pleiotropic effects will be included and different modular genetic architectures are tested for their influence on the distribution of fitness effects of mutations and the rate of adaptation of a population.
Depending on the complexity of the organism and the distance to the fitness optimum the distribution of fitness effects of mutations is expected to change for different genetic architectures. Genetic correlations among traits may increase adaptation if selection favors phenotypic integration, otherwise they may impede adaptation.
Incorporating recent results on the distribution of pleiotropic effects from experimental studies into a theoretical model leads to a better understanding how modularity affects the adaptation to changing environments.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy22-i005-E*

Symposium 22
Environment, G matrices and adaptation

The quantitative genetics of sperm traits in a simultaneous hermaphrodite

Ramm SA[1], Vizoso DB[1], Janicke T[1], Kölliker M[1], Schärer L[1]
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Summary statement:

We estimate G and GxE effects (where E is the social environment) for sperm production and morphology in the marine flatworm Macrostomum lignano.

Abstract:

Post-copulatory sexual selection is clearly established as a major selective agent generating diversity in reproductive traits. However, the phenotypic expression of reproductive traits often depends on the social environment in which they are expressed, and it is increasingly recognised that in order to understand their evolution, phenotypic studies of individual reproductive traits have significant limitations. The existence of functional and genetic trade-offs between different traits implies that more comprehensive studies that jointly consider whole suites of traits and explicitly incorporate the estimation of genetic correlations between traits are now required. We study the free-living flatworm Macrostomum lignano, a simultaneous hermaphrodite exhibiting a complex sperm design and considerable plasticity in gamete production in response to varying social group size (as predicted by both sperm competition and sex allocation theory). We are using this model system to understand the genetic architecture of sexual traits (sex allocation, sperm morphology, sperm production etc.), as well as the genetics of phenotypic plasticity in these traits. We report progress on quantitative genetic experiments designed to address these issues, and discuss how the patterns of genetic variation we observe impact on how these traits can evolve in response to post-copulatory sexual selection.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy22-i010-R*

Symposium 22
Environment, G matrices and adaptation

The quantitative genetic basis of adaptive divergence in frogs and stickleback: Implications for divergent selection and gene flow

Räsänen K[1]
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Summary statement:

Variation in the quantitative genetic basis of trait divergence is shown in Rana arvalis and Gasterosteus aculeatus. Implications for selection and gene flow are discussed.

Abstract:

The quantitative genetic basis (i.e. the relative contribution of additive and non-additive genetic, maternal and environmental effects) of adaptive divergence provides important insight to how phenotypic diversity arises and is maintained. I present empirical evidence for variation in the quantitative genetic basis of trait divergence from common garden studies and reciprocal crosses i) between three divergent population pairs of the moor frog (Rana arvalis) in embryonic acid stress tolerance and larval life-history traits, and ii) between lake and stream stickleback (Gasterosteus aculeatus) ecotypes in key foraging-related morphological traits. Together these studies suggest that adaptive divergence can be mediated by additive, non-additive and/or maternal effects, and that their relative contribution can strongly depend on the particular population pair, the rearing environment and the trait under study. I discuss the implications of these findings for divergent selection and gene flow, in particular in the context of fitness of migrants and hybrids.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy22-i011-R*

Symposium 22
Environment, G matrices and adaptation

Environmental quality interacts with genetic variance and gene expression in a tropical butterfly adapted to two seasonal environments

Saastamoinen M[1], Brommer JE[1], Wheat CW[1], Oostra V[2], Brakefield PM[3], Zwaan BJ[4]
[1]University of Helsinki, Department of Biosciences, Helsinki, Finland, [2]Leiden University, Leiden, Netherlands, [3]University of Cambridge, Cambridge, United Kingdom, [4]University of Wageningen, Wageningen, Netherlands

Summary statement:

Genetic variance and gene expression vary across temperature and nutritional condition in the seasonally plastic butterfly, Bicyclus anynana

Abstract:

The tropical butterfly Bicyclus anynana exhibits two seasonal morphs, which vary in numerous life history and morphological traits, as an adaptation to alternate wet and dry seasonal environments. Full-sib families were exposed to a complete two-factorial (nutritional stress × dry/wet season) conditions. The experience of nutritional stress during development had a great impact on the resulting phenotype, with some variation between the sexes and seasons. Heritability estimates for all traits (life history and morphology) were significant, and for some the estimates were environment and nutrition specific. Although no strong evidence of Genotype*Season interaction was found for development time, pupal mass or thorax ratio, we did find evidence for Genotype*Stress interaction in one or both of the seasons for metabolic rate and fat allocation. Results from a microarray study will reveal how gene expression varies across these environmental conditions. Understanding how environmental quality interacts with genetic variation and gene expression is crucial in determining the evolutionary potential and dynamics of populations inhabiting heterogeneous environments.

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SUN 21 AUG at 1610 - Room N9
Oral presentation *A4-Sy22-1610-O*

Symposium 22
Environment, G matrices and adaptation

Estimation evolutionary changes of age-structured populations in fluctuating environments

Sæther B-E[1], Engen S[1]
[1]Norwegian University of Science and Technology, Centre for Conservation Biology, Trondheim, Norway

Summary statement:

We estimate evolutionary responses to selection on quantitative characters into age-specific components using contributions to the total reproductive value of the population

Abstract:

We analyze weak fluctuating selection on a quantitative character in an age-structured population not subject to density regulation. We assume that early in the first year of life before selection, during a critical state of development, environments exert a plastic effect on the phenotype which remains constant throughout the life of an individual. Age-specific selection on the character affects survival and fecundity, which have intermediate optima subject to temporal environmental fluctuations. Weighting individuals by their reproductive value, as suggested by Fisher, we show that the expected response in the weighted mean character has the same form as for models with no age structure. Environmental stochasticity generates stochastic fluctuations in the weighted mean character following a first order autoregressive model with a temporally autocorrelated noise term and stationary variance depending on the amount of phenotypic plasticity. The parameters of the process are simple weighted averages of parameters used to describe age-specific survival and fecundity. The {em age-specific selective weights} are related to the stable distribution of reproductive values among age classes. This allows partitioning of the change in the weighted mean character into age-specific components We use this method to quantitatively estimate the evolutionary responses to age-specific selection on quantiative characters of house sparroes and moose

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MON 22 AUG at 1400 - Room N9
Invited talk *B3-Sy22-1400-I*

Symposium 22
Environment, G matrices and adaptation

Genetic architecture of local adaptation in Arabidopsis thaliana

Schmitt J[1], Fournier-Level A[2], Korte A[3], Cooper M[2]
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Summary statement:

The genetic basis of local adaptation differs across geographic regions.

Abstract:

Adaptation to local environments has been observed experimentally in many organisms, and will be critical for species persistence in the face of rapid environmental change. However, the genetic mechanisms underlying local adaptation are still largely unexplored. Here we report that the genetic basis of fitness in the genetic model species Arabidopsis thaliana varies among natural environments across the species' native European range, and that fitness-associated loci exhibit both geographic and climatic signatures of local adaptation. A genome-wide association study of survival and lifetime reproduction in common garden field experiments in Finland, England, Germany, and Spain revealed that effect sizes of the SNPs associated with fitness were weakly correlated across field sites, ranging from weakly negative correlations between climatically distant sites to weakly positive correlations between more similar sites, and very few of the most strongly associated SNPs for each trait were common across sites. Thus distinct environment-specific loci contributed to fitness variation in each field site. Cross-environment genetic correlations of fitness phenotypes across environments exhibited similar patterns. Alleles conferring higher fitness within each site were distributed significantly closer to that site than genomic controls in all sites except Finland, providing a geographic signature of local adaptation.

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MON 22 AUG at 1500 - Room N9
Oral presentation *B3-Sy22-1500-O*

Symposium 22
Environment, G matrices and adaptation

Multivariate phenotypic divergence due to fixation of beneficial mutations in experimentally evolved lineages of filamentous fungus

Schoustra SE[1,2], Punzalan D[3], Dali R[4], Rundle HD[2], Kassen R[2]
[1]Wageningen University, Laboratory of Genetics, Wageningen, Netherlands, [2]University of Ottawa, Biology, Ottawa, Canada, [3]Royal Ontario Museum, Natural History, Toronto, Canada, [4]McGill University, Montreal, Canada

Summary statement:

We used a divergence matrix D to study multivariate phenotypic divergence due to fixation of beneficial mutations in experimentally evolved lineages of filamentous fungus.

Abstract:

The potential for evolutionary change is limited by the availability of genetic variation. Mutations are the ultimate source of novel genetic variation, yet there have been very few experimental investigations of the role of novel mutations in phenotypic evolution. Here, we evaluated the degree of multivariate phenotypic divergence observed in a long-term experimental evolution study over 800 generations using two different bottleneck treatments, whereby replicate lineages of the filamentous fungus Aspergillus nidulans were derived from a single genotype and were allowed to fix novel, beneficial mutations. We measured fitness and phenotypic values for 6 traits, 4 of which are expected to be correlated with fitness. Using a divergence matrix (D*matrix), we asked (1) whether the degree of phenotypic divergence among lineages was limited by the supply of mutations, (2) whether divergence occurred in a deterministic/repeatable direction and (3) whether the extent of divergence was related to the margin of fitness gain. Results show that (1) bottleneck treatments differed in the average degree of divergence but (2) exhibited very similar divergence (D) matrices, the latter result indicating some conserved patterns of divergence (i.e. covariance structure of D), regardless of mutation supply. Curiously, the extent to which divergence conferred adaptation (i.e. the phenotype-fitness relationship) differed between treatments, potentially due to drift. These results are discussed in the context of evolution of complex phenotypes and adaptive landscapes.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy22-i012-R*

Symposium 22
Environment, G matrices and adaptation

Environment matters to monarchs and their parasites

Sternberg ED[1], Lefevre T[1], de Roode JC[1]
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Summary statement:

We focus on how variation in biotic environmental factors can modulate infection of the monarch butterfly (Danaus plexippus) by a protozoan parasite (Ophryocystis elektroscirrha).

Abstract:

Environmental conditions can significantly affect interactions between hosts and parasites, consequently shaping host-parasite coevolution. If parasites adapt not only to local host genotypes but also to the surrounding environment, then these environmental conditions can drive local adaptation in host-parasite systems. We focus on how variation in biotic environmental factors modulates infection of the monarch butterfly (Danaus plexippus) with a protozoan parasite (Ophryocystis elektroscirrha). In addition, we discuss patterns of local adaptation in this system and whether these patterns are consistent with what is known about the environmental conditions experienced by the different monarch populations. Generally we emphasize that the environment must be taken into consideration when studying the evolutionary dynamics of hosts and parasites.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy22-i013-R*

Symposium 22
Environment, G matrices and adaptation

Comparing environmental and genetic variance as adaptive response to fluctuating selection

Svardal H[1], Rüffler C[1], Hermisson J[1]
[1]University of Vienna, Faculty of Mathematics, Vienna, Austria

Summary statement:

Low heritability is favored if environmental fluctuations are similar to the Gaussian environmental variance, but high heritability is favored if the fluctuations are asymmetric.

Abstract:

Phenotypic variation within populations has two sources: genetic variation and environmental variation. Here we investigate the co-evolution of these two components under fluctuating selection. Our analysis is based on the lottery model for which it is known that genetic polymorphism can be maintained by negative frequency-dependent selection, while environmental variation can be favored due to bet-hedging. In our model phenotypes are characterized by a quantitative trait under stabilizing selection with the optimal phenotype fluctuating in time. Genotypes are characterized by loci determining an individuals phenotypic offspring distribution, which is assumed to be Gaussian with heritable variation for its mean and variance. Polymorphism in the mean corresponds to genetic variance while the width of the offspring distribution corresponds to environmental variance. We show that increased environmental variance is selectively favored whenever fluctuations in the selective optima are sufficiently strong. Given the environmental variance has evolved to its optimum, whether genetic polymorphism can still emerge depends on the skewness and kurtosis of the distribution of selective optima over time. A large mismatch between the Gaussian offspring distribution and the distribution of selective optima favors genetic polymorphism. All results are based on analytical approximations and complemented by individual based simulations.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy22-i014-R*

Symposium 22
Environment, G matrices and adaptation

Reduced genetic variance of gmax among high fitness individuals: evidence of mutation-selection balance for sexually selected traits

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Summary statement:

We provide evidence from an unmanipulated population of Drosophila serrata for mutation-selection balance of a male sexual display.

Abstract:

Directional selection is common in nature and often strong, but in the absence of environmental change it appears insufficient to cause sustained trait evolution.
Instead, phenotypes in nature tend to remain remarkably constant over various time scales, suggesting an evolutionary limit. Such a limit may arise as a consequence of widespread pleiotropy, which can cause the appearance of stabilizing selection on measured traits. In particular, at mutation-selection balance the pleiotropic effects of alleles underlying a specific measured trait can be summarized into a net deleterious effect on fitness. Because individuals with more extreme values of the trait tend to carry more mutations, this is predicted to generate apparent stabilizing selection on the trait and hence an asymmetry in genetic variance among high and low fitness genotypes. Using a half-sib breeding design in Drosophila serrata we tested the latter prediction, to provide insight into the evolutionary limit of a male sexual display consisting of a suite of contact pheromones (i.e. cuticular hydrocarbon or CHCs). Consistent with the signature of stabilizing selection, we found that the genetic basis of CHCs differed between high and low fitness males, with unfit males having significantly more additive genetic variance than high fitness males. Stabilizing selection was not detected in phenotypic analyses, indicating that it arose from the pleiotropic effects of the underlying alleles on other traits. Our results suggest that male sexual displays in this unmanipulated population are at mutation-selection balance, providing a potential explanation for their lack of response to directional sexual selection in this population.

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SUN 21 AUG at 1710 - Room N9
Oral presentation *A4-Sy22-1710-O*

Symposium 22
Environment, G matrices and adaptation

What is the role of phylogeny and ecology in shaping G matrices? Insights from wild bird populations

Teplitsky C[1], Tarka M[2], Charmantier A[3], Nakagawa S[4], Becker PH[5], de Lope F[6], Gustafson L[7], Mills JA[8], Møller AP[9], Schroeder J[1]0
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Summary statement:

Coupling interspecific and interpopulation comparisons, we investigate differentiation of G matrices for morphology and life history traits and how much G may constrain adaptation.

Abstract:

G matrices are a crucial element in understanding evolutionary trajectories, as correlations between traits may act to constrain or facilitate responses to selection. Some theoretical work was undertaken to understand the stability of G matrices, but there is still unconclusive evidence as to whether these matrices are stable or not in wild populations. Here, to disentangle the effects of ecology and phylogeny, we investigate how G matrices differ between species and among populations of the same species for a set of four morphological traits (beak length, tarsus length, wing length and weight) and two life history traits (laying date and clutch size) in several bird species for which long term data and pedigree were available. In order to include confidence intervals, we use a Bayesian approach to run animal models needed to estimate G matrices. We compare results for morphological and life history traits, highlighting to which extent genetic correlations may constrain responses to selection in these populations. First results on migration syndromes in two barn swallow populations already show stronger differentiation between G matrices for life history traits than for morphological traits. Furthermore, genetic correlations between life history traits halved the expected rate of adaptation in one of the two populations. These differences are probably to be linked to the between populations differences in migration distances and timing.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy22-i006-E*

Symposium 22
Environment, G matrices and adaptation

Climatic niche divergence or conservatism? Environmental niches and northern range limits in ecologically similar damselflies

Wellenreuther M[1], Larson KW[1], Svensson EI[1]
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Summary statement:

Although C. virgo and C. splendens are strongly sexually isolated from each other, that they show only modest niche differentiation in general, and almost none in sympatry.

Abstract:

The ecological factors that determine species' range limits are of central interest to evolutionary biologists. One particularly interesting group are odonates (dragonflies and damselflies), which show large differences in secondary sexual traits and respond quickly to changes in climatic factors, but which are also thought to show minor interspecific ecological niche differences, thus challenging models of species co-existence that are based on niche divergence. Here, we quantify environmental niches at two different scales and investigate the factors that influence range limits and local co-existence of the two congeneric damselflies Calopteryx splendens and C. virgo. Using environmental niche modelling, we quantified the amount of niche divergence (i) across the whole geographic range in Fennoscandia and (ii) in the area of sympatry. We found evidence for interspecific divergence along the axes of temperature and precipitation across Fennoscandia, but negligible niche differences in zone of sympatry, suggesting that adaptation to colder and wetter climate might have allowed C. virgo to expand further north than C. splendens. The shared niche preferences in sympatry result in strong interspecific sexual interactions, thereby likely affecting sexual divergence and mate preferences at the local level. Niche differences across Fennoscandia vs. the sympatric Fennoscandian zone point towards species differences in physiological tolerances.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy22-i015-R*

Symposium 22
Environment, G matrices and adaptation

Predicting evolutionary response to rapid environmental change: genetic variation of a natural amphibian population under stress

Winkler JD[1], Van Buskirk J[1]
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Summary statement:

Stressful conditions influence genetic variation in tadpole behavior, morphology and life history traits. This may be important for adaptation under future environmental change.

Abstract:

Genetic variation and heritability are condition-dependent. Estimates of genetic variation under diverse environments are important for understanding the evolutionary impacts of rapid environmental change. Our study was designed to determine whether stressful or novel environments typically lead to increased or decreased genetic variance. We raised Rana temporaria tadpoles originating from artificial crosses under five ecologically-relevant treatments varying in stress. There were large changes in the genetic variation of many traits and in genetic covariances among traits. The results generate predictions about univariate and multivariate responses to selection, and indicate that certain types of environmental variation may have consistent effects on heritability.

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Symposium 23

Climate change and evolution

Talks: *Room N2*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Ground floor campus canteen *Mensa*

Invited Speakers:

Juha Merilä, Ary Hoffmann

Organizers:

Klaus Fischer, Stephanie S Bauerfeind, Wolf U Blanckenhorn

Description:

Evolutionary change (rather than short-term responses as plasticity and movement) has been assumed to be too slow to keep pace with the rapidly changing environment. This symposium will bring together new insights in understanding evolutionary responses to global environmental changes, and outline chances for as well as limits to such evolutionary change and the implied system-wide consequences.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

Ground floor lecture hall centre *HZ*
Essence poster *E-Sy23-i001-E*

Symposium 23
Climate change and evolution

Evolutionary potential of the reintroduced large blue butterfly in the U.K.

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Summary statement:

Conservation genetics of reintroduced populations of Large Blue butterflies in the U.K. and their source in Sweden will test the ability of a bottlenecked species to quickly adapt.

Abstract:

The Large Blue butterfly Maculinea arion is an obligate social parasite of the ant Myrmica sabuleti. Populations of the butterfly are highly fragmented, as it can only exist where the distributions of its host ants and its initial host plants overlap. The species went extinct in the UK in 1979 and was subsequently reintroduced in 1983,using source individuals from Öland, Sweden. The source populations on Öland have a somewhat different phenology, and experience different climatic conditions than the extinct U.K. populations. Recent surveys, however, indicate that there have been shifts in host plant use and flight times of reintroduced U.K. populations of the Large Blue, as well as changes in dispersal ability, allowing natural recolonization of suitable habitat.
The aims of this study are: 1) To characterize the population genetic structure of the poorly studied M. arion population on Öland, 2)To reconstruct the levels of genetic diversity in this population over the last 28 years, 3) To examine the levels of genetic diversity in the introduced populations in the U.K., and, 4) To examine the relationship between genetic diversity and the observed changes in life-history traits in some U.K. populations. The study will allow us to test the effect of known bottleneck events on the long-term diversity of the Large Blue butterfly, and how they may affect its ability to adapt to different conditions and food plants.Our results will be valuable not only for future reintroductions of this threatened species, but also for assessing the potential of the Large Blue butterfly to adapt to climate change.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy23-i001-R*

Symposium 23
Climate change and evolution

Impact of larval exposure to an antiparasitic drug (Ivermectin) on thermal stress resistance in geographic populations of Yellow Dung Flies (Diptera: Scathophagidae)

Bauerfeind SS[1], Berger D[2], Broder ED[3], Blanckenhorn WU[2]

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Summary statement:

Thermotolerance in the yellow dung fly depends on geographic origin and is affected by the exposure of the dung-feeding larvae to the veterinary drug Ivermectin.

Abstract:

Global warming can result in a local increase in the frequency and magnitude of thermal extremes, and thus exposes ectotherms to temperature conditions exceeding their tolerance limits beyond which survival declines rapidly. Plastic responses in thermotolerance and subsequent genetic accommodation depend on the population genetic background and may be affected by interfering environmental factors. The larvae of the yellow dung fly (Scathophaga stercoraria) feed and develop in cow dung and may be exposed to veterinary drugs that are excreted unmetabolised by treated livestock, which have been shown to affect performance of non-target invertebrates in the dung. Exposure to Ivermectin (a common anthelmintic drug) may affect stress resistance via a reduction in overall condition or via its effect on the expression on heat shock proteins hsp, which are intimately connected to thermotolerance. We here link geographic variation in thermal tolerance to the effects of Ivermectin employing a common garden design including six populations sampled over a wide latitudinal range in Europe. Heat tolerance significantly differs locally, though not in accordance to geographic regions, and is enhanced by exposure to Ivermectin; cold tolerance is slightly lower in southern populations as compared to northern populations, and both regions respond differently to exposure to Ivermectin. Thus, our results demonstrate (1) asymmetric geographic patterns in heat and cold tolerance of yellow dung flies, (2) plastic responses in thermal tolerance facing exposure to Ivermectin, which (3) depend on the geographic origin.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy23-i002-R*

Symposium 23
Climate change and evolution

Asymmetric thermal performance curves and response to selection

Berger D[1], Walters RJ[1], Blanckenhorn WU[1]
[1]University of Zurich, Institute for Evolutionary Biology and Environmental Studies, Zurich, Switzerland

Summary statement:

We estimate assymetry in thermal reaction norms and G matrixes for physiological traits and relate them to geographic differentiation and laboratory evolution responses.

Abstract:

Evolutionary responses to climate change may be limited if strong selection in the past has eroded genetic variance for physiological traits. Thermal performance curves are typically asymmetric in shape, a pattern that has been attributed to underlying metabolic properties of temperature sensitive enzymes. In particular, physiological performance tends to display a steep decline at temperatures above the thermal optimum. In theory this could potentially limit the amount of genetic variance available to selection under climate warming. In contrast, models based upon biophysical principles predict that pleiotropy could be instrumental in maintaining genetic variance at high temperatures. We here used the dung fly Sepsis punctum to evaluate a model incorporating assumptions on metabolic constraints and enzyme kinetics developed to predict the amount of genetic variance in thermal reaction norms for ectotherm growth and development . We further test whether the amount of temperature-specific genetic variance differs among geographical regions. Finally we relate G matrix estimates to trait responses under laboratory evolution in four thermal regimes varying in mean temperature and the mode of temporal variation.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy23-i003-R*

Symposium 23
Climate change and evolution

Long distance dispersal as a mechanism to maintain genetic diversity during range expansion

Bialozyt RB[1]
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Summary statement:

This work highlights the special importance of colonisation and gene flow events during past migrations, thereby improving the genetic basis for adaptation at the range edge.

Abstract:

Currently many attempts are made to reconstruct the colonization of plant and animal species in Europe and in other temperate regions after the last ice age. A surprising finding is that genetic diversity did not decreased as much as expected during colonization. In a former study we examined the role of long distance seed dispersal (LDD) events in the unexpected maintenance of genetic diversity during range expansion. The simulations revealed a non-linear relationship between the frequency of LDD events and the amount of genetic diversity preserved during range expansion. Using very low amounts of LDD events may result in a complete loss of genetic diversity. However, increasing the rates of LDD events results in a mosaic of variants to persist across the landscape and thus maintaining diversity at a regional scale.

In another study, we separated these LDD events into two categories. There are LDD events that correspond to the colonisation of new habitats (pure colonisation – PC) and others that land in a already occupied patch (pure gene flow – PGF). We performed simulations using both types of LDD events, either separately or together. We measured diversity parameters: allelic richness (AR), genetic diversity (HT) and genetic differentiation (GST). Whereas diversity in the complete system is mainly driven by PC events, allelic richness follows the same dynamics as PGF events, except in the case of the embolism effect described in the previous paper. The simulation show that a low frequency of PC events is sufficient to affect diversity parameters, whereas a fair amount of PGF events is necessary to observe a significant response.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy23-i002-E*

Symposium 23
Climate change and evolution

What do allele frequencies tell us about the past?

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Summary statement:

We are interested in the influence of range expansions on the genetic composition of populations.

Abstract:

Many species have undergone range expansions in their evolutionary history. A prominent example is the colonization of previously uninhabitable regions after a climate change. Research has revealed that neutral mutations occurring at the front of such expanding populations can reach frequencies higher than expected in populations with a stable demography. This effect is now known as gene surfing.
Gene surfing also affects standing variation --- i.e. different variants of a gene already present in the population. We show using computer simulations that gene surfing has a stronger influence on standing variation than on mutations that occur during a range expansion. Therefore we study how range expansions act on already existing variation, and quantify the influence of migration processes on the frequency of neutral and disadvantageous mutations. Our results will help to interpret spatial distributions of genetic variants in extant populations and to uncover past migration events.

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TUE 23 AUG at 1500 - Room N2
Oral presentation *C3-Sy23-1500-O*

Symposium 23
Climate change and evolution

Adaptive chromosomal inversions differ in their basal expression of HSP70

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Summary statement:

Significant differences in HSP70 basal expression between warm and cold adapted inversions in D. subobscura might be related to latitudinal inversion frequency clines.

Abstract:

Chromosomal inversion polymorphism has been identified in different organisms as drivers of environmental adaptation and speciation. Studies in several Drosophila species have determined their adaptive role although the bases of this adaptation remain elusive. In Drosophila subobscura latitudinal clines in the frequency of different gene arrangements have been detected and proved to be related to increasing global warming. Genes encoding heat shock proteins are obvious candidates for thermal adaptation. These genes encode for molecular chaperones, some of which are expressed during a stress response and help to maintain the natural conformation of proteins inside the cells. Here we present data on HSP70 expression levels, a protein encoded by a gene located in a rich inversion region in D. subobscura. We studied the levels of expression in individuals carrying warm and cold adapted chromosomal arrangements in order to determine if there is an association between particular gene arrangements and HSP70 expression levels. The assays have been performed on homozygous (inbred and outbred) and heterozygous individuals. Our results show that there is no difference in induced levels of HSP70 (i.e. after a heat shock). However, the different arrangements differ statistically in their basal levels of HSP70, with O3+4 (typically considered as warm adapted) showing higher levels of expression. These higher levels of protein expression might be beneficial for flies carrying the O3+4 arrangement in warmer settings, which could overcome the cost associated with the expression of hsp70 and help to explain the latitudinal frequency clines of some chromosomal arrangements.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy23-i004-R*

Symposium 23
Climate change and evolution

The effect of diurnal temperature fluctuations on Aedes aegypti biology and dengue transmission dynamics

Carrington LB[1], Lambrechts L[2], Scott TW[1]
[1]University of California Davis, Entomology, Davis, California, United States, [2]Institut Pasteur, Virology, Paris, France

Summary statement:

The longevity and life history traits of Aedes aegypti, as well as their vector competence for transmitting the dengue virus, are influenced by diurnal temperature fluctuations.

Abstract:

There are few vector competence studies that have considered the effect of real-world daily temperature fluctuations on the transmission of vector-borne diseases. Most studies focus on constant temperatures, yet the vectors are rarely ever exposed to such conditions in nature. High and low dengue transmission seasons in Thailand associate with small and large daily fluctuations respectively, even though the average temperature during both seasons is the same (≈26°C).
Here we investigate the effect of diurnal temperature fluctuations on dengue infection and transmission, and life history traits, in the primary dengue vector Aedes aegypti. We use environmentally relevant temperature profiles, with diurnal temperature ranges of 10°C and 20°C around a common mean of 26-°C, relative to a control temperature regime, of constant 26°C. We test the hypothesis that the magnitude of diurnal temperature fluctuations may be the cause of seasonal changes in dengue transmission dynamics in Thailand. Our experiments show that aspects of vector competence, longevity and numerous mosquito life history traits negatively associate with the magnitude of diurnal temperature ranges.
This awareness of how realistic temperature fluctuations influence the vector biology of Ae. aegypti and vector-virus interactions allow us to understand how dengue transmission dynamics might be affected by large magnitude temperature fluctuations, the potential for the vector and virus to adapt to climatic changes, and subsequently to better strategize vector control in the future.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy23-i005-R*

Symposium 23
Climate change and evolution

Adaptive potential of Atlantic salmon populations to hypoxia during embryo development

Côte J[1], Roussel J-M[1], Evanno G[1]
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Summary statement:

We studied the resistance to hypoxia of embryos from four populations of Atlantic salmon (Salmo salar) by a common garden approach involving within and among population crosses.

Abstract:

Studying the adaptive potential of organisms to global changes is a major issue in conservation biology. Aquatic ecosystems have been strongly impacted by disturbances induced by human activities. Atlantic salmon (Salmo salar) is an ectothermic organism whose embryonic development depends on environmental conditions. A frequent cause of population decline is a degradation of the freshwater salmon habitat. Hypoxia rates often reach lethal levels during embryonic development hence hypoxia is a strong selective agent in salmon populations. We studied the resistance to hypoxia of embryos collected in four populations with constrated environments using a common garden experiment. Factorial mating designs were made within and among populations to separate genetic, maternal, and environmental effects. Over 7000 embryos were reared under normoxic or hypoxic conditions and we measured the following life history traits: survival, size and embryo development rates. In normoxic conditions, size and embryo development rates differed among populations. In hypoxic conditions, survival was slightly lower, embryos were smaller and hatched later than under normoxic conditions. Significant populations x treatment interactions were detected for size and embryo development rates. Embryos from among populations crosses developed faster and were larger than those from within population crosses suggesting the occurrence of hybrid vigour. Overall these results demonstrate that salmon populations can differ in their adaptation to hypoxia. This suggests variations in adaptive potential to global changes which are further corroborated by differences in heritability estimates among populations.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy23-i006-R*

Symposium 23
Climate change and evolution

Climate-driven evolution? The success of alternative sexuality and unfaithfulness in arctic-alpine plants

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[1]UNIS-The University Centre in Svalbard, Arctic Biology Department, Longyearbyen, Norway, [2]NCB - National Centre for Biosystematics, Natural History Museum, University of Oslo, Oslo, Norway

Summary statement:

Polyploidisations, some sexual reproduction, and hybridization events generate genetic diversity and evolutionary potential within mainly asexual arctic-alpine plant species

Abstract:

Arctic-alpine areas provide unfavorable conditions for sexual reproduction in plants: Few pollinators, low nutrient levels, long winters and short growing seasons makes sexual reproduction challenging. Due to these conditions, asexual reproduction, or vegetative persistence, has been recognized as the dominant method of reproduction in arctic-alpine areas. However, asexuality, in the long run, is regarded as an evolutionary dead end. How can some of the most successful arctic-alpine species be mainly asexual – and still be extremely genetically diverse, widespread and persistent through extreme climatic oscillations, like the Pleistocene glaciations? Alternative sexuality and unfaithfulness, combined with efficient dispersal, seem to be the recipe for success. Through studies of several arctic-alpine plant species and species complexes, we have found several examples of overwhelmingly complex evolutionary paths based on recurrent polyploidisations, (occasionally) sexual reproduction, and hybridization events. These events have been driven by range shifts and changing climatic conditions through recurrent glaciation events. Today, global warming is on of the major challenges for arctic-alpine plants. The ability to achieve genetic diversity in various ways, and thus evolutionary potential, might be the answer. We present results based on studies of Saxifraga cernua, Bistorta vivipara, Vaccinium uliginosum, Betula nana and B. pubescens, using AFLPs (amplified fragment polymorphisms), microsatellites, DNA sequencing of nuclear and chloroplast regions, and DNA content estimations.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy23-i003-E*

Symposium 23
Climate change and evolution

Migration history and dispersal potential of Puccinellia phryganodes

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Summary statement:

AFLP analysis of the circumpolar, clonal, salt mash-grass Puccinellia phryganodes, facing different climatic systems and human influence, identified several genetic lineages.

Abstract:

The circumpolar, clonal grass Puccinellia phryganodes is a key species in arctic salt marshes, and a favorable food source of geese. Puccinellia phryganodes lives towards the tidal zone and are able to survive among the driftwood brought onshore by storms and high tides. It is suggested that it disperses its vegetative clones by ocean currents.
Spitsbergen is the largest island of Svalbard, situated between the Arctic Ocean, Barents Sea, Greenland Sea and Norwegian Sea. The west coast of Spitsbergen is influenced of the warm West Spitsbergen Current while the east coast in influenced by the cold Arctic Current. The aim for the study is to investigate whether these two current systems, representing different climatic conditions, have a different impact on the migration and establishment pattern, and thus the genetic structure, of P. phryganodes. We will also evaluate the migration pattern in relation to the human impact and geese migration route.
We have sampled and analyzed 28 populations along the west and east coast of Spitsbergen using APLPs (Amplified Fragment Length Polymorphisms), and in reference areas in Russia, Canada and Scandinavia. Our Preliminary results based on 96 individuals from 12 populations identify several genetic groups with more genetic groups co-occurring in areas with human influence.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy23-i005-E*

Symposium 23
Climate change and evolution

The genomics underpinning adaptive responses to global warming in Daphnia magna

Geerts A[1], Orsini L[1], De Meester L[1]
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Summary statement:

Using paleogenomics and resurrection ecology, we reconstruct micro-evolutionary responses to global warming and link those responses to candidate genes.

Abstract:

During the past decades global warming has significantly impacted species diversity and the structure and functioning of ecosystems. This emphasizes the importance of insights into eco-evolutionary dynamics to understand biological responses to climate change. Water fleas (Daphnia) are exceptional model organisms because of their ecological importance, their amenability to evolutionary ecological research, and the presence of layered egg banks that provides an archive of past evolutionary changes. We will reconstruct micro-evolutionary responses to increased temperature due to global warming and link these responses to candidate genes.
We will sample layered dormant eggs to contrast populations from the coldest (1955-1965) and the warmest (2000-present) decades of the last century. Populations will be hatched (resurrection ecology) from sediment cores from six different lakes intensively studied from a paleolimnological perspective, providing us with strong background information on ecological conditions. The sediment cores originate from lakes with varying specific histories; this will allow us to detect a recurrent climate change signal and to distinguish it from other temporally variable selection pressures. Contrasting populations from the two time periods in common garden experiments, we will quantify micro-evolutionary responses in ecologically relevant traits (e.g. thermal tolerance) and the relative performance (fitness) of genotypes isolated from the warm and the cold era. Finally, we will apply a functional paleogenomic approach, linking candidate genes to traits under selection with a promise to reconstruct evolutionary dynamics over several hundreds of years.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy23-i007-R*

Symposium 23
Climate change and evolution

Adaptive response of parasitoid insect populations to climate change

Gibert P[1], Delava E[1], Fleury F[1], Allemand R[1]
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Summary statement:

We investigate the consequences of the recent invasion of a Mediterranean species on the Drosophila larval parasitoids community, probably related to increasing temperature

Abstract:

Faced with the ongoing climate change, ectothem species will exhibit two kinds of not mutually exclusive responses: either changing their geographical range or maintaining their repartition range by genetic adaptations or phenotypic plasticity. Studies on the indirect effects of global warming taking into account several species of the community as well as the genetic response of the populations and the associated modification of the interactions, are scarce because few model systems allow this kind of global approach. In this purpose, some insect communities in which phytophagous species are regulated by several parasitoid species are good models because the specific nature of relationships makes it possible to identify a small number of interacting species, which all have to face direct and indirect effects of temperature. We are interested on the community of frugivorous Drosophila larval parasitoids in South-East of France, transition area between Mediterranean and continental climate. In this region, those communities experience the recent invasion (within 10 years) of a species of Mediterranean parasitoid (Hymenoptera) probably related to increasing temperature. This progression that mimics a situation of invasion gave the opportunity to study not only the adaptability of this species to a new environment, but also the consequences of its arrival on the composition of local populations and communities and the interspecific co-adaptations. We analyzed this complex situation by investigating both populations differentiation (LHT, molecular markers) and phenotypic plasticity in order to determine how temperature increase will act at the level of the whole community.

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MON 22 AUG at 1650 - Room N2
Oral presentation *B4-Sy23-1650-O*

Symposium 23
Climate change and evolution

How sexual selection shapes adaptation during rapid temperature change in small insect populations

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Summary statement:

Using experimental evolution with increasing and fluctuating temperatures we assess the role of sexual selection in adaptation to climate change in flour beetles.

Abstract:

Natural populations face rapid environmental change, such as warmer temperatures and longer heat periods. Can small populations with low genetic diversity adapt during rapid warming? Are there factors, which aid the adaptation process or lead to higher extinction risk? We have evidence that red flour beetles benefit from sexual selection (SS) if temperature increases. There is a survival cost of reproduction at standard 30°C, but not at elevated temperature. In addition, although total reproductive success is similar at standard temperature, at elevated temperature there is a significant benefit of polyandry (SS present) compared to monogamy (SS absent). To follow up on these findings, we used experimental evolution to assess adaptation to temperature change. We subjected established selection lines with or without SS to three temperature regimes: constant 30°C, gradually increasing and fluctuating temperature. In every regime there were populations with polyandry and populations with enforced monogamy. After 6 generations we performed two common garden experiments at 30°C and 35°C. There we assessed female fitness via mating rates, fecundity, hatching rate, reproductive success and survival. We document responses to selection under different temperature regimes and according to the presence or absence of SS. Interestingly the two common gardens highlighted responses in distinct traits. In general, the expectation that SS plays a role in adaptation to rapid change was met. This study further underlines the importance of phenotypic adaptation, such as via adaptive plasticity, in the face of climate change.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy23-i008-R*

Symposium 23
Climate change and evolution

Pollinators impose different selection pressure on floral scent and size at different altitudes

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Summary statement:

Pollinator-mediated selection varies at different altitudes, indicating that global warming may change selection on floral traits.

Abstract:

Pollinators prefer specific floral traits and select for these. Therefore, they play an important role in the evolution of floral variation in plants. Pollinator guilds may differ regionally and thus may select for different floral traits. Climate change, especially an increase in ambient temperature, may affect pollinator communities, which impacts on selection on floral traits. We quantified phenotypic selection on floral scent as well as plant, inflorescence, and flower size in the rewarding orchid Gymnadenia odoratissima in Swiss lowland and mountain populations. As an estimate of fitness, we determined relative fruit set. There was positive directional selection both on some floral scent compounds (especially physiologically active compounds) and on plant, inflorescence, and flower size. However, there was negative directional selection on some other floral scent compounds and some flower size measurements, probably due to antagonistic impacts on pollinators. Selection pressure differed in strength and direction among populations, especially in mountain populations. Moreover, the strength and direction of selection pressure differed between lowland and mountain populations. Thus, our results suggest that pollinator-mediated selection varies at different altitudes. Such investigations of plant-pollinator interactions at different altitudinal and thus temperature levels may allow predicting selection changes in the view of global warming.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy23-i009-R*

Symposium 23
Climate change and evolution

Rapid microevolution in response to climate change?

Haenel S[1], Tielboerger K[1]
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Summary statement:

In this study we assess the phenological, morphological and reproduction related traits of annual plants in response to climate change.

Abstract:

Climate change, expressed as increasing temperatures, decreasing annual precipitation and larger variability in rain events will strongly impact plant communities in the Mediterranean basin. In situ adaptation may be the only way for plants to persist under environmental change. We study possible rapid selection after 9 years of rain manipulation in Mediterranean and semi-arid field sites in Israel. We look at phenotypic and genetic shifts in key adaptive traits for dominant annual plant species exhibiting different life history strategies. Differences in traits among rainfall manipulations detected in the field are tested in a two-generation-experiment to distinguish between plastic response and genetically fixed adaptation. Our initial results suggest differences in traits that are indicative for an adaptive response for some species and selected traits, but no response for other species, indicating the importance of a community-wide approach to studying selection under climate change.

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MON 22 AUG at 1610 - Room N2
Oral presentation *B4-Sy23-1610-O*

Symposium 23
Climate change and evolution

Selection in a fluctuating environment leads to decreased genetic variation and facilitates the evolution of phenotypic plasticity

Hallsson LR[1], Björklund M[1]
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Summary statement:

Fluctuations in a changing environment have major impact on a population's potential to respond to selection, environmental sensitivity and the evolution of phenotypic plasticity.

Abstract:

The global environment is changing, characterized, for instance, by an increase in temperature, and the resulting environmental conditions are novel, often suboptimal or even stressful. These changes in the environment are expected to create changes in the quantitative genetic variation, which influences the ability of a population for adaptive evolutionary change. Furthermore the environment is not constant in time, but is fluctuating. Here we investigate the effect of rapid, continuous and/or fluctuating temperature changes on mass at emergence, developmental time, fecundity and hatching success in the seed beetle Callosobruchus maculatus. An evolution experiment over 18 generations followed by a split brood experiment allowed for estimates of phenotypic, genetic, environmental and plastic responses to a change in temperature environment. We found individuals to respond in a plastic way and an overall higher potential to respond to selection after a rapid change in the environment. However, after selection in an environment with increasing temperature, especially when fluctuations are added, we found significant changes in a set of quantitative genetic parameters (genetic and environmental variance, gene by environment interactions and genetic correlations). Changes indicate that the exact pattern of the selective past matters for a population's response to environmental change and most importantly, that fluctuations in the environment have a major impact on the potential to respond to selection, environmental sensitivity and the evolution of phenotypic plasticity.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy23-i010-R*

Symposium 23
Climate change and evolution

Adaptive divergence in response to direct and indirect effects of acidification in the moor frog (Rana arvalis)

Hangartner S[1], Egea-Serrano A[2], Laurila A[3], Räsänen K[1]
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Summary statement:

We found evidence for adaptive divergence in response to direct (acid stress) and indirect (prevailing predation regime) effects of acidification in the moor frog (Rana arvalis).

Abstract:

The ongoing environmental changes expose contemporary populations increasingly to a range of environmental stressors. These changes, such as acidification, can cause strong selection both through the direct effects of a stressor (e.g. low pH) and through correlated abiotic and biotic environmental changes (e.g. altered predator communities). We studied adaptive divergence to acidification in eight moor frog (Rana arvalis) populations differing in breeding pond pH (pH 4.0 to 7.5). We used common garden laboratory experiments to study divergence in response to pH per se (exp I) and interactions between pH and predators (exp II). In exp I, embryos and tadpoles were reared at two contrasting pH's (pH 4.0 or 4.3 and 7.5) and measured for embryonic survival and larval life-history traits. In exp II, tadpoles were reared at two pH´s (4.5 and 7.5) and two predation (presence and absence of a caged dragonfly larva) treatments and measured for inducible defenses and larval life-history traits. Subsequently, the relative fitness (survival) of tadpoles from different predator treatments and populations were tested under direct predation. We found that acid and neutral origin populations have diverged in embryonic acid tolerance, larval life-history traits and in inducible defenses, and that acid origin tadpoles have higher survival under predation than tadpoles from neutral populations. Our results suggest that acid (and predator-rich) origin R. arvalis populations are adapted to both acid stress and the prevailing predation regime, emphasizing the need to study responses to interacting direct and indirect effects of environmental stressors.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy23-i011-R*

Symposium 23
Climate change and evolution

Modeling the evolution of diapause timing

Hazel WN[1], Smock R[2]
[1]DePauw University, Biology, Greencastle, United States, [2]DePauw University, Mathematics, Greencastle, United States

Summary statement:

We present a general model that treats the timing of diapause as an environmentally cued threshold trait and ask how the timing will evolve in response to climate change.

Abstract:

The timing of diapause induction has been implicated as a major target of natural selection in response to climate. We present a general model that treats the timing of diapause as an environmentally cued threshold trait. We use the model to predict how the timing of diapause is likely to evolve under different climate change scenarios and under different assumptions about how climate change will impact other life history traits. The model suggests that not only will selection be fluctuating in the short term, but in some circumstances even more so in the long term, depending on how changes other life history traits affect fitness.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy23-i012-R*

Symposium 23
Climate change and evolution

The adaptation of Daphnia galeata to climate change

Henning N[1], Cordellier M[1], Streit B[2], Schwenk K[3]
[1]Biodiversity and Climate Research Centre, Frankfurt am Main, Germany, [2]Goethe University, Department of Ecology and Evolution, Frankfurt am Main, Germany, [3]University Koblenz-Landau, Institute for Environmental Sciences, Frankfurt am Main, Germany

Summary statement:

We studied potential adaptations in life history traits of Daphnia galeata to local environmental changes (temperature), with respect to the impact of latitude (origin of clones).

Abstract:

To estimate the impact of current and future climate changes on ecosystems it is essential to understand the adaptation potential of species. In our experiments we compare life history traits of Daphnia galeata clones from different time periods to measure the differential response to variation in temperature. We exposed D. galeata individuals (hatched from resting eggs of different sediment layers) to various temperature regimes in a common-garden experiment (flow-through-system). Sediment samples were taken from lakes along a latitudinal gradient across Europe to compare locally adapted populations ranging from Italy to Sweden. Elevated water temperatures were shown to result in a reduced number of offspring, a lower survival rate, an increased somatic growth rate and according to that an earlier age at maturity. We discuss potential adaptations in life history traits to local environmental changes (temperature) within the last 50 years and with respect to the impact of latitude (origin of clones).

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TUE 23 AUG at 1400 - Room N2
Invited talk *C3-Sy23-1400-I*

Symposium 23
Climate change and evolution

Assessing the likelihood of evolutionary adaptation under climate change

Hoffmann A[1]
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Summary statement:

Evolutionary considerations tend to have been ignored in discussions on management strategies for the conservation of biodiversity; is this justified?

Abstract:

There are now a few cases where evolutionary adaptation under recent climate change has been demonstrated, however it is not at all clear how often species are likely to be able to adapt. This issue is particularly important when assessing the vulnerability of threatened taxa as well as species living in threatened habitats like the tropics and high elevation sites. I provide a brief overview of models and data that have been used to assess evolutionary potential and then focus on some of our recent work on Drosophila in suggesting a way forward for assessing vulnerability. Finally some of the ways that evolutionary considerations can be incorporated into biodiversity management strategies are discussed.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy23-i006-E*

Symposium 23
Climate change and evolution

Life history evolution in a changing world: the impact of environmental variance on optimal plasticity in a fecundity – somatic maintenance trade-off

Hoffmeister TS[1], Coquillard P[2], Vet LEM[3], Wajnberg E[2]
[1]University of Bremen, Population Ecology & Evolutionary Ecology Group, Bremen, Germany,
[2]I.N.R.A., Sophia Antipolis, France, [3]Netherlands Institute of Ecology, Wageningen, Netherlands

Summary statement:

Using evolutionary algorithms we analysed optimal trade-offs, and their optimal plasticity, for insects facing increased variance in resource availability due to global change.

Abstract:

One of the most important effects of global change may be the increased variance in environmental conditions organisms are exposed to within and across generations. For instance, imagine a large continuous environment with more or less constant resource availability contrasted with habitat islands in which, due to environmental fluctuations, resources might be present at one time and sparse or absent at other times. The latter may allow animals to forage locally in one generation but forces them to disperse to other such habitat islands in other generations. In such a situation, many insects that forage for oviposition resources like butterflies searching for host plants and parasitoid wasps hunting for host insects face the dilemma that they need to trade-off fecundity against the lifetime they can invest into foraging for oviposition sites. With decreasing predictability of resource availabilities, foragers might be forced to allocate increasingly into somatic maintenance rather than fecundity. Using evolutionary algorithms we analysed optimal trade-offs for insects facing different environments, and the optimal plasticity – the capability of adjusting the fecundity-survival trade-off within a lifetime – when such plasticity is costly.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy23-i007-E*

Symposium 23
Climate change and evolution

High degree of genetic differentiation of northern Swedish Arabidopsis thaliana

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[1]Vetmeduni Vienna, Institut für Populationsgenetik, Vienna, Austria, [2]Gregor Mendel Institute of Molecular Plant Biology GmbH, Vienna, Austria, [3]Max F. Perutz Laboratories, Vienna, Austria

Summary statement:

A northern Swedish population of A. thaliana shows low diversity and is highly differentiated compared to a diverse panel of Eurasian populations.

Abstract:

The weed Arabidopsis thaliana is endemic to all of Eurasia and North Africa. After the last glaciation 10,000 years ago it also colonized the most northern parts of Europe and it is not entirely clear yet, from where those plants came. To address this question we analyzed 120 Arabidopsis thaliana accessions from Sweden and compared them with an European/Asian sample of 80 accessions. Amongst the Swedish plants 81 are from the south, 10 from the middle and 29 from the north. All accessions are part of the 1001 genomes project and we are grateful to having access to whole genome sequence data.

On the one hand the southern Swedish plants have a high diversity and are closely related to other western and middle European plants. On the other hand, the northern Swedish plants are much less diverse and also genetically more diverged. Generally, geographic and genetic distance correlate well in these data, confirming that most of the population structure in Arabidopsis thaliana can be explained through isolation by distance. However, the data suggest tentatively that such a model fits the northern Swedish plants less well. It remains to speculate whether this can be seen as evidence for two colonization events of Scandinavia: One from the south, via Denmark, and one from the north via Russia and Finland.

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MON 22 AUG at 1440 - Room N2
Oral presentation *B3-Sy23-1440-O*

Symposium 23
Climate change and evolution

Speeding up microevolution: The effects of increasing temperature on selection and genetic variance in a wild bird population

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Summary statement:

We show that expression of genetic variance and strength of selection is temperature dependent causing positive covariance between them that may speed-up evolutionary adaptation.

Abstract:

The amount of genetic variance underlying a phenotypic trait and the strength of selection acting on that trait are two key parameters that determine any evolutionary response to selection. Despite substantial evidence that, in natural populations, both parameters may vary across environmental conditions, very little is known about the extent to which they may covary in response to environmental heterogeneity. Here we show that, in a wild population of great tits (Parus major), the strength of the directional selection gradients on timing of breeding increased with increasing spring temperatures, and that genotype-by-environment interactions also predicted an increase in additive genetic variance, and heritability, of timing of breeding with increasing spring temperature. Consequently, we therefore tested for an association between the annual selection gradients and levels of additive genetic variance expressed each year; this association was positive, but non-significant. However, there was a significant positive association between the annual selection differentials and the corresponding heritability. Such associations could potentially speed up the rate of micro-evolution and offer a largely ignored mechanism by which natural populations may adapt to environmental changes.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy23-i008-E*

Symposium 23
Climate change and evolution

Evolutionary history of an endemic alpine plant, Cardamine nipponica (Brassicaceae), at the range periphery of arctic-alpine sister species, Cardamine bellidifolia

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Summary statement:

Using multilocus sequences, our study elucidated phylogenetic as well as speciation history of Cardamine nipponica, an alpine plant endemic to Japan.

Abstract:

Endemic alpine plants in high mountains at lower latitude, such as Japanese archipelago, may have originated from arctic-alpine plants. To address this hypothesis, the phylogenetic history of the Japanese alpine endemic species, Cardamine nipponica (Brassicaceae) was elucidated using equence variation in 10 nuclear genes. A species-tree estimated by Bayesian procedure (BEST) showed a sister relationship between C. nipponica and C. bellidifolia, a species distributed in arctic-alpine regions. This suggests that endemic alpine plant to Japan, C. nipponica, would have evolved from species with widespread distribution, C. bellidifolia. In addition, Bayesian clustering implemented by STRUCTURE showed the distinct genetic structures between the two sister species. However, model parameters estimated under isolation with migration (IM) model showed that introgression occurred from C. nipponica to C. bellidifoliolia. Considering the current allopatric distribution of each species, introgression may have occurred following range expansion during the last glacial period. Thus, Pleistocene climatic oscillations would be involved in the speciation history of between the endemic and widespread species.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy23-i013-R*

Symposium 23
Climate change and evolution

Effects of seasonally varying environments and timing-dependent competition on ESS phenologies

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Summary statement:

We explain how phenological responses are modified by timing-dependent competition and how they, depending on baseline environment, may differ from shifts in environmental optima.

Abstract:

We present a game-theoretic model for studying phenological responses to environmental changes. We study a scenario with birds competing for territories during spring, but the model can represent many other situations as well. We study how the ESS phenology depends on the season length, on the timing and width of the larval resource peak as well as on the pace of improvement of abiotic conditions early in season. Thereby we can also assess how different environmental changes affect the ESS phenology. Under strong competition the ESS phenology responds weakly to changes in the timing of the resource peak but strongly to changes in the onset of favorable conditions. In general, shifts in the ESS phenology may differ substantially from shifts in the environmental optimum. As an example, an increase of the season length may not necessarily change the environmental optimum, but if competition is strong it will still advance the ESS phenology noticeably. Conversely, even if a change in the timing of a narrow resource peak may shift the environmental optimum considerably, it may leave the ESS phenology unaffected. In some situations the ESS phenology and the environmental optimum may even respond in different directions. Our study highlights that changes in timing in other trophic levels, changes in the environmental optimum and expectations from the full eco-evolutionary game need to be separated when predicting phenological responses to changed environments.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy23-i030-R*

Symposium 23
Climate change and evolution

Temperature adaptation and speciation within a geothermal system from a freshwater snail (Radix balthica) perspective

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Summary statement:

Temperature variation has evoked relatively little interest in speciation research but the demand for this knowledge is increasing in view of global warming.

Abstract:

Although temperature variation has evoked relatively little interest in speciation research, several interesting questions related to temperature adaptation can be posed in this context. The freshwater lake Mývatn in northern Iceland is situated on the Mid-Atlantic Ridge and is therefore subjected to geothermal activity with several warm (24°C) and cold (6°C) springs within and around the lake. As fluctuations in water temperature in the vicinity of springs are small, aquatic life close to the outflow of cold and warm water can hence be expected to have adapted to the relatively stable temperature environment. Connecting these areas of small temperature variation are areas of seasonal temperature variation. Here the conditions are different and therefore the selection pressure on the aquatic life is altered. In order to investigate these differences in evolutionary forces the pulmonate freshwater snail Radix balthica will be sampled along the shoreline of Lake Mývatn. A pilot study in Lake Mývatn based on 88 Amplified Fragment Length Polymorphism (AFLP) markers and six populations (two warm, intermediate and cold locations) showed that snails from cold and warm locations are differentiated by an average Φpt of 0.157 indicating strong divergence along a short geographic distance (7 km). Future experiments will give valuable information regarding species formation in relation to temperature and how adaptation to different temperature regimes take place in the presence of gene flow. Such information is increasingly important in the face of global warming.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy23-i014-R*

Symposium 23
Climate change and evolution

Ecological and evolutionary responses to global warming in the seaweed Fucus serratus, a key foundational species in the North Atlantic intertidal

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Summary statement:

If genetic change in F. serratus cannot mitigate its predicted northward niche shift due to ocean warming, the N-Atlantic intertidal ecosystem may undergo substantial restructuring

Abstract:

Marine intertidal ecosystems are likely to be profoundly affected by climate change because human impacts have already undermined their resilience and capacity to buffer additional environmental stresses. Global environmental change invokes two basic responses of organisms: ecological (dispersal, phenotypic plasticity) and evolutionary (genetic change), both of which are integrated into a “move, be plastic, or evolve” strategy. We investigate ocean warming responses in the seaweed Fucus serratus, a key ecosystem engineer of North Atlantic rocky shores with focus on: (1) predicting distributional changes under three IPCC scenarios by ecological niche modeling using the program Maxent and (2) identifying loci under selection in four populations that were sampled at the beginning and end of the current decade and genotyped for 31 microsatellite loci. Our ecological niche models forecast a substantial northward shift of the fundamental niche of F. serratus with rocky shores below 45° latitude becoming uninhabitable by the end of this century. Furthermore, each of the four populations revealed significant genetic changes over the past decade that were inversely related to genetic diversity. Outlier loci coincide only partly between populations, suggesting alternative microevolutionary responses. Common-garden heat-stress experiments will address the hypothesis that revealed genetic changes are adaptive to ocean warming. If F. serratus is unable to adapt rapidly to increasing temperature, its predicted absence from North Atlantic rocky shores below 45° latidude may result in substantial ecosystem restructuring with potential societal and economic impacts.

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TUE 23 AUG at 1440 - Room N2
Oral presentation *C3-Sy23-1440-O*

Symposium 23
Climate change and evolution

Identifying phylogenetic and ecological constraints limiting species distributions: A 100 Drosophila species comparison

Kellermann V[1], Loeschcke V[1], Kristensen TN[2], David JR[3], Svenning J-C[1], Fløjgaard C[1], Hoffmann AA[4], Overgaard J[1]
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Summary statement:

A combination of phylogenetic and ecological constraints, in thermal related traits, were found to limit species ability to adapt to changing environments.

Abstract:

The capacity to tolerate stressful climatic conditions helps to define the fundamental niche of a species, and consequently species distributions are often linked to the degree to which they have evolved tolerance to climatic stress. Evolutionary history as well as current selection pressures may constrain the development of stress tolerance across phylogenies and lead to niche conservatism. Understanding the prevalence of niche conservatism is important for predicting how species will respond to climate change. To investigate the putative constraints of ecological and evolutionary history in limiting stress tolerance, we assessed heat, cold and desiccation resistance in 103 Drosophila species while controlling for environmental acclimation, phylogeny and spatial variation. Cold and desiccation resistance proved vital for shaping Drosophila distributions and the strong phylogenetic signal found for these traits was associated with phylogenetically structured adaptation rather than phylogenetic constraints. In contrast to expectation, heat resistance was associated with low environmental precipitation rather than high ambient temperature per se. Phylogenetic constraints were detected for heat resistance. Irrespective of phylogeny, species from tropical habitats were less resistant to environmental stress and their tolerance was entirely independent of environmental variability. These findings point to both ecological and phylogenetic constraints dictating species tolerance levels and highlight likely limits in adapting to rapid future climatic change.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy23-i015-R*

Symposium 23
Climate change and evolution

Fisher´s geometric model with a moving optimum

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Summary statement:

We use Fisher´s geometric model to make theoretical predictions about the genetic basis of phenotypic adaptation to gradual environmental change.

Abstract:

Predicting the consequences of global change requires a better understanding of adaptation and its genetic basis. For example, it is still unclear to what degree adaptive evolution proceeds through small or large mutational steps. A simple yet powerful tool for studying this kind of question is Fisher´s geometric model. This model views adaptation as a "walk" through a multidimensional trait space, in which large steps are likely to have deleterious side effects (due to pleiotropy). For adaptive walks towards a constant optimum (e.g., after an abrupt environmental change), Fisher´s model predicts that the distribution of step sizes is exponential: Most steps are small, but some are quite large and make up a large portion of the total distance covered. However, many aspects of global change are gradual rather than abrupt, such that populations must "chase" a moving optimum rather than approach a constant one. Furthermore, the perceived speed of the optimum depends on the generation time of the study species. We will present a moving-optimum version of Fisher´s geometric model, which shows how the genetic basis of adaptation depends on the speed of environmental change, its direction relative to the direction of genetic correlations (the "genetic line of least resistance"), and the number of traits under selection ("complexity"). One result is that, under moving-optimum selection, the majority of adaptive steps have intermediate size.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy23-i016-R*

Symposium 23
Climate change and evolution

A phylogeographic dissection of the recent range expansion of the spider Argiope bruennichi - a consequence of climate change?

Krehenwinkel H[1], Tautz D[1]
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Summary statement:

A spider's recent range expansion can not be satisfactorily explained by climate change alone. Instead adaptive evolution might have played an important role.

Abstract:

The recent pole ward range expansion of various species is commonly attributed to global warming. However, the role of genetic adaptations in the success of such invasions remains to be discussed. Originally inhabiting the Mediterranean and few warm regions in central Europe, the thermophilic wasp spider Argiope bruennichi has greatly expanded its range in the past century. Today, it can be found nearly everywhere in central Europe as far north as Finland. The cause of the spider's spread remains unknown. But the spiders colonized regions, in which their persistence is hard to explain merely by global warming. In order to trace the expansion genetically we reconstructed the Europe-wide phylogeography of Argiope bruennichi. Our results point to a single glacial refugium for European wasp spiders in the near East, from which they recolonized the Mediterranean region. Within Europe, a phylogeographic split occurs between Mediterranean and Western Oceanic, vs. North-Eastern Continental climatic zones. The spider´s body size follows a clear latitudinal gradient, which is further enhanced by the transition from Western to Northeastern Europe. Climate driven range expansion might thus culminate into differential adaptation in this species.
Currently we are conducting common garden experiments to confirm potential genetic factors, involved in the observed size gradient. Further morphological and ecological analysis might highlight adaptive characters in newly established spider populations.

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TUE 23 AUG at 1650 - Room N2
Oral presentation *C4-Sy23-1650-O*

Symposium 23
Climate change and evolution

What are the consequences of being a 'thermal generalist' at the 'warm edge' of a population's range? Insights from the eukaryotic microbe Paramecium caudatum

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Summary statement:

European paramecia constitute a 'thermal generalists' subpopulation and only genotypes at the southern, 'warm edge' of the subpopulation's range may suffer from global warming.

Abstract:

Latitudinal thermal heterogeneity could act as a driver of evolutionary temperature adaptation and may lead to locally-adapted phenotypes. Due to the apparent impact of climate change on Earth's ecological and biological systems, studies investigating such adaptation patterns have become a renewed important topic. Especially ectothermic organisms are of interest, because their physiological performance is, in general, highly dependent on environmental temperature. Surprisingly, very little is known about thermal adaptation patterns of globally distributed eukaryotic microbes. Whether subpopulations of such ubiquitous species are adapted to their respective temperature regime or if a global population consists of thermal generalists are pivotal questions to estimate the impact of environmental change on species' distribution and genetic diversity.
Here, we investigated the thermal tolerance of the ciliate Paramecium caudatum along a latitudinal transect in Europe and included tropical strains as a phenotypic and genetic outgroup. Further, the sensitivity of the different genotypes to current and future temperatures of their natural habitats was estimated by calculating thermal safety margins and maximum warming tolerances.
Our data suggest a 'thermal generalist' pattern among all investigated European P. caudatum clones, while the Indonesian clones seem to be adapted to the tropical temperature regime. Because of the generalist pattern among the European clones, only paramecia currently living at the southern edge of the European subpopulation's range may suffer from the occurrence of predicted extreme hot summer temperatures if they cannot adapt to warming environments.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy23-i017-R*

Symposium 23
Climate change and evolution

Synergistic effects of temperature stress and veterinary pharmaceuticals on yellow dung flies

Kunce W[1], Lindgren B[1], Kiehl B[1], Bussière LF[1,2], Laugen AT[1]
[1]Swedish University of Agricultural Sciences, Department of Ecology, Uppsala, Sweden, [2]Stirling University, School of Natural Sciences, Stirling, United Kingdom

Summary statement:

We assess the combined effects of two human-induced stresses on the survival of yellow dung flies larvae and discuss implications for population persistence under climate change.

Abstract:

In the face of global environmental change, wild animal populations are frequently subjected to multiple environmental stressors. While a population may remain healthy under the pressure of one stressor, it could be devastated under the negative influence of combined or synergistic effects of multiple stressors with different modes of action. The knowledge and techniques required to investigate the effects of stressors likely to be found together in nature cross academic disciplines and are thus are seldom brought together in the necessary interdisciplinary approach. The trans-generational effects of multiple stressors must also be examined in order to appropriately assess the sustainability of the stressed populations. For example, it is possible that offspring of mothers who survived being raised in the stressful temperature might outperform their peers whose mothers were not. Using yellow dung flies (Scathophaga stercoraria) as a model system we tested the combined effects of two anthropogenic stressors on larval survival and development time and also how the environment experienced by the parents influenced offspring performance. In a common garden experiment, we used the common paraciticide ivermectin, which is known to have detrimental effect on many dung organisms. Since yellow dung flies are known to be cold-tolerant and generally avoid high temperatures we also subjected them to a high temperature stress to simulate a climate change stressor. We quantify the synergistic effect of two multiple coincident stresses and discuss the potential repercussions for wild populations.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy23-i010-E*

Symposium 23
Climate change and evolution

Trans-Arctic invasion of the Pacific herring (Clupea pallasii) to North-East European seas

Laakkonen H[1], Lajus D[2], Strelkov P[2], Hardman M[1], Väinölä R[1]
[1]University of Helsinki, Finnish Museum of Natural History, Helsinki, Finland, [2]St. Petersburg State University, Department of Ichthyology and Hydrobiology, St. Petersburg, Russian Federation

Summary statement:

We use mtDNA sequence data and coalescent analyses to trace the inter-oceanic history of the Pacific herring in NE Europe.

Abstract:

For most of the boreal marine fauna, the Arctic basin today presents a dispersal barrier that isolates the Atlantic and Pacific oceans from each other. Yet the existence of shared taxa shows that dispersal opportunities have earlier existed, whereas the dynamics of such trans-Arctic connections remain unclear. Understanding the control and consequences of the dispersal has become even more topical with the ongoing warming of global and Arctic waters and new navigation practices. The Pacific herring Clupea pallasii is a sister species of the Atlantic herring C. harengus; these species have evolved in isolation from each other in the two oceans for some 3 million years. However, the Pacific herring is currently also present in NE Europe, e.g. in the White and Barents Seas, along with the Atlantic herring. We use mtDNA sequence data and coalescent analyses to trace the inter-oceanic history of the Pacific herring. Data shows a very close relationship, probably of early post-glacial age, between the European White Sea C. pallasii and herring that now inhabit the Russian Pacific coast. In the process of recent invasion to Europe, the colonizers have lost a major part of the ancestral Pacific mtDNA variability, and already acquired some new by mutation. Considerable differences are also found among different NE European stocks. The inferred history is similar to that earlier described for the similarly distributed boreal molluscs Macoma and Mytilus.

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TUE 23 AUG at 1630 - Room N2
Oral presentation *C4-Sy23-1630-O*

Symposium 23
Climate change and evolution

Changes in the genetic variance-covariance matrix across multiple stressful environments and the implications for evolutionary response to climate change

Laugen AT[1], Kunce W[1], Kiehl B[1], Lindgren B[1], Bussière LF[1,2]
[1]Swedish University of Agricultural Sciences, Department of Ecology, Uppsala, Sweden, [2]University of Stirling, School of Natural Sciences, Stirling, United Kingdom

Summary statement:

We assess the magnitude of changes in the genetic variance – covariance matrix for traits under selection across environments featuring coincident multiple stresses.

Abstract:

Global climate change will not only drastically alter ambient temperatures but also impose additional environmental stressors on living organisms. We know little about how wild populations respond to the appearance of multiple new stresses particularly when they exert contrasting selection pressures. Predicting evolutionary responses by simply using genetic correlations between characters is futile because the genetic variance-covariance matrix (G) may vary across environments. Using the cold-tolerant yellow dung flies (Scathophaga stercoraria) as a model system we estimated G for larval development, growth and survival as well as morphology of emerging adults. Additionally we estimated how G varies across multiple experimental treatments. To simulate an environment with increased ambient temperature we subjected half-sib families of yellow dung fly to two different temperature treatments one of which was stressfully high. Additionally, to provide estimates of G across multiple stressful environments we spiked half of the replicates from each family with Ivermectin, an antiparasite pharmaceutical known to negatively affect the survival of many dung organisms. We discuss the magnitude of the changes in G we observed and their relevance for wild populations. Together with linear and non-linear coefficients of selection obtained from the field, these estimates of G across environments will improve our ability to predict the evolutionary response of populations to multiple human-induced disturbances.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy23-i018-R*

Symposium 23
Climate change and evolution

Species interactions alter evolutionary responses to environmental change

Lawrence D[1], Fiegna F[1], Phillimore AB[1], Bell T[2], Barraclough TG[1]
[1]Imperial College, Ascot, United Kingdom, [2]Oxford University, Oxford, United Kingdom

Summary statement:

We present evidence that evolutionary dynamics of an experimental microcosm are affected by species inteactions and this has knock-on effects on ecosystem function.

Abstract:

Studies of evolutionary responses to changing environments typically consider single species or perhaps pairs of interacting species. However, all organisms co-occur with many other species, resulting in evolutionary dynamics that might not match those predicted using single species approaches. Recent theories predict that species interactions in diverse systems can influence how component species evolve during periods of environmental change. In turn, evolution might have knock-on effects for ecosystem functioning. We used experimental communities of 5 bacterial species to investigate the effects of species interactions on adaptation to a novel environment in the laboratory. Overall, we found that the evolutionary response was altered by co-occurring species because of a trade-off between adaptation to physical and biotic components of the environment. Most species adapted by using resources produced by other species, and consequently became less effective at metabolising the culture medium. These evolutionary changes had significant repercussions for the functioning of these experimental ecosystems: communities assembled from isolates that had evolved in polyculture were more productive than those that had evolved in monoculture. Our results show that species interactions can greatly influence evolutionary dynamics. Moreover, predicting how functioning of complex ecosystems will respond to environmental change requires knowing how interactions among component species will evolve.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy23-i019-R*

Symposium 23
Climate change and evolution

Limits to evolution at range margins: testing evolutionary hypotheses about species borders in Drosophila serrata

Lee FH[1], Sgro C[1]
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Summary statement:

Using a quantitative genetic approach and distribution modeling, we attempt to elucidate whether adaptation and/or climate change is facilitating the range expansion of D. serrata.

Abstract:

In the absence of geographic barriers, what stops species expanding beyond their current range?
Using the Australian endemic Drosophila serrata as our model, we found the species has expanded its range by 300 km in the last decade.
Using a quantitative genetic approach and distribution modeling, we are currently trying to elucidate whether adaptation and/or climate change is facilitating the rapid expansion of the species.
The results suggest that cold and desiccation resistance are probable selection pressures limiting their distribution. In addition, we found low to no heritable genetic variation for cold resistance in the species, suggesting a limited potential of the species to increase cold resistance.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy23-i020-R*

Symposium 23
Climate change and evolution

How to prepare for the winter when the major cue is missing? The latitudinal range expansion of a beetle

Lehmann P[1], Sinisalo T[1], Lyytinen A[1], Lindström L[1]
[1]University of Jyväskylä, Department of Biological and Environmental Science, Jyväskylä, Finland

Summary statement:

How to time overwintering when the information from the photoperiod changes? A study of adaptation, bet-hedging and plasticity in a beetle undergoing latitudinal range expansion.

Abstract:

Many animals use the photoperiod to assess seasonal progression and to time their life-cycle. However, animals undergoing rapid latitudinal range expansions often face a change in the prevalent photoperiod. This can have serious effects on their ability to correctly predict and respond to seasonal changes. We investigated the effect of different photoperiods on traits important for diapause survival in the invasive beetle Leptinotarsa decemlineata, which has undergone rapid range expansion during the last 100 years in Europe.

Field studies have shown this species to display bet-hedging behaviour between reproduction and overwintering, and the physiological grounds for this remain elusive. In light of climate change, with warmer winters and longer growth periods predicted for high latitudes, we are interested in how well one can anticipate the continued range expansion and population dynamics of this pest species. Beetles from a marginal and a central European population were reared in short day (12h light) and long day (18h light) photoperiods. Adult beetles of three different ages were used in the analyses and sampled at time points where critical developmental and behavioural commitments are taking place. Growth rate, total abdominal lipid content as well as neutral- and phospholipid fatty acid composition in the fat body was measured. We report population dependent differences in growth rate and total lipid content and show fatty acid profiles. The results are discussed in light of rapid evolution, strong selection (by insecticides) and evolutive potential.

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TUE 23 AUG at 1710 - Room N2
Oral presentation *C4-Sy23-1710-O*

Symposium 23
Climate change and evolution

You or your offspring - Immune defense and reproduction under high temperatures

Leicht K[1,2], Jokela J[3], Seppälä O[3]
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Summary statement:

We examined the effect of high temperature (25°C) on reproduction and immune parameters in a freshwater snail. Immune defense decreased while reproduction increased.

Abstract:

Extreme weather conditions (e.g. heat waves) are predicted to become more frequent in near future due to climate change. Exposure to high temperature is known to be stressful for many organisms, but detailed information about its influence on ecological interactions is still limited. Here, we examined the effects of high ambient temperature on immune function and reproduction of the great pond snail (Lymnaea stagnalis) in order to test whether temperature stress can predispose snails to pathogen infections, and how this is related to other changes in snail life histories. Over a period of 10 days, we exposed snails to a non-stressful temperature (15°C) and to a high temperature (25°C) that occurs in small ponds and in shallow lakes during hot summers. During the experiment, we measured haemocyte concentration, phenoloxidase activity, and antibacterial activity of snail haemolymph in order to estimate snail immune function, and counted the number of produced eggs. We could show that exposure to high temperature reduces phenoloxidase activity and haemocyte concentration, whereas antibacterial activity was not affected. However, number of produced eggs increased in high temperature. This result can be seen as altered energy allocation between life history traits under high ambient temperature.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy23-i011-E*

Symposium 23
Climate change and evolution

Nucleotide diversity in candidate genes for drought stress response in European silver fir (Abies alba Mill.) across its western distribution range

Liepelt S[1], Zimmermann H[1], Roschanski A[1], Fettweis K[1], Ziegenhagen B[1], Hasenkamp N[1,2]
[1]University of Marburg, Conservation Biology, Marburg, Germany, [2]Max Planck Institute for Evolutionary Biology, Evolutionary Genetics, Ploen, Germany

Summary statement:

At this point, the results from only two candidate genes provide little evidence for local adaptation of silver fir to drought stress.

Abstract:

Forest ecosystems face great challenges in the future according to predictions of global climate change and it is of crucial importance for conservation and management to gain information about the adaptive potential of keystone species. Most forest trees will not be able to track the predicted rapid climate change by migrating towards cooler regions. This problem is reinforced by intensive land use and high levels of fragmentation in many regions of the world, especially in Europe.
Knowledge about variation in genes involved in the response to environmental stress is a first step in understanding past evolutionary processes and ultimately the adaptive potential of populations.
We re-sequenced two candidate genes for drought stress response (COMT and erd3) in approximately 130 individuals from 10 regions across the western distribution range of A. alba. The same populations were analysed with nuclear microsatellite markers. Population structure and genetic diversity were estimated for candidate genes and microsatellite markers. Neutrality tests were performed with the candidate gene data. Further re-sequencing work of additional candidate genes is ongoing.
Levels of nucleotide diversity similar to other conifer species were observed and overall population structure was weak although some population pairs were significantly differentiated for single genes. Only one region, in southeastern France, exhibited a significant deviation from standard models of neutral variation in the gene COMT indicating balancing selection. The analysis of nucleotide variation in more genes will provide a more detailed picture about signatures of selection in A. alba.

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MON 22 AUG at 1550 - Room N2
Oral presentation *B4-Sy23-1550-O*

Symposium 23
Climate change and evolution

Rapid evolution of a key phytoplankton species: 500 generations in a high CO2 world

Lohbeck KT[1], Riebesell U[1], Reusch TBH[1]
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Summary statement:

We experimentally studied rapid evolution of a key phytoplankton species and investigated the role of novel mutation over genotypic selection under a climate change scenario.

Abstract:

The uptake of anthropogenic CO2 by the surface ocean changes seawater carbonate chemistry, namely it leads to increased carbon availability and a lowered pH. This process is called ocean acidification. While numerous studies have shown effects of ocean acidification on a variety of marine organisms, the potential for rapid evolutionary changes has been widely neglected. Considering the short generation time of unicellular algae, this group lends itself for testing the evolutionary potential to respond to projected future ocean changes. Using freshly isolated strains of the calcifying microalgae Emiliania huxleyi we designed a replicated laboratory selection experiment under ambient and predicted future CO2 levels over ~500 generations. The experiment was performed as semi-continuous batch cultures with equal contribution of 6 clones as starting conditions and with high inocula sizes to keep the mutational target high and genetic drift effects low. We also performed a replicated single-clone experiment in order to assess the relative role of novel mutations over genotypic selection among clones. To test for adaptation, growth rate was measured as fitness proxy in reciprocal experiments every ~100 generations. Calcification rates, as biogeochemically relevant phenotypic trait, of evolved and non-evolved lines were determined after appropriate acclimation under reciprocal CO2 conditions. Thus, our experiments provide first insights into the role of rapid evolution for modulating the physiological response of a key calcifying phytoplankton species in a high CO2 ocean.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy23-i021-R*

Symposium 23
Climate change and evolution

Chronicle of an adaptation foretold: Individual-based analysis of rapid life-history evolution in wild male guppies

Lopez-Sepulcre A[1], Bentzen P[2], Ghalambor CK[3], Gordon SP[4], Torres-Dowdall J[3], Handelsman C[3], Bassar RD[4], Torres-Mejia M[4], Furness A[4], Reznick DN[4]

[1]Ecole Normale Superieure, Paris, Ecology and Evolution, Paris, France, [2]Dalhousie University, Marine Gene Probe Lab, Halifax, Canada, [3]Colorado State University, Biology, Fort Collins, United States, [4]University of California, Riverside, Biology, Riverside, United States

Summary statement:

Common garden evidence of rapid evolution after experimental introduction of guppies to a new environment is compared to individual-based analyses of selection and heritability.

Abstract:

Understanding the selective and genetic factors behind rapid evolution is key to predict the fate of populations under environmental change. Long-term studies on individually monitored populations have proven that selection and heritability can be strong, yet none show unequivocal evidence of a subsequent evolutionary (i.e. genetic) response. Our best examples of rapid evolution come from common garden comparisons of introduced populations, but these lack the individual-based data needed to understand the selective mechanisms. We bridge both approaches in a system where rapid evolution of life histories have repeatedly been demonstrated: the Trinidadian guppy. When released from predation, guppies evolve a higher age and size of maturation. This change can be attributed to either a decrease in mortality rate or increased competition for resources given higher population densities. We performed two translocations experiments in the wild, moving uniquely marked guppies from high to low predation environments. We trimmed the canopy above one of the streams to increase light and hence the level of basal resources. Since the introduction individuals have been monitored monthly, and their pedigree reconstructed. After a year, individuals from the control stream but not the treatment stream, show significantly bigger maturation sizes in a common garden. Individual-based analysis show strong heritability of the trait and strong selection only on the control stream. Evolutionary inferences using the animal model on the wild data, however fail to demonstrate evolutionary change. The consequences of this result for our understanding of rapid evolution in the wild will be discussed.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy23-i022-R*

Symposium 23
Climate change and evolution

Life-history trade-offs' shift in response to community changes: The case of the Drosophila parasitoids from the Rhône Valley

Martel V[1], Vayssade C[2], Moiroux J[1], Fauvergue X[2], van Alphen JJM[1], van Baaren J[1]
[1]CNRS / Université de Rennes I, Ecobio, OSUR, Rennes, France, [2]INRA PACA, UMR Interactions Biotiques et santé végétale, Sophia-Antipolis, France

Summary statement:

The life-history trade-offs were examined in populations of parasitoids differing in their community composition (i.e. presence/absence of a competitor).

Abstract:

Life-history traits are linked to fitness and are influenced by both biotic and abiotic environmental factors. Organisms should display an optimal life-history in a given environment, within the limits of certain internal constraints. Changes in a parasitoid community is expected to influence life-history traits, and consequently modify trade-offs between maintenance, reproduction and dispersal. In this study, we investigated the impact of a community change (the presence of a migrating species following global changes) on the life-history traits of Drosophila larval parasitoids in the Rhône valley in France. Two native species, Leptopilina heterotoma and Asobara tabida are present all along the valley while a third species, L. boulardi, is slowly extending its distribution towards the North of the valley. This species being competitively superior and bringing high levels of parasitism of Drosophila larvae, we expect life-history to be different in southern populations where mortality is likely to be higher. As predicted, investment in reproduction was higher in southern populations for both native species, coupled with higher dispersal potential. However, only A. tabida showed a shorter longevity as predicted by the trade-off between fecundity and longevity. Female L. heterotoma use a different mechanism to be able to invest more in reproduction: they have a lower metabolic rate consuming less lipids.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy23-i023-R*

Symposium 23
Climate change and evolution

The influence of temperature on fertilisation success in three-spined sticklebacks (Gasterosteus aculeatus)

Mehlis M[1], Bakker TCM[1]
[1]University of Bonn, Insitute for Evolutionary Biology and Ecology, Bonn, Germany

Summary statement:

Increasing temperatures can be both disadvantageous and beneficial in a sperm competition context in three-spined sticklebacks (Gasterosteus aculeatus).

Abstract:

Increasing water temperatures, caused by climate change, may especially affect organisms which live in a fluctuating environment, e.g. in the shallow shore region. The three-spined stickleback (Gasterosteus aculeatus) is a fish that breeds from April through July. During this time males establish riparian territories and build a nest composed of filamentous algae in which several gravid females spawn. In this species stealing of fertilisations, so-called sneaking, is a common behavioural tactic, which consequently results in sperm competition. Furthermore, males have a fixed number of sperm during the breeding season and they are able to adjust their ejaculate size depending on rival context. In many species fertilisation success is suggested to follow a raffle-principle. In detail, the chances of fertilisation are equivalent to one's own sperm number in proportion to the total sperm number. In the present study, ten different sperm numbers (ranging from 5,000 to 5,000,000 sperm per egg) were used to fertilise the same female's eggs in vitro at two different temperatures. The results revealed that in the 25°C treatment a lower number of sperm was sufficient to fertilise 50% of the eggs than in the 17°C treatment. However, when the number of sperm increased the fertilisation success also increased in the 17°C treatment almost reaching 100% whereas the fertilisation success in the 25°C treatment saturated at about 75%. In summary, ambient temperature conditions have an effect on fertilisation success in three-spined sticklebacks and could thus influence sperm allocation and accordingly the outcome of sperm competition.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy23-i012-E*

Symposium 23
Climate change and evolution

Host adaptation and preference of beetles occurring on a native and a non-native host plant

Meijer K[1], Beukeboom L[1], Schilthuizen M[2]
[1]University of Groningen, Evolutionary Genetics, Groningen, Netherlands, [2]Netherlands Centre for Biodiversity Naturalis, Leiden, Netherlands

Summary statement:

Gonioctena quinquepunctata beetles occur on both the native rowan and the non-native black cherry. We try to answer if they adapted to and have a preference for either host plant.

Abstract:

Gonioctena quinquepunctata beetles (Coleoptera: Chrysomelidae) occur in Western Europe on both the native rowan (Sorbus aucuparia) and the non-native black cherry (Prunus serotina, originally from the USA). Here we study the host adaptation and the host preference of this beetle to either host plants. Field observations showed that Gonioctena occurs on both host plants in equal numbers, but is absent on all other shrub and tree species in the same area, including native cherry species (P. padus, P. avium). The fact that this beetles is using P. serotina as a host plants is rather surprising. P. serotina is only moderately related to S. aucuparia, P. serotina leafs contain high levels of prussic acid (hydrogen cyanide; HCN), and the beetles do not occur on other Prunus species (in which the levels of prussic acid is much lower).
We tested if Gonioctena beetles (adults and larvae) have a specific host preference, do ´S. aucuparia-beetles´ prefer Sorbus and do ´P. serotina-beetles´ prefer P. serotina? Furthermore we tested larval survival in a cross-rearing experiment.

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MON 22 AUG at 1400 - Room N2
Invited talk *B3-Sy23-1400-I*

Symposium 23
Climate change and evolution

Detecting climate change responses in the wild: Problems and prospects

Merilä J[1]
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Summary statement:

Climate change impose directional selection on heritable phenotypic traits, but expected evolutionary responses are often not observed. I discuss possible explanations for this.

Abstract:

Climate change, human induced habitat changes and harvesting are all factors that impact upon wild populations creating directional selection on heritable phenotypic traits. Since heritable phenotypic traits should respond on directional selection, evolution in response to these human induced selection pressures should be of commonplace occurrence. However, detecting these evolutionary responses is technically challenging because we typically lack means to verify the genetic basis for the observed phenotypic shifts. An additional complication in interpretation of many datasets resides on the realization that evolutionary dynamics of heritable traits under selection are subject to various complexities stemming from inheritance patterns as well as to interactions among genes and environment. In my presentation, I will illustrate and discuss upon the problem of detecting evolutionary changes in response to climate change mediated selection by utilizing examples from long-term genetic studies of natural vertebrate populations.

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MON 22 AUG at 1500 - Room N2
Oral presentation *B3-Sy23-1500-O*

Symposium 23
Climate change and evolution

Geographical variations in the level of phenotypic plasticity: Does reproductive strategy or climate variation explain it in parasitic wasps?

Moiroux J[1], van Baaren J[2], van Alphen JJ[3]
[1]University of Rennes 1, UMR ECOBIO, Rennes, France, [2]University of Rennes 1, UMR 6553 ECOBIO, Rennes, France, [3]University of leiden, Institute of Biology, Leiden, Netherlands

Summary statement:

The level of phenotypic plasticity of egg load and egg size is primarily affected by climate variation and not egg maturation strategy in drosophila parasitoids.

Abstract:

Climate variation is known to affect the level of phenotypic plasticity, represented by the slope of a reaction norm. A flat reaction norm is generally observed in variable climates, where fitness-related traits are buffered against variations. Life history may also affect this plasticity´s level. In parasitoids, two reproductive strategies exist: proovigenic females emerge with all their eggs mature and are unable to produce more as adult whereas synovigenic females can produce eggs as adult. A flat reaction norm may thus be expected in proovigenic wasps as their initial fecundity should be maximised in every environment.

In this study, we investigated the relative role of climate variation and egg maturation strategy in the selection of the level of plasticity of egg load and egg size in drosophila parasitoids. To address this question, we compared thermal reaction norms of these traits of proovigenic and synovigenic populations from a variable or stable climate.

In proovigenic and synovigenic populations from the stable climate, egg load and egg size showed strong variations, whereas reaction norms were flatter in wasps from the variable environment. These results indicate that the level of plasticity is primarily affected by climate variation and not reproductive strategy in parasitoids. In populations from the stable climate, we observed a strong decrease in egg load and an increase in egg size with an increase in temperature. This reaction norm may be an adaptation to the effect of temperature on the host´s size. As smaller hosts occur at higher temperature, parasitoids may lay bigger eggs to compensate for the lower amount of nutrients provided by the host.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy23-i024-R*

Symposium 23
Climate change and evolution

Colaescence times in expanding populations

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Summary statement:

We use the coalescent approach to describe the influence of range expansion on neutral genetic diversity.

Abstract:

Range expansions are an ubiquitous phenomenon in natural populations. They can be induced e.g. by changing habitats - notably climate change - or adaptation. Their strong impact on neutral genetic variation is caused by repeated bottleneck effects. Coalescence time distributions can be used to analyse patterns of genetic diversity.
In spatially structured populations, coalescence times particularly depend both on the relative sampling locations of the individuals, and on the boundaries of the habitat.
Here we study the influence which expansion fronts have on the coalescence time distributions in structured habitats. We derive characteristic scales, and a cutoff for coalescence times and identify two separate regimes of the coalescence process. Simulation data supports these findings.
Our results complement findings obtained from the serial founder model as well as from models with fixed habitat boundaries. Based on our results, future studies aim at identifying range expansions in natural populations and to estimate parameters such as population densities, migration rates, and expansion velocities.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy23-i013-E*

Symposium 23
Climate change and evolution

Latitudinal variation in photoperiodic induction of diapause in parasitoid Nasonia vitripennis

Paolucci S[1], Salis L[1], Van de Zande L[1], Beukeboom L[1]
[1]University of Groningen, Evolutionary Genetics – CEES, Groningen, Netherlands

Summary statement:

Photoperiodic induction of diapause in natural populations of Nasonia vitripennis shows latitudinal cline as a result of adaptation to seasonal cycles at different latitudes

Abstract:

Adaptation of diapausing species to ultradian conditions at different latitudes requires the evolution of different strategies for optimal synchronization of life cycle with seasonal cycles. Photoperiod represents the most reliable signal for upcoming seasonal change and is used by many organisms as a cue for optimal timing of diapause induction. The effect of photoperiod on the induction of diapause in the parasitoid wasp Nasonia vitripennis collected at various locations along a latitudinal gradient in Europe was investigated. Adult females were exposed to eight photoperiodic conditions (Light/Dark cycles in 24 hours period) ranging from L:D 8:16 to L:D 18:6 and lifetime diapausing offspring production was scored. We found clear latitudinal clines in the effect of maternal age on diapause induction in offspring, overall diapause incidence and in critical photoperiod inducing diapause. Crosses between individuals from the two extremes of the cline (Oulu, Finland and Corsica, France) were performed in order to investigate the underlying genetics. The results indicate that photoperiodic inducton of diapause most likely has a polygenic basis.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy23-i025-R*

Symposium 23
Climate change and evolution

Reduced responses to selection and inbreeding depression after species range expansion

Pujol B[1]
[1]French CNRS-University of Toulouse Paul Sabatier, Lab. Evolution & Diversité Biologique, Toulouse, France

Summary statement:

Here, we bring empirical evidence that range expansion depleted the evolutionary potential of plant populations to respond to selection and their inbreeding depression.

Abstract:

Many species expanded their geographic ranges from core ‘‘refugium’’ populations when the global climate warmed after the Pleistocene. The bottlenecks that occur during such range expansions diminish neutral genetic variation in marginal populations. It is commonly expected that such depletion affects the evolutionary potential of populations but no clear evidence of such evolutionary response was brought so far. Here, we show that range expansion strongly depleted the ability of populations to respond to directional selection and inbreeding depression on size and reproductive traits. We compared the response to directional selection and inbreeding depression among 20 populations across the expanded range of a common European plant, and found that marginal populations had greatly reduced inbreeding depression. Similar patterns were also revealed by multilocus computer simulations. Certainly, the depletion of heritable variation in marginal populations is likely to be a common feature in species that have expanded their range by passing through genetic bottlenecks. Such populations may face a higher risk of extinction if they are less able to respond to selection under a changing environment. Our results also expose a remarkable aspect of reproductive evolution at range margins, where a history of expansion can reverse the direction of selection on the mating system. Low inbreeding depression is predicted to ease conditions for the evolution of self-fertilization, and selfing is known to be particularly frequent in marginal populations. Our findings therefore provide a novel parsimonious explanation for the high incidence of selfing in marginal populations.

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MON 22 AUG at 1630 - Room N2
Oral presentation *B4-Sy23-1630-O*

Symposium 23
Climate change and evolution

Dynamics of temperature adaptation over 130 generations in a wild population of Artemia franciscana

Rode NO[1], Charmantier A[1], Lenormand T[1]
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Summary statement:

We study the evolution of thermal tolerance breadth in A. franciscana (Crustacea) transferred from temperate to tropical salterns, by reviving dormant cysts sampled over 20 years.

Abstract:

Tolerance curves are central for predicting responses to temperature change in ectotherms. However, little is known about their evolution in the wild, for which most data is comparative and interspecific. Models predict either a shift in optimal temperature or an increased plasticity (and tolerance) following abrupt environmental change. Testing for these processes in the wild requires longitudinal data over many generations and is hampered by the difficulty to accurately estimate breeding values in an uncontrolled environment. “Resurrection ecology” (revival of resting stages) represents a good alternative to these shortcomings. We study adaptation to temperature over 130 generations in natura, reviving dormant cysts from an Artemia franciscana population transferred from temperate to tropical salterns in the mid 80’s. Comparison of ancestral and recent genotypes raised in the lab at different temperatures allowed us to document the evolutionary changes in this population. This situation represents an unprecedented opportunity to study the strength and speed of evolution of tolerance curves in the course of adaptation.

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TUE 23 AUG at 1610 - Room N2
Oral presentation *C4-Sy23-1610-O*

Symposium 23
Climate change and evolution

How do genetic correlations affect species range shifts in a changing climate? A theoretical model.

Ronce O[1], Duputié A[2,3], Massol F[3,4], Chuine I[2], Kirkpatrick M[3]
[1]CNRS Université Montpellier 2, ISEM UMR 5554, Montpellier, France, [2]CNRS Université Montpellier 2, CEFE UMR 5175, Montpellier, France, [3]University of Texas at Austin, Section of Integrative Biology, Austin, United States, [4]CEMAGREF, UR HYAX, Aix-en-Provence, France

Summary statement:

Our demogenetic model allows studying the joint adaptation of multiple traits in a species confronted to climate change, tracking favourable conditions through space.

Abstract:

Natural selection imposed by local climate affects many different phenotypic traits (e.g. water use, phenology, allocation to growth versus resistance, seed size). Optimal combinations of traits vary in space along climatic gradients of altitude or latitude. Climate change projections predict shifts in those optima, sometimes of hundreds of kilometres in only a century. Several demo-genetics models have explored how migration and selection interact in species confronted to such shifts in selection pressures, in space and in time. Yet, none of such spatial models integrated the multivariate nature of adaptation to climate. It is well known that genetic correlations and selective interactions among traits can slow down or accelerate evolutionary responses to new selection pressures. Here, we develop a theoretical model that allows studying the joint adaptation of multiple traits in a species confronted to climate change, which is tracking favourable conditions through space. There is a critical rate of climate change per generation above which extinction of the whole species is certain. We show how this critical rate of change depends on the species basic growth rate and migration rate, but also on how patterns of genetic and phenotypic covariation align with variation of selection through space. Our model provides a framework to better evaluate the potential demographic impact of genetic and selective interactions in real-case examples where the multiple targets of climate-driven selection have been identified. We look forward to the conference to make contact with empiricists interested in applying our model to their data.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy23-i026-R*

Symposium 23
Climate change and evolution

Living with environmental change: causes and consequences of rapid range expansion by the dragonfly Crocothemis erythraea

Sánchez-Guillén RA[1], Ott JR[2]
[1]Universidad Nacional autónoma de México, Evolutionary Ecology, México, Mexico, [2]University of Landau, Ecology Department, Landau, Germany

Summary statement:

Evolutionary consequences and responses to climate change

Abstract:

Rising global temperatures have substantially altered many species' ranges, with ectotherms, such as insects, being particularly susceptible to temperature effects. Evolutionary consequences and responses to climate change include altered timing of major life history events, such as migrations and/or reproduction. The dragonfly Crocothemis erythraea elicits a strong response to climate, shows the capacity for high dispersal and has recently and quickly colonized central and northern Europe. To identify the evolutionary features of the range expansion of C. erythraea in central Europe we sampled and analysed 42 populations all over Europe and also Africa, and we sequenced two mitochondrial genes: Cytochrome b and NADH Dehydrogenase 1. In this study we have proposed two main objectives: 1) investigate phylogeographic structure over a large part of its geographic range to infer the pattern of colonisation and 2) investigate the pattern of genetic diversity to infer whether central and edge of range populations differ in their level of neutral and adaptive diversity. Preliminary results have showed a high genetic diversity along much of its distribution, which is a typical pattern of a species that is completing a rapid range expansion in large numbers and/or from several regions. To predict the evolutionary response to climatic change is necessary to improve our knowledge on ecology, physiology and genetics in as many species as possible.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster ***B5-Sy23-i027-R***

Symposium 23
Climate change and evolution

Intraspecific genetic variance in soil - what soil organisms tell us about the past

Schaefer I[1], Rosenberger M[1], Maraun M[1], Scheu S[1]
[1]Georg-August-University Goettingen, Ecology, Goettingen, Germany

Summary statement:

Genetic diversity of below-ground organisms offers new insights into the glacial history of Europe and the assembly of present day communities.

Abstract:

Knowledge on how ice-ages influenced the biodiversity in Europe mainly comes from studies on above-ground organisms. For interpreting their response to climatic changes one has to consider that above-ground organisms often are interdependent. If hostile conditions eradicated animal or plant species, the respective consumers were also affected. In contrast, most below-ground organisms are generalist feeders or decomposers, and therefore do not depend on the presence of certain prey species or living resources. Further, soil-living species include a high number of parthenogenetic species that have a colonization advantage compared to sexual species. The presented results on the genetic variation of below-ground organisms on a pan-European scale suggest that the common view on extinction during and recolonization after glaciation events needs to be reconsidered. The intraspecific genetic structure of two sexual and two parthenogenetic oribatid mite species (Acari, Oribatida) indicate that (i) species co-occuring in the same habitat today differ in their colonization history, (ii) genetic diversity in soil animal species is exceptionally high (>19% p-distances), and (iii) parthenogenetic lineages are more susceptible to selective sweeps than sexual species. The results indicate that soil animals radiated predominantly in pre-Quaternary times and survived Pleistocene glaciations in refugia in Central Europe. Overall, below-ground animals need to be included for a comprehensive view on the glacial and pre-glacial history of Europe and to understand how post glacial communities in Europe assembled.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy23-i028-R*

Symposium 23
Climate change and evolution

Understanding climate change related shifts in phenology in a wild bird population

Schmoll T[1], Winkel W[2], Kruuk LEB[3]
[1]University of Bielefeld, Evolutionary Biology, Bielefeld, Germany, [2]Institute of Avian Research 'Vogelwarte Helgoland', Wilhelmshaven, Germany, [3]University of Edinburgh, Institute of Evolutionary Biology, Edinburgh, United Kingdom

Summary statement:

Analysis of relative role of individual phenotypic plasticity, demography & microevolution for a flycatcher population characterised by massive forward shift in phenology.

Abstract:

Recent climate change profoundly affects the phenology of life cycle events in variety of taxa. In particular, many bird species have responded to increasing spring temperatures by shifting their timing of reproduction towards earlier breeding over the last decades. However, the relative contributions of phenotypic plasticity, changing demography and microevolutionary responses for the widely observed trends on the phenotypic level remain unclear. Disentangling these mechanisms and quantifying their relative importance is of crucial importance for predicting how populations will respond to future climate change and for informing managing decisions.
Here we analyse a longterm data set of more than 3400 breeding events from a German pied flycatcher Ficedula hypoleuca population that is characterised by a massive forward shift in reproductive phenology over the last 37 years. Random regression analysis of multiple observations of known-age individuals in different environments allow quantifying the role of individual phenotypic plasticity and demography for the observed changes in key reproductive traits like laying date, clutch size or duration of the incubation period. In addition, quantitative genetic analysis will reveal whether also microevolution has the potential to contribute to the observed trends in the phenotype over time.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy23-i031-R*

Symposium 23
Climate change and evolution

Addressing clinal variation: the relative role of evolutionary history and adaptation to a novel environment

Simões P[1], Fragata I[1], Lima M[1], Cunha ML[1], Kellen B[1], Bárbaro AM[1], Santos J[1], Matos M[1]
[1]Faculdade de Ciências da Universidade de Lisboa, Centro de Biologia Ambiental, Departamento de Biologia Animal, Lisbon, Portugal

Summary statement:

Confined to the same environment: breaking down the differences in inversion frequencies between clinally divergent populations

Abstract:

Latitudinal clines are well-known and described phenomena, although it remains a mystery how and why they are maintained. Chromossomal inversions in Drosophila are one of the most emblematic cases of such clinal variation and strong evidence supports an adaptive cause for the evolution and maintenance of inversion polymorphisms. It has been thought that temperature plays a major role in the formation of these latitudinal clines. In fact, recently it has been found that the inversion polymorphisms are now shifting, in what is thought to be an adaptive response to global warming, reinforcing this potential causality. Nevertheless, though experimental thermal evolution studies showed changes in inversion frequencies between regimes, they were not in the expected direction. Altogether, it is still unclear what are the underlying adaptive processes involved in clinal variation of inversions. A different approach to address this issue is to study the evolutionary dynamics of chromosomal inversions of populations initially differentiated along a cline, during adaptation to a novel, common environment. We use this strategy analyzing laboratory adaptation in Drosophila subobscura founded from contrasting European latitudes. Will natural selection in the new environment overcome the initial differences between the populations, leading to convergence of inversion frequencies? Or is the adaptive potential of the populations constrained by their evolutionary history?

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy23-i032-R*

Symposium 23
Climate change and evolution

More sun, more kills. The influence of light/temperature conditions during development on the survival of newt larvae

Smolinský R[1], Gvoždík L[1]
[1]Institute of Vertebrate Biology Academy of Sciences of the Czech Republic, v.v.i., Department of Population Biology, Koněšín, Czech Republic

Summary statement:

Variation in the exposure of pools to sun during the development of newt larvae affects their short-term survival under the presence of a predator.

Abstract:

Recent theory views phenotypic plasticity as an important pacemaker of thermal adaptation to sustaining climate change. An adaptive plastic response moves mean phenotype towards a new phenotypic optimum, and thereby accelerates (partial response) or decelerates (fully compensatory response) an adaptive evolutionary change. In turn, a maladaptive plastic response generally reduces the population size, but may sometimes induce the evolution of phenotypic novelty through the expression of cryptic genetic variance. Under climate change, organisms face not only the directional selection pressure of changing temperature and precipitation but also a higher frequency of extreme climatic events that act as a stabilizing selection with large random shifts in local phenotypic optima. In temperate areas, a typical extreme event represents windstorms that cause large tree falls, and consequent changes in sun exposure of forest microhabitats, such as temporary pools. Using a mesocosm experiment, we examined the development of newt larvae in artificial pools with various sun exposures on their short-term survival under the presence of predator (dragonfly nymph). Previous studies showed that newt larvae respond to the variation in sun exposure by various physiological and morphological modifications. As the gradient in mean temperature and diel thermal fluctuations increased, newt larvae that developed in shaded pools (i.e. natural conditions) survived better than larvae from sun-exposed pools. This suggests that extreme climatic events may induce a maladaptive plastic response that ultimately leads to population extinction or the evolution of new phenotypic variants.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy23-i016-E*

Symposium 23
Climate change and evolution

Recent divergence and rapid expansion of the rare peat moss Sphagnum wulfianum in northern Europe

Stenøien HK[1], Shaw J[2], Stengrundet K[1], Flatberg KI[1]
[1]Norwegian University of Science and Technology, Systematics and Evolution Group, Section of Natural History, Department Museum of Natural History and Archaeology, Trondheim, Norway,
[2]Duke University, Department of Biology, Durham, United States

Summary statement:

The peat moss Sphagnum wulfianum is mostly found in northern parts of Europe covered by ice during last glacial period. However, the species has not survived last glacial period in these northern areas.

Abstract:

An increasing number of studies reveal putative glacial refugia and post-glacial colonization patterns for several types of organisms in the northern hemisphere. Nevertheless, comparably little is still known about origin, survival and historical migration routes of moss species during late Pleistocene and Holocene. It is of interest to elucidate to what extent vascular and nonvascular plants differ regarding historical causes of current distributions. More specifically, recent studies have indicated that nonvascular plants have survived periods of extreme climatic conditions better than vascular plants in northern parts of Europe. We have studied genetic structuring in the haploid and rarely spore producing peat moss Sphagnum wulfianum. This species is mostly found in areas covered by ice during the last glacial period. A low genetic variation is observed in microsatellite markers, possibly due to bottlenecks and recent colonization by founder events. The two major genetic clusters observed within the species have diverged recently, most likely in late Holocene. The results give no support for survival in possible Scandinavian refugia during the last glacial period. Rather, the species may have survived in southern and possibly eastern regions of Europe with subsequent establishment in Scandinavia via two post-glacial immigration routes, one from East Europe through Finland and one from the Baltic states.

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TUE 23 AUG at 1550 - Room N2
Oral presentation *C4-Sy23-1550-O*

Symposium 23
Climate change and evolution

Adaptation and extinction risk under climate change: Integrating insights from metabolic theory

Walters R[1], Berger D[1], Blanckenhorn W[1]
[1]University of Zürich, Institute of Evolutionary Biology and Environmental Studies, Zurich, Switzerland

Summary statement:

We integrate predictions from metabolic theory into a quantitative genetics framework to generate evo-ecological forecasts of extinction risk under climate warming.

Abstract:

Global climate change threatens to commit many species to extinction; for those with nowhere left to go only adaptation can mitigate this risk. Evolutionary responses to recent climatic changes are already evident but to what extent responses will be sufficient to prevent extinction remains unclear. Although evolutionary biologists have developed quantitative genetics models to predict persistence time, macroecologists in general have yet to account for evolutionary processes in their ecological forecasts. In part this is because the data required to parameterise such models are lacking for most organisms. However, recent developments in metabolic theory have provided a potential unifying framework for understanding global patterns of biodiversity in terms of microevolutionary dynamics. The biochemical kinetics of metabolism fundamentally constrain the rate at which individuals can take up, transform, and expend energy and materials and so are predicted to impact upon on all aspects of fitness. Pertinent to evolutionary rate are the allometric and temperature dependence of development time, mutation rate and maximal population growth rate. Here we demonstrate how these predictions can be integrated within an existing quantitative genetics framework to infer broad scale ecological forecasts of extinction risk under climate warming.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy23-i033-R*

Symposium 23
Climate change and evolution

Detecting climate signals in genomes: A GWA approach to find footprints of climate selection in the Arabidopsis thaliana genome using new measures of climatic variability

Wang G[1], Stegle O[2], Rowan BA[1], Dillon ME[3], Weigel D[1]
[1]Max Planck Institute for Developmental Biology, Molecular Biology, Tuebingen, Germany, [2]Max Planck Institute for Biological Cybernetics, Tuebingen, Germany, [3]University of Wyoming, Department of Zoology and Physiology, Laramie, United States

Summary statement:

We use population-structure-controlled GWA studies to detect historical bouts of climate selection in Aradidopsis thaliana, using new measures of climate variability.

Abstract:

Climate change has had strong and varied effects on natural and domesticated populations of plants and animals and on human health. Although climate has been shown to be associated with specific ecologically and physiologically important traits, the impacts of past climate change on entire genomes are relatively unknown. Here, we investigate the historic selective effects of climate on the Aradidopsis thaliana genome using a Genome Wide Association (GWA) approach. We use new measures of worldwide cyclic and stochastic climate variability directly in a population-structure-controlled GWA model. We are thus able to detect genomic regions that are associated with specific climatic measures. Furthermore, we extend our GWA methods to detect changing influences over time. We find that GWA studies utilizing environmental variables as inputs are a promising methodology for identifying genes that are most sensitive to the environment, and thus most likely to be affected by our changing climate.

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MON 22 AUG at 1710 - Room N2
Oral presentation *B4-Sy23-1710-O*

Symposium 23
Climate change and evolution

Unveiling the effect of climate dynamics on species diversification during the Cenozoic

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Summary statement:

Analyzing the role of climate change in species diversification in the Cenozoic from two methodological approaches, reveals distinct responses among 50 time-calibrated phylogenies.

Abstract:

Environmental change is recognized as an important factor promoting species evolution. Our knowledge of past environmental change has improved greatly thanks to the development of palaeoclimatological research and recent interest in global climate change. Methodological progress in phylogenetics also allows for estimation of diversification times and rates of evolution. Here the impact of past climate dynamics on biological diversification is investigated from two methodological approaches: Bayesian Estimation of Diversification Rates and Climatic scenario comparison. Robust time-calibrated phylogenies of 50 taxa were analyzed. The datasets comprise terrestrial, freshwater and marine organisms distributed in different regions around the world. We tested whether diversification rates are constant through time and evaluated the temporal dynamics of species diversification in relation to important climatic events. Additionally, node-ages in phylogenies were constrained to times that reflect diversification under a certain climatic scenario (rapid change vs slow change; glacial periods vs interglacial periods). Bayes Factors were calculated to compare among scenarios and to select the best hypothesis explaining the data. Results suggest that rates of diversification have remained constant in many groups throughout the Cenozoic and the pace of climate change seems to have affected taxa in different ways. During the Quaternary, the response of organisms to glacial or interglacial periods is varied. Climate changes probably promoted diversification in some taxa without following a geographic or taxonomic pattern. Thus, taxa seem to respond individualistically to climate change.

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Symposium 24

Adaptation in large populations

Talks: *Room N9*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Ground floor campus canteen *Mensa*

Invited Speakers:

Nick Barton, Joachim Hermisson

Organizers:

Nicolas Bierne, Denis Roze

Description:

The dynamics of adaptation in large populations has been the subject of substantial recent interest. In large populations mutation is not a limiting factor to adaptation, and many beneficial alleles can segregate simultaneously and interact. Standard results of the neutral theory are invalid under these conditions. This symposium welcomes both theoretical and empirical contributions to this issue.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

TUE 23 AUG at 1400 - Room N9
Invited talk *C3-Sy24-1400-I*

Symposium 24
Adaptation in large populations

Hitch-hiking in genetically structured populations

Barton N[1]
[1]IST Austria, Klosterneuburg, Austria

Summary statement:

Hitch-hiking is complicated by demography, multiple mutations, response from standing variation, background selection, etc. How can we can disentangle these complex processes?

Abstract:

There is intense interest in the effect of adaptive substitutions on the rest of the genome, both because such hitch-hiking may be the main cause of random drift in large populations, and because it may allow us to detect recent selective sweeps. Although the basic process is simple, it is complicated by several factors: demographic and spatial structure, multiple adaptive mutations, response from standing variation, background selection, and so on. Even given complete genome sequences, it is not clear whether we can disentangle these complex processes.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy24-i001-E*

Symposium 24
Adaptation in large populations

The hitchhiking effect of adaptive introgression in a mosaic hybrid zone

Bierne N[1], Fraisse C[1], Welch J[2]
[1]University of Montpellier 2, CNRS, SETE, France, [2]University of Cambridge, Cambridge, United Kingdom

Summary statement:

Introgression differentials have been scanned in a mosaic hybrid zone and the hitchhiking effect of adaptive introgression investigated.

Abstract:

Adaptive introgression is a special case of the propagation of a favourable allele in a subdivided population. In the native genetic background, the favourable allele might have fixed a long time ago and the neutral neighbourhood have converged back to the mutation-drift equilibrium. When the favourable allele introgresses into a foreign genetic background, the selective sweep can start from a single chromosome if introgression levels are very low but more likely involves multiple copies of the favourable allele generating a so-called “soft sweep”. There are only a few examples of adaptive introgression, and even fewer examples of the hitchhiking effect of adaptive introgression. We scanned introgression differentials in the mosaic hybrid zone between Mytilus edulis and M. galloprovincialis. We identified a locus with a distinctly strong level of introgression in a M. galloprovincialis patch of populations enclosed in the mosaic zone in Brittany relative to the external patch in Portugal. This pattern is explained by adaptive introgression. The study of DNA sequence polymorphisms allowed us to verify how much of the heterospecific diversity hitchhiked during adaptive introgression.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy24-i001-R*

Symposium 24
Adaptation in large populations

The unforeseen history underlying the differentiation of two high Fst outlier loci in the mussel Mytilus galloprovincialis

Gosset CC[1]
[1]Université Montpellier 2, Sète, France

Summary statement:

A genome scan allowed us to investigate the genetic basis and history of adaptive differentiation in a species with large population sizes.

Abstract:

Scanning genomes for loci with high levels of population differentiation has become a standard of population genetics. Fst outlier loci are traditionally interpreted as being under local selection. However, a strong genetic structure at specific loci can be the consequence of a variety of scenarios. Here, we tried to identify further the genetic basis and history underlying the differentiation of high Fst outlier loci in Mytilus galloprovincialis. A genome scan has been conducted between Atlantic and Mediterranean populations. The differentiation was low overall, but 2% of loci were Fst outliers. We then analyzed DNA sequence polymorphism. The genetic structure proved to be the consequence of differential introgression of alleles from the sister hybridizing species M. edulis. While the contact zone between the two species is nowadays localised along the Atlantic coasts of France and the British Isles, the most introgressed population was the Mediterranean one.
Introgression was historical and implies a contact between M. edulis and Mediterranean M. galloprovincialis probably during the last glacial period while population distribution was shifted southward. However, it proved difficult to disentangle two hypotheses: (i) introgression was adaptive, implying some edulis alleles were favoured in Mediterranean populations, (ii) or the genetic architecture of the barrier to gene flow was different between the two M. galloprovincialis backgrounds. Our study highlights the importance of history, and probably of the genetic architecture of reproductive isolation, in the genesis of strong genetic structure at specific loci.

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TUE 23 AUG at 1630 - Room N9
Oral presentation *C4-Sy24-1630-O*

Symposium 24
Adaptation in large populations

Interference amongst new mutations, finite structured populations, and selection for sex

Hartfield M[1], Otto SP[2], Keightley PD[1]
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Summary statement:

Using computer simulations, we investigate how costly sex is maintained in large finite populations, if it is subdivided in different ways.

Abstract:

The evolution of sex is a major open problem in evolutionary genetics. An appealing widespread explanation is that sex, coupled with recombination, breaks down interference ("Hill-Robertson" effects) among multiple, linked loci subject to selection. However it has yet to be shown whether this mechanism can select for costly sex with realistic parameters and population structure. We investigated whether structured obligate sexual populations can resist the invasion of an asexual lineage. Despite a twofold cost, we find that sex is maintained in sufficiently large populations with a deleterious mutation rate of $U = 1.0$, and realistic values of population subdivision (as measured by Fst). We also find that as the overall population size increases, the level of subdivision needed to maintain sex decreases. The combined effect of advantageous and deleterious mutations can thus be sufficient to maintain sex in weakly structured populations by breaking down interference amongst linked loci.

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TUE 23 AUG at 1440 - Room N9
Invited talk *C3-Sy24-1440-I*

Symposium 24
Adaptation in large populations

Genetic footprints in large panmictic populations

Hermisson J[1]
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Summary statement:

All about soft selective sweeps

Abstract:

The typical genetic footprint of positive selection in large populations deviates significantly from the classical "hard selective sweep"-pattern. In my presentation I will give an intuitive overview based on coalescent theory of the different types of "soft selective sweep"-phenomena that may occur.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy24-i002-R*

Symposium 24
Adaptation in large populations

The substitutional load under hard and soft selection

Kessinger TA[1], Masel J[1]
[1]The University of Arizona, Department of Ecology and Evolutionary Biology, Tucson, United States

Summary statement:

Haldane´s "substitutional load" is studied in the context of selection that is permitted to vary between hard and soft extremes with implications for the rate of adaptation.

Abstract:

Haldane (1957) introduced the concept of the "substitutional load" or the "cost of natural selection" and showed that, in a scenario where survival is based only on the absolute fitness of an individual, an upper limit on the rate of adaptation can be calculated based on the number of deaths required for fixation of a beneficial allele. Ewens (1970) demonstrated that, when the relative fitness of an individual is what matters, the rate of adaptation is much higher, and many loci can segregate simultaneously. These typify the extremes of "hard" and "soft" selection, respectively. We develop a Moran-type model in which selection is permitted to vary between these two extremes and study the relevant substitutional load, i.e., the reproductive excess that is required for the population to undergo a selection event, as well as the extent to which this limits the rate of adaptation.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy24-i003-R*

Symposium 24
Adaptation in large populations

The accumulation of genetic incompatibilities in large parapatrically subdivided populations

Loire E[1,2], Bierne N[2], Roze D[1]
[1]CNRS, Station Biologique de Roscoff, équipe BEDIM, Roscoff, France, [2]CNRS, Institut des Science de l'Evolution de Montpellier, Sète, France

Summary statement:

Accumulating genetic incompatibilities in large parapatrically subdivided populations and the coupling with local adaptation genes: implications for interpreting FST outliers.

Abstract:

Genome scan studies often highlight local adaptation as the prime interpretation of increased genetic differentiation. Here we consider an alternative interpretation: the accumulation of Dobzanhsky-Muller (DM) incompatibilities in large parapatrically subdivided populations.
Our results show significant departure from the previous prediction of a linear rate of accumulation of DM substitutions in parapatry. On one hand we show that drift and asymmetry in the selective advantage of DM substitutions tend to lower this rate. On the other hand, genetic coupling between loci, which occurs when the relationship between fitness and heterozygosity is not additive (e.g. multiplicative fitness) self-reinforce the accumulation of DM incompatibilities by generating spatial aggregation patterns ("accumulation nuclei"). Interestingly, a local adaption cline can serve as an accumulation nucleus within which DM incompatibilities couple. We discuss how the interplay of exogenous and endogenous factors can potentially obfuscate Fst outliers interpretation.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy24-i004-R*

Symposium 24
Adaptation in large populations

Geographic variation of stamen number in an invasive plant Cardamine hirsuta

Matsuhashi S[1], Hay A[2], Kudoh H[3], Maki M[1], Tsiantis M[2], Sakai S[1]
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Summary statement:

The inconsistency between geographic variation and the genetic structure suggests that plasticity of the stamen number in Cardamine hirsuta has evolved after invasion of Japan.

Abstract:

Invasive species are expected to show evolutionary changes rapidly in the invaded environments. Cardamine hirsuta (Brassicaceae) has invaded Japan several decades ago. Flowers of other Brassicaceae, in general, have 6 stamens, but C. hirsuta have variations in the stamen number showing 4, 5, and 6 stamens of a flower. In Japan, populations of this species are classified two types: population where most flowers have 4 stamens and those where flowers have 4-6 stamens. The latter type has temperature dependency of the stamen number. If this differentiation occurred after invasion to Japan, it is possible to detect the evolutionary process of the stamen number and to be useful to understand how phenotypic plasticity is acquired and influences evolution of traits. To examine whether phenotypic plasticity in the stamen number has evolved after invasion of Japan, we examined the geographic variations in the stamen number and their inheritance. We then conducted clustering populations in Japan by SSR markers.
Populations with 4 stamens-flowers were distributed northeast region, whereas those with 4-6 stamens-flowers were distributed southwest region. The stamen number of flowers did not change in the experimented plants from plants in their original populations, suggesting that the stamen number is determined genetically. According to the SSR analysis, populations in Japan could be divided into four genetic clusters. However, these clusters did not correspond to the geographic variation of the stamen number. These results may suggest that phenotypic plasticity in the stamen number has evolved after invasion.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy24-i007-R*

Symposium 24
Adaptation in large populations

Different types of life strategies from salmon fishes as a base of microevolution of high-latitude species

Melnikova M[1], Pavlov S[1], Senchukova A[1], Pivovarov E[1]
[1]Lomonosov Moscow State University, Ichthyology, Moscow, Russian Federation

Summary statement:

The genetic investigations of different life strategy forms P. (O.) mykiss has shown that these forms possibly only adaptive.

Abstract:

As we now, the same genotype can formed different phenotypes, according to conditions of environment. The range of these phenotypes within one species also calls as adaptive norms or life strategies of this species (Mednikov 1987). Usually, this strategies can be separate by morphology and physiology, but genetic nature this differences still unknown.

The species P. (O.) mykiss have about seven different life strategies. Two of them are mostly separate and have cultivate resident and anadromous forms. This forms clear recognizable according morphometric, scale structure, others parameters. We tried to search genetic differences between them.

Resident and anadromous forms from different west and east coast populations of Kamchatka peninsula were investigated by allozyme loci (Pavlov et al., 2000), sites of mitochondrial DNA (Pavlov et al., 2004), different sites of nuclear DNA (Pavlov et al. 2010, Melnikova et al. 2010, Semenova et al. 2010). The forms of closely related north american trout's and cherry salmon (O. masu) were used as a reapers.

There are no differences between separate forms inside one population were revealed. It can be supposes that different life strategy forms of Kamchatka mykiss and other salmonides, detect by gene diversity of these species and specific environmental conditions. Thus, there have epigenetic mechanism of adjusting and determine the ways of microevolution species.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy24-i005-R*

Symposium 24
Adaptation in large populations

Microevolution of the blackcap (Sylvia atricapilla) at two migratory divides

Mettler RD[1], Schaefer HM[1], Segelbacher G[2]
[1]University of Freiburg, Ecology and Evolutionary Biology, Freiburg, Germany, [2]University of Freiburg, Wildlife Ecology and Management, Freiburg, Germany

Summary statement:

This study investigates temporal, genotypic, and phenotypic divergence of traits at two migratory divides of a European warbler species, the blackcap (Sylvia atricapilla).

Abstract:

Blackcaps (Sylvia atricapilla) breeding in central Europe have recently established a north-western (NW) migratory route and over-winter in Britain in addition to the traditional Mediterranean wintering grounds, resulting in a north-west/south-west migratory divide in central Europe. Due to differences in migratory distances, it has been suggested that a temporal difference in spring arrival to the breeding grounds may facilitate assortative mating in this species, potentially contributing to reproductive isolation between migrants from different winter origins. Evidence has been found for restricted gene flow and phenotypic divergence among subpopulations of breeding blackcaps in southern Germany. North of the Alps, an additional south-east/south-west migratory divide is proposed for this species, with easterly breeding birds migrating south-east (SE) and wintering in East Africa and westerly breeding birds migrating south-west (SW). This current study aims at comparing population genetics and morphological variation in breeding populations of blackcaps in both southern Germany (NW/SW divide) and northern Austria (SE/SW divide) to investigate genotypic and/or phenotypic divergence at two migratory divides. Stable isotope analysis is utilized for geographic assignment of individuals to their respective wintering grounds, while microsatellite allele frequencies and standard morphometrics are compared within and between breeding populations. Our results will provide a better understanding of the migratory behavior in this warbler species, and the potential ecological and evolutionary consequences of the divergence in traits related to migration.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy24-i003-E*

Symposium 24
Adaptation in large populations

Zooplankton populations isolated in marine lakes: natural laboratories of evolution?

Peijnenburg KTCA[1], Batistić M[2], Becking LE[3], Garić R[2], Anisimova M[4]
[1]Institute for Biodiversity and Ecosystem Dynamics/ University of Amsterdam, Evolutionary Biology, Amsterdam, Netherlands, [2]Institute for Marine and Coastal Research/ University of Dubrovnik, Dubrovnik, Croatia, [3]National Center for Biodiversity Naturalis, Department Zoology, Leiden, Netherlands, [4]Swiss Federal Institute of Technology Zurich, Department of Computer Science, Zurich, Switzerland

Summary statement:

We present evidence of fast adaptive evolution in an isolated marine lake population of the planktonic chaetognath Sagitta setosa.

Abstract:

Marine species that drift with the currents all of their lives (plankton) are traditionally thought to have large populations and high levels of gene flow. Therefore, the classical interpretation is that the open sea habours relatively few and slowly evolving species. An important prediction from evolutionary theory however, states that natural selection should be stronger in large populations than in smaller ones, which may lead to elevated evolutionary rates in species with very large populations. Understanding evolutionary processes in the open sea is particularly difficult because barriers to migration are often obscure and fossil records are typically lacking. We have studied populations of the copepod Calanus helgolandicus and the chaetognath Sagitta setosa isolated in marine lakes in Ireland and Croatia. Marine lakes provide extraordinary opportunities to study evolution of zooplankton because populations have invaded these lakes by known and dated flooding events (during the Holocene) from ancestral populations in the adjacent sea. Results (based on mitochondrial gene sequences) suggest that zooplankton populations in the Irish lakes are not significantly isolated from the adjacent sea, whereas populations in Croatian lakes are strongly differentiated. Furthermore, we found preliminary evidence of fast adaptive evolution of S. setosa populations isolated in the Croatian lakes based on morphometric (17 measurements), nuclear DNA (four microsatellites), and mitochondrial DNA (two genes) data. These findings force a careful re-evaluation of the tempo and mode of marine zooplankton evolution.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy24-i006-R*

Symposium 24
Adaptation in large populations

The evolution of stress-induced hypermutation in bacteria

Ram Y[1], Hadany L[1]
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Summary statement:

We use deterministic and stochastic models to show that stress-induced hypermutation is favored by natural selection and can evolve in bacteria due to its adaptive value.

Abstract:

Stress-induced hypermutation is common among different species of bacteria, but we still do not understand the evolutionary forces driving this surprising phenomenon, despite knowledge about some of the involved genetic pathways. Primarily, it is unclear whether stress-induced hypermutation is an adaptive trait, or merely a by-product of stress. Using mathematical models and simulations we found that alleles coding for stress induced hypermutation are expected to evolve in bacterial populations, and result in increased average fitness for the population as a whole. This was shown for an extremely wide range of scenarios and parameters, including both constant and changing environments, competitions with non-mutators as well as many types of uniform mutators, and in finite and infinite population models. Our model does not assume any extrinsic pleiotropic costs or benefits for hypermutation, thus showing that stress-induced hypermutation can evolve due to its adaptive value per se. Furthermore, the advantage we demonstrate is not restricted to stressful periods or environments. Our results directly relate to questions such as the emergence of drug-resistance in bacteria and host-parasite co-evolution. But most importantly, they suggest a paradigm shift in the way we view mutation: namely, we should expect mutation to be more common in individuals and populations that are maladapted to their environments. This is very different from the classic view of mutation as an inevitable copying error which is kept at a minimal level through accurate replication and sophisticated error correction mechanisms.

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TUE 23 AUG at 1650 - Room N9
Oral presentation *C4-Sy24-1650-O*

Symposium 24
Adaptation in large populations

Large populations sizes predict the distribution of asexuality in scale insects

Ross L[1,2], Hardy N[3], Okusu A[4], Normark BB[5]
[1]University of Massachusetts, Organismic and Evolutionary Biology, Amherst, United States, [2] University of Oxford, Department of Zoology, Oxford, United Kingdom, [3]Queensland Primary Industries and Fisheries, Entomology, Indooroopilly, Australia, [4]University of Massachusetts, Department of Plant Soil and Insect Sciences, Amherst, United States, [5]University of Massachusetts, Department of Plant Soil and Insect Sciences and Graduate Program in Organismic and Evolutionary Biology, Amherst, United States

Summary statement:

Using a comparative approach on scale insects we show that species with large population sizes are more likely to reproduce asexually and additionally are often highly polyphagous.

Abstract:

Understanding why some organisms reproduce by sexual reproduction while others can reproduce asexually remains an important unsolved problem in evolutionary biology. Simple demography suggests that asexuals should outcompete sexually reproducing organisms, because of their higher intrinsic rate of increase. However, the majority of multicellular organisms have sexual reproduction. The widely accepted explanation for this apparent contradiction is that asexual lineages have a higher extinction rate. It has recently been suggested that population size might play a crucial role in the evolution of asexuality, as the strength of processes that could lead to extinction of asexual species is reduced when the population size is very large. Here we use a comparative approach using scale insects (Coccoidea, Hemiptera) to show that asexuality is indeed more common in species with larger population density and geographic distribution and we also show that asexual species tend to be more polyphagous. Finally we discuss the implication of our findings for previously observed patterns of asexuality in agricultural pests.

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TUE 23 AUG at 1710 - Room N9
Oral presentation *C4-Sy24-1710-O*

Symposium 24
Adaptation in large populations

Balancing selection in the experimental evolution of C. elegans populations under alternative mating systems

Teotonio H[1], Chelo IM[1]
[1]Instituto Gulbenkian de Ciencia, Oeiras, Portugal

Summary statement:

We will provide an experimental evolution example that maintenance of genetic variation in large populations involves selection on non-additive gene interactions.

Abstract:

Maintenance of genetic variation in large populations is determined by balancing selection on heterozygosity counteracting directional selection promoting homozygosity. We will present an example of both maintenance and increase of ancestral diversity by balancing selection at one or two loci, during a 100 generation experiment with C. elegans populations segregating abundant genetic variation under alternative mating systems, androdioecy and dioecy. Three replicate populations were used (N=10E4) under well defined demographic conditions for each mating system. The trajectories of SNP markers covering two chromosomes (~1/3 of the genome) were measured during evolution in large individual samples. Analysis of the data reveals that directional selection diminishes with time, and that inbreeding by self-fertilization is correlated with lower adaptive rates because a high variance of heterozygosity among individuals is being maintained during evolution. At a region of 10cM, balancing selection on single SNPs or pair-wise SNPs is modeled with overdominant viability heterozygous effects in individual forward simulations of experimental evolution. Since meiotic crossover rates are known, we are able to show that androdioecious populations maintain ancestral linkage disequilibrium across the whole region if selection occurs at only at one locus. With dioecy and random mating, balancing selection with diminishing-returns epistasis between two loci better explains the increase in haplotype diversity observed in these populations, than single locus overdominant selection. These results will be discussed in the context of confounding directional selection for homozygosity.

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TUE 23 AUG at 1550 - Room N9
Oral presentation *C4-Sy24-1550-O*

Symposium 24
Adaptation in large populations

The rate of adaptation in large sexual populations

Weissman DB[1], Barton NH[1]
[1]IST Austria (Institute of Science and Technology Austria), Klosterneuburg, Austria

Summary statement:

In a large, rapidly adapting population, recombination is needed to break up clonal interference. We calculate the limit that this puts on the rate of adaptation.

Abstract:

In a large population, multiple beneficial mutations may arise simultaneously. In order for them all to fix, they must occur in the same individual or be brought together by recombination. This requirement sets an upper limit to the rate of adaptation. We calculate the dependence of the rate of adaptation on population size, mutation rate, strength of selection, and recombination rate in a toy model of adaptation. We find that for a broad range of parameters, adaptation in very large populations is primarily recombination-limited: the rate of adaptation increases only slowly with increasing population size, mutation rate, and selection strength, but increases nearly linearly with increasing recombination rate. This increase saturates when recombination is frequent enough that competing beneficial mutations are almost always unlinked.

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TUE 23 AUG at 1610 - Room N9
Oral presentation *C4-Sy24-1610-O*

Symposium 24
Adaptation in large populations

Interpreting Fst outlier loci in large structured populations

Welch JJ[1]
[1]University of Cambridge, Department of Genetics, Cambridge, United Kingdom

Summary statement:

Theoretical study of the effects of selective sweeps on genetic differentiation in large structured population.

Abstract:

Genome scans of populations connected by gene flow, often reveal marker loci with greatly enhanced differentiation between populations, as measured, for example, by Wright's F statistics. Such Fst outlier loci are often interpreted as demonstrating local adaptation (i.e., the selective maintenance of different alleles in different populations). However, the same pattern can be generated in several other ways. These include incorrect assumptions about the null distribution of Fst values, the segregation of intrinsically incompatible alleles, replicated selective sweeps in different populations, and a single sweep passing between populations. Some theoretical results will be presented, with the aim of understanding the conditions under which each of these processes can produce Fst outliers and of devising methods of distinguishing between the different scenarios. The results will help us to improve inferences from genomic data about the form of natural selection acting on wild populations.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy24-i008-R*

Symposium 24
Adaptation in large populations

Identification and validation of novel SNP markers in European populations of marine mussels Mytilus

Zbawicka M[1], Drywa A[1], Wenne R[1]
[1]Institute of Oceanology Polish Academy of Sciences, Sopot, Poland

Summary statement:

The discovery of 21 novel SNPs in Mytilus genome using Sequenom MassARRAY iPLEX genotyping. The usefulness of novel SNPs as the species markers was assessed.

Abstract:

Mussels Mytilus are widespread in northern and southern hemispheres. These mussels are known for two types of mitochondrial genomes called F and M, which are transmitted through females and males, respectively. The Mytilus species are very important component of marine coastal ecosystems and are morphologically inseparable in European waters.
Sequencing and Sequenom MassARRAY iPLEX genotyping technology was used to identify and verify novel SNP markers in three taxa of Mytilus.
SNPs were localised in coding and noncoding sequences of some functionally important genes.
24 samples of mussels Mytilus, were studied.
The percentage of polymorphic SNPs ranged from 19 to 100%. Populations from Scotland, Mecklenburg Bight and Norway had over 90% polymorphic loci. Most loci were in Hardy-Weinberg Equilibrium except sample from Scotland. The highest percentage of heterozygotes were observed in Atlantic (Banyuls, Vigo) and North Sea (Tjarno, Westerschelde) populations. The excess of homozygotes were notice in samples from Scotland, Norway and Barents Sea.
Correspondence and Structure analysis used in the present study show also great heterogeneity of these three samples.
Eight SNPs localised in histone, hsp 70 and p53 genes were discovered as novel Mytilus genus markers on a large European scale.
Five of them distinguished M. trossulus genome, two M. galloprovincialis and one M. edulis. Other SNPs differentiated individuals and populations within species.
Genotype data clearly differentiated M. edulis, M. trossulus and M. galloprovincialis.
SNPs data were a very useful tool to study population structure of European mussels Mytilus.

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Symposium 25

Evolutionary systems biology

Talks: *Room N1*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Ground floor campus canteen *Mensa*

Invited Speakers:

Jennifer Reed, Andreas Wagner

Organizers:

Laurence Loewe, Orkun Soyer

Description:

An aim of evolutionary systems biology is to extend molecular systems biology models to predict fitness correlates. These can enable new insights into the adaptive landscape and genotype-phenotype maps and may thus be used to address problems in population genetics. Such work can inspire mechanistic simulations of evolution, testing increasingly detailed evolutionary hypotheses.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy25-i001-R*

Symposium 25
Evolutionary systems biology

How the gametophytic self-incompatibility system works with multiple pollen genes

Aguiar B[1], Vieira J[1], Fonseca NA[2], Raspé O[3], Vieira CP[1]
[1]IBMC, Porto, Portugal, [2]CRACS-INESC, Porto, Portugal, [3]National Botanic Garden of Belgium, Meise, Belgium

Summary statement:

Multiple F-box genes are involved in the gametophytic self-incompatibility system in Pyrinae (Maloideae).

Abstract:

S-RNase-based gametophytic self-incompatibility (GSI) evolved once before the split of the Asteridae and Rosidae, about 120 million years ago. In Prunus (Amygdaloideae) the S-pollen is a single F-box gene that presents the expected evolutionary signatures for the S-pollen. In Malus and Pyrus (Pyrinae) however, clusters of F- box genes (at least ten SFBB genes per S-haplotype) are described. Although polymorphic, these genes present levels of diversity lower than those observed at the S-RNase gene. They have been suggested as putative S-pollen genes. A detailed characterization of SFBB-like genes in Sorbus aucuparia (Pyrinae) revealed a minimum of 16 genes. For five genes that are in linkage with the S-RNase gene, low levels of diversity, evidence for intragenic recombination, and positively selected amino acid sites are observed. Furthermore, there is no evidence for trans-specific evolution for two genes where data exists to address this issue. These observations are incompatible with one gene determining S-pollen GSI specificity. Building on the biochemical work performed in Petunia, a hypothesis involving multiple S-pollen genes is presented. This hypothesis can account for many otherwise puzzling observations, such as the presence of identical S-pollen gene sequences in individuals not having the same S-RNase allele and that the deletion of one S-pollen gene in one haplotype causes no change in the recognition of the S-pollen by the pistil carrying that haplotype but the pollen is rejected by the pistils having a different haplotype, and that there are different organization of the S-pollen genes in the different S-haplotypes.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy25-i002-R*

Symposium 25
Evolutionary systems biology

Evolution of the pollen competitive ability in Oxalis alpina, a tristylous species

Baena FS[1], Fornoni J[1], Márquez-Guzmán J[2], Pérez-Ishiwara R[3], Domínguez CA[4]
[1]Instituto de Ecología, UNAM, Evolutionary Ecology, Mexico, Mexico, [2]Facultad de Ciencias, UNAM, México, Mexico, [3]Instituto de Ecología, UNAM, México, Mexico, [4]Instituto de Ecología, UNAM, Mexico, Mexico

Summary statement:

Evolution of the pollen competitive ability in an heterostylous species, representing the evolutionary transition between tristyly to distyly within the Sky Island region.

Abstract:

The stigma and the style of Angiosperms are the arena where pollen competes for the access to the ovules. Competitive ability of the pollen depends on its capacity to germinate and on the pollen tube growth rate. The first step in this process is highly dependent on the pollen grain reserves, so the pollen grain size could be very important in pollen competition. Oxalis alpina is a heterostylous species with tristylous and distylous populations (characterized by the loss of the mid morph), representing the evolutionary transition between these heterostylous reproductive systems. The loss of the mid morph is accompanied by strong modifications in the incompatibility system, changes in floral morphology and on the patterns of pollen flow; which in turn, increase the frequency of illegitimate crosses (between different anther levels and styles) and thus producing competition among pollen grains formerly adapted to grow in different style lengths. In this study we evaluated whether pollen size is related with the pollen tube growth rate and if this relationship changes along the tristyly-distyly evolutionary gradient. Preliminary analyses show that there is a positive correlation between pollen size and pollen tube growth rate and length. We also observed modifications in pollen size along this evolutionary gradient that are consistent with the evolution of a distylous phenotype.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy25-i003-R*

Symposium 25
Evolutionary systems biology

Stepping back for a closer look: Classical evolutionary theory drives a systems and computational approach to the aging paradox

Bolt K[1]
[1]Albert Einstein College of Medicine, Systems and Computational Biology, Bronx, United States

Summary statement:

Williams' theory of Antagonistic Pleiotropy inspires a high-throughput analysis of empirical data to offer new insights into the mechanisms and persistence of human aging.

Abstract:

To the disciple of Natural Selection, aging presents itself as a paradox. How does a process that so favors reproductive success and survival overlook a decline in fitness so great as to have death as its endpoint? In 1957, George C. Williams published his theory of Antagonistic Pleiotropy, suggesting that a gene will face positive selective pressure as long as its net effect on fitness is positive. For example, a gene exerting late-acting detrimental effects on fitness would be maintained in the gene pool if it were to also imbue an early-acting, beneficial effect.
Our research implicates the phenomenon now known as alternative splicing as a validating, molecular mechanism for the theory of Antagonistic Pleiotropy. Using alternative transcript data for the human genome, we have examined the prevalence of alternative splicing in aging-related (AR) genes as compared to the remaining human gene set (non-AR genes). We have revealed a significant tendency for AR genes to have higher numbers of splice variants than non-AR genes (p=2.63x10-4). A similar trend has been revealed for degree of pleiotropy (measured as the number functional categorizations) of AR versus non-AR genes (p=4.6x10-113). We now investigate the relationships between splice variants; functional diversity; connectivity; expression; and mutation susceptibility and impact in AR and non-AR gene sets. Examination of these functional and structural characteristics may reveal pervading features exclusive to the otherwise motley collection of AR genes, enabling their identification by characteristic features rather than by mutant models, and substantially hastening our understanding of the aging process.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy25-i004-R*

Symposium 25
Evolutionary systems biology

Plasticity of combination prophylaxis provided by symbiotic streptomycetes in solitary wasps

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Summary statement:

We investigated the plasticity of the defense provided by Streptomycete symbionts of different diggerwasp host species and potential adaptations to environmental conditions.

Abstract:

Female digger wasps of the genera Philanthus and Trachypus (“beewolves”; Hymenoptera, Crabronidae) cultivate symbiotic Streptomyces- bacteria in specialized antennal gland reservoirs. They secrete the symbionts into their subterranean brood cells, where the bacteria are taken up by the larvae and incorporated into their cocoons. On the cocoon, the symbionts produce a mixture of at least nine antibiotic substances, comprising streptochlorin and eight different piericidin derivatives, which significantly reduce the risk of pathogen infestation for the beewolf offspring in the cocoon. Thus, by means of their symbionts, beewolves evolved a strategy that is very similar to the ‘combination prophylaxis’ used in human medicine.
Here, we investigated the plasticity of the defense provided by the symbionts of different host species and potential adaptations to environmental conditions. Using LC-ESI-MS/MS, we analyzed the antibiotic cocktail on cocoons or in female antennae of several beewolf species across a range of different geographic locations. Despite some quantitative variation, the antibiotic blend qualitatively showed a surprisingly high level of conservation across species, suggesting that it provides an efficient defense against pathogens over a wide range of geographic and environmental conditions.

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SUN 21 AUG at 1440 - Room N1
Oral presentation *A3-Sy25-1440-O*

Symposium 25
Evolutionary systems biology

Reverse-engineering the evolutionary and developmental dynamics of the gap gene network

Jaeger J[1]
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Summary statement:

I present an integrative and quantitative study, based on data-driven modeling, of the evolution and developmental function of a developmental gene regulatory network.

Abstract:

Evolutionary developmental biology tries to close the gap between molecular evolution and phenotypic change. This requires a quantitative systems-level understanding of the gene networks underlying development across multiple levels from the molecular to the organismic. Obtaining such an understanding is challenging due to the large number of factors involved. We depend on computational models for this task. I present a reverse-engineering approach, where gene regulatory interactions are inferred from quantitative expression data, using data-driven mathematical models (called gene circuits). Gene circuit models of the gap gene network of Drosophila reproduce observed gene expression with high precision and temporal resolution and reveal a dynamic mechanism for the control of positional

information through shifts of gap gene expression domains. We are extending this approach to a comparative study of the gap gene network between different species of dipterans (flies, midges and mosquitoes). I present preliminary results on data quantification and modeling for gap genes in the scuttle fly Megaselia abdita, and the moth midge Clogmia albipunctata. Our approach yields predictions of how changes of gene regulatory feedback affect the timing and positioning of expression domains. These predictions will be tested experimentally using RNA interference in all three species. No such quantitative systems-level analysis of an evolving gene regulatory network has been achieved to date.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy25-i006-R*

Symposium 25
Evolutionary systems biology

On executable models of molecular evolution

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Summary statement:

We discuss the key characteristics that a standardised framework for evolutionary systems biology should possess in order to be maximally applicable and useful.

Abstract:

Recent years have witnessed an increased interest in addressing questions of molecular evolution using the techniques of systems biology. At the heart of these efforts lies the realisation that the key evolutionary duality between genotype and phenotype is akin to the distinction between a formal model and the outcome of its execution. In other words, a formal model can serve as a proxy for genotype and its execution as a proxy for development, i.e. the determination of phenotype. With reactive computational models used by systems biology one can thus gain insight into the mechanics of development and the causal links between genotype and phenotype, all of which is inaccessible to the established purely mathematical formalisms.

In this presentation, we advocate development of a generic framework for evolutionary systems biology and discuss in some detail the key characteristics it should possess to be maximally applicable and useful. Ideally, it would play a role similar to that which SBML plays in systems biology, enabling the researches to exchange and reuse their models. We argue, among other things, that a framework for evolutionary systems biology should be based on an intermediate molecule-centric specification language and offer multiple execution paradigms for a single model. We offer one such prototype framework ourselves, and evaluate it with a case study of a mitogen-activated protein kinase cascade.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy25-i007-R*

Symposium 25
Evolutionary systems biology

Estimating the fraction of adaptive mutations from mechanistic models

Loewe L[1]
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Summary statement:

An evolutionary systems biology approach to estimating the distribution of adaptive mutational effects

Abstract:

How many advantageous mutations exist? This question is of pivotal importance for understanding evolution and has been the subject of numerous studies in population genetics. Unfortunately, mutations causing large fitness advantages are very rare and mutations with small fitness advantages are extremely difficult to observe in experiments due to experimental noise. Thus recent population genetics work has developed approaches to infer the fraction of adaptive substitutions from DNA sequence data. Results have consistently found that a substantial fraction of substitutions were caused by adaptive mutations, but usually involve assumptions that are often difficult to check. Furthermore, any descriptive approach does not yield any mechanistic insight into why so many advantageous mutations might exist. Here I present a new approach that extends existing systems biology models to include fitness correlates that can then be used for analyzing how many random changes in biochemical reaction rates might lead to an advantageous outcome for the system. Using the circadian clock of the green algae Ostreococcus as an example, I will show that a surprisingly large number of random changes of biochemical reaction rates is advantageous from a mechanistic point of view.

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SUN 21 AUG at 1650 - Room N1
Oral presentation *A4-Sy25-1650-O*

Symposium 25
Evolutionary systems biology

The genetic basis of gene expression divergence between closely related Drosophila species

Meiklejohn CD[1], Coolon JD[2], Hartl DL[3], Wittkopp PJ[2]
[1]University of Rochester, Biology Department, Rochester, United States, [2]University of Michigan, Ecology and Evolutionary Biology, Ann Arbor, United States, [3]Harvard University, Organismic and Evolutionary Biology, Cambridge, United States

Summary statement:

We detect the rapid accumulation between Drosophila species of substantial and largely sexually dimorphic divergence in gene expression due to changes in both cis and trans.

Abstract:

Gene expression is a quantitative and evolutionarily dynamic trait that influences the majority of organismal phenotypes. Understanding the genetic basis of transcriptional divergence between species therefore has the potential to provide insight into basic principles of phenotypic evolution. Using hybrid introgression genotypes of Drosophila simulans in which a small segment of their genome has been replaced with the homologous region from their sister species, D. mauritiana, we examined the effects of interactions between these two species´ genomes on gene expression. From these experiments we estimate that 1/4 to 1/3 of all genes in the genome have acquired cis-regulatory mutations that detectably alter gene expression between these two species. Furthermore, sufficient divergence in trans-regulatory factors has accumulated between these two species that introgression of 5% of the genome from one species to the other detectably influences the expression of hundreds of genes. This suggests that over extremely short evolutionary timescales, there may be sufficient trans-regulatory divergence to account for differential expression of a species´ entire transcriptome. The vast majority of divergent gene regulation in both cis and trans is sexually dimorphic, confirming an important role for sex-specific regulation in the evolution of gene expression. Finally, a large majority of genes differentially expressed in these introgression hybrids are misexpressed when compared to both parental species, suggesting that divergence in gene regulation may be a significant source of hybrid incompatibilities.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy25-i001-E*

Symposium 25
Evolutionary systems biology

The evolution of natural selection

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Summary statement:

Fauceir theory considers natural selection a fauceir and a subject to evolution, too. Principles and outcome are modeled mathematically.

Abstract:

Fauceir theory considers natural selection a fauceir and a subject to evolution, too. Principles and outcome are modeled mathematically.
Natural selection differs depending on a fauceir´s complexity. For instance, while the selection of viruses occurs mainly for single base exchanges that affect antigenic proteins, in bacteria, selection for entire resistance genes is common. Furthermore, in a populations of higher eukaryotes selection affects more complex traits that often involve many genes.
Next, while in bacteria it is entirely possible that a single individual is selected and originates a new colony, in higher eukaryotes individuals are selected statistically, maintaining genetic variability.
A mathematical model characterizes the parameters of such developments and illustrates the cut-off when natural selection in a given fauceir setting peters out. This is when symbiogenesis, the generation of new fauceirs, takes place to revive the impact of natural selection. Such developments are theorized at molecular level [1] and cellular level [2], and anticipated at social level [3].

1. Michael W Gray, Science 330, 920-921.
2. Lynn Margulis, Symbiotic Planet: A New Look At Evolution, (Basic Books, 1999).
3. Nagel M, Current Research Journal of Social Sciences 4, (2010): 255-261.

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SUN 21 AUG at 1500 - Room N1
Oral presentation *A3-Sy25-1500-O*

Symposium 25
Evolutionary systems biology

Novel methods for constructing genotype-phenotype maps from genomic data

Nelson RM[1], Shen X[2], Carlborg Ö[1,2]
[1]Swedish University of Agricultural Sciences, Department of Animal Breeding and Genetics, Uppsala, Sweden, [2]Uppsala University, Uppsala, Sweden

Summary statement:

Genotype-phenotype maps as basis for understanding evolution of epistasis from large-scale genomic data.

Abstract:

The genomics revolution has provided a powerful toolbox for genetic dissection of complex traits. By performing Genome Wide Association Studies (GWAS) with hundreds of thousands of markers in thousands of individuals, researchers aim to identify causal loci and understand the path from genotype to phenotype. Both mapping and explaining trait variation has, however, proven to be more difficult than anticipated. Many of the phenotypic traits and congenital diseases have been under no, or weak selection during our recent evolutionary history. Theory suggests that weak selection could lead to the build-up of complex epistatic networks rather than simple additive gene associations with a phenotype. This means there may be a number of undiscovered epistatic networks governing multiple phenotypes, which cannot be detected by current analysis tools. Classical genetic theory also suggests that the continuous nature of phenotypic variation may lie in epistasis. Using newly developed analysis methods, combined with detailed simulation of genomic data, as well as empirical data, we are able to test multiple genes and construct genotype-phenotype maps as a model free approach to study current and future genomics data. Studying gene variation in context of the rest of the genome provides opportunities to improve our understanding of evolution of molecular networks under weak and strong selection.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy25-i002-E*

Symposium 25
Evolutionary systems biology

Multilocus phylogenetic hypothesis testing in a cryptic species complex: The case of Iberian and North African Podarcis

Pereira C[1], Kaliontzopoulou A[1,2], Rocha S[1,3], Carretero MA[1], Harris DJ[1], Pinho C[1]
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Summary statement:

Using a multilocus approach, we reconstruct the species tree of a lizard cryptic species complex and discuss the implications to the study of speciation in this system.

Abstract:

Reconstructing phylogenetic relationships in cryptic species complexes tend to be a challenging task, since the discrimination of evolutionary entities based on morphological traits is always problematic. Moreover, given the typical recent nature of the divergence process, incomplete lineage sorting and gene flow may lead to incongruence among loci, providing limited views on both phylogeny and speciation scenarios, when only few markers are considered.

Iberian and North African Podarcis wall lizards are subject to all these difficulties, and therefore constitute a striking example of how intricate the study of speciation processes can be. Previous works using not only mitochondrial DNA (mtDNA) but also some nuclear markers were not enough to clarify the controversial relationships within this clade.

Here, we aim to provide new insights about the evolutionary dynamics of Iberian and North African Podarcis, through an exhaustive nuclear multilocus approach. To do so, sequence data for twenty nuclear markers was collected from individuals representing all known mtDNA lineages and further analysed using state of the art species tree reconstruction tools. Additionally, we tried to unravel the relative influence of incomplete lineage sorting and gene flow in the clade's history.

Our results illustrate the phylogenetic complexity underlying the evolutionary lineages within the Iberian and North African Podarcis species complex, highlighting the puzzle of approximating species trees in contexts where both historical isolation and gene flow seem to have been important factors.

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SUN 21 AUG at 1400 - Room N1
Invited talk *A3-Sy25-1400-I*

Symposium 25
Evolutionary systems biology

Using computational models to explore and leverage biochemical networks

Reed JL[1,2]
[1]University of Wisconsin-Madison, Madison, United States, [2]Great Lakes Bioenergy Research Center, Madison, United States

Summary statement:

Models can be used to predict cellular phenotypes and model-data discrepancies can be used to improve them. These models can also be used to design strains with desired phenotypes.

Abstract:

Integrated genome-scale models of metabolism and transcriptional regulation can be used to predict cellular phenotypes. Model development is currently a challenge since computational methods that automate the refinement of such integrated models are not available. We recently developed an algorithm, GeneForce, which pinpoints what model aspects cause incorrect predictions. We used the approach to refine integrated models of Escherichia coli metabolism and regulation, and experimentally confirmed some of the suggested refinements. After making the model refinements the model’s accuracy improved to (~80.0%) when comparing predictions to over 50,000 measured phenotypes. We believe that this general computational approach will enable the rapid development of integrated genome-scale metabolic and regulatory network models. Since such models can be constructed from genome annotations and cis-regulatory network predictions, they can be developed for less characterized microorganisms. Once accurate integrated metabolic and regulatory models are constructed, our recently developed computational methods can be used to propose metabolic engineering strategies to improve chemical production using these models. The genetic strategies identified can include deletion of transcription factors and metabolic genes, as well as over expression of metabolic genes. Using this approach we have identified strategies for improving chemical production by E. coli. Together approaches can be applied to improve our understanding of metabolism and regulation in microbial organisms and to improve production of a wide variety of compounds through modification of metabolic and regulatory networks.

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SUN 21 AUG at 1710 - Room N1
Oral presentation *A4-Sy25-1710-O*

Symposium 25
Evolutionary systems biology

Genetic variability in primary metabolism genes of Arabidopsis accessions

Schwarte S[1], Stange M[1], Wegner F[1], Brust H[2], Steup M[2], Tiedemann R[1]
[1]University of Potsdam, Evolutionary Biology, Potsdam, Germany, [2]University of Potsdam, Plant Physiology, Potsdam, Germany

Summary statement:

The analysis of primary metabolism genes revealed a nucleotide diversity similar to already investigated genes of secondary metabolism among accessions.

Abstract:

Primary metabolism has been defined as those essential reactions involving compounds that are formed as part of the normal anabolic and catabolic processes, i.e., assimilation, respiration, transport, and differentiation. Due to their essential function, genes involved in primary metabolism have been assumed to be more conserved than secondary metabolism genes. Most investigations of intraspecific variability among accessions of A. thaliana were performed on secondary metabolism genes. We could demonstrate that some genes involved in primary metabolism exhibit similar sequence variation among accessions. In general, genes where alleles separate out into two or more groups have higher nucleotide diversities than genes with only singleton polymorphisms. Here, two or more distinct evolutionary lineages are maintained in the species, presumably by disruptive selection.

For an increasing number of A. thaliana accessions, full genomes become accessible. However, our gene-specific approach frequently reveals additional genetic variation not reported in freely available genome-wide data sets. This becomes particularily apparent with regard to rearrangements in the genomic structure of gene families. As an example, within the Rubisco small subunit family, we just recently revealed that rbcS-1b was lost, while rbcS-2b was duplicated in some accessions. This phenomen had gone undetected in previous genome-wide analyses.

Funding is acknowledged from the German Federal Ministry of Research (BMBF, Grant Number: 313924) within the GoFORSYS systems biology initiative.

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SUN 21 AUG at 1630 - Room N1
Oral presentation ***A4-Sy25-1630-O***

Symposium 25
Evolutionary systems biology

Molecular evolution of stochastic switching

Soyer OS[1], Kuwahara H[2]
[1]University of Exeter, Systems Biology, Exeter, United Kingdom, [2]Carnegie Mellon University, Ray and Stephanie Lane Center for Computational Biology, Pittsburgh, United States

Summary statement:

Bistability and stochastic switching in a gene regulatory network emerge as a byproduct of evolution of evolvability under fluctuating selection

Abstract:

While fitness benefits of phenotypic variance (i.e. stochastic switching) under fluctuating environments has been shown both experimentally and theoretically, it is not well understood if fluctuating environments can result in incremental evolution of molecular mechanisms that underpin this phenomena. A potential molecular mechanism that can lead to stochastic switching is noisy bistable dynamics in gene regulation. In this talk, I will summarise results from an in silico evolution study where we have simulated molecular evolution of a simple regulatory network consisting of a single gene under fluctuating selection on gene expression levels. We find that the main outcome of fluctuating selection is the evolution of increased evolvability in the network; system parameters evolve towards a nonlinear regime where small changes cause large changes in expression level. In contrast to this broad observation of increased evolvability, we find that bistability evolves only under environments with specific type of fluctuations and in presence of noise. We find that both evolvability and bistability evolve only in a range of specific environmental fluctuation rates, however, once evolved they are maintained under a broader range of rates. These results provide the first direct evidence that bistability and stochastic switching in a gene regulatory network can emerge as a mechanism to cope with fluctuating environments.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy25-i008-R*

Symposium 25
Evolutionary systems biology

Genetic variability of Calvin cycle genes in accessions of Arabidopsis accessions

Stange M[1], Schwarte S[1], Wegner F[1], Grodzicki S[1], Tiedemann R[1]
[1]University of Potsdam, Evolutionary Biology, Potsdam, Germany

Summary statement:

The analysis of starch metabolism genes revealed a remarkable number of nonsynonymous substitutions in functional domains of respective proteins.

Abstract:

The Calvin cycle is the essential pathway for carbon fixation in green plants and belongs to primary metabolism. 14 genes coding for 11 enzymes which catalyze 13 reactions in the Calvin cycle, additional two genes which encode for regulatory enzymes, were chosen for research on genetic variation. We investigated 26 A. thaliana accessions with respect to the number of substitutions, nucleotide diversity, and haplotype diversity in different functional domains. The nucleotide diversity of all analyzed genes ranges within the level of nucleotide variation found in genes of secondary metabolism, as for example phenylproponoid pathway genes. Several polymorphisms were detected in functional relevant regions. Using straightforward physical and comparative considerations for the prediction of possible impact of an amino acid substitution on the structure and function of a protein, some of these polymorphisms found in coding regions were predicted to have possibly or probably implications on protein structure and hence on protein function. In addition, we tested which kind of selection acts on Calvin cycle genes. A one-tailed Z-test fails to reject the null hypothesis of neutral evolution for 5 genes. The remaining 11 genes are under purifying selection. A Tajima’s D test supports the findings of the Z-test. In general, all genes underlie different pressures of selection, which lead to different tolerance towards SNPs in coding regions, although all genes are essential in this primary pathway.
Funding is acknowledged from the German Federal Ministry of Research (BMBF) within the GoFORSYS systems biology initiative.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy25-i004-E*

Symposium 25
Evolutionary systems biology

Ecological factors and phylogenetic assembly of plant communities in three landscape units in Central Amazonia

Umaña MN[1], Norden N[1], Cano A[1], Stevenson PR[1]
[1]Universidad de los Andes, Biological Sciences, Bogotá, Colombia

Summary statement:

To better understand plant distribution patterns is highly relevant to take into account the existence of different forest types across the Amazonia.

Abstract:

The Amazon harbours one of the richest ecosystems on earth and is composed by a mosaic of heterogeneous forests, structured by multiple ecological and historical processes. However, we do not fully understand the relative contribution of these components. We evaluated patterns of phylogenetic structure and variability in abiotic factors to determine how the ecological and evolutionary processes shape plant community assembly in three types of forest: hills and terraces in terra firme and flooded forest. We established two 1-ha plots at each forest type in the Caparú Biological Station, Colombia, and we measured edaphic, topographic and light variables. Floristic composition showed important differentiation among forest types, particularly between terra firme and flooded forests. Edaphic variables were strongly associated with such differentiation supporting the prevalence niche-based processes over neutral ones. In terms of phylogenetic structure, Igapó, showed significant phylogenetic clustering, whereas the terra firme forests showed phylogenetic overdispersion, suggesting that habitat filtering processes govern the stressful flooded communities, and competition seems more important in terra firme. We conclude that Amazonian plant assemblages are highly dependent on ecological factors, mainly under stressful conditions, and stochastic processes play significant roles when the environment is not stressful. For this reason Amazonia have to be considerate as a mosaic of forest assembled by different processes.

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SUN 21 AUG at 1550 - Room N1
Invited talk *A4-Sy25-1550-I*

Symposium 25
Evolutionary systems biology

The origins of evolutionary innovations

Wagner A[1]
[1]University of Zurich, Inst. of Evolutionary Biology and Environmental Studies, Zurich, Switzerland

Summary statement:

A synthetic view of evolutionary innovation in different classes of systems where epistasis plays an important role in genotypic change.

Abstract:

Life can be viewed as a four billion year long history of innovations. These range from dramatic macroscopic innovations like the evolution of wings or eyes, to a myriad molecular changes that form the basis of macroscopic innovations. We know many examples of innovations -- qualitatively new phenotypes that can provide a critical advantage in the right environment -- but have no systematic understanding of the principles that allow organisms to innovate. Most phenotypic innovations result from changes in three classes of systems: metabolic networks, regulatory circuits, and protein or RNA molecules. I will discuss evidence that these classes of systems share two important features that involve epistasis, and that are essential for their ability to innovate.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy25-i009-R*

Symposium 25
Evolutionary systems biology

The evolution of a signal: Silken web decorations in orb web spiders

Walter A[1], Elgar MA[1]
[1]University of Melbourne, Zoology, Parkville, Australia

Summary statement:

Many hypotheses address the maintenance of web decoration in orb web spiders without explaining its evolutionary origin. Thus, we provide model of the evolutionary progression.

Abstract:

Contemporary animal signals may derive from an elaboration of previous forms or may be an innovation. Unravelling the evolution of the latter is challenging because the signalling effect may have evolved from a non-signalling biological trait. The web decorating behaviour of orb web spiders represents an intriguing model system to investigate innovative signals. For over 100 years, biologists have struggled to explain why spiders decorate their webs with additional threads of silk, paradoxically producing a conspicuous signal on a construction whose function is to entangle unsuspecting prey. The numerous explanations for the maintenance of this behaviour starkly contrast with the absence of a plausible explanation for its evolutionary origin. Our review of web decorating behaviour highlights the difficulties in discriminating between the evolution and maintenance of animal signalling, and inferring the causative arrow – even from experimental studies. Drawing on recent research that focuses on physiological processes, we provide a novel model of the evolutionary progression of web decorating behaviour.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy25-i010-R*

Symposium 25
Evolutionary systems biology

Genetic variation in starch metabolism genes of Arabidopsis accessions

Wegner F[1], Schwarte S[1], Brust H[2], Steup M[2], Tiedemann R[1]
[1]University of Potsdam, Evolutionary Biology, Potsdam, Germany, [2]University of Potsdam, Plant Physiology, Potsdam, Germany

Summary statement:

The analysis of starch metabolism genes revealed a remarkable number of nonsynonymous substitutions in functional domains of respective proteins.

Abstract:

Starch is the most abundant storage carbohydrate in photoautotrophic eukaryots. It enables the organisms to sustain metabolism and growth during those periods that are unfavorable for photosynthesis. In higher plants, starch is formed as water-insoluble particles in the stroma of plastids and consists of two types of high molecular weight homoglucans, i.e., amylopectin and amylose. The metabolism of native starch requires the cooperation of 30 to 40 distinct (iso)enzyme activities. We sequenced a number of gene family members of ADP-glucose pyrophosphorylase (AGPase: APL1-4, APS1,2), inorganic pyrophosphorylase (siPPiase: PPA1-6), starch synthase (SS1-4, GBSS), branching enzyme (BE1-3), debranching enzyme (ISA1-3), and glucan phosphorylase (PHS1,2) of 30 worldwide distributed accessions of Arabidopsis thaliana. A remarkable number of substitutions were found in the coding sequence of each gene. We identified amino acid substitutions in catalytic domains and discuss possible implications on the protein level. For some genes, two distinct groups of haplotypes were detected. Single gene trees are, however, neither congruent nor do they follow any evident geographic or ecological pattern. We discuss this phenomenon in the light of natural selection and recombination across accessions.
Funding is acknowledged from the German Federal Ministry of Research (BMBF) within the GoFORSYS systems biology initiative.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy25-i005-E*

Symposium 25
Evolutionary systems biology

Phylogeographic patterns and investigation of hybrid zones in sympatric populations of Vriesea carinata and V. incurvata (Bromeliaceae) in the Brazilian Atlantic Rainforest

Zanella CM[1], Goetze M[1], Pinheiro FG[1], Buttow MV[1], Palma-Silva C[2], Bered F[1]
[1]UFRGS, Genetics, Porto Alegre, Brazil, [2]Intituto de Botânica, São Paulo, Brazil

Summary statement:

We are interested in identification of possible hybrid zones between V. carinata and V. incurvata and in investigating the extend of inter-specific gene flow.

Abstract:

Vriesea carinata and V. incurvata are two bromeliad species of the Tillandsioideae subfamily (Bromeliaceae) with high ornamental appeal, suffering impacts with the illegal extraction. Both species are distributed along the Brazilian Atlantic Rainforest, with populations occurring in sympatry. These bromeliads showed a sequential flowering along the year, with a short period of flowering overlap, and share the same floral visitor; both were pollinated by hummingbirds (Phaethornis eurynome). We are interested in identification of possible hybrid zones between V. carinata and V. incurvata since individuals with intermediate morphologies were found in wild populations of these species, and in investigating the extend of inter-specific gene flow. A phylogeographic approach and aspects of population genetics will be also evaluated. We sampled 582 individuals from ten sympatric and six allopatric populations across the geographical range of both species along Brazilian Atlantic Rainforest. To test the strength of their reproductive barriers, a combined data set of nuclear and chloroplast microsatellites will be used. Until now we have tested 26 microsatellite loci developed for species of bromeliads and suitable amplification were obtained in nine nuclear and four plastid loci in both species. The results achieved will help to elucidate evolutionary process of these species and will be of great importance in understanding reproductive barriers, introgression and speciation processes in Neotropical species.

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Symposium 26

Parallel evolution

Talks: *Room N7*

Essence posters: Ground floor lecture hall centre *HZ*

Regular posters: Ground floor campus canteen *Mensa*

Invited Speakers:

Hopi E Hoekstra, Louis Bernatchez

Organizers:

Walter Salzburger, Moritz Muschick

Description:

Parallel evolution is the emergence of the similar phenotypes in independent lineages. The evolution of parallel (or convergent) morphologies can be a response to similar selection pressures. Alternatively, developmental or genetic constraints could lead to convergence. This symposium focuses on the genetic and developmental basis as well as on the ecological circumstances of parallel evolution.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

WED 24 AUG at 1200 - Room N7
Oral presentation *D2-Sy26-1200-O*

Symposium 26
Parallel evolution

Catching convergent evolution in the act? Different mutant wing morphologies in two populations of crickets have the same phenotypic effect in both: loss of song

Bailey NW[1]
[1]University of St Andrews, School of Biology, St Andrews, United Kingdom

Summary statement:

I present a morphometric analysis of a wing mutation occurring in different populations of field crickets, with the aim of testing a scenario of rapid, convergent evolution.

Abstract:

Studies of convergent evolution often rely on inferences made from sequence data and reconstruction of historical character states, and documenting this phenomenon in real-time, in the wild, is challenging. I will discuss evidence for rapid convergent evolution in wing morphology in the cricket Teleogryllus oceanicus. These crickets range across the Hawaiian archipelago, and in 2003 a mutation that eliminates sound-producing structures on male wings arose and spread on the island of Kauai. The mutation is likely maintained because of the presence of acoustically-orienting parasitoid flies on the Hawaiian islands. However, it is now present on two different islands with similar ecological conditions, which affords an opportunity to test whether it arose once and spread, or whether it has arisen independently on separate islands. I will present evidence that the wing morphologies of mutant males from the two islands are different, even though all mutant males experience the same loss-of-function which protects them from attack by the parasitoid fly. This surprising result suggests that different genetic mechanisms may be involved, or that epistatic interactions produce different phenotypes when the mutation is expressed in different genomic backgrounds. I will discuss the results in the context of what is known about the genetic architecture of the wing mutations, focusing on how this system can be used to distinguish different types of homoplasy with a resolution that has been difficult to achieve previously.

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WED 24 AUG at 1010 - Room N7
Oral presentation ***D1-Sy26-1010-O***

Symposium 26
Parallel evolution

Parallel evolution in Neotropical crater lake cichlids

Barluenga M[1], Muschick M[2], Salzburger W[2], Harrod C[3], Meyer A[4]
[1]Museo Nacional de Ciencias Naturales CSIC, Dept. Biodiversity and Evolutionary Biology, Madrid, Spain, [2]University of Basel, Zoological Institute, Basel, Switzerland, [3]Queen's University Belfast, Belfast, United Kingdom, [4]University of Konstanz, Konstanz, Germany

Summary statement:

Evolution repeating itself - cichlid fishes

Abstract:

Evolution sometimes repeats itself producing the same phenotypic adaptations in independent lineages exposed to similar environmental conditions. These striking examples of parallel evolution emphasize the central role of natural selection in speciation, but also support the notion of a deterministic, predictability to evolution. A classic textbook example of parallel evolution are cichlid fishes of the East African Great Lakes Tanganyika and Malawi, where remarkably similar trophic morphologies and coloration types have evolved from different founder lineages within a few million years. Here we report a striking case of parallel speciation in small volcanic crater lakes in Nicaragua, Central America, over a period of no more than just a few thousand years. Several ecologically and morphologically equivalent species of Midas cichlids (Amphilophus spp.) have evolved independently in several Nicaraguan crater lakes. Moreover, the speciation events follow the exact same succession in independent radiations, adaptations to alternative lake regions occurring first and specializations to alternative trophic resources within habitats happening only later. Natural selection through ecological specialization to newly available niches is the likely force driving sequential parallel ecological speciation in crater lake cichlid fishes.

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TUE 23 AUG at 1550 - Room N7
Invited talk *C4-Sy26-1550-I*

Symposium 26
Parallel evolution

Testing for differential extent of parallelism in phenotypic, transcriptomic and gene variation in sympatric whitefish species pairs (Coregonus sp.)

Bernatchez L[1]
[1]Université Laval, Biologie, Québec, Canada

Summary statement:

I will test the general hypothesis that parallelism should be more pronounced at the phenotypic than at the gene polymorphism level, with gene expression being intermediate.

Abstract:

Parallel evolution is considered as one of the hallmarks of natural selection, which is predicted to drive the evolution of similar phenotypes under similar selective regimes. In contrary, it is widely accepted that stochastic processes such as genetic drift are unlikely to cause the independent evolution of similar phenotypes. Recent studies have also investigated the occurrence of parallelism to the level of both gene polymorphism and expression, which provided mixed evidence at these functional levels. In this talk, I will revisit data and present new results pertaining to our research program on the ecological speciation of whitefish (Coregonus sp.) in order to test the general hypothesis that, since phenotypes represent the ultimate integrated target of selection, parallelism should be expected to be more pronounced at this functional level than at the gene polymorphism level, with gene expression being intermediate. Such differential pattern of parallelism would also be in line with Lynch's (2007) hypothesis that convergent (or parallel) phenotypic evolution can result from non-adaptive shaping of genome architecture in independently evolved lineages.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy26-i001-R*

Symposium 26
Parallel evolution

In what sense QTL are context-dependent and in what sense not: Replication of genetic effects on mandible shape between a Chromosome Substitution Strain (CSS) panel and a QTL study

Boell LA[1], Forejt J[2], Gregorova S[2], Tautz D[1]
[1]Max-Planck-Institute for Evolutionary Biology, Plön, Germany, [2]Institute of Molecular Genetics, Academy of Sciences of the Czech Republic, Department of Mouse Molecular Genetics, Prague, Czech Republic

Summary statement:

Relative genetic effect sizes on mouse mandible shape are replicated between a CSS panel and a QTL study, but epistasis may modulate the direction of QTL effects.

Abstract:

The mouse (Mus musculus) mandible has been much investigated as a paradigm for the genetic architecture and evolution of shape. An advantage of shape over univariate traits in studies of genetic architecture is that effects on shape have not only a magnitude, but also a direction in multivariate space. This makes them attractive as paradigms of organism´s structural complexity. Furthermore, mandible shape has been found to have a complex multigenic genetic architecture in numerous QTL mapping studies.

Is parallel evolution, i.e. implication of the same genes in independent instances of evolutionary change, to be expected for such a complex phenotype?

Using a CSS panel, we analyze the genetic effects of PWD (M. m. musculus) chromosomes in a C57BL/6J (M. m. domesticus) background on mandible shape and compare them to the results of a previously published QTL mapping study (Klingenberg et al. 2004) describing variation within M. m. domesticus.

We find that the distribution of genetic effects across the genome is consistent between the studies (implying involvement of the same loci), while the specific shape changes associated with the chromosomes seem to be different. Furthermore, our results imply pervasive epistasis in the genetic architecture of shape.

Thus, the same loci might contribute to evolutionary change of the same anatomical structure in different directions. To make this possible may constitute one aspect of the evolutionary importance of epistasis.

Klingenberg, C. P., Leamy, L. J., Cheverud, J. M. (2004): Integration and modularity of quantitative trait locus effects on geometric shape in the mouse mandible. Genetics 166: 1909-1921.

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TUE 23 AUG at 1710 - Room N7
Oral presentation *C4-Sy26-1710-O*

Symposium 26
Parallel evolution

Selecting for Giants: Genetic dissection of an adaptive complex trait in laboratory and wild mice

Chan YF[1], Bünger L[2], Tautz D[1]
[1]Max Planck Institute for Evolutionary Biology, Department of Evolutionary Genetics, Ploen, Germany, [2]Scottish Agricultural College, Animal Breeding and Development Team, Midlothian, United Kingdom

Summary statement:

Using parallel longterm selection and haplotype association, this study achieves high-resolution identification of a large number of orchestrator genes with pleiotropic effects.

Abstract:

Adaptation underlies much evolutionary diversity. Yet, we know little about the genetic architecture underlying adaptation. We used growth as a model complex trait to ask, how repeatable is genetic adaptation? Is body size controlled by many loci of infinitesimal effects? Or by few loci of large effects? Gigantism in house mouse represents an ideal system: it occurs repeatedly during island colonisation and can be readily mimicked by artificial selection. Using seven pairs of long-term selection lines, here we conduct a specialized form of association mapping we call “parallel association”. We have identified 67 loci (FDR 0.01) broadly distributed across the genome showing allele-sharing across high body weight selected lines, yet rare or missing among their sibling control or low body weight lines. To confirm these regions, we also genotyped one longterm selection experiment at different time intervals to detect allele frequency change through time. Consistent with adaptation, these regions show characteristic evidence for selective sweeps. Mapping resolution achieved by parallel association compares favorably with conventional QTL mapping, often achieving sub-megabase resolution. Although numerous, these loci show strong clustering and contain genes regulating growth and metabolic pathways, suggesting that clusters of favorable alleles of orchestrator genes may be repeatedly involved in adaptation. By applying these loci to an independent mouse dataset, we are able to predict body weight with >90% accuracy. These results show that adaptive strategies may rely broadly on standing variations and adaptive evolution may proceed through many loci of significant effects.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy26-i002-R*

Symposium 26
Parallel evolution

Removal of selection pressure leads to convergent male behavior in Caenorhabditis

Chang AS[1], Rockman MV[1]
[1]New York University, Biology/ Genomics and Systems Biology, New York, United States

Summary statement:

The availability of an alternative mating system and genetic tools makes the C. elegans species group an ideal model for examining the genetic basis of convergent evolution.

Abstract:

Selection on male traits that assure paternity is thought to be prevalent in gonochoristic species. The removal of male-specific selection should lead to decreased efficiency in mate searching and/or copulation. Whether particular behavioral phenotypes are especially susceptible to breakdown is unknown. The C. elegans species group offers a unique opportunity to examine how lack of selection on males affects phenotypes in multiple lineages. While most species within the group are gonochoristic, hermaphroditism has evolved independently multiple times. In hermaphroditic species, males occur at very low frequencies and are rarely found in nature and hermaphrodites are primarily self-fertilizing; thus selection on male traits is presumably largely absent.
Caenorhabditis males typically deposit a copulatory plug over the vulvae of their mates upon completion of sperm transfer. However, in a strain of the hermaphroditic species C. elegans, males frequently deposit the plug over the excretory pore of other males when hermaphrodites are absent. This “head plugging” behavior is possibly a consequence of relaxed selection on male function. Here, we survey the prevalence of mis-plugging behavior in multiple strains and species and show that it has evolved multiple times only in the hermaphroditic species. Additionally, we map the genomic region responsible for head-plugging behavior in C. elegans to a single locus on chromosome II. Using these results and a combination of transgenics and next-generation sequencing, we will be able to determine whether breakdown in the same genetic pathways has generated convergent behavioral phenotypes in multiple lineages.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy26-i003-R*

Symposium 26
Parallel evolution

Intercontinental parallel evolution: Two cichlid species with hypertrophied lips

Colombo MG[1], Muschick M[1], Diepeveen E[1], Salzburger W[1]
[1]University of Basel, Zoological Institute, Basel, Switzerland

Summary statement:

Studied a intercontinental parallel evolution scenario using morphometrics (pharyngealjaws and body),stomach content analyses and population genetics.

Abstract:

Parallel evolution provides natural replicates of trait evolution and is, therefore, an exciting field within evolutionary biology. Although cichlids are very diverse, there are examples of convergence between and even within lake radiations. A textbook example is the recurrent evolution of body shapes and colorations found in the cichlid species flocks of the Great Lakes of East Africa. Less attention has been paid to the intercontinental parallel evolution of cichlid fishes, involving species from Central America and East Africa. These clades got separated 110-130 million years ago when the supercontinent Gondwana broke apart.
In our project, we investigate the possible parallel evolution between a Central American crater lake cichlid species, Amphilophus labiatus, found in Nicaragua and a species from the East African Lake Tanganyika, Lobochilotes labiatus. These two species share an eye-catching feature: both have big, fleshy, hypertrophied lips, a remarkable feature that distinguishes them from other cichlid species found in the same habitat. We assume that these lips are an adaptation to their feeding behaviour since we found that both species prey on hard shelled food.
We analysed the lower pharyngeal jaws and the body shape of the fish using geometric morphometrics, conducted stomach content analyses and used nuclear genetic loci to perform population genetic analyses.
Furthermore, we analysed RNA extracted from the lips of L. labiatus. Using Solexa sequencing of cDNA, we tried to reveal the genetic basis of hypertrophism in these lips by comparing the lip-tissue specific gene expression of L. labiatus with that of a small-lipped relative, Astatotilapia burtoni.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy26-i004-R*

Symposium 26
Parallel evolution

Comparative analysis and differential gene expression of multiple reproductive strategies of Lake Tanganyika lamprologine cichlids

De Maddalena J[1], Gante H[1], Salzburger W[1]
[1]University of Basel, Zoological Institute, Basel, Switzerland

Summary statement:

Analysis of number of origins of different reproductive behaviours in cichlids and quantification of expression levels of genes possibly involved in changes of egg adhesiveness.

Abstract:

The impressive diversity of cichlid fish assemblages in the Great East African Lakes is a textbook example of adaptive radiation, among which the lamprologines are the major substrate-breeding tribe in Lake Tanganyika. Lamprologines show several reproductive strategies, such as the peculiar adaptation to live and breed in empty gastropod shells, or in tunnels built in mudflats, allowing these species to colonize multiple new habitats. Furthermore, distinct levels of egg adhesiveness are observed across these reproductive strategies, reflecting the nature of breeding substrate.
We investigate how many times the different reproductive behaviours arose in the evolution of Tanganyikan lamprologines, based on phylogenies generated from multiple nuclear loci. To understand how differences in egg adhesiveness are achieved, quantification of differences in gene expression among adhesive and non-adhesive eggs is examined following a candidate gene approach using quantitative real time polymerase chain reaction.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy26-i005-R*

Symposium 26
Parallel evolution

Global analysis of genes involved in freshwater adaptation in threespine sticklebacks (Gasterosteus aculeatus)

DeFaveri J[1], Shikano T[1], Shimada Y[1], Goto A[2], Merilä J[1]
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Summary statement:

The results conform to the view that evolutionary adaptation to similar challenges posed by the environment can be achieved through multiple genetic pathways.

Abstract:

Examples of parallel evolution of phenotypic traits have been repeatedly demonstrated in threespine sticklebacks (Gasterosteus aculeatus) across their global distribution. Using these as a model, we performed a targeted genome scan – focusing on physiologically important genes potentially related to freshwater adaptation – to identify genetic signatures of parallel physiological evolution on a global scale. To this end, 50 microsatellite loci, including 26 loci within or close to (< 6 kb) physiologically important genes, were screened in paired marine and freshwater populations from six locations across the Northern Hemisphere. Signatures of directional selection were detected in 24 loci, including 17 physiologically important genes, in at least one location. While no loci showed consistent signatures of selection in all divergent population pairs, several outliers were common in multiple locations. In particular, seven physiologically important genes, as well as reference ectodysplasin gene (EDA), showed signatures of selection in three or more locations. Hence, while these results give some evidence for consistent parallel molecular evolution in response to freshwater colonization, they suggest that different evolutionary pathways may underlie physiological adaptation to freshwater habitats within the global distribution of the threespine stickleback.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy26-i006-R*

Symposium 26
Parallel evolution

Use it or lose it: Parallel loss of an essential metabolic trait in parasitic insects

Ellers J[1], Visser B[1], Le Lann C[1], Harvey J[2], van Alphen J[3]
[1]VU University, Amsterdam, Netherlands, [2]NIOO, Heteren, Netherlands, [3]Universite de Rennes, Rennes, France

Summary statement:

Lipid synthesis has repeatedly been lost in the evolution of insect parasitoids. We present ecological correlates and underlying molecular mechanisms of this parallel evolution.

Abstract:

Evolutionary loss of traits can result from negative selection on a specific phenotype, or because the phenotype associated with the trait has become redundant. Even essential traits may be lost if the resulting phenotypic deficiencies can be compensated for by the environment or a symbiotic partner. In parasitoids, a large number of species have lost the ability to biosynthesize lipids. We test the hypothesis that lack of lipogenesis in insect parasitoids is a case of parallel evolution of compensated trait loss, and we study the underlying ecological, molecular and physiological mechanisms. Phylogenetic analyses of more than 70 species, showed that lack of lipogenesis has evolved independently four times within the insects, and is concurrent with the evolution of parasitism in insects. Parasitoid larvae live inside their host and can manipulate their host's physiology to increase lipid availability, which presumably facilitates redundancy of traits that are involved in lipid production. Gene expression profiling showed downregulation of key enzymes involved in lipid synthesis. Furthermore, parasitoids that were fed isotope-labelled intermediate compounds of the lipid pathway did not show incorporation of the label into body lipids, indicating that the lack of lipogenesis is caused by a mutation upstream in the lipid synthesis pathway.
We conclude that trait loss through environmental compensation is often unnoticed at the phenotypic level, therefore it may be more common than currently anticipated, especially in species involved in intricate symbiotic relationships with other species.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy26-i007-R*

Symposium 26
Parallel evolution

Shared environment in a host-parasite relationship leads to adaptive evolution of immune system genes

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Summary statement:

Host- and cuckoo-bumble bees share substitution patterns in immune system genes indicating parallel evolution caused by a shared environment.

Abstract:

Coevolutionary arms races between host and parasite seem to be one of the driving forces in evolution. Species sharing the same microhabitat and being exposed to the same microbiome might adapt their defense mechanisms in a similar way – by parallel or convergent evolution. In order to test this form of adaptive evolution a suitable test system is needed fulfilling several criteria: 1) exposition to the same microhabitat, 2) decoupling of relatedness from co-occurrence and 3) a suitable phenotype.

We have chosen a test system that fulfills these criteria – bumble bees and their socially parasitic cuckoo bumble bees. The latter form a monophyletic group within the bumble bees whereas their hosts are scattered throughout the tree. The relationship between host and parasite is specific with every cuckoo bumble bee being specialized on a certain host species sharing a nest site and thus both being exposed to the same microbiome.

We sequenced 3 antimicrobial peptide genes (abaecin, hymenoptaecin, defensin), all being effector genes of the innate immune system, in 6 couples of bumble bee host and the respective cuckoo bumble bee species. We took advantage of the haplo-diploid system of hymenopteran insects using haploid males for sequencing.

All immune genes evolved at higher rates compared to 4 non-immune genes. Highest variability was found for defensin and hymenoptaecin. Reconstruction of ancestral amino acids for variable sites revealed parallel evolution to occur in certain species pairs of host and parasite. This in turn shows that the shared environment can have a strong impact on the selective pressure on parts of the genome like the immune system.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy26-i008-R*

Symposium 26
Parallel evolution

Rapid evolution of fire melanism in replicated populations of pygmy grasshoppers

Forsman A[1], Karlsson M[1], Wennersten L[1], Johansson J[1], Karpestam E[1]
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Summary statement:

We demonstrate rapid and parallel shifts in colour morph frequencies in response to divergent and fluctuating selection associated with spatiotemporal environmental changes.

Abstract:

Evolutionary theory predicts an interactive process whereby spatiotemporal environmental heterogeneity will maintain genetic variation, while genetic and phenotypic diversity will buffer populations against stress and allow for fast adaptive evolution in rapidly changing environments. Here we study colour polymorphism patterns in pygmy grasshoppers (Tetrix subulata) and show that the frequency of the melanic (black) colour variant was higher in areas that had been ravaged by fires the previous year than in non-burned habitats, that, in burned areas, the frequency of melanic grasshoppers dropped from ca. 50% one year after a fire to 30% after four years, and that the variation in frequencies of melanic individuals among and within populations were genetically based and represented evolutionary modifications. Dark coloration may confer a selective benefit mediated by enhanced camouflage in recently fire-ravaged areas characterized by blackened visual backgrounds before vegetation has recovered. These findings provide rare evidence for unusually large, extremely rapid adaptive contemporary evolution in replicated natural populations in response to divergent and fluctuating selection associated with spatiotemporal environmental changes.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy26-i009-R*

Symposium 26
Parallel evolution

Parallel evolution vs. introgression at wing pattern loci in mimetic Heliconius butterflies

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Summary statement:

We investigate the introgression of adaptive alleles to promote adaptive morphological evolution as a possible mechanism involved in the parallel evolution in Heliconius mimicry.

Abstract:

Heliconius are Amazonian butterflies that are unpalatable and exhibit warning wing coloration and patterns learned by predators. Heliconius butterflies have undergone rapid speciation (adaptive radiation), but show spectacular convergence in wing pattern due to mimicry between species. Although most species only display one mimetic pattern locally, Heliconius numata (H.n.) species shows up to seven discrete wing colour patterns segregating in a single locality. Each morph is a precise mimic of local species and races of Melinaea butterflies (Nymphalidae: Ithomiinae). Other closely related Heliconius species also join those mimicry rings. Specifically, the morphs H. n. tarapotensis and H. n. aurora have similar patterns as those of H. pardalinus sergestus and butleri, respectively, with which they are sympatric. In contrast, the morph H. n. silvana is distinct of any other Heliconius species in sympatry, but resembles the pattern of its sister species H. ismenius. In H. numata, wing pattern variation is entirely controlled by one single supergene, P. With a comparative phylogenetic approach for markers at the colour-pattern-determining locus (P), and genes in flanking regions or scattered around the genome, we investigated the evolutionary history of mimicry within the Heliconius species history. We examined the importance of introgression of adaptive alleles from the genomes of co-mimics to promote adaptive morphological evolution (mimicry), as a possible mechanism involved in the widespread parallel evolution in Heliconius mimicry.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy26-i001-E*

Symposium 26
Parallel evolution

Morphological evolution of male genitalia in Tephritoidea and Nothyboidea

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Summary statement:

Family structure of Tephritoid flies and Nothyboid flies was specified more exactly by studying morphological evolution of genitalia.

Abstract:

Tephritoidea and Nothyboidea are considered to be sister groups. We reviewed genitalia of 16 families belonging to these two groups. These two superfamilies are characterized by own ground plan of genital structures. Genitalia of Tephritoidea differ by reduction of hypandrial sclerites, decrease of hypandrium, enlargement of epandrium, aedeagus elongating. In basal group of Tephritoidea (Piophilidae) aedeagus keeps a structure, typical for Tephritoidea, but relatively short, hypandrial sclerites present. Genitalia of sister group Nothyboidea: Nerioidea have genitalia with long two-parted aedeagus, connected with a pair of sclerites (homologised as parameres). There is a pair of narrow connecting sclerites ("x" sclerites sensu Griffits, 1972), joined bases of parameres and hypandrium. In basal group of Nothyboidea (Diopsoidea) aedeagus is short, connecting sclerites in some species present.

Elongating aedeagus of Tephritoidea can be due to sclerotising of ovipositor of females, and this can be due to larvae phytophagy. Similar process of elongating of aedeagus (but exemplified in another form) is mentioned in Psilid genus Psilosoma Zettershtedt and due to strongly sclerotising of ovipositor.

We made following conclusions. In evolution of Tephritoidea s.l. can be distinguished basal group, including Piophilidae and Pallopteridae, and monophyletic group, containing Ulidiidae, Platystomatidae, Tephritidae, Pyrgotidae. In evolution of Nothyboidea also can be distinguished basal group Diopsoidea, including Diopsidae, Psilidae, and monophyletic Nerioidea, including Tanypezidae, Strongylophthalmyiidae, Megamerinidae, Syringogastridae, Neriidae, Cypselosomatidae, Pseudopomizidae.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy26-i010-R*

Symposium 26
Parallel evolution

Retracing the genetic origins of enamel loss during the evolutionary history of xenarthran mammals

Gibb G[1], Sérol D[1], Tibi A[1], Tilak M-K[1], Sire J-Y[2], Delsuc F[1]
[1]University of Montpellier 2, Montpellier, France, [2]Université Pierre et Marie Curie, Paris, France

Summary statement:

Examination of the main structural proteins comprising enamel and dentin in mammals uncovered pseudogenes and relaxed selection pressure after enamel loss in xenarthrans.

Abstract:

Mammals present a variety of dental morphologies associated with the adoption of varied diets that have certainly played a major role in the success of their evolutionary radiation. Teeth development is controlled by genetic pathways that are well characterized in humans, and many mutations leading to dental abnormalities have been identified in genes involved in the formation of dentin and enamel layers. Among placentals, xenarthrans (armadillos, anteaters, and sloths) are noteworthy in that anteaters have completely lost teeth, and armadillos and sloths have teeth composed only of dentin. In this work, we studied the molecular evolution of the main structural proteins making up the enamel and dentin layers in mammals in order to retrace the genetic origins of enamel loss in xenarthran mammals. Our results show that all genes involved in enamel formation are present as pseudogenes in xenarthran genomes as the result of the relaxation of selection pressures following enamel loss. Moreover, although most are also involved in osteogenesis, the genes involved in dentin formation show signs of relaxed selection in xenarthrans in which the dentin layer presents a particular structure.

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WED 24 AUG at 0910 - Room N7
Oral presentation *D1-Sy26-0910-O*

Symposium 26
Parallel evolution

The role of introgression and standing genetic variation in the emergence of parallel evolution on islands

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Summary statement:

Both introgression within and among islands may reveal a spurious patterns of independent parallel divergences.

Abstract:

The observation that species diverge independently in similar directions on separate islands has led evolutionary biologist to conclude that evolution is not random. Both developmental constraints and recurrent adaptive radiation to occupy similar niches have been put forward as major arguments to explain such parallel divergences.
Based on a presumed parallel radiation of wolf spiders and caterpillar hunters from the Galàpagos, we argue that introgression both between as within islands may greatly alter our interpretation of island monophyly as a signal of independent evolutionary histories. First, we show that within island hybridisation among the divergent taxa can erode neutral genetic divergence, resulting in a spurious phylogenetic signal of sym/parapatric divergence even when the initial divergence is allopatric. Second, we demonstrate that colonization events on each island can be followed by subsequent ongoing gene flow between the islands. This greatly enhances the role of introgression of adaptive genetic variation in producing phenotypic similar species. The combination of those two mechanisms could not only be pivotal to explain the relatively common observation of phenotypic parallelisms in island situations, but also questions the validity of phylogenetic patterns based on neutral genes to explain recently evolved parallel radiations.

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TUE 23 AUG at 1630 - Room N7
Invited talk *C4-Sy26-1630-I*

Symposium 26
Parallel evolution

Convergence in pigmentation at multiple levels: mutations, genes and function

Hoekstra HE[1]
[1] Harvard University, Department of Organismic & Evolutionary Biology

Summary statement:

Phenotypic convergence can occur at many levels--from mutations to genes to function--I will provide examples and discuss the implications for understanding evolutionary process.

Abstract:

Convergence—the independent evolution of the same trait by two or more taxa—has long been of interest to evolutionary biologists, but only recently has the molecular basis of phenotypic convergence been identified. Here, I will discuss studies of rapid evolution of cryptic colouration in vertebrates to demonstrate that phenotypic convergence can occur at multiple levels: mutations, genes and gene function. I will first show that different genes can be responsible for convergent phenotypes even among closely related populations, but by contrast, the exact same mutation can create similar phenotypes in distantly related species. Second, I will show that different mutations in the same gene need not be functionally equivalent to produce similar phenotypes. Finally, mutations that alter the expression of a gene in different ways can nevertheless result in similar phenotypes. Together these studies underscore the importance of identifying not only the genes but also the precise mutations and their effects on protein function that contribute to adaptation and highlight how convergence can occur at different genetic levels.

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WED 24 AUG at 1120 - Room N7
Oral presentation *D2-Sy26-1120-O*

Symposium 26
Parallel evolution

The genomics of parallel evolution in the threespine stickleback

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[1]Stanford University, Developmental Biology, Stanford, United States, [2]Max-Planck Institute for Evolutionary Biology, Plön, Germany, [3]Broad Institute of Harvard and MIT, Cambridge, United States, [4]HudsonAlpha Institute for Biotechnology, Huntsville, United States, [5]Stanford University, Biological Sciences, Stanford, United States

Summary statement:

Genomic sequencing of natural stickleback populations identifies, with very high resolution, multiple loci and intricate genomic architecture underlying parallel evolution.

Abstract:

Sticklebacks provide a unique opportunity to identify the genomic regions that underlie parallel evolution of traits in natural populations. We have previously shown that parallel evolution of armor and pigment traits in sticklebacks has occurred by repeated fixation of ancient standing variants that preexist at low levels in marine ancestors. Selection from standing variation gives rise to a characteristic pattern of SNP and haplotype sharing among parallel evolved populations. We have now scanned the entire genome for regions that underlie parallel evolution of marine-freshwater divergence, using next-gen sequencing of natural populations. We surveyed the morphology of 54 marine and freshwater populations and chose 10 marine-freshwater pairs for study. We generated 48x combined sequence coverage from 21 individuals sampled from diverse Northern hemisphere locations. Finally, we developed statistical methodologies that identify, with kilobase resolution, genomic regions that are shared among parallel evolving phenotypes. Our methods recover the previously known locus underlying parallel evolution of armor plates in sticklebacks. We also recover more than 30 new regions across the genome. The properties of these regions indicate that regulatory differences and chromosomal inversions play a role in the evolution of parallel marine-freshwater differences. Our study suggests that adaptation of sticklebacks to marine and freshwater environments involves dynamic reassemblies of multiple distinct loci, and highlights the importance of reuse of standing genetic variation for rapid adaptation to dramatic environmental change.
Broad Institute Whole Genome Sequencing and Assembly Team

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy26-i011-R*

Symposium 26
Parallel evolution

Ecomorphology of fire-salamander larvae: a geometric morphometric approach

Keckeis S[1], Mitteröcker P[1], Gollmann G[2]
[1]University of Vienna, Department of Theoretical Biology, Vienna, Austria, [2]University of Vienna, Department of Evolutionary Biology, Vienna, Austria

Summary statement:

We analyse variation in body shape of fire-salamander larvae from different habitats using advanced methods of geometric morphometrics

Abstract:

Shifts in life histories, from lotic to lentic larval habitats or to direct development, have been important events in evolutionary diversifaction of salamanders. Recently, a habitat change from streams to ponds in fire-salamanders in Western Germany has been discussed in the context of sympatric speciation. To probe the generality of patterns of adaptive change, we investigate a similar situation in Vienna (Austria), where fire-salamanders have colonized standing water bodies. Here, we describe variation in body shape of larvae from a gradient of habitats, ranging from fast running streams over intermittent streams to stagnant pools, using advanced methods of geometric morphometrics.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy26-i012-R*

Symposium 26
Parallel evolution

Adaptive introgression of anticoagulant rodent poison resistance between Old World mice

Kohn MH[1]
[1]Rice University, Department of Ecology & Evolutionary Biology, Houston, United States

Summary statement:

Adaptive introgressive hybridization with the Algerian mouse (Mus spretus) promoted the evolution of anticoagulant rodenticide resistance in house mice (M. musculus domesticus).

Abstract:

Evolution of new traits due to adaptive interspecific introgression between reproductively isolated species is seldom well-documented in animals. We studied the Western European house mouse (Mus musculus domesticus) in Europe and show that genetic variants have been introgressed from the Algerian mouse (M. spretus) into the house mouse over ~20.3 megabases (Mb) on chromosome 7, including the vitamin K 2,3-epoxide reductase subcomponent 1 gene (vkorc1) which is the target of anticoagulant rodenticide. This introgressed vkorc1 variant confers rodenticide resistance in house mice, is under selection, and has spread from its geographic origin where house mouse and Algerian mouse are sympatric. Our study highlights an additional path for the evolution of adaptive traits in animals, in which divergent foreign alleles, acquired by hybridization, provide a substrate on which selection may act.

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WED 24 AUG at 0950 - Room N7
Oral presentation *D1-Sy26-0950-O*

Symposium 26
Parallel evolution

Strength of natural selection associated to the parallel evolution of lateral body armor in the threespine stickleback

Le Rouzic A[1,2], Østbye K[2], Klepaker TO[3], Hansen TF[2], Bernatchez L[4], Schluter D[5], Vøllestad LA[2]
[1]CNRS, LEGS, Gif sur Yvette, France, [2]University of Oslo, Center for Ecology and Evolutionary Synthesis, Oslo, Norway, [3]University of Bergen, Institutt for biologi, Bergen, Norway, [4]Université Laval, Department of Biology, Québec, Canada, [5]University of British Columbia, Department of Zoology, Vancouver, Canada

Summary statement:

From two independent evolutionary time series, we estimated the similarities and the differences in the selection strengths that have induced parallel evolution.

Abstract:

Parallel evolution occurs when populations or species are subject to identical selection pressures in similar environments. In this work, we analyse the characteristics of selection for morphological change (lateral-plate reduction) in the threespine stickleback Gasterosteus aculeatus. Adaptation to freshwater, leading to the reduction or loss of the bony lateral armor, has occurred in parallel on numerous occasions in this species.

We estimated the strength and the characteristics of natural selection in favor of the freshwater-type fish (which have reduced armor compared to the marine forms) from two independent time series in which phenotypic change was tracked for up to 20 generations: an experimental pond in Bergen (Norway) in which fish were introduced artificially, and the published time series of the Loberg Lake (Alaska) involving a natural colonization event. Our population genetics models include information about the genetic architecture of the trait, which is known to involve a major gene (Ectodysplasin-A), genotyped in the artifical pond population.

Our results show that the fitness advantage of the freshwater morph and the freshwater genotype is substantial in both populations (20 to 90% depending on the details of the model). The observed trends are better explained when this fitness advantage decreases in the course of time, as expected if selection is frequency-dependent. However, selection happened to be stronger in the natural lake, leading to faster evolutionary dynamics in spite of a similar selection pattern.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy26-i004-E*

Symposium 26
Parallel evolution

Evolutionary origin and function of the xenosensor CAR in amphibia

Mathäs M[1], Burk O[2], Qiu H[1], Nußhag C[1], Gödtel-Armbrust U[1], Baranyai D[1], Deng S[1], Römer K[1], Nem D[1], Windshügel B[3], Wojnowski L[1]
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Summary statement:

CAR, previously described only in mammals, is a functional PXR equivalent in amphibians and constitutes a first major xenobiotic receptor in this class of vertebrates.

Abstract:

Background: Pregnane X receptor (PXR) is considered the most important sensor of natural and anthropogenic xenobiotics. Amphibian PXR plays a role in neural development and it is irresponsive to xenobiotics.
Methods/Results: We report a first broad-spectrum amphibian xenobiotic receptor, which is a homolog of the mammalian constitutive androstane receptor (CAR). The low basal activity and pronounced responsiveness to activators such as drugs and steroids displayed by the amphibian CAR resemble PXR, which both trace back to a common ancestor early in the radiation of land vertebrates. The constitutive activity of CAR emerged first in reptiles and it is common to all fully terrestrial land vertebrates. This activity can be mimicked by humanizing just two amino acids of the amphibian CAR.
Conclusions: These results demonstrate a remarkable plasticity of CAR which enabled its employment as amphibian xenosensors. They open way to toxicogenomic and bioaugmentation studies in amphibians, a critically endangered class of land vertebrates.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy26-i013-R*

Symposium 26
Parallel evolution

Ecological speciation at flooded habitats in plants of the genus Ainsliaea (Asteraceae)

Mitsui Y[1], Setoguchi H[2]
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Summary statement:

Adaptation to flooded habitats can facilitate parallel phenotypic evolution of narrow leaf shape and may lead to rapid speciation in plants.

Abstract:

The flood-resistant riparian plants referred to as “rheophytes” are diversified throughout the world across various angiosperm and pteriodphyte taxa. The rheophytic plants provide good opportunities for assessing ecological process of population differentiation and speciation because natural selection (water pressure) and the corresponding adaptive traits (narrow leaves) are explicit, and closely related taxa with contrasting broader leaves often coexist within the same geographic ranges. We investigated the origin and process of speciation in multiple lineages of flood-resistant riparian plants and non-riparian (inland) relatives in Ainsliaea (Asteraceae) by modeling population demographic parameters using a multilocus data set of nuclear gene sequences. The results of coalescent simulation analyses estimated that the two riparian species A. faurieana and A. oblonga distributed in the Ryukyu Islands, Japan, were estimated to have diverged from sister inland species quite recently; ca. 25,000 years ago for A. faurieana and ca. 9,000 years ago for A. oblonga. In addition, statistical tests provided evidence of significant post-divergence gene flow between each of the riparian species and its sister species. The present shared distribution of riparian and inland species within each island and the historical gene flow suggest that parapatric speciation across riparian-forest habitats occurred independently on each island. Thus, our results indicate that adaptation to flooded habitats triggered phenotypic evolution and speciation in Ainsliaea within relatively short evolutionary time scales.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy26-i014-R*

Symposium 26
Parallel evolution

Evidence that parallelism in primate brain expansion has a conserved genetic basis

Montgomery SH[1], Mundy NI[1]
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Summary statement:

Brain size has expanded multiple times across primates, we explore whether these parallel expansions have a conserved genetic basis.

Abstract:

The expansion of the brain is a major hallmark of primate evolution. However, whether brain expansion is limited to a few lineages or is a ubiquitous trend across the primate phylogeny is not clear. Using phylogenetic methods and published datasets of brain size we have reconstructed the evolutionary trajectories of brain size in primates. Our results show that, from a small-brained ancestor, brain size has increased multiple times independently across primate lineages and may be driven by directional selection on total neuron number. However, despite a general trend to expand, brain size does decrease in some lineages.

We subsequently explored whether the parallel evolution of increased brain size is due to parallelism at the molecular level by studying the molecular evolution of candidate genes, with known roles in neurogenesis, across a broad selection of species representing all major clades of anthropoids. Using molecular tests for selection, we show that many of these loci have been under pervasive positive selection across anthropoids. Furthermore we found that the molecular evolution of several is positively associated with neonatal brain size, suggesting a role in prenatal development that is consistent with a direct effect on neuronal proliferation. We have subsequently complemented this candidate gene approach with a transcriptome-wide analysis of species pairs representing independent episodes of brain expansion. This study demonstrates that brain expansion has occurred in parallel across primates and that the genetic basis of brain size evolution may be partially conserved.

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WED 24 AUG at 0930 - Room N7
Oral presentation *D1-Sy26-0930-O*

Symposium 26
Parallel evolution

A conserved genetic basis underlies parallel evolution of melanic polymorphism in pomarine (Stercorarius pomarinus) and arctic skuas (S. parasiticus)

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[1]University of Cambridge, Zoology, Cambridge, United Kingdom, [2]Tromsø University Museum, Natural Sciences, Tromsø, Norway

Summary statement:

Pomarine and arctic skuas show a striking example of parallel evolution at the phenotypic and genetic level down to the same mutation in two closely related species.

Abstract:

The evolutionary lability of melanic coloration and its genetic tractability make it an excellent system for studying parallel evolution. Skuas are one of several bird genera to exhibit parallel evolution of melanic polymorphism. In arctic skuas, adults of either sex vary in the amount of dark melanin in the ventral plumage. The polymorphism is probably maintained by balancing selection, and we previously showed that it is largely attributable to variation at the MC1R locus. Here we investigate the genetic basis of a similar polymorphism in the pomarine skua. We show that, as in arctic skuas, variation at the MC1R locus is strongly associated with colour variation in pomarine skuas. Reconstruction of MC1R evolution clearly shows that parallel phenotypic evolution occurred, i.e. an independent origin of the polymorphism in the two species rather than separate speciation from a polymorphic ancester. Finally, at least one amino acid site at MC1R has evolved in parallel. Thus these skuas show a striking example of parallel evolution at the phenotypic and genetic level down to the same mutation in two closely related species.

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WED 24 AUG at 1140 - Room N7
Oral presentation *D2-Sy26-1140-O*

Symposium 26
Parallel evolution

The genetic and molecular basis of parallel evolution in egg-spots of cichlid fishes

Santos E[1], Celozzi R[1], Salzburger W[1]
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Summary statement:

We uncover and compare the genetic networks involved in the development of a secondary sexual trait that independently emerged in two cichlid lineages.

Abstract:

The exceptionally diverse assemblages of cichlid fishes in the East African Great Lakes are an ideal system to study the molecular mechanisms that underlie the evolutionary parallelisms in independent radiations. One characteristic feature of the most species-rich group of cichlids, the haplochromines, are egg-spots on male anal fins, which play an important role in the breeding cycle of these mouthbrooding fishes. This structure serves as intra-specific sexual advertisement and maximizes breeding success. Egg-spots evolved independently in another cichlid lineage, the ectodines. It has previously been shown that the same pigmentation gene, csf1ra, is expressed in both kinds of egg-spots, suggesting that the same developmental cascades might be used to form this trait in both lineages. However, csf1ra is rather downstream in the morphogenesis of egg-spots. Here, we uncover the genetic networks involved in egg-spot formation using a combination of quantitative next generation sequencing and qPCR mediated gene expression experiments of RNA from eggspot tissue in the haplochromine Astatotilapia burtoni and ectodine Ophthalmotilapia ventralis. Our large-scale survey reveals molecular similarities but also differences in the morphogenesis of egg-spots between these two cichlid lineages.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy26-i015-R*

Symposium 26
Parallel evolution

Ecomorphological divergence of omnivorous fish in response to structural complexity of lake nearshore zones

Scharnweber K[1], Wanke T[1], Syväranta J[2], Mehner T[1]
[1]Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Biology and Ecology of Fishes, Berlin, Germany, [2]University of Jyväskylä, Biological and Environmental Science, Jyväskylä, Finland

Summary statement:

We observed phenotypical divergence (resource polymorphism) of omnivorous fish in response to structural complexity of lake nearshore zones.

Abstract:

Nearshore zones of shallow lakes can be structurally complex if macrophytes dominate due to clear water, whereas in turbid, phytoplankton-dominated lakes these zones are devoid of macrophytes. Benthic macroinvertebrates dominating in complex habitats are bigger, but less dense than zooplankton species that are typical for unstructured habitats. We hypothesize that feeding and swimming in complex habitats induce morphological adaptations in omnivorous fish (roach, Rutilus rutilus) which differ from those observed in roach from turbid lakes. Therefore, we compared spatial distribution, diet composition, morphology (landmark-based geometrics) and structure of gill rakers (horny filaments on the branchial arches used in fish feeding) between roach from a macrophyte-dominated and a turbid lake. We found surprisingly little differences in diet and distribution of roach between both lakes. However, gill raker numbers were higher and distances lower in roach from the turbid lake. First morphological analyses suggest that roach from the macrophyte-dominated lake had a deeper body that assures higher manoeuvrability. These data show ecomorphological divergence of omnivorous fish in response to structural complexity of habitats. To evaluate genetic divergence between populations, we generate additionally genetic markers (amplified fragment length polymorphism, AFLP).

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WED 24 AUG at 1100 - Room N7
Oral presentation *D2-Sy26-1100-O*

Symposium 26
Parallel evolution

Parallelism and divergence in the transition from sexual reproduction to asexuality

Schwander T[1]
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Summary statement:

Results report on parallel and divergent proximate mechanisms underlying the transition from sexual reproduction to asexuality in stick insects.

Abstract:

Parallel evolution is the acquisition of similar adaptive traits in independently evolving lineages. Understanding whether analogous genetic and developmental changes underlie phenotypes that evolved in parallel in different lineages can shed light on the degree of evolutionary constraints. Asexual reproduction has evolved in many independent lineages derived from sexual ancestors. However, the proximate changes underlying the evolution of asexuality remain elusive. The transition from sexual to asexual reproduction can be achieved by diverting different aspects of the meiotic divisions so that diploid eggs instead of haploid gametes are produced. As a consequence, intermediate steps in such transitions may diverge among species. Here, we analyze parallel and divergent proximate mechanisms underlying the transition from sexual reproduction to asexuality in the stick insect genus Timema. We inferred the cellular and molecular processes underlying asexuality in five independently derived lineages by investigating the chromosome dynamics during egg production in combination with molecular sequence analysis of genes involved in meiosis. We discuss the rates of parallel and convergent evolution between lineages, and how these rates are affected by inter-specific divergence levels.

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Symposium 27

Selective sweeps

Talks: *Room N4*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Ground floor campus canteen *Mensa*

Invited Speakers:

Luis-Miguel Chevin, Wolfgang Stephan

Organizers:

Kristan Schneider, Yuseob Kim

Description:

This symposium aims to present recent empirical and theoretical advancements in detecting selective sweeps in complex biological settings and furthermore inferring parameters of biological contexts under which directional selection occurs. Possible topics include geographic structure of populations, epidemiological processes, epistasis and other non-standard assumptions of directional selection.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy27-i009-R*

Symposium 27
Selective sweeps

A simulation comparison of methods to detect selective loci using dominant markers

Caballero A[1], Pérez-Figueroa A[1], Vilas A[1], García-Pereira MJ[1], Saura M[1], Rolán-Alvarez E[1]
[1]Universidad de Vigo, Vigo, Spain

Summary statement:

We compare the efficiency of three alternative programs to detect loci under directional selection from genome-wide scans.

Abstract:

We carried out a simulation study to compare the efficiency of three alternative programs (DFDIST, DETSELD and BAYESCAN) to detect loci under directional selection from genome-wide scans using dominant markers. We also evaluated the efficiency of correcting for multiple testing those methods that use a classical probability approach. Under a wide range of scenarios, we conclude that BAYESCAN appears to be more efficient than the other methods, detecting a usually high percentage of true selective loci as well as less than 1% of outliers (false positives) under a fully neutral model. In addition, the percentage of outliers detected by this software is always correlated with the true percentage of selective loci in the genome. Our results show, nevertheless, that false positives are common even with a combination of methods and multitest correction, suggesting that conclusions obtained from this approach should be taken with extreme caution.

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SUN 21 AUG at 1440 - Room N4
Invited talk *A3-Sy27-1440-I*

Symposium 27
Selective sweeps

Selective sweeps under polygenic adaptation

Chevin L-M[1]
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Summary statement:

I will present theoretical and empirical arguments that suggest polygenic responses to selection may limit the importance of strong selective sweeps for understanding adaptation.

Abstract:

The advent of population genomics has fostered the hope that scans for signatures of selection on molecular polymorphism could provide insights on the genetic basis and phenotypic spectrum of adaptation. However this approach largely ignores that most multicellular sexual organisms for which selective sweeps are searched exhibit polymorphic responses to selection for many ecologically important traits. I will present an investigation of the influence of background genetic variance of a polygenic trait on the sweep of a focal mutation at a locus affecting this trait. The joint dynamics of the mean phenotype and allelic frequency at the focal locus are derived using a model that combines the quantitative and population genetics versions of adaptive surfaces. Background genetic variance due to other loci causes evolution of the mean background phenotype, resulting in a change in time of the selection coefficient of the focal mutation. Importantly, the dynamics of the selective sweep and its overall hitchhiking effect on neutral polymorphism depend on the shape of the fitness-trait relationship. This model illustrates that characters for which selective sweeps are detected can be a biased subset of all ecologically important traits, in terms of both their genetic architecture and form of selection. I will also discuss recent empirical examples from the literature that suggest polygenic responses to selection may limit the importance of strong selective sweep signatures for understanding adaptation.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy27-i002-R*

Symposium 27
Selective sweeps

Non-neutrality of the mitochondrial genome underlies discordance in phylogeographic patterns between mitochondrial and nuclear genes in the marine clam Ruditapes decussatus

Cordero D[1], Saavedra C[1], Peña JB[1]
[1]CSIC - Instituto de Acuicultura de Torre la Sal, Ribera de Cabanes, Spain

Summary statement:

Hitchhiking on the mitochondrial genome appears as the main cause of discordance of phylogeographic patterns between mitochondrial and nuclear genes in a marine clam.

Abstract:

We have carried out a phylogeographic study of the clam Ruditapes decussatus from the Mediterranean and nearby Atlantic. Eleven localities were sampled along the species´ geographic range. A fragment of 459 bp of the COI gene was sequenced, and 6 nuclear genes were scored for size variability (1 gene) or restriction fragment size polymorphisms(5 genes). The analysis of variability at nuclear genes indicated a significant geographic structure, with genetic differentiation between the Atlantic and the Mediterranean representing on average 13.9 % of total variability. At the mitochondrial gene, two clades separated by an uncorrected distance of 3% were found. Clade A was present in all the samples, and clade B was present in the Aegean sea only. There was significant differentiation in clade A haplotype frequencies among populations (Φst = 0.61), but differentiation between the Atlantic and the Mediterranean was nonsignificant. Fst distribution across nuclear loci was consistent with neutrality expectations. However, we found negative values of Tajima's D and Fu and Li's D statistics for the mitochondrial gene in all but one populations, which were significant in 6 cases. This could be a signature of natural selection or past demographic expansion, but mismatch analyses indicated poor fit to population growth models. On the other hand, Fay and Wu's H statistic, which is relatively insensitive to demography and reflects the effect of hitchhiking selection, was significant in 4 populations. Our results underline the convenience of not relying only on mitochondrial markers and carrying out adequate neutrality testing in phylogeographic studies.

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SUN 21 AUG at 1710 - Room N4
Oral presentation *A4-Sy27-1710-O*

Symposium 27
Selective sweeps

Insights into the evolution and epidemiology of drug resistance in clinical Leishmania donovani strains from whole-genome sequencing and SNP genotyping

Downing T[1], Imamura H[2], Decuypere S[2], Clark TG[3], Coombs GH[4], de Doncker S[2], Maes I[2], Quail MA[1], Rijal S[5], Sanders M[1], Schonian G[6], Stark O[6], Sundar S[7], Vanaerschot M[2], Hertz-Fowler C[8], Dujardin J-C[2], Berriman M[1]

[1]Wellcome Trust Sanger Institute, Parasite Genomics, Cambridge, United Kingdom, [2]Institute of Tropical Medicine, Department of Parasitology, Antwerp, Belgium, [3]London School of Hygiene and Tropical Medicine, London, United Kingdom, [4]University of Strathclyde, Strathclyde Institute of Pharmacy & Biomedical and Sciences, Glasgow, United Kingdom, [5]B.P. Koirala Institute of Health Sciences, Ghopa, Dharan, Nepal, [6]Charité Universitätsmedizin Berlin, Institut für Mikrobiologie & Hygiene, Berlin, Germany, [7]Banaras Hindu University, Institute of Medical Sciences, Varanasi, India, [8]University of Liverpool, Centre for Genomic Research, Liverpool, United Kingdom

Summary statement:

Sequencing the genomes of clinical Leishmania donvani strains identifies SNP, structural, chromosome and episome variation illuminating the genetics of drug responses & evolution.

Abstract:

Visceral leishmaniasis is a potentially fatal disease endemic to tropical regions of Asia and Africa caused primarily by the parasite Leishmania donovani. We sequenced, assembled and annotated the genome of a Nepalese L. donovani strain that was used as a high-quality reference for detecting variation in 16 other genome-sequenced samples. Diversity in a further 13 Nepalese and 8 other strains from Europe, Africa and Asia was assessed using genome-wide SNP genotyping. All parasites were isolated from independent patients with visceral leishmaniasis and showed diverse responses to drug treatments in vitro despite coming from population with low genetic variability. Evidence of adaptive evolution was discovered at surface- and transport-related genes, including those linked to drug resistance. Extensive variation in the copy number of entire chromosomes was matched by structural mutations at protein-coding loci, some of which discriminated drug-resistant from drug-susceptible isolates. This contrast between groups was preserved at an episome, an extended circularised extrachromosomal segment of chromosomal DNA that was present in multiple copies. Placing the population-level diversity in a global context led to the identification of divergent lineages from a small geographic region, illuminating the evolutionary history and modern-day epidemiology of this pathogen. This study provides a basis for more powerful profiling of visceral leishmaniasis outbreaks using approaches based on deep genome sequencing and demonstrates the feasbility of using this a basis for continuous surveillance for novel and emerging drug-resistant strains and their threat to public health.

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SUN 21 AUG at 1610 - Room N4
Oral presentation *A4-Sy27-1610-O*

Symposium 27
Selective sweeps

Estimating demographic and selective sweep parameters with likelihood free ABC and SGA

Ewing GB[1], Futschik A[2], Hermisson J[1]
[1]Mathematics and BioSciences Group, University of Vienna, Mathmatics, Vienna, Austria, [2]University of Vienna, Statistics, Vienna, Austria

Summary statement:

We estimate both demographic and selection parameters simultaneously with the likelihood free methods, ABC and SGA using msms for fast forward simulations with selection.

Abstract:

Considerable work has been done estimating demographic parameters from genetic data. However when selection is considered, much of the work is restricted to tests of selection rather than directly estimating parameters from the models. We consider the case of estimating both demographic and selection parameters simultaneously from genetic data. This is done with likelihood free methods, Approximate Bayesian Computation (ABC) and the Stochastic Gradient Algorithm (SGA), where both methods rely on forward simulations using msms, a fast coalescent simulator that includes selection. We consider complex demographic models with simple and complex selection scenarios, such as locally adaptive sweeps. The selection parameters estimated include the time of the sweep and deme specific selection strength. We show both the effectiveness and limitations of the estimation methods and consider possible improvements. Finally, we discuss the sensitivity of successful inference on the choice of summary statistics and distance metrics.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy27-i003-R*

Symposium 27
Selective sweeps

Finding the traces of selection in the genome of Arabidopsis thaliana

Günther T[1], Cao J[2], Korbinian S[2], Ossowski S[2], Weigel D[2], Schmid KJ[1]
[1]University of Hohenheim, Stuttgart, Germany, [2]Max Planck Institute for Developmental Biology, Tübingen, Germany

Summary statement:

An analysis of genome-wide data from Arabidopsis thaliana in order to identify the signature of positive and purifying selection in the genome.

Abstract:

The recent publication of several whole genome sequences and genome-wide SNP data provide sufficiently large data sets for the genome-wide detection of natural selection in Arabidopsis thaliana. Demographic effects and population structure affect both, the effectivity of selection and our ability to detect the signature of selection. We analyzed the genome-wide data sets from A. thaliana and detected some species-wide and population specific signals of positive as well as purifying selection. Some genomic regions in A. thaliana show a strong haplotype structure, low diversity and/or high differentiation between populations, which are genetic signatures of selection. We identified candidate genes for positive selection which may be involved in pathogen defense and response to climatic conditions. Additionally, we show a strong correlation between the effectivity of purifying selection and the size of a population as well as the influence of ecological constraints in plants.

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SUN 21 AUG at 1630 - Room N4
Oral presentation *A4-Sy27-1630-O*

Symposium 27
Selective sweeps

Characterizing the influence of effective population size on the rate of adaptation: Gillespie's Darwin Domain

Jensen JD[1]
[1]University of Massachusetts, Bioinformatics & Integrative Biology, Worcester, United States

Summary statement:

Characterizing the role of effective population size in dictating the rate of adaptive evolution remains a major challenge in evolutionary biology.

Abstract:

Characterizing the role of effective population size in dictating the rate of adaptive evolution remains a major challenge in evolutionary biology. Depending on the underlying distribution of fitness effects of new mutations, populations of different sizes may differ vastly in their rate of adaptation. Here, we collect polymorphism data at over one hundred loci for two closely related Drosophila species with different current effective population sizes, Drosophila miranda and Drosophila pseudoobscura, to evaluate the prevalence of adaptive evolution versus genetic drift in molecular evolution. Utilizing these large and consistently sampled datasets, we obtain greatly improved estimates of the demographic histories of both species. Specifically, while current Ne differs between these species, their ancestral sizes were much more similar. We find that statistical approaches capturing recent adaptive evolution (using patterns of polymorphisms) detect higher rates of adaptive evolution in the larger D. pseudoobscura population. In contrast, methods aimed at detecting selection over longer time periods (i.e., those relying on divergence data) estimate more similar rates of adaptation between the two species. Our results suggest an important role of effective population size in dictating rates of adaptation and highlight how complicated population histories, as is probably the case for most species, can effect rates of adaptation. Additionally, we also show how different methodologies to detect positive selection can reveal information about selective sweeps across different evolutionary time scales.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy27-i002-E*

Symposium 27
Selective sweeps

Temporal variation of MHC-I alleles (Major Histocomplatibility complex class I) in an island population of house sparrows (Passer domesticus)

Karlsson M[1], Burke T[2], Nakagawa S[3], Westerdahl H[4]
[1]Biologoical institution Lund university, Lund, Sweden, [2]University of Sheffield, Department of Animal and Plant Science, Sheffield, United Kingdom, [3]University of Otago, Department of Zoology, Dunedin, New Zealand, [4]Biologocal Intitution Lund University, Lund, Sweden

Summary statement:

In present study we have measured MHC polymorphism in an island population of house sparrows, and compared the selected MHC diversity with that of neutral microsatellite markers.

Abstract:

The MHC genes are the most polymorphic genes known in vertebrates and considerable research has been done to understand how this polymorphism can be maintained over time in theory. However, much less work has been done to investigate maintenance of MHC polymorphism over time in natural populations. In present study we have measured MHC polymorphism over 12 years in an island population of house sparrows, and compared the selected MHC diversity with that of neutral microsatellite markers.
An initial characterization of MHC-I (exon 2-4) showed that two distinct groups of alleles can be distinguished; on less variable and one highly variable group. We focused on the alleles in the variable group since only these MHC alleles showed classical MHC characteristics and evidence of strong positive selection. We used the reference strand conformational analysis (RSCA) to screen for MHC genotypes. The mean number of MHC alleles was stable over the years although the frequency of the alleles fluctuated. The observed variation could be an effect of pathogen mediated selection favoring different MHC alleles in different years.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy27-i004-R*

Symposium 27
Selective sweeps

The effect of recombination, linkage disequilibrium and epistasis on fixation probability of an advantageous mutation in a three-locus model

Kermany AR[1], Lessard S[1]
[1]Université de Montréal, Département de mathématiques et de statistique, Montréal, Canada

Summary statement:

We discuss a new method to approximate the fixation probability of an advantageous mutation in a three locus system using ancestral graphs.

Abstract:

In this talk, we present a new method to approximate the fixation probability of a new advantageous mutation arising in linkage with two other loci on which previous beneficial mutations have occurred some time in the past. Using the Ancestral Recombination-Selection Graph (ARSG) we derive an analytical approximation for the fixation probability of the new mutation in terms of the intensity of natural selection, recombination rate and epistatic interaction among loci under study. The expression for the leading terms of the fixation probability shows that the sign of epistasis and linkage disequilibrium determine whether recombination increases the chance of fixation of the new advantageous mutation or if it is detrimental to its success. Moreover, in the absence of epistatic interactions we show that recombination has a positive effect on the fixation probability of the new advantageous mutation which is an analytical confirmation of the Hill-Robertson effect. In addition, the fixation probability of a neutral mutation that increases the rate of recombination is discussed and the effect of selection, epistasis, linkage disequilibrium and dominance of the modifier on its success in the population is discussed.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy27-i005-R*

Symposium 27
Selective sweeps

Dynamics of positive selection on the mammalian tree: episodic selection and co-evolution

Kosiol C[1]
[1]Vetmeduni Vienna, Institute of Population Genetics, Vienna, Austria

Summary statement:

We present a new Bayesian approach to analyse episodic selection histories and co-evolution on the mammalian phylogeny.

Abstract:

In genome-wide analysis for natural selection, we often identify the same genes to be under recent positive selection by population genetic scans (Bustamante et al., 2005; Sabeti et al., 2007) as well as under lineages and clade specific selection by phylogenetic scans (Kosiol et al, 2008). Furthermore, we observe that several pathways are strongly enriched for positive selected genes (PSGs), suggesting possible co-evolution of interacting genes. Thus selection histories often considerably more complex than expected for an idealized model of a selective sweep or simple lineage specific selection.

To gain further insight into the dynamics of selection on the mammalian tree, we devised a novel Bayesian approach to describe the possible histories of positive selection. Unlike the standard likelihood ratio tests for lineage specific positive selection (which are simple one-sided hypothesis tests and are not necessarily conservative about rejection of the null hypothesis) this framework consider all candidate selection histories symmetrically, and allows for soft (probabilistic) choices of history at each gene. Briefly, a probabilistic model is defined in terms of a switching process for the evolutionary mode (selected or non-selected) along the phylogeny. The inferred rates of gain and loss of positive selection were quite large, suggesting that positive selection tends to occur in bursts or episodes, and our observations are qualitatively compatible with Gillespie´s theoretical model (1984) of an episodic molecular clock. We also discuss similarities of the individual most likely selection histories for particular PSGs involved in the same complement immunity pathway.

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SUN 21 AUG at 1650 - Room N4
Oral presentation *A4-Sy27-1650-O*

Symposium 27
Selective sweeps

Fitness overdominance as a generic feature of adaptation in diploids

Messer PW[1], Sellis D[1], Callahan BJ[2], Petrov DA[1]
[1]Stanford University, Biology, Stanford, United States, [2]Stanford University, Applied Physics, Stanford, United States

Summary statement:

We argue that fitness overdominance should emerge naturally in diploids from the primary importance of the heterozygote fitness for the invasion of new mutants.

Abstract:

Fitness overdominance can maintain genetic variation in diploid organisms but is generally considered infrequent due to the detriment of segregation load. This notion has been corroborated by the absence of widespread signatures of long-term balanced polymorphisms in genomic scans. Here we reassess the role of fitness overdominance in the context of adaptation. We show that in the presence of stabilizing selection, fitness overdominance should emerge naturally in diploids from the primary importance of the heterozygote fitness for the invasion of new mutants. We derive this explicitly in the framework of Fisher´s influential geometric model of adaptation. We further argue that because of the universality of the underlying mechanism fitness overdominance should be a general feature of most reasonable models of adaptation in diploids. We find that the frequent fitness overdominance during adaptive walks generates a diversity advantage in fast changing environments that more than compensates for the attendant segregation load. Moreover, the resulting balanced states are short-lived, making them invisible to current scans for signatures of long-term balancing selection. Instead, these ephemeral balanced polymorphisms should leave the signatures of partial selective sweeps, which appear to be common in a number of organisms. Our results raise the possibility that balancing selection, as a natural by-product of frequent adaptation, might play a more prominent role among the forces underlying genetic variation than commonly acknowledged.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy27-i006-R*

Symposium 27
Selective sweeps

Selective sweeps under skewed offspring distributions

Moreno S[1], Wakeley J[2]
[1]Universidad de los Andes, Biology, Bogotá, Colombia, [2]Harvard University, Organismic and Evolutionary Biology, Cambridge, United States

Summary statement:

It is shown that the dominance coeffcient has a minor effect on the probability of soft sweeps and that they are least likely in populations with skewed offspring distributions

Abstract:

After a selective sweep the extent of reduction in nearby variation decreases with the number of copies of the advantageous mutation that are fixed. If there is more than one copy, different genetic backgrounds are going to be selected so the variation in close genomic regions does not decrease considerably. This is known as a soft sweep. This work explores the effect of the dominance coefficient in the dynamics of selective sweeps. Using a computational approach, it is shown that the dominance coefficient has only a minor effect in the probability of a soft sweep. This is especially valid for low selection coefficients. Furthermore, selective sweeps from new mutational input in populations with skewed offspring distributions are characterized. High variance in reproductive success is a common characteristic of biological populations, especially of species with large numbers of offspring as some plants and marine organisms. A skewed offspring distribution arises when there is a non negligible probability of some individuals having many descendants. We show that, although the effect of reproductive skew on the dynamics of selective sweeps depends on the dominance coefficient, the probability that more than one copy of an advantageous mutation is present after selection is always lower in populations with reproductive skew. This means that the molecular signature of selection from new mutational input in populations with skewed offspring distributions is stronger.

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SUN 21 AUG at 1550 - Room N4
Oral presentation *A4-Sy27-1550-O*

Symposium 27
Selective sweeps

Detecting and characterizing sweeps using the frequency spectrum of rare haplotypes

Neher RA[1], Messer PW[2]
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Summary statement:

Novel sequencing technologies allow us to survey rare variation in populations. We developed a method that exploits this rare variation to measure selection coefficients of sweeps.

Abstract:

We present a method that allows to detect selective sweeps and estimate the selection coefficients driving individual sweeps. The method uses the frequency spectrum of rare haplotypes which arose during the sweep through mutation or recombination of the haplotype on which the beneficial mutation arose. The interplay of this diversification and the exponential amplification of the beneficial mutation results in a characteristic haplotype spectrum: The abundance of the ith most abundant haplotype is proportional to 1/i. The constant of proportionality is given by the ratio of the overall mutation/recombination rate in the haplotype and the coefficient of selection. Given an independent estimate of the mutation rate, we can therefore estimate the strength of selection. Furthermore, we present a statistic of the pairwise distances between rare haplotypes which allows us to detect sweeps and soft sweeps. We exemplify this method with deep sequencing data from HIV populations and discuss how it can be used to analyze data from population scale re-sequencing projects in other organisms such as the human 1000 Genomes project.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy27-i007-R*

Symposium 27
Selective sweeps

Natural variation on a genomic scale in Drosophila mauritiana

Nolte V[1], Betancourt AJ[1], Kofler R[1], Pandey RV[1], Kapun M[1], Visnovska M[1], Schlötterer C[1]
[1]Vetmeduni Vienna, Institut für Populationsgenetik, Wien, Austria

Summary statement:

We provide a genomic reference sequence of Drosophila mauritiana and determine patterns of genome-wide polymorphism in this species using sequencing of pooled individuals.

Abstract:

Drosophila mauritiana is the last species of the D. melanogaster complex with no genomic sequence available. We determined the genomic sequence of D. mauritiana and used Pool-Seq to obtain genome-wide patterns of polymorphism in this species. In comparison to D. melanogaster, centromeric suppression of recombination is much less pronounced in D. mauritiana. We show that this pattern is well-reflected in the polymorphism pattern in these regions. Furthermore, D. mauritiana has experienced a major selective sweep, resulting in an exceptionally large (> 600 kb) window of reduced variation on the X chromosome. We discuss the involvement of the Winters sex-ratio distorter system as a driver for this selective sweep.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy27-i008-R*

Symposium 27
Selective sweeps

The hitchhiking effect in multi-locus models

Pavlidis P[1], Metzler D[2], Stephan W[2]
[1]HITS gGmbH, The Exelixis Group, Heidelberg, Germany, [2]Ludwig Maximillian University, Munich, Germany

Summary statement:

A study of trajectories of alleles, coalescent trees, and polymorphism patterns in multi-locus models.

Abstract:

We study the trajectories of a mutation that affects a quantitative trait which is determined by multiple loci. Given the trajectory, we analyze the properties of the coalescent trees around the new mutation, and compare them with those of classical selective sweeps. Coalescent trees and neutral polymorphism patterns have been implemented conditioning on the trajectory. The fitness function of the trait is Gaussian. The model assumes that the population size is finite; the recombination rate between two adjacent loci is arbitrary. We aim at scrutinizing the similarities and differences between the multi-locus model affecting a quantitative trait and the classical one-locus selective sweep model, and consequently to study whether statistical tests that have been developed to detect one-locus selective sweeps are useful for the multi-locus scenario. In the case of multi-locus scenarios, the trajectories of a new mutation, even beneficial, might not reach fixation. The alleles of the loci compete against each other and a polymorphic equilibrium may be obtained. In general, the trajectories that reach polymorphic equilibria generate different polymorphism patterns than the trajectories that result infixation. If the polymorphic equilibrium point has been reached recently, then the coalescent trees and the polymorphism patterns resemble those of standard neutral model. Consequently, current neutrality tests would not be able to detect a large proportion of selective events in multi-locus models. On the other hand, if fixation is achieved then the polymorphism patterns are similar to the classical one-locus selective sweeps and neutrality tests can detect the selective event.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy27-i001-R*

Symposium 27
Selective sweeps

Adaptation on two islands with successional beneficial mutations

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Summary statement:

We use the ancestral selection graph in order to study fixation times of selective sweeps, both in panmictic and in structured populations.

Abstract:

We consider a population evolving on two islands with symmetric migration. Each beneficial mutation has the same selective advantage and both neutral and deleterious mutations are ignored. We assume, that the population evolves in the successional mutations regime (Desai,M.M.,and Fisher, D.S., Genetics(176) 2007), i.e. it takes a long time to establish a mutation but a short time to fix it. Under these assumptions the rate of adaptation can be computed. If the migration rate is small, almost half of the mutations get lost as a migrant displaces all mutations which fixed in the target island before. The rate of adaptation tends to the rate of adaptation of an island population. If the migration rate is large almost all mutations which could fix in one of the islands can also fix in the other island. As a consequence the rate of adaptation coincides with that of a panmictic population of the same size.

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SUN 21 AUG at 1400 - Room N4
Invited talk *A3-Sy27-1400-I*

Symposium 27
Selective sweeps

Population genomic approaches to map recent positive selection

Stephan W[1]
[1]University of Munich, Biocenter, Planegg, Germany

Summary statement:

Methods for mapping footprints of adaptations in the genome of sexual species are presented, with applications to Drosophila melanogaster.

Abstract:

In several model organisms (whose genome has been sequenced) scans of DNA sequence variation have been carried out to elucidate the recent demographic and adaptive histories of these species. Using selective sweeps, it is possible to identify adaptive events in the genome. I will describe the theoretical basis of these mapping methods and present results from our work on Drosophila melanogaster. I show that (1) selective sweep analysis can be used to accurately map targets of positive selection in the genome, and (2) it can be combined with QTL mapping to determine the phenotype selection has been operating on.
Two case studies will be highlighted:
(1) the divergence of the tandemly duplicated polyhomeotic (ph) genes under positive selection, and
(2) the localization of candidate genes for cold tolerance.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy27-i003-E*

Symposium 27
Selective sweeps

Impact of selection pressure exerted by host resistance gene on population genetic structure of a plant pathogen

Valade R[1], Ducasse A[2], Maisonneuve B[3], Neema C[1]
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Summary statement:

We studied the impact of selection exerted by host resistance genes on population genetic structure of a plant pathogen, and on pathogen effectors polymorphism.

Abstract:

Most pathogens are submitted to high selection pressure which can be induced by several variables (climatic, biotic, anthropogenic…) according to their life traits. In the case of plant pathogens, host resistance may be considered as the main driving force of pathogen evolution, with pathogens evolving to overcome host resistance strategies. In the model system, Bremia lactucae, the causal agent of downy mildew on Lactuca sativa, several specific resistance genes are used to counter this pathogen with a heterogeneous spatial distribution in crops. In turn, pathogens showed a rapid adaptation to host resistances, and characterisation of population genetic structure could be an important step to identify evolutionary strategy used by pathogens to overcome host resistance.
More than four hundred isolates were recovered in France from different regions and different varieties (carrying different resistance genes) of L. sativa. Microsatellites markers were developed to study genetic diversity of this biotrophic, heterothallic and diploid pathogen, and to identify the impact of selection pressure of resistance gene on the population structure of B. lactucae in France. Moreover, polymorphism and selection signature in RxLR candidate pathogen effectors were studied in different populations of B. lactucae.
Results showed high clonality in populations, important gene flow between populations and a role of selection pressure of resistance gene on population structure of Bremia in France.
These results will be discussed regarding impact of directional selection on evolutionary strategy used by pathogens to breakdown new host resistances.

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Symposium 28

Functional population genomics

Talks: *Room N4*

***Essence posters**:* Ground floor lecture hall centre *HZ*

***Regular posters**:* Ground floor campus canteen *Mensa*

Invited Speakers:

Axel Meyer, Chris Jiggins

Organizers:

Jay F Storz, Jeffrey M Good

Description:

This symposium showcases research in 'functional population genomics', an emerging subdiscipline of evolutionary systems biology. The symposium emphasizes integrative studies of pathway function that investigate the fitness consequences of transcriptomic and proteomic variation. A chief goal is to relate changes in pathway or network function to evolutionary changes in whole-organism phenotypes.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy28-i001-R*

Symposium 28
Functional population genomics

Sequence and expression divergence of the foraging gene between African and European populations of Drosophila melanogaster

Catalan A[1], Müller L[2], Parsch J[2]
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[2]Ludwig-Maximilians-Universität München, Planegg-Martinsried, Germany

Summary statement:

We found that foraging gene in Drosophila melanogaster shows an expression divergence between two populations and that this difference is putatively driven by natural selection.

Abstract:

The colonization of new habitats by an organism usually involves the occurrence of specific adaptations, some of which may occur at the level of gene regulation. Using microarray analysis and quantitative RT-PCR, we detected significant differences in foraging expression between an ancestral African and a derived European population of Drosophila melanogaster. Interestingly, the inter-population expression difference shows the opposite pattern in the two sexes. In females, foraging expression is significantly higher in Africa, while in males it is significantly higher in Europe. These results suggest that foraging expression may be subject to population-specific sexual antagonism. The foraging gene encodes a cGMP-dependent protein kinase (PKG). Larvae and adults show differences in feeding behavior, memory, learning and nutrient storage that correlate with PKG expression levels and which could be targets of natural selection. To examine this possibility, we are surveying DNA sequence polymorphism at the foraging locus in the African and European populations and its relationship to gene expression variation. In addition, we are investigating differences in transcript- and tissue-specific expression between the two populations and how these relate to differences in foraging-related behaviors between African and European Drosophila.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy28-i002-R*

Symposium 28
Functional population genomics

Origins of distinct patterns of gene expression in a hybrid species of fish (Cottus sp.)

Czypionka T[1], Cheng J[1], Pozhitkov A[1], Nolte AW[1]
[1]Max Planck Institute for Evolutionary Biology, Evolutionary Genetics, Plön, Germany

Summary statement:

Analysis of expression patterns of parent species, F2s and a young invasive hybrid lineage regarding how hybridization might have allowed the latter to adapt to a new habitat.

Abstract:

Successful hybrid speciation is thought to be facilitated by novel combinations of parental characters that permit an emerging species to invade a new niche. An example of ongoing hybrid speciation is found in genus Cottus, where the parental species (C.rhenanus and C.perifretum) are confined to small streams. In contrast, the hybrids appear to be adapted to big rivers that tend to have higher water temperatures during summer month. This poses the question, whether hybridization has caused the emergence of adaptive traits. In order to identify candidate adaptive traits in which the hybrid lineage differs from both parental species, we used gene expression profiling to screen more than 11000 genes. Secondly, artificial F2 crosses were used to test whether the distinct features result directly from the admixture of parental genomes or may be the result of secondary evolutionary processes. A set of 17 genes in which the hybrid fish differ from both parental species in nature and in the laboratory was identified. Enrichment-analysis for GO-terms and the gene functions point towards adaptive functions that are relevant to understand the colonization of the novel habitat. This includes genes that are involved in hypoxia stress response which may facilitate the colonization of warmer waters as it was documented for the hybrids. Further, gene expression in artificial F2 crosses recreated distinct patterns in natural hybrids, which supports the hypothesis that hybridization has generated evolutionary novelty in hybrid sculpins.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy28-i003-R*

Symposium 28
Functional population genomics

Signs of adaptation in interacting genes

Daub J[1,2], Cutivet E[1], Robinson-Rechavi M[2,3], Excoffier L[1,2]
[1]University of Bern, Institute of Ecology and Evolution, Bern, Switzerland, [2]Swiss Institute of Bioinformatics, Lausanne, Switzerland, [3]University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland

Summary statement:

Using a variant of the Gene Set Enrichment Analysis we found gene sets enriched for adaptive signals among human populations.

Abstract:

In order to find genes that are involved in adaptive events, studies generally focus on single genes or restricted genic regions. These attempts often result in the discovery of only a small number of ´significant´ genes. However, many small effect mutations can have a large effect on a given pathway involving several genes. We therefore propose to uncover signals of natural selection in pathways or gene sets instead of looking at single independent genes. We use a variant of Gene Set Enrichment Analysis (GSEA) to identify gene sets enriched for adaptive signals among human populations. First results reveal a few candidate pathways for having been the target of positive and balancing selection in recent human evolution. The genes that give the enrichment signal in these pathways are found on different chromosomes, suggesting functional epistatic interactions.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy28-i004-R*

Symposium 28
Functional population genomics

Natural variation in the regulation of commensal gut bacteria in the fruit fly, Drosophila melanogaster

Early AM[1], Clark AG[2]
[1]Cornell University, Field of Ecology and Evolutionary Biology, Ithaca, United States, [2]Cornell University, Department of Molecular Biology and Genetics, Ithaca, United States

Summary statement:

This project uses SNP, microarray, and qPCR analyses to investigate how natural variation in the innate immune response affects growth of commensal gut bacteria in the fruit fly.

Abstract:

In addition to defending against invading pathogens, the immune system acts on a more constitutive basis to regulate commensal bacterial populations. While this regulation is necessary for maintaining the organism's health, it also comes with a cost: the production of bactericidal compounds such as anti-microbial peptides and reactive oxygen species cause both direct and indirect self-harm. As a step toward understanding the evolutionary trade-offs inherent in this process, we have quantified commensal gut bacterial growth in 38 fully sequenced, inbred lines of Drosophila melanogaster. By first rendering the flies completely bacteria-free, we have established in these flies commensal populations of a single bacterial species of our own choosing. Then using a combination of qPCR and standard plate counting, we quantified bacterial growth in each fly-bacterium combination and found significant inter-line variation. Leveraging the full genome sequences available for each of these fly lines, preliminary SNP, microarray and qPCR analyses suggest the genetic basis for this trait, giving us a first look at how natural genetic variation in tissue-specific immune expression affects Drosophila's microbiota.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy28-i005-R*

Symposium 28
Functional population genomics

The role of gene expression regulation in male-female mating interactions

Fricke C[1], Green D[1], Chapman T[1]
[1]University of East Anglia, School of Biological Sciences, Norwich, United Kingdom

Summary statement:

At mating receipt of seminal fluid proteins changes fruit fly female physiology and behaviour. We study how receipt of one, the sex peptide, affects regulation of gene expression.

Abstract:

Mating profoundly changes female physiology and behaviour. We aim to understand the changes in gene expression that underlie these observed physiological and behavioural responses. In Drosophila melanogaster we know that mating results in subtle but widespread and measurable changes of the female transcriptome. Combined with the knowledge that female physiological and behavioural responses are often mediated by the receipt of many seminal fluid proteins transferred by males at mating, we investigate how the receipt of one functionally significant seminal protein, the sex peptide, alters female gene expression. More specifically we are interested in how mating affects the regulation of gene expression by studying candidate microRNAs and their role in the expression of known sex peptide mediated female mating responses.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy28-i002-E*

Symposium 28
Functional population genomics

Hemocyanin evolution and the adaptation of stoneflies (Insecta, Plecoptera) under hypoxic conditions

Gamboa MA[1], Monaghan MT[1]
[1]Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Abt 2, Shallow lakes, Berlin, Germany

Summary statement:

Hemocyanin and Hexamerin proteins were found in both Nemouroidea and Perloidea suborder. Presence of Hemocyanin in a different locus could implicate a new protein function.

Abstract:

Respiratory proteins have long been considered unnecessary in most insects because the tracheal system was thought to be sufficient for oxygen supply. Studies of stoneflies have discovered an ancestral and functional Hemocyanin (Hc) in the haemolymph of nymphs, similar to crustaceans, suggesting that certain basal insects have retained an ancestral blood-based mechanism of gas exchange. In normal conditions functional Hc is present in the Perloidea suborder but lost in the Nemouroidea. We characterized Hc in stoneflies under hypoxia using nitrogen gas in laboratory experiments. Our results suggest that in 13 genera of stoneflies (from both Perloidea and Nemouroidea suborder) two types of proteins are present, an invariable Hemocyanin type and a species-specific Hexamerin, suggesting a novel hypothesis for the protein function.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy28-i003-E*

Symposium 28
Functional population genomics

A gene expression analysis of inbreeding effects in Drosophila melanogaster

Garcia C[1], Avila V[2], Caballero A[2], Quesada H[2]
[1]Santiago de Compostela University, CIBUS, Santiago de Compostela, Spain, [2]University of Vigo, Department of Biochemistry, Genetics and Immunology, Vigo, Spain

Summary statement:

The ability to make the gene expression adjustments appropriate to cope with inbreeding could be an important source of variation in inbreeding depression.

Abstract:

The genomic understanding of fundamental genetic and evolutionary phenomena such as inbreeding depression is still limited. We used Affymetrix 2.0 arrays to study the gene expression profiles of four Drosophila melanogaster inbred lines, each divided in three most and three least depressed sublines. The overall comparison between inbred and control flies found that inbreeding affected the majority of genes expressed, the greatest proportion of changes corresponding to over expressions. In the comparison between most and least depressed sublines, genes over expressed in the most depressed ones were related with cell and tissue growth control, lipid catabolism, immune response and response to nutrient levels. Genes underexpressed in the same most depressed sublines were mostly related with Endoplasmic reticulum and Golgi apparatus, and their functions of protein synthesis, modification, maturation and transport, and with the synthesis of carbohydrates and their addition to proteins in Glycosylation reactions. This suggested that inbreeding depression could be in part generated by inefficiency in the production of functional proteins and in the processing of defective ones. In addition, in the genes showing significant effects of the amount of depression, the most depressed sublines' expressions clearly tended to be intermediate between those of controls and the least depressed. This suggested that these genes have a role in protecting the organism against the consequences of inbreeding, and that the observed increase in depression was related to an inability to do the appropriate expression adjustments.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy28-i006-R*

Symposium 28
Functional population genomics

The influence of sex-biased transcription on rates of molecular evolution in Drosophila

Grath S[1], Parsch J[2]
[1]University of Münster, Institute for Evolution and Biodiversity, Münster, Germany, [2]University of Munich (LMU), Department of Biology II, Munich, Germany

Summary statement:

Influence of degree and conservation of sex-biased expression on molecular evolution and evidence for faster-X evolution using whole genome data for two Drosophilid lineages

Abstract:

Sex-biased gene expression (i.e., the differential expression of genes between males and females) is a widespread phenomenon within eukaryotes. However, genes often differ in their sex-bias classification or degree of sex-bias between species. Furthermore, especially male-biased genes are not evenly distributed across the genome. We used whole-genome species-specific expression data and evolutionary rate estimates for two Drosophilid lineages, melanogaster and obscura, spanning an evolutionary time scale of around 50 million years to investigate the influence of sex-biased gene expression on the rate of molecular evolution. Data from Drosophila ananassae were used to infer gains or losses of sex-biased gene expression within this time frame. In both lineages, the rate of protein evolution was positively correlated with the male/female expression ratio. However, the two lineages differed in the magnitude of this correlation, with there being a stronger correlation in the melanogaster lineage. Further, male-biased genes with a higher degree of sex-bias or with conserved male-biased gene expression over larger evolutionary time scales showed faster rates of evolution. Interestingly, we found evidence for a ´fast-X´ effect in which the rate of evolution was greater for X-linked than for autosomal genes. This pattern was particularly pronounced for male-biased genes. Genes located on the obscura ´neo-X´ chromosome, which originated from a recent X-autosome fusion, show rates of evolution that are intermediate between genes located on the ancestral X-chromosome and on the autosomes. This suggests that the shift to X-linkage led to an increase in the rate of molecular evolution.

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TUE 23 AUG at 1610 - Room N4
Oral presentation *C4-Sy28-1610-O*

Symposium 28
Functional population genomics

Sleeping beauties: the evolution of seasonal dormancy characteristics mediates metabolic demand, life history timing, and adaptive divergence in the apple maggot

Hahn D[1], Ragland G[2], Berlocher S[3], Feder J[4]
[1]University of Florida, Entomology and Nemato9logy, Gainesville, United States, [2]University of Florida, Gainesville, United States, [3]University of Illinois, Urbana, United States, [4]University of Nortre Dame, South Bend, United States

Summary statement:

Metabolic efficiency and cell cycle control have emerged as two classes of mechanisms associated with adaptive divergence in life history timing in the apple maggot.

Abstract:

The apple maggot, Rhagoletis pomonella, a text-book model for sympatric speciation and adaptive genetic divergence has recently (~200ya) expanded its host range from native hawthorns to domesticated apples. Apples flower and fruit earlier in the summer than hawthorns and to synchronize themselves with the novel plant apple flies undergo a longer, more metabolically demanding diapause. To compensate, we expected apple pupae would: 1) tank up with more fuel reserves (greater lipid storage), or 2) use their fuel reserves more judiciously (decreased metabolic rates).We have shown that field-collected apple race individuals have significantly greater lipid reserves than hawthorn race individuals. But, are apple race individuals more efficient? First, we use microarrays to characterize the tanscriptome of diapausing and non-diapausing individuals, indentifying several candidates for adaptive shifts in diapause in metabolic, endocrine, and stress resistance pathways. Second, we assay variation in diapause metabolic rates in a large group of individuals, clearly identifying classes of individuals with greater or lesser metabolic depression. We also identify important mechanisms associated with diapasue termiantion and seasonal phenology. Climate change will affect the phenology of plants and their insect herbivores, potentially yielding both rapid adaptive change in life history timing and novel interactions; this work bridges the gap between physiological and genetic mechanisms underlying the evolution of diapause timing, host plant shifts, and diversification.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy28-i007-R*

Symposium 28
Functional population genomics

A dictionary of genetic effects, and its relationship to natural variation

Houle D[1], Nye J[1], Márquez E[1]
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Summary statement:

We are generating a dictionary of genetic effects in the Drosophila melanogaster wing by quantitatively manipulating the expression of individual genes.

Abstract:

A central challenge in biology is the elucidation of the genotype-phenotype map. Current efforts to do so depend on mutations of large effect or natural variation, each furnishing a narrow view of the the map. We are generating a dictionary of genetic effects in the genotype-phenotype map by quantitative, targeted knockdowns of the expression of individual genes in Drosophila melanogaster, followed by high-dimensional characterization of the effects on wing size and shape. We present initial results from this work, including genes from several major pathways known to affect wing size and vein configuration. A phenotypic response to perturbation of expression has been observed in about half of the genes manipulated. The correspondence between a priori knowledge of gene function or expression domain and wing shape is modest. When responses are observed, they can be gradual (e.g., rho), discrete (e.g., hpo, Dll), asymptotic (e.g., en), or subject to a perturbation threshold (e.g., vg). The correspondence of the dictionary results to that of a genome-wide association study using the Drosophila Genome Reference Panel is generally good, suggesting that these results are predictive of variation in natural populations. High-dimensional characterization of the effects of changes in gene expression is a promising step toward the elucidation of the G-P map.

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TUE 23 AUG at 1420 - Room N4
Invited talk *C3-Sy28-1420-I*

Symposium 28
Functional population genomics

The upstream and downstream of wing pattern variation in Heliconius butterflies

Jiggins C[1]
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Summary statement:

Heliconius butterflies are brightly coloured and show Mullerian mimicry. Here I discuss how the genetic control of convergent evolution commonly uses the same genetic pathways.

Abstract:

Heliconius butterflies are brightly coloured and famous for their Mullerian mimicry. Over recent years we have been studying the genetic loci that regulate polymorphism in wing pattern across the genus, and have shown that a few narrow regions of the genome control variation in wing pattern in parallel across both divergent and convergent phenotypes. Here I will present gene expression and population genomic evidence for the role of multiple genes across these narrow regions in wing pattern development. I also show that patterns of expression in downstream pigmentation pathways are shared across the genus, with the melanin pathway genes, ebony and tan, expressed in a the same patterns associated with particular colour patches across independent lineages. Overall, despite independent convergent evolution of mimetic wing patterns in multiple lineages, the genetic control of these patterns is strikingly predictable.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy28-i004-E*

Symposium 28
Functional population genomics

Isolation after colonization: Midas cichlid fishes in Nicaraguan crater lakes

Kautt AF[1], Elmer KR[1], Meyer A[1]
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Summary statement:

We infer the evolutionary history of the Amphilophus citrinellus species complex in allopatry and sympatry using coalescent analyses.

Abstract:

Biological systems with replicated colonization and recent speciation events are promising contexts for identifying the genetic mechanisms and ecological circumstances leading to adaptive radiation. Neotropical Midas cichlid fishes (of the Amphilophus citrinellus species complex) have independently colonized several isolated crater lakes (aged 1.2 to 23 kya) from one ancestral population. Adaptive speciation has occurred within some of these crater lakes, including the independent repeated evolution of phenotypically parallel species´ phenotypes. However, the role of single vs. multiple colonization events, and the timing of these colonization events, remains unquantitated for at least some of the crater lakes. Knowledge about past demographic processes is crucial to understanding the demographic and geographic conditions and speed of speciation, including the potential for sympatric speciation and parallel evolution. This study makes use of coalescent theory and a comprehensive molecular data set (>1000 individuals, 14 microsatellite loci and mtDNA sequence) of Midas cichlids from six crater lakes and the ancestral population. Together with knowledge about the geological age of the lakes, we estimate the colonization time and use measures of effective population sizes and migration rates to make inferences about past demographic processes. We infer the order of divergence of sympatric species in lakes containing multiple described species of Midas cichlids. Reconstructing the evolutionary history of this species complex is important for elucidating the genetic and demographic factors underlying rapid speciation and parallel evolution.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy28-i005-E*

Symposium 28
Functional population genomics

Network-level and population genetics analysis of the insulin/TOR signal transduction pathway (IT pathway) across human populations

Luisi P[1], Alvarez-Ponce D[2,3], Dall'Olio GM[4], Sikora M[5], Bertranpetit J[4], Laayouni H[4]
[1]Institute of Evolutionary Biology, Evolutive Biolology, Barcelona, Spain, [2]National University of Ireland Maynooth, Department of Biology, Maynooth, Ireland, [3]Universitat de Barcelona, Departament de Genètica, Barcelona, Spain, [4]CEXS-UPF-PRBB, IBE-Institute of Evolutionary Biology, Barcelona, Spain, [5]Stanford University School of Medicine, Department of Genetics, Stanford, United States

Summary statement:

IT pathway analysis across human populations shows potential positive selection pattern for 13 genes presenting greater information control and encoding interacting proteins.

Abstract:

We aim at assessing the relevance of the "thrifty genes" hypothesis that assume that human populations must have been adapted for efficient genes in energy acquisition and / or storage and / or expenditure through episodes of lack of food. For that purpose we analysed the patterns of molecular evolution of 67 genes, belonging to 24 paralogous groups, involved in the human insulin/TOR signal transduction pathway. Both mTOR and insulin have relevant functions related to the obesity phenotype. This pathway plays a major role in controlling critical energy functions such as glucose and lipid metabolism and it elicits a diverse array of biological responses to energy intake. It is also involved in the control of cell growth and proliferation in response to nutrients. Using genotyping data from 7 main geographic areas all around the world (Human Genome Diversity Panel), we applied usual methods for population genetics to detect recent natural selection events. We identified signatures of potential positive selection on 13 of the studied genes. Analysis taking into account features of the genes within the network show that (i) genes encoding physically interacting proteins tend to present similar pattern of positive selection; (ii) genes for which we detected signatures of positive selection tend to have a greater information control within the pathway according to the network centrality measures. Moreover, we observed most of the potential adaptation signals within the Middle East and North Africa, European and Central South Asia populations.

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TUE 23 AUG at 1710 - Room N4
Oral presentation *C4-Sy28-1710-O*

Symposium 28
Functional population genomics

Testing hypotheses about localized morphometric effects in genome-wide functional genomic studies

Marquez EJ[1], Cabeen R[2], Woods RP[2], Houle D[1]
[1]Florida State University, Biological Science, Tallahassee, United States, [2]UCLA, Brain Research Institute, Los Angeles, United States

Summary statement:

We discuss new methods for the extraction of local shape information from morphological data and their application to test functional hypotheses based on genomic data.

Abstract:

Functional genomics has emerged as a powerful tool for studying the causes of phenotypic variation. In the case of morphological variation, understanding the link between genomic and phenotypic variation often requires the decomposability of phenotypic variation into factors linked to specific mechanisms or allelic varieties. Dominant methods for the analysis of shape variation, however, are suitable for capturing components of global variation and it is not obvious how they can be used to localize variation information to specific parts of the form. We have developed new methods, based on mathematical interpolation, that allow shape differences to be decomposed into local changes while incorporating information contained in the full set of landmarks. These methods depart from other approaches which define localized regions as subsets of landmark positions, thus ignoring the dependence of local shape differences on their global context. We demonstrate how these methods can be applied in the formulation and testing of hypotheses based on gene function and network topology to explain morphometric variation in the context of a genetic-wide association study of the Drosophila wing.

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TUE 23 AUG at 1400 - Room N4
Invited talk *C3-Sy28-1400-I*

Symposium 28
Functional population genomics

Population genomic analyses of parallel adaptations and sympatric speciation in repeated adaptive radiations of crater lakes cichlids in Nicaragua

Meyer A[1], Elmer K[1], Fan S[1]
[1]University of Konstanz, Biology, Konstanz, Germany

Summary statement:

De novo mutations in different genes, and possibly alternative developmental pathways led to the evolution of parallel adaptations in crater lakes within only a few thousand years.

Abstract:

A natural experiment is taking place in Nicaragua. From the ancestral populations of the large and old Lakes Managua and Nicaragua at least six young (between 1200 and 23000 years of age) crater lakes have been colonized by a particular lineage of cichlid fish, the Midas cichlid (Amphilophus ct. citrinelllus). Small adaptive radiations (of up to 6 species) formed by sympatric speciation in each these crater lakes in a predictable manner. In several of these species flocks the parallel adaptations to life in their new environments led first to the evolution of a limnetic species with an elongated body form and then several deeper-bodied benthic species with different dentitions and dietary preferences diverged next. What is the genetic basis of these parallel adaptations? Are they caused by the same beneficial alleles that originated from standing genetic variation in the ancestral population? Or do de novo mutations in the same or different genes account for the repeated evolution of similar phenotypes? Given that there is a common source population and that the speciation and evolution of parallel phenotypes took place exceedingly fast, one might have predicted that standing genetic variation would be the basis of this case of repeated evolution. Surprisingly however, our preliminary evidence, based on comparative transcriptomics and AFLP genome scans, leads us to conclude that different genes and possibly new mutations are involved in bringing about parallel adaptations and new species within only a few thousand generations under sympatric conditions in several small crater lakes.

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TUE 23 AUG at 1650 - Room N4
Oral presentation *C4-Sy28-1650-O*

Symposium 28
Functional population genomics

Population transcriptomics of Drosophila melanogaster females

Müller L[1], Hutter S[1], Stamboliyska R[1], Saminadin-Peter S[2], Stephan W[1], Parsch J[1]
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Summary statement:

Survey of gene expression levels among strains of an ancestral and a derived population of D. melanogaster shows substantial expression divergence between the populations.

Abstract:

Variation at the level of gene expression is abundant in natural populations and is thought to contribute to the adaptive divergence of populations and species. Gene expression also differs considerably between males and females. Here we report a microarray analysis of gene expression variation among females of 16 Drosophila melanogaster strains derived from natural populations, including eight strains from the putative ancestral range in sub-Saharan Africa and eight strains from Europe. Gene expression variation among males of the same strains was reported previously. We detected relatively low levels of expression polymorphism within populations, but much higher expression divergence between populations. A total of 569 genes showed a significant expression difference between the African and European populations at a false discovery rate of 5%. Genes with significant over-expression in Europe included the insecticide resistance gene Cyp6g1, as well as genes involved in proteolysis and olfaction. Genes with functions in carbohydrate metabolism and vision were significantly over-expressed in the African population. There was little overlap between genes expressed differently between populations in females and males. Our results suggest that adaptive changes in gene expression have accompanied the out-of-Africa migration of D. melanogaster. Comparison of female and male expression data indicates that the vast majority of genes differing in expression between populations do so in only one sex and suggests that most regulatory adaptation has been sex-specific.

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TUE 23 AUG at 1630 - Room N4
Oral presentation *C4-Sy28-1630-O*

Symposium 28
Functional population genomics

Teleost fish salinity adaptation: a proteomics perspective

Papakostas S[1], Vasemägi A[1], Peil L[2], Himberg M[3], Vähä J-P[1], Primmer CR[1]
[1]University of Turku, Turku, Finland, [2]University of Tartu, Tartu, Estonia, [3]Åbo Academy University, Turku, Finland

Summary statement:

Using a label-free proteomics experiment, new insights were gained about the molecular mechanisms behind brackishwater adaptation in a salmonid species (Coregonus lavaretus).

Abstract:

Systems-wide proteomics research became possible lately, inaugurated mostly by recent developments in high resolution mass spectrometry (MS). As a result, the study of changes in protein expression, post-translational modifications (PTMs) and protein-protein interactions (PPIs) is finally within the reach of evolutionary biologists even in non-model species. Combined with transcriptomic and genomic information, the molecular genetic basis of adaptive traits can now be viewed in a more comprehensive systems biology context. Here we employ such an approach to investigate the molecular mechanisms behind salinity adaptation in teleost fish. We focus on brackishwater adaptation in whitefish (Coregonus lavaretus), a species renowned for its adaptive radiation across different environmental gradients. A label-free proteomics experiment was conducted, using hatch-stage larvae from 1 freshwater & 1 brackishwater population that were reared in 2 salinity treatments (0 & 10 ppt). Overall, 384 LTQ Orbitrap runs (32 biological samples) enabled the quantification of more than 1500 proteins. Over 100 proteins showed significant differential expression between salinities, many of which concerned genes never reported before to be involved in salinity tolerance response. Enrichment tests, PTMs and PPIs highlighted an extensive signaling crosstalk network behind salinity adaptation. For example, G-protein coupled salinity sensors interact closely with signaling pathways such as the glucorticoid, to activate mitochondrial and cellular proton pumps towards a viable osmoregulatory response. Evidently, MS proteomics can now be used for the study of adaptive traits even in non-model species.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy28-i009-R*

Symposium 28
Functional population genomics

Comparative proteome analysis of two convergent morphotypes from two marine snail species living in sympatry with different reproductive strategies

Perez Diz A[1], Dominguez Garcia S[1], Rolan Alvarez E[1]
[1]University of Vigo, Department of Biochemistry, Genetics and Immunology, Vigo, Spain

Summary statement:

Understanding adaptive convergence mechanisms of two marine snail species living in sympatry with different reproductive strategies through a comparative proteomics approach.

Abstract:

Littorina saxatilis and Melarhaphe neritoides are both marine snails living sympatrically on intertidal rocky shores and present two distinctly adapted morphotypes cohabiting at the upper-sheltered and lower-exposed side. Both species follow an internal fertilization but while L. saxatilis holds their non-planktonic shelled embryos in a brood pouch, M. neritoides follows a planktotrophic larvae-stage development. It can be hypothesised that these different reproductive strategies might have some effects at gene expression level as far as level of gene flow is different within each species. Likewise, molecular mechanisms of the two morphotypes to adapt to distinct environments might be different in both species. Proteomics approaches has been scarcely used to address evolutionary questions in order to unraveling the molecular mechanisms underlying adaptation and speciation processes, despite natural selection acts at first instance over the molecular phenotype rather than at DNA level. Proteins are thus good candidates to complement DNA/RNA studies. Proteomics studies has recently showed extraordinary differences at proteome level between the two morphotypes of L. saxatilis, a well studied case of incomplete sympatric speciation. Such differences are mainly explained by genetic variation rather than phenotypic plasticity, and maintained across different life-stages. Similar studies in M. neritoides allow us in addition to make a comparative proteomics assessment. Thus some interesting hypothesis can be tested, such as, whether or not the two different morphotypes within each species show a similar level of variation and/or molecular mechanisms of adaptation.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy28-i010-R*

Symposium 28
Functional population genomics

Nonlinear fitness landscape of a molecular pathway

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Summary statement:

We use the biophysical processes affecting the lac proteins to explain the fitness effects of expressing the lac operon in different environments and uncover a nonlinear landscape.

Abstract:

Genes are regulated because their expression involves a fitness cost to the organism. The production of proteins by transcription and translation is a well-known cost factor, but the enzymatic activity of the proteins produced can also reduce fitness, depending on the internal state and the environment of the cell. Here, we map the fitness costs of a key metabolic network, the lactose utilization pathway in Escherichia coli. We measure the growth of several regulatory lac operon mutants in different environments inducing expression of the lac genes. We find a strikingly nonlinear fitness landscape, which depends on the production rate and on the activity rate of the lac proteins. A simple fitness model of the lac pathway, based on elementary biophysical processes, predicts the growth rate of all observed strains. The nonlinearity of fitness is explained by a feedback loop: production and activity of the lac proteins reduce growth, but growth itself also affects the concentration of these molecules. This nonlinearity has important consequences for pathway function and evolution. It generates a critical activation threshold of the lac operon, above which bacterial growth drops to low values. Furthermore, the nonlinearity determines how the fitness of operon mutants depends on the inducer environment. We argue that fitness nonlinearities, growth thresholds, and gene-environment interactions are generic features of fitness landscapes for metabolic pathways and discuss their implications for the evolution of regulation.

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TUE 23 AUG at 1500 - Room N4
Oral presentation *C3-Sy28-1500-O*

Symposium 28
Functional population genomics

Genetics and robustness of a developmental network under environmental change

Runcie D[1], Garfield D[1], Babbitt C[1], Wray G[1]
[1]Duke University, Biology Department, Durham, United States

Summary statement:

Buffering in the sea urchin endomesoderm gene regulatory network explains patterns of natural variation under changing environments.

Abstract:

The relationship between genetic and phenotypic variation is critical for understanding evolutionary change. However, this relationship is not only indirect, it can be exceptionally sensitive to the environment. The well-studied endomesoderm gene regulatory network in the purple sea urchin is an ideal model system for linking variation in outbred individuals under realistic environments to the molecular interactions underlying development. Here, we combined quantitative genetics with a systems biology approach to investigate how naturally segregating genetic variation is buffered and propagated within a gene regulatory network following a shift in environmental temperature. We documented considerable variation in the responses of genetically distinct embryos to changes in temperature for a variety of traits including morphology, the induction of a heat shock response, and the expression of key developmental genes. We observed striking correlations in the responses of genes that interact directly, suggesting an influence of the endomesoderm network structure on developmental plasticity. More interestingly, the predictive power of the network model was strongest in the cultures most affected by higher temperatures. This suggests that environmental stress can increase the extent to which variation is propagated within a developmental gene regulatory network, providing a possible molecular explanation for a phenomena associated with a breakdown of robustness including the release of cryptic variation following an environmental shift.

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TUE 23 AUG at 1550 - Room N4
Oral presentation *C4-Sy28-1550-O*

Symposium 28
Functional population genomics

A genomic and functional analysis of reproductive diapause in Drosophila melanogaster

Schmidt P[1], Zhao X[2], Behrman E[2], Brisson D[2], Gregory B[1]
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Summary statement:

Here we report on the ecological and evolutionary significance of variation in the transcriptome and proteome in response to photoperiod, temperature, and diet in Drosophila.

Abstract:

While genetic and genomic resources in non-model organisms continue to develop at an increasing rate, the genetic models remain understudied from an ecological genetics perspective. In Drosophila melanogaster, the expression of reproductive diapause is a central component in a suite of traits involved in the adaptation to seasonal, temperate environments. While several genes for diapause have been identified, the mechanisms by which environmental stimuli are differentially perceived and integrated remains unknown. Similarly, the downstream pathways associated with the diapause phenotypic cascade (i.e., the traits that promote overwintering survivorship) have not been investigated in a comprehensive way utilizing the platform and strengths of a genetic model. Here, we use a combination of mapping techniques, RNAseq, and proteomics to 1) evaluate the functional significance of molecular polymorphism on environmental sensing, 2) examine the transcriptome and proteome in response to temperature, photoperiod, and dietary manipulations; and 3) identify the pathways and networks associated with diapause expression and temperate adaptation.

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TUE 23 AUG at 1440 - Room N4
Oral presentation *C3-Sy28-1440-O*

Symposium 28
Functional population genomics

Population genomics of metabolic adaptation to high-altitude in deer mice

Storz JF[1], Cheviron Z[1]
[1]University of Nebraska, Lincoln, United States

Summary statement:

Here we present the results of an RNA-Seq analysis of wild-derived deer mice to identify the transcriptional underpinnings of physiological adaptation to high-altitude hypoxia.

Abstract:

High-altitude environments provide ideal testing grounds for investigations of mechanism and process in physiological adaptation. For air-breathing vertebrates that live at high-altitude, hypobaric hypoxia is an unremitting environmental stressor that cannot be mitigated by behavioral avoidance. Some of the best prospects for identifying adaptive mechanisms of hypoxia tolerance are afforded by genomic studies of population-level variation in species that are continuously distributed across steep altitudinal gradients. Many mechanisms of physiological adaptation involve modifications of regulatory networks, and newly developed genomic technologies provide a means of investigating the nature of these modifications. In particular, genomic technologies such as RNA-Seq that permit the simultaneous analysis of sequence variation and expression profiles for a set of genes in the same pathway can be used to identify both structural and regulatory mechanisms of physiological adaptation. Here I present the results of an RNA-Seq analysis that was conducted as part of a large-scale common garden experiment to disentangle the genetic and environmental components of gene expression differences between high- and low-altitude deer mice (Peromyscus maniculatus). The study was designed to identify the specific genes and specific pathways that contribute to adaptive variation in hypoxia tolerance in these animals.

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Symposium 29

Can drift facilitate adaptive evolution?

Talks: *Room N9*

Essence posters: Ground floor lecture hall centre *HZ*

Regular posters: Ground floor campus canteen *Mensa*

Invited Speakers:

Joanna Masel, Merijn Salverda

Organizers:

Bas Zwaan, Arjan de Visser

Description:

How predictable is the outcome of selection depending on the effective population size and the target trait? Can low effective population size facilitate adaptive evolution via accumulation of near-neutral mutations? How does the nature of genetic variation influence the outcome of natural selection? These questions will be addressed to highlight the interplay between all four forces of evolution.

The following abstracts are sorted by first author last name in alphabetical order within this symposium (independent of contribution type). Use the search function on your computer to locate specific authors or keywords. Jumping between symposia is facilitated by the pdf bookmarks.

SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy29-i001-R*

Symposium 29
Can drift facilitate adaptive evolution?

Paradox dispersal: protracted larval stages and the adaptive radiation of Antarctic notothenioid fishes

Damerau M[1], Matschiner M[2], Salzburger W[2], Hanel R[1]
[1]Johann Heinrich von Thuenen Institute, Federal Research Institute for Rural Areas, Forestry and Fisheries, Institute of Fisheries Ecology, Hamburg, Germany, [2]University of Basel, Zoological Institute, Basel, Switzerland

Summary statement:

Comparative population genetics in Antarctic fish reveal high gene flow among populations and gives clues about the process of their adaptive radiation.

Abstract:

Notothenioidei (Perciformes) are the most prominent group of fish on the shelves and slopes of the Antarctic region. The evolution of antifreeze glycoproteins within their lineage enabled them to survive in the cold, ice-laden waters, which remain hostile to most fishes since approximately 25-20 million years ago. With few competitors for ecological niches, they radiated into more than 130 species known today. However, their development usually includes a protracted larval stage of several months, during which they are likely to drift away from the spawning grounds on the shelves into the open ocean or to distant habitats. Larvae as dispersal units are hence likely to increase gene flow and counteract speciation processes. In a comparative study, we here investigate the role of larvae in population structuring and the consequences on adaptive radiation in the Antarctic realm.

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WED 24 AUG at 1200 - Room N9
Oral presentation *D2-Sy29-1200-O*

Symposium 29
Can drift facilitate adaptive evolution?

Limited impact of effective population size as the major determinant of the rate of adaptive evolution in eukaryotes

Gossmann TI[1], Eyre-Walker A[1]
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Summary statement:

We investigate the relationship between Ne and adaptive evolution and do not find conclusive evidence that differences in Ne translate into similar levels of adaptive changes.

Abstract:

The role of adaptive evolution is one of the fundamental questions in population genetics. Theory suggests that species with large effective population sizes undergo more adaptive evolution than species with low effective population sizes. Advances in sequencing technology open up the opportunity to verify this hypothesis for a growing number of species. By comparing mouse and human and two species of the plant family Brassicaceae we show that differences in the effective population do not translate into comparable differences in the rate of adaptive evolution. We investigate the relationship between rate of adaptive evolution and effective population sizes in more depth by looking across 17 eukaryotic species. Even though there seems to be evidence that some species with large effective population size have undergone substantial adaptive evolution an overall significant relationship does not emerge. Therefore we conclude a limited role for effective population size as the major determinant in adaptive evolution and suggest that other factors may be as important in determining the rate of adaptive evolution.

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WED 24 AUG at 1100 - Room N9
Oral presentation *D2-Sy29-1100-O*

Symposium 29
Can drift facilitate adaptive evolution?

Invasion biology of Cirsium arvense: Insights from common garden experiments, microarray analyses, DNA fingerprinting and next-generation sequencing

Guggisberg A[1], Horvath D[2], Rieseberg L[1]
[1]University of British Columbia, Botany Department, Vancouver, Canada, [2]ARS-USDA, Fargo, United States

Summary statement:

This project aims at identifying the phenotypic and genetic changes associated with the evolution of invasiveness in Cirsium arvense.

Abstract:

Cirsium arvense (Compositae) is native to temperate Eurasia, but it has been introduced into the other four continents, where it became one of the worst weeds. This project aims at (i) determining whether introduced, North American (NA) populations have traded investment in defence/tolerance for increased growth/reproduction, by comparing their survival, growth rates, reproductive output, and gene expression profiles to those of native populations using common garden and microarray experiments, and (ii) assessing the genetic composition and adaptive potential of these introduced populations, using microsatellites (SSRs) and population-level chloroplast (cpDNA) genome sequences. Preliminary results from morphological data fail to detect any difference in stress response between the two ranges, but indicate a five- to ten-fold higher variance among native populations. Whether this conclusion holds at the gene expression level is currently being analysed. Results from SSR fingerprinting show that NA populations originated from Western Europe and experienced a strong bottleneck upon their introduction. Despite this apparent drop in population size, C. arvense spread under new abiotic conditions (bigger temperature and precipitation shifts, as well as colder and drier seasons), and it remains unknown which adaptive traits may have evolved. To more accurately reconstruct the invasion routes of C. arvense and identify eventual signs of positive selection in its organelles, sequence data from whole cpDNA genomes are currently under investigation.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy29-i002-R*

Symposium 29
Can drift facilitate adaptive evolution?

Spatial fragmentation and local adaptation in Mediterranean Parsley frog, Pelodytes punctatus

Jourdan-Pineau H[1,2], Folly J[2], Crochet P-A[2], David P[2]
[1]Université de Lausanne, Ecology and Evolution, Lausanne, Switzerland, [2]CEFE - CNRS UMR 5175, Montpellier, France

Summary statement:

Habitat fragmentation and small population size induce genetic drift and differentiation both at genetic and phenotypic levels in Parsley frog populations.

Abstract:

In Mediterranean regions, the Parsley frog, Pelodytes punctatus, inhabits fragmented environments consisting in small ponds. Habitat fragmentation is expected to decrease effective population size and migration which in turn may increase genetic drift and inbreeding. Using microsatellite markers, we investigated the impact of fragmentation on genetic differentiation on inbreeding. Then, in lab rearing experiments, we looked for potential local adaptation in larval traits using Fst-Qst comparisons.

In the studied area (15 ponds, mean distance = 20.5 ± 12.8 km), we found low but significant genetic differentiation between sites (mean Fst = 0.07 ± 0.04). Comparing temporal samples, we showed that drift occurred but genetic identity of the ponds remained through time. Although effective population sizes were low (8 to 50 individuals), there was no inbreeding hence no inbreeding depression. Surprisingly, in one pond, heterozygosity/fitness correlations rather indicated outbreeding depression which could be considered as the result of local adaptation on size at metamorphosis.

Qst values obtained for larval period and size at metamorphosis were higher than Fst for most pairs of sites. However, larval period showed a large variability within site whereas size at metamorphosis varied mostly between sites. Thus size at metamorphosis is probably shaped by local adaptation although maternal effects may also be implied.

We conclude that habitat fragmentation plays a role both on genetic structure and phenotypic differentiation of Parsley frog populations. But, in this fragmented environment and despite low effective population size, Parsley frog doesn’t exhibit inbreeding.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy29-i003-R*

Symposium 29
Can drift facilitate adaptive evolution?

Climate-forced temporal variation in population structuring in the face of contemporary adaptation to divergent thermal habitats in grayling

Junge C[1], Barson NJ[1], Haugen TO[1,2,3], Primmer CR[4], Saetre G-P[1], Jaime O[1], Kausrud KL[1], Leder EH[4], Vøllestad LA[1]

[1]University of Oslo, Centre for Ecological and Evolutionary Synthesis (CEES), Oslo, Norway, [2]Norwegian Institute for Water Research, Oslo, Norway, [3]Department of Ecology and Natural Resource Management (INA), Norwegian University of Life Sciences, Aas, Norway, [4]Department of Biology, University of Turku, Turku, Finland

Summary statement:

Habitat specific adaptation in this young system has preceded the development of consistent population structuring, despite high levels of gene flow from divergent environments.

Abstract:

The relationships between adaptive divergence, genetic drift and gene flow can be complex. Genetic drift can aid divergence but might oppose adaptation due to its random nature. Gene flow on the other hand has the potential to both constrain and facilitate adaptation to local environmental conditions. Investigating temporal variation in gene flow during the initial stages of population divergence can therefore provide insights to the role of gene flow in adaptive evolution. Since the recent colonization of Lake Lesjaskogsvatnet in Norway by European grayling (Thymallus thymallus), local populations have been established in over 20 tributaries. Multiple founder events appear to have resulted in reduced neutral variation. Nevertheless, there is evidence for local adaptation in early life history traits to different temperature regimes. Microsatellite data from almost a decade of sampling revealed strong gene flow and a lack of stable stable population structure. Decomposed pairwise regression analysis showed differing patterns of genetic structure among local populations and indicated that migration outweighs genetic drift in the majority of populations. Subsequently, several climate factors were used to estimate the onset of spawning and calculate a spawning time difference index. Our results suggest that the temporal variation in population structuring seems to be driven by climate-induced differences in reproductive timing. In conclusion, this indicates that habitat specific adaptation in this system has preceded the development of consistent population sub-structuring, despite high levels of gene flow from divergent environments.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy29-i004-R*

Symposium 29
Can drift facilitate adaptive evolution?

Limited gene flow may enhance adaptation to local optima in isolated populations of Roesel´s bush cricket (Metrioptera roeselii)

Kiehl B[1], Kaňuch P[2], Cassel-Lundhagen A[1]
[1]Swedish University of Agricultural Sciences, Department of Ecology, Uppsala, Sweden, [2]Institute of Forest Ecology, Slovak Academy of Sciences, Zvolen, Slovakia

Summary statement:

Local selection pressures and gene flow interact to create latitudinal patterns in adaptive morphology of M. roeselii and seem to be enhanced by isolation.

Abstract:

Variation in morphological traits along latitudinal gradients often manifests as size clines. In insects both positive and negative correlations are observed. The mechanism behind the response is unclear and may even differ between organisms. Different mechanisms may also interact and this can create variation in responses, even among populations within species. Size variation may, for example, be determined by physiological constraints or selection pressures acting to favour larger or smaller individuals. These processes may also be affected by gene flow from surrounding populations. We studied variation in seven morphological traits of Roesel's bush cricket, Metrioptera roeselii, measured on wild caught and lab reared individuals originating from two latitude-matched-pair populations that were either geographically isolated from or connected to the species continuous distribution range. Data from field-collected specimens sampled in seven latitude-matched-pair populations indicates that size clines are apparent in the isolated populations while no such trend was found in the continuous area. Data from lab reared individuals was then used to evaluate if variation in trait means originates from plastic responses to the environment or genetic adaptation to local conditions. The combined morphological data from wild caught and lab reared individuals will allow us to discriminate between alternative mechanisms and to what extent gene flow has any influence on the pattern.

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WED 24 AUG at 1120 - Room N9
Oral presentation *D2-Sy29-1120-O*

Symposium 29
Can drift facilitate adaptive evolution?

Mechanism for a drift-induced evolutionary advantage of small populations in complex fitness landscapes

Krug J[1], Jain K[2], Park S-C[3]
[1]University of Cologne, Institute for Theoretical Physics, Köln, Germany, [2]Jawaharlal Nehru Centre for Advanced Scientific Research, Bangalore, India, [3]Catholic University of Korea, Bucheon, Korea, Republic of

Summary statement:

We show theoretically that drift may facilitate the adaptation of small populations in complex environments by helping the population to evade trapping at local fitness peaks.

Abstract:

The speed of adaptation of a population placed into a new environment is generally expected to increase with increasing population size, for at least two reasons: The supply of beneficial mutations is proportional to population size, and the probability of fixation of deleterious mutations is negligible in large populations. Contrary to this expectation, recent experiments on microbial populations have shown that small populations evolving in a complex nutrient medium may achieve a higher fitness than large ones due to the increased heterogeneity of adaptive trajectories. We introduce a class of haploid three-locus fitness landscapes that allows to investigate this scenario in a precise and quantitative way. Our main result derived analytically shows how the probability of choosing the path of largest initial fitness increase grows with the population size. This makes large populations more likely to get trapped at local fitness peaks and implies an advantage of small populations at intermediate time scales. Additional studies using ensembles of random fitness landscapes show that the results achieved for a particular choice of three-locus landscape parameters are robust and also persist as the number of loci increases. Our study indicates that an advantage for small populations is likely whenever the fitness landscape contains local maxima. The advantage appears at intermediate time scales, which are long enough for trapping at local fitness maxima to have occurred but too short for peak escape by the creation of multiple mutants.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Sy29-i005-R*

Symposium 29
Can drift facilitate adaptive evolution?

Genetic bottlenecks do not increase invasiveness in natural populations of the invasive garden ant Lasius neglectus

Larsen RS[1], Mosbacher J[1], Holman L[1], Pedersen JS[1]
[1]University of Copenhagen, Centre for Social Evolution, Department of Biology, Copenhagen, Denmark

Summary statement:

Unlike the Argentine ant we found no association of genetic diversity, variation of recognition cues and worker aggression in this invasive species.

Abstract:

Previous studies on the invasive Argentine ant Linepithema humile have shown that laboratory colonies become more aggressive towards conspecifics when genetic diversity, and consequently the diversity of chemical recognition cues such as cuticular hydrocarbons, is reduced. Hence, in an encounter the least diverse colony is more likely to be the aggressor, thus conferring a competitive advantage. This raises the hypothesis that invasive ability mediated by such polarized aggression paradoxically may increase over time in introduced populations when colonies go through more genetic bottlenecks.

This hypothesis was tested in natural populations of the invasive garden ant Lasius neglectus representing four independent introductions into Europe. When possible we collected live ants from the oldest and largest colony and from a young and small colony to represent different invasion stages. Behavioral tests were performed to detect polarized aggression among L. neglectus colonies (intraspecific), and to detect differences in aggression towards other local ant species that are likely competitors (interspecific). Furthermore, the genetic (11 microsatellite loci) and chemical (cuticular hydrocarbon) diversity of colonies was analyzed.

Young and old colonies did not differ significantly in genetic diversity or in aggression towards either conspecifics or local ant species. Furthermore, the colony genetic diversity did not correlate with aggression or the variation of cuticular hydrocarbons.

This indicates that polarized aggression mediated by genetic bottlenecks is not an important factor increasing invasiveness in introduced populations of this species.

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WED 24 AUG at 0910 - Room N9
Invited talk *D1-Sy29-0910-I*

Symposium 29
Can drift facilitate adaptive evolution?

Evolution of molecular error rates and the consequences for evolvability

Masel J[1], Rajon E[1,2]
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Summary statement:

Either low error rates or more benign cryptic sequences may evolve to mitigate gene expression errors. The latter drive evolvability, especially in large populations.

Abstract:

Making genes into gene products is subject to predictable errors, each with a phenotypic effect that depends on a normally cryptic sequence. The distribution of fitness effects of these cryptic sequences, like that of new mutations, is bimodal. For example, a cryptic sequence might be strongly deleterious if it causes protein misfolding, or it might have only a minor effect if it preserves the protein fold and tweaks function. Few sequences have effect sizes that fall in between.
Strongly deleterious sequences can be subject to some selection even while they are cryptic, and expressed only at low levels that depend on a molecular error. Strongly deleterious effects can be avoided globally by avoiding making errors (e.g., via proofreading machinery) or locally by ensuring that each error has a relatively benign effect. The local solution requires powerful selection acting on every cryptic site, and so evolves only in large populations. Small populations with less effective selection evolve global proofreading solutions. However, we also find that for a large range of realistic intermediate population sizes, the evolutionary dynamics are bistable and either solution may result. The local solution, which does not occur in very small populations, facilitates the genetic assimilation of cryptic genetic variation and therefore substantially increases evolvability.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy29-i001-E*

Symposium 29
Can drift facilitate adaptive evolution?

Drosophila subobscura in America: Molecular evidence of colonization

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[1]Universitat de Barcelona, Genetica, Barcelona, Spain, [2]Generalitat Valenciana, Centro Superior de Investigación en Salud Pública, Valencia, Spain, [3]Universitat de València, Institut Cavanilles de Biodiversitat i Biologia Evolutiva, Valencia, Spain

Summary statement:

Molecular evidence indicates a possible western Mediterranean origin of the colonization of America by D. subobscura.

Abstract:

The recent colonization of America by D. subobscura is a great opportunity for evolutionary biology studies. The knowledge of the populations from which the colonization started would allow understanding how genetic composition changed during the new environment adaptation. To this aim, a 793 nucleotide fragment of the Odh gene was sequenced in 66 chromosomal lines from Barcelona (western Mediterranean) and in 66 from Mt. Parnes (Greece, eastern Mediterranean). For both populations the estimates of nucleotide polymorphism were higher than those obtained in American populations. With the exception of O3+4+1, no associations between chromosomal inversions and Odh sequences were observed. No sequence of Odh fragment was identical in Barcelona or Mt. Parnes with those previously obtained in America. However, an Odh sequence from Barcelona differed in only one nucleotide with another found in American populations. In both cases, the chromosomal lines presented the same inversion, O7, being the Odh gene located inside this inversion. This is an evidence of a possible western Mediterranean origin of the colonization. From molecular and inversion data it seems that the colonization has not presented multiple reintroductions and thus, the genetic composition derived from the original population (probably from the western Mediterranean) was enough to assure the colonization success.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Sy29-i002-E*

Symposium 29
Can drift facilitate adaptive evolution?

Genetic drift widens the expected cline but narrows the expected cline width

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Summary statement:

Drift shifts clines from side to side, alters their width, and distorts their shape. We quantify the expected effects on the shape and position of a cline, and their variance.

Abstract:

Random genetic drift shifts clines from side to side, alters their width, and distorts their shape. Such random fluctuations complicate inferences from cline width and position, but may themselves be used to infer rates of gene flow, drift and selection. More important, genetic drift is expected to reduce local diversity, and so to make selection less effective, thereby interfering with adaptation to local conditions. We extend the previous results beyond the effect of genetic drift on the "expected cline" in a one-dimensional habitat, giving the relation between the deterministic cline width, the expected cline width and the width of the expected cline: With step change in selection, while random drift on average broadens the overall cline in expected allele frequency by a factor (1-‹F›)-1/2, it narrows the width of any particular cline by the inverse of this factor. Here, ‹F› is the standardised variance of fluctuations in the cline, averaged across the habitat with the weight of the product of expected allele frequencies. The apparently opposite effect arises because fluctuations in position make the expected cline wider. However, locally, drift drives alleles towards local fixation, so that individual clines are, on average, narrower. We also estimate the expected variance in the position and width of a cline.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Sy29-i006-R*

Symposium 29
Can drift facilitate adaptive evolution?

Strong neutral genetic- and morphological divergence in small islet populations of Podarcis gaigeae: Effects on pre-mating isolation and morph fixation

Runemark A[1], Hansson B[1], Svensson EI[1]
[1]Lund University, Department of Biology, Lund, Sweden

Summary statement:

Small islet populations of the Skyros wall lizard are strongly diverged in sexually selected traits. This divergence could potentially provide a basis for assortative mating.

Abstract:

Small isolated islet populations of the Skyros wall lizard Podarcis gaigeae show substantial morphological and behavioural divergence from geographically close mainland populations. We found strong neutral genetic divergence, significant differences in frequencies of throat colour morphs, in pheromone composition and in interest in sex pheromones between populations. Variation in colour morph frequencies and pheromone divergence among islet populations exceeded that between mainland populations, indicating accelerated phenotypic divergence in the islet populations. Both divergence in colour morph frequencies and pheromone composition were significantly correlated with neutral genetic divergence, and FST for colour morph fell within the lower part of the neutral FST-distribution. These patterns presumably reflect the combined effects of local selection and/or genetic drift. However, in behavioural assays investigating sexual interest islet lizards preferred the scent from other islet lizards regardless of population origin, whereas mainland animals were less discriminant. This is unexpected, since the difference in pheromone composition is larger between islet- than mainland populations, with few parallel changes in the pheromone composition between islands. The highly divergent pheromone composition on the islets indicates that sexually selected traits can diverge in arbitrary directions in small subdivided populations, potentially providing a basis for assortative mating and reinforcement. A possible loss of three out of six throat colour morphs in the closely related subspecies P. g. weigandi might also partly be due to stochasticity in combination with local selection.

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WED 24 AUG at 0950 - Room N9
Invited talk *D1-Sy29-0950-I*

Symposium 29
Can drift facilitate adaptive evolution?

Can drift facilitate adaptive evolution? Empirical insights from an antibiotic resistance gene

Salverda M[1], Koomen J[1], de Visser A[1]
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Summary statement:

In vitro evolution of an antibiotic resistance enzyme is used to answer questions about the role of drift in enzyme evolution.

Abstract:

TEM-1 β-lactamase is one of the best studies antibiotic resistance enzymes around. It confers resistance to ampicillins and early cephalosporins, while the resistance spectrum of the ~170 different variants of the enzyme that have been isolated in hospitals around the world has fanned out to monobactams and more modern cephalosporins like cefotaxime. Next to this well described 'natural' evolution, TEM-1 has been the focus of attention in many biochemical and biotechnological studies, leading to a high degree of understanding of which mutations in the enzyme alter its function and why they do so. We have previously used in vitro evolution of TEM-1 to study its adaptive pathways towards increased resistance to cefotaxime, and demonstrated that negative interactions between alternative initial mutations can cause diversification of the adaptive pathways. In this talk I will focus on experiments carried out to further clarify the role of drift in enzyme evolution. What is the effect of population size on the adaptive trajectories followed? And to what extent can an initial mutation determine the qualitative and quantitative outcome of evolution?

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WED 24 AUG at 1140 - Room N9
Oral presentation *D2-Sy29-1140-O*

Symposium 29
Can drift facilitate adaptive evolution?

Stochastic variation in individual fitness components and a neutral theory for life-histories

Steiner U[1], Tuljapurkar S[2]
[1]INSERM, U1001, Paris, France, [2]Stanford University, Biology, Stanford, United States

Summary statement:

The observed and predicted amounts of neutral stochastic variation in life histories amplifies drift and make it hard to detect selective variation in natural populations.

Abstract:

Stochastic variation among individuals within populations drives evolutionary and ecological dynamics. However, we lack an expectation of the stochastic neutral variation in fitness components. We present formulas to compute exactly the variance in fitness components among individuals with identical vital rates (assuming a common genotype) using matrix models. We illustrate the outcome and consequences of neutral and non-neutral variation for a natural population of a seabird bird species, and some E. coli strains in the lab using microfluidics devices. Non-neutral differences among genotypes increase variances in fitness components only modestly. The expected and observed amount of neutral variation predict small heritabilities for fitness components (which is in fact the case); small selective differences in quantitative characters will be hard to measure; and the effects of random drift will be amplified. Our findings highlight the challenge in disentangling demographic stochasticity, environmental stochastic effects, and genetic variation in natural populations.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Sy29-i007-R*

Symposium 29
Can drift facilitate adaptive evolution?

Fixation of slightly beneficial alleles in finite-size structured populations: Effects of life history

Vindenes Y[1,2], Lee AM[1], Engen S[3], Sæther B-E[1]
[1]Centre for Conservation Biology, Norwegian University of Science and Technology, Department of Biology, Trondheim, Norway, [2]Centre for Ecological and Evolutionary Synthesis, University of Oslo, Department of Biology, Oslo, Norway, [3]Centre for Conservation Biology, Norwegian University of Science and Technology, Department of Mathematical Sciences, Trondheim, Norway

Summary statement:

The fixation rate of beneficial alleles is shown to depend on reproductive value and demographic variance, two important life history characteristics in structured populations

Abstract:

The rate of evolution varies considerably between species and between populations. Explaining this variation requires knowledge of how the two main underlying processes, the rate of formation of new mutations and the rate of fixation of beneficial mutations, depend on life history characteristics. We focus on the latter process, revisiting the classic problem of finding the fixation probability of a slightly beneficial allele. Earlier results are extended to a model with overlapping generations and general stage structure, finite population size and stochastic fluctuations. The approach is based on diffusion approximation using recent results from stochastic demography, and we consider both the haploid and diploid case. The results, which are verified by computer simulation, indicate that even with complex life histories only two demographic parameters are sufficient to give an accurate approximation of the fixation probability. These are
1) the reproductive value of the stage in which the allele first occurs, and
2) the demographic variance of a subpopulation of mutants, defining the variance effective population size.
Both parameters depend on the general life history characteristics of a species. For instance, the demographic variance tends to be high and the reproductive value of newborns tends to be low in species with fast life histories characterized by low survival probability and high fecundity. Our results show that the fixation probability is low in such cases, and we hypothesize that this may explain part of the observed variation among species in rates of evolution.

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General session

Talks: *Room N2, N3, N4, N5, N6, N7*

Essence posters*:* Ground floor lecture hall centre *HZ*

Regular posters*:* Ground floor campus canteen *Mensa*

Organizers:

Local scientific committee

Description:

The general sessions address all topics relevant to Evolutionary Biology that are not sufficiently covered by the contributed symposia 1 to 29.

MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i001-R*

General sessions

The evolution of alternative developmental pathways in a butterfly: Footprints of ongoing selection on life history traits

Aalberg Haugen IM[1], Gotthard K[1]
[1]Stockholm University, Department of Zoology, Stockholm, Sweden

Summary statement:

Evolution of pathway-specific expression of three life history traits in the speckled wood butterfly.

Abstract:

In polyphenic traits alternative phenotypes are expressed depending on an environmental variable. Organisms with polyphenisms may frequently end up in environments where only one of the alternative phenotypes is expressed. In such situations only the developmental pathway leading to the expressed phenotype is subjected to selection; the unexpressed trait will be subject to relaxed selection and change only due to correlated evolution and genetic drift. Many insects have alternative developmental pathways leading to either diapause or direct development allowing alternative developmental regulation downstream of the diapause/direct decision producing adaptive phenotypic differences. To what degree such differences will be eroded when one of the pathways is never expressed has not been studied in any detail. We compare the alternative expression of life history traits along direct and diapause pathways in two populations of Pararge aegeria, one bivoltine and one univoltine. Direct development was associated with faster larval development and growth as well as a smaller pupal weight compared to pupal diapause. In the population with selection on both developmental pathways the difference between pathways in growth rate was larger while the difference in size was smaller, compared with the population in which direct development is rarely expressed. This suggests that relaxed selection has allowed these traits to drift. Selection on the direct development pathway appears to favor fast growth and a large size; the results also indicate that because of genetic correlations among pathways this selection may have influenced body size in the alternative developmental pathway.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i002-R*

General sessions

Ecological and evolutionary determinants of disease distribution in a natural host-pathogen system

Abbate JL[1]
[1]University of Virginia, Biology, Charlottesville, United States

Summary statement:

Temperature-induced pathogen suppression may limit anther-smut disease to high-elevation Silene vulgaris populations, and mean resistance shows no change across the gradient.

Abstract:

The ability to predict range limits for pathogens offers an important tool for targeting disease prevention and control strategies. Both ecological and evolutionary factors are important for species range distributions. This research investigated what factors determine the restriction of anther smut disease, Microbotryum spp., to high-elevation populations within the natural range of the host, Silene vulgaris. As a well developed model for host-pathogen dynamics, anther-smut in Silene is an ideal system for testing hypotheses empirically. Through a series of laboratory and field studies, I have found that high inoculation temperatures reduce infectivity rates, and cause suppression of disease symptoms and transmission opportunity through the hottest summer months. This implies the potential restriction of disease to higher elevations if climate change causes increased daytime temperatures along the gradient. Interestingly, I have shown that even though the hosts at the two elevations have separate evolutionary and disease exposure histories, lower elevation hosts are just as susceptible to disease as high-elevation hosts. While the limit to disease distribution might be tightly correlated with temperature effects along the elevational gradient, these results raise interesting questions about the effects of reduced disease prevalence on the evolution of resistance genes in nature.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i003-R*

General sessions

Not only the fed die young: Interactions of developmental and adult dietary restriction

Adler MI[1], Cassidy E[1], Bonduriansky R[1]
[1]University of New South Wales, Evolution & Ecology Research Centre, Sydney, Australia

Summary statement:

Manipulating diet at two key life history stages reveals a complex picture of resource scheduling, with sex-specific effects on multiple fitness-related traits.

Abstract:

Life history effects of dietary restriction in adulthood are well established in the evolution of ageing literature, but less is known about how dietary restriction in development affects life history traits, or how developmental and adult diets may interact. We manipulated both larval diet (high vs low concentration of nutrients) and adult diet (sugar-only vs sugar + protein) in Telostylinus angusticollis, a neriid fly that exhibits strong, sex-specific effects of condition on a variety of morphological and life history traits. We also manipulated the opportunity for reproduction. We measured effects on lifespan, ageing, reproductive performance, and somatic deterioration. In line with previous findings, our adult dietary restriction (sugar-only diet) resulted in a significant lifespan extension effect in both sexes. However, only males could successfully reproduce without protein in the adult diet, indicating that the sexes have very different dietary needs. Surprisingly, developmental dietary restriction (low carbohydrate and protein concentration) resulted in qualitatively different effects from those of adult dietary restriction, and revealed complex, sex-specific interactions between developmental and adult diets. Thus, the effects of both larval and adult diets were strongly sex-specific, and varied among fitness-related traits. Our findings suggest an intricate picture of resource allocation and life history scheduling that is responsive to multiple environmental variables.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i004-R*

General sessions

Genome size variability among phylogenetically distinct groups including sexual, diploid asexual and triploid asexual lineages

Adolfsson S[1], Lamatsch DK[2], Paczesniak D[3], Michalakis Y[4], Martens K[5], Schön I[5], Butlin RK[6], Jokela J[3]
[1]Uppsala University, EBC, Dep. of Evolutionary Biology, Uppsala, Sweden, [2]Institute for Limnology, Austrian Academy of Sciences, Mondsee, Austria, [3]EAWAG, IBZ, Zurich, Switzerland, [4]CNRS, IRD, Montpellier, France, [5]RBINS, Brussels, Belgium, [6]University of Sheffield, Sheffield, United Kingdom

Summary statement:

We use a phylogenetic approach to evaluate genome size change in respect to genetic divergence and discuss the effects of asexual transitions, often involving ploidy elevations.

Abstract:

Drift and adaptive processes can both account for genome size variation but an assessment of their relative importance is challenging. We use a phylogenetic approach to quantify and discuss the extensive variation in genome size within a species group. If genome size change correlates with phylogenetic distance between groups of organisms, then genetic distance between organisms could be employed to infer genome size evolution at different scales of divergence. We examined genome size variation using flow cytometry in European populations of the freshwater ostracod Eucypris virens, an especially interesting species complex since multiple transitions to diploid and triploid asexual lineages have occurred from shared sexual ancestors. We then linked the individual genome sizes to lineages defined by mitochondrial sequence, covering a total of eight divergent clusters. We found that the genome sizes of sexual diploid males were significantly smaller than those of sexual diploid females of the same population, in accordance with the expectations for species with X0 or XY sex chromosomes. The sexual diploid females had, in turn, a smaller genome size than the asexual diploid females, suggesting that transitions to asexuality can have an influence on genome size. Finally, we found a high variability in genome size among lineages within each reproductive mode and ploidy group and a significant correlation between genetic distance and difference in genome size. Comparisons to other species indicate that the absolute rate of genome size change in E. virens seems not to be exceptional.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i005-R*

General sessions

The fate in the wild of an MHC allele shared with a domesticated species: combining short- and long-term evidence for selection

Aeschbacher S[1,2], Grossen C[3], Biebach I[4], Keller LF[4], Barton NH[2]
[1]University of Edinburgh, Institute for Evolutionary Biology, Edinburgh, United Kingdom, [2]Institute of Science and Technology Austria, Klosterneuburg, Austria, [3]University of Lausanne, Lausanne, Switzerland, [4]University of Zurich, Zurich, Switzerland

Summary statement:

Combining short- and long-term signals, we found evidence for selection at the MHC class IIa gene DRB in a structured population of Alpine ibex (Capra ibex) in the Swiss Alps.

Abstract:

We found evidence for selection at the Major Histocompatibility Complex (MHC) gene DRB in a structured population of Alpine ibex (Capra ibex) in the Swiss Alps. DRB is an MHC class IIa gene and biallelic in ibex. One of the alleles is shared with domestic goat (C. aegagrus hircus), either as an ancestral polymorphism or due to more recent introgression. The known history of reintroduction of Alpine ibex into Switzerland allowed us to condition inference on detailed demographic information. We set up a drift-migration-selection model and numerically iterated the transition matrices to obtain joint and marginal likelihoods of parameters. In principle, the allele frequency spectrum was compatible with various dominance schemes and, therefore, a wide range of selection coefficients. Considering additional short-term signals of selection, we concluded that the allele shared with domestic goat had likely been under spatially homogeneous selection (Ne*s ~ 1 to 100) in the wild during the last 50 to 100 years, and that there was either underdominance or directional selection against it. This findings would exclude overdominance as a mechanism for the maintenance of diversity at DRB in Alpine ibex. Further, negative selection against the shared allele would support recent introgression, rather than an ancestral polymorphism. Migration tended to reduce estimated selection coefficients, but could not explain the data equally well on its own.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i006-R*

General sessions

Eggs choose the sperm that produce the best quality offspring

Aguirre JD[1], Blows MW[1], Marshall DJ[1]
[1]The University of Queensland, School of Biological Sciences, Brisbane, Australia

Summary statement:

The compatibility of sperm and eggs at fertilisation determines the fitness of offspring in a broadcast spawning marine invertebrate.

Abstract:

In sexual selection, females can choose to mate with either males of higher genetic quality, or more genetically compatible males. Choice for both male quality and male compatibility increase female reproductive success by increasing the genetic quality of her offspring. Studies on broadcast spawning species have shown that species recognition happens at the level of gametes – eggs can recognise sperm of the same species, and it appears that this gamete-level choice also occurs within species. Some male x female combinations of gametes result in higher fertilisation success than others, but whether this reflects male quality effects or genetic compatibility remains unknown. Here, we examined the consequences of female choice on offspring quality, and thus female reproductive success in the broadcast spawning tunicate Ciona intestinalis. Using a half-sib breeding design we found that male genetic quality effects were either weak or non-significant, whereas male compatibility effects were strong and persistent. Moreover, we find there is a positive relationship between male x female compatibility at fertilisation and post-fertilisation offspring performance. Overall, our results suggest that gametes that are more compatible at fertilisation produce better performing offspring, and provide evidence that mate-choice can occur in the ancestral reproductive strategy of broadcast spawning.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i001-E*

General sessions

Sex and origin matter - The influence of predator regime and sex on the behaviour and mortality of a freshwater amphipod, Gammarus pulex

Ahlgren J[1], Åbjörnsson K[1], Brönmark C[1]
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Summary statement:

Tthere are general differences in behaviour traits, both between predator regimes and sexes in G. pulex.

Abstract:

In species with restricted dispersal, traits may become genetically fixed leading to local adaptations. Therefore, predator avoidance in a prey species may differ between populations experiencing different predator regimes, but also between sexes within a population due to different vulnerability to predators. In this study we used male and female Gammarus pulex from two different predator regimes: fishless ponds, where invertebrates are the dominant predators and ponds with predatory fish. In the laboratory we examined refuge use, mortality, leaf decomposition rate and pairformation in G. pulex when exposed to predator cues from either invertebrate predators or fish. Individuals from fish ponds spent more time in refuge and had a higher mortality than those from fishless ponds independent of predator cues. There was no effect of pond predator regime or predator cues on leaf decomposition rates. Further, fewer individuals formed pairs in G. pulex from fish ponds than from fishless ponds. Male G. pulex had a higher mortality and a higher decomposition rate than females independent of predator cues. However, there was no difference in refuge use between sexes. We found that there are general differences in behaviour traits, both between predator regimes and sexes in G. pulex.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i003-E*

General sessions

Metabolic rate and energy consumption in an aphid parasitoid

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Summary statement:

An investigation of whether metabolic rates influence energy consumption rates in an aphid parasitoid, and if such relation varies according to body size.

Abstract:

It is widely known that metabolic rates and energy reserves are key elements to understanding fitness in ectotherms, as they affect important life history traits, such as longevity, dispersal and fecundity. In some insect species, lipid reserves are fixed at birth or nymphal emergence, inducing high selective pressure on metabolic rates and organism maintenance. Considering such a species, an aphid parasitoid, we investigated the effects of metabolic rate on the speed of energetic resource consumption, and how different body sizes may influence that relation.
For this purpose, we considered male and female parasitoids and measured their (1) longevity under starvation conditions, (2) metabolic rate at 1 day old, (3) body size and (4) initial lipid reserves. Results were analysed in order to find potential correlations between those traits, in an attempt to better understand the mechanisms by which pre-emergency energy intake and lipid synthesis as well as metabolic rates affect fitness. We also examined those results in light of two current hypotheses: (1) the absolute energy demand (AED) hypothesis, which predicts that smaller organisms are advantaged by their lesser energy requirements, and (2) the relative efficiency (RE) hypothesis, which predicts that larger individuals are favoured by their more efficient resource consumption rate. Both hypotheses are related to metabolic rates, however the conditions to which they apply are yet to be fully understood.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i007-R*

General sessions

Population history and evolution of colour variation of European Barn Owls: Insights from an approximate Bayesian computation approach

Antoniazza S[1], Neuenschwander S[2], Kanitz R[2], Burri R[3], Fumagalli L[2], Roulin A[2], Goudet J[2]
[1]University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland, [2]University of Lausanne, Lausanne, Switzerland, [3]Uppsala University, Uppsala, Sweden

Summary statement:

We used an Approximate Bayesian Computation approach on microsatellites data in European Barn Owl to unravel past history and understand the evolution of a colour polymorphism.

Abstract:

Understanding the evolution and maintenance of phenotypic variation in space requires a deep comprehension of past demographic and evolutionary history. Reconstructing past demographic history is notoriously difficult. While several analytical techniques exist for simple scenarios, complexes real world cases are difficult to study analytically. In these cases, Approximate Bayesian Computation (ABC) techniques provide a flexible and powerful alternative. The rationale of ABC is to compare the observed summary statistics of genetic variation in a study organism with those obtained from simulated data generated under different models and parameters values. These comparisons allow inferring which historical scenario matches best the current observed data. In this study, we performed an ABC analysis in European Barn Owls in order to understand how a strong cline in melanin-based colouration known to be under selection at the scale of Europe can be maintained despite very low differentiation for neutral genetic markers. We will particularly test whether these patterns are best explained by an expansion after the end of last glacial maximum from one or two refugees and attempt to date the onset of colonisation.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i004-E*

General sessions

Detecting a reproductive fitness difference in the wild: power analysis and its application to salmon populations

Araki H[1], Njenga P[1], Adjei B[1]
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Summary statement:

To evaluate the best means of detecting fitness difference in the wild, power analyses were performed under realistic conditions, followed by its application to salmon populations.

Abstract:

Fitness difference of living organisms in the wild is of central interest in evolutionary biology. While theoretical studies suggest that even a small difference in fitness, especially in reproductive fitness, can have a profound impact on the evolutionary process, our ability to identify them in natural environment is often quite limited. Furthermore, it is not clear how best one can statistically test such a difference in reproductive fitness between the groups of interest. To address this issue, we performed power analyses on several statistical tests under realistic conditions. Our results suggest that not only the number of parental samples but also the number of offspring samples are important to obtain a sufficient power in the tests, and that the fitness distribution plays a critical role in the power. Some tests provided a higher power than the others, but the statistical significance should be taken into account with care because it occasionally comes with a risk of a higher type-I error rate than expected under certain conditions. Using empirical examples from salmonid fish populations, we discuss how one should test the difference in reproductive fitness in the wild.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i008-R*

General sessions

Superior quality of extrapair nestlings in blue tit – good genes interact with environment?

Arct A[1], Drobniak SM[1], Podmokła E[1], Cichoń M[1]
[1]Jagiellonian University, Institute of Environmental Sciences, Krakow, Poland

Summary statement:

Our study indicate that the fitness benefits of extra-pair mating are likely to be context dependent.

Abstract:

Extra-pair matings constitute a relatively frequent reproductive strategy in a number of species. This strategy may considerably improve reproductive success of males, but the reasons of why females might be interested in extra-pair matings is not such clear. The good genes hypothesis is usually invoked to explain such female behavior, but empirical evidence supporting existence of any benefits in females remains elusive. It is possible that any benefits of extra-pair matings may come into play only in adverse environments. In order to test this prediction we manipulated environmental conditions by altering brood sizes of blue tits and compared phenotypic characteristics of within pair offspring (WPO) and extra-pair offspring (EPO) in mixed-paternity broods. We found that extra-pair young were larger than WPO independent of environmental condition. They also exhibited improved immune response in comparison to WPO, but this was only apparent among nestlings from enlarged broods. These results indicate that any benefits of extra-pair mating are likely to be context dependent, and that genetic effects may be more apparent when conditions are relatively unfavourable.

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SUN 21 AUG at 1140 - Room N6
Oral presentation *A2-Ge05-1140-O*

General sessions
Disease and immunity

Specific immune priming and the evolution of Dscam across the arthropods

Armitage SAO[1], Glander S[1], Freiburg R[1], Bravo IG[1,2,3], Kurtz J[1]
[1]Institute for Evolution and Biodiversity / University of Münster, Münster, Germany, [2]Genomics and Health / Centre for Public Health Research (CSISP), Valencia, Spain, [3]Unit of Infections and Cancer / Catalan Institute of Oncology (ICO), L'Hospitalet de Llobregat, Spain

Summary statement:

Specific immune priming and the evolution of Dscam across the arthropods.

Abstract:

Innate immunity is evolutionarily ancient; it is the first line of defence for vertebrates and invertebrates against parasites. To understand how the insect innate immune system combats parasites it is necessary to have an insight into both immunological mechanisms, and into how the evolutionary pressures of abundant and rapidly evolving parasites have shaped immune defence. Key to this understanding is knowledge about how the immune system recognises parasite antigen diversity: Downs syndrome cell adhesion molecule (Dscam) has been proposed as a candidate for recognition of specific antigens by insects and may also be involved in immune priming (phenomenologically similar to immune memory in vertebrates). I will first present experimental data on the phenomenon of specific immune priming in Drosophila melanogaster. Second, I will present an analysis of the evolution of the Dscam gene family across the arthropods. Some Dscam exons have undergone massive expansions resulting in mutually exclusive alternative splicing that in D. melanogaster can potentially result in thousands of different isoforms, and can putatively provide diversity for parasite recognition; we therefore also examined the evolution of the alternatively spliced exons across arthropod species.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i005-E*

General sessions

Can sperm competition cause evolution of faster sperm in polygamous compared to monogamous guppies?

Aronsen T[1], Fossøy F[1], Rudolfsen G[2], Egset CK[1], Rosenqvist G[1]
[1]NTNU, Biology, Trondheim, Norway, [2]NRPA, Tromsø, Norway

Summary statement:

We have investigated sperm ejaculate characteristics of male guppies from generation 12 of polygamous and monogamous populations of guppies.

Abstract:

Sperm competition is the form of postcopulatory sexual selection that occurs when ejaculates from several males competes to fertilize the ova of a female. Sperm competition is common in many animal taxa, and a powerful evolutionary force. Sperm competition theory predicts that the strength of sperm competition will affect sperm characteristics. Specifically, evolution by sperm competition should favour traits that enhance male fertilization ability. Sperm velocity has earlier been shown to determine fertilization success across several taxa.
In this study we investigate how sperm competition may influence the velocity and number of sperm of captive bred guppies (Poecilia reticulata). We compare sperm ejaculates from guppies from replicated populations that have been mated either polygamously or monogamously for 12 generations. We predict that postcopulatory sexual selection have lead to the evolution of ejaculates with higher competitive abilities (faster and more sperm) in polygamous populations, compared to the ejaculates of males from populations that have experienced enforced monogamy for many generations.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i006-E*

General sessions

Ontogeny of the immune function relative to developmental periods in avian offspring

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Summary statement:

This study shows the results of a comparative study relating multiple immune responses with life history and ecological traits in nestlings of tropical and temperate bird species.

Abstract:

Variation in ontogeny and investment in immune defense mechanisms can be integrally related to variation in life history strategies and determined by trade-offs during development. The nestling period in birds, represents a critical window of vulnerability to pathogens because the immune system is still developing. Therefore, the ability to resist infections during the juvenile period is expected to be under intense selection pressure. However, little is still known about the ontogeny of immune function in wild birds, especially in a comparative context across species with diverse life history strategies. Here I present the results of a taxonomically broad comparative study relating multiple types of immune responses with life history and ecological traits in nestlings of tropical and temperate bird species. I examined several components of the constitutive and induced immune response in relation to developmental stage in 22 Passerine species sampled in tropical Venezuela and north temperate Arizona. The results show activity of constitutive components of the immune defense as early as 1-3 days post-hatching, and an increase in immune activity with age. This increase indicates that immune function in older nestlings reflects intrinsic development and not maternal effects. Nestlings sampled in Venezuela had higher natural antibody levels than nestlings from Arizona. However, this difference was not related to variation in developmental periods across species or sites.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i010-R*

General sessions

Drosophila melanogaster develops aversive behaviour after interacting with a virulent pathogen

Babin A[1], Schneider F[1], Dolivo V[1], Kawecki TJ[1]
[1]University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland

Summary statement:

Fruit flies develop avoidance of food contaminated with the entomopathogen Pseudomonas entomophila.

Abstract:

Animals are permanently exposed to pathogens which may cause diseases. Upon encountering a pathogen, an animal faces two non-mutually exclusive options: to activate its immune system to eliminate the source of infection, or to express an aversive behaviour to prevent infection by the pathogen. Drosophila melanogaster lives on decaying and fermenting fruit, and is likely to ingest pathogens, such as the highly virulent bacterial entomopathogen Pseudomonas entomophila. Fruit flies are also well-known for their ability to learn in different contexts (mating, oviposition, foraging). In this study, we tested whether flies have evolved the ability to learn to avoid pathogens which contaminate their food patches. In one experiment, flies were given a choice between a non-contaminated food source and a food source contaminated with either a pathogenic strain or a harmless mutant strain of P. entomophila. In a second experiment, flies had a binary choice between two contaminated food sources, one with the pathogenic strain of P. entomophila and the other one with the harmless mutant. We found that in both types of binary choice tests, flies developed an aversive behaviour towards food sources contaminated with the pathogenic strain of P. entomophila over time, while their preference did not change after exposure to the harmless mutant of P. entomophila. Our results showed that fruit flies are able to modify their preference for food sources to avoid pathogens, and further suggest that they may be able of associative learning in this context.

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WED 24 AUG at 1440 - Room N5
Oral presentation *D3-Ge09-1440-O*

General sessions
Evolution of sex

Delineating arenas of recombination in bacterial populations using multilocus sequence typing data

Balbi KJ[1], Aswad A[1], Barraclough TG[1]
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Summary statement:

We present a method for identifying groups of closely related bacteria, within a named species or species complex, which are recombining only within themselves.

Abstract:

The concept of a species in bacteria has been hotly debated and many approaches rely up on setting an arbitrary threshold for sequence similarity.

However there are now a large number of Multilocus Sequence Typing (MLST) databases, each database containing hundreds or thousands of sequence profiles for isolates of a given named bacterial species or species complex. These databases open up the opportunity to examine whether subgroups can be reliably identified using the MLST profiles and sequence data, based on biologically relevant criteria.

To that end we present a bioinformatics approach based upon the microepidemic adaptation of the neutral infinite alleles model (IAM), as proposed by Fraser et al (2005), which determines a distribution of the number of mismatched alleles within population as a function of both the mutation and recombination rate.

ur method uses a phylogenetic tree as guide to successively partition the dataset and, assuming that recombination between clades is minimal, to optimize an independent IAM fit to each clade. In this way the dataset is continually subdivided until no improvement is achieved in the log likelihood scores of all the optimized IAMs, revealing groups of isolates which show no / minimal signs of genetic exchange via recombination.

We demonstrate this approach using a Bacillus cereus dataset, using both the standard housekeeping genes and several ecologically relevant genes.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i007-E*

General sessions

How mammals grow large brains: brain size, maternal investment and life histories in eutherian mammals

Barton RA[1]
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Summary statement:

We use phylogenetic comparative analysis to examine developmental mechanisms underlying brain size evolution in eutherian mammals

Abstract:

Brain size variation in mammals correlates with life histories: larger-brained species have longer gestations, mature later and have increased lifespans. Explanations for these patterns have been framed in terms of both developmental costs (larger brains take longer to grow) and cognitive benefits (large brains enhance survival and increase lifespan). In support of the developmental cost hypothesis, we show that evolutionary changes in pre- and post-natal brain growth correlate specifically with duration of the relevant phases of maternal investment (gestation and lactation respectively). We also find support for the hypothesis that the rate of fetal brain growth is related to the energy turnover of the mother. In contrast, we find no support for hypotheses proposing that costs are accommodated through direct trade-offs between brain and body growth, or between brain growth and litter size. Once the duration of maternal investment is taken into account, however, adult brain size is uncorrelated with post-weaning life history traits and lifespan. Hence, the general pattern of slower life histories in large-brained species appears to be a direct consequence of developmental costs.

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MON 22 AUG at 1100 - Room N3
Oral presentation *B2-Ge02-1100-O*

General sessions
Life-history

Experimental evidence for Crozier´s paradox: somatic fusion in fungi as a model for the evolution of cooperation and kin recognition

Bastiaans E[1], Debets AJM[1], Aanen DK[1]
[1]Wageningen University, Laboratory of Genetics, Wageningen, Netherlands

Summary statement:

We show that fungal fusion is cooperative, leading to loss of recognition types on the short term, as Crozier predicted. This contrasts with the many recognition types in nature.

Abstract:

Cooperative behaviors, behaviors that benefit other individuals, are widespread. However, to understand cooperation we have to explain how cheating, i.e. profiting without contributing, is kept at low frequency. Kin selection is the predominant solution for this problem. Kin selection requires that cooperation is preferentially directed towards related individuals, and one way to achieve this is via genetic kin recognition. However, Crozier argued that in the short term positive frequency dependent selection will eliminate the genetic polymorphism required for such recognition, since common genotypes will experience more cooperation and thereby increase in frequency. Here we study somatic fusion as a model for cooperation and kin recognition. Sharing somatic tissue via fusion seems to be an extreme form of cooperation, but the fitness consequences of fusion are unknown. In fungi, successful somatic fusion is usually restricted to clonally related individuals, regulated by highly polymorphic recognition loci. We study somatic fusion between mycelia of the fungal species Neurospora crassa. First we show that there is a highly significant positive correlation between total fitness and the degree of successful fusion. This result demonstrates that fusion between genetically identical mycelia is net beneficial (i.e. B-C>0) and thus cooperative. We then show experimental evidence for Crozier’s theoretical prediction that, in the short term, positive frequency dependent selection acts against polymorphism of recognition alleles. With these findings we discuss which counteracting evolutionary forces maintain the extensive recognition polymorphism observed in nature.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i008-E*

General sessions

Inbreeding and inbreeding depression in an open population of dippers (Cinclus cinclus)

Becker P[1], Hegelbach J[1], Keller L[1], Postma E[1]
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Summary statement:

We test for effects of inbreeding on morphological and life-history traits in the Eurasian dipper, and discuss our findings in terms of the evolution of mate choice and dispersal.

Abstract:

The negative effect of inbreeding (i.e. inbreeding depression) has been studied intensively over the last decades. Inbreeding depression has been shown to affect e.g. birth weight, survival or resistance to disease in various taxa of animals and plants. However, most studies in the wild have focused on small and isolated populations. Here we use a long term data set for a Swiss population of Eurasian dippers (Cinclus cinclus), a bird species which lives along streams and rivers. Mark-recapture data reveal high levels of gene flow between the different rivers which constitute our study area. Nevertheless, extensive pedigree data show high levels of inbreeding. Here we first test whether inbreeding in this system is higher than expected under random mating, and second, whether there are negative effects of inbreeding on morphological traits, survival and life-time reproductive success. We discuss our findings within the light of the evolution of mate choice and dispersal behavior as potential mechanisms for inbreeding avoidance.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i011-R*

General sessions

Parasites cause spatially fluctuating selection on MHC (Major Histocompatibility Complex) genes in Eurasian perch (Perca fluviatilits)

Behrmann-Godel J[1], Oppelt C[1]
[1]University of Konstanz, Limnological Institute, Konstanz, Germany

Summary statement:

We empirically show that variability in local parasite-host interaction can cause spatially fluctuating selection on Major Histocompatibility Complex genes in perch

Abstract:

Parasites affect the fitness of their hosts and thus can be seen as major selective agents for the evolution of defence mechanisms. Parasites have a patchy distribution and due to their complex life cycles, parasite communities of local host populations can be very variable. Thus local selection by parasites can result in a geographic mosaic of adaptations in the host population. MHC class II genes are perfect candidates to study adaptive traits in parasite host interaction and coevolution. They code for receptors that present parasite-derived antigens to immune cells and induce the adaptive immune response.

We analysed the local parasite communities of perch at 10 different locations within one large lake and found differences between locations. High allele variability of MHC class II genes was found for perch with 8 loci and 41 alleles. However, only a subset of loci and alleles was expressed at the locations studied, and we found local differences in allele pattern and frequencies of expressed alleles. This was in sharp contrast to neutral markers (10 microsatellite loci) that showed no population substructuring between any of the local perch stocks. Similarity in MHC allele pattern between individual fish was correlated with similarity of their parasite community. Moreover we found significant associations between several alleles and parasite species. Thus the presence of specific MHC class II alleles was positively or negatively correlated with a higher or lower abundance of specific parasites. Our results indeed indicate fluctuating selection in space and will be discussed in terms of parasite host interaction, coevolution, local adaptation and speciation.

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WED 24 AUG at 1400 - Room N4
Oral presentation *D3-Ge04-1400-O*

General sessions
Evolutionary genetics

The origin of novelty through the evolution of novel expression domains or novel pathway regulators of conserved genetic circuitry

Beldade P[1,2], Saenko SV[2]
[1]Instituto Gulbenkian de Ciencia, Oeiras, Portugal, [2]Institute of Biology, Leiden University, Leiden, Netherlands

Summary statement:

The evolution of novelties via the acquisition of novel expression domains or novel regulators of conserved developmental genetic circuitry.

Abstract:

Comparative studies of anatomy and development have suggested that the extraordinary diversity in animal form is not matched by equivalent levels of diversity in underlying "building blocks" and mechanisms. The same body structures and the same cellular and molecular mechanisms are used to produce different body parts in single organisms and different body plans across species. Even the evolutionary origin of novel adaptive traits seems to rely largely on "teaching old genes new tricks". The genetic and developmental basis of the formation and diversification of such novelties is a crucial topic in evo-devo whose resolution will require a wider sampling of phylogenetic and morphological diversity. We will discuss the redeployment of conserved developmental genes and pathways (specifically, the Hox gene Antennapedia and the Wingless signaling pathway) to the formation of novel, complex traits (specifically, butterfly wing color pattern elements called eyespots). Our analysis shows that the recruitment of Antennapedia to the early specification of eyespot organizers proceeded via the acquisition of a novel and unique expression domain, and that this occurred only in a specific lineage having eyespot-bearing butterflies. We also show that the involvement of Wingless signaling in the later specification of color rings seems to have involved a novel regulator for this widely studied pathway. The genomic location of this locus furthermore suggests that it is a putative "hotspot" for wing pattern diversification. Together, our results illustrate different genetic mechanisms whereby shared genetic circuitry can be involved in the origin and diversification of novel traits.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i012-R*

General sessions

The population genetics of positive but deteriorating mutations

Bengtsson BO[1]
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Summary statement:

Not all mutations are consistently good or bad. What are the evolutionary effects of mutations, for exemple asexual clones, that start as good but rapidly deteriorate in fitness?

Abstract:

Some positive mutations decline in fitness soon after they have become induced. Examples of mutations that may show such behaviour are polyploids, asexual clones, biochemical opportunists that deteriorate their own cellular environment, mutations causing trinucleotide repeat expansion, and so on. I have analysed the population genetics of such mutations, making only a minimal number of assumptions.

In an infinitely large population with recurrent mutations, an equilibrium state will be reached if and only if the loss of fitness to the mutant type is greater than μ within a bounded number of generations (where μ is the mutation rate). Many properties of this equilibrium state can be described, corresponding to the properties of the standard mutation-selection balance under fixed fitness values. With a smooth change in fitness, the most common class of mutations will have fitness close to normal. From empirical data it can therefore be difficult to grasp the complex dynamics underlying the population variation.

In finite populations, a mutation of the assumed kind may go to fixation before it turns deleterious. Probabilities for this to happen have been estimated using computer simulations.

For mutations that stay positive until they drastically drop in fitness additional results can be obtained. Their behaviour is, for example, more determined by the time to the fitness drop than by the actual fitness values. Modifier selection will increase the time to the fitness drop in sexual populations but will not affect it in asexual populations.

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MON 22 AUG at 1120 - Room N7
Oral presentation ***B2-Ge04-1120-O***

General sessions
Evolutionary genetics

An evolutionary model of genome streamlining in free-living prokaryotes

Bentkowski P[1], Williams HTP[2], Mock T[1], Lenton TM[1]
[1]University of East Anglia, School of Environmental Sciences, Norwich, United Kingdom, [2]University of East Anglia, School of Computing Sciences, Norwich, United Kingdom

Summary statement:

An agent-based model was developed to test if the variability of the environmental conditions can drive the genome streamlining in prokaryotes.

Abstract:

The size of the genomes of known free-living prokaryotes varies from ~1.3 Mb to ~13 Mb (Koonin & Wolf, 2008). We would like to propose an explanation of this variation due to variability of the physical conditions of the environment. In a stable environment the competition for the resource becomes the main force of selection and smaller (cheaper) genomes are favoured. In more variable conditions larger genomes will be preferred, as they have a wider range of response to a less predictable environment.

We have developed an agent-based model (ABM) of genome evolution in an aquatic prokaryotic population. Using a classic Hutchinson niche space model (1957), we defined a gene as a Gaussian function over a corresponding niche dimension. The cell can have more than one gene along a given dimension, and the envelope of all the corresponding responses is considered a full description of a cell´s phenotype over that dimension. Gene deletion, gene duplication, and point mutations are permitted during reproduction, so the number of genes and their phenotypic effect (height and position of the Gaussian envelope) are free to evolve. The surface under the curve is fixed to prevent ´supergenes´ from occurring. Change of the environmental conditions is simulated as a bounded random walk with a varying length of the step (a parameter representing variability of the environment).

Using this approach we are able to reproduce the phenomenon of genome streamlining in more stable environments (e.g. oligotrophic gyre regions of the ocean) and genome complexification in variable environments.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i013-R*

General sessions

Selection against inbreeding in a natural house sparrow population

Billing AM[1], Lee AM[1], Skjelseth S[1], Borg ÅA[1], Pärn H[1], Ringsby TH[1], Sæther B-E[1], Jensen H[1]
[1]Norwegian University of Science and Technology, Centre for Conservation Biology, Trondheim, Norway

Summary statement:

No inbreeding avoidance led to high levels of inbreeding and reduced female reproductive success during the decade after a new population was founded.

Abstract:

Inbreeding is one of the most important genetic processes affecting the persistence of small and threatened populations. Inbreeding usually has a negative effect on individual fitness and causes loss of biodiversity at all levels of organization, i.e. genes, populations, species and communities. In this study we investigated the effects of inbreeding on fitness in a wild, highly inbreed house sparrow (Passer domesticus) population. After the founding event in 1998 (by one female and three males) the adult population size rapidly increased to more than 30 individuals. At the same time the mean inbreeding coefficient among adults increased to a level of approx. 0.06 in 2002, and thereafter fluctuated between 0.06 and 0.10, indicating a highly inbred population. We found a negative effect of inbreeding on the total production of recruits over an individual's lifespan, i.e. a reduced lifetime reproductive success. Furthermore, analyses suggested that there was selection against inbreeding in females but that this effect was less clear in males. In addition, we compared observed inbreeding and kinship coefficients in the population with those obtained from simulations of random mating. This did not indicate that mating in the population had been non-random with respect to inbreeding. We conclude that there was selection against inbreeding in females in this population and that this was due to lower reproductive success of highly inbred females. Despite this birds did not seem to actively avoid mating with close relatives, perhaps as a consequence of constraints on mating possibilities in such a small population.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i009-E*

General sessions

Modeling the evolution of concealed ovulation

Birand A[1]
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Summary statement:

We model the conditions under which concealed ovulation could evolve where females stop advertising their estrus.

Abstract:

Mammalian females usually mate during a brief period around ovulation, usually called estrus. In some anthropoid primates, however, there is a tendency to mate at times when conception is not possible such as during the luteal phase of the ovarian cycle, and pregnancy. In addition to non-reproductive mating or prolonged sexual receptivity, in some anthropoid primates ovulation is not advertised by external visual signs, while other species have marked sexual swellings. Evolution of concealed ovulation presents a dilemma since the females that show no or reduced signs of ovulation should be selected against. Here, we model under what conditions could concealed ovulation evolve, and evaluate the plausibility of two competing hypotheses, viz. parental investment hypothesis and the reduced infanticide hypothesis. The former hypothesis suggests that concealed ovulation forces males into consort relationships longer, which decreases the opportunity to for males to mate with other females and potentially increases males wilingness to invest in their offspring. The latter hypothesis suggests that concealed ovulation and promiscuity combined confuse males about paternity and reduce infanticide.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i014-R*

General sessions

When evolutionary theory meets reality: Population dynamics and genetic variation in an endangered shorebird

Blomqvist D[1], Pauliny A[1], Borlid J[1]
[1]University of Gothenburg, Department of Zoology, Gothenburg, Sweden

Summary statement:

Long-term data from a declining bird population provide striking support for theoretical predictions, e.g. the influence of population structure and genetics on local extinctions.

Abstract:

Theory predicts that small populations should suffer from loss of genetic diversity through inbreeding and genetic drift. The reduced genetic variation is expected to lower individual fitness, but it may also eventually erode the population's mean fitness and thereby increase the likelihood of its extinction. However, detailed tests in natural populations are scarce. We used long-term data to examine population dynamics in a critically endangered shorebird, the southern dunlin (Calidris alpina schinzii). Our study population consists of several sub-populations, whose fates appeared to support predictions from classical metapopulation theory. Sub-populations inhabiting small and relatively isolated habitat patches received fewer immigrants than those inhabiting larger and less isolated sites. Consequently, both patch area and degree of isolation were correlated with the likelihood of local extinction. Further supporting theoretical predictions, we found a marked increase in the level of inbreeding over time. These matings resulted in more homozygous offspring that suffered from reduced fitness in early and probably also later life stages. Since the population-level of genetic variation has been suggested to influence mating patterns and sexual selection, we are also examining patterns of genetic parentage.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i015-R*

General sessions

When to be neighbourly: exploring cooperative territory defence in fiddler crabs

Booksmythe I[1], Hayes C[1], Jennions MD[1], Backwell PRY[1]
[1]Australian National University, Research School of Biology, Canberra, Australia

Summary statement:

Fiddler crabs support theoretical predictions that it can be less costly to help defend a neighbour´s territory than to establish new territory boundaries with a successful usurper.

Abstract:

Fiddler crabs defend individual territories, and fight repeatedly with their neighbours to establish and maintain territory boundaries. Despite this intense competition between neighbours and the costs of territory defence, residents will sometimes help their neighbours to repel intruding individuals. Cooperative territory defence is predicted when the cost of helping a neighbour is less than the cost of establishing new boundaries with a successful usurper of a neighbouring territory. In fiddler crabs cooperative defence occurs within and between the sexes and across species, but in almost all cases depends strongly on the sizes of participants: larger crabs will help their smaller neighbours against intermediate-sized intruders. Simply meeting these size criteria does not, however, guarantee that helping occurs, and additional factors are likely to determine the net benefit of helping a neighbour. In this talk I will explore the conditions necessary for cooperative territory defence and factors influencing the likelihood that help is provided, and consider why cooperative defence is not more common in other, similarly territorial species. I will present the results of an experimental study that simulated territory intrusions to investigate the effects of neighbour familiarity and size on helping behaviour.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i010-E*

General sessions

Analysis of the diversity and the genetic structure of Cystoseira Amentacea var. stricta (Phaephyceae: Fucales)

Bottin L[1], Robvieux P[2], Thibaut T[2], Meinesz A[2]
[1]Laboratoire ECOMERS UE 4228, Nice Cedex, France, [2]Laboratoire ECOMERS, UE 4228, Nice, France

Summary statement:

Population genetic study of the brown algae Cystoseira amentacea var. stricta, a major species of the sublittoral zone, on the French Mediterranean coast.

Abstract:

In the Mediterranean Sea, Fucales (Phaeophyceae) are mainly represented by the genus Cystoseira (Sargassaceae). Cystoseira amentacea var. stricta is among the most vulnerable species in the genus Cystoseira. This species can form continuous or fragmented belts in the sublittoral zone. Human activities such as sewage outfalls along with the nature and topography of the substrate (e.g sand coasts or overhanging cliffs) can result in belts fragmentation. This study aimed at studying the genetic structure and diversity of the French Mediterranean populations of Cystoseira amentacea var. stricta.
This analysis was based on 8 microsatellites and was performed on 56 populations along the French coast. This was the first time so many microsatellites were developed for a Cystoseira species.
The number of alleles in the studied populations varied between 9 and 25. The rate of observed heterozygosity ranged from 0.140 to 0.505 which was significantly low compared to the expected ratio. The fixation index values (Fis) in each population varied from 0.279 to 0.623, implying a strong intrapopulation structure. This might be partly explained by the very low dispersal rate of the zygotes. In C. amentacea, a when a zygote is released, it directly sinks on the substrate and exsudes a substance fixing it onto the substrate. The intrapopulation differentiation within the total population was significant (Fst = 0.172), suggesting a low gene flow between populations. This could be partially due to the low dispersal ability of zygotes, and to past glaciations or global warming events.

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MON 22 AUG at 1140 - Room N4
Oral presentation *B2-Ge03-1140-O*

General sessions
Population ecology

What are the determinants of the ´chaotic genetic patchiness´ observed in marine species?

Broquet T[1], Yearsley J[2], Viard F[1]
[1]CNRS Station Biologique de Roscoff, Roscoff, France, [2]University College Dublin, School of Biological Sciences, Dublin, Ireland

Summary statement:

Local genetic drift combined with propagule-pool dispersal may generate chaotic genetic patchiness, as observed in marine species with a bentho-pelagic life cycle.

Abstract:

We currently have an incomplete understanding of the processes controlling genetic variation in marine species with a bentho-pelagic life-cycle (i.e. with a sessile adult benthic phase and a free-floating larval phase). In particular, empirical observations of the genetic structure in these species rarely fit the predictions from classical models of neutral population genetics. Such observations find that genetic differentiation between two samples of individuals is not a simple function of distance between the samples and is not stable in time (termed ´chaotic genetic patchiness´). They also suggest that effective dispersal is not correlated with the pelagic larval duration. Understanding the processes underlying such complex patterns matters not only to evolutionary biology but also to molecular ecology (e.g. to determine what information about life-history processes such as reproduction and dispersal can be inferred from genetic data when the genetic structure is chaotic).Results from previous studies have suggested that genetic drift during reproduction interacts with complex patterns of dispersal (and thus gene flow) to create chaotic genetic patchiness. We used analytical and simulation-based approaches to formally test this idea. In particular, we show how genetic drift (created by the small local effective population sizes of the sessile phase due to highly variable reproductive success) in combination with non-random dispersal of the larval phase (propagule pool dispersal of related individuals) can generate chaotic genetic patchiness, as observed in marine species with a bentho-pelagic life cycle.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i011-E*

General sessions

Morphological and bioacoustic diversification in the neotropical poison frog Oophaga granulifera

Brusa O[1]
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Summary statement:

Oophaga granulifera has been discovered to be polymorphic and new colour morphs are described. The different colour morphs are diversified morphologically and bioacoustically.

Abstract:

The species Oophaga granulifera, is found on the pacific side of Costa Rica, with a range of distribution North-South mainly along the Coast of about 160 Km in length.
The species previously thought to be essentially monomorphic has been found to be polymorphic in the present study.
Three main colour morphs were identified according to the dorsal colour phenotype: red, typical of the southern populations; green, in the northern part of the distribution and a variable intermediate phenotype in the contact area.
The level of diversification between colour morphs in terms of morphology and bioacoustics were investigated in 7 populations in an 80 Km area around the contact zone.
Twenty morphometric traits were measured in 13 to 20 frogs per population and the male advertisement call recorded in 3 to 6 frogs per populations. The statistical analysis revealed a significant level of differentiation for morphology and calls characteristics between the red colour morph and the intermediate-green morph.
The results can be interpreted considering that the different colour morphs can be a result of an incipient diversification process.
This would explain the highly variable colour phenotypes of the intermediate populations.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i016-R*

General sessions

Insights about the phylogeny of Lake Malawi cichlids

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[2]Departamento de Biologia, Faculdade de Ciências da Universidade do Porto, Porto, Portugal,
[3]Department of Genetics, Rutgers, the State University of New Jersey, New Jersey, United States

Summary statement:

In order to reconstruct the Malawi cichlids species tree and to assess speciation modes, more than a hundred genealogies for several individuals were sequenced.

Abstract:

Cichlid fishes from the Great African lakes are known for their explosive radiation and rapid speciation. So far, the mechanisms that drove this extraordinary diversification are largely unknown. Particularly, in Lake Malawi, because speciation is very recent, there is a great deal of variation still shared by different species. Thus, there is no reliable phylogenetic tree for the Malawi cichlids making it difficult to assess speciation models and divergence times.
Our intent with this project is to decipher the phylogeny of Lake Malawi cichlid species. With this purpose, we collected DNA sequences for 102 genomic regions for several individuals representing the cichlid species diversity in the lake. The obtained results illustrate the complexity of cichlid speciation and provide new insights about the speciation modes and key events.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i078-R*

General sessions

Opposing effects of a single nucleotide substitution on fitness in different environments: Insights from the aldehyde dehdrogenase locus in Drosophila melanogaster

Chakraborty M[1], Fry JD[1]
[1]University of Rochester, Department of Biology, Rochester, United States

Summary statement:

A replacement substitution at the Aldh locus of D. melanogaster gives rise to a functional trade-off. The fitness effects of the substitution will be reported.

Abstract:

The enzyme aldehyde dehydrogenase (DmALDH) is necessary for metabolism of ethanol in Drosophila melanogaster; without it, flies are killed by ethanol concentrations typical of decaying fruits. In a recent worldwide survey, we found an amino-acid substitution ('Leu' to 'Phe') at the 479th residue of DmALDH in natural populations. The frequency of the 'Phe' allele increases in populations with higher ethanol resistance, and purified enzyme encoded by the allele detoxifies acetaldehyde (the breakdown product of ethanol) more quickly than that encoded by the ancestral 'Leu' allele. The 'Leu' allele, however, is in high frequency in all natural populations examined, raising the question of why the 'Phe' allele does not become fixed despite its advantage in ethanol metabolism. One possibility is that DmALDH has a conserved function unrelated to ethanol metabolism, and the 'Leu' allele is superior to the 'Phe' allele for that function. A good candidate for such a function is detoxification of large aldehydes produced endogenously when reactive oxygen species attack lipids. Consistent with this, flies lacking DmALDH are highly sensitive to oxidative stress; moreover, enzyme encoded by the 'Leu' allele detoxifies large aldehydes more quickly than that encoded by the 'Phe' allele, the opposite of the result for acetaldehyde. We have created transgenic fly lines differing only in the nucleotide position causing the amino acid substitution, and are using them to determine whether the observed kinetic trade-off results in a trade-off between resistance to ethanol and resistance to oxidative stress in vivo. Results of these experiments will be reported at the conference.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i017-R*

General sessions

Non-infective parasite environment during rearing and future resistance in a (social) insect-trypanosome parasite system

Cisarovsky G[1], Schmid-Hempel P[1], Sadd BM[1]
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Summary statement:

Rare cases of apparent acquired resistance were found, but many groups exhibited higher susceptibility, indicative of a cost of being reared in a parasite loaded environment.

Abstract:

The environment surrounding an individual can have a profound effect on immunity or parasite resistance. The abiotic environment and also previous parasite encounters have been shown to be important. In a social insect colony parasite resistance may be further mediated by interactions with the mother queen and siblings. In bumblebees, using a bacterial based immune challenge transfer of immunity between mother and offspring has been shown. However, a more typical natural scenario will be where individuals are raised surrounded by nursing siblings carrying a particular natural parasite infection. Even where infection of the focal individual cannot take place, for example due to life-stage incompatibility, exposure to parasitised siblings has the potential to influence future resistance. Yet, the exact nature of the influence is hard to predict, with it being a balance between the potential benefits of acquired resistance and the costs associated with being raised in a parasite loaded environment. This situation was investigated by raising bumblebee larvae nursed by either uninfected siblings or siblings infected with one of two strains of the adult-only-infecting parasite, Crithidia bombi. After emergence as adults experimental infections in a fully crossed design tested for the effects of rearing environment. It was found that the response of parasite resistance to rearing environment was not consistent across colonies (families). While rare cases of apparent acquired resistance were found to exist, several groups exhibited increased susceptibility relative to controls that is indicative of a cost of being reared in a parasite-loaded environment.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i013-E*

General sessions

Modularity and the evolution of fast movements

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Summary statement:

The evolution of fast biomechanical mechanisms results from developmental modularity and mechanical connectivity.

Abstract:

Biological structures that produce extremely fast movements can be divided into three functional regions: an “engine” (muscle) that loads an “amplifier” (spring) which drives a “tool” (hammer). Although their biomechanics are well-studied, little is known about the processes that drive the evolution of fast movements. Using the hammer-like raptorial appendage of a mantis shrimp, Gonodactylaceus falcatus (Crustacea, Stomatopoda), we tested whether each of these three regions could be considered as independent developmental entities (modules). Then, using over 60 species we tested whether these regions could evolve independently or whether the appendage evolved as one integrated unit. Analyses of G. falcatus shape showed that the functional regions belonged to independent developmental modules. Using phylogenetic comparative methods on geometric morphometric shape data across species, we found that the evolution of the three regions was correlated. Finally, a measure of the shape disparity across superfamilies for each region was indicative that the amplifier, which was more disparate for some superfamilies than the other two regions, was more propitious to greater shape variation. This last result indicated that even if these three regions coevolved, some regions are capable of greater innovation than others, suggesting an underlying modularity. In conclusion, the raptorial appendage might owe its novel and diverse designs to an underlying developmental modularity. Nonetheless, the overriding mechanical connections necessary for the proper functioning of the power amplification system as a whole may drive the broader coevolution of the engine, amplifier and tool.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i014-E*

General sessions

Fisher and wright reconsidered: The concepts of mean fitness and adaptation in genetics, evolution and ecology

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Summary statement:

Long term persistence of species may be independen from the fitness maximizing genetic selection witin species.

Abstract:

The fitness of any allele is defined by the relative change in the proportion of the allele in the next generation. These measures have been misrepresented when applied to the concepts of mean fitness and mean adaptation, which led to major misleading inconsistencies in the theory of population genetics:

The Mean Genetic Fitness of all alleles or genotypes in any one generation equals 1.0 by definition at all selection regimes, which cannot increase by any changes in the selection regime.

Selection cause a proportional decrease of the additive genetic variance in fitness of the selected variables, but the implied Fundamental Theorem of Natural Selection that the Mean Fitness of a population increases by selection is flawed.

The fitness of any allele or genotype is defined only relative to that of the mean fitness of all the alleles or genotypes in the population. Selection increases or decreases the frequency or expression of alleles or traits with mean conditional fitness larger or smaller than the population mean fitness = 1.0. Stabilizing selection at a genetic equilibrium maintains and defines an equal fitness = 1.0 for all the polymorphic alleles and the frequency dependent traits.

The relative fitness of alleles over a sequence of generations is well defined by the Geometric Mean of the per generation fitness. The long term weighted mean of the Geometric Mean Fitness of all the alleles necessarily equals 1.0, even in populations undergoing genetic changes by selection.

The ecological growth rate of all populations is defined by the geometric mean also equals 1.0, and cannot be used to define the ecological adaptation of different species.

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SUN 21 AUG at 1100 - Room N7
Oral presentation *A2-Ge04-1100-O*

General sessions
Evolutionary genetics

Dissecting the causes of rate variation in the molecular clock

Comper V[1], Cotton J[1], Nichols R[1]
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Summary statement:

New bayesian approach uses vast number of loci and multiple species pairs to estimate population genetics parameters while including variation in coalescence and substitution rate

Abstract:

Molecular-dating techniques can enable us to estimate the ages of important evolutionary events and can allows us to study the evolutionary history of related species when a fossil record is absent or poor. However, these techniques assume that molecular evolution occurs at a steady rate over time. Variation in this clock have been observed not only between species but also between genes and sections of genes. This project tries to model the molecular clock and tries to understand the causes of this variation. When the causes are found they could be incorporated into new molecular-dating techniques and hopefully will enable us to more accurately estimate evolutionary history.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i019-R*

General sessions

Age and reproductive effort in metapopulation

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Summary statement:

We investigate how metapopulation dynamics affect classic life history theory predictions on the evolution of age-specific reproductive effort.

Abstract:

Classic life history theory predicts that reproductive effort should increase with age in a single large undisturbed population. We used a metapopulation model to investigate how the extinction-colonization dynamics influence the distribution of the reproductive effort along life. If only the juveniles disperse, the extinction-recolonization dynamics generate a disequilibrium in the age structure, such that the age of the individual becomes a cue of the age of the population where it lives. We show that in a metapopulation with partial dispersal of juveniles, the reproductive effort of young adults is increased as the latter are mostly found in recently colonized sites with favorable recruitment conditions. We further study the joint evolution of reproductive effort with the dispersal rate of juveniles, when both vary with the age of the mother. Under a wide range of parameters, the dispersal rate increases with maternal age, unlike previous studies. Change in dispersal with maternal age, in turn, makes the evolution of age-specific reproductive effort resemble more what is expected in a single large undisturbed population. Our study emphasizes the need to study the joint evolution of life history traits at different scales and illustrates how metapopulation processes could modulate classic predictions on life history.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i015-E*

General sessions

Competition among foraging adult female parasitoid wasps

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Summary statement:

Value of the ressource affects behaviour and competition among foraging adult female parasitoid wasps.

Abstract:

The parasitoid wasp Hyposoter horticola forages for eggs of the butterfly Melitaea cinxia. It monitors the locations of multiple potential hosts for up to several weeks before the hosts become susceptible to parasitism and return to previously found hosts, increasing the amount of time available for foraging. As a result, the location of each potential host is known by several wasps. Since each egg cluster can only be parasitized by a single wasp, the hosts are a limiting resource and there is strong competition between individual adult female wasps. We tested the hypothesis that competition intensity increases with host egg age. We carried out a behavioural experiment in a large field enclosure. Individually marked wasps were observed visiting plants with host eggs of different ages upon them. We recorded the frequency and duration of visits and the interactions among wasps. We found that both egg age and the presence of competitors influenced the behaviour of H. horticola. Overall the wasps were more interested (visited for longer, probed more...) in old eggs than young eggs, especially if several wasps were present, supporting the idea that as the eggs age and are closer to being available to parasitize they become more valuable.

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WED 24 AUG at 1440 - Room N6
Oral presentation *D3-Ge07-1440-O*

General sessions
Primates

Natural and sexual selection in a monogamous human population

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[1]University of Sheffield, Department of Animal and Plant Sciences, Sheffield, United Kingdom, [2]University of Turku, Turku, Finland, [3]University of Helsinki, Helsinki, Finland, [4]University of Oxford, Oxford, United Kingdom, [5]University of Sheffield, Sheffield, United Kingdom

Summary statement:

We measured variance in fitness in a historical human population with sequential monogamy. We show that opportunity for sexual and natural selection was high, especially for men.

Abstract:

Whether and how human populations exposed to agricultural revolution are still affected by Darwinian selection fuels controversy among social scientists, biologists and the general public. While advances in molecular genetics and epidemiological analyses suggest recent selection on specific loci or traits, the overall strength of selection remains unmeasured in humans. Using longitudinal data on historical Finns we show that individual differences in early survival and fecundity induced large variance in reproductive success, even among wealthier individuals. Variance in mating success influenced reproductive success in both sexes, but men had greater variance in mating and reproductive success than women, despite a monogamous marriage system. Our results demonstrate an opportunity for intense natural and sexual selection and contradict claims for minimal evolution in agricultural societies.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i020-R*

General sessions

A repeatedly evolved host-specific ectosymbiosis between groundwater amphipods and sulfur-oxidizing bacteria

Dattagupta S[1], Bauermeister J[1], Ramette A[2], Flot J-F[1]
[1]University of Goettingen, Courant Centre Geobiology, Goettingen, Germany, [2]Max Planck Institute for Marine Microbiology Bremen, Microbial Habitat Group, Bremen, Germany

Summary statement:

We report a host-specific ectosymbiosis involving groundwater amphipods that is widespread and has evolved independently in at least two different host and symbiont lineages.

Abstract:

Amphipods of the genus Niphargus are the most common groundwater fauna in Europe and dominate invertebrate communities of the sulfide-rich Frasassi caves in Italy. Molecular and morphological investigations showed that three partially sympatric Niphargus species occur within this cave ecosystem. Using a combination of microscopy, DNA sequencing and fingerprinting, we found that all three species harbor ectosymbiotic bacteria belonging to the sulfur-oxidizing clade Thiothrix. Despite co-occurrence of host species as well as competition from diverse free-living Thiothrix phylotypes, the symbionts are strictly host-specific and maintained over generations. Phylogenetic analyses revealed that the symbiosis has evolved independently in at least two different host and symbiont lineages in Frasassi. Following this discovery, we examined Niphargus species collected from other locations in Europe. We found that although the closest relatives of the Frasassi-dwelling species are symbiont-free, many others carry Thiothrix- ectosymbionts. Therefore, the Niphargus–Thiothrix association appears to be widespread and has originated multiple times by convergent evolution.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i021-R*

General sessions

Patterns of genome introgression between wheat and a wild relative

Définod C[1], Parisod C[1], Arrigo N[1], Sarr A[1], Felber F[1]
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Summary statement:

Assessment of introgression between cultivated hexaploid and tetraploid wheats, and its wild relative Aegilops triuncialis, using chromosome-specific markers.

Abstract:

Gene flow between crops species and their wild relatives is a subject of growing interest since transgenic crops have been introduced in agriculture. The major concern is that the transgene might escape from genetically modified plants into wild populations of relatives, and could modify the fitness of the introgressed species and for instance increase its invasiveness. No genetically modified wheat is commercialized yet, allowing for risk assessment of introgression from wheat to wild before the release of transgenic wheat.
Here we assess gene flow between conventional hexaploid and tetraploid wheats, respectively Triticum aestivum (genome BBAADD) and Triticum turgidum (genome BBAA), and one of the most common tetraploid wild relative, Aegilops triuncialis (genome CCUU). For this purpose, we validated a set of chromosome specific EST-SSR markers from hexaploid wheat that display different alleles in reference wheat versus pure Aegilops triuncialis accessions. In populations from Aegilops triuncialis collected close or distant to wheat fields in the Mediterranean area and in North America, individuals showing evidence of introgression were genotyped to assess chromosome and genome-specific patterns of gene flow. These results will contribute to develop containment strategies.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i022-R*

General sessions

Post-copulatory sexual selection: widespread among social insects?

den Boer SPA[1,2,3], Jaffé R[1,2], García-González F[2], Boomsma JJ[3], Simmons LW[2], Baer B[1,2,3]
[1]The University of Western Australia, ARC Centre for Plant Energy Biology, Crawley, Australia, [2]The University of Western Australia, Centre for Evolutionary Biology, Crawley, Australia, [3]University of Copenhagen, Centre for Social Evolution, Copenhagen, Denmark

Summary statement:

Our findings imply that post-copulatory sexual selection and sexual conflict may have played an important role in the evolution of eusociality and mating systems in social insects.

Abstract:

Multiple mating is known to generate selection for behavioural, physiological, and morphological traits in males and females to optimize reproductive success. In the social Hymenoptera (the ants, bees and wasps), post-copulatory sexual selection has been assumed to be largely absent or not a major selective force. Here, we demonstrate that post-copulatory sexual selection is actually more widespread than so far acknowledged. First, we show in an analysis of multiple ant, bee and wasp species that the evolution of increased mating frequency is associated with a decrease in paternity skew. This implies that sperm competition or cryptic female choice are significant selective forces in species with low queen re-mating rates (biasing paternity towards a single or few males), while sexual conflict is likely important in the highly polyandrous species, as queens generally keep paternity skew below levels predicted by sperm competition or random processes, thereby assuring high genetic diversity among offspring. Second, we provide some evidence on how post-copulatory sexual selection could operate; we show that ejaculates consist of distinct parts, how they are assembled during ejaculation and how this influences paternity success. We also show that glandular secretions provided to sperm (seminal fluid from males or ovarian / spermathecal fluid from queens) significantly affect ejaculate function.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i023-R*

General sessions

Experimental evolution of antimicrobial peptide resistance in Staphylococcus aureus: costs, cross-resistance and ecology

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[1]University of Sheffield, Animal & Plant Sciences, Sheffield, United Kingdom, [2]Medical University of Gdansk, Gdansk, Poland, [3]University of Sheffield, Molecular Biology & Biotechnology, Sheffield, United Kingdom

Summary statement:

Evaluating the evolutionary ecology of pathogens selected for resistance to immune analogues developed as novel antibiotics.

Abstract:

Antimicrobial peptides (AMPs) have been proposed as a new class of therapeutic antibiotics, since as innate immune effectors they are ancient and ubiquitous but still highly effective. However, AMPs are not 'resistance-proof', and their use as antimicrobial drugs could select for bacteria that are AMP-resistant and thus better able to survive immune responses. Therefore we exposed the pathogen Staphylococcus aureus to increasing doses of AMPs and established antibiotics to select for resistance. S aureus showed similar or greater acquisition of resistance to AMPs than to established antibiotics. However S aureus evolved resistance to combinations of AMPs more slowly. These results suggest that the rarity of natural AMP resistance is likely driven by its costliness and spatio-temporal patterns in AMP synthesis. We also show that AMP resistance is associated with fitness costs. Critically, resistance to AMPs can confer cross-resistance to others, which could allow them to better survive AMPs deployed in an immune response, although AMP resistant clones showed no enhanced survival or virulence after injection into mealworms or zebrafish. We conclude that in natural infections, costs of resistance and the multiplicity of antimicrobial effectors transcribed after inoculation are likely factors in the lack of observed AMP resistance. Crucially, resistance to one AMP can in principle translate into elevated resistance to others, suggesting that their use as drugs could potentially select for recalcitrant persistent pathogens.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i024-R*

General sessions

Carotenoid-based signalling of blood parasite infection status in the blue tit

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Summary statement:

In blue tit (Cyanistes caeruleus) females carotenoid-based breast feather colouration may reflect blood parasite infection status.

Abstract:

Carotenoids are commonly used by animals to provide the colour of different body structures. In birds, carotenoids are often deposited in feathers and plumage colouration has been shown to reliably reflect body condition, foraging efficiency and survival. Feather colour may also predict reproductive success and the quality of parental effort. The direct mechanism underlying these relationships remains, however, unclear. Presumably, it may involve the effects of parasitic infections. On one hand, parasites negatively affect the expression of carotenoid-based plumage colouration, and on the other hand, carotenoids play an important role in the stimulation of the immune function, and consequently in the protection against parasitic infections. Here, we tested whether carotenoid-based breast feather colouration may be a reliable indicator of blood parasite infection status in the blue tit (Cyanistes caeruleus). We tested this relationship under the conditions of natural and increased probability of infection as induced by brood size enlargement. We found that in females the relationship between the colour tone and the probability of infection differed between unmanipulated and enlarged broods: in the former group this probability tended to decrease with increasing colour tone, while in the latter group – it tended to increase. There was also a tendency, regardless of the brood size type, for less intensly coloured females to have higher probability of infection. Overall, these results suggest that in the blue tit female plumage coloration may be used as an indicator of blood parasite infection status.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i025-R*

General sessions

The evolution of Apomixis in ferns

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Summary statement:

Using results of molecular systematic and AFLP studies, i will introduce hypotheses on the evolution of Apomixis and reproductive strategy within the Asplenium monanthes complex.

Abstract:

It has long been argued that the greater genetic diversity that is afforded by recombination has led to the evolutionary success and diversification of sexually reproducing organisms. Paradoxically, there are numerous examples across the eukaryotic tree where organisms have lost sexual reproduction and become asexual. This evolutionary reversion is relatively prevalent in plants and especially within ferns with up to 10% of the ~ 9,500 fern species exhibiting facultative or obligate apomixis. The aim of my project is to investigate the evolution of apogamous reproduction, a form of apomictic/asexual reproduction, in a well-defined lineage of ferns know as the Asplenium monanthes complex. Within this complex of ~15 taxa there are at least 2 species of long-lived obligate apomicts that are morphologically variable and locally common across Mesoamerica. To study the evolution of apomixis in this fern complex I am employing a robust phylogenetic framework based on DNA sequence data from the plastid and nuclear genomes that includes reticulate evolution as a major phylogenetic process in this lineage. This framework will be used to develop and test hypotheses on the evolution of apomictic taxa within this complex. The lineage is well suited to study these questions due to the occurrence of species of different reproductive strategies, varying from obligate apomicts, facultative apomictics and vegetative to sexually reproducing taxa. In this presentation, I will outline my research approach using the results of molecular systematic and AFLP studies to introduce a number of hypotheses on the evolution of Apomixis and reproductive strategy within this complex.

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WED 24 AUG at 1400 - Room N7
Oral presentation *D3-Ge05-1400-O*

General sessions
Disease and immunity

Parasites in ecological speciation; heritability of parasite resistance in the three-spined stickleback, Gasterosteus aculeatus, explored through line-cross analysis

El Nagar A[1], de Roij J[1], MacColl A[1]
[1]University of Nottingham, Biology, Nottingham, United Kingdom

Summary statement:

Parentals, F1, F2, and backcrosses were infected experimentally to determine how the resistance trait is genetically controlled and how this affects fitness.

Abstract:

The role of parasites as potential drivers in ecological speciation has been studied less than other causes of divergent selection. In order to understand whether parasites contribute towards ecological speciation, it must initially be ascertained whether they can influence the diversification of populations.
Populations of the three-spined stickleback Gasterosteus aculeatus are highly diverse in the wild, and carry different species and abundances of parasites. Infection experiments on progeny of various populations has shown that resistance to parasites is genetically determined because when treated equally and exposed to the same parasite strains, resistance differed.
The next step is to understand how the resistance trait is genetically determined. Investigating how the quantitative trait works can reveal whether hybridization between populations influences fitness, and if this could create a breeding barrier. Line-cross analysis between a resistant and susceptible population was conducted. Parentals, F1, F2, and backcrosses were bred and infected experimentally with a digenean trematode Diplostomum pseudospathaecum and a monogenean trematode Gyrodactylus gasterostei. Results show how the resistance trait may be genetically controlled, and how fitness of the crosses differs to parental fitness.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i073-R*

General sessions

Selection pressure on wing morphology in Calopteryx damselflies

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[1]Lund University, Department of Biology, Lund, Sweden, [2]Ohio University, Department of Biological Sciences, Athens, United States

Summary statement:

We combine geometric morphometrics with drop-escape tests and field observations to link wing morphology of Calopteryx damselflies to flight performance and field survival.

Abstract:

Damselflies of the genus Calopteryx are highly aerial creatures that depend on their flight capabilities for hunting, territory defense, courtship displays, mating success and predator avoidance. All these requirements put selective pressure on wing morphology, although potentially in opposing directions. While we have a good conceptual understanding of the consequences of wing shape on flight performance, few studies have shown a direct link between wing morphology, flight performance and individual fitness and survival in the field.
Our study system comprises of two sympatric damselfly species: Calopteryx splendens, and C. virgo for which previous studies suggest differential selection pressure on wing morphology by avian predators. We use geometric morphometric methods to analyze variations in wing morphology, both between and within the species, and combine these data with flight performance parameters (speed acceleration and force production) from a drop-escape test and field measurements of predation and survival to quantify selection pressure on wing morphology.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i026-R*

General sessions

Multiple functionally divergent and conserved copies of alpha tubulin are present in bdelloid rotifers

Eyres I[1]
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Summary statement:

Cloning and genomic data have revealed that multiple functionally divergent and conserved copies of alpha tubulin are present in bdelloid rotifers.

Abstract:

Bdelloid rotifers are microscopic aquatic invertebrates of particular interest for two features of their lifestyles. First, they have persisted for over ~80my and diversified into nearly 450 recognized species, despite the apparent absence of meiosis and sex. Second, adult bdelloids can survive complete desiccation in a state known as anhydrobiosis. Moreover, bdelloid genomes show a number of unusual features (degenerate tetraploidy, gene conversion and uptake of foreign genes) that might relate to their long-term asexuality and ability to survive desiccation. Understanding these features can shed light not only on bdelloids´ unusual lifestyle, but also on the range of mechanisms by which animal genomes can evolve.
We used cloning and preliminary transcriptome and genome data to characterize alpha tubulin copies in several monogonont and bdelloid rotifer species. The monogononts had up to two copies with very similar amino acid sequence (each presumably representing a single diploid locus). Contrary to the four or eight copies expected if bdelloids retained copies from their tetraploid ancestor, we found 11 to 15 copies in each of four species of bdelloids. Relationships among species indicate that multiple copies were inherited from the common ancestor. Approximately half of the copies retained amino acid sequences similar to the monogonont copies, whereas the rest had diverged in amino acid sequences and predicted biochemical properties. The findings confirm current understanding of bdelloid genome organization, but show how further duplication events in the ancestor of bdelloids led to proliferation in both conserved and functionally divergent copies of this gene.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i027-R*

General sessions

Ecological consequences of a transgene in a hybrid between wheat and its wild relative, Aegilops cylindrica

Felber F[1], Guadagnuolo R[1], Arrigo N[1], Senerchia N[1], Sarr A[1], Parisod C[1]
[1]University of Neuchâtel, Institute of Biology, Neuchâtel, Switzerland

Summary statement:

Fitness of transgenic and nontransgenic hybrids between hexaploid wheat and a wild relative, Aegilops cylindrica, were compared in an experimental field for 3 years.

Abstract:

Gene flow from crops to wild relatives through sexual reproduction is one of the major issues in risk assessment for the cultivation of genetically engineered plants. Fitness of hybrids and subsequent backcrosses will drive the persistence of the transgene in wild populations.Investigations of natural populations indicated extensive gene flow during the long cohabitation of wheat and wild relatives (Aegilops sp.), especially in the Mediterranean area.
Here, we compared fitness of hybrids between Aegilops cylindrica and respectively transgenic and nontransgenic hexaploid wheat in an experimental field during three years. Transgenic wheat expressed wheat powdery mildew resistance (Pm3 resistance gene). Fitness of hybrids varied according to environmental conditions, in particular between years. Hybrids between Ae. cylindrica and wheat were generally less fit than their parents, suggesting that they should not persist in wild populations. No evidence of the influence of the transgene was found. Nevertheless, some hybrids had much higher fitness values than others, even higher than wild Ae. cylindrica. Consequently, risk of introgression from transgenic wheat to natural populations of Ae. cylindrica exists when both species coexist.

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WED 24 AUG at 1420 - Room N6
Oral presentation *D3-Ge07-1420-O*

General sessions
Primates

Out of Africa – But how and when? Insights from Hamadryas baboons

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[1]German Primate Center, Cognitive Ethology, Göttingen, Germany, [2]Max Planck Institute for Evolutionary Anthropology, Department of Primatology, Leipzig, Germany, [3]German Primate Center, Primate Genetics, Göttingen, Germany

Summary statement:

We investigate the dispersal history of hamadryas baboons from Africa to Arabia, compare our results to paleoecological data and discuss their implications for human evolution.

Abstract:

When anatomically modern humans dispersed out of Africa is still a central question in the study of human evolution. Recently discovered archaeological evidence points to a presence of modern humans in Arabia much earlier than previously thought (by about 125 kya), possibly not migrating via the Sinai Peninsula into the Levant but crossing the southern Red Sea via the Bab al Mandab Strait during hyperarid periods when sea-levels were low. Baboons have been proposed as an analogous model for human evolution as they evolved in the same period and habitats. Hamadryas baboons (Papio hamadryas) are the only baboon taxon that also migrated out of Africa and still inhabits parts of the Arabian Peninsula. Investigating their dispersal history can potentially help us elucidate the evolution of our own species. In this study we investigate the Arabian origin of hamadryas baboons using mitochondrial sequence data of nearly 300 samples collected non-invasively in Arabia and north-eastern Africa. Using (Approximate) Bayesian computation, we specifically test (i) via which route, (ii) when and (iii) how often baboons colonized the Arabian Peninsula. We compare our results to paleoecological data and migration scenarios of other Afro-Arabian mammals and discuss their implications for human population history.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i017-E*

General sessions

Genetic analysis of inter-demic processes in a metapopulation of Silene latifolia

Fields PD[1], Taylor D[1]
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Summary statement:

Spatiotemporal character of a Silene latiofolia metapopulation is found to be important, but marker dependent, in understanding population genetic differentiation.

Abstract:

Many recent advances in the study of the causes and consequences of population structure have used a Bayesian model-based approach. We applied this advanced approach to an unprecedented spatiotemporally defined demographic and genetic dataset of a well-characterized plant metapopulation of Silene latifolia in Southwest Virginia, USA. We conducted a genetic analysis of 16 microsatellite markers, identifying the direction and magnitude of effect of population specific connectivity, population age, and population size as significant factors in generating population genetic differentiation. All three spatiotemporal parameters were important in explaining genetic differentiation of anonymously derived microsatellites, while connectivity, a quantitative measure of potential for gene flow, was by far the most important factor describing the genetic differentiation of EST-SSRs. We suggest potential factors driving the difference in inference of the factors driving genetic structuring, as well as suggest approaches to dealing with molecular markers undergoing distinct evolutionary processes, thereby allowing for full and simultaneous inference within a single Bayesian analysis.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i028-R*

General sessions

Evolution of plasticity windows and age-dependent phenotypic plasticity

Fischer B[1]
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Summary statement:

This study addresses the question why organisms possess time windows of phenotypic plasticity and more generally why age-dependent plasticity might evolve.

Abstract:

Phenotypically plastic organisms are favored by selection in a variable environment. Often the plasticity of a trait varies during lifetime. Many organisms adjust traits in response to environmental cues only during a specific window of plasticity, which can vary greatly in length across species. When exposed to an environmental cue at a time outside the plasticity window, no adjustment occurs. This study addresses the question why windows of plasticity exist, and which processes govern the evolution of age-dependent plasticity.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i029-R*

General sessions

Behavioural mechanisms that mediate inbreeding depression for male fitness

Forstmeier W[1], Janker S[1], Martin K[1], Kempenaers B[1]
[1]Max Planck Institute for Ornithology, Behavioural Ecology and Evolutionary Genetics, Seewiesen, Germany

Summary statement:

We study how variation in male heterozygosity affects male courtship and mate-guarding behaviour, as well as female promiscuity and discrimination behaviour.

Abstract:

Inbreeding depression for fitness is a very widespread phenomenon, but the behavioural mechanisms that lead to the lower fitness of inbred individuals have rarely been studied in detail. In socially monogamous birds it is often found that males with reduced heterozygosity suffer increased loss of paternity in their own nest and are less successful at siring offspring outside their social pair bond (extra-pair paternity). Based on extensive observational data on domesticated zebra finches breeding in large communal aviaries, we study the male courtship and female discrimination behaviour in relation to male inbreeding coefficients (pedigree-based) and heterozygosity (marker-based). We test whether inbred or more homozygous males show reduced within-pair and extra-pair courtship rates, reduced courtship persistence, or reduced mate-guarding efforts. We test whether females discriminate against inbred extra-pair males and also against inbred social partners. Finally, we examine whether females that are socially mated to inbred males show elevated rates of extra-pair courtship and responsiveness towards extra-pair males.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i030-R*

General sessions

Effects of outbreeding on an inbreeding insect

Fountain T[1], Otti O[1], Butlin RK[1], Reinhardt K[2]
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Summary statement:

By mimicking gene flow in naturally inbreeding bedbug populations we assess effects of outbreeding on fitness and population structure.

Abstract:

In some species populations with few founding individuals can be apparently resilient to even extreme inbreeding, despite the loss of any heterozygote advantage and/or increased expression of deleterious alleles. Such inbreeding populations seem to be the norm in the common bedbug, Cimex lectularius, but infestations can rapidly grow and persist successfully. Bedbugs are flightless and movement often involves passively dispersing individuals, which are increasingly reported on public transport. This allows gene flow between distant geographic locations, potentially leading to loss of local adaptation or genetic incompatibility between populations. To date no work has addressed how outbreeding may impact population structure in the bedbug. Here we compared fitness traits of lines that were either inbred or outbred for several generations. We also present data on behavioural inbreeding avoidance and of the population genetic structure of natural populations of bedbugs. Comparing these aspects should allow us to estimate the significance of outbreeding in the wild.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i018-E*

General sessions

Recent demographic history of cactophilic Drosophila species can be related to the Quaternary paleoclimatic changes in South America

Franco FF[1], Sene FM[2], Manfrin MH[2]
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Summary statement:

In this work is discussed the causal effect of the Quaternary paleoclimatic changes on the geographic distribution of five cactophilic species of Drosophila in South America

Abstract:

The genetic based data have been providing a large amount of information about the past demographic history of extant species. These data have been contributing to the discussion about the causal effect of the Quaternary paleoclimatic changes on the geographic distribution of the Neotropical biomes. The D. serido haplogroup (D. serido, D. gouveai, D. seriema and D. borborema species) and D. antonietae haplogroup (D. antonietae species) represents sister lineages within D. buzzatii species cluster. These species are naturally endemics of Neotropical region and associated to xerophitic vegetation as they are cactophilic. Here we present phylogeographic analysis with species of D. serido and D. antonietae haplogroups. The main conclusion is that all of the species analyzed experienced populations expansions during the Pleistocene period. Bottleneck events in Holocene period were inferred for only two of these species namely D. seriema and D. antonietae. We suggest that this fact should be related to ecological factors due some particularities related to the geographical distribution of their cacti hosts. Finally, we suggest that the major vicariant events between the D. serido and D. antonietae haplogroup as well as the demographic fluctuations within the each species of these lineages could be related to the spatial dynamic of Seasonally Tropical Dry Forest in Brazil. This is in general agreeing with Pleistocene arc hypothesis.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i031-R*

General sessions

Genetic evidence for past hybridisation between illegally reintroduced English wild boar and domestic pigs

Frantz AC[1], Massei G[2], Burke T[3]
[1]Ernst-Moritz-Arndt-Universität Greifswald, Zoologisches Institut, Greifwald, Germany, [2]The Food and Environment Research Agency, Sand Hutton, York, United Kingdom, [3]University of Sheffield, Sheffield, United Kingdom

Summary statement:

We show that wild boar from an accidentally establish population in the UK were not pure-bred wild boar, but had a mixed wild boar-domestic pig ancestry

Abstract:

In the UK, some wild boar have escaped from captivity and managed to establish some breeding populations. Wild boar farmers often cross a male wild boar with a domestic pig sow in order to produce a hybrid with increased productivity. The aim of this work was to investigated whether the escaped wild boar were genetically 'pure', or whether we could find evidence of past hybridisation with domestic pigs. We sequenced part of the mitochondrial control region, the MC1R coat-colour gene and the pseudo-gene GPIP in 20 wild boars from the Forest of Dean. We found that about half the individuals had a sequence of Asian origin, which must have originated from domestic pigs, at the control region and GPIP. However, all 20 individuals had the wild boar wild type coat colour gene. We conclude that the escaped wild boars have been crossed with domestic pigs in captivity and that the coat colour gene alone is not very useful to identify hybrids.

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SUN 21 AUG at 1200 - Room N7
Oral presentation *A2-Ge04-1200-O*

General sessions
Evolutionary genetics

Sex and social environment strongly influence the additive genetic architecture of lifespan in Drosophila melanogaster

Friberg U[1], Lehtovaara A[1], Flis I[1]
[1]Uppsala University, Evolutionary Biology, Uppsala, Sweden

Summary statement:

Genetic variation in lifespan is highly dependent on sex and social environment in Drosophila melanogaster.

Abstract:

Understanding the genetic architecture of lifespan is important since this trait sums over all genetically influenced disease phenotypes. Lifespan is in addition a central life-history trait, making it interesting also from the perspective of evolutionary biology. In virtually all taxa lifespan is sexually dimorphic, presumably because selection acts differently on males and females for traits affecting lifespan. Different selection operating on males and females may result in a sex-specific genetic architecture of lifespan. In this study of Drosophila melanogaster we measured additive genetic variation in lifespan, separately in males and females, in two different social environments (individuals were either housed with individuals of the same sex or with individuals of the opposite sex). We find significant additive genetic variation for lifespan for males as well as females. This variation does however strongly interact with sex, either because different sets of genes influence lifespan in males and females or because variation in the same genes has different effect depending on what sex they are expressed in. We further find that social environment has a large impact on the additive genetic architecture of lifespan in females but not in males. In sum our results show that lifespan is a very complex trait, and that the expression of genetic components underling variation in lifespan may be highly context dependent.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i032-R*

General sessions

Bateman gradients: A comparative study of sex-role-reversal

Fritzsche K[1], Arnqvist G[1]
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Summary statement:

We assess the evolution of sex-role-reversal and test Bateman's principle by comparing variation in mating success in four seed beetle species with different mating systems.

Abstract:

We are currently re-evaluating our view of the evolution of sex-role-reversed mating systems and their importance to shed light upon unresolved questions in sexual selection. In these systems, females actively court males and males discriminate among mates. Theory predicts that females should have a higher expected variance in mating success due to male mate choice. However, empirical evidence for this prediction as well as assessments of Bateman gradients are currently scarce and the role of additional factors (e.g. mate quality variance) is unclear. In the sex-role-reversed honeylocust beetles Megabruchidius dorsalis and M. tonkineus, males choose females actively and females compete for the access to males and their nutritious ejaculates. We measured intra-sexual variation in mating success of honeylocust beetles and in two closely related seed beetles (Callosobruchus maculatus and C. chinensis), which show conventional sex roles (courting males, choosy females). We recorded mating success and reproductive success in a competitive setting which allowed for mate choice, and measured traits that are likely to be under sexual selection in each species. Our key prediction is that the positive relationship between mating success and fitness (i.e. Bateman gradients) will be steeper in females than in males for sex-role-reversed beetles, while the opposite should hold true in the other species. Our results provide novel insights into the evolution of sex-role-reversal and constitute a strong and direct test of the generality of Bateman's principle and of sexual selection gradients.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i033-R*

General sessions

Molecular Phylogenetics of Neotropical Oryzomyine Rodents (Muridae: Sigmodontinae). Evidence of 3 mtDNA genes with parsimony and probabilistic methods

Garcia LF[1]
[1]Universidad Nacional de Colombia, Department of Biology, Bogota, Colombia

Summary statement:

mtDNA phylogenetics of oryzomyine rodents reveals good divergence values and phylogenetic resolution to study different splitting events through the time of evolution of the tribe

Abstract:

The tribe Oryzomyini belongs to the subfamily Sigmodontinae a successful and highly diversified group of mammals which inhabit a variety of habitats and food niches from northern Colombia to southern Argentina. The relationships among the oryzomyine genera has been better understood with several studies including mainly nuclear evidence. The recognition of the genus Oryzomys as a polyphyletic taxon led to the division of the genus in 10 new genera for the tribe. Thus, currently there are about 26 genera included in the tribe. However, there are still unresolved taxonomic issues as well as the historic scenary of the evolution of the group. In order to better understand the intergenic relationships of the Oryzomyini and estimate divergence times for the tribe and the genera, I used three different mtDNA genes: Cytochrome B, Cytochrome Oxidase I, and the ribosomal unit 16S. A wide taxonomic range from the Oryzomine and other Sigmodontine tribes were included in the analysis. The three genes were phylogenetic informative at different scales and provided a good range in sequence divergence and phylogenetic resolution to study different splitting events through the time of evolution of the tribe Oryzomyini. Parsimony and probabilistic methods established different degrees of support for the different identified clades. The monophyly of the tribe Oryzomyini and most of the genera were supported. Cyt B appear to be highly effective but COI performed relatively poorly when considered alone in the analyses. Combined data sets provided a better picture for the genealogical relationships despite the apparent evidence of heterogeneity among data sets.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i034-R*

General sessions

An empirical test of polyandry as a bet-hedging strategy

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Summary statement:

We investigate whether polyandry via bet-hedging enables females to increase their fitness. We discuss bet-hedging mechanism underlying the evolution of polyandrous behaviour.

Abstract:

Polyandry may provide females with genetic benefits. Multiple mating as bet-hedging represents a female strategy that deals with sampling errors arising from inaccurate information on male quality and with the unpredictability of the future environmental conditions that the offspring will experience. The genetic bet-hedging hypothesis predicts that polyandrous females reduce the probability that all their eggs are fertilized by a male of poor genetic quality. The genetic diversity bet-hedging hypothesis focuses on variation in fitness across environments, and suggests that, due to the diversity of paternal genotypes in the offspring of a polyandrous female, the likelihood that at least some offspring will be viable in a changing environment is higher than when offspring genotypes are less diverse. Here we use the Australian sea urchin Heliocidaris erythrogramma to test both hypotheses. Our use of a modified maternal half-sib design enables us to measure fitness in the same female genotypes following both a monandrous and a polyandrous strategy.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i035-R*

General sessions

First report in Atlantic of the cryptic invasive species: The Rhodophyta Polysiphonia morrowii Harvey

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[1]Station Biologique de Roscoff, CNRS-UPMC, Roscoff, France, [2]Muséum National d'Histoire Naturelle, Paris, France

Summary statement:

We used two genetic markers (rbcL) and (cox1) to detect the occurrence of Polysiphonia morrowii, a cryptic invasive species in Northern Atlantic.

Abstract:

Species delineation is one of the major challenges for systematics which has recently received an increased level of attention in the context of the barcoding approach. In red algae, many species limits are poorly delineated due to the relatively small number of diagnostic characters available compared to the high number of species described and their wide range of distribution. In the genus Polysiphonia, the precise taxonomic identification is often problematic, or nearly impossible, due to the lack of diagnostic criteria. Recently, the invasive species Polysiphonia morrowii Harvey (Rhodomelaceae) originaly from Northwestern Pacific (Japan, Korea) was identified using barcoding approach in different regions across the Pacific Ocean (Chile, New Zealand).

The genus Polysiphonia is well represented in Brittany with more than 18 different morphological species of which two species, Polysiphonia stricta and Polysiphonia atlantica, are morphologically similar to Polysiphonia morrowii. In this study, we used two genetic markers (rbcL) and (cox1) to detect the occurrence of this cryptic invasive species in Northern Atlantic. The cox1 locus was found to be highly informative at the infra specific level: 9 haplotypes were found over the whole dataset. The relatively high genetic diversity (sequence divergence) observed within populations suggests that P. morrowii, previously unnoticed in Brittany, was probably overlooked. The occurrence of multiple introductions is discussed in the light of our results.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i036-R*

General sessions

Subspeciation in Carabus (Chrysocarabus) auronitens in western Europe results from genetic structuring over several glacial periods and from hybridization

Gilabert A[1,2], Deuve T[2], Veuille M[1,2]
[1]EPHE, Paris, France, [2]Muséum National d'Histoire Naturelle, Systematic and Evolution, Paris, France

Summary statement:

The genetic diversity of C. auronitens is the result of historic events such as fragmentation, range expansions and hybridization, reflecting recent climatic fluctuations.

Abstract:

The study of speciation must integrate the complex changes in the evolution of geographical barriers resulting from the glaciations of the recent million years. The golden-glow ground-beetle Carabus (Chrysocarabus) auronitens is a wingless predator of the litter of European forests. It has been subdivided into a number of local forms from its diverse color variations. We recorded its polymorphism at COI, ITS and nine microsatellite loci in eleven populations covering most of its distribution in France. An early split of the species corresponds to a classic morphological distinction between populations, based on the color of their tibiae. Another split associates populations from western Massif Central and Brittany. A third split separates populations from Central France and Normandy. These populations were probably isolated during the last glacial maximum. Eastern populations from between the Alps and Northern France belong to a chain of closely related populations which probably expanded and differentiated at the postglacial period. The Pyrenean population, hitherto believed to belong to a different taxon (C. punctatoauratus), was not found to be genetically more distinct than the sampled C. auronitens populations, despite large geographical distances between them. Our data also suggests introgressive hybridization events with the related species C. splendens. The history of C. auronitens appears as a sequence of different kinds of events constrained by climatic fluctuations: ancient fragmentation, hybridization, range expansion, retraction. They resulted in a complex geographical structure which may have generated the amazing phenotypic variability of this species.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i037-R*

General sessions

Inferred invasion history of Silene latifolia into North America utilizing population genetic data and approximate Bayesian computation

Gilbert KJ[1], Keller SR[2], Fields PD[1], Taylor DR[1]
[1]University of Virginia, Biology, Charlottesville, United States, [2]University of Minnesota, St. Paul, United States

Summary statement:

Population genetic analysis of species invasion in the plant Silene latifolia

Abstract:

Species invading new ranges are subject to a series of demographic events that can strongly shape genetic diversity, such as founder effects, multiple introductions from different native range sources, and genetic admixture. Describing this demographic history is important for understanding where invasive species come from and how they spread, and is also critical to robustly testing hypotheses of post-invasion adaptation. Here, we report on our latest efforts using population genetic data to gain insight into the invasion history of the global weed, Silene latifolia (Caryophyllaceae). We genotyped 393 individuals of S. latifolia from 40 populations spanning both Europe (native) and North America (introduced) at 16 microsatellite markers and one chloroplast marker. Bayesian clustering and PCA revealed strong population structure in Europe and the presence of genotypes from multiple native sources in North America. Using approximate Bayesian computation (ABC), we modeled the evolution of population structure during the post-glacial expansion of S. latifolia in Europe. We then used ABC to compare support for different invasion scenarios into North America, including the number and size of independent introduction events, and the amount of admixture occurring between the sources of introduced genotypes. Our results highlight the flexibility of the ABC approach for gaining insight into the demographic events accompanying species invasions, and provide guidance for future tests of contemporary evolution among introduced S. latifolia populations.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i038-R*

General sessions

Withstanding being sick: compensatory foraging behaviour to put up with sexual activities

González-Tokman DM[1], González-Santoyo I[1], Lanz-Mendoza H[2], Córdoba-Aguilar A[1]
[1]Universidad Nacional Autonoma de Mexico, Instituto de Ecología, Mexico, Mexico, [2]Instituto Nacional de Salud Pública, Cuernavaca, Mexico

Summary statement:

Infection effects on feeding and territorial behaviour in a predatory insect in the wild

Abstract:

Sick animals can change their feeding behaviour adaptively to deal with infections. However, there is no information in relation to: a) whether predator animals exhibit such changes; b) changes in feeding behaviour in the wild; c) effects on other costly behaviours at the time of infection, and d) effects on physiological components of condition. We experimentally infected males of the predator territorial damselfly Hetaerina americana in a field experiment with the hypothesis that infected animals will show adaptive feeding and reproductive changes in response to the infection. It is predicted that infected animals will reduce feeding and territorial activities, increase immune response (in the form of phenoloxidase [PO] activity), and show depleted fat reserves and flight-associated muscle mass (two traits usually traded off with immunity and territorial behaviour). We also infected males but in a laboratory experiment, to control for food supply and territorial activity, and took the same physiological measures. Contrary to prediction, infected males from the field experiment increased their feeding behaviour but did not modify their territorial activities. Muscle mass was reduced in the field but not in the lab, due probably to the energetically-exhaustive territorial activities. In the lab, starvation led to reduced PO activity in infected males and fat was depleted by infection but not by starvation. Our results support the idea of compensatory resource intake as an adaptation to deal with infections in predators, although we do not discard the possibility that there could be a phase of an infection where illness induced anorexia can be adaptive.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i039-R*

General sessions

Evolutionary ecology of sex-linkage in wild Trinidadian guppies

Gordon SP[1], Lopez Sepulcre A[2], Roughton A[1], Reznick DN[1]
[1]University of California, Riverside, Biology, Riverside, United States, [2]Ecole Normale Supérieure, Paris, Ecologie et Evolution, Paris, France

Summary statement:

Novel introduction of guppies to new environments is used to explore relationship between sex linkage and selective pressures influencing evolutionary rates in the wild.

Abstract:

Numerous studies have documented contemporary evolution in the wild. While the selective factors behind such rapid changes are often studied, it is rarely explored how differences in the mode of inheritance can influence the speed of evolutionary change. For example, theory suggests that sexually-selected dimorphic traits should have a faster rate of evolution if linked to the sex chromosomes versus the autosomes. Here we use Trinidadian guppies (Poecilia reticulata) to examine important ideas from theory regarding the relationship between sex-linkage and selective pressures, which together influence evolutionary rates in wild populations. In the guppy many traits have already been shown to rapidly evolve when fish are introduced to new environments, but has been shown to be quite variable for one such trait (male coloration). We here study the mode of inheritance of male coloration in various high- and low-predation guppy populations across Trinidad and then closely track changes in male coloration in a novel introduction of high-predation guppies into two new low-predation environments. Our results indicate consistent geographic variation of sex-linkage in guppies between high- and low-predation environments. Moreover, in the two introduced, individually-monitored and pedigreed populations, color is already changing after less than two years. Common garden experiments show these changes have a genetic basis. By then combining information on sex-linkage and the individual-based data in the wild, this study can evaluate the importance of genetic architecture in facilitating or constraining evolutionary processes.

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SUN 21 AUG at 1140 - Room N5
Oral presentation *A2-Ge06-1140-O*

General sessions
Development

Spatiotemporal variation in colour patterning in the Trinidadian guppy: Exploring a selection mosaic

Gotanda KM[1], Hendry AP[1]
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Summary statement:

Using adaptive traits of guppies as a proxy for selection, we document variation through space and time, which indicates that selection should be viewed as a spatiotemporal mosaic.

Abstract:

Recent work has suggested that selection is more variable through time than had been appreciated. To date, however, there is no clear understanding of the relative amount of spatial versus temporal variation in selection. Given the difficulties of accurately measuring selection in nature, we quantify spatial and temporal variation in an adaptive trait as a proxy for spatial and temporal variation in selection. We focused on Trinidadian guppies, Poecilia reticulata, where previous work has described a spatially varying balance between natural and sexual selection: females generally prefer males with brighter colour spots (sexual selection), but this colour might increase their mortality at sites with strong predators (natural selection). More recent work, however, suggests substantial temporal variation in selection within sites. To formally evaluate these spatial and temporal contributions to trait variation, we partition the variance in male colour pattern between six sites (across two rivers and two predation intensities), six consecutive years, and the interaction between site and year. We find that site effects, especially those related to predation, are indeed an important determinant of male guppy colouration, supporting previous findings based on a single time period. However, we also find a strong interaction between site and year, which implies that selection varies temporally in direction and strength both within and between sites. These results indicate that spatial and temporal variation are both important to the dynamics of selection and adaptation, and we discuss potential underlying causes of this variation.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i040-R*

General sessions

The hidden cost of avoiding nest predators: offspring pay a long-term fitness cost for parental behaviours which reduce nest predation risk

Griesser M[1,2], Panagakos A[2]
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Summary statement:

Nest predation avoidance strategies reduce nestling feather quality, which have a negative impact on offspring fitness by increasing their risk of being killed by a predator.

Abstract:

Open-nesting bird species have evolved multiple strategies to reduce nest predation such as nesting in dense habitat patches, or avoid visiting the nest in presence of predators. While these strategies effectively reduce nest predation rates, the long-term costs thereof to nestlings remain unknown. We used ptilochronology to investigate the consequences of parental nest predation avoidance strategies on feather growth and quality (the number of faulty growth bars) of Siberian jay Perisoreus infaustus nestlings. Earlier studies showed that jays breed in dense, colder patches and feed more irregularly under high predator abundance, which is predicted to reduce nestling condition. We found that nestlings born on unmanaged territories with a late onset of snowmelt grew shorter and smaller, but heavier feathers of higher quality compared to nestlings from managed territories. Moreover, increased predator abundance (territories close to human settlements) had a negative effect on feather growth and on feather quality. This suggests that a colder microclimate reduces nestling feather growth while irregular feeding reduces feather quality. Given that low feather quality increases mortality of Siberian jays during the first year of life, parental nest predation avoidance strategies can have a negative impact on offspring fitness.

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MON 22 AUG at 1140 - Room N7
Oral presentation *B2-Ge04-1140-O*

General sessions
Evolutionary genetics

Gene expression trade-offs and the evolution of pleiotropy

Guillaume F[1], Otto SP[2]
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Summary statement:

Conditions for the evolution of pleiotropy of coding genes are shown using a modifier locus approach. Traits robust to changes in gene allocation favor the evolution of pleiotropy.

Abstract:

Pleiotropy, the capacity of a gene to affect more than a single trait, is a universal property of the genes. Yet, there is ample variation in pleiotropic degree among genes, with many genes seemingly affecting 1-3 characters while a handful of genes affect many characters (10´s to 100´s). Although the evolutionary consequences of variational pleiotropy is thought to be central for concepts such as evolvability or adaptive constraints, the evolutionary mechanisms leading to such variation are less well known.

We use a population genetics approach to model the evolution of pleiotropy where a regulatory sequence (modifier locus) epistatically influences the pleiotropic action of coding genes. By tracking fitness changes caused by substitution at the modifier locus, we delineate the conditions for the evolution of resource allocation of protein coding sequences to two different traits or functions. Pleiotropy is favored when traits are robust to changes in expression levels (concave fitness curve), with loci with higher expression evolving to be more pleiotropic. Genetic constraints acting on the modifier locus (positive correlation among the pleiotropic degree of each coding gene) also favors transitions towards increased gene pleiotropy. On the other hand, coding gene specialization and a decrease in pleiotropy evolves when the traits are sensitive to variation in gene expression (convex fitness curve). Evolution by gene duplication (sub or non-functionalization) can be considered as a special case of our model.

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SUN 21 AUG at 1120 - Room N5
Oral presentation *A2-Ge06-1120-O*

General sessions
Development

Exploring the molecular basis of differential jaw outgrowth in half beaks

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Summary statement:

We examined the developmental genetic basis of heterochronic growth in the jaws of a half beak fish, and identified Calmodulin as a good candidate.

Abstract:

Heterochronic shifts in growth can lead to morphological innovations that are achieved through simple developmental switches. Understanding the nature of these switches can allow us to gain insight into the molecular mechanism of evolutionary change. Fishes from the suborder Belonioidei achieved a vast array of craniofacial morphologies that appear to have arisen through a series of heterochronic shifts. In some species (needlefishes) both the upper and lower jaws are highly elongated and in others, only the lower jaw is (half-beaks). We examined the molecular basis of accelerated heterochronic growth in the lower jaw, relative to the upper jaw in the half beak Dermogenys pusilla, and compared it to a member of their sister group, the Adrianichthyoidei (medaka), where this trait is ancestral, i.e., both jaws are equally long. We used qRT-PCR analyses to examine the expression of craniofacial patterning genes between the upper and lower jaws of medaka and D. pusilla, during key stages of jaw outgrowth in D. pusilla, and stage-matched medaka samples. Calmodulin shows a strong difference in expression between the upper and lower jaws of D. pusilla, which agrees with observations that this gene is important for beak elongation in Darwin's finches, and jaw width in cichlid fishes. We also compared skeletal development between D. pusilla and medaka, using methods that include morphometric measurements of the upper and lower jaws and histological sectioning. These different lines of evidence point towards a candidate gene for differential jaw growth rates leading to the derived morphologies found in Beloniform fishes.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i042-R*

General sessions

Gene movement between chromosomes in Drosophila miranda

Gurbich T[1], Bachtrog D[1]
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Summary statement:

We describe patterns of gene movement between the chromosomes of Drosophila miranda, particularly focusing on the young neo-X chromosome.

Abstract:

Evolutionary patterns on the X chromosome differ from those on the autosomes. Several recent studies in Drosophila have shown that genes with sex-biased expression are distributed non-randomly among chromosomes, and there is a paucity of male-specific genes on the X chromosome. Often this pattern is a result of relocation of male-biased genes from the X chromosome onto the autosomes. What exactly causes this pattern, however, is unclear. Here, we present data on gene traffic between chromosomes utilizing the genome sequence of Drosophila miranda. Drosophila miranda has recently evolved neo-sex chromosomes, which were formed about 1 million years ago by the fusion of Muller element C, an autosome, to the ancestral Y chromosome, and are still in the process of acquiring characteristics of fully differentiated sex chromosomes. The young age of Drosophila miranda's neo-X chromosome provides an excellent system for analyzing early evolution of an X chromosome. We combine the pattern of gene movement with data on gene expression, X chromosome inactivation regions and dosage compensation to investigate which forces are driving male-specific genes off the X chromosome.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i043-R*

General sessions

Genetic characterization of a breeding system polymorphism in Daphnia

Haag CR[1], Galimov Y[2], Haag-Liautard C[1], Walser B[1], Fasel D[1], Roulin A[3], Routtu J[3]
[1]University of Fribourg, Ecology & Evolution, Fribourg, Switzerland, [2]Institute of Developmental Biology Russian Academy of Sciences, Moscow, Russian Federation, [3]Zoological Institute, University of Basel, Basel, Switzerland

Summary statement:

A locus with a dominant male suppression allele on chromosome 4 of Daphnia magna determines a breding system intermediate between enviornmental and genetic sex determination.

Abstract:

In Daphnia (Cladocera, Crustacea), parthenogenetic reproduction alternates with sexual reproduction. Individuals of both sexes that belong to the same parthenogenetic line are genetically identical and their sex is determined by the environment. Here we describe the existence of non male producing (“NMP”) genotypes in Daphnia magna, which can only persist through phases of sexual reproduction if they co-occur with normal (“MP”) genotypes that produce both males and females. We find that this breeding system polymorphism, which is similar to the well-known gynodioecy (coexistence of females with hermaphrodites) in plants, is determined by a single, nuclear locus (or a tight linkage group) with NMP being dominant over MP. We mapped this locus to linkage group 4 of D. magna, and we are currently trying to identify candidate loci that may contain the mutation(s) causing the NMP phenotype. We also show that the NMP phenotype is likely to have evolved several times independently within the species. As a similar breeding system polymorphism is also known from D. pulex, which shared a common ancestor with D. magna more than 100 MY ago, these results suggest that the evolution of NMP genotypes in cyclical parthenogens may be more common than previously thought. Moreover, MP genotypes that coexist with NMP genotypes may have responded to the presence of the latter by partially specializing on male production. Hence this breeding system polymorphism may be a model for an evolutionary transition from a purely environmental to a partially genetic sex determination system.

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MON 22 AUG at 1100 - Room N4
Oral presentation *B2-Ge03-1100-O*

General sessions
Population ecology

The “singles bar” hypothesis for pollinator-flower coevolution

Hadany L[1], Hendrix S[2], Lachmann M[3]
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Summary statement:

We propose that pollinators visit flowers not only for food, but sometimes for meetings with potential mates. We present models and empirical data supporting this hypothesis.

Abstract:

Why do pollinators visit flowers? The answer to this question seems simple: they are looking for food. We propose that by effectively advertising themselves, flowers also offer pollinators a natural meeting place with potential mates, thus serving as ´singles bars´ rather than just ´restaurants´. We develop a simple mathematical model to study the ‘singles bar’ scenario and derive predictions that differentiate it from the ´restaurant´ one. We test and validate these predictions using an extensive set of observations of flower visitation by multiple species of bees. The singles bar interpretation puts flower-pollinator interactions in a new perspective, suggesting, for example, that sexually reproducing bees can have very different flower preferences in comparison with non-reproductive workers, and that large floral display might sometimes be an “unfakable signal” of attractiveness.

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MON 22 AUG at 1200 - Room N7
Oral presentation *B2-Ge04-1200-O*

General sessions
Evolutionary genetics

Positive and negative selection in murine ultra-conserved noncoding elements

Halligan DL[1], Oliver F[1], Guthrie J[1], Stemshorn KC[2], Harr B[2], Keightley PD[1]
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Summary statement:

A phylogenetically independent comparison shows that sections of noncoding DNA absolutely conserved across mammalian orders are subject to strong negative and positive selection.

Abstract:

There are many more selectively constrained noncoding than coding nucleotides in the mammalian genome, but most mammalian noncoding DNA is subject to weak selection, on average. One of the most striking discoveries to have emerged from comparisons among mammalian genomes are the hundreds of noncoding elements of more than 200bp in length that show absolute conservation among mammalian orders. These elements represent the tip of the iceberg of a much larger class of conserved noncoding elements (CNEs). Much evidence suggests that CNEs are selectively constrained and not mutational cold-spots, and many CNEs have been shown to play a role in the regulation of development. Here, we quantify negative and positive selection acting in murine CNEs by analysing within-species nucleotide variation and between-species divergence of CNEs identified by a phylogenetically independent comparison. The distribution of fitness effects of new mutations in CNEs, inferred from within-species polymorphism, suggests that CNEs receive a higher number of strongly selected deleterious mutations and many fewer nearly neutral mutations than amino acid sites of protein-coding genes or regulatory elements close to genes. Paradoxically, however, we also show that CNEs experience a far higher proportion of adaptive substitutions in murids than any known category of genomic sites. The absolute rate of adaptation of CNEs is similar to that of amino acid sites of proteins. This result suggests that there is widespread adaptation in mammalian conserved noncoding DNA elements that are implicated in the regulation of crucially important processes, including development.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i019-E*

General sessions

Sexual selection and the evolution of sexually dimorphic appendages in amphipods

Handschuh S[1,2], Nemeschkal HL[1], Metscher BD[1], Mitteröcker P[1], Müller GB[1,2]
[1]University of Vienna, Department of Theoretical Biology, Vienna, Austria, [2]Konrad Lorenz Institute for Evolution and Cognition Research, Altenberg, Austria

Summary statement:

We analyze the contribution of sexual selection to the evolutionary modification of amphipod trunk appendages, using microCT-based measurements of mated specimens from 50 pairs.

Abstract:

We investigate the evolution of trunk appendages in Amphipoda (Malacostraca, Crustacea) using three-dimensional microCT imaging for quantitative measurements at microscopic scales. The sample for this study consists of 200 microCT scans from 100 specimens (50 matched pre-copula pairs) of the invasive freshwater gammarid Dikerogammarus villosus (Sowinski, 1894). To our knowledge, this is the largest (microscopic) tomographic sample hitherto acquired for an evolutionary investigation of mated pairs. We analyze phenotypic integration of body appendages as well as correlation patterns between mated specimens of the two sexes. Ultimately we intend to show how sexual selection contributes to the evolutionary modification of amphipod trunk appendages. The two pairs of gnathopods (second and third pereon appendages) are sexually dimorphic in this species (as in many other amphipods). Their function in pre-copulatory mate guarding and mating behaviour, during which they serve the males as prehensile organs, is fairly well known. We present preliminary data regarding sexual selection on the size of male gnathopods, to provide an insight into the process of how these highly dimorphic characters might have evolved. We discuss the implications of our findings in a synthetic evolutionary context.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i044-R*

General sessions

Phylogeny and population genetics of green monkeys (Chlorocebus) – Is there evidence for hybridization?

Haus T[1], Roos C[2], Zinner D[3]

[1]German Primate Center, Cognitive Ethology / Primate Genetics, Göttingen, Germany, [2]German Primate Center, Primate Genetics, Göttingen, Germany, [3]German Primate Center, Cognitive Ethology, Göttingen, Germany

Summary statement:

Here we present our results of phylogeny and population genetics of green monkeys and discuss the degree of interspecific gene flow across contact zones in West and East Africa.

Abstract:

Within the genus Chlorocebus currently at least 6 species are recognized. The parapatric species inhabit wide ranges of sub-Saharan Africa. In the past several authors described hybridization between most species in contact zones in Ethiopia and Uganda, and genetic exchange was also suggested in the respective contact zone in West Africa. Hybridization became obvious to play an important role in evolutionary processes of several primate species, even in the human lineage. To study the impact and extent of hybridization on the evolution of green monkeys, we investigate phylogenetic and population genetic patterns. We therefore collected faecal samples in two potential hybrid zones along the Volta River in Ghana and Burkina Faso where C. sabaeus and C. tantalus meet, and in Ethiopia within the contact zones of C. aethiops, C. pygerythrus and C. djamdjamensis. By analyzing various nuclear and mitochondrial loci we will estimate the degree of interspecific gene flow across contact zones. Furthermore, we will reconstruct the phylogeny of green monkeys by including respective samples from the whole distribution range of the genus.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i045-R*

General sessions

Origin and evolution of the bacterial component of eukaryotic proteome

He D[1], Baldauf S[1]
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Summary statement:

A phylogeneitc pipeline to investigate the origin and evolution of bacterial component of eukaryotic proteome.

Abstract:

The chimera of eukaryotic genomes reflects the complex evolutionary history of eukaryogenesis that suggests there were more than two (alpha-proteobacteria gave the birth of mitochondria and cyanobacteria gave the birth of chloroplast) groups of bacteria involved. To understand the early evolutionary history of eukaryotic proteome I have chosen the universal EUkaryotic BActerial Component (EUBAC) as the material, using phylogenetic approaches to investigate the eukaryotic proteome in terms of their respective bacterial groups. The phylogenetic signal of a gene is often very week for confidently detecting deep phylogeny. In this study I have applied a pipeline to enhance the phylogenetic signal by concatenating clusters of genes based on the profiles of their bacterial orthologs. The results show that weak phylogenetic signals could be retrieved indicating they have common underline evolutionary (phylogenetic) history. This is especially very important for ancient phylogenetics that normally could not be picked up by a single gene tree. Moreover, it might be more important to find the proper clusters of genes that are phylogenetically congruent than just combining them all as “phylogenomics”.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i046-R*

General sessions

Reproduction in vole populations versus the monogamy gene avpr1a

Heckel G[1,2], Gschwind A[1,2]
[1]University of Bern, Institute of Ecology and Evolution, Bern, Switzerland, [2]Swiss Institute of Bioinformatics, Lausanne, Switzerland

Summary statement:

Association of avpr1a polymorphism with different traits of social behavior in common voles is highly dependent on statistical treatment.

Abstract:

The extent of genetic control of behavior is a long standing question in sociobiology and behavioral ecology. Innate components of behavior are evident at all evolutionary levels but the complexity and interdependence of behavioral traits makes it difficult to assess the contribution of particular genes. An exception is the arginine vasopressin 1a receptor gene (avpr1a) which has been associated with individual variation in social behavior of several mammalian species. Several studies have linked length variation of a repetitive element (STR) in the regulatory region of avpr1a with e. g. sexual fidelity and pair-bonding in voles and humans. Here we tested for an association of avpr1a STR polymorphisms with social parameters such as the number of mating partners or offspring in male and female common voles under quasi-natural conditions. Field observations and parentage data spanning three years and 2000 individuals detected considerable variation in social and mating system parameters and avpr1a STR polymorphism. Multivariate analyses resulted in several sex-specific associations between STR polymorphisms and social traits very similar to reports on avpr1a in other species. However, we detected also a strong dependency of the associations on the statistical treatment of the genetic and behavioral data. Our results show that the impact of avpr1a STRs on the social behavior of common voles is - at best - very weak in natural populations, and it is questionable whether the effects of the avpr1a system are stronger in other mammalian species.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i020-E*

General sessions

The taxonomic subdivision and population structure of the greylag goose

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[1]University of Oulu, Department of Biology, Oulu, Finland, [2]University of Aberdeen, Department of Archaeology, Aberdeen, United Kingdom, [3]Cornell University, Department of Ecology and Evolutionary Biology, Ithaca, United States

Summary statement:

We studied the taxonomy and population structure of the greylag goose throughout its distribution area by using both modern and museum samples.

Abstract:

The greylag goose (Anser anser) has a disjunct Palearctic distribution. It breeds widely at boreal and temperate latitudes across Europe and Asia and winters south to North Africa, the Middle East, India and southern China. It has two recognized subspecies, the western form is the nominate form A. a. anser and the eastern form is A. a. rubrirostris. However, there is also third subspecies A. a. sylvestris mentioned in literature. The taxonomic status of A. a. sylvestris is questionable and if such a subspecies really exists, it would be desirable to reassess the current population boundaries of different subspecies. Another important factor concerning current populations of greylag goose is the introductions that have been carried out in Western Europe in the 20th century. Overall, we wanted to find out the taxonomic subdivisions and population structure and interactions of the greylag goose. To answer these questions, we sampled both modern geese and museum specimens throughout the species' distributional area. Based on mitochondrial control region sequences we clarified the taxonomy and the population genetic structure of the species.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i021-E*

General sessions

Male genital length affects individual fitness in wild Trinidadian guppies (Poecilia reticulata)

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[1]North Carolina State University, Department of Biology, Raleigh, United States, [2]W.M. Keck Center for Behavioral Biology, Raleigh, United States, [3]Ecole Normale Supérieure, Paris, France, [4]Colorado State University, Fort Collins, United States, [5]Dalhousie University, Halifax, Canada, [6]University of California, Riverside, United States

Summary statement:

We show for the first time that male genital length influences probability of survival and reproduction for guppies in a long-term, individually based field study.

Abstract:

Genitalia evolve extremely rapidly and divergently among internally fertilizing taxa such that many closely related species are only distinguishable by genital morphology. This pattern suggests an important link between genital diversification and speciation, though the mechanism and fitness consequences of genital evolution remain poorly understood. Potentially important influences on genital evolution include selection on survival (e.g., locomotor performance) and reproduction (e.g., female preference). Here, we investigated the effect of male genital length on survival and reproduction in two wild, experimental populations of Trinidadian guppies (Poecilia reticulata). We introduced native guppies into two natural Trinidadian streams previously devoid of guppies. Subsequently, we monitored each individual by conducting a monthly mark-recapture and reconstructing the genetic pedigree. We measured gonopodium (sperm transfer organ) and body (standard) length of each mature male from mark-recapture photographs. We predicted that short gonopodia males would have a higher probability of survival while long gonopodia males would have a higher probability of reproduction. Our results revealed that overall, males possessing small gonopodia relative to body size are both more likely to survive and to sire at least one offspring that survives until sexual maturity. However, the magnitude and sign of this reproductive pattern varies seasonally. Our findings suggest a strong, but temporally variable, directional selection on male genital length that may prove to be an important factor in promoting reproductive isolation.

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WED 24 AUG at 1500 - Room N6
Oral presentation *D3-Ge07-1500-O*

General sessions
Primates

Effects of sex-biased evolution on patterns of diversity in apes

Hellmann I[1], Thalmann O[2], Fischer A[3], Vigilant L[4]
[1]Max F. Perutz Laboratories, Mathematics and Biosciences Group, Vienna, Austria, [2]University of Turku, Turku, Finland, [3]African Insect Science for food and Health, Molecular Biology and Biotechnology, Nairobi, Kenya, [4]Max Planck Institute for Evolutionary Anthropology, Primatology, Leipzig, Germany

Summary statement:

X/Autosome ratios of diversity in great ape populations differ a lot and might be indicative of sex biased migration.

Abstract:

Apes show striking variability in the reproductive strategies that underlie their social systems. For example, behavioral studies suggest that most offspring in a gorilla group are sired by one dominant male, while bonobos are relatively promiscuous. Furthermore, observational data also suggest that apes have a strong sex bias in their migration patterns. Here we investigate potential long-term effects of reproductive strategies and female-biased migration on levels of diversity by comparing sequence data from mitochondria, autosomes, X- and Y-chromosome. To do so, we sequenced ten 5kb loci on the X and Y in ~10 bonobos, eastern, western and central male chimpanzees as well as ~10 male mountain and lowland gorillas, and then combined this with previous studies of autosomal and mitochondrial data.

We have too little data to detect a significant departure from the X/A of 0.75, which would be expected given no sex biases. However, the general pattern of X/A-ratios appears to be dominated by female biased migration rather than a big difference in reproductive variance between males and females.

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MON 22 AUG at 1100 - Room N2
Oral presentation *B2-Ge01-1100-O*

General sessions
Behaviour

Is Australia a hotspot for deception: the evolution of deceptive signals in spiders and orchids

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[1]Macquarie University, Biological SCiences, Sydney, Australia, [2]University of Auckland, Biological Sciences, Auckland, New Zealand

Summary statement:

We present cases studies of deception in Australian spiders and orchids and discuss hypotheses why deception in these systems is so common in Australia.

Abstract:

Australia is curious place characterised by long evolutionary isolation, extreme ecological conditions and high levels of diversity and endemisms. Deceptive systems, that lure insects to their detriment are surprisingly common in Australian crab spiders and orchids. Australian crab spiders reflect UV-light thereby attracting pollinators to the flowers they forage on. Australian sexually deceptive orchids mimic the scent, colour and possibly shape of female wasps to attract males that attempt pseudo-copulation thereby transferring orchid pollen. In some cases the decpetion is so convincing that males ejaculate.
We present data to illustrate this deceptive exuberance in these systems and offer several hypotheses why deception may be selected for in spiders and orchids. While some of the hypotheses we offer are specific to the system, others may work across several systems. We argue that Australia offers a natural advantage to study the evolution and maintenance of deceptive signals.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i022-E*

General sessions

The influence of UV-signalling in female mate-choice of three-spined sticklebacks from different photic habitats

Hiermes M[1], Bakker TCM[1]
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Summary statement:

Stickleback females from clear-water and tea-stained lakes were compared with respect to mate-choice when males were presented under UV-poor and UV-rich conditions.

Abstract:

Ultraviolet (UV) signals have been shown to be of importance in mate-choice contexts in numerous species, amongst others the three-spined stickleback (Gasterosteus aculeatus L.), which is able to transmit and perceive in the UV-wave range. The benefits of private UV-signalling and the costly expression and receipt of UV-signals are a function of the prevailing ecological conditions. A decisive factor for colour signalling is the photic environment, especially in aquatic habitats, as the visibility of colour signals, and thus costs and benefits of signals are instantaneously influenced by it. The island of North Uist (Outer Hebrides), Scotland, comprises bodies of water ranging from clear-water to turbid, tea-stained lakes. The latter are characterised by strong absorption and scattering of short wavelengths, especially UV-wavelengths, and thus the lakes across the island possess great variation in their UV-transmission. We examined female sticklebacks of six populations, three of which originated from tea-stained lakes and the other three from clear-water lakes, with respect to their preferences to court males viewed under UV-rich and UV-poor conditions. The results are discussed in the context of differences in UV-signalling and UV-preferences between the two habitat types, and possible evolutionary adaptations.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i048-R*

General sessions

Benchmarking de novo RNA-seq analysis in non-model species using H. sapiens as a proxy

Hornett EA[1], Wheat C[1]
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Summary statement:

For non-model species with no genomic reference, de novo transcriptomes can be utilised in gene expression studies. Here we assess their performance and discuss the implications.

Abstract:

As high-throughput sequencing technologies advance, obtaining large quantities of RNA-seq data becomes more achievable for researchers studying non-model species, such as ecological geneticists investigating the genetic variation underlying their phenotype of interest. There are however still many challenges in analysing expression data, one of the most common being the lack of a reference genome. An alternative route for measuring gene expression levels is to map RNA-seq reads to a de novo transcriptome. We here assess the performance of de novo RNA-seq using genomic resources available for H. sapiens as a proxy, thereby obtaining detailed insights not possible in non-model species. Eleven different transcriptomes using varying amounts of Illumina and 454 data were assembled and their exact amount of gene model coverage quantified, in terms of total base pairs and number of unique genes. Each assembly's utility as a mapping scaffold for RNA-seq data was then investigated across independent technical runs, comparing these expression levels with those obtained using the predicted gene set from the H. sapiens WGS data. Variation in expression levels among technical replicates was low when mapping reads to the same assembly, but comparisons across assemblies were on the same order of difference as among microarray experiments (c. R2 = 0.80). We then extend this analysis by using increasingly divergent genomic reference species (25, 50, 75 million years) as proxy. These results are then compared back to those from H. sapiens, and the loss of expression signal assessed across GO functional categories. The implications for de novo RNA-seq in non-model species are discussed.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i049-R*

General sessions

Life-history plasticity in semelparous organisms

Hughes PW[1], Simons AM[1]
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Summary statement:

We examine phenotypic plasticity of life-history characters in semelparous organisms using an experimental manipulation of the monocarpic biennial Lobelia inflata.

Abstract:

Semelparous life-histories are characterized by a single, fatal reproductive episode that accounts for 100% of their reproductive investment in offspring. Mathematical modelling has provided a basis for understanding the general selective forces favouring semelparous life-histories, but yet life-history characters can remain highly plastic, even in key life-history traits (i.e. offspring quality). Some semelparous individuals survive terminal senescence to reproduce a second time, others spread their "single episode" over long periods of time, and plants bolted under different flowering conditions elicit widely varying flowering phenologies. What factors account for this variation?
Our work examines the phenotypic plasticity of key life-history characters though a series of manipulation experiments on the monocarpic (semelparous) biennial Lobelia inflata. In this paper, we: (i) explain the phenomenon of secondary (i.e. post-senescent flowering), (ii) define and metricize degrees of semelparous behaviour expressed along different time scales and (iii) investigate the temporal norms of reaction for key reproductive characteristics.

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WED 24 AUG at 1400 - Room N2
Oral presentation *D3-Ge08-1400-O*

General sessions
Human impact

The effects of ecology and chemotherapy on the evolution of drug resistance

Huijben S[1], Sim D[1], Chan B[1], Read A[1]
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Summary statement:

We reason that current drug use practices are poor resistance management strategies developed in a knowledge vacuum. Empirical data from our rodent malaria model support this view.

Abstract:

The evolution of drug resistant pathogens is one of the major challenges for 21st century medicine. We reason that there is poor theoretical and empirical justification for current drug use practices as a resistance management strategy. For instance, rapid and complete elimination of pathogens is advocated as a way to reduce the probability that de novo resistance mutations occur. Yet, this ‘radical pathogen cure’ strategy maximizes the evolutionary advantage of any resistant pathogens that are present.

We studied this apparent paradox in a rodent malaria model. The fitness of resistant pathogens is dependent on tradeoffs between the cost of resistance in untreated hosts and the benefit under drug pressure. In the case of malaria, both the cost and drug pressure are dynamical processes strongly dependent on in-host ecology. We studied the selective pressures on resistant parasites in a variety of infection ecologies, such as multi-genotype infections, variable genotype frequencies and under varying drug pressures.

All these ecological factors had a marked impact on the fitness of resistant parasites, but not always in intuitive ways. Altering the within-host ecology by administrating drugs invariably resulted in strong positive selection for drug-resistant parasites. Reduction of drug pressure led to significant decreases in selection for resistance, while being equally as effective, or sometimes better, at improving host health and reducing infectiousness. These experiments confirm our view that much public health orthodoxy about evolution is developed in a knowledge vacuum.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i050-R*

General sessions

Ploidally antagonistic selection maintains stable genetic polymorphism

Immler S[1], Arnqvist G[1], Otto SP[2]
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Summary statement:

We explore the potential for the maintenance of genetic polymorphisms assuming both ploidally antagonistic and sex-specific selection under autosomal, X-, and Y-linked inheritance.

Abstract:

Understanding the maintenance of genetic variation in the face of selection remains a key issue in evolutionary biology. One potential mechanism for the maintenance of genetic variation is opposing selection during the diploid and haploid stages of biphasic life cycles universal amongst eukaryotic sexual organisms. If gene expression occurs during the haploid phase, selection can act in both phases, potentially in opposing directions. In addition, the potential for sex-specific selection is large during haploid phases simply because male and female gametophytes/gametes tend to have contrasting life histories. We explored the potential for the maintenance of a stable polymorphism under ploidally antagonistic selection as well as sex-specific selection. Furthermore, we examined the potential influence of the chromosomal location of alleles (autosomal or sex-linked). Our analyses show that the most permissible conditions for the maintenance of polymorphism occur under negative ploidy-by-sex interactions, where an allele favoured by selection in the haploid phase of one sex is simultaneously disfavoured by selection in the diploid phase of the other sex. With constant fitnesses, ploidally antagonistic selection can maintain stable polymorphisms for autosomal and X-linked genes but not for Y-linked genes. We discuss the implications of our results and put them into a biological context.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i023-E*

General sessions

Is the fate of harbour seals sealed? Population structure and genetic diversity of (Phoca vitulina) in the UK

Islas-Villanueva V[1], Hall AJ[1], Graves JA[2]
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Summary statement:

This study seeks to determine if genetic diversity and population structure of harbour seals in the UK have been recently altered due to previous mass mortality events.

Abstract:

Harbour seal (Phoca vitulina) distribution in Europe has been influenced both by glaciations and by antropogenic factors. Population substructure and genetic diversity will reflect both past and present events such as colonisation, bottlenecks and migration. The identification of current differentiated populations is crucial for management purposes and it can also give us an insight into the rapid response of wild populations to accelerated antropogenic processes such as: climate change, reduced habitat, reduced food resources, etc. In 1988 over 18000 harbour seals in the North Sea died, due to a PDV (Phocine distemper virus) epizootic. Goodman et al. (1998) analyzed 1029 samples of harbour seals, with 7 microsatellites from 12 different locations. Most of these samples were from animals that died during the epizootic. This study identified six population units of harbour seals in the UK and Europe. Since this mass mortality event harbour seal populations have been declining in the UK, in addition to the first PDV epizootic there was a second outbreak in 2002, which was less severe. Harbour seal populations in the UK might also be affected by competition with grey seals and predation from killer whales. Our study is investigating the population structure and genetic diversity of harbour seals around the UK in more detail, particularly around Scotland. A total of 345 wild harbour seals have been analyzed for twenty-six polymorphic microsatellites. The goal is to determine if genetic diversity and population structure have been significantly altered, in this short period of time, due to PDV mass mortality and the factors driving the current decline of the populations.

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SUN 21 AUG at 1140 - Room N3
Oral presentation *A2-Ge02-1140-O*

General sessions
Life-history

Quantitative test of sex allocation theory in a simultaneous hermaphrodite

Janicke T[1], Marie-Orleach L[1], De Mulder K[2], Berezikov E[2], Ladurner P[3], Vizoso DB[1], Schärer L[1]
[1]University of Basel, Zoological Institute, Basel, Switzerland, [2]Hubrecht Institute, Utrecht, Netherlands, [3]University of Innsbruck, Institute of Zoology, Innsbruck, Austria

Summary statement:

Focal individuals with fluorescent sperm allow us to study how mating group size and skews in sperm-transfer success influence sex allocation.

Abstract:

Classical sex allocation theory for simultaneous hermaphrodites predicts that the optimal resource allocation into the male and the female sex function depends on the number of mates an individual acquires (also termed mating group size). However, more recent theoretical work suggests that paternity skews (e.g., due to sperm displacement or random events) can also have strong effects on the optimal sex allocation, which until now has been largely ignored in empirical studies. Using the outcrossing simultaneously hermaphroditic flatworm Macrostomum lignano, we here provide a quantitative test of the classical resource allocation model for simultaneous hermaphrodites, which predicts 1) that the male allocation increases with increasing mating group size and 2) that the resources put into the male function never exceed 50% of the available reproductive resources (i.e., sex allocation saturates with increasing mating group size). Moreover, we test how skews in the number of sperm that a focal individual manages to store in its mates can affect the link between mating group size and the sex allocation. For this we raised one GFP-expressing focal worm per treatment group together with varying numbers of wild-type worms to generate different social and mating group sizes. The detection of GFP-expressing sperm in wild-type worms allowed us to obtain both a measure of the mating group size and the number of successfully stored sperm by focal worms. Thereby we tested how these measures translate into a phenotypically plastic response in sex allocation. To our knowledge, this is the first quantitative test of the resource allocation model in a simultaneously hermaphroditic animal.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i051-R*

General sessions

The importance of evolutionary reservoirs for pathogen emergence: Experimental evolution of pathogenic bacteria within immunocompromised C. elegans hosts

Jansen G[1]
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Summary statement:

The role of immunodeficient hosts as incubators for novel pathogen strains was studied using experimental evolution of bacteria within C. elegans nematode hosts.

Abstract:

Infectious diseases incur a large biological and economic burden on society. The emergence of previously unknown or medically unimportant strains as new disease causing agents is particularly worrisome. These strains are sporadically traced back to initial infections of patients suffering from AIDS, leishmaniasis or other diseases, to weakened patients in intensive care units or to hosts treated with immunosuppressing drugs. Epidemiological models confirm that opportunistic bacteria may be able to persist in patients with an inefficient immune system and emerge as pathogens after an adaptive stage in immunocompromised hosts.

These observations and predictions have not been tested experimentally. In this study an empirical model system was developed to understand the emergence and evolution of disease agents. As a model host the genetically tractable model nematode Caenorhabditis elegans was chosen. Immunocompromised hosts were produced by knocking down central genes in conserved innate immunity signalling cascades (TGF-ß and ILR pathways). These host lines were subsequently infected with several strains of bacteria (a.o. Staphylococcus aureus, Pseudomonas aeruginosa). After repeated infection of non-evolving hosts with evolving populations of pathogens, those adapted to immunocompromised hosts are expected to have become more pathogenic. The first results of the outcome of this evolution experiment are presented here.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i052-R*

General sessions

Migratory behaviour of birds affects their coevolutionary relationships with blood parasites

Jenkins T[1,2], Thomas GH[3], Hellgren O[4], Owens IPF[1]

[1]Imperial College, Silwood Park, Ascot, United Kingdom, [2]University of Bern, Institute for Ecology and Evolution, Bern, Switzerland, [3]University of Bristol, School of Biological Sciences, Bristol, United Kingdom, [4]University of Lund, Animal Ecology Group, Lund, Sweden

Summary statement:

We present cophylogenetic analyses investigating the congruence between phylogenies of Leucocytozoon parasites and their avian hosts and relate this to host migration.

Abstract:

Migratory birds may facilitate the dispersal of disease causing parasites, potentially transferring infection both across geographic areas and between host species. There is however, little quantitative information on whether the migratory behaviour of hosts affects the macro-evolutionary outcome of host-parasite associations. In this study, we considered Leucocytozoon blood parasites of birds, a group closely related to avian malaria, to study host-parasite coevolution in relation to host migratory behaviour using a phylogenetic comparative approach. We reconstructed molecular phylogenies of both the hosts and parasites and used cophylogenetic tools to assess whether each host-parasite association contributed significantly to the overall congruence between the two phylogenies. We found evidence for a significant fit between the two phylogenies, and showed that this was due only to associations between non-migrant parasites and their hosts. We also showed that migrant bird species harboured a greater genetic diversity of parasites compared with non-migrant species. Taken together, these results confirm that migratory habits of birds influence their coevolutionary relationship with their parasites: this has not been shown at the macro-evolutionary scale, and could have implications on parasite range expansion.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i024-E*

General sessions

Strategic ejaculation: a meta-analysis of the numbers

Jennions MD[1], Kelly CD[2]

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Summary statement:

We present meta-analyses of evidence for four claims about social situations where males should strategically adjust the number of sperm ejaculated. Some are support, others not.

Abstract:

In four meta-analyses we quantify the evidence that sperm competition (SC) favours greater sperm number in specific social situations using data from studies of strategic ejaculation. Differential investment into ejaculates occurs if males exhibit phenotypic plasticity in ejaculate properties in response to the likely risk and/or intensity of sperm competition after a given mating. Theoretical models have been developed that predict how ejaculate size will be strategically adjusted in relation to: (a) the number of immediate rival males, with a distinction made between 0 versus 1 rival ('risk' of SC) and 1 versus several rivals ('intensity' of SC); (b) female mating status (virgin or previously mated); and (c) female phenotypic quality (e.g. female size or condition). Some well-known studies have reported large adjustments in ejaculate size depending on the relevant social context. This has led to widespread acceptance of the claim that strategic sperm allocation occurs in response to all of the proposed factors. It is necessary, however, to test each claim separately because it is easy to overlook studies with weak or negative findings. We will present results that show some claims are well supported, while others are not. Our results highlight how meta-analysis can reveal unintentional biases in narrative literature reviews, as well as in how results are presented.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i053-R*

General sessions

Effects of population size and dispersal on genetic variation in a house sparrow metapopulation

Jensen H[1], Torvik Kristiansen A[1], Ringsby TH[1], Pärn H[1], Sæther B-E[1]
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Summary statement:

In a natural house sparrow metapopulation dispersal counteracted the loss of genetic diversity and genetic differentiation caused by genetic drift.

Abstract:

Many human activities lead to increased habitat fragmentation and reduced size of natural populations. Dispersal and random genetic drift are expected to become increasingly important processes for the persistence of fragmented and small populations. However, little is known about the relative importance of immigration and population size for intra- and inter-population genetic variation in natural populations. In this study we used empirical data from an insular house sparrow (Passer domesticus) metapopulation in northern Norway. In this metapopulation good estimates on local population sizes and dispersal were available through extensive capture-mark-recapture in 18 populations across almost 20 years. Genetic variation within and between populations was estimated at three-year intervals to reduce bias due to overlapping generations (generation time is approx. 2 years). Gene diversity (i.e. expected heterozygosity) within populations and Fst between populations was estimated using individual information on 14 neutral microsatellite loci. Our results showed that gene diversity increased with population size and number of immigrants. However, the effect of immigration on gene diversity was strongest when the number of immigrants was small. On the other hand, genetic differentiation between populations was reduced mainly by dispersal. Consequently, our results suggest that dispersal is an important process in structured populations, counteracting the loss of genetic diversity and genetic differentiation caused by genetic drift in small populations. Dispersal may reduce negative effects of fragmentation and small population size, and thus reduce loss of biodiversity.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i025-E*

General sessions

Protective coloration in the Shieldbug Graphosoma lineatum

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Summary statement:

These findings gives support for a general pattern of avoidance learning and generalization in avian predators.

Abstract:

There are many ways to lower the risk of predation. Protective coloration such as crypsis and aposematism are two strategies commonly used in predation avoidance. The chosen strategy depends on the possibilities and constraints to the animal. Consequently, insects often change strategy between life stages, but a switch in strategy within a life stage is quite uncommon. In the Swedish shieldbug Graphosoma lineatum we see a colour change from the pre-hibernating to the post-hibernating adults that alters their protective strategy from cryptic to aposematic. By measuring the attack latencies of naïve great tits red and pale adults and last-instar larvae (black and brown), we investigate avoidance learning and generalisation between the three forms of the shieldbug. Great tits hesitated more before attacking the red form, and hesitated longer before attacking both adult forms than the larva. Birds learnt to avoid both adult forms, but learnt to eat the larvae. There was positive generalization from larvae to adults and negative from adults to larvae. These findings are very similar to experiments with G. lineatum on domestic chicks, giving support for a general pattern of avoidance learning and generalization in avian predators.

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WED 24 AUG at 1440 - Room N3
Oral presentation *D3-Ge10-1440-O*

General sessions
Inbreeding

The influence of maternal effects on inbreeding depression in Mimulus guttatus

Jordan CY[1], Hodgins K[1], Ally D[2], Otto S[1]
[1]University of British Columbia, Department of Zoology, Vancouver, Canada, [2]San Diego State University, Biology, San Diego, United States

Summary statement:

We test whether maternal effects influence the expression of inbreeding depression, and discuss the evolutionary implications for such maternal effects.

Abstract:

Many experiments show that Inbreeding depression differs among environments, and generally suggest that it is greater under more stressful conditions. However, such experiments often do not control for maternal effects, which can be substantial in plant populations. Therefore, we tested whether maternal effects influence inbreeding depression in Mimulus guttatus in two greenhouse environments (benign and low water), using multiple independent genetic lines. Preliminary results show that maternal effects influence inbreeding depression for total biomass but not flower number. We will present complete analyses for these and other traits, and discuss the implications of these findings both for understanding the effect of stress on inbreeding depression, and potential evolutionary consequences of such maternal effects.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i054-R*

General sessions

Seasonal sex allocation in Gambusia holbrooki

Kahn AT[1], Kokko H[1], Jennions MD[1]
[1]Australian National University, Research School of Biology, Canberra, Australia

Summary statement:

Seasonal birth sex ratio shifts are well known but poorly understood. Our data and model suggest operational sex ratio variation drives these shifts in fish populations.

Abstract:

Birth sex ratio (BSR) biases in vertebrates are rare. With the exception of a few cases, the BSR biases that do occur tend to be weak and idiosyncratic. Seasonal trends in BSR have been demonstrated in several bird and mammal species but few have considered: what happens when the operational sex ratio (OSR) and hence sex-specific mating opportunities vary seasonally due to differential mortality? Generally, adult mortality is not expected to affect the optimal BSR, but when generations overlap this is not always the case. We produced a periodic non-linear two-sex matrix model for life-histories where the sexes suffer differential mortality that varies seasonally (i.e. seasonal variation of the OSR). Seasonal shifts in BSR are predicted – alternating between an overproduction of sons and of daughters. We tested this model in 3 populations of the freshwater fish Gambusia holbrooki in southeastern Australia. The OSR of populations varied seasonally in a consistent way, albeit to different extents. Significant BSR biases were observed: up to ~ 60% sons in spring and ~ 70% daughters in autumn. These biases were significantly correlated with those predicted by our model.

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WED 24 AUG at 1440 - Room N4
Oral presentation *D3-Ge04-1440-O*

General sessions
Evolutionary genetics

Non-random gene loss from the Drosophila miranda neo-Y chromosome

Kaiser VB[1], Zhou Q[1], Bachtrog D[1]
[1]University of California, Integrative Biology, Berkeley, Canada

Summary statement:

Gene loss from the Drosophila miranda neo-Y chromosome is non-random; highly expressed, broadly expressed and male-biased genes remain functional for longer.

Abstract:

Suppressed recombination leads to the degeneration of an evolving Y chromosome. However, it is not known whether gene loss is a largely random process and primarily driven by the order in which mutations occur, or whether certain categories of genes are lost less quickly than others; the latter would imply that selection counteracts the degeneration of Y chromosomes to some extent. We investigated the relationship between putative ancestral expression levels of neo-Y-linked genes in Drosophila miranda and their rates of degeneration. We used RNA-Seq gene expression data of neo-Y homologues in Drosophila pseudoobscura to show that genes that have become non-functional on the D. miranda neo-Y had, on average, lower ancestral expression levels and were expressed in a lower number of tissues compared to genes with intact reading frames. We also show that male-biased genes are retained on the neo-Y for longer compared to female-biased genes. Our results imply that gene loss on the neo-Y is not a purely random, mutation-driven process. Instead, selection is, at least to some extent, preserving the function of genes that are more costly to lose, despite the strongly reduced effective population size of the neo-Y chromosome.

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WED 24 AUG at 1400 - Room N6
Oral presentation *D3-Ge07-1400-O*

General sessions
Primates

Estimation of demographic parameters in the evolution of modern humans: A geographically-explicit Approximate Bayesian Computation approach

Kanitz R[1], Antoniazza S[1], Neuenschwander S[1], Goudet J[1]
[1]University of Lausanne, DEE, Lausanne, Switzerland

Summary statement:

We used geographically-explicit simulations to compare alternative scenarios of human evolution and estimate demographic parameters underlying the colonization of the world.

Abstract:

The combination of genetics and informatics has been of great relevance in the studies of human evolution during the last years. The increase in computational power allowed new and more complex methods to be applied to the ever-growing genetic data available for our species. The goal of the present study is to combine for the first time the genetic data from 346 microsatellite loci available for 78 populations distributed worldwide (including the Americas) with a geographically-explicit ABC approach. We modelled the world map with 20’272 demes comprising all inhabited continents. We then compared two competing scenarios of human evolution – the Recent African Origin vs. the Multiregional Origin – by setting the colonization origin, either in Sub-Saharan Africa only, or in Sub-Saharan Africa plus Europe and Asia, respectively. For the best supported of these scenarios, further estimations of six demographic parameters were made: (1) the onset of this expansion; (2) the initial (3) and current population sizes; and finally the (4) migration, (5) growth, and (6) mutation rates. The results of these analyses shall, not only shed some light on interesting details of human evolution, but also serve as groundwork for building more realistic models of modern human evolution.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i055-R*

General sessions

Fine-scale elytral morphology with a sexually antagonistic function in female diving beetles (Dytiscidae)

Karlsson Green K[1], Kovalev A[2], Svensson EI[1], Gorb SN[2]
[1]Lund University, Department of Biology, Lund, Sweden, [2]University of Kiel, Department of Zoology, Kiel, Germany

Summary statement:

We measured the adhesive performance of male diving beetles suction cups on females to infer the function of the rough elytral structures present on some female morphs.

Abstract:

Under a sexual conflict scenario, males and females are expected to evolve traits and behaviours with a sexually antagonistic function. It has recently been proposed that there is an ongoing sexually antagonistic coevolution between male and female diving beetles (Dytiscidae). Male diving beetles posses numerous suction cups on their forelegs, which they use to capture a female during mating, and females commonly have rough structures on their elytra. These rough structures have been suggested to obstruct adhesion from male suction cups and thus to repel male mating attempts. This antagonistic function of the dorsal structures has, however, not been tested before. Some diving beetle species are dimorphic where one female morph possesses a rough elytra and the other has a smooth elytral surface. Here, we compared the adhesive performance of male suction cups on the elytral surfaces of two female morphs to infer the function of the rough elytral modifications. We measured adhesion on both the elytra and the pronotum and did so both on the two female morphs and on males. The study was done in two species of diving beetles: Dytiscus lapponicus and Graphoderus zonatus. We found that, in both species, the adhesive force generated on the rough structures was much lower than on other surfaces. The rough female structures are thus likely to obstruct male mating attempts. These findings strongly support the recent suggestion of sexual conflict among diving beetles and a sexually antagonistic function of the female elytral modifications.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i056-R*

General sessions

Evolution of morphology and molecular phylogeny of green euglenoids

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[1]University of Warsaw, Department of Plant Systematics & Geography, Warsaw, Poland, [2]Michigan State University, East Lansing, United States

Summary statement:

Mapping of morphological characters onto well-resolved phylogenetic tree enabled tracing the evolutionary trends in green euglenoids used as a model of photosynthetic eukaryotes.

Abstract:

Green euglenoids (Euglenea) are a monophyletic group inside Euglenida. This single-celled photosynthetic eukaryotes acquired chloroplast as a consequence of a single endosymbiotic episode between a heterotrophic euglenoid and a chlorophycean alga. Once photosynthesis was established in a previously phagotrophic cell, the evolutionary pressures on the cytoskeletal systems involved in locomotion and feeding changed. This gave rise to fundamental modifications of cell structures found in the descendants of these chimeric cells. Moreover, during the evolution of green euglenoids they took possession of the freshwater environments which probably also had huge impact on their morphology. The morphological diversity present in this group provides an excellent system for demonstrating evolutionary transformations of morphological characters. This diversity also offers essential criteria for major events in the evolution of photosynthetic eukaryotes, such as effects of secondary endosymbiosis.
We constructed the first molecular phylogeny of the green euglenoids with parallel nuclear SSU and LSU rDNA, hsp90 and psbO and plastid 16S rDNA data sets. Based on well-resolved tree, we mapped morphological characters and established crucial features such as the shape and metaboly of the cell, chloroplasts (their number, size, shape, location and presence or absence of pyrenoids), the morphology and size of paramylon grains (reserve material) and the presence and shape of mucus bodies. We found that most of the characters (i.e. rigid cells, big paramylon grains or mucocysts) evolved many times independently and we haven't found a good explanation for this phenomenon yet.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i026-E*

General sessions

The role of the circadian clock and photoperiodic timer in adaptation to seasonally changing environment in Drosophila montana

Kauranen H[1], Hoikkala A[1]
[1]University of Jyväskylä, Department of Biology and Environmental Science, Jyväskylä, Finland

Summary statement:

We study how the circadian clock and the photoperiodic timer regulate daily and annual rhythms in the behavior and development of D. montana both at phenotypic and neuronal level.

Abstract:

Living in an environment with high daily and annual changes in temperature and light conditions sets challenges for organisms' survival and reproduction. Adaptation to these changes is especially important at high latitudes, where the climate conditions change drastically throughout the year. Daily rhythms in many physiological and behavioral traits are known to be under the control of organisms' endogenous genetic clock, the circadian clock, while annual rhythms (e.g. reproductive diapause) are likely to be regulated by the photoperiodic timer. The molecular basis of the circadian clock is already well-known, but the functional basis of the photoperiodic timer is still under debate. The object of the study is to find out how the circadian clock and the photoperiodic timer mechanisms regulate daily and annual rhythms in the behavior and development of D. montana flies, and to trace connections between the two clock mechanisms. D. montana has spread around the northern hemisphere adapting to different kinds of environmental conditions. We are exploring the basic characteristics of the circadian clock in this species by studying the locomotor activity and eclosion rhythm of the flies in different environmental conditions and photoperiodically controlled reproductive diapause of the females. We also study the structure and function of some of the circadian clock neurons to gain better understanding on the genetic basis of the circadian clock in D. montana. Information on changes in the function of the key neurons playing a role in daily and annual rhythms is of utmost importance for examining possible connection between the circadian clock and the photoperiodic timer.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i057-R*

General sessions

Phosphorus limitation and individual growth rate across ploidy levels in a freshwater snail – implications for the maintenance of sex

Kay AD[1], Neiman M[2], Krist A[3]
[1]University of St. Thomas, Biology, Saint Paul, United States, [2]University of Iowa, Biology, Iowa City, United States, [3]University of Wyoming, Zoology and Physiology, Laramie, United States

Summary statement:

We show that tetraploid Potamopyrgus antipodarum snails are more sensitive to phosphorus scarcity than are triploids. These results have implications for the maintenance of sex.

Abstract:

It is surprising that most eukaryotes reproduce sexually because of profound demographic costs for sexual females resulting from the production of males. Most research on the advantages of sex has focused on explicitly genetic mechanisms that offset male production costs. A novel complementary hypothesis posits that competitive interactions between sexual and asexual animal taxa may be mediated by the availability of dietary phosphorus (P). The role of P is suggested because 1) many asexual animals have higher ploidy than sexual counterparts, 2) P is an important component of nucleic acids, and 3) P is often a limiting nutrient. One basic prediction of this hypothesis is that if increased ploidy confers more stringent dietary requirements for P, growth rate will decrease more with P scarcity as lineage ploidy level increased. Here we test this prediction using the New Zealand freshwater snail Potamopyrgus antipodarum, a focal system for research on the maintenance of sex that contains both obligately sexual diploid and asexual triploid and tetraploid individuals. We used dietary P manipulations to test whether individual growth rate in 20 triploid and 5 tetraploid lineages is differentially affected by P limitation. We found a significant interactive effect of ploidy level and dietary P on growth rate, as growth was particularly low for tetraploid lineages in low-P conditions. These results suggest that P-limitation could influence the distribution and relative frequency of asexual P. antipodarum differing in ploidy, and suggest the possibility that ploidy differences between sexual and asexual lineages could affect P-mediated competitive dynamics in this system.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i027-E*

General sessions

Considering the evolution of social interactions affects evolutionary dynamics

Kazancioglu E[1], Klug H[2], Alonzo SH[2]
[1]Uppsala University, Evolutionary Biology Centre, Uppsala, Sweden, [2]Yale University, Ecology and Evolutionary Biology, New Haven, United States

Summary statement:

Evolutionary dynamics of traits whose value is partly determined by the phenotype of the social partner are changed qualitatively when social interactions are allowed to evolve.

Abstract:

In many traits involved in social interactions, such as courtship and aggression, the phenotype is an outcome of interactions between individuals. Such traits whose value in an individual is partly determined by the phenotype of its social partner are termed “interacting phenotypes”. Quantitative genetic models of interacting phenotypes suggested that these traits can evolve much faster than traits that are not involved in social interactions. Current models, however, consider the interaction between the phenotypes of social partners as a fixed phenotypic response rule. Here, we incorporate the response of an individual to the phenotype of its social partner as a trait that can evolve. We find that an evolving response rule can change qualitatively the predictions about the evolution of interacting phenotypes. For example, in contrast to previous models that predict that reciprocal interactions between the phenotypes of social partners would lead to a greater exaggeration of traits, we find that an evolving phenotypic response rule can limit or even reverse the predicted change in trait values. We argue that it is crucial to determine whether and how the phenotypic response of an individual to its social partner can evolve to make accurate predictions about the evolution of traits involved in social interactions.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i058-R*

General sessions

Both male and female sexual ornaments are honest indicators of offspring quality in whitefish

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[1]University of Eastern Finland, Department of Biology, Joensuu, Finland, [2]University of Oulu, Department of Biology, Oulu, Finland

Summary statement:

We studied mutual sexual ornamentation in the whitefish. We found that both male and female ornaments signal swimming performance and predator avoidance ability of the offspring.

Abstract:

In many species secondary sexual ornaments are expressed in both sexes (mutual ornamentation). Despite this fact the signalling function of female ornamentation is only rarely studied. We studied the indicator value of male and female sexual ornaments in a mutually ornamented fish, the whitefish Coregonus lavaretus. We crossed 10 males and 10 females in all possible combinations (North
Carolina II design), and partitioned fitness variation among good genes, compatible genes, and maternal environmental effects. We found that highly ornamented females, males, and their parental combinations had offspring with better swimming performance and predator-avoidance ability than less ornamented individuals or combinations. In addition, highly ornamented females had larger offspring that also had higher yolk volume than less ornamented individuals. Swimming performance was not related to offspring size and was only weakly affected by yolk volume, which suggest that swimming performance and measured morphological traits are independent indicators of offspring fitness. Taken together, our results clearly indicate that mutual ornamentation of whitefish signal offspring quality, which may indicate ongoing directional selection for these ornamental traits. However, we also found that genetic compatibility effects may weaken the directional selection and the indicator value of the ornamentation.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i059-R*

General sessions

Post-pollination fitness traits in hybridizing distylous Primula species - Differential performance of F1- and later generation hybrids modulate reproductive isolation

Keller B[1], Conti E[1]
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Summary statement:

Data from hand-pollination experiments reveal that information about hybrid fitness is crucial to understand speciation and hybridization in a Primula species complex.

Abstract:

Reproductive isolation is a fundamental factor in speciation, for it reduces or prevents hybridization. It is composed of pre- and postzygotic components. Information about hybrid fitness is crucial to estimate the degree of postzygotic isolation and understand the processes of hybridization and speciation. Natural hybridization between closely related Primula elatior, P. veris, and P. vulgaris occurs in various extents when species occur in sympatry. We performed a literature review and re-analyzed available data from hand-pollination experiments in a comparative way. We compared fitness components (fruit set, seed set, seed weight, seed viability, and germination rate) of parental species and hybrids, estimated total fitness of hybrids, and calculated the strength of postzygotic reproductive isolation. We found that hybrids had a reduced fitness compared to their parents. F1-hybrids were the least fit, mainly due to low germination rates. Fitness of later generation (Fx-)hybrids was overall higher than in F1-hybrids, but more variable. Total fitness of Fx-hybrids between P. elatior and P. veris was almost as low as in F1-hybrids. Fx-hybrids between P. elatior and P. vulgaris, however, were as fit as their parents (or more fit). Accordingly, postzygotic isolation was strongest between P. elatior and P. veris and most weak between P. elatior and P. vulgaris. Our results show that postzygotic isolation between closely related Primula species pairs is high, but variable, and that after overcoming the first step of hybridization (F1-hybrid production) Fx-hybrids may be produced more readily, enabling introgression between species pairs.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i028-E*

General sessions

Exploring sex-specific mutational effects on life history in Drosophila melanogaster

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Summary statement:

We investigated the sex-specific effects of the same spontaneous mutations on life histories in Drosophila melanogaster, with emphasis on longevity and age-specific reproduction.

Abstract:

Evolutionary theories of ageing depend on the existence of mutations with age-specific effects, but there is relatively little empirical characterization of this class of allele. We increasingly recognize the importance of sex differences and conflict in other aspects of life history, but for ageing the role of sex conflict is a germinal idea. Research in our laboratory has shown that the same mutations can have markedly different impacts on early reproduction in each sex. The degree to which these differences extend to later parts of life histories remains unknown. Filling this knowledge gap is crucial to understanding how mutational properties affect life history evolution. To this end, we used hemiclone analysis to sample a series of nearly complete haploid genotypes from an outbred Drosophila melanogaster population. This technique allowed for replicates of the same genotypes to be maintained under both control and mutation accumulation (MA) regimes. The latter relaxed selection against spontaneous mutations through single-genome bottlenecking every generation. The same set of mutations was then expressed in flies of each sex. By measuring the reproductive output of both control and MA genotypes across their lifespan, we investigated whether sex-specificity of mutational effect extends into later reproductive life. Measurement of how the same mutations affect both adult fitness and longevity will also be presented, broadening our understanding of the complex genetic relationship between these two key life history traits. This experimental system represents a particularly powerful tool for investigating how the same alleles affect whole life histories in each sex.

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WED 24 AUG at 1500 - Room N5
Oral presentation *D3-Ge09-1500-O*

General sessions
Evolution of sex

Parasites, sex and clonal diversity in natural snail populations

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Summary statement:

We address whether clonal diversity in a snail is maintained by coevolving parasites (i.e., Red Queen) or by the input of clones by mutation from sympatric sexual progenitors.

Abstract:

Under the Red Queen hypothesis, host-parasite coevolution selects against common host genotypes. While this mechanism might underlie the persistence of sexual reproduction, it might also maintain high clonal diversity. Alternatively, clonal diversity might be maintained by multiple origins of parthenogens from conspecific sexuals, a feature in many animal groups. We addressed the maintenance of overall genetic diversity by coevolving parasites in host populations comprised of a mix of clonal and sexual individuals. We specifically examined the contribution of parasites to host clonal diversity and sexual frequency in natural stream populations of Potamopyrgus antipodarum snails. We also tested the alternative hypothesis that clonal diversity is maintained by the input of clones by mutation from sympatric sexuals. Infection frequency was positively related to clonal diversity and the frequency of sexual individuals, and explained 37% and 27% of their variation, respectively. Surprisingly, although clones are derived by mutation from sexual snails, parasites explained more of the genotypic variation among parthenogenetic subpopulations. Our findings are consistent with the Red Queen hypothesis and highlight the importance of parasites as drivers of clonal diversity, as well as sex.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i060-R*

General sessions

Consistent individual differences in anti-predator behaviour in mealworm beetles Tenebrio molitor

Kivleniece I[1], Znotina S[1], Frolkova V[1], Krams I[1,2], Krama T[1], Rantala MJ[2]
[1]University of Daugavpils, Institute of Systematic Biology, Daugavpils, Latvia, [2]University of Turku, Department of Biology, Section of Ecology, Turku, Finland

Summary statement:

We found consistent individual differences in anti-predator behaviour of mealworm beetles Tenebrio molitor.

Abstract:

When predators such as birds and rodents attack, mealworm beetles usually feigns death by entering a state known as tonic immobility. In a series of experiments we placed adult mealworm beetles in conical Eppendorf test tubes, which were used as insect chambers. Tonic immobility was evoked by hitting the tube which mimics a bird landing or a rodent jump. We observed time to reach immobility and the duration of tonic immobility in mealworm beetles at 23˚C. During the experimental trials the tube containing a beetle was connected to microrespirometer and the CO2-emission was recorded. The respirometric device was combined with an infrared optical system using infrared diodes which were placed on the sides of the insect chamber. We repeated the trials 6 days later. Time until immobility was repeatable between the trials, and the duration of immobility was also found to be highly repeatable. After being shaken, most of the immobile beetles reduced the CO2 release for 10-15 s and it was followed by a large burst of gas which was not associated by abdominal pulsations. We also exposed the beetles to diurnal (great tits) and nocturnal predators. Our results suggest that anti-predator responses of mealworm beetles may be individually consistent and adaptive: rats killed active beetles more often than immobile individuals, while great tits killed mostly the beetles which did not dig in the bran layer.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i029-E*

General sessions

The winner takes it all! Evolutionary consequences of double infections in a trematode/snail system

Klappert K[1], Jokela J[1]
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Summary statement:

Multiple infections with trematodes of snail hosts are extremely rare. An experiment to investigate competition between parasites for the exclusive use of the host is presented.

Abstract:

Trematode parasite larvae commonly attack aquatic snails. An infection usually results in castration and damage to internal organs of the snail host, thus lowering its fitness dramatically. Since space and resources within a snail are highly restricted inter- and intraspecific competition for hosts is expected to be fierce. In an earlier study on a very large data set we found that double infections with any given pair of several trematode species occur significantly less often than expected. So far, it is not known which mechanisms prevent snails from acquiring multiple infections, but direct competition between the parasite species is possible and has been reported in other snail-trematode systems. Here we experimentally test a hypothesis on competition between parasites for the exclusive utilisation of a snail host: Notocotylus gippyensis (M2) redia should be able to feed on competing parasitic larvae and thus prevent double infections directly. Some double infections with M2 and Microphallus spec (mic) have been found in nature so we chose those two species for our experiment. M2 co-occurs with mic in the same lake habitat and both use ducks as final hosts. Ducks defecate parasite eggs, but while M2 eggs produce a free swimming miracida that actively intrudes the snail mic infections are caused by embryonic eggs that are ingested by the snail. This particular difference in life history allowed us to control the infection risk a snails suffers from M2 or mic larvae, respectively. The results of this currently still running experiment will be presented and discussed with respect to the consequences for the evolution of virulence and interspecific-competition avoidance.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i030-E*

General sessions

Genetic coupling of natal dispersal and exploration behaviour?

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Summary statement:

Using data from a long-term population study on a wild songbird, the great tit, we test for the first time whether dispersal and exploration behaviour are genetically correlated.

Abstract:

Natal dispersal, the movement of individuals from their place of birth to the place where the will breed, is an important ecological parameter that influences the dynamics of, and gene flow between, natural populations. Often there is marked variation in the dispersal distances covered by different individuals. Part of the individual variation in dispersal behaviour may be due to genetic differences, but this has rarely been tested. Individual variation in dispersal distances has also been suggested to relate to consistent differences between individuals in their behavioural responses to novel environments. Here, we use a multigenerational pedigree and dispersal data from a long-term individual-based study on a wild great tit (Parus major) population near Antwerp, Belgium, to estimate the heritability of natal dispersal distance. Furthermore, we estimate the heritability of exploration behaviour measured in a standardised novel environment test. Finally, we test whether natal dispersal distance and exploration behaviour are genetically correlated.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i061-R*

General sessions

Assortative mating by sexually developmental time in a Japanese human population

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Summary statement:

Positive assortative mating was found for sexually matured age between husband and wife in a Japanese human polations.

Abstract:

Assortative mating has widely been known for non-biological traits such as social status, income,educational level, religion, occupation in human populations. For biological traits such as body size, skin color and IQ, several reserchers reporte the positive assortative mating, whereas random mating has been assumed as to the genetic variation such as blood type or isozyme type. The author presents an evidence for non-random mating for sexually developmental time in a Japanese human population. The age at menarche for wives and the age at the first ejaculation for husbands were respectively adopted as developmental rate. Correlation coefficient in sexually matured age between husband and wife was disclosed to be 0.395. This correlation is statistically significant and it is higher than those in morphological traits such as body weight, height and BMI(body mass index).

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i062-R*

General sessions

Environmental and genetic effects on brain size and brain morphology in Coho Salmon

Kotrschal A[1], Sundström FL[1,2], Brelin D[1], Devlin RH[2], Kolm N[1]
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Summary statement:

We use a transgenic salmon to demonstrate how environmental and genetic factors, which modulate somatic growth rate, have strong influence on brain size and structure development.

Abstract:

The close allometric relationship between vertebrate body size, brain size and brain structures indicates that brains evolve under a strong body size constraint. Since a change in somatic growth rate can alter those allometries, differences in previous growth may critically influence relative brain and structure size diversity. As growth is determined by both environmental and genetic factors, differences in brain size or structures may partly arise due to altered growth rates. Transgenic Coho salmon genetically modified to overexpress growth hormone show dramatically increased growth rates compared to wild type salmon. Since their growth rates can be normalized by food restriction, they provide an ideal model for investigating how genes coding for somatic growth and environmental factors influence brain development. We raised transgenic and wild type salmon in hatchery and near-natural stream conditions and determined their brain and structure sizes. Here we show that fish raised in hatcheries grow larger and develop relatively larger brains. Remarkably, transgenic salmon have smaller brains than wild type fish. We also demonstrate that the optic tectum of both genotypes increases when raised in hatcheries and that the cerebellum of transgenic fish grows smaller in near-natural streams. Finally, opposite to theoretical predictions, transgenic fish develop a markedly larger telencephalon than wild type fish in hatchery conditions. We conclude that, apart from the environment, also genetic factors modulating somatic growth rate have strong influence on brain size and structure and that genetically determined fast growth may hamper brain development.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i063-R*

General sessions

Guppy golden and blue mutants provide novel insights into pattern formation of coloration

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Summary statement:

Analysis of guppy (Poecilia reticulata) pigment mutants revealed that golden and blue are required for normal pattern formation of coloration in this species.

Abstract:

Juvenile and adult guppies (Poecilia reticulata) of both sexes are camouflaged by an inconspicuous reticulate pattern. Additionally, guppy males develop exceptionally colorful and highly variable ornamental patterns during puberty. Sex-linked inheritance of several guppy color traits has been demonstrated, but the developmental pathways forming the guppy color pattern have not yet been discovered. We have investigated two independently segregating autosomal genes designated golden and blue. Golden guppies lack almost all melanophores at birth, but acquire some melanophores dorsally at later stages that eventually form an incomplete reticulate pattern in adults. This indicates that golden is crucial for specification, migration, differentiation or survival of embryonic melanophores. Further, early golden-dependent and late differentiating golden-independent melanophore populations may exist in the guppy. The male ornamental melanophore pattern is also affected in golden fish. In blue fish, a recessive mutation leads to almost complete loss of xanthophores. Adult blue males therefore lack orange spots. In addition, the black ornamental pattern of blue males is changed substantially compared with the wild-type, suggesting that both golden and blue play a significant role in the development of the guppy reticulate and male specific ornamental pattern. We have taken a candidate gene approach to identify the molecular basis of these mutations and have detected potential splicing defects and frameshift mutations in candidate genes.

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WED 24 AUG at 1500 - Room N4
Oral presentation *D3-Ge04-1500-O*

General sessions
Evolutionary genetics

Is the distribution of fitness effects of new mutations multimodal?

Kousathanas A[1], Keightley PD[1]
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Summary statement:

We introduce a method that can accurately infer the properties of the distribution of fitness effects of new mutations even if it is multimodal.

Abstract:

Knowing the distribution of fitness effects of new mutations (DFE) is of fundamental importance for many evolutionary genetics research topics, including estimating rates of adaptive evolution at the molecular level. More specifically, the DFE is central to disentangling the effects of positive and negative selection on molecular variability, and understanding how the rate of adaptation is influenced by effective population size. Existing computational methods that infer the DFE from DNA polymorphism data, have made the assumption that the true DFE can be approximated by a gamma distribution. However, if the true DFE is multimodal, the assumption of a gamma distribution could lead to misleading results about its properties. We show that if the DFE is multimodal, fitting a gamma distribution produces inaccurate estimates of the mean effect of a new mutation, and increasing the number of sequenced sites and alleles does not improve the accuracy of the estimates. We develop a model that approximates the DFE by fitting multiple uniform distributions of varying locations and densities (“steps” model). We find that the “steps” model, given sufficient amounts of data, accurately recovers the mean of the simulated DFE, even when the simulated DFE is multimodal. Finally, we apply the “steps” model to infer the DFE for protein-coding and non-coding DNA, using published polymorphism data from a variety of species (including Drosophila, mice and humans), and examine whether there is evidence for multimodality.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i031-E*

General sessions

Sexual selection and the function of the genitalic claws of male guppies (Poecilia reticulata)

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Summary statement:

We examined the selective mechanisms acting upon the genitalic claw structure, and its evolutionary divergence among populations of Poecilia reticulata.

Abstract:

One of the most widespread and intriguing evolutionary patterns is the rapid divergence of male genitalia in species with internal fertilization and promiscuous mating systems. In the family Poeciliidae, there is remarkable diversity in the male intromittent organ, the gonopodium, which is a modified anal fin employed in sperm transfer. Species-specific diversity in structures at the distal tip of the gonopodium can include variation in claws, hooks, distal serrae, palps, and/or spines. Although there are extensive descriptions of this gonopodial variation, the functions of these traits remain unclear. Here, the selective mechanisms acting upon the claw structure in guppies were studied. Specifically, we performed an experimental study testing three possible functions of the claw: female stimulation, sperm transfer, and/or grasping of females. To distinguish between these functions, clawed and declawed males were mated to receptive and unreceptive females, and the numbers of sperm transferred were quantified. We also looked for associations among sperm counts, genital morphology, and male reproductive behaviours.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i064-R*

General sessions

How and why the weeping lizard cry

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[1]Universidad de Chile, Santiago, Chile, [2]University of Oslo, Oslo, Norway, [3]Universidad Mayor, Santiago, Chile

Summary statement:

We study the function of vocalization in a non-gekkonid lizard.

Abstract:

Among lizards, Gekkonidae is the taxon best known for acoustic communication, but there is an increasing number of reports of vocalizations in many other lizards families, suggesting that vocalization has evolved multiple times. Nevertheless, the selective pressures that have affected the evolution of vocalization in non-gekkonid taxa, remain unclear. There are indications that vocalizations tend to occur when lizards are in risk of predation, and they may thus functions as: 1- predator deterrents and/or 2- alarm calls to conspecifics. Here, we study the evolution of vocalization in the “weeping or shrill lizard”, Liolaemus chiliensis. The genus Liolaemus has more than 200 species, and this is the only species in the genus that is known to vocalize. We found seven different patterns of vocalizations, and the two most common constituted 55% of the total, and some of the vocalizations (4%) reach the ultrasound spectrum. Lizards confronted by models of their two main predators (a raptor and a snake) did not scream. A high frequency of screams (88%) was obtained when animals were gently taken by the researcher. Thus, vocalizations may function as a last-chance predator deterrent. We also demonstrated that lizards react to the vocalizations of other individuals. Hence, conspecifics may use the scream to assess predation risks, and it may possibly function as a warning call. Finally, lizards respond to the vocalization with immobility, regardless if these were presented or not together with visual cues (e.g. presence of predators). This suggests that the weeping lizard does rely mainly on acoustic information, to assess predation risk. Funds: Fondecyt 1090251.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i065-R*

General sessions

Cassiopea andromeda – why all these colors?

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Summary statement:

In the light of global climate change our study system, the Cassiopea/Symbiodinium symbiosis, is remarkable as it is maintained even under stressful environmental conditions.

Abstract:

Many cnidarians live in symbiosis with dinoflagellates of the genus Symbiodinium. Symbiodinium are photosynthetically active and provide their hosts with fixed carbon. A disturbance of the symbiosis by stressful environmental conditions e.g. unusually high temperatures or high levels of irradiation often ultimately leads to the death of the holobiont (bleaching). Bleaching is therefore directly linked to climate change.

Cassiopea andromeda, the up-side-down jellyfish, is remarkable, because it occurs in shallow lagoon waters at high temperatures and high levels of irradiation and still maintains its symbiosis. Cassiopea shows a wide range of individually distinct tentacle colors. As in corals host color pigments can influence photosynthetic activity in symbiotic dinoflagellates, we assumed an influence of host color on the Symbiodinium clade present in the host. However, we found no correlation of Symbiodinium clade and Cassiopea color morph – all Cassiopea collected in the field were always associated with Clade A, irrespective of individual color. As host color morph does also not change in association with changing environmental conditions and can be determined very early during development, we expect a genetic mechanism to underlie the different colorations.

While the adaptive value of host color polymorphism still remains unclear, further studies of the symbiotic system of Cassiopea and Symbiodinium promise to provide valuable information about a successful co-operation under stressful environmental conditions. This knowledge might help us to understand the bleaching events seriously endangering coral reefs world wide.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i066-R*

General sessions

Evolution and Development of Drosophila pachea asymmetric genitalia

Lang M[1], Orgogozo V[1]
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Summary statement:

We aim to identify genes involved in the establishment of Drosophila pachea asymmetric epandrial lobe development and study their evolution.

Abstract:

Recent progress has been made on the developmental pathways responsible for establishment and maintenance of left-right differences during development of otherwise bilateral organisms. However, how such an asymmetry arises in the first place during evolution remains a mystery. As opposed to its closely-related species, Drosophila pachea has a striking directional left-right asymmetry in malegenitalia external lobes, with the left lobe being 1.49± 0,08 (SD) times longer and thinner than the right lobe. To better understand how such a novel asymmetry arises during evolution, we aim to identify genes involved in the establishment of D. pachea asymmetric lobe development and study their evolution. Two approaches are ongoing, mapping of a mutation producing D. pachea males with symmetric lobes and comparative transcriptomics from left and right developing lobes. We are also investigating the function of asymmetric lobes during copulation. We observed that at the onset of copulation D. pachea adopts an asymmetric mating posture with the male always shifted towards the females right side. Given these preliminary results, we hope that our study will also clarify the relationships between morphological diversification of male genitalia and mating behaviour.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i032-E*

General sessions

No experimental evidence for sneaking in a West African cichlid with extraordinarily long sperm

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Summary statement:

We provide microsatellite and behavioural evidence of a lack of sneaking, thus genetic monogamy in a cichlid fish with extraordinarily long sperm.

Abstract:

Alternative reproductive tactics, e.g. sneaking, are widespread in fishes. Due to the diversity of mating systems and fertilisation mechanisms in fishes the potential for sperm competition is high. In some cichlid species sneaked fertilisations were detected, while in others no evidence for alternative reproductive tactics was found, suggesting genetic monogamy. In cichlids the sperm competition risk is very divergent and large sperm are usually interpreted as an adaptation to sperm competition. The West African cichlid Pelvicachromis taeniatus is a socially monogamous cave breeder with biparental brood care that shows size and colour dimorphism. Its small relative testis size indicates low gonadal investment, which is typical for genetically monogamous species. In contrast, the total sperm length is extraordinarily long, possibly as an adaptation to strong sperm competition. Here we examined whether sneaking tactics exists in P. taeniatus. We observed the reproductive behaviour of ten equally composed groups under semi-natural conditions over a period of several weeks 24h a day via digital video recording. After spawning, eggs were removed and paternity tests were conducted using six to ten microsatellites. Additionally, video recordings were analysed to identify sneaking attempts during the spawning events. The results suggest an absence of sneaking during spawning, thus genetic monogamy in this population of P. taeniatus. No evidence for sperm competition was found, assuming that other selection pressures have to be responsible for the evolution of long sperm in P. taeniatus.

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WED 24 AUG at 1420 - Room N7
Oral presentation *D3-Ge05-1420-O*

General sessions
Disease and immunity

Population genetic structure of Crithidia bombi, a parasite of bumblebees (Bombus sp.) reveals selective pressures shaping parasite distribution

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[1]Martin-Luther-Universität Halle-Wittenberg, Institut für Biologie, Molekulare Ökologie, Halle (Saale), Germany

Summary statement:

Crithidia bombi, a parasite of bumblebees shows indications for sexual reproduction, high levels of horizontal transmission and a lack of local adaptation.

Abstract:

Social insects seem to be prone to invasion by parasites and pathogens. Nests of these insects provide a rich resource of food and brood, which might attract parasites. The high density of individuals within nests enhances the transmission of parasites. The host colony shows defence mechanisms in terms of an advanced system of behaviour of adults, individuals having an immune system and group level effects (social immunity). The genetic structure of the colony might also influence the degree of parasite invasion.
The genetic structure of parasite populations has been studied less. Most microbial pathogens are clonally propagating with short generation times resulting in huge population sizes which allow for rapid evolutionary responses towards the hosts defence mechanisms.
We studied the population genetic structure of Crithidia bombi, an intestinal pathogen of bumblebees (Bombus sp.). Several host species were sampled during 3 years at 3 locations and microsatellite analysis of the parasite was used to infer key parameters of its population structure. A large amount of distinct genotypes of C. bombi have been identified. The parasite populations are in Hardy-Weinberg equilibrium showing no linkage disequilibrium indicating sexual reproduction as an alternative reproductive strategy. Population differentiation is observed between samples of different years, indicating that the hibernation of queens exhibits a bottleneck for the C. bombi population. The occurrence of clones is rare. Their distribution across hosts indicates high levels of horizontal transmission indicating a lack of local adaptation.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i033-E*

General sessions

Male genitalia (titillators) selected to prolong copulation durations across bushcrickets

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Summary statement:

The internal titillators in bushcrickets fulfil predicted criteria of morphological traits under sexual selection.

Abstract:

Copulation duration varies greatly between species, as does the complexity of male genitalia. Where mating is costly for males, for example in regard to the production of large spermatophores, males are predicted to invest more into female stimulation. Few studies have tested the hypothesis that complex genitalia may allow the male to extend copulation duration to ensure this stimulation of the female. An alternative function of extended copulation prior to ejaculate transfer is that this represents a mate assessment period for the male. We examined the relationship between copulation duration, genital (titillator) complexity, spermatophore mass and male body mass across 54 species of bushcricket using phylogenetic comparative analyses. While copulation duration was much longer in species with titillators as opposed to without, it was no longer in species with complex compared to simple titillators. Titillator complexity also affected the spermatophore size/copulation duration relationship. In general, copulation duration prior to spermatophore transfer was longer in species with larger spermatophores. However, the relationship between copulation duration and spermatophore size was actually steeper in species with simple rather than complex titillators.

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WED 24 AUG at 1420 - Room N5
Oral presentation *D3-Ge09-1420-O*

General sessions
Evolution of sex

Anisogamy as a gateway in the the evolution of sex

Lehtonen J[1], Kokko H[1]
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Summary statement:

Explaining the evolution of sex becomes much easier when we realize that anisogamy can only evolve in obligately sexual species.

Abstract:

The evolution of sex remains one of the biggest unresolved questions in evolutionary biology. It is difficult to overcome the two-fold cost of sex: the cost of production of males who cannot themselves directly reproduce.

This cost only applies when males exist, i.e. it requires anisogamy. The problem is greatly diminished in isogamous species. This has been ignored in some treatments of the evolution of sex: they talk about sex as if it always had to involve males.

One possible explanation for the maintenance of sex (after its initial evolution before the two-fold cost existed) is that transitions from sexual reproduction back to asexual reproduction are constrained to a low rate. This can explain the pattern of sexuality and asexuality that we see today in anisogamous organisms. Yet we lack evolutionary explanations for the low transition rate itself, and for how obligate sexuality can become prevalent in the first place. Also, a low transition rate in itself offers no solution to the apparently contradictory observation that facultative sexual reproduction is more common in isogamous organisms than anisogamous ones.

Here we show that if sex has a slight advantage (between 1 and 2) to partially counter its two-fold cost, the evolution of anisogamy can act as a ‘gateway’ through which only obligately sexual species with low transition rates to asexuality can pass. Obligate sexual reproduction and a low transition probability to asexuality are then prerequisites for anisogamy to evolve in given species. This offers an explanation for the pattern of sexual vs. asexual reproduction as well as the pattern of facultative vs. obligate sex.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i067-R*

General sessions

Sexual selection and senescence in mammals

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Summary statement:

Understanding senescence is a long-standing goal in evolutionary biology. We present new findings relative to the relationship between sexual selection and senescence in mammals.

Abstract:

Understanding patterns of variation in actuarial senescence (i.e. increase in mortality rate with age) is a long-standing goal in evolutionary biology. Although empirical evidence of actuarial senescence in wild populations has increased steadily thanks to a higher number of long-term detailed studies, how sexual selection shapes between-sex differences in patterns of age-specific mortality remains unknown. In the present work, we used available information in the literature to measure both the age at the onset of actuarial senescence and the rate of aging in a wide range of mammalian species. We measured the intensity of sexual selection using different indicators of both pre- and post-copulatory competition. These included sexual dimorphism in size, testes mass, and mating tactics. We tested the effects of the intensity of sexual selection on the strength of actuarial senescence. We first investigated how sexual competition influenced male and female senescence patterns separately. We then tested for a role of the intensity of sexual selection on between-sex differences in the strength of senescence. Our comparative analysis based on > 100 mammalian populations was performed using phylogenetically-controlled methods. Our analysis provides new insights on the relationships between sexual selection and senescence that we discuss in the context of current theory on life history evolution.

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MON 22 AUG at 1200 - Room N3
Oral presentation *B2-Ge02-1200-O*

General sessions
Life-history

The determinants of reproductive success in male Tree swallows

Lessard A[1], Garant D[1]
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Summary statement:

Reproductive success in male Tree swallows: which traits affect the number of offspring produced in a species with frequent extra-pair fertilization?

Abstract:

Reproductive success is a key parameter to obtain when assessing individual fitness and predicting population persistence in the wild. In birds with high rates of extra-pair fertilization, different traits could potentially maximize intra and extra pair success. Tree swallow (Tachycineta bicolor) shows one of the highest rates of extra-pair fertilization in birds, which potentially generate a great variance in male reproductive success. Here we studied a tree swallow population over 5 years and performed genetic analyses to assess the extent of variation and determinants of reproductive success in males. We used data obtained from more than 750 reproductive events and found that extra-pair young represented over 50% of the total number of offspring analysed and occurred in more than 85% of nests. Further analyses will aim at evaluating the relative effects of male genetic and phenotypic characteristics on the number of within-pair young, extra-pair young and the total number of offspring produced. In doing so, we will test for the presence of a trade-off, for males, between the number of offspring obtained within and among nests. Finally, the temporal stability of the patterns observed among and within males will also be discussed.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i068-R*

General sessions

Genetic relationship between male signaling and female preference traits in the context of sexual selection in an acoustic pyralid moth, Achroia grisella

Limousin D[1], Streiff R[2], Greenfield MD[1]
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Summary statement:

Highlighting of quantitative trait loci influencing male song and female preference to explore the genetic correlation between these traits involved in the sexual selection process

Abstract:

Models of indirect (genetic) benefits sexual selection predict linkage disequilibria between genes that influence male traits and female preferences, owing to either non-random mate choice or physical linkage. Such linkage disequilibria (genetic correlation) can promote and accelerate the evolution of male traits and female preferences to exaggerated levels. Relatively few empirical studies have measured the genetic correlation between male traits and female responses in natural populations, and fewer have determined whether such an observed correlation was the result of either non-random mate choice or physical linkage. We studied signals and preferences in an acoustic pyralid moth, Achroia grisella, in which males attract females with a rhythmic train of sound pulses and females prefer songs that are loud and delivered at a faster rhythm. Both male acoustic signal characters and female preferences are repeatable and heritable traits. In addition, female choice is based largely on male song, while males do not appear to provide direct benefits at mating in this species. In this context some genetic correlation between song and preference traits is thus expected. We employed a standard crossing design between inbred lines of A. grisella and used AFLP loci in two segregating broods to build the first genetic map for this species and locate quantitative trait loci (QTL) that influence male song and female preference. We also examined whether genetic correlation between these traits exists by virtue of physical linkage. Our results provide an improved understanding of the nature of traits involved in the sexual selection process.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i069-R*

General sessions

Testing the role of plasticity for local adaptation: a life-history approach in locally adapted populations of the common frog

Lind MI[1,2], Johansson F[2]
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Summary statement:

In a novel approach using development and growth rate data we have developed and successfully tested a conceptual model for the role of life-history plasticity in local adaptation.

Abstract:

Phenotypic plasticity can be important for local adaptation, since it enables individuals to survive in a novel environment until genetic changes have been accumulated by genetic accommodation. By analyzing the relationship between development rate and growth rate, it can be determined if plasticity is caused by changed physiology or behaviour. We extended this to examine if plasticity had been aiding local adaptation, by investigating if the plastic response had been fixed in locally adapted populations. Tadpoles from island populations of Rana temporaria, locally adapted to different pool drying regimes, were monitored in a common garden. Individual differences in development rate were caused by different foraging efficiency. However, developmental plasticity was physiologically mediated by trading off growth against development rate. Moreover, the physiological life-history shift mediated by plasticity was consistently expressed in populations locally adapted to pool drying. Our results suggest that adaptation to pool drying was caused by genetic accommodation.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i034-E*

General sessions

Frequency-dependent mating success of personality types

Løvlie H[1,2]
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Summary statement:

The study experimentally shows that the mating success of personality types is context dependent in free-ranging groups of fowl.

Abstract:

Animal personality (i.e. when individuals differ consistently in behavioural responses across context or time) generates puzzles over the evolution of such limited behavioural plasticity. Nevertheless, we observe individuals –from insects to primates- to have personality. A frequently suggested, however not yet explored, process maintaining variation in personality is negative frequency-dependent selection.

I experimentally altered frequencies of personalities (majority of members being shy, or bold) in free-ranging groups of fowl, Gallus g. domesticus, revealing that mating success of types depend both on own and other group-members' personality. For example, groups with majority of shy males had overall higher mating success compared to groups with more bold birds. However, shy males had reduced mating success in groups where other members were bold, showing that the success of personality types is frequency-dependent.

Not only being the first empirical test of frequency-dependent effects of personality, these results also suggests an explanation for the maintenance of personalities and thus how personality can evolve. Moreover, these results also offer potential sources of variation in individuals' reproductive success; a trait still challenging to explain how remains so highly variable.

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SUN 21 AUG at 1100 - Room N4
Oral presentation *A2-Ge03-1100-O*

General sessions
Population ecology

The role of phenotypic plasticity and heritability in the early stages of ecological divergence

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Summary statement:

We test if phenotypic divergence in invasive stickleback results from plasticity or genetic predisposition. We find that adaptive diversification can exist in invasive species.

Abstract:

In their early stages, adaptive radiations are characterized by divergent adaptation to several different new environments. Such adaptation is driven by divergent selection and typically requires standing genetic variation, but can be importantly facilitated by phenotypic plasticity. Although an extensive theoretical framework on ecological diversification exists, empirical test of the relative importance of these mechanisms in the early stages is rare. We identified several candidate cases for ecotype divergence on a historical time scale in invasive threespine stickleback in Switzerland. Here we studied one of these cases, where we have one lake population and many stream populations that differ in their feeding-related morphology. Because divergence began only 150 generations ago, we can here investigate the relative proportion of plasticity and genetic evolution in the early stage of adaptive radiation. Using a common garden setup, we test if the phenotypic divergence that we observe between populations from different habitats results from phenotypic plasticity or from genetic predisposition. In addition, we estimated growth rates on alternative dietary resources to test for divergent adaptation. Our data suggest that the early stage of ecological adaptation is characterized by an interaction of plasticity and divergent evolution but that the relative importance of either differs among the traits studied. Moreover we find evidence for divergent adaptation that has emerged within less than 150 generations. We suggest that adaptive diversification may not be uncommon in invasive species.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i035-E*

General sessions

Early reproductive investment decreases age-specific survival and fitness in female Asian elephants

Lummaa V[1], Mar KU[2], Robinson MR[2], Russell AF[3]
[1]University of Sheffield, Department of Animal and Plant Sciences, Sheffield, United Kingdom, [2]University of Sheffield, Sheffield, United Kingdom, [3]University of Exeter, Penryn Cornwall, United Kingdom

Summary statement:

High early-life fecundity in elephant females has no effect on age-specific declines in fecundity or offspring quality, but it impairs a female's own subsequent survival.

Abstract:

While a growing number of studies on natural populations of vertebrates have shown early reproduction to impair measures of later-life performance, little is known of the selection affecting such outcomes, and how the findings apply to vertebrates with extreme longevity. Here we use an extensive longitudinal dataset on semi-captive Asian elephants (Elephas maximus) to investigate the effects of early-life reproduction on subsequent female age-specific survival, offspring number, quality and annual fitness. Females show clear reproductive priming followed by subsequent senescence, with age-specific fecundity peaking at age 30 and declining thereafter. While high early-life (< 30 years) fecundity has no effect on age-specific declines in fecundity or offspring quality (recruitment probability), it significantly impairs a female's own subsequent survival. Consequently, annual fitness gains decline after age 30 with those investing in early reproduction showing fastest age-specific fitness declines in old age. Age-specific fitness of high and low early-investment mothers cross after peak reproduction but despite this high early-investment females still achieve greater overall reproductive success. Our results document age-specific fitness declines following high early-life reproduction and selection on such strategies, and highlight the generality of the processes underpinning ageing. Furthermore, that maternal survival and performance in elephants depend on age and previous investment has implications for the success of (semi)-captive breeding programmes of this critically endangered species.

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SUN 21 AUG at 1140 - Room N4
Oral presentation *A2-Ge03-1140-O*

General sessions
Population ecology

A theory or partial migration

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Summary statement:

We present a general theory of partial migration.

Abstract:

Partial migration, i.e., when a segement of a population is sedentary and another is (seasonally) migratory, is an ubiqutous phenomenon. We here present a general theory of the evolution of this dimorphism and how pure sedentary and migratory strategies are ends of a continuum. Both density- and frequency-dependence are critical forces, wheres environmental stochasticity is not. The theory explains data from mammals, birds and fish and it highlights the potential conflict between evolutionary optimality (frequency-dependent selection) at the individual level and population consequences.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i036-E*

General sessions

An incipient case of cactophilic Drosophila population differentiation revealed by the presence of microsatellite null allele

Machado LPDB[1], Simão DP[1], Mateus RP[1]
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Summary statement:

No allele amplification in a microsatellite locus is an indicative of incipient differentiation for Drosophila antonietae populations from Iguassu river basin in South America.

Abstract:

Drosophila antonietae (Diptera; Drosophilidae) is a South American cactophilic species that is found associated with the cactus species Cereus hildmaniannus within the Parana-Uruguay Rivers basin. In this work, three populations recently discovered in the Iguassu river basin, located intermediatly compared with the previous surveyed populations, had their genetic variability analyzed using seven microsatellite loci described for this species. Low genetic differentiation among these populations of the Iguassu river basin was found (Fst = 0.0491) and they form a separated branch when analysed together with other Parana-Uruguay river basin populations through Neighbor-Joining grouping using Fst. This higher differentiation is likely to be a result of the non-amplification of the HaeIIIanto-2 locus in almost all samples, probably caused by the presence of null allele(s). Microsatellite null alleles are resulted of one or multiples mutation at flanking regions, which prevent primers annealing during PCR amplification reactions and it could, in time, become fixed on populations. The detection of this null microsatellite "locus" indicates an incipient stage of population differentiation in D. antonietae. This way, although no allele amplification at microsatellite loci demands caution in parentage and populational studies, null allele is an indicative of incipient population differentiation.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i070-R*

General sessions

Sex allocation in haplodiploids is mediated by egg size : Evidence in the spider mite Tetranychus Urticae

Macke E[1]
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Summary statement:

Egg size determines sex-specific egg provisioning, sex and offspring sex ratio in the haplodiploid spider mite Tetranychus Urticae.

Abstract:

Haplodiploid species display extraordinary sex ratios. However, a differential investment in male and female offspring might also be achieved by a differential provisioning of eggs, as observed in birds and lizards. We investigated this hypothesis in the haplodiploid spider mite Tetranychus urticae, which displays highly female-biased sex ratios. We show that egg size significantly determines not only larval size, juvenile survival and adult size, but also fertilization probability, as in marine invertebrates with external fertilization, so that female (fertilized) eggs are significantly larger than male (unfertilized) eggs. Moreover, females with on average larger eggs before fertilization produce a more female-biased sex ratio afterwards. Egg size thus mediates sex-specific egg provisioning, sex and offspring sex ratio. Finally, sex-specific egg provisioning has another major consequence: male eggs produced by mated mothers are smaller than male eggs produced by virgins, and this size difference persists in adults. Virgin females might thus have a (male) fitness advantage over mated females.

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SUN 21 AUG at 1100 - Room N2
Oral presentation *A2-Ge01-1100-O*

General sessions
Behaviour

Mate choice and sexual antagonism during pollen competition

Madjidian JA[1], Lankinen Å[2]
[1]Lund University, Department of Biology, Lund, Sweden, [2]Swedish University of Agricultural Sciences, Department of Plant Protection Biology, Alnarp, Sweden

Summary statement:

Assessment of co-occurrence of mate choice and sexual antagonism during pollen competition in relation to degree of stigma receptivity in Collinsia heterophylla.

Abstract:

Partner choice and sexual antagonism may act simultaneously, but few empirical studies have investigated how these two selective forces interact. Furthermore, empirical evidence of sexual antagonism is scare in plants. The hermaphroditic Collinsia heterophylla shows delayed stigma receptivity, a female choice character that intensifies pollen competition. We have previously demonstrated a potential sexual conflict over timing of stigma receptivity, as pollen from certain pollen donors can grow in the pistil at early floral development, at a maternal cost of lowered seed set. Here, we will present a study assessing the co-occurrence of mate choice and sexual antagonism during pollen competition. In a greenhouse experiment we performed controlled two-donor crosses at several stages of floral development in order to investigate siring success across varying degrees of stigma receptivity. We further compared siring success to the sexually antagonistic traits of the two sexual functions, namely, the ability of pollen to germinate early, and the ability of pistil to delay stigma receptivity in presence of pollen (evaluated in a separate crossing experiment). In order to explore benefits of delaying stigma receptivity (female choice character) we measured fitness of the resulting offspring. The results suggest that both mate choice and sexual antagonism occur during pollen competition in C. heterophylla, indicating that sexual conflicts may have important evolutionary consequences also in plants.

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MON 22 AUG at 1100 - Room N6
Oral presentation *B2-Ge05-1100-O*

General sessions
Disease and immunity

Frequency-dependent selection shaping optimal immune response in female mammals

Mappes T[1], Koskela E[2], Mills SC[3], Poikonen T[2]
[1]University of Jyvaskyla, Centre of Excellence in Evolutionary Research, Jyvaskyla, Finland, [2]University of Jyvaskyla, Jyvaskyla, Finland, [3]University of Perpignan, Perpignan, France

Summary statement:

Individuals with lower immunocompetence increase in frequency if they are rare in the population consisting mainly of high immunity individuals.

Abstract:

Immunocompetence, the ability to produce an effective immune response following exposure to an antigen, is a central character affecting the fitness of an individual. Immucompetence is costly and thus the optimal allocation to immune response should depend on the current risk of infections . As pathogens are mainly transmitted from neighbouring individuals, the susceptibility to diseases should be affected not only by the immunity of the individual itself but also by the immune status of its neighbours. Here we show that individuals with lower immunocompetence increase in frequency if they are rare in the population consisting mainly of high immunity individuals. This negative frequency-dependent selection was shown in the field experiment on wild rodents where the survival and reproductive success of females from two artificially selected immune groups (high or low immunity) and in different frequencies (rare or common) were monitored both in parasite-free environment (generated by antiparasite medication) and in control conditions. The experimental design revealed the advantage of the rare type both for survival and reproductive success. Potentially, individuals with lower immunity can allocate their resources to other traits (e.g. intraspecfic resource competition abilities) explaining their higher success in the populations of lower infection risk. In wider context, our results suggest that high proportion of highly immunocompetent individuals in the population can decrease the transmission of diseases in wild animals. Frequency-dependent selection thus plays a pivotal role in determining the optimal level of parasite resistance in the wild.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i072-R*

General sessions

Drosophila/cactus interaction plays an important role in the population phenotypic diversification

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Summary statement:

There is Drosophila-cactus specificity with a host shift for D. antonietae, and an interespecific and intraspecific variation of the wing and aedeagus size and shape.

Abstract:

The genetic basis of phenotypic divergence in the process of speciation and population diversification accompanying the cladogenesis are controversial, both with respect to the number of genes (many or few) and with respect to their effects (large or small). Within this context, phytophagous insects represent an excellent model system as the host plants constitute an immediate environmental factor that can affect early stages of the life cycle. Currently, there is a secondary contact zone without hybrid formation on the southern coast of Brazil, formed by the presence of two species of Drosophila buzzatii cluster, D. serido and D. antonietae, where they can be obtained from two different types of preferred host plants, Opuntia monacantha and Cereus hildmaniannus. Thus, the objective of this work was to evaluate, from the host plant utilization pattern, the genetic and ecological diversification process of these species. Our results showed that there is a certain specificity of D. antonietae with Cereus and D. serido with Opuntia. However, considering that there was a recent expansion from south to north on the southern coast of Brazil for D. antonietae, there has been a host shift for this species at this location without an influence of sympatry with D. serido (reinforcement effect) despite the relatively short period of time. Our results also indicated a potential role of environmental heterogeneity (represented by different cactus hosts) in the maintenance of interespecific and intraspecific variation of the wing and aedeagus size and shape. This Drosophila/cactus interaction seems to be important and probably played a significant role in the history of these species.

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MON 22 AUG at 1200 - Room N4
Oral presentation *B2-Ge03-1200-O*

General sessions
Population ecology

Great reduction in fitness in an old isolated butterfly population

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Summary statement:

We report on a case study examining the joint effects of drift, inbreeding and local adaptation in a small, completely isolated butterfly population.

Abstract:

Loss and fragmentation of natural habitats is a major cause of population and species extinctions. In countless cases, populations have become completely isolated. Small isolated populations, where gene flow is entirely absent, may suffer of inbreeding depression and the loss of genetic variation due to drift. On the other hand, isolation may enhance fitness through local adaptation. While many studies focus on any one of these evolutionary forces alone, empirical studies on natural populations examining the joint effects of drift, inbreeding and local adaptation are scarce. Here, we report on a case study of a small population of the Glanville fritillary butterfly, which has persisted on an island in the Baltic Sea completely isolated from conspecific populations for at least 75 years. We examined signs of inbreeding depression and local adaptation in a large number of fitness components, covering the entire life cycle of the species from larval development to adult morphology, metabolic capacity, flight and reproductive performance. The results demonstrate greatly reduced absolute fitness, which is most likely due to large genetic load (fixation of deleterious alleles). There were no obvious indications of local adaptation.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i074-R*

General sessions

Natural variation in Pristionchus pacificus dauer formation reveals cross-preference rather than self-preference of nematode dauer pheromones

Mayer MG[1], Sommer RJ[1]
[1]Max Planck Institute for Developmental Biology, Department of Evolutionary Biology, Tübingen, Germany

Summary statement:

Most Pristionchus pacificus strains show a higher formation of dauer larvae in response to dauer pheromones from other strains than in response to their own pheromone.

Abstract:

Evolutionary ecology investigates how the developmental response to the environment and the ecological interactions of an organsism shape the evolution of new phenotypes. Under harsh environmental conditions, the nematode Pristionchus pacificus can arrest its development in the third larval stage and form dauer larvae. The assosciation of P. pacificus with scarab beetles is exclusively in the dauer stage, indicating that the dauer stage is essential not only for enduring unfavorable conditions but also for dispersal.

We have investigated the ability of P. pacificus to enter and exit the dauer stage by using a natural variation approach. The supernatant prepared from P. pacificus liquid cultures contains dauer pheromone, which induces dauer formation. We isolated dauer pheromone from 16 P. pacificus strains and tested for natural variation in pheromone production and sensitivity in cross-reactivity assays. Surprisingly, 13 out of 16 strains produce a pheromone that induces the highest dauer formation in individuals of other strains, showing clear cross-preference as opposed to self-preference of dauer pheromones. We will also report recombinant-inbred-line experiments, which try to identify the molecular basis of natural variation in dauer pheromone production and sensitivity. Furthermore, the analysis of survival, recovery, and fitness after dauer exit of eight P. pacificus strains revealed that dauer larvae can survive for up to one year under experimental conditions.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i075-R*

General sessions

Population genetics and gene expression analysis of the cbf genes in wild tomatoes

Mboup MK[1]
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Summary statement:

Using a candidate approach we investigated the selective forces acting on the CBF gene family in wild tomatoes. These genes evolved differently and are induced by abiotic stresses.

Abstract:

Abiotic stresses such as drought, extreme temperatures and salinity have a strong effect on plant development. They act as strong selective forces on the evolution of plant physiology and morphology. These selective constraints leave peculiar footprints that can be detected at the sequence level using population genetics tools. Using a locus candidate approach we investigated signatures of adaptation in two wild tomatoes species: Solanum Peruvianum and Solanum Chilense. These species are native from Western South America and constitute a good model system to study adaptation for their ability to colonize a large range of habitats. We have determined the selective forces acting upon the CBF gene family, which is known to be involved in tolerance to abiotic stresses and mainly in cold tolerance. We also looked at the expression pattern of these genes after drought and cold stresses. We found that CBF1 and 3 have evolved under purifying selection, whereas CBF2, their putative regulator is under balancing selection. This is the first study reporting that the CBF genes are cold induced in wild tomatoes. So far all the studies have reported that only CBF1 was cold induced in tomato. Interestingly the CBF genes are also induced by drought.

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MON 22 AUG at 1120 - Room N2
Oral presentation *B2-Ge01-1120-O*

General sessions
Behaviour

Cooperation and the evolution of intelligence

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[2]University of Edinburgh, Centre for Immunity, Infection and Evolution, School of Biological Sciences, Edinburgh, United Kingdom

Summary statement:

We use simulation models to show that cooperative behaviours may be key in the evolution of advanced intelligence.

Abstract:

The high levels of intelligence seen in humans, other primates, and certain cetaceans and birds remains a major puzzle for evolutionary biologists, anthropologists and psychologists. One of the leading theories is the "social intelligence hypothesis", which holds that the evolution of intelligence is driven by a need to process and memorise the intricate social interactions that occur in these taxa. In recent years decision-making in the context of cooperative social interactions has been conjectured to be a possible source of selective pressures leading to greater cognitive abilities. We use an artificial neural network model to show that selection for efficient decision-making in social interactions can give rise to selection pressures for greater cognitive abilities, despite individuals paying a fitness penalty for higher levels of intelligence. These selection pressures are maximised during transitions to cooperative behaviour. Furthermore, we show that intelligent strategies can themselves select for greater intelligence, leading to a Machiavellian arms race. Our results provide, to our knowledge, the first mechanistic support for the social intelligence hypothesis, highlight the importance of cooperative behaviour in the evolution of intelligence and help to explain the bimodal distribution of cooperation with intelligence across taxa.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i076-R*

General sessions

Negative frequency dependent selection of sexually antagonistic alleles: Insights from experimental field data and mathematical modeling

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Summary statement:

We present an experiment and mathematical model that show negative frequency dependent selection maintains sexually antagonistic alleles in the field.

Abstract:

Recent empirical work has revealed that a major portion of genetic fitness variation is sexually antagonistic (SA). Yet, how this SA genetic variation is maintained remains an unresolved question, especially in light of the various sex-specific selection processes that affect males and females. We designed an integrated empirical-theoretical study to assess whether frequency dependent selection can maintain SA alleles in a population. By selecting a small mammal, the bank vole (Myodes glareolus) in the lab first, we created populations in which the males were dominant and their sisters had low fecundity (and vice versa). By manipulating their frequencies in semi-natural field enclosures, we discovered that males were negatively frequency dependent, such that dominant males were only the most successful when rare in the population. However, females showed selection for higher fecundity regardless of frequency in the population. We derived parameter estimates from our field data for our mathematical model that incorporates diploid genetics and frequency dependence into the investigation of sexual antagonism. The model revealed that negative frequency dependence can maintain SA alleles over many generations in stable equilibria, when run with the parameters obtained from the field data. In the absence of frequency dependence, the alleles would go to fixation/elimination. We will discuss the implications of our study in the broader context of selection theory.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i077-R*

General sessions

Untangling hybridization in a genus of New Zealand plants

Monaghan J[1], Shepherd L[1], Hendy M[1], Holland B[2]
[1]Massey University, Palmerston North, New Zealand, [2]University of Tasmania, Hobart, Australia

Summary statement:

The application of next-generation sequencing techniques to the development of a multi-locus dataset for the study of hybridization in New Zealand tree genus Pseudopanax.

Abstract:

Hybridization plays a key role in generating biodiversity. However, as hybrids inherit genetic material from two parent species, they are hard to detect using a single gene. The use of multi-locus datasets may result in a more accurate species phylogeny if hybridization has taken place. Hybridization occurs between some species of Pseudopanax, an endemic New Zealand tree genus. A previous phylogeny for the genus, constructed from AFLP-DNA fingerprinting data, recovered each species as a cohesive genetic grouping, and revealed strong phylogenetic support for higher-level relationships. However, intermediate relationships (amongst species within the two principal groups) were not confidently resolved. In order to explore this result further we are developing a multi-locus sequence dataset for Pseudopanax using the Illumina Solexa NGS platform. We sequenced restriction-digested and size-selected DNA from four Pseudopanax species, of which at least two species are known to hybridize extensively. We will identify variable loci across the resulting sequence alignments of these species, and develop primers to amplify these regions in all 12 Pseudopanax species. Future work will include development of a hybrid evolution simulator, in order to allow identification of the levels and modes of hybridization that can be detected (along with more specific questions regarding hybridization). The Pseudopanax dataset generated here will provide an ideal system to compare with these simulations, improving our understanding of the complex evolution of this genus, as well as the many other plant radiations currently being studied in New Zealand and around the world.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i079-R*

General sessions

Diversification patterns in Drosophila

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Summary statement:

We present a study of the rates of diversification of Drosophila with the goal of understanding the factors that promote the species richness of this group of organisms.

Abstract:

The lineage of Drosophila is widely distributed and its members show a large diversity of ecological niches. We present a study of the rates of diversification of the Drosophila groups with the goal of understanding the factors and processes that promote the origin of biodiversity and with what frequency adaptive radiations have occurred in this group of organisms. For that purpose, we have estimated and dated the phylogeny of Drosophila using *BEAST v1.6.1 with data sequence for three genes obtained from the GenBank. Patterns and rates of diversification have been analysed using MEDUSA, the MCCR test and the temporal method BDL, which was used to test different diversification models in LASER. The D. repleta group has been identified as evolving under a density-dependent model, suggesting an adaptive radiation for this group of species. The members of the D. repleta group are all cactophilic species, and it was therefore tested whether adaptation to cacti was an innovation key that triggered an increase in the speciation rate of this group. Results of the comparative method BiSSE showed no relationship between the speciation rates of cactophilic and non-cactophilic species. Therefore, cactophily provides a weak explanation for the patter of richness of this group.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i080-R*

General sessions

Dollo's law and the re-evolution of aquatic larvae in plethodontid salamanders

Mueller H[1]
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Summary statement:

The re-evolution of aquatic larvae in plethodontid salamanders is investigated, which has been proposed to represent an instance of a violation of Dollo´s Law.

Abstract:

Dollo's Law states that complex structures are unlikely to be regained in the same form, once they are lost during evolution. This notion has been seriously challenged recently by studies indicating a re-evolution of an aquatic larva from direct developing ancestors in plethodontid salamanders and marsupial frogs. While the phylogenetic evidence seems compelling, we have currently little understanding of the evolutionary and developmental mechanisms that would enable such a re-evolution. I investigated the development of the cranial skeleton and its associated musculature in desmognathid and other plethodontid salamanders and present morphological and developmental evidence that enables a better understanding of the evolution of direct development and its potential reversal. It appears as if desmognathid salamanders did indeed re-evolve an aquatic larva from a direct developing ancestor. Direct developers closely related to desmognathids do, however, retain a number of larval in their ontogeny, which seem to have elaborated again in Desmognathus. It is therefore debatable whether this re-evolution of an aquatic larva does indeed qualify as a violation of Dollo's Law.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i081-R*

General sessions

How does phenotypic plasticity evolve? Genetics of the mouth‑form dimorphism in Pristionchus pacificus

Müller MR[1], Ragsdale EJ[1], Sommer RJ[1]
[1]Max Planck Institute for Developmental Biology, Department of Evolutionary Biology, Tübingen, Germany

Summary statement:

A forward genetic approach is used to investigate genes involved in the development of a phenotypically plastic mouth‑form dimorphism in the nematode Pristionchus pacificus.

Abstract:

The hermaphroditic nematode Pristionchus pacificus is a model system for comparative studies to Caenorhabditis elegans, with well-developed genetic, genomic, and transgenic tools. The availability of tools for functional investigations makes P. pacificus ideal for the genetic investigation of ecologically relevant traits. Under stress conditions P. pacificus forms resistant dauer larvae, a case of phenotypic plasticity in nematodes. A second type of phenotypic plasticity in P. pacificus is a dimorphism in its feeding structures, an evolutionary novelty of the family Diplogastridae. The mouth‑form dimorphism decision is made during larval development and is irreversible. The dimorphism consists of a stenostomatous (“St”) and a eurystomatous (“Eu”) form, which differ in the number and shape of teeth and by the width of the buccal cavity. Dauer larva formation and mouth‑form dimorphism share common environmental and molecular switches, suggesting partial co‑option of the dauer formation pathway in mouth‑form dimorphism evolution. Here we present a first approach to the identification of genes specific to the mouth‑form phenotype execution. Using a forward genetic approach, we identified eight mutant strains that are strongly biased to the Eu mouth form. Dauer formation in these mutants is normal, suggesting that the mutants are specific to the mouth-form dimorphism. Another screen for mutants that show a high frequency of St animals is currently ongoing. Mapping and cloning these mutants will provide unprecedented insight into the genetic mechanisms controlling of a polyphenic novelty.

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MON 22 AUG at 1120 - Room N4
Oral presentation *B2-Ge03-1120-O*

General sessions
Population ecology

Early life climatic conditions and survival in Asian elephants (Elephas maximus) from Myanmar

Mumby HS[1], Mar KU[1], Lummaa V[1]
[1]University of Sheffield, Animal and Plant Sciences, Sheffield, United Kingdom

Summary statement:

We studied the effect of early life climatic conditions on infant mortality, age-specific survival rates and survival during adverse climatic events in elephants from Myanmar.

Abstract:

Conditions in early life are known to have immediate effects on survival in both wild animals and lab studies, and they may also have long term effects on survival, reproduction and later life health. Early life effects are of particular importance in long lived species such as the Asian elephant (Elephas maximus) in which individuals must respond to fluctuating environmental conditions over a long lifespan and offspring are highly vulnerable to extreme climatic events such as drought. However, little is known of how these effects produce long term impacts on survival, and it is uncertain whether poor conditions in early life improve or reduce the ability of individuals to cope with harsh conditions later in life.

We use individual-based longitudinal data for >1000 semi-captive logging elephants from Myanmar, that occupy regions with a tropical monsoon climate and extreme fluctuations in rainfall across and within years, to investigate immediate and long term life history responses to early life climatic conditions. Climatic data consist of monthly rainfall and mean temperature records collected for four regional elephant camps over a 35 year period. We first test the effect of climatic variation during early life on age-specific survival rates in the infant, juvenile and adult stages. We then test the predictive adaptive response hypothesis by assessing the effect of early life conditions on the probability of surviving adverse environmental events later in life. Finally, we study whether effects differ by sex, or depend on whether the individual's mother was born in captivity or wild-captured.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i082-R*

General sessions

Evolution of mating strategies and ornamentation in conventional and sex-role reversed dance flies (Diptera: Empididae)

Murray RL[1], Bussiere LF[1]
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Summary statement:

A comparison of mating strategies, including sex ratios, sexual dimorphism and mating behaviour, in conventional and sex-role reversed dance flies (Diptera: Empididae).

Abstract:

Sexual ornaments are among the most striking and diverse morphological adaptations in the animal kingdom. The theory of sexual selection helps to explain how diverting resources away from survival to costly reproductive traits could evolve because mate attraction more than compensates for the fitness costs to other traits. Dance flies (Diptera: Empididae) are a group that displays remarkable diversity in mating systems, including sex-role reversal, nuptial gifts and female ornaments. We used a combination of natural history observations and phylogenetically independent contrasts of species with a variety of mating strategies to better understand the trade-offs associated with producing costly secondary sexual characteristics. Here, we present results contrasting species sex ratios, sexual dimorphism and mating behaviour in conventional and sex-role reversed taxa.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i083-R*

General sessions

Demographic parameter estimation can be both fast and accurate

Naduvilezhath L[1], Rose L[2], Metzler D[1]
[1]LMU, Biocenter, Planegg, Germany, [2]Heinrich-Heine-Universität, Düsseldorf, Germany

Summary statement:

We developed Jaatha to estimate demographic parameters (e.g. population size, divergence time, migration rate) from sequence data. Simulations show Jaatha is fast and accurate.

Abstract:

While information about a species' demography is interesting in its own right, it is an absolute necessity for certain types of population genetic analyses. The most widely used methods to infer a species' demographic history do either not take intralocus recombination or recent divergence into account and some methods take several weeks to converge. Here we present Jaatha, a fast composite-likelihood method which does incorporate recent divergence and intralocus recombination. The accuracy of Jaatha is comparable to that of other currently available methods, though it is superior under certain conditions, especially when divergence is very recent. As a proof of concept, we apply this new method to estimate demographic parameters for two closely related wild tomato species, Solanum chilense and S. peruvianum.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i084-R*

General sessions

Cryptic diversity of endemic Indirana frogs of the Western Ghats biodiversity hotspot

Nair A[1], Gopalan SV[2], George S[2], Kumar KS[2], Teacher AGF[1], Merilä J[1]
[1]University of Helsinki, Department of Biosciences, Helsinki, Finland, [2]Rajiv Gandhi Center for Biotechnology, Chemical Biology, Thiruvananthapuram, India

Summary statement:

Taxomomy of Indirana frogs need revision, detailed genetic studies across Western Ghats might yet uncover additional new candidate species from this poorly studied endemic genus.

Abstract:

Recent studies have shown that the number of amphibian species in biodiversity hotspots may be heavily underestimated, and many new species are constantly being reported from these hotspots. For successful conservation and management strategies to be implemented within these hotspots, better understanding of the species diversity and their evolutionary relationships is required. Frogs of the genus Indirana belong to the endemic family Ranixalidae, and are found exclusively in the Western Ghats biodiversity hotspot, in southern India. We used three mitochondrial (16S, 12S and CO1), and two nuclear (rag1 and rhodopsin) gene fragments to investigate the genetic diversity within the endemic Indirana genus, using Bayesian, maximum likelihood and maximum parsimony methods. The results suggest that the species diversity within the Indirana is much higher than previously anticipated. Instead of the previously expected six species within this region, the analyses identified eleven clades with high levels of sequence divergence. Hence, each of these clades is likely to represent a distinct species .In general, the results suggest the existence of multiple unrecognised cryptic lineages within Indirana, which are likely to have narrower distribution ranges and lower abundance than the taxonomic units into which they are currently assigned.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i085-R*

General sessions

Does linkage has an effect on the reliability of genome scans?

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Summary statement:

Using simulations we show that linkage disequilibirum between markers may have a significant effect on the accuracy of genome scans.

Abstract:

Nowadays genome scans, taking advantage of the fact that selection affects the allele frequencies of involved loci, whereas demographic history affects the allele frequencies of the entre genome, are widely used to detect the genetic basis of local adaptation. To characterize a locus as an outlier, and thus as a candidate locus for selection most often a measurement based on Wright's inbreeding coefficient Fst is used. The genome wide Fst-distribution has been shown to be quite robust to many demographic assumptions being an ideal measurement for genome scans. However recently it has also been shown that although robust the genome wide Fst-distribution may be misleading if the underlying demographic model is wrong. But so far it has never been investigated if linkage disequilibrium (statistical and physical) has an effect on genome scans. In our study we address this question using individual-based simulations.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i038-E*

General sessions

Preconditioned reaction norm of developmental phenotypic plasticity

Nishimura K[1], Kuwano S[2], Kishida O[3]
[1]Hokkaido University, Graduate School of Fisheries Sciences, Hakodate, Japan, [2]Hokkaido University, Graduate School of Fisheries Sciences, Hakodate, Hokkaido, Japan, [3]Hokkaido University, Teshio Experimental Forest, Field Science Center, Horonobe, Hokkaido, Japan

Summary statement:

Developmental reaction norm is preconditioned before hatch, and the norm is correlated with egg size.

Abstract:

Consistency and modification of phenotypic expression of individuals with an identical set of genes in response to environmental changes remind us organismal integrity, and it is referred as ‘reaction norm’. In some organisms, developmental reaction norm prepares alternative developmental pathways according to experiencing environment of the individual. The dynamical reaction norm is referred to as ‘phenotypic plasticity’. In some case, not all individual take alternative developmental pathway in a given environment. The facultative plasticity hinges on individuals’ physiological and physical conditions before the developmental differentiating timing. It comes as a reminder of an aspect of elaboration of reaction norms, that is, adjustment in the way of development. We investigated variation of reaction norm among individuals in larvae of salamander Hynobius retardatus. In crowd condition, some larvae of the salamander develop to a cannibalistic morph and rest of the larvae develops to a non-cannibalistic morph, and it makes trophic dimorphic population. We found that the reaction norm generating the facultative development of either cannibal or non-cannibal is preconditioned. Developing embryos form larger egg prepared morph tend to become cannibal in endogenous developmental period, in which the embryos have no cue to induce the cannibal morph. In the subsequent exogenous developmental period, larvae adjust to develop either of cannibal or non-cannibal morph depending on experiencing external and internal conditions. It comes as a reminder of relationships of individuals’ developmental reaction norm with genomic or un-genomic maternal inheritance.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i086-R*

General sessions

Female fineries - but not at all costs

Nordeide JT[1], Kekäläinen J[2], Kortet R[2]
[1]University of Nordland, Faculty of Biosciences and Aquaculture, Bodø, Norway, [2]University of Eastern Finland, Department of Biology, Joensuu, Finland

Summary statement:

Recently published empirical studies which are in direct conflict with the "direct selection hypothesis" to explain the evolution of ornaments in females, are presented.

Abstract:

"The direct selection hypothesis" of sexual ornamentation predicts that both sexes benefit from displaying an ornament and that female ornaments have evolved as a response to sexual selection from males. The hypothesis has become popular, since it was advocated in two influential papers which review literature on evolution of female ornaments. However, based on the new evidence the direct selection hypothesis can potentially be questioned, especially on carotenoid-based signalling systems. Since animals cannot synthesize carotenoids and thus must acquire these pigments from food, carotenoids are believed to be energetically costly to the individuals. This means that the carotenoid resources allocated to elaborate ornamentation should reduce resources available for other purposes. This trade off is expected to be especially critical in females that usually invest significant amount of their resources in offspring. Resources allocated to ornaments are expected to constrain female fecundity, which in turn should lead to selection for dishonest female signalling. This study highlights recent independent data sets that suggest negative fitness consequences of elaborate female ornaments in mutually ornamented species. Acknowledging these findings is important, since they challenge the generality of the direct selection hypothesis as an explanation for the evolution of female ornaments in species where females trade-off resources between ornaments and eggs.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i120-R*

General sessions

Hox gene cluster in ontogenesis of Alitta (Nereis) virens and Platynereis dumerilii (Annelidae, Polychaete)

Novikova E[1], Bakalenko N[1], Kulakova M[1]
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Summary statement:

Two polychaete Hox genes are collinearly expressed in larvae and form gradients in adult bodies. Larval and postlarval developmental programs differ in expression of Hox genes.

Abstract:

Hox cluster of the common ancestor of Eubilateria consisted at least of 7 genes. The first five genes (PG1-5) are the most conservative and are shared by representatives of different evolutionary branches. Medial (PG 6-8) and posterior (PG 9-14) Hox genes originate from ancestral sequences, which independently diversificate in different phyla of Eubilateria.

Alitta (Nereis) virens and Platynereis dumerilii are homonomously segmented polychaetes with two larval stages – spherical trochopore and segmented nechtochaete, which forms all its segments from the cells of vegetal plate. In the juvenile worm the new segments appear from posterior growth zone.

We found, Alitta virens and Platynereis dumerilii Hox genes are collinearly expressed in segmented larvae. Nvi-Hox1-5, Lox5 and Post2 act in larval ectoderm. Nvi-Hox2, Nvi-Hox4 и Nvi-Lox5 are also expressed in larval mesoderm in collinear manner.

In juvenile worms patterns of Hox gene expression form oppositely directed gene-specific gradients. The medial genes Nvi-Hox7, Nvi-Lox4 and Nvi-Lox2 begin to express in postlarval segments of A. virens. Patterns of expression quickly react to the changes of body length and proportions, resulted from the loss and regeneration of posterior segments.

Thus, larval and postlarval developmental programs differ in the number and expression patterns of Hox genes, that might be the result of structural and functional evolution of lophotrochozoan Hox cluster.

The work is supported by Russian Fund for Fundamental Researches (RFFR), grant 09-04-01322a.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i087-R*

General sessions

Nymphalid butterflies and their host plants - evolutionary conservatism and transient dynamics

Nylin S[1], Janz N[1], Wahlberg N[2]
[1]Stockholm University, Department of Zoology, Stockholm, Sweden, [2]University of Turku, Department of Biology, Turku, Finland

Summary statement:

Nymphalid butterflies show strong conservatism in host plant utilization, with few shifts to novel hosts. The apparent conservatism may however be misleading.

Abstract:

As new and better resolved phylogenies become available for nymphalid butterflies, an interesting picture emerges regarding the evolution of host plant associations in this species-rich family. It appears that this group of butterflies has been associated with "urticalean rosid" plants (nettles, elms etc) ever since the family diverged from other butterflies in the Cretaceous, perhaps 90 Mya. This association persists in many modern taxa. However, there has also been some radiations after host shifts. I present the patterns that can now be reconstructed and investigate the relative roles of such rapid diversification after colonizations of novel hosts and the less spectacular process of transient increases in host range and plasticity - followed by re-specialization on ancestral or novel hosts (the "oscillation hypothesis" of Janz & Nylin).

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SUN 21 AUG at 1200 - Room N4
Oral presentation *A2-Ge03-1200-O*

General sessions
Population ecology

The geography of adaptive radiation: Insights from willow-galling sawflies

Nyman T[1], Roininen H[1], Zinovjev AG[2], Collet DM[3], Price PW[4]
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Summary statement:

A phylogenetic analysis of >200 willow-galling sawfly species indicates that speciation in the group is driven by both allopatric divergence and shifts among host species.

Abstract:

Most plant-feeding insects are very specialized in their use of available plants, and shifts among plant taxa may constitute an important driver of insect speciation. However, the frequency of sympatric, shift-associated speciation, as opposed to ´ordinary´ allopatric speciation, is still unclear. Willow-galling sawflies (Hymenoptera: Tenthredinidae) constitute a highly suitable model system for studying the relative importance of niche shifts vs. geographic isolation for insect speciation: this holarctically distributed monophyletic group contains an estimated 400-500 species, many of which are strict specialists on single willow species. Different species-rich galler clades induce distinct galls on willows; in essence, this means that the different gall-type groups represent replicated radiations across the common resource base formed by over 500 northern Salix species. We studied the geography of adaptive radiation by using sequence data from two mitochondrial and one nuclear gene to reconstruct the phylogeny of >200 willow-galling sawfly species collected from numerous different willow species across Europe, Asia, and North America. The phylogeny demonstrates that large-scale distributional shifts have occurred in all main gall-type groups. Frequent interchange between Eurasia and North America indicates that allopatric speciation has been commonplace within most galler taxa. Nevertheless, some galler clades are composed of closely related species or host races that are found on different willows in geographically restricted areas, suggesting that host-shifting among willow species may also contribute to galler speciation.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i088-R*

General sessions

Developmental patterns of the bizarre 2-sex / 2-morph polyphenism in the ant Cardiocondyla obscurior

Oettler J[1], Schmidt CV[1], Platschek T[1], Heinze J[1], Abouheif E[2]
[1]Universität Regensburg, Regensburg, Germany, [2]McGill University, Montreal, Canada

Summary statement:

The ant Cardiocondyla obscurior is a unique model for the study of phenotypic plasticity. We describe caste differences in wing development and adult morphology.

Abstract:

Eusociality in the Hymenoptera is generally correlated with polyphenism where workers are the extended phenotype of queens. The study of the underlying mechanisms of polyphenism will allow to understand the processes that led to and continue to maintain eusociality. Usually ants have winged males and females (queens) and wingless workers. Species of the ant genus Cardiocondyla (Formicidae: Myrmicinae) are characterized by the derived condition of wingless males, which stay inside the maternal nest and mate with closely related virgin queens. In addition, some species within this genus have retained the standard winged males. This unique system allows for comparing intraspecific sex-dependent development. Using morphometrics of adults and in-situ hybridization in late larvae we studied growth patterns of workers, queens, wingless males and winged males. We asked whether castes develop according to reaction norms or discrete phenotypes, and how the interruption of wing development is regulated in wingless males and workers. Surprisingly, interruption of wing development in workers is upstream compared to wingless males. Our study of male plasticity adds a new facet to the known extreme degree of female plasticity in the Formicidae.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i117-R*

General sessions

Adaptive trait evolved in digestive assimilation of a dominant seabird in cooler current

Oka N[1]
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Summary statement:

Nestling obesity evolved in pelagic birds was accelerated by high ability to assimilate krill, which trait was an important factor to keep them dominant in cooler currents.

Abstract:

Oceanic bird chicks such as albatrosses and shearwaters accumulate large amount of lipid. This obesity functions as a buffer against parental irregular attentiveness to provision meals, however, yet surprisingly the assimilation mechanism to attain obesity remains unclair. This study presents the first measurements in assimilation efficiency (AE) in relation to nestling ages and diet kinds through a long nestling period of a shearwater species that utilizes marine organisms in lower trophic level. To determine AE and diet effects on growth, short-tailed shearwater chicks, a cooler current species, were fed in captivity with three taxa diets of marine organisms. The younger chicks showed higher AE than those at older chicks. It was noted that the krill-fed chicks (KC) showed consistently higher AE than those of the squid- (SC) or fish-fed (FC) chicks. Krill diet contributed to the better growth in body mass, while the SC and FC groups grew slowly. The diet effects on feather growth did not parallel to those in body mass increments. The SC had similar growth in their feathers to those of the KC, whereas the FC often vomited food, given large amount of meal, and had slower feather growth. This suggested that chicks needed parent fluids to digest large amount of fish, while were competent to digest krill and squid on their own. The chicks, thus, have well assimilation abilities at early nestling stage, that resulted in obesity to bear up the fast and may tolerate their parents to forage far to the nutritive waters. Furthermore this study showed that they have highly adaptive potential to assimilate krill at higher rate.

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WED 24 AUG at 1500 - Room N7
Oral presentation *D3-Ge05-1500-O*

General sessions
Disease and immunity

Sex differences in telomere selection in free-ranging sand lizards

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Summary statement:

We show that telomere selection is much stronger on female than male wild lizards.

Abstract:

Telomere length is restored primarily through the action of the reverse transcriptase telomerase, which may contribute to a prolonged lifespan in some but not all species and may result in longer telomeres in one sex than the other. To what extent this is an effect of proximate mechanisms (e.g., higher stress in males, higher estradiol/estrogen levels in females), or is an evolved adaptation (stronger selection for telomere length in one sex), usually remains unknown. Sand lizard (Lacerta agilis) females have longer telomeres than males and better maintain telomere length through life than males do. We also show that telomere length more strongly contributes to life span and lifetime reproductive success in females than males and that telomere length is under sexually diversifying selection in the wild. Finally, we performed a selection analysis with number of recruited offspring into the adult population as a response variable with telomere length, life span and body size as predictor variables. This showed significant differences in selection pressures between the sexes with strong ongoing selection in females, with these three predictors explaining 63% of the variation in recruitment. Thus, the sexually dimorphic telomere dynamics with longer telomeres in females is a result of past and ongoing selection in sand lizards. Finally, we compared the results from our selection analyses based on Telometric-derived data to the results based on data generated by the software ImageJ. ImageJ resulted in shorter average telomere length, but this difference had virtually no qualitative effect on the patterns of ongoing selection.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i089-R*

General sessions

Hormonal control of seasonal polyphenism: flexibility and integration of a suite of morphological and life history traits sharing a hormonal regulator

Oostra V[1], De Jong MA[1,2], Mateus ARA[1,3], Invergo BM[4], Wende F[5], Beldade P[1,3], Brakefield PM[1,6], Zwaan BJ[1,7]
[1]Institute of Biology Leiden, Leiden, Netherlands, [2]Department of Biological and Environmental Sciences, University of Helsinki, Helsinki, Finland, [3]Instituto Gulbenkian de Ciência, Oeiras, Portugal, [4]Institut de Biologia Evolutiva (CSIC-UPF) CEXS-UPF-PRBB, Barcelona, Spain, [5]Department of Animal Ecology I, University of Bayreuth, Bayreuth, Germany, [6]University Museum of Zoology Cambridge, Cambridge, United Kingdom, [7]Laboratory of Genetics, Wageningen University and Research Centre, Wageningen, Netherlands

Summary statement:

A threshold reaction norm of ecdysteroid hormones underlies seasonal polyphenism in a butterfly, but does not constrain independent, trait-specific responses to the environment.

Abstract:

Polyphenisms – the expression of discrete phenotypic morphs in response to environmental variation – are a key adaptation to predictable environmental heterogeneity. Hormones are essential mediators of polyphenisms, coordinating the expression of physiological, behavioural and morphological traits into an integrated life history. The butterfly Bicyclus anynana has evolved phenotypic plasticity of a suite of traits as adaptation to its habitat´s contrasting seasonal environments. The polyphenism is induced by temperature during development and mediated by ecdysteroid hormones. We study the role of hormones in interpreting the environment during development and inducing changes in adult traits involved in the seasonal adaptation. We measured thermal reaction norms for ecdysteroids and adult fitness traits. Ecdysteroids showed a binary response to the linear temperature gradient, demonstrating that hormones can translate a linear environmental gradient into a discrete signal and, thus, that polyphenic differences between adult morphs can already be programmed at the stage of hormone signalling during development. Several adult traits (e.g. relative abdomen mass) responded in a similar, dimorphic manner, while others (e.g. wing pattern) showed a linear response. Furthermore, ecdysteroid injections during development altered these traits in a time- and temperature dependent manner, revealing both shared regulation and independent, trait-specific windows of sensitivity to the hormone. This suggests that rather than constraining environmental responses, the hormone system allows for both flexibility and integration of traits underlying adaptations to divergent environments.

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MON 22 AUG at 1140 - Room N6
Oral presentation *B2-Ge05-1140-O*

General sessions
Disease and immunity

Male and female fitness effects of sperm-microbe interactions

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[1]University of Sheffield, Sheffield, United Kingdom, [2]Uni Tuebingen, Tuebingen, Germany

Summary statement:

Through artificially introducing microbes into mated females we investigated male and female fitness effects of sperm-microbe interactions.

Abstract:

Male reproductive traits, including seminal fluids or sperm cells are generally thought to be under sexual selection rather than natural selection. However, microbes that live in the male or female body, and particularly those that are sexually transmitted, frequently meet with sperm cells and could be agents of natural selection. If such microbes impair sperm function one can predict effects on either male or female fitness. One can further predict that male and female traits exist to counteract such fitness costs, such as immune active seminal fluid. In bedbugs males transmit several microbe species during mating and these co-occur with sperm in the female body for several hours. 1. We found that the seminal fluid of bedbugs has antimicrobial properties and tested its effects in vitro on sperm performance in the presence and absence of bacteria. 2. Injecting realistic concentrations of this antibacterial substance into females we found that the immune active ejaculate substance did not release females from a costly immune response and had no effect on female fitness. 3. In vivo, microbes caused direct effects on sperm function after physical contact, and indirect effects when they co-occur in the body via infection costs to females. Sperm and microbe encounters are very widespread, and our data suggest that their interactions may have more widespread fitness consequences than is currently appreciated.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i041-E*

General sessions

Wide variation in reproductive success among asexual clones of a New Zealand freshwater snail

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Summary statement:

The Red Queen remains a possibility favouring sexual reproduction in P. antipodarum, as only a few clones out of the diverse clonal population have high relative fitness.

Abstract:

Asexually-reproducing organisms should have a reproductive advantage over sexuals because they do not waste resources on sons. Under the Red Queen hypothesis, sexuals can persist because they can escape parasites by producing offspring with novel or rare genotypes with which their parasites are unfamiliar. However, the Red Queen hypothesis fails to explain the maintenance of sex if asexual population is very diverse, presenting a multitude of rare genotypes that should still capitalize on the cost of sex.
Sexual and asexual Potamopyrgus antipodarum, a New Zealand freshwater snail, frequently coexist. The persistence of sexual reproduction may be due to negative frequency-dependent selection on clones caused by a castrating trematode parasite. However, the very high genetic diversity of asexual P. antipodarum poses a challenge for this hypothesis, since rare clones should be favoured along with sexuals. Here, we wanted to test whether all the clones have high relative fitness and are thus potentially able to outcompete the sexual population.
We measured fitness of asexual clones in the wild by culturing isofemale lineages in underwater cages and measuring population growth after one year. We found that there are very few clones with high fitness, and the majority of asexual genotypes have low fitness.
These results indicate that the truly competitive asexual genetic diversity is much lower that the observed, and implies that high clonal diversity is not as serious of a threat for coexisting sexual P. antipodarum as initially assumed.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i090-R*

General sessions

Hybridization and introgression of sympatric bromeliad species (Pitcairnia spp.): mechanisms involved in species cohesion and reproductive isolation in Neotropical inselbergs

Palma-Silva C[1], Wendt T[2], Pinheiro F[3], Barbara T[4], Fay M[5], Cozzolino S[6], Lexer C[4]
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Summary statement:

We show that long-term gene exchange across complex species barriers forms an integral aspect of a Neotropical radiation in island-like environments.

Abstract:

The roles of intra- and inter-specific gene flow in maintaining species cohesion and integrity are of great interest in current evolutionary genetics. It is widely accepted that species are cohesive units that are held together by gene flow and kept apart from other species by reproductive barriers. We studied four sympatric species adapted to inselbergs (“island” like environments) using plastid and nuclear microsatellites. Spatial patterns of haplotype sharing and nuclear admixture indicate persistent interspecific gene exchange in the face of extremely low levels of gene flow within species. In contrast to plastid DNA, nuclear markers revealed clearly distinct genetic pools corresponding to morphologically diagnosed species. Patterns of nuclear genomic admixture and cross-pollination experiments indicate that species integrity is maintained by the simultaneous action of multiple prezygotic barriers, including flowering phenology, pollinator isolation, and divergent mating systems. Postzygotic Bateson-Dobzhansky-Muller incompatibilities appear to contribute to isolation, as suggested by asymmetric introgression rates of single loci. Our results suggest that hybridization and introgression form integral aspects of adaptive radiation in Neotropical inselberg archipelagos.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i091-R*

General sessions

Host - parasite interaction in Drosophila melanogaster

Paparazzo F[1], Tellier A[1], Hutter S[1], Stephan W[1]
[1]Ludwig Maximillian University, Biology 2, Planegg-Martinsried, Germany

Summary statement:

Resistance to fungal infection and post-infection changes in gene expressionis are assessed in Drosophila melanogaster populations from different geographic locations.

Abstract:

Drosophila melanogaster is a model organism to study innate immunity in invertebrates. Parasite pressure varies between different environments and can determine level of host investment in defence. It is expected that host-parasite interactions are more intense at tropics than under temperate latitudes, given the higher species richness and climatic stability, though empirical evidence is scarce. Beauveria bassiana is a world-wide distributed enthomopatogenic fungus and in a previous study (Tinsley et al, 2006) a trend for increased resistance to B. bassiana in tropical D. melanogaster populations was found. We infected two tropical and two temperate D. melanogaster outcross populations with two B. bassiana strains and present results of mortality rates due to infection. Then, we perform a micro-array experiment to assess inter-populations variability in transcriptional response to infection and its correlation with resistance to infection. Preliminary qPCR results investigating post-infection changes in gene expression are presented.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i092-R*

General sessions

Gene flow between wheat and wild relatives

Parisod C[1], Arrigo N[1], Définod C[1], Sarr A[1], Guadagnuolo R[1], Felber F[1]
[1]University of Neuchatel, Evolutionary Botany, Neuchatel, Switzerland

Summary statement:

Surveys of natural populations with different molecular markers revealed extensive gene flow between cultivated wheats and selected wild relatives of the genus Aegilops.

Abstract:

The domestication of tetraploid (4x) and hexaploid (6x) wheat involved Aegilops species. Despite observation of intergeneric hybrids along wheat fields and great concern for risk assessment associated with the potential release of transgenic wheat, natural introgression involving wheat and Aegilops is poorly documented.
We surveyed natural populations of four Aegilops species - Ae. cylindrica (4x), Ae. geniculata (4x), Ae. triuncialis (4x) and Ae. neglecta (6x) - across the native European and the invasive American ranges. Samples were collected along wheat fields and in areas isolated from agriculture. They were genotyped with AFLP, chromosome-specific EST-SSR markers from wheat as well as wheat-specific TE insertion sites, in order to assess the presence of wheat genome subregions in Aegilops populations. Level and patterns of introgression varied according to Aegilops species, proximity to wheat cultivations and wheat ploidy level. While Ae. geniculata showed limited evidence of gene flow from wheat, numerous wheat genetic markers were commonly observed in the other Aegilops species. Most introgressed samples were collected near to crop cultivations and, in some cases, revealed relatively ancient hybridization events. Our results indicated that reproductive barriers have been regularly bypassed during the long history of sympatry between wheat and Aegilops species.
As field experiments showed that hybrids between Ae. cylindrica and transgenic wheat can have relatively high fitness, risk of introgressing transgenes into natural populations of Aegilops exists and should be considered in the context of commercialization of transgenic wheat.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i093-R*

General sessions

Genetic consequences of natal dispersal in a house sparrow metapopulation

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Summary statement:

Dispersal decrease mate relatedness in a house sparrow metapopulation and may thus reduce risks of inbreeding depression.

Abstract:

Human-induced loss and fragmentation of critical habitat types pose a serious threat to many wild populations. In small, subdivided populations the probability of mating between related individuals is high. This may cause reduction in fitness through inbreeding depression and loss of genetic variation, which in turn influence long-term population persistence. Inbreeding may select for mechanisms that reduce the probability of mating with close relatives, such as natal dispersal, i.e. movement away from the place of birth to the place of breeding. Still, little is known about the genetic consequences of dispersal in natural populations. In this study, we used data from a long-term study on an insular metapopulation of house sparrows Passer domesticus to investigate the relationship between relatedness and individual dispersal behaviour. In the study area, inbreeding occurs and has negative fitness consequences. Accordingly, dispersal may be a way to escape such costs of inbreeding. On the natal island, mean relatedness to individuals of the opposite sex (i.e. potential mates) was higher for individuals that dispersed from the island than for individuals that remained on their natal island. On the breeding island, relatedness to potential mates was lower for immigrants than for resident birds. Furthermore, the relatedness between mates in actual breeding pairs was lower in pairs in which at least one mate was immigrant than in pairs where both mates were residents. Our results support the view that dispersal reduces the costs of inbreeding.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i094-R*

General sessions

A transcriptome-based phylogenetic analysis of Pucciniales within the Basidiomycota

Paulo OS[1], Vieira A[1,2], Talhinhas P[2], Silva DN[1,2], Azinheira H[2], Silva MC[2], Fernandez D[3], Duplessis S[4], Batista D[2]
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Summary statement:

A transcriptome-wide screening to infer the evolutionary relationships among the Pucciniales (rust fungi) within the Basidiomycota.

Abstract:

Rust fungi (Pucciniales) represent a large group of plant pathogens causing disease on a variety of host plants, including several important crops such as cereals, legumes, forest trees and coffee. The huge economic impact of these pathogens led to several studies that provide a wide range of information about their lifestyle, available namely in the form of EST databases. Several studies aiming to unravel the phylogenetic relationships between the rust species and other basidiomycota have already been performed, although they relied on a very limited number of loci. However, in molecular systematics, it is becoming increasingly accepted that one can only accurately infer evolutionary relationships between taxonomic groups when using a representative portion of the genome in such analyses. Thus the main goal of this study is to unveil the evolutionary relationships among rusts and other basidiomycota using an EST mining strategy to suppress high incongruencies and recover the most robust phylogeny. Moreover, this new approach could provide new insights on the phylogenetic relationships between the different taxonomic groups. Preliminary results suggest a clear divergent and monophyletic clade for the Pucciniales within the Basidiomycota, in which Hemileia seems to be the most ancestral lineage. We expect that this transcriptome-wide screening will contribute to a more complete view of the evolutionary relationships among these pathogenic fungi and the related taxa.

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WED 24 AUG at 1400 - Room N5
Oral presentation *D3-Ge09-1400-O*

General sessions
Evolution of sex

Hidden epistasis: The search for the function of sex and recombination

Peck JR[1]
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Summary statement:

Current experimental data are largely irrelevant to determining whether fitness landscapes favour the evolution of sex and recombination. More revealing experiments are suggested.

Abstract:

For the last several decades, experimentalists have been trying to understand how deleterious mutations combine together to affect fitness. This attention has been motivated by a desire to solve a variety of vexing evolutionary questions. For example, one possible type of interaction has been called "negative epistasis", and it occurs when deleterious mutations cause the greatest loss in fitness if they occur in genomes that are already "contaminated" with many other deleterious mutations. Negative epistasis is required for some of the leading hypotheses regarding the evolution of recombination, the evolution of sex, and a variety of other phenomena. However, the best-controlled experiments have not, in general, supported the idea that negative epistasis is common. Here, biologically-motivated "fitness landscapes" are considered that are more complex than those examined in most previous studies. (A fitness landscape describes the relationship between genotype and fitness.) The results show that, in some cases, a fitness landscape can produce a very strong advantage for sex and recombination even though, at equilibrium, experimental analysis is unlikely to find any trace of negative epistasis. Indeed, there are landscapes that strongly favour sex and recombination even though experimental study is likely to suggest that positive epistasis is common (positive epistasis means that deleterious mutations are most harmful in the least contaminated genomes). The results suggest what features a complex fitness landscape must have if it is to favour the evolution of sex and recombination, and experiments are proposed that could reveal whether such landscapes are common in nature.

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WED 24 AUG at 1420 - Room N3
Oral presentation *D3-Ge10-1420-O*

General sessions
Inbreeding

Effects of inbreeding and between-population hybridization on fitness of individuals and viability of populations

Pekkala N[1], Knott KE[1], Kotiaho JS[1], Puurtinen M[1]
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Summary statement:

Using experimental Drosophila littoralis populations of different sizes, we studied the effects of low to high levels of inbreeding and hybridization between isolated populations.

Abstract:

Our knowledge on the effects of different rates of inbreeding on population persistence is still insufficient in order to reliably predict the future of increasing number of plant and animal populations that are decreasing in size and becoming isolated from each other. Also, information about the consequences of increased gene flow between populations is urgently needed to make well-founded and accurate conservation decisions possible. I will present results from experimental studies of the short- and long-term effects of small population size and hybridization between isolated populations on the fitness of individuals and viability of populations. Replicated Drosophila littoralis populations were established in four different sizes (N2, N10, N40, and an outbred control). The effect of varying rate of inbreeding on offspring production and extinction risk of the isolated populations was measured. The long-term effects of between-population hybridization were studied by establishing hybrid populations from the isolated N10 populations at varying levels of inbreeding and measuring offspring production and extinction risk of the populations for seven generations after the hybridization event. Further, the effects of the level and the rate of inbreeding on drift load, inbreeding depression, and heterosis were studied by making controlled crosses outside the isolated populations and recording the fitness of the progeny (egg-to-adult survival and a measure of female reproductive output). The measures of genetic variation at 11 microsatellite loci give an additional estimate for inbreeding rate, to be compared with inbreeding rate estimated from population genetic theory.

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WED 24 AUG at 1420 - Room N2
Oral presentation *D3-Ge08-1420-O*

General sessions
Human impact

How interrupting antiretroviral treatment can lead to faster evolution of drug resistance in HIV

Pennings PS[1]
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Summary statement:

I show how interrupting treatment (and therefore selection pressure), can speed up evolution if the population grows and genetic variation can build up during the interruption.

Abstract:

Treatment interruptions lead to faster evolution of drug resistance, which is usually attributed to intermediate drug levels or effective monotherapy after stopping therapy. Using a stochastic model I show that treatment interruptions can lead to resistance in a different way, when they allow the viral population to grow. The growth of the population leads to the build-up of standing genetic variation on which selection can act when treatment is restarted. Analysis of published data shows that, indeed, longer interruptions lead to a higher risk of drug resistance. Data also show that the risk due to a long interruption is similar to the risk of starting therapy for the first time. Strategies to avoid the evolution of drug resistance are discussed.

In general, the model suggests that adaptation can be, under some circumstances, faster in a system with varying selection pressures than in a system with a constant selection pressure, if times of relaxed selection allow for population growth. These results can help us understand seemingly contradicting results, such as the observation that using more antibiotics generally leads to more resistance, whereas using more antiretrovirals generally leads to less resistance.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i095-R*

General sessions

Phylogeography and genetic differentiation along the distributional range of the orchid Epidendrum fulgens: a Neotropical coastal species not restricted to glacial refugia

Pinheiro F[1], Barros FD[2], Palma-Silva C[2], Fay MF[3], Lexer C[4], Cozzolino S[5]
[1]Instituto de Botanica, Nucleo de Pesquisa do Orquidario, Sao Paulo, Brazil, [2]Instituto de Botanica, Sao Paulo, Brazil, [3]Royal Botanic Gardens Kew, Jodrell Laboratory, London, United Kingdom, [4]University of Fribourg, Unit of Ecology and Evolution, Fribourg, Switzerland, [5]Università degli Studi di Napoli Federico II, Dipartimento di Biologia Strutturale e Funzionale, Napoli, Italy

Summary statement:

This study indicates the long-term persistence of a sand-dune orchid in regions where forest retraction and fragmentation were inferred for forest-dwelling species.

Abstract:

Phylogeographic studies in the Brazilian Atlantic Rainforest have only been conducted with forest-dwelling species, suggesting that a significant component of the evolutionary history of taxa associated to grassland and sand dune plant communities has hitherto been largely overlooked. This study examines the phylogeography of the orchid Epidendrum fulgens, in order to identify major genetic disjunctions across the range of the species and to investigate genetic signatures of past range contraction and expansion events. We used nine nuclear and four plastid microsatellite loci to genotype 424 individuals from 16 populations. We estimated genetic diversity and population differentiation, testing for a north-south gradient of genetic diversity. A haplotype network was inferred based on the plastid haplotypes. For nuclear markers, we used a Bayesian assignment analysis to infer population structure. Demographic changes were tested using a coalescent approach. The microsatellite data sets suggest a low level of population differentiation (GST = 0.097) and low inbreeding coefficient (f = 0.079). There was no significant evidence of phylogeographic structure in either nuclear and plastid markers. The results are consistent with the long-term persistence of E. fulgens in many regions where forest retraction and fragmentation were inferred for species associated with forest habitats. Bottlenecks were detected in populations from areas where population expansion events were also detected previously for other animals and plant species, suggesting that forest expansion after the LGM played a role in population fragmentation and decrease in genetic diversity in this species.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i042-E*

General sessions

The role of sexual and non-sexual selection in reducing mutational load in the Bulb mite (Rizoglyphus robini)

Plesnar A[1], Radwan J[2]
[1]Jagiellonian University, Institute of Environmental Sciences, Cracow, Poland, [2]Jagiellonian University, Cracow, Poland

Summary statement:

We tested a role of sexual and nonsexual selection in reducing mutation load
on irradiated males' progeny. Our result suggests greater role of fecundity than sexual selection.

Abstract:

It has been hypothesized that competition between males for mates decreases mutational load of the population more than do other components of natural selection. To test the role of sexual and ecological selection in purging the genome of deleterious mutations we conducted an experiment on the bulb mite (Rizoglyphus robini). The progeny (F1) of males irradiated with ionizing radiation was divided into three treatments. In sexual selection treatment five males competed for the access to five females. In fecundity selection treatment sexual competition between males was experimentally eliminated. However, female fecundity selection was present in both the above treatments, as sampling of progeny was proportional to female fecundity. In MCN treatment, both sexual competition and fecundity selection were eliminated by enforcing monogamy and sampling progeny irrespective of female's fecundity. Identical treatments with non-irradiated males' progeny were carried out as a control for maternal effects. Following the treatments, fecundity of females was assayed in the F2 generation. Difference in this fitness component between control and irradiation treatments was higher in MCN than in selection treatments, and nearly the same for SS+ and SS-. However, neither the effect of treatment nor irradiation*treatment interaction was significant. These preliminary results nevertheless suggest that sexual selection does not significantly increase the efficiency of natural selection in reducing mutational load.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i043-E*

General sessions

Ornamentation, condition, immunity and haematopoiesis in Scarlet rosefinch (Carpodacus erythrinus)

Poplová J[1], Albrecht T[1,2], Schnitzer J[1], Vinkler M[1,2]
[1]Charles University in Prague, Department of Zoology, Prague, Czech Republic, [2]Academy of Sciences of the Czech Republic, Institute of Vertebrate Biology, Brno, Czech Republic

Summary statement:

Proportion of immature erythrocytes among red blood cells is a condition-dependent trait in Scarlet rosefinch which might be associated with the individual metabolic rate.

Abstract:

Haematological methods form one of the most basic attitudes to the physiological state assessment in vertebrates. Besides plasma proteins also blood cells may provide important information on individual health, metabolism or stress. Current immunoecology and ecotoxicology utilise only few of these techniques among which the investigation of heterophil : lymphocyte ratio (H/L) is most common. Less widespread traits may, however, provide additional information on other aspects of individual physiology. It has been assumed that the proportion of immature developmental stages of erythrocytes may be indicative of haematopoiesis rate in birds. In this contribution we describe a novel and easy method for examination of immature erythrocytes' frequencies in avian blood. We report ornamental, immunological and other condition-dependent traits associated with the frequency of immature erythrocytes in peripheral blood in Scarlet rosefinch. Our results suggest that the immature erythrocytes count is a condition-dependent trait which may be associated with the individual metabolic rate. Nevertheless, this hypothesis requires further testing.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i044-E*

General sessions

Variation in phenotypic plasticity and selection for breeding time among blue tit populations

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Summary statement:

An assessment of the differences in the extent of phenotypic plasticity and the strenght of selection for breeding time in blue tits.

Abstract:

Wild organisms continually face spatio-temporal variation in resource abundance and abiotic conditions. An important mechanism allowing individuals to face these variations is phenotypic plasticity, or the ability of a genotype to change its phenotype across environmental conditions. Yet, despite the growing interest of evolutionary ecologists for the study of phenotypic plasticity, relatively little is known regarding the causal mechanisms of plasticity in life-history traits in the wild, and the extent of within-species variation in plasticity patterns. We compared phenotypic plasticity and selection for breeding time (egg-laying date) in four Mediterranean populations of blue tits (Cyanistes caeruleus) in heterogeneous habitats, using data collected from 1976-1998 to 2010. Timing of breeding is a key life-history trait strongly related to fitness in many animal species, and has been shown to be very sensitive to environmental conditions. Using a sliding-window approach, we determined which temperature window best explained variation in mean annual laying date in each population. We found significant individual level responses of laying date to temperature in every population, with females breeding earlier in warmer years. However, significant inter-individual variation in laying date plasticity was present in only two out of four populations. Interestingly, we found significant directional selection for earlier laying date only in populations where there was no inter-individual differences in plasticity. Our results show that considerable differences in phenotypic plasticity patterns can exist between populations of the same species, even at a small geographical scale.

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WED 24 AUG at 1400 - Room N3
Oral presentation *D3-Ge10-1400-O*

General sessions
Inbreeding

Combining marker and pedigree data to unravel the genetic architecture of inbreeding depression in a wild bird population

Postma E[1], Nietlisbach P[1], Camenisch G[1], Keller LF[1]
[1]University of Zurich, Institute of Evolutionary Biology and Environmental Studies, Zurich, Switzerland

Summary statement:

Using QTL linkage mapping, we infer the non-additive genetic architecture of fitness traits, providing a mechanistic understanding of inbreeding depression in the wild.

Abstract:

Despite a century of research on the genetic basis of inbreeding depression, i.e. the reduced fitness of individuals with related parents, the relative importance of the various underlying mechanisms continues to be debated. So despite its ubiquity, we still lack a truly mechanistic understanding of inbreeding depression, especially in natural populations. Here we present a unique dataset consisting of a combination of extensive pedigree, microsatellite and fitness data for a natural population of song sparrows (Melospiza melodia). Using quantitative trait locus (QTL) linkage mapping, we infer not only the (additive) genetic architecture of a number of fitness traits, but also the (non-additive) genetic architecture of inbreeding depression in these traits. In particular, we estimate the number of loci involved and the distribution of their effects, as well as the relative importance of dominance versus overdominance in shaping inbreeding depression. We compare our findings to those from inbred lab populations, and discuss the implications for our understanding of the evolutionary genetics of natural populations in general.

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MON 22 AUG at 1140 - Room N2
Oral presentation *B2-Ge01-1140-O*

General sessions
Behaviour

Temporal shifts in queen number in a socially polymorphic ant population

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Summary statement:

Since 2000, the frequency of ant colonies with multiple queens has increased through queen adoption and colony turnover in Valais, providing insight into factors favoring polygyny.

Abstract:

In social insects, the maintenance of colonies with multiple queens requires additional evolutionary explanations compared to single queen colonies where all workers are siblings. Positive selection favoring multiple queens is needed to counteract the cost of sharing reproduction and cooperating with more distant relatives or non-kin. For example, multiple queen colonies may be favored in risky or saturated environments, because young queens are able to join pre-existing colonies and new nests often form by budding off from established nests. We investigate a Formica selysi population that contains both single-queen (monogyne) and multiple-queen (polygyne) colonies. Ultimately, we seek to determine what factors favor each social structure and how these two forms co-occur in the same environment. In this study, we explore whether the social polymorphism is stable through time. To this end, we compare the genetic structure of colony members collected from marked nests from 2000 to 2010 at 11 polymorphic microsatellite loci in order to identify changes in social structure and in relatedness among colony members. In our population, monogyne colonies appear to be more likely to become polygyne than the reciprocal shift. The monogyne colonies gain queens either through queen adoption or colony turnover. Given the apparent lack of genetic differentiation between social forms shown in previous studies and the directional shift in queen number that we document here, we consider whether the hypotheses that have been proposed to explain polygyny in other species are applicable to F. selysi. We explore the potential role of habitat instability in maintaining this polymorphism.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i096-R*

General sessions

Experimental evidence for stabilizing selection on avian brood sex ratios

Radersma R[1], Ubels R[1], van der Velde M[1], Tinbergen JM[1], Komdeur J[1]
[1]University of Groningen, Centre for Ecological and Evolutionary Studies, Groningen, Netherlands

Summary statement:

Brood sex ratios at parity maximise parental fitness. This constrains facultative sex allocation and might preserve chromosomal sex determination.

Abstract:

While sex allocation theory is successful in predicting sex ratio variation in some taxa (e.g. haplodiploid insects), it poorly predicts sex ratio variation in birds and mammals. An important reason for this discrepancy may be that most models do not take the complex life-history of birds and mammals into account. To reveal the adaptive significance of sex allocation in birds and mammals, we conducted an experimental study on great tits (Parus major) in which we investigated the effect of manipulated brood sex ratios on long-term fitness benefits accrued to both male and female parents. Offspring raised in broods with equal sex ratios had higher fecundity than offspring raised in broods with extreme biased sex ratios. Since offspring recruitment, parental survival and parental fecundity were not affected by the brood sex ratio these results mean that there was stabilizing selection for an equal brood sex ratio. We argue that this effect can provide an explanation why sex allocation in birds and mammals is often subtle. Higher benefits for equal brood sex ratios counteract selection for facultative sex allocation and might play a role in the preservation of chromosomal sex determination in birds and mammals.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i045-E*

General sessions

Effects of ionizing radiation on mutation rates: a meta-analysis of Chernobyl studies

Randic S[1], Møller AP[1]
[1]Université Paris-Sud XI, Laboratoire Ecologie, Systématique et Evolution, Orsay Cedex, France

Summary statement:

A meta-analysis examining impact of radiation on mutation rates across a taxa, using data from Chernobyl, revealed a surprisingly large mean effect size.

Abstract:

Mutation is the cause of novel genetic variation, but most mutations are deleterious, so selection has led to systems that are buffered against mutation via proofreading and repair mechanisms. Mutation rates differ widely among even closely related taxa, and it remains unclear why species differ in their resistance to environmental mutagens, such as radiation. Numerous studies have examined the consequences of radioactive fallout resulting from the Chernobyl disaster. Surprisingly, there are no quantitative meta-analyses attempting to summarize the entire literature. Therefore, our goal was to analyze data from a large number of available studies, and use a meta-analytical quantitative approach to examine the relationship between radiation and mutation rates. 48 published studies were included in the analysis. The results of all reported statistical tests were converted to z-transformed correlation coefficients (Zr). We found a very large overall effect size of radiation on mutation rates (E=0.804, 95% CI: 0.677 to 0.932), accounting for 64% of the total variance. The fail-safe calculations (Rosenthal's method: 8412.8 at P=0.05; Orwin's method: 450.1 at En = 0.2) show the robustness of this finding. The effect of radiation varied among taxa, but effect size did not depend on radiation intensity. The surprisingly high effect size suggests the possibility of a strong impact of radioactive contamination on individual fitness, as well as potentially significant population-level consequences, even beyond the area contaminated with radioactive material. Furthermore, our study affirms that there doesn't seem to be a threshold effect when it comes to impact of ionizing radiation.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i097-R*

General sessions

No simple relationship between male mating attraction and parental care: an example in a fish with exclusive male care

Rasotto MB[1], Pizzolon M[1], Locatello L[1]
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Summary statement:

Analysis of the interplay among male attraction traits, parental effort, fertility and health status in the peacock blenny, Salaria pavo.

Abstract:

Recent theoretical models posit that, in species with exclusive male care, male attractiveness reliably indicates paternal care effort and may also signal male quality. Here we perform a comprehensive analysis of the interplay among male mating attraction and parental care but also fertility and health status in a blenny species, Salaria pavo. In this fish, males are larger than females, exhibit two sexually dimorphic traits (head crest and anal glands) and solely care for eggs. We recorded parental behaviours (fanning, cleaning, and spreading of antimicrobials on eggs) in the field, and in the lab we measured sperm number, viability, and velocity as proxies of fertility, and nitric oxide concentration as a proxy of stress level. We generated a male attractiveness index through principal component analysis of morphological traits and quantifed parental care effort as the total time spent in egg fanning, cleaning and rubbing. We found that male attractiveness is a reliable indicator of fertility, in terms of sperm number, but is unrelated to stress level and parental care effort, with males able to perform high levels of care regardless of their level of advertisement. However, a single male trait involved in mating attraction, the head crest, appears to be traded-off with parental care investment. If females base their evaluation of prospective mates exclusively on head crest expression (in this species males often protrude only their head at the nest entrance), they may be faced with conflicting information on male qualities.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i098-R*

General sessions

Phenotypic plasticity and local adaptation in a multiple predator environment

Reger J[1], Robinson M[1], Slate J[1], Beckerman A[1]
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Summary statement:

We use a novel statistical approach to show that plasticity of the G matrix differs between Daphnia populations that have been subject to long histories of contrasting predation.

Abstract:

Evaluating the impact of environmental heterogeneity on evolutionary processes is important to understand how organisms adapt to variable environments. While we know that phenotypic plasticity allows organisms to respond to fluctuating environments, we have a limited understanding of its genetic basis and its role in local adaptation. Here we focus on Daphnia pulex and their vertebrate and invertebrate predators. Specifically, we are interested in genetic and phenotypic responses of D. pulex to chemical signals from each predator in a multivariate set of behavioural, life historical and morphological traits during development. We present results from Bayesian Markov chain Monte Carlo multivariate mixed models combined with eigenvector analyses, which provide novel insight into the adaptive value of predator induced phenotypic plasticity by detailing genetic relationships among traits across different predation treatments. We show that the plasticity of the G matrix differs between natural populations that have been subject to long histories of contrasting predation regimes. By combining these results with findings from a QST – FST analysis, we are able to infer that diversifying selection drives G matrix differentiation between Daphnia populations from different predation backgrounds. Our results suggest that G matrix plasticity may play a major role in local adaptation.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i041-R*

General sessions

UV and long wavelengths aid visual foraging in a fish

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Summary statement:

Very short (UV) and long wavelengths (´red´) are of relative importance in visual foraging in three-spined sticklebacks (Gasterosteus aculeatus).

Abstract:

Visual signalling can be affected by both the intensity and spectral distribution of environmental light. In shallow aquatic habitats the spectral range available for visually mediated behaviours such as foraging can reach from ultraviolet (UV) to long wavelengths in the human-visible range. However, the relative importance of different wavebands in foraging behaviour is generally unknown. Here, we test how the spectral composition of ambient light influences behaviour of three-spined sticklebacks (Gasterosteus aculeatus) when foraging for live cladoceran Daphnia magna. While paying particular attention to the UV we measured foraging preferences of sticklebacks for prey presented under four different spectral conditions. These conditions selectively blocked one part of the stickleback visible spectrum corresponding to the sensitivity of the four retinal cones. The removal of UV and long wavelengths strongly reduced prey attractiveness for G. aculeatus compared to conditions without short and medium wavelengths suggesting that very short (UV) and long (’red’) wavelengths are of particular importance in a foraging context. The effects are also mirrored in chromatic contrast values between prey and the experimental background as calculated for each lighting condition using a physiological model of stickleback perception.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i099-R*

General sessions

Bet-hedging as a strategy, and as a game

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Summary statement:

We demonstrate the possible simultaneous evolution of risk avoiding, diversified and coin-flipping strategies. The inevitable frequency dependence of bet-hedging is discussed.

Abstract:

Bet-hedging theory addresses how individuals should optimize fitness in varying and unpredictable environments by sacrificing mean fitness to decrease variation in fitness. So far, three main bet-hedging strategies have been described: conservative bet-hedging (play it safe), diversified bet-hedging (don't put all eggs in one basket) and adaptive coin-flipping (choose a strategy at random from a fixed distribution). The possible evolution of adaptive coin-flipping implies that phenotypic variation within a population, often assumed to be due to non-adaptive variation, instead can be a result of individuals 'choosing' phenotypes at random.

Within this context, we have modeled the trade-off between many small eggs (or seeds) and few large, given an unpredictable environment. In our individual based model a combination of all three bet-hedging strategies evolves, which means a relatively large mean egg size, but variation both within clutches and between years.

We also discuss the definition of bet-hedging strategies, in particular their frequency dependence. Given density and frequency dependent selection, the very same strategy can be considered 'bet-hedging' in some circumstances, and not in others, all depending on what other strategies occur in the same population.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i100-R*

General sessions

The influence of spermatophore consumption on paternity outcome in the two-spot ladybird beetle Adalia bipunctata

Rödenbeck I[1,2], Perry J[2,3], Rowe L[2]
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Summary statement:

We investigated if spermatophore consumption by females in the ladybird A. bipunctata has an effect on paternity after double mating. First male paternity was highly heterogeneous.

Abstract:

This study tests whether spermatophore consumption has an influence on paternity outcome in the two-spot ladybird beetle Adalia bipunctata. In several insect species, the reproductive behaviour of females can be influenced by nuptial gifts. In A. bipunctata, males give females a spermatophore during mating. After mating, the female ejects the spermatophore and it is consumed. To determine the effect of the spermatophore on paternity, females were mated twice. A melanic male was used as a marker for paternity. In different treatments, females were allowed or prevented from consuming the spermatophore. Paternity was determined by looking at the phenotype of the offspring. The paternity of the first male was highly heterogeneous, and no difference between the different treatments was detected. These results imply that the spermatophore has no direct impact on paternity, but leaves room to speculate about other possible roles of the spermatophore in A bipunctata.

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SUN 21 AUG at 1120 - Room N3
Oral presentation *A2-Ge02-1120-O*

General sessions
Life-history

The effect of drift and selection on life-history traits among managed and natural populations of sea trout Salmo trutta

Rogell B[1], Dannewitz J[1], Palm S[1], Petersson E[2], Laurila A[1]
[1]Uppsala University, Population Biology, Uppsala, Sweden, [2]Uppsala University, Animal ecology, Uppsala, Sweden

Summary statement:

Evidence for local adaptations in life-history traits across managed and natural populations of sea trout.

Abstract:

Several endangered or economically important populations are today managed by ex-situ rearing. If the ex-situ rearing conditions induces specific adaptations, this management strategy may be sub-optimal or even harmful for the part of the population facing native selection pressures. Few studies have examined the environmental dependency of local adaptation across rearing conditions (ex-situ vs. natural conditions), and local adaptations in plastic responses across rearing conditions. In Sweden the sea trout (Salmo trutta) is managed by rearing parts of the populations in hatchery between the egg and the smolting stage, that is released into the stream. Here we employ a QST-FST approach to investigate local adaptations in survival until, and size at, the smolting stage across managed and unmanaged populations of the sea trout. A common garden experiment with two rearing environments was used: a hatchery setting and a close to natural experimental stream. We found evidence for local adaptations in survival and size (with the exception of survival in the second year) in both years and rearing environments with the managed populations having a larger probability for survival and a larger size. There were weak differences in QST across the rearing environments and proof for local adaptation in the plastic response across the rearing environments in size the first year. The results indicate that different management strategies may induce local adaptations in life history traits.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i101-R*

General sessions

Temporal variability of genetic diversity of Finnish wolf population during the last 150 years

Roininen E[1], Ruokonen M[1], Aspi J[1]
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Summary statement:

We present our results of temporal genetic variability of Finnish wolf population during the last 150 years based on analyses of 113 museum samples.

Abstract:

Reconstruction of population history based solely on modern genetic data is often skewed reflecting recent or extreme events. With the development of novel laboratory techniques and analytical methods, museum specimens have become an important tool for conservation genetics as they enable direct comparison of population structure and genetic diversity between historical and present-day populations.

Extensive hunting led to almost complete eradication of the Finnish wolf population by the end of 19th century. After over 100 years of low population size and consequential bottlenecks and with at least 23,000 wolves killed, more stringent management actions together with immigration from neighboring large Russian population contributed to population growth and wolves started to regularly reproduce in Finland in 1995. Today, population is considered as endangered and consists of approximately 140 individuals. Excessive hunting is still a serious threat as population has almost halved during a last couple of years.

For this study 113 historical wolf samples (mostly teeth) from 1854 to 1993 were collected from zoological museums in Finland and studied with genetic markers (mtDNA and microsatellites). Contemporary Finnish wolf samples (N = 298, 1995 - 2009) collected after the permanent re-establishment of the population were used as a reference in this study. We will present our results from genetic analyses of this data during the congress.

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MON 22 AUG at 1120 - Room N6
Oral presentation *B2-Ge05-1120-O*

General sessions
Disease and immunity

Bateman´s principle and immunity in a sex-role reversed pipefish

Roth O[1], Scharsack JP[2], Keller I[1], Reusch TBH[1]
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[2]Westfaelische Wilhelms University Münster, Münster, Germany

Summary statement:

In sex-role reversed pipefish males have a stronger and more specific immune defence than females- this suggests sexual immune dimorphism to depend directly on life-history strategy.

Abstract:

In diverse animal species, from insects to mammals, females have a more efficient immune defence than males. Bateman´s principle posits that males maximize their fitness by increasing mating frequency whilst females gain fitness benefits by maximizing their lifespan, which requires a more efficient immune system. Because in most extant animals, provisioning of eggs and higher parental investment are correlated within the female, sex-role reversed species are required to demonstrate that immune dimorphism depends on life-history and not on sex per se. In the broad-nosed pipefish Syngnathus typhle, males brood the eggs in a paternal brood pouch and thus, invest more into reproduction than females. Concordant to an extension of Bateman's principle, we found males to have a more active immune response both in field data from four populations, and also in an experiment under controlled laboratory conditions. This applied to four different measures of immunocompetence, using parameters of the innate as well as from the adaptive immune system. We further determined the specificity of mounting immune responses after a fully factorial primary and secondary exposure to a common marine pathogen Vibrio spp. Here, we found males to not only have a more active but even a more specific immune defence than females.

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SUN 21 AUG at 1200 - Room N5
Oral presentation *A2-Ge06-1200-O*

General sessions
Development

Natural modifiers of hybrid necrosis in Arabidopsis thaliana

Rowan BA[1], Bomblies K[1,2], Schneeberger K[1,3], Ossowski S[1,4], Lanz C[1], Weigel D[1]
[1]Max Planck Institute for Developmental Biology, Molecular Biology, Tuebingen, Germany, [2]Harvard University, Organismal and Evolutionary Biology, Cambridge, United States, [3]Max Planck Institute for Plant Breeding Research, Plant Developmental Biology, Cologne, Germany, [4]Center for Genomic Regulation, Barcelona, Spain

Summary statement:

Three-way epistasis modulates aberrant immune responses associated with genetic incompatibilities.

Abstract:

The maintenance of allelic diversity at loci encoding components of the non-self recognition system is expected to be evolutionarily favorable because it allows individuals within a species to recognize and defend themselves against a broad range of pathogens. However, such diversity can also inadvertently lead to the formation of reproductive barriers, as was observed for an intraspecific cross between the Uk-1 and Uk-3 accessions of Arabidopsis thaliana. The F1 hybrid progeny exhibited a constitutively active pathogen defense response that led to reproductive failure during growth at the ecologically relevant temperature of 16°C. This incompatibility, known as hybrid necrosis, was due to an epistatic interaction between two loci associated with the pathogen defense response, suggesting that diversification of pathogen recognition loci could result in the restriction of gene flow among individuals within a species. This restriction could be reinforced or overcome, however, by the presence of alleles at additional loci that enhance or suppress deleterious hybrid phenotypes. Here, we report that the Er-0, Hl-0, Dr-0, and Is-0 accessions of A. thaliana carry dominant suppressors of the Uk-1/Uk-3 hybrid necrosis, while dominant enhancers are carried by the Bur-0 and Jl-2 accessions. Using high-throughput sequencing of pooled individuals with a complex genetic make-up, we mapped the Er-0 suppressor to a roughly 500-kb interval on chromosome 5. Ongoing work towards identifying the genes that modify hybrid necrosis will provide insight into the evolutionary forces that lead to reproductive isolation and may uncover novel components of the plant defense response mechanism.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i102-R*

General sessions

Sperm evolution in passerine birds

Rowe M[1], Laskemoen T[1], Kleven O[1], Johnsen A[1], Rudolfsen G[2], Lifjeld JT[1]
[1]University of Oslo, Natural History Museum, Oslo, Norway, [2]Norwegian Radiation Protection Authority, The Polar Environmental Center, Department for Environmental Radioactivity, Tromsø, Norway

Summary statement:

We examine the evolutionary consequences of sperm competition for sperm phenotype and show how selection may have shaped contemporary variability in sperm size and performance.

Abstract:

Despite their common role as fertilisers of ova, sperm cells exhibit considerable interspecific variability in size, structure and performance. Recent studies suggest that sperm competition is an important driver of evolutionary change in sperm traits. Under conditions of sperm competition, longer, faster and longer-lived sperm are expected to gain a greater share of fertilisation success; though whether selection acts on multiple traits or generates trade-offs between traits is unclear. For species with internal fertilisation and prolonged sperm storage, theory predicts that sperm competition will promote long-lived, fast sperm. Alternatively, there may be a trade-off between longevity and speed if fast sperm utilise energy reserves more quickly without compensatory increases in energy production. We used data from 73 passerine species to examine the effects of sperm competition and sperm storage duration on multiple ejaculate traits: sperm size, velocity and longevity. We found that species experiencing higher levels of sperm competition had longer and faster sperm, but not longer-lived sperm. Moreover, we found that sperm velocity was positively correlated with sperm size, implying a functional relationship between these traits. In addition, our data show that sperm velocity and longevity are positively correlated, but that species with a longer duration of sperm storage have slower and shorter-lived sperm. Finally, using ancestral state reconstruction to determine the likelihood of directional evolution in sperm traits, we show how selection may have acted over evolutionary time to shape contemporary interspecific variation in sperm phenotype.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i047-E*

General sessions

Constraint and adaptation: incomplete loss of a family-level diagnostic trait in Arabidopsis thaliana

Royer A[1], Conner JK[1], Schemske D[1]
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Summary statement:

In Arabidopsis thaliana, production of non-functioning short stamens is variable; adaptive loss may be constrained by low genetic diversity and the trait’s complex genetic basis.

Abstract:

Despite three decades of interest starting with Gould and Lewontin´s Spandrels paper, our mechanistic understanding of constraints on adaptive evolution remains poor. These mechanisms are important for describing patterns of past evolution as well as predicting future change. Conserved traits are excellent systems for studying the mechanisms of constraint.
Tetradynamy, the presence of four long and two short stamens within a flower, is highly conserved in the mustard family, but has no known function. Existing adaptive hypotheses address how it may increase pollen export by pollinators, but cannot explain its maintenance in self-pollinating species.
In the highly selfing Arabidopsis thaliana, we performed stamen removal experiments showing that short stamens do not contribute to seed set, so there should be selection to eliminate them. We then grew 46 populations from latitudinal and longitudinal transects of the native range in a common environment, and found short stamen loss is widespread and increases at lower latitudes. Ovule counts across populations are negatively correlated with stamen number, providing further evidence for selection against short stamen production.
The results of a QTL analysis suggest that a complex genetic architecture combined with a lack of outcrossing may be slowing the loss of short stamens in A. thaliana. In the north, this constraint is likely magnified by the well-documented decrease in genetic diversity due to bottleneck events during post-glaciation recolonization. Insight into genetic mechanisms of constraint on adaptive evolution can help us understand both the history of life and modern challenges to natural populations.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i048-E*

General sessions

Persistence of biased sex ratios in widely distributed dioecious plant Mercurialis perennis

Rubinjoni L[1], Jovanović V[2], Cvetković D[1]
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Summary statement:

Sex ratios remain significantly biased in majority of analysed populations of M. perennis, but the direction of bias changed only in high altitude populations.

Abstract:

In dioecious plants, variation in sex ratios (SR) is the issue of special interest. Our recent research on Mercurialis perennis L., a dioecious anemophilous species, revealed significantly biased SR in populations occupying wide altitudinal range. The direction of bias was correlated with altitude – lowland populations were male biased, while in montane populations females tended to prevail.
The aim of this study was to explore the persistence of deviations from the unity sex ratio, both in terms of direction and extent. During period 2006–2010, we investigated populations of M. perennis in Serbia, from a wide variety of altitudes and habitats. Interannual patterns of variation in SR (expressed as percent of males), as well as in sexual size dimorphism (SSD) were analysed in 9 populations for which data was available for minimum 4 consecutive years.
In the analysed period, significant deviations from unity SR were found in majority (67%-87%) of populations. The bias was more pronounced in lowland populations. Although it tended to decrease with time, SR in all lowland populations (< 500m asl) remained significantly male biased. Montane populations showed more interannual variation, but most prominent changes in the direction of bias were found only in high altitude populations occupying exposed grasslands. All populations exhibited moderate values of male-biased SSD in height (the only exception was the highest-altitude population) and a decreasing trend in SSD values with time.
Conclusion: In the analysed period, SR remained significantly biased in majority of analysed populations, but the direction of bias changed only in high altitude populations on exposed grasslands.

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MON 22 AUG at 1100 - Room N7
Oral presentation *B2-Ge04-1100-O*

General sessions
Evolutionary genetics

Evolution of de-novo overlapping genes

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Summary statement:

Evolutionary analysis of genes, which originated de-novo, embedded within an existing gene, in an overlapping reading-frame.

Abstract:

How does a new gene originate and evolve? Numerous efforts have been made to search and characterize molecular mechanisms by which new genes could originate. So far, most of the detected new genes were found to originate through mechanisms that involve modifications of existing genes, such as gene duplication, gene fusion, or incorporation of a non-coding sequence (e.g., mobile elements). Consequently, very little is known about de-novo origin of genes, the case where a completely new gene originated. Unlike cellular organisms, on which most of the studies of new genes have focused, the genomes of viruses contain high number of genes, which originated de-novo, embedded within an existing gene, in an overlapping reading-frame. We reconstruct the ancestral sequences of de-novo overlapping genes to examine the rate of adaptation during the evolution of new genes.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i103-R*

General sessions

Interactions and coevolution in co-infecting viral species of wild cucurbits

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[1]Pennsylvania State University, Entomology Department, State College, United States, [2]Université Paris Sud XI, Laboratoire Ecologie, Systematique et Evolution, Orsay, France

Summary statement:

We investigated how two viruses frequently co-infecting host plants interact for their aphid transmission and what coevolutionary processes might be involved in their association.

Abstract:

Parasites, like their hosts, interact with the community of species that share the same habitat. Co-infection of a single host by multiple parasite strains or species thus raises questions about how interactions among them may alter the phenotype of the co-infected host and the transmission of the parasite competitors. Two potyviruses, Zucchini Yellow Mosaic Virus (ZYMV) and Watermelon Mosaic Virus -2 (WMV-2), commonly infect wild and cultivated cucurbits and can be frequently found co-infecting the same host plant in many locations—they also share similar host exploitation strategies and are vectored by the same aphids. Thus, we expect that they are under selective pressure to outcompete one another, which may yield coevolutionary dynamics similar to those observed between parasites and their hosts. A hypothesis arising from this expectation is virus strains that frequently co-infect the same hosts should be better adapted to their matched local competitor than to other less-frequently encountered strains. In order to test this hypothesis, we collected strains from singly- and co-infected host populations, and studied how pairs of virus species from "local" vs. "distant" associations performed on squash hosts. As these two viruses are transmitted by an overlapping range of aphid species, we also compared the attractiveness of singly- vs. co-infected plants to aphid vectors, their suitability for aphid colony establishment and growth, and the success of aphid transmission for each parasite species relative to the competitor.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i104-R*

General sessions

Costs of plastic responses to a changing social situation in a simultaneous hermaphrodite

Sandner P[1], Vizoso DB[1], Schärer L[1]
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Summary statement:

We report significant but small production costs of plastic responses to fluctuating social group size, and we discuss their impact on the evolution of phenotypic plasticity.

Abstract:

The ability of individuals to adjust their sex allocation in a phenotypically plastic way to fluctuations in the current environmental conditions – such as the level of sperm competition – has been proposed as an important advantage of simultaneous hermaphroditism over gonochorism (separate sexes). However, this argument only holds if the possible benefits of such plasticity are not countered by equivalent costs. The simultaneously hermaphroditic flatworm Macrostomum lignano can plastically adjust its sex allocation – measured as testis size over the sum of testis size and ovary size – to its current social group size. Here, we experimentally test for production costs (but not maintenance costs) of phenotypic plasticity by exposing individuals to repeated changes in social group size (i.e., alternating between pairs and octets), or to a constant social group size (i.e., either stable pairs or stable octets). We used hatchling production as a fitness-proxy and found a significantly lower hatchling production in the alternating compared to the stable treatment, suggesting costs of adjustments to the social environment. We suggest that these costs may derive from modulation of gonad activity and/or gonad size, and that they also include a time-lag of phenotype-environment mismatch when facing a new social situation. Moreover, as predicted by sex allocation theory for simultaneous hermaphrodites, hatchling production was highly significantly lower in stable octets than in stable pairs, while the observed costs of plasticity were comparatively small. We discuss the implications of this result for the evolution of plasticity in this free-living flatworm.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i105-R*

General sessions

Colonisation and diversification of the endemic Monomorium ants on the Canary Islands

Savolainen R[1], Vepsäläinen K[1], Espadaler X[2]
[1]Department of Biosciences, University of Helsinki, Finland, [2]C.R.E.A.F., Autonomous University of Barcelona, Bellaterra, Spain

Summary statement:

A phylogenetic–phylogeographic analysis suggests that Tenerife, the largest island in the middle of the archipelago, was the source of colonisations to the other islands.

Abstract:

The Canary Island archipelago lies in the Atlantic Ocean, ca. 110 km west of Africa, and includes seven major islands. All islands were formed in the past 20 million years by volcanic eruptions, the youngest island being only one million years old. The archipelago is rich in endemics, including five apterous species of the ant genus Monomorium of which only one species is found on each island. We investigated the evolutionary history of the Monomorium endemics in a phylogenetic–phylogeographic analysis, sampling all species from the seven islands, in total 31 samples. We sequenced mitochondrial and nuclear genes and analysed the data with Bayesian phylogenetic inference. Preliminary results suggest that colonisation of Monomorium did not follow a simple stepping-stone model from older islands in the east to younger islands in the west. Instead, Tenerife, the largest island of ca. 11 million years in the middle of the archipelago, seems to have been the source of colonisations to the other islands. We will discuss our results and a likely scenario for colonisation and diversification of Monomorium on the Canary Islands in the light of available geological and biogeographic information.

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SUN 21 AUG at 1200 - Room N2
Oral presentation *A2-Ge01-1200-O*

General sessions
Behaviour

Neighbors reduce the cost of predation deterrence by public information in a colonial breeding cichlid, Neolamprologus caudopunctatus

Schädelin FC[1], Fischer S[2], Wagner RH[3]
[1]University of Vetrinary Medicine Vienna, Intergrative Biology and Evolution, Vienna, Austria, [2]University of Bern, Behavioural ecology, Bern, Switzerland, [3]University of Vetrinary Medicine Vienna, Integrative Biology and Evolution, Vienna, Austria

Summary statement:

The colonial cichlid Neolamprologus caudopunctatus choose to breed near conspecific neighbours by public information and thereby benefits from a reduced investment in nest defence.

Abstract:

Although colonies are a widespread phenomenon amongst animals, evolutionary causes for colony formation are still controversial. Many bird species are colonial despite negative crowding effects such as higher competition and an increased pathogen transmission rate. For fishes, it is generally assumed that ecological constraints lead to breeding aggregations without further examination. However, we show in this study that public information on conspecific behaviour may be the main determinant in colony formation. In our first experiment with our model species Neolamprologus caudopunctatus, a monogamous, biparental cichlid from Lake Tanganyika, we found that they choose to breed near conspecific neighbours. We show that these new neighbours thereby benefit from a reduced investment in nest defence which is complemented by their neighbour's defence activities. In our second experiment, we investigate in how far public information on conspecific nest defence activity determines aggregation preferences. We can conclude that settling near another breeding pair may evolve even if communal group defense or mobbing recruitment is not observed, as the selfish nest defense of neighbors allows a reduction in nest defense investment while keeping the predator threat constant.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i106-R*

General sessions

Hydra – a “simple” animal?

Schaible R[1], Kramer BH[1], Ringelhan F[1]
[1]Max Planck Institute for Demographic Research, Rostock, Germany

Summary statement:

Hydra shows no senescence, providing the unique opportunity to gain insights into the role that tradeoffs play in shaping age specific life histories.

Abstract:

Hydra presents an interesting deviation from typical life-histories: It appears to show no senescence, providing an outstanding opportunity to gain insights into the role that trade-offs may play in shaping age-specific life-histories.

In order to disentangle the evolutionary processes that could be responsible for the lack of senescence in Hydra, we conducted a series of experiments to tease apart the influences of stochastic events and environmental and genetic effects on life-history traits.

A first set of laboratory experiments involved keeping individuals of Hydra polyps in identical and constant environments to investigate asexual reproduction and age at first reproduction of isogenic polyps in the course of time and among several asexuals generations. We observed a high phenotypic plasticity in the reproductive traits among isogenic Hydra..Thus, stochasticity seems to be an important variable for Hydra’s fitness. We assume that this plasticity is adaptive as a bet-hedging strategy to unpredictable environmental changes.

A second set of experiments investigated how trade-offs between reproduction and maintenance are modified under environmental stresses. The results of the study show that asexual reproduction and maintenance of Hydra depends on fluctuation in environmental conditions and can increase simultaneously in both components of fitness, asexual reproduction and maintenance. We propose that this non-trade-off effect is related to a hormetic stress response, resulting in an increase in organismic efficiency.

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MON 22 AUG at 1140 - Room N3
Oral presentation *B2-Ge02-1140-O*

General sessions
Life-history

Phenotypic engineering of sperm-production rate supports evolutionary predictions for fitness returns of male reproductive allocation

Schärer L[1], Sekii K[1], Vizoso DB[1], Kuales G[2], de Mulder K[2,3], Arbore R[1], Beisel C[4], Berezikov E[3], Ladurner P[2]

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Summary statement:

Dosage-dependent RNAi allows experimental manipulation of sperm-production rate in a flatworm, leading to predicted variation in paternity success

Abstract:

Male reproductive allocation towards sperm production is a key parameter in many models of sexual selection and sex allocation. However, in animals it is notoriously difficult to manipulate, because it represents an internal allocation decision. Here we experimentally manipulated sperm-production rate in the free-living flatworm Macrostomum lignano. We used RNA interference (RNAi) by soaking worms in a solution of double-stranded RNA (dsRNA) of a testis-specific gene (macbol1). Specifically, we took advantage of a dsRNA-dosage-dependent RNAi response to quantitatively manipulate sperm-production rate via a more or less leaky male-sterility phenotype. Using this approach we provide support for two key predictions of sex allocation theory for simultaneous hermaphrodites:
1) that competitive fertilization success scales positively with male allocation to sperm production, and
2) that under low levels of sperm competition this relationship shows diminishing returns.
This, to our knowledge, is the first study to use phenotypic engineering to test predictions from sperm competition theory. Finally, we report on an ongoing transcriptome-profiling (RNAseq) project that aims at identifying other target genes, which should allow manipulating other important reproductive traits, thus clearly documenting the striking versatility of this emerging model organism for sexual selection research.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i049-E*

General sessions

Sex allocation adjustment in lab vs wild simultaneous hermaphrodites

Schleicherova D[1], Lorenzi MC[1], Sella G[1]
[1]University of Turin, Department of Animal and Human Biology, Torino, Italy

Summary statement:

Long-term lab-rearing in hermaphrodites does not change the ability to adjust sex allocation as a function of mating regimes.

Abstract:

Sex allocation theory predicts that simultaneous hermaphrodites share reproductive resources between the two sexual functions and adjust the proportions of resources allocated to each sex as a function of the mating regime. According to Charnov, in monogamous regimes, hermaphrodites increase their investment in eggs and limit the male function. In contrast, in promiscuous regimes hermaphrodites increase their male function at the expense of egg production to face competition for the male role. Empirical studies in a small hermaphroditic polychaete worm Ophryotrocha diadema supported Charnov's theory: hermaphrodites reared in promiscuity produced significantly fewer cocoons and exhibited more "male" aggressive behaviours than hermaphrodites reared in monogamy. This opens the question that results obtained may be due to selective pressures specific to the lab. For example, in the lab worms are kept mostly in large masses and occasionally breed in pairs. Therefore they have usually high and occasionally low mating opportunities. These fluctuations may have favoured a high plasticity in sex allocation which may be absent in wild populations. Therefore, in the present study we compare sex allocation in lab and wild strain under high and low mating opportunities. Our results revealed that there was no difference between strains in sex allocation adjustments. Both strains changed their allocation to the female function decreasing it under high mating opportunities and increasing it under low mating opportunities. These results suggest that lab conditions have not altered sex allocation plasticity of wild hermaphroditic populations.

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SUN 21 AUG at 1200 - Room N6
Oral presentation *A2-Ge05-1200-O*

General sessions
Disease and immunity

Genome-wide inference of transposon distribution in natural Drosophila melanogaster populations

Schlötterer C[1], Kofler R[1], Nolte V[1], Betancourt A[1]
[1]Vetmeduni Vienna, Institut für Populationsgenetik, Wien, Austria

Summary statement:

A novel approach based on Pool-Seq to infer TE frequencies in natural populations

Abstract:

With the increasing popularity of the new sequencing technologies it has become possible to infer genome-wide patterns on a population scale. For transposable elements various approaches have been introduced that describe the distribution of TEs annotated in a reference genome in population samples. Here, we introduce the first method that permits the inference of TE population frequencies independent of their presence in the reference genome. Using pair-end Illumina reads from a cosmopolitan D. melanogaster population we will highlight differences between TE families and discuss how the distribution of TEs is shaped by positive and purifying selection.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i107-R*

General sessions

Breeding system and evolutionary history: a success story of Arabidopsis thaliana´s wild relatives

Schmickl R[1], Koch MA[1]
[1]Centre for Orgamismal Studies Heidelberg (COS Heidelberg), Biodiversity and Plant Systematics, Heidelberg, Germany

Summary statement:

Both widespread and endemic Arabidopsis species exhibit a sporophytic self-incompatibility system by the majority.

Abstract:

To be a selfer or not is a crucial aspect for the present and future dynamics of plant populations. The breeding system affects the adaptive potential of a plant species because of its influence on effective population sizes, levels of heterozygosity, and cohesive gene flow. The evolution of the breeding system in concert with life-history traits plays an important role in a species´ fate to become widely distributed or endemic. In this study we used population genetics, based on nuclear microsatellites and cpDNA sequence data, to unravel the evolutionary history of wild populations within the genus Arabidopsis. We studied populations from all the three main and widespread species lineages (A. arenosa, A. halleri, A. lyrata) inclusive numerous, more local subspecies of these lineages. Additionally, results from two narrow endemics (A. cebennensis, A. pedemontana) were included here for the first time. Besides parameters of population genetics, selfing and artificial crossing experiments contributed to demonstrate functional sporophytic self-incompatibility in the majority of analysed populations.

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SUN 21 AUG at 1100 - Room N6
Oral presentation *A2-Ge05-1100-O*

General sessions
Disease and immunity

Excessive polymorphism: How can the trypanosome Crithidia bombi persist in its host populations (Bombus spp.)?

Schmid-Hempel P[1], Tognazzo M[2], Schmid-Hempel R[2]
[1]ETH Zürich, Institute of Integrative Biology (IBZ), Zürich, Switzerland, [2]ETH Zürich, Zürich, Switzerland

Summary statement:

The trypanosome, C. bombi, has a host escape strategy as it frequently undergoes genetic exchange in co-infections and shows excessive polymorphism.

Abstract:

C. bombi infects its bumblebee hosts regularly and at high prevalences. Infections are characterized by an unusually strong specificity. In fact, each host colony contains its own, distinct ´cocktail´ of infections. Trypanosomes are generally considered to be clonal, but the same parasite genotype of C. bombi is rarely recovered in a population and less so across years. The question is therefore how this parasite can persist in its host populations? We have studied this problem for a number of years. The data now show that C. bombi has excessive strain variation in field populations of its hosts. This pattern suggests a highly dynamic host-parasite interaction at the epidemiological and evolutionary level. We present experimental evidence to show that genetic exchange among strains underlies this high degree of diversity. C. bombi is unusual in this respect as genetic exchange seems frequent and also leads to the emergence of completely novel types. The findings converge to a comprehensive picture of how this host-parasite system functions in the wild. We will also compare the escape strategies of C. bombi with those of the better known African trypanosomes.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i108-R*

General sessions

Anti-malarial drug resistance in P. falciparum vs. P. vivax

Schneider KA[1]
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Summary statement:

A comparison between the evolution of drug-resistance in P. falciparum and P. vivax (the clinically most important types of human malaria).

Abstract:

Aims: Malaria is among the most devastating human diseases, and it is still a threat to the public health in large areas of the developing world. Malaria control is highly dependent on the use of drugs, which clear out parasites in infected hosts. However, many important drugs have been rendered useless because parasites evolved resistance against them. The economic damage is tremendous, and treatment policies are challenged, because of the limited repertoire of effective, and affordable anti-malarial drugs. How can we understand the underlying evolutionary process?
Methods: We introduce two models for the evolution of anti-malarial drug resistance. One tailored to the details of P. falciparum and one to that of P. vivax (the clinically most important types of human malaria). We also link the evolution of drug-resistance to genetic hitchhiking. Genetic hitchhiking might provide a means to indirectly reconstruct the evolutionary history of drug resistance in the absence of reliable clinical and epidemiological long-term data.
Results: From the respective transmission cycles, we deduce that selection for drug-resistant parasites is much stronger in P. falciparum than in P. vivax. Immanent in the transmission cycle, genetic hitchhiking associated with drug resistance in P. vivax is less pronounced than in P. falciparum (even if the strengths of selection were the same). While a genome-wide reduction in genetic variability can occur in P. falciparum if selection is sufficiently strong, this is impossible for P. vivax.
Conclusions: The differences in strengths and pattern of selection need to be taken into account when reconstructing the dynamics of drug-resistance evolution.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i050-E*

General sessions

Selfish females on the nest – incubating Brown Thornbills distinguish danger posed by different predators to maximise their own survival

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Summary statement:

Incubating females of closed nest species access predation danger outside the nest and trade-off their own survival prior to their brood.

Abstract:

In bird species nesting in cavities and closed nests incubating females have only limited information about current risks outside the nest. Thus it would be adaptive for them to have evolved behavioural mechanisms to access and respond to these risks. In the presence of a predator incubating females have to trade off their own survival versus that of the brood: they can either escape from the nest and disclose its location to the predator or stay cryptic and increase the own risk in case the predator finds the nest. For long-lived species life-history theory predicts that breeders in such a situation should value their own survival over that of their brood. This trade-off has so far not been investigated as most studies concentrate on parent-brood interactions after hatching. We investigated the resolution of this trade-off in Brown Thornbills, a long-lived Australian passerine, which builds closed dome nests in dense vegetation. We filmed female Thornbills during incubation and exposed them to the playback of a nest predator, a predator of adults, and a control species close to the nest. Females significantly increased their level of alertness in the presence of both predator species by looking up and out of the nest. Females reacted strongest to the presence of a predator of adults by looking out longer and more often, also after the end of the simulated predator presence. This suggests that incubating females are on the watch striving to maximise their own survival according to life-history theory predictions.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i109-R*

General sessions

Sexual selection and adaptation in fluctuating environments

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Summary statement:

Using three-spined stickleback, we relate resource availability and heterozygosity to the expression of male colouration, female mate choice, and reproductive fitness.

Abstract:

Although natural selection's role in adaptation to changing environments is well studied, the consequences of sexual selection for population persistence remains relatively unexplored. We here apply genomic and experimental methods to determine the relationship between sexual selection and fitness using three-spined stickleback (Gasterosteus aculeatus). Despite considerable knowledge relating environmental variation to sexual signals, less is known about the gene-by-environment effects. This study explores the potential impact of environmental change on the long-term population consequences of mate choice. Male stickleback exaggerate mating signals (red colour) with carotenoids found in their diet. Because carotenoids also enhance immunological function, females can use this signal to ensure high quality offspring. The context-dependence of the maintenance of this signal also provides the opportunity for deception of low-quality males under conditions of plentiful resources, however. If females cannot discriminate or detect differences between an honest and a dishonest male signal, the result will be offspring of low fitness. Here, we present results of an experiment that manipulates body condition, the opportunity for sexual selection, and the intensity of sexual signals. We further relate genome-wide individual heterozygosity to the expression of sexual signals, individual preference functions, and reproductive fitness. This study demonstrates a so far unexplored genomic scale understanding of the direct influences of sexual selection on fitness, and importantly, how even small temporal environmental changes can influence this relationship.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i110-R*

General sessions

The many ways to delimit species: hairs, genes and surface chemistry

Seppä P[1], Helanterä H[1], Trontti K[1], Punttila P[2], Chernenko A[1], Martin SJ[3], Sundström L[1]
[1]University of Helsinki, Dept. Biosciences, Helsinki, Finland, [2]Finnish Environment Institute, Helsinki, Finland, [3]University of Sheffield, Dept. Animal and Plant Sciences, Sheffield, United Kingdom

Summary statement:

Cuticular hydrocarbons, morphology, and genetic markers separate ants Formica fusca and F. lemani, but they are closely related (FST=0.12) and hybridization cannot be ruled out.

Abstract:

Species identification forms the basis for understanding the diversity of life, but it is also required for understanding evolutionary patterns and processes. The most promising approach to correctly delimit and identify species is to integrate many types of information in the same study. We test how cuticular hydrocarbons, traditional morphometrics, genetic polymorphisms in nuclear markers (allozymes, DNA microsatellites) and DNA barcoding (sequencing of a mt COI gene) perform in delimiting species. As an example, we use two closely related Formica ants, F. fusca and F. lemani, sampled from a sympatric population in the northern part of their distribution. Morphological characters vary and overlap in different parts of their distribution, but cuticular hydrocarbons include a strong taxonomic signal and we test the degree to which morphological and genetic data correspond to the chemical data.

In the morphological analysis, species were best separated by the number of hairs on promesonotum, but individual workers were overlapping in our study area. Nests were separated according to species but not clustered in a PCA made on nuclear data, but Bayesian clustering resulted in perfect separation of the species. Furthermore, F. fusca and F. lemani did not share any mt haplotypes, and they were perfectly separated in a phylogenetic tree. We conclude that F. fusca and F. lemani are valid species that can be separated in our study area relatively well with all methods employed. However, the small genetic differentiation in nuclear markers (FST=0.12) shows that they are closely related, and occasional hybridization between F. fusca and F. lemani cannot be ruled out.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i111-R*

General sessions

When does immune defence determine your success?

Seppälä O[1,2], Leicht K[1,3], Karvonen A[3], Haataja M[4], Kuosa M[3], Jokela J[1,2]
[1]Eawag, Department of Aquatic Ecology, Dübendorf, Switzerland, [2]ETH Zürich, Institute of Integrative Biology, Zürich, Switzerland, [3]University of Jyväskylä, Department of Biological and Environmental Science, Jyväskylä, Finland, [4]University of Helsinki, Faculty of Biological and Environmental Sciences, Helsinki, Finland

Summary statement:

Ecological factors rather than host immune defence may be most important in determining host susceptibility to infections and impose strongest selective pressures on parasites

Abstract:

Evolutionary ecological research on host–parasite interactions typically focuses on immune function and parasite resistance of hosts. This is because host immune defence is often considered as the main barrier against parasites. We propose that also other factors than host immune defence can play important roles in determining host and parasite fitness. Here we present results from experiments designed to investigate the effect of resource (i.e. food) availability on the susceptibility of an aquatic snail Lymnaea stagnalis to infection by a trematode parasite Echinoparyphium aconiatum. In this system, food limitation is known to reduce snail immune function. However, our results indicate that contrary to general expectations, fed snails are most susceptible to infection by free-swimming parasite transmission stages. Furthermore, this effect is mainly dominated by factors related to food processing rather than body condition of the snails. Although the detailed mechanisms leading to this effect remain to be investigated, our data indicate that food consumption modifies host finding by parasite larvae. Thus, our results suggest that the importance of host immune defence may vary across different ecological conditions, and also other factors than host immune function can be crucial in determining the selection gradients under which parasites evolve.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i112-R*

General sessions

Fertile women choose partners with high level of anti-body based immunity

Skrinda I[1], Rantala MJ[2], Krams I[1,2], Kecko S[1], Krama T[1], Kivleniece I[1], Gavarane I[1]
[1]University of Daugavpils, Institute of Systematic Biology, Daugavpils, Latvia, [2]University of Turku, Department of Biology, Section of Ecology, Turku, Finland

Summary statement:

The cyclic shift in women preference towards facial masculinity may be an adaptation for identifying high-quality mates with strong anti-body based immunity.

Abstract:

It has been suggested that the attractiveness of men's faces reveals their immunological status. We experimentally tested whether the attractiveness of male faces is associated with the strength of male immune defence. This was done by photographing and vaccinating 74 young men with hepatitis B vaccine, and measuring the amount of specific antibodies produced. We found that the immune responsiveness (the amount of antibodies produced) correlated positively with facial masculinity and facial attractiveness. We also found the attractiveness rating of men faces by women who were at the fertile phase of their menstrual cycle correlated positively with facial masculinity, but among women who were at the non-fertile phase of the cycle the attractiveness rating did not correlated with facial masculinity, supporting the hypothesis that women increase their preference for facial masculinity during the fertile phase of menstrual cycle. Thus, the cyclic shift in women preference towards facial masculinity might be an adaptation for identifying high-quality mates with strong immune responses.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i113-R*

General sessions

Host range evolution in the Vanessa group

Slove J[1], Eriksson T[2], Nylin S[1], Janz N[1]
[1]Stockholm University, Department of Zoology, Stockholm, Sweden, [2]Natural History Museum, Stockholm, Sweden

Summary statement:

Phylogenetic comparison of host plant use in two closely related butterfly genera, aiming to examine the dynamics of host range evolution, and the generality of those dynamics.

Abstract:

Host plant shifts and range expansions are likely important drivers of the exceptional diversity of herbivorous insects. In order to understand the source of this diversity we therefore need to understand the dynamics of host range evolution. Specialists are ubiquitous and their prevalence may have masked the importance of changes in host plant use. This is a complex trait, that is in itself the combined outcome of many interrelated traits, such as female preference and larval ability to feed, grow and survive. Yet frequent changes in host use are found, at least in some groups, suggesting that adding new plants to the range might not be as difficult as one might expect.
By conducting a case study on two closely related butterfly genera, and including available data on larval feeding ability, as well as plants used in the field, we can describe and compare the evolutionary changes in host range. A Bayesian model of character change was first constructed using the genus Polygonia, and the resulting model was then applied to the closely related Vanessa genus to see how well it could explain the dynamics of host use in this group.

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WED 24 AUG at 1420 - Room N4
Oral presentation *D3-Ge04-1420-O*

General sessions
Evolutionary genetics

Complex evolutionary events at a tandem cluster of Arabidopsis thaliana genes resulting in a single-locus genetic incompatibility

Smith LM[1], Bomblies K[1,2], Weigel D[1]
[1]Max Planck Institute for Developmental Biology, Molecular Biology, Tübingen, Germany, [2]Harvard University, Cambridge, United States

Summary statement:

Our work provides insights into how tandem arrays, which are particularly prone to complex rearrangements, can produce genetic novelty.

Abstract:

Non-additive interactions between genomes have important implications not only for practical applications such as breeding, but also for understanding evolution. In extreme cases, interactions between genes from different genomic backgrounds may present as incompatibilities that compromise normal development or physiology. Despite their importance, only a few cases of genetic over- or underdominance affecting plant growth or fitness are understood at the level of individual genes. Moreover, the relationship between biochemical and fitness effects may be complex: genetic overdominance, that is, increased or novel activity of a gene may lead to evolutionary underdominance expressed as hybrid weakness. We describe a non-additive interaction between alleles at the Arabidopsis thaliana OAK (Outgrowth Associated Kinase) gene. OAK alleles from accessions Bla-1 and Sha interact in F1 hybrids to cause a variety of aberrant growth phenotypes that depend on a recently acquired promoter with a novel expression pattern. The OAK gene, which is located in a highly variable tandem array encoding closely related receptor-like kinases, is found in one third of A. thaliana accessions, but not in the reference accession Col-0. Besides recruitment of exons from nearby genes as promoter sequences, key events in OAK evolution include gene duplication and divergence of a potential ligand-binding domain. OAK kinase activity is required for the aberrant phenotypes, indicating it is not recognition of an aberrant protein, but rather a true gain of function, or overdominance for gene expression, that leads to this underdominance for fitness.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i114-R*

General sessions

Effects of sequential diets in the comma butterfly: Testing predictions from gene expression

Soderlind L[1], Janz N[1], Nylin S[1]
[1]Stockholm University, Department of Zoology, Stockholm, Sweden

Summary statement:

P. c-album larvae are surprisingly good at adjusting to new diets, considering there are differences in midgut gene expression depending on the host plants.

Abstract:

Phenotypic plasticity is advantageous in variable environments since only gene products necessary for specific conditions are produced and phenotypes match environmental demands. We have previously found differences in gene expression in the midgut of larvae of the comma butterfly (Polygonia c-album) among host plant diets. These results suggested that there might be special patterns of gene expression used for feeding on Urticalean Rosids (nettle, elm) and others for utilizing trees (elm, sallow). From this we predicted that diet switches between nettle/sallow would be more difficult in terms of larval performance than switches between nettle/elm and elm/sallow, since hosts are neither closely related or share a common growth form and similarities in gene expression are fewer.

The consequences of sequential diets on larval life history performance were investigated by 3 experiments: diet was changed (1) once in the 3rd larval instar, (2) once in the 4th instar, and (3) on a daily basis between two of the hosts.

In both experiments with a single host switch there were few significant differences in performance between treatment individuals and controls. These differences were probably due to host intrinsic quality rather than to the diet change per se. Results from the more stressful experiment, (3), initially revealed fitness consequences in the nettle/sallow diet switch, in accordance with our theory. However, this pattern could not be confirmed when the experiment was repeated. Larvae seem to adapt amazingly well to changing diets, which suggests rapid adaptation of midgut gene expression. Ecological and evolutionary implications of the results are discussed.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i051-E*

General sessions

The effect of metabolic theory on life histories

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[2]J.F. Blumenbach Institute of Zoology and Anthropology / George August University of Goettingen, Göttingen, Germany

Summary statement:

An explicit resource-consumer model based on metabolic theory leads to Cope´s rule and to a larger life span under food restriction.

Abstract:

We explore the consequences of metabolic theory on life histories and life history evolution. We use a mathematical model for an iteroparous species and its resources, taking into account the allometric scaling of consumption, metabolism and mortality with consumer body mass. Mortality is assumed to be density-dependent, and the dynamics of resources are modelled explicitly. We find that populations that have more or faster growing resources have a shorter life span and a higher mortality, and that populations with a larger adult biomass have a larger number of offspring per female and a larger biomass density. When we allow the adult body mass to evolve, it increases with time without limits. When we allow the offspring body mass to evolve, it becomes smaller. Both trends result from the allometric scaling of mortality and are kept in limits by trade-offs other than those included in our model.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i115-R*

General sessions

Parasites shape the genetic structure of natural Daphnia populations

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[1]Eawag, Aquatic Ecology, Duebendorf, Switzerland, [2]Ludwig-Maximilians-Universität München, Department Biologie II, Evolutionsökologie, Planegg-Martinsried, Germany

Summary statement:

Both in the field and in experiments in the laboratory we could show evidence for coevolution between waterfleas (Daphnia) and their parasites.

Abstract:

The Red Queen coevolutionary hypothesis predicts that parasites drive oscillations in host genotype frequencies due to frequency-dependent selection where common hosts are at disadvantage. However, examples of this phenomenon in natural populations are scarce. To examine if the Red Queen theory operates in the wild, we studied the genetic structure of populations of the crustacean waterflea (Daphnia), in relation to their infection levels, for which we collected multiple samples from a variety of lakes. Furthermore we investigated whether previous epidemics selected for higher resistance to novel parasite isolates in Daphnia by comparing susceptibility of host clones from populations with varying epidemic history.

The most common clone in a given population was often under infected. This advantage, however, did not remain stable over time. Instead, the most common clone decreased in frequency over subsequent generations, indicating that parasites can track common clones. Such decreases were not observed in uninfected populations. In our experiment we found that Daphnia originating from lakes with previous epidemics better resist infection. Our results strongly suggest that Red Queen dynamics do operate in the wild.

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SUN 21 AUG at 1140 - Room N7
Oral presentation *A2-Ge04-1140-O*

General sessions
Evolutionary genetics

The importance of ancestral polymorphism in testing for "snowballing" hybrid incompatibility between Solanum species

Städler T[1], Florez-Rueda AM[1], Paris M[1]
[1]ETH Zurich, Institute of Integrative Biology, Zurich, Switzerland

Summary statement:

We show that recent claims of "snowballing" seed sterility factors between Solanum species are flawed and quantitatively assess the pivotal role of ancestral sequence polymorphism

Abstract:

Two prominent recent studies claimed to find support for a faster-than-linear accumulation of hybrid incompatibility factors (the "snowball" effect), a pattern predicted by the Dobzhansky-Muller model that posits that postzygotic incompatibilities arise due to deleterious epistatic interactions among two or more loci. Both studies, however, used raw interspecific divergence at synonymous sites as a proxy for time since divergence.
Most importantly, this approach assumes that sequence divergence at the time of lineage divergence was zero, i.e. it neglects ancestral polymorphism. Extant wild tomato species (Solanum section Lycopersicon) exhibit abundant nucleotide polymorphism; moreover, the many segregating S-alleles at the locus mediating self-incompatibility, jointly with phylogenetic reconstruction, demonstrate that effective population size must have been substantial during the relevant divergence events.
We thus undertook a reanalysis of the Solanum study using more comprehensive sequence data and explored the impact of a wide range of potential ancestral polymorphism on model comparison. Our reassessment uncovers large discrepancies with the published study by Moyle and Nakazato (Science 2010), in that support for the "claimed" quadratic model under their divergence estimates decreases dramatically under even low levels of ancestral polymorphism. In contrast, we found that levels of ancestral polymorphism exceeding 0.013 are required to favor a linear accumulation of incompatibilities. Considering plausible ancestral parameters, however, the currently available phenotypic and molecular data cannot justify strong claims regarding the snowball effect in Solanum.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i116-R*

General sessions

Novel hypotheses for explaining patterns of fleshy fruit color diversity

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[1]University of Freiburg, Ecology and Evolutionary Biology, Freiburg, Germany, [2]Yale University, Ecology and Evolutionary Biology, New Haven, United States

Summary statement:

Is the diversity of fleshy fruit colors random? We provide insights and novel hypotheses for explaining the evolution of diversity in a visual signal.

Abstract:

The color of fleshy fruits is considered to be a signal to seed dispersing frugivores that promotes the detection of fruits. The diversity of the colors of fleshy fruits is generally thought to have evolved through a process of coevolution between plants and seed dispersing frugivores. A recent study, however, suggests that the color diversity of fleshy fruits dispersed mainly by birds is not higher in tropical regions with more frugivore bird species, as predicted by a coevolutionary model. Moreover, until now it has not been investigated whether fruit color diversity follows a pattern different from that expected by random processes. In our study we used reflectance spectra of 250 fleshy-fruited plant species of six communities dispersed mainly by birds and an avian color space model to analyze patterns of fruit color diversity. We show that the observed fleshy fruit color diversity differs from simulated random fruit communities where potential biochemical and/or physiological constraints on color production are accounted for. We also propose two possible alternative hypotheses for explaining the observed fruit color diversity. First, we suggest a cooperative model in which plant species converge to a few, similar signals thus reducing searching effort for the avian frugivores and enhancing their own dispersal success. Second, we describe a marketplace model in which fruit color diversity is shaped through the competition of plant species for the attention of consumers. We conclude that further research is needed to understand the processes leading to the observed, non-random diversity of this signal.

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WED 24 AUG at 1440 - Room N2
Oral presentation *D3-Ge08-1440-O*

General sessions
Human impact

Sexual signalling in a changing environment

Sundin J[1], Rosenqvist G[2], Aronsen T[2], Berglund A[1]
[1]Uppsala University, Ecology and Genetics/Animal Ecology, Uppsala, Sweden, [2]Norwegian University of Science and Technology, Department of Biology, Trondheim, Norway

Summary statement:

Pipefish avoid phytoplankton blooms and filamentous algae. If no choice exists, turbidity affects the genetic mating system, mate choice- and search, and reproductive success.

Abstract:

One of the oldest and most well studied topics in biology circles around the understanding of adaptation to different environments. In a simplified way one could say that organisms living in a variable environment evolved to cope with changes, whereas organisms living in a stable environment became specialist. Because of human induced environmental change, both stable and variable environments are becoming increasingly unpredictable. In order to persist, both opportunists and specialists respond to these changes. We use pipefish as our study organism, which is a group of highly specialized marine fish, focusing on the interaction between the mechanistic how and the behavioural, evolutionary why. Pipefish have evolved in close relation to seagrass, which they mimic in colour, shape and behaviour. Their vision system is highly sophisticated, with eyes that can be moved independent of each other. Pipefish are dependent on vision when they feed, but also during courtship and mating. Eelgrass meadows are exposed to human induced changes, amongst all in the form of eutrophication and over fishing, which leads to phytoplankton blooms and extreme growth of filamentous algae. Water turbidity reduces visibility and such changes may in turn affect animal behaviour as well as evolutionary processes that are dependent on visual stimuli. We have shown that pipefish strongly avoids this new environment if possible, but in the case of no choice we show the effects of turbidity on the genetic mating system, mate choice- and search, as well as reproductive success.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i118-R*

General sessions

Local adaptation mediates life history trade-offs in obligate pathogen

Susi H[1], Laine A-L[1]
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Summary statement:

I studied trade-offs between infectivity and transmission in an obligate parasite on sympatric and allopatric hosts.

Abstract:

Trade-offs in life history traits are suggested to maintain variation in populations. In parasites, the most important trade off is assumed to be between infectivity and transmission. To date, empirical studies show conflicting results regarding trade-offs in parasite life-history traits.
I studied pathogen infectivity, aggressiveness, time to infection and sporulation in the Plantago lanceolata-Podosphaera plantaginis interaction. I used 35 fungal lines from eight populations from Åland in inoculation experiments on detached leaves from both sympatric and allopatric hosts. Preliminary results indicate that there was no evidence of trade-offs on sympatric hosts. Typically high fitness in one trait correlated positively with other traits. However, the same positive correlations were not observed on allopatric hosts which may be evidence of local adaptation. However, in natural populations parasites occur often as co-infections and hence, parasites evolve in presence of competitors. To better understand which life history traits are linked in trade-offs under competition and if there is a trade-off between competitive success of the parasite and other life history traits, more empirical studies are needed.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i119-R*

General sessions

Does high metabolic rate (RMR) increase survival rate due to resistance to parasite infection?

Szafranska PA[1], Kloch AM[2], Konarzewski M[1]
[1]Polish Academy of Sciences, Mammal Research Institute, Bialowieza, Poland, [2]Copernicus Science Center, Warsaw, Poland

Summary statement:

Resting metabolic rate is positively correlated with survival rate. Animals with high RMR are resistant to parasites what is an effect of costs of immunological response.

Abstract:

Resting metabolic rate (RMR) determines minimal energy demands and is treated as an indicator of metabolic condition of an individual. One of the components which make up the RMR is activation and maintenance of an immune system. In a wild population of root voles Microtus oeconomus we found positive correlation between RMR and survival rate. Thus we hypothesized that high metabolic rate could be associated with the resistance to parasite infection. We therefore measured RMR in free living voles and screened their excrements for three groups of parasites (coccidium, tapeworms and nematodes). We carried out our study in early winter, when voles' energy budgets are especially difficult to balance. We found that infected and uninfected animals did not differ with respect to body mass (F(1,50) = 2.18 p = 0.1), but infected ones had lower RMR ((F(1,50) = 6.17, p = 0.02, body mass corrected) . There was no correlation between RMR (body mass corrected) and the intensity of infection. Our results suggest that individuals with high RMR can have more competent immune system, which in turn increases winter survival rates.

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WED 24 AUG at 1500 - Room N3
Oral presentation *D3-Ge10-1500-O*

General sessions
Inbreeding

Inbreeding and the role of kin selection in outbreeding species

Szulkin M[1]
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Summary statement:

We ask whether kin selection theory can be used to explain why in some outbreeding species females mate with relatives more often than expected.

Abstract:

Avoiding the deleterious consequences of inbreeding is a considerable driving force in mate choice. In birds, constraints on social mate choice can lead to the expectation that extra-pair copulations provide a mechanism to avoid inbreeding and inbreeding depression in offspring. By contrasting broods of related and unrelated breeding pairs, we asked whether great tits (Parus major) have a higher number of extra-pair young when mating with relatives. Contrary to expectations, we found that broods sired by related mates have fewer extra-pair young than broods of unrelated partners. Moreover, we also found that despite substantial inbreeding depression observed in this population, great tits bred with close relatives more often than expected, and divorced them less often than outbreeding individuals. This case study is representative of an often overlooked but recently growing body of evidence suggesting that various animal taxa characterised by an outbreeding mating system actively engage in mating with genetically similar partners more often than expected. I discuss the extent to which a kin-selection approach can be used to explain mating patterns governed by genetic [dis]similarity in outbreeding species.

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WED 24 AUG at 1440 - Room N7
Oral presentation *D3-Ge05-1440-O*

General sessions
Disease and immunity

Spatial variation in parasite sexual reproduction creates coevolutionary hotspots and coldspots

Tack AJ[1], Laine A-L[1]
[1]University of Helsinki, Department of Biosciences, Helsinki, Finland

Summary statement:

Parasite life history, host genotype and the environment explain substantial variation in host-parasite coevolutionary dynamics during the crucial overwintering stage.

Abstract:

Aims: While overwintering success is often assumed to be an inherently random process, we here investigate whether spatial variation in pathogen life-history may explain overwintering hotspots and coldspots.
Methods: A recent epidemiological model shows that local persistence of the biotrophic fungal pathogen Podosphaera plantaginis varies substantially across the metapopulation of its host, Plantago lanceolata. We then use a field survey and reciprocal transplants to disentangle how host-plant genotype, parasite genotype, and the environment (GxGxE) explain spatial variation in parasite overwintering success.
Results: There is large variation across the metapopulation in overwintering strategy of the host parasite, where the production of sexual resting spores is positively correlated with the persistence of the local parasite population. Moreover, the reciprocal transplants show that the environment and host plant genotype can strongly affect overwintering success.
Conclusion: While overwintering success is often assumed to be a highly stochastic process, we here show that parasite life history, host plant genotype, and the environment can explain host-pathogen coevolutionary dynamics during this crucial but rarely studied epidemiological phase.

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SUN 21 AUG at 1100 - Room N3
Oral presentation *A2-Ge02-1100-O*

General sessions
Life-history

Frequency-dependent selection: linking plasticity and dynamics

Takahashi Y[1], Yoshimura J[2], Morita S[2], Watanabe M[3]
[1]Tohoku University, Sendai, Japan, [2]Shizuoka University, Hamamatsu, Japan, [3]University of Tsukuba, Tsukuba, Japan

Summary statement:

Frequency-dependent selection (FDS) is powerful selective force maintaining polymorphisms. We fully demonstrated FDS in a female-dimorphic damselfly.

Abstract:

Frequency-dependent selection (FDS) is one of the most powerful selective forces maintaining genetic polymorphisms in nature. Recently many prospective cases of polymorphisms by FDS have been reported. Some of them are very complicated, though strongly supportive of FDS. Here we investigate FDS in wild populations of the damselfly, Ischnura senegalensis, where females exhibit color dimorphism (an andromorph and a gynomorph) that is considered to be an evolutionary response to sexual conflict. Males selectively harassed to the common female morph in the population, hindering them from ovipositing and foraging activities. Consequently, the fitness of each morph was an inverse function of own frequency in a population, and the equilibrium morph frequency was predicted about 1:1, where each morph has an equal reproductive success. The long-term field surveys showed that the morph frequencies oscillate with a period of two generations, as predicted by mathematical model. Therefore, female dimorphism in I. senegalensis must be maintained by FDS. This example is the simplest confirmed cases of FDS maintaining genetic polymorphisms in nature.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i121-R*

General sessions

Role of seed exchanges and farmers practices in crop metapopulation evolution

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Summary statement:

In the context of farmer-led on-farm conservation, we show that the evolution of a crop metapopulation is mainly explained by social network information.

Abstract:

Metapopulation is acknowledged to be a powerful conceptual tool for characterizing mechanisms of evolutionary process into wild populations. Crop metapopulation was recently used to describe the behavior of crop species evolution within traditional farming systems. However, a given on-farm system needs to be characterize both at the genetic and social level to fully demonstrate its metapopulation functioning. To this aim, we present the first study of a crop metapopulation (bread wheat: Triticum aestivum L.) where we characterized farmer practices, seed exchanges and sub-population genetic diversity over time and space.

With an interdisciplinary approach crossing ethno-botany and population genetics, we analyzed the extent to which the dynamics of this new farmers´ network contribute to maintain and shape genetic diversity in this crop metapopulation. For that, we combine two promising graph theory-based method (population graph and shared haplotype network) to analyse population structure and gene flow among the 19 sub-populations studied. We show that the structure of genetic diversity of these sub-populations is mostly explained by the social network rather than related to spatial information. These results illustrate that it is critical to consider farmers networks as key actors in the sustainable management of agrobiodiversity.

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SUN 21 AUG at 1140 - Room N2
Oral presentation *A2-Ge01-1140-O*

General sessions
Behaviour

Mate-choice trade-offs in a cichlid fish with mutual mate choice

Thuenken T[1], Bakker TCM[1], Meuthen D[1], Baldauf SA[1]
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Summary statement:

We provide experimental evidence for sex-specific trade-offs between mating preferences for relatedness and quality traits in a cichlid fish with mutual mate choice.

Abstract:

Mating preferences for genetic compatibility are fundamentally different from preferences for quality traits like body size or ornamentation because of their relative character, i.e. their strict dependence on the genotype of the choosing individual. As a consequence, the most compatible partner is on average not that of the best quality and vice versa. This problem of conflicting preferences has received considerable theoretical attention, but is less well experimentally studied. Here, we examine this conflict while investigating the interplay of mating preferences for large body size (a quality trait) and relatedness (a compatibility criterion) in Pelvicachromis taeniatus, a cichlid fish with mutual mate choice. In previous experiments, both sexes showed mating preferences for large or related partners, when these criteria were tested in separate experiments controlling for variation in the other trait. In the present mate choice experiment test individuals were exposed to a situation in which preferences for both criteria could not simultaneously be satisfied: They were given the choice between a small, related individual and a large, unrelated individual of the opposite sex. We show that P. taeniatus trade-off mating preferences for quality against that for relatedness and that the trade-off is sex-specific. For males, female body size gained greater importance than relatedness, whereas the opposite was true for females suggesting that different benefits are associated with the choice decisions of males and females.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i122-R*

General sessions

Interactions between immunity and ageing in Drosophila melanogaster.

Tinsley MC[1]
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Summary statement:

We show that the immune system deteriorates in response to ageing, but furthermore it also acts to accelerate the ageing process in Drosophila melanogaster.

Abstract:

We have investigated the interactions between the immune system and the ageing process in Drosophila melanogaster. We demonstrate that parasite defence senesces rapidly as flies age, rendering older individuals more likely to die following pathogen exposure. Key aspects of the cellular immune response deteriorate in parallel with this increase in pathogen susceptibility. By studying multiple wildtype genotypes we shown that considerable genetic variation exists in natural fly populations for the rate at which parasite defence senesces. This genetic variation is partly caused by the action of loci which have specific effects the ageing of the immune system but also by loci which influence declining disease defence through their general impact on the physiology of ageing. Finally, we demonstrate that as well as being influenced by the ageing process, the activity of the immune system in flies also contributes to the rate at which animals age. When the expression of key genes regulating immune system function were knocked down reducing immune responsiveness, the rate of senescence in fly populations slowed. This demonstrates that an important and perhaps fundamental cost of immune system activity is a detrimental effect on the rate at which individuals age.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i123-R*

General sessions

Sexual reproduction of the powdery mildew Podosphaera plantaginis. Consequences for evolution and epidemiology

Tollenaere C[1], Laine A-L[1]
[1]University of Helsinki, Metapopulation Research Group, Helsinki, Finland

Summary statement:

Experimental, field and molecular work investigate sexual reproduction of an pathogen, along with its evolutionary and epidemiological consequences.

Abstract:

The interaction between the host plant Plantago lanceolata and its obligate fungal pathogen Podosphaera plantaginis has been intensively surveyed in the Åland archipelago (10 years occurrence data in about 4000 host populations). Experimental infections and epidemiological modelling revealed evidence of ongoing co-evolution between the host and its pathogen. Sexual reproduction is critical in this pathosystem, not only because of its consequences on genetic diversity, but also because it allows pathogen over-wintering. In spite of its evolutionary potential and epidemiological consequences, this stage remains unexplored until now.

Field observations revealed that sexual structures (cleistothecia) were produced frequently, but with high variability among populations. The frequency of cleistothecia was positively linked with the model prediction of overwinter survival, emphasizing the role of sexual reproduction in perennation. It was also correlated with the intensity of infection, which could be interpreted as an evidence of heterothallism. However, mating experiments revealed that sexually produced spores can be obtained from pure strains, revealing selfing capacity in P. plantaginis (homothallism).

Further investigation will involve mating-type loci sequencing in order to investigate the importance of selfing in natural populations, as well as the evolution of sexual reproduction in this species.

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SUN 21 AUG at 1100 - Room N5
Oral presentation *A2-Ge06-1100-O*

General sessions
Development

Gene expression divergence recapitulates the developmental hourglass

Tomancak P[1], Kalinka AT[1], Varga KM[1], Gerrard DT[2], Ohler U[3], Bergman CM[2]
[1]Max Planck Institute of Molecular Cell Biology and Genetics, Tomancak lab, Dresden, Germany, [2]The University of Manchester, Faculty of Life Sciences, Manchester, United Kingdom, [3]Duke University, Institute for Genome Sciences and Policy, Durham, United States

Summary statement:

We show how modern, molecular, comparative genomics technologies help elucidate classic biological questions concerning the broad relationship between evolution and development.

Abstract:

The observation that animal morphology tends to be conserved during the embryonic phylotypic period led to the proposition that embryogenesis diverges more extensively early and late than in the middle, known as the hourglass model. This pattern of conservation is thought to reflect a major constraint on the evolution of animal body plans. Despite a wealth of morphological data confirming that there is often remarkable divergence in the early and late embryos of species from the same phylum, it is not yet known to what extent gene expression evolution, which plays a central role in the elaboration of different animal forms, underpins the morphological hourglass.
We address this question using species-specific microarrays designed from six sequenced Drosophila species separated by up to 40 million years. We quantify divergence at different times during embryogenesis, and show that expression is maximally conserved during the arthropod phylotypic period. By fitting different evolutionary models to each gene, we show that at each time point more than 80% of genes fit best to models incorporating stabilising selection, and for genes whose evolutionarily optimal expression level is the same across all species selective constraint is maximised during the phylotypic period. The genes that conform most to the hourglass pattern are involved in key developmental processes.
These results indicate that natural selection acts to conserve patterns of gene expression during mid-embryogenesis, and provide a genome-wide insight into the molecular basis of the hourglass pattern of developmental evolution.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i053-E*

General sessions

Structure and variability of Toll-like receptor genes in Grey Partridge (Perdix perdix)

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[2]Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, v.v.i., Brno, Czech Republic

Summary statement:

We present identification of Toll-like receptor-coding genes (ppTlrs) in Grey Partridge (Perdix perdix) together with revealed ppTlr4 polymorphism.

Abstract:

Due to their ability to recognise pathogen associated molecular patterns, Toll-like receptors (TLRs) belong to crucial immunity elements in detection of most pathogens. Despite the growing interest in TLRs in medical and veterinary research, only limited attention has been paid to these molecules in ecological and evolutionary studies. There is hence still lack of information about TLR evolution in free-living animals. In birds, TLR repertoire has been fully described only in domestic chicken (Gallus gallus) and Zebra Finch (Taeniopygia guttata). In order to research the importance of TLR polymorphism in free-living birds, we first focused on identification of Grey Partridge (Perdix perdix) orthologues of chicken Tlrs (chTlrs). To identify Grey Partridge TLR-coding genes (ppTlrs), we used primers designed on the basis of known chTlrs. All ppTlrs sequences obtained showed high similarity to their chicken counterparts. Prediction of domain composition of the resultant proteins by SMART software revealed conserved general features in all ppTLRs, including extracellular region with leucine rich repeats (LRRs), transmembrane domain and cytoplasmic Toll/interleukin-1 receptor (TIR) domain. To confirm close proximity of ppTlrs, chTlrs and other known galliform Tlrs, we performed phylogenetic analysis of all currently known avian Tlrs. Subsequently, we cloned and sequenced ppTlr4 from samples of several individuals from free-living population in the Czech Republic for the purpose of revealing the allelic variability at the population level and its possible fitness consequences.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i054-E*

General sessions

Optimal resource allocation to survival and reproduction in a serotinous plant species. Consequences for population viability under different fire regimes

Tonnabel J[1], Van Dooren T[2], Midgley J[3], Haccou P[4], Mignot A[1], Ronce O[1], Olivieri I[1]
[1]University of Montpellier 2, CNRS, ISEM, Montpellier, France, [2]Ecole Normale Supérieure, Ecology & Evolution laboratory, Paris, France, [3]University of Cape Town, Department of Botany, Cape Town, South Africa, [4]University of Leiden, Leiden, Netherlands

Summary statement:

We investigate how fire regime affects optimal resource allocation of a serotinous plant between growth, production of new seeds and maintenance of seeds in the canopy seed bank.

Abstract:

In fire-prone environments, the evolution of life histories is strongly influenced by fire regimes. One adaptation to fire, called serotiny, consists in the retention of seeds in closed fruits within the crown. Such aerial seed banks might be advantageous because (1) seeds are more protected from predation, unlike soil-stored seed banks and (2) seeds are released when the environment is the most favourable to recruitment. Indeed, during the inter-fire period, seedling establishment is less likely because of competition with adult plants. A disadvantage of serotiny is that plants must stay alive until the arrival of fire otherwise the stored seeds are released during the unfavourable inter-fire period. As a consequence, strong serotiny, i.e. retention of all seeds produced until the next fire, would appear as the best strategy. However, the level of serotiny varies from weak to strong in the South African fynbos. We built a life-history optimization model based on dynamic programming to find the optimal resource allocation (between growth, production of seeds and maintenance of stored seeds) for a plant under a particular fire regime. Our study highlights the importance of fire regimes in the evolution of different levels of serotiny. Unlike earlier studies, we use realistic modelling of fire intervals, in particular we investigate the effect of their variance. We find that a low level of serotiny should evolve whenever the variance of fire interval is large or fire occur at high frequencies, whereas strong serotiny should evolve when the variance is low. Our study points to the importance of the trade-off between current and future reproduction in serotinous species.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i124-R*

General sessions

Parasite-mediated selection acting on the innate immunity gene Toll-like receptor 2 (TLR2) in wild rodents

Tschirren B[1,2], Westerdahl H[2], Råberg L[2]
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Summary statement:

We show how parasite-mediated selection acts on an important receptor of the innate branch of the immune system within and across wild rodent populations.

Abstract:

Patterns of selection acting on immune defence genes have recently been the focus of considerable interest. Yet, when it comes to vertebrates, studies have primarily focused on the acquired branch of the immune system. Consequently, the direction and strength of selection acting on genes of the vertebrate innate immune defence remain poorly understood. Here, we present a study in which we analysed patterns of parasite-mediated selection acting on the innate immune gene Toll-like receptor 2 (TLR2) in free-living rodents at different levels: i) across species, ii) across populations, and iii) within populations. We demonstrate that positive selection has shaped TLR2 during the evolutionary history of rodents. Furthermore, by comparing patterns of diversity and divergence between populations at TLR2 and neutral markers, we show that contemporary selection acts in dramatically different ways on TLR2 in ecologically similar and sympatric rodent species, and that pronounced TLR2 population differentiation occurs even at a small geographical scale. Finally, the results of a large capture-mark-recapture study within a rodent population provide evidence for a close association between TLR2 genotype and parasitism. Together, these results highlight that TLR2 plays an important role in host-parasite interactions in wild rodents and that vertebrate innate immune genes can be evolutionarily much more dynamic than often assumed.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i055-E*

General sessions

Host condition mediates within-host parasite reproductive rate in two host-parasite systems

Tseng M[1], Myers JH[1]
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Summary statement:

Parasites in two host-parasite systems have higher total reproduction, but lower within-host reproductive rate when reared in better condition hosts.

Abstract:

Conventional wisdom holds that poor-condition organisms suffer more from parasitism compared to those in better condition. Accordingly, tests of this assertion in host-parasite systems have demonstrated that parasitized hosts reared under limited food or crowded conditions show overall lower fitness than parasitized hosts reared in better conditions. Here we turn the tables and ask the overlooked question: do parasites reared in poor condition hosts have lower fitness compared to parasites reared in good condition hosts? We conducted experiments in two host-parasite systems: mosquito/protozoan (Aedes albopictus/Ascogregarina taiwanensis), and cabbage looper/virus (Trichoplusia ni/AcMNPV). Mosquito larvae and looper larvae were infected with their respective parasites, and then hosts were reared under two or three food levels respectively. We found that in both host parasite systems, total parasite reproduction was higher in high condition hosts, but within-host parasite reproductive rate varied according to host food availability. In the mosquito experiment, parasite reproductive rate was higher in the low-host food treatment than in the high-host food treatment. In the T. ni experiment, parasite reproductive rate was higher in the intermediate-host food treatment than in the other two food levels. These results demonstrate that parasites have higher total reproductive output when reared in well-fed hosts, but that parasites reproduced faster in intermediate or lower condition hosts. Overall, like their hosts, parasites have higher fitness when reared in better conditions, but parasite reproductive rate is mediated by host condition.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i056-E*

General sessions

Are Hsp70 and Hsp90 biochemical adaptations in natural populations of Iris pumila?

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[1]Sinisa Stankovic Institute for Biological Research, Evolutionary Biology, Belgrade, Serbia

Summary statement:

The Hsp70 and Hsp90 level in reciprocally transplanted genotypes were higher in local than in alien genotypes at original habitats, likely due to divergent selection.

Abstract:

Molecular chaperones are biochemical machinery that prevents fitness reduction in fluctuating environments. They assist in the folding, disaggregation or degradation of aggregated proteins. Since their beneficial effects in all organisms are probable identical as the benefits that initially favoured their evolution, molecular chaperones are referred as biochemical adaptations. We tested this prediction by investigating variation in the level of two heat-shock proteins, Hsp70 and Hsp90 that exhibit chaperone properties. To detect local adaptation for Hsp level, we implemented a reciprocal transplant experiment conducted in the wild. Samples of Iris pumila genotypes from contrasting light environments were reciprocally transplanted between their original habitats. The Hsp concentration was assessed by a Western blot analysis using one developed leaf from each genotype once during spring and summer. To distinguish the pattern of local adaptation, two diagnostic approaches were applied: „local“ vs. „foreing“ and „at home“ vs. „away“. We revealed that local genotypes of I. pumila exhibited significantly higher amounts of all three Hsps in their own habitats than the foreign genotypes. Similarly, a single genotype produced more Hsps within its native habitat in both seasons relative to the non-native one. Theoretically, a higher performance in the native environment compared to the non-native environment is the evidence of local adaptation. Since adaptations are the product of natural selection, it is likely that different concentrations of Hsps observed in the I. pumila populations could be causally related to divergent selection operating within alternative light habitats.

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SUN 21 AUG at 1120 - Room N4
Oral presentation *A2-Ge03-1120-O*

General sessions
Population ecology

Behavioural differentiation of stickleback populations in response to human-induced eutrophication

Tuomainen U[1], Sylvin E[1], Candolin U[1]
[1]University of Helsinki, Biosciences, Helsinki, Finland

Summary statement:

The differentiation of threespine stickleback reproductive behaviour could explain the ability of the species to adjust to different conditions in the Baltic Sea.

Abstract:

Human actions are changing habitats rapidly. A major current problem in aquatic environments is increased nutrient input from anthropogenic sources that promotes algae and vegetation growth in the water. Fishes with visually based mating systems, such as the threespine stickleback (Gasterosteus aculeatus), are likely to be affected by these changes in their breeding habitats. The intensity of eutrophication varies locally and this local variation could over time lead to locally diverged populations. Here we investigated if threespine sticklebacks from areas of varying levels of eutrophication on the Finnish south coast differ in their expression of sexually selected traits. Interestingly, it seems that eutrophied areas induce higher courtship activity in the males. A higher courtship level is required to attract females under poor visibility. Predation risk is also lower in eutrophied areas allowing more conspicuous displays. Thus, the differentiation could increase fitness of the local populations.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i125-R*

General sessions

Behavioural consistency arising from the state-dependent costs of parasitism and predation

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Summary statement:

Results of evolutionary modelling of behaviour in relation to immunocompetence will be presented together with our idea that parasites may drive the evolution of personality.

Abstract:

Positive feedback loops between current and future state can lead to behaviour that is consistent over time and individually characteristic. Our recent paper suggests that ubiquitous parasites and pathogens may provide an ultimate explanation for the existence of initial immunological state differences among individuals. Such initial differences may induce the development of stable behavioural trajectories via state-dependent, active behaviours that increase the efficiency of condition-dependent immune function. In addition, rapid growth may aid individuals to escape from some size-limited predators. Evolutionarily stable behavioural trajectories are dependent on initial state differences, so we predict that intrinsically immunocompetent individuals will be more active and bolder than less immunocompetent individuals. We will present the first results of our evolutionary modelling of boldness-associated behaviours under the risk of parasitism and size-dependent predation.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i126-R*

General sessions

Spatial and temporal variation in genetic diversity of an endangered freshwater seal

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Summary statement:

MtDNA diversity of the Saimaa ringed seal was studied to assess long- and short-term changes in the gene pool of a small and isolated population.

Abstract:

Past and present demography, geography, and genetic diversity are all important factors contributing to the survival of populations. Especially in small and isolated populations, the magnitude and pace of genetic changes can be high. Molecular-genetic assessments of demographic history and geographic structure in natural populations are, however, often hampered by lack of information on isolation time, initial diversity, and migration rates. The landlocked ringed seal population inhabiting Lake Saimaa in southeastern Finland offers a unique model for studying the aforementioned processes in small populations. It has remained completely isolated since the last ice age, information on its initial diversity can be inferred from the large marine source population in the Baltic Sea, and its ecology is well studied. We analyzed mitochondrial DNA diversity in 215 Saimaa ringed seals from three decades in order to assess long- and short-term changes in the gene pool of this isolated and critically endangered population. The mtDNA diversity of the Saimaa ringed seal is low, consisting of only eight unique haplotypes. Nevertheless, coalescent simulations show that the diversity is unexpectedly high when contrasted with the > 800 generations of isolation and the estimated historical carrying capacity of the lake. In the short term, high temporal and spatial differentiation was observed among three decades and four regions of Lake Saimaa, suggesting extremely low effective subpopulation sizes and limited migration within the lake. Our study clearly shows that enhancing gene flow and population growth is crucial in maintaining genetic diversity and viability of the Saimaa ringed seal.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i127-R*

General sessions

The function of the public good of sociable weavers

van Dijk RE[1], Hatchwell BJ[1]
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Summary statement:

Communal nests of sociable weavers are public goods with variable thermoregulatory benefits. We investigate what determines access to these benefits.

Abstract:

The tragedy of the commons is a widespread phenomenon that can be observed at many levels of social organisation. Although widespread, it is still poorly understood how the tragedy may be averted through mutualistic (or agonistic) interactions among members of a social group, leading to cooperative investment in public goods. The aim of this study was to investigate the function of the extraordinary communal nests of sociable weavers, Philetairus socius, and to determine the factors influencing individual access to this public good. Sociable weavers build massive, communal nests consisting of individual nest chambers used for breeding and roosting by one or more individuals, and a communal thatch overarching the chambers. First, we investigated the function of the thatch, showing its thermoregulatory benefits in buffering ambient temperature, and demonstrating that these benefits vary in relation to the position of nest chambers within the communal structure. Second, we investigated the factors that determine which individuals gain access to this variable public good, focusing in particular on the roles of age, morphology and kinship. Our results indicate that there is competition for access to the best positions within the communal nest. This competition is likely to have a profound influence on the social organisation of the colony, and also to influence who contributes to the maintenance of the public good.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i128-R*

General sessions

Dams and their effect on the adaptation and fragmentation of riverine fish populations in northern Chile

Veliz D[1,2], Muñoz P[1,2], Quezada-Romegialli C[1,2], Vila I[1], Copaja S[3]
[1]Universidad de Chile, Departamento de Ciencias Ecologicas, Santiago, Chile, [2]Instituto de Ecologia y Biodiversidad, Santiago, Chile, [3]Universidad de Chile, Departamento de Quimica, Santiago, Chile

Summary statement:

Dams not only disrupt the movement of riverine fish; they also reduce the effective size of fragmented populations and impose new selective conditions, above and below reservoirs.

Abstract:

The effects of human activity are reducing the size of natural populations, restricting migration rates and changing selective pressures, which results in a net reduction of genetic diversity and a loss of capacity to adapt to new environmental changes. It is generally agreed that one of the great environmental modifiers of freshwater systems is dam construction. The objective of this study is to quantify the effects of dams on their rivers over time, both those on the discontinuity of populations which they impose and on the habitat quality of the rivers, by comparing the river above and below the dams. Five dams were studied in north central Chile, involving three main aspects: a) the effects on population fragmentation over time by using a population genetic approach with two fish species, Basilichthys microlepidotus (silverside) and Trichomycterus areolatus (catfish); b) the effects on habitat changes by comparing physical and chemical features of the habitat above and below dams and c) the bioavailability of metals in the habitat produced by the observed changes in the chemical composition of the water. Our results showed low genetic differentiation above and below dams but strong reduction of the effective population size above the dams. Below the reservoir, changes in water chemistry and sediment are bioavailable some metals, which accumulate in fish. In northern Chile, the dams not only impose new selective regimes in the riverine species inhabiting below the reservoir, but also produce dramatic changes in the effective size of the remaining populations above the dam.
Financial support: Fondecyt 1100341, PFB-23, ICM P05-002.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i057-E*

General sessions

Phylogenetic patterns in Beta section (Subfamily Betoideae, Amaranthaceae) as inferred from chloroplast and nuclear DNA sequences

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Summary statement:

Phylogenetic patterns in Beta section as inferred from chloroplast (matk, rbcl, trnH-psbA) and nuclear (ITS) DNA sequences.

Abstract:

The phylogenetic relationships between the six species in Beta section, (Amaranthaceae) and their putative relatives (Patellifolia; Aphanisma; Oreobliton; Hablitzia and Acroglochin) from Subfamily Betoideae are investigated based on an extensive geographic sample, using DNA sequence data from the chloroplast genome and the nuclear ribosomal ITS region. The results revealed low genetic differentiation for the regions matK and rbcL being difficult to use in species delimitation. These results also suggest that interspecific hybridization might occur within this complex. Other cpDNA regions (e.g. trnH-psbA) and nuclear DNA (ITS region) are being investigated in a larger sampling range in order to obtain a better picture of the genetic differentiation within this complex. With the information gathered so far we provide valuable data for future studies on the distribution and ecology of each species, and thus contribute with important knowledge for the conservation of wild Beta populations in Macaronesian Islands.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i058-E*

General sessions

Health and ornamentation in Grey partridge (Perdix perdix)

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Summary statement:

In Grey partridge we have found that both carotenoid- and melanin-based ornamentation involved in sexual selection may indicate health state and immune function.

Abstract:

Grey partridge (Perdix perdix) is a non-migratory terrestrial game-bird species. Its reproduction system is social monogamy with male-male competition and female choice determining the sexual selection outcome. Both males and females possess multiple ornamental traits involved in sexual selection: a melanin-pigmented horseshoe-shaped breast feather patch and a carotenoid-based eye-ring. In this study we have investigated whether these traits are associated with the health state revealed by several haematological (differential leukocyte count, absolute leukocyte count, proportion of immature erythrocytes, haematocrit) and immunological markers (PHA skin swelling test, complement activity). Our results suggest that all three components of the carotenoid-based colouration (hue, saturation and brightness) as well as the size of the melanin-based ornamentation may serve as good indicators of the physiological state of the animal. The positive association between ornamental hue and PHA-induced response indicates that magnitude of the response may be in fact a sign of impaired health in this species. Innate immunity (such as complement activity) may have an important role in good health maintenance as suggested by the relationship between complement activity and carotenoid-based ornament expression. These results help to understand the physiological background behind the ornament-based sexual selection in this species.

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SUN 21 AUG at 1200 - Room N3
Oral presentation *A2-Ge02-1200-O*

General sessions
Life-history

Senescense, family relations and oxidative stress in a social mammal

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Summary statement:

We investigate effects of social interactions on rates of aging, and the role of oxidative stress in mediating these in a cooperatively breeding mammal, the banded mongoose.

Abstract:

What causes variation in aging rates across individuals and taxa is a major question in evolutionary biology. Life-history theory predicts trade-offs between investment in reproduction and cellular maintenance, oxidative stress being a candidate mechanism in mediating the trade-offs. Most studies so far have been conducted under laboratory conditions, offering limited insight into life-history evolution in natural populations. We investigate effects of oxidative stress on aging in a natural population of banded mongooses, a cooperatively breeding mammal. Banded mongooses are an excellent system for studying these questions, as there is extensive variation in reproductive effort between mature individuals. Individuals also differ in the amount of help they give to and receive from other group members, potentially causing variation in the extent to which individuals are exposed to deleterious effects of oxidative stress. Furthermore, males and females differ in their reproductive strategy: females start reproducing early, while males queue to gain dominance and access to females, which may lead to evolved differences between the sexes in their rate of senescence. Here we present the results of long-term observations on over 1000 individuals monitored through their life span coupled with longitudinal blood sampling of target individuals. We quantify changes in blood levels of markers for oxidative stress, and relate these to detailed observations on behaviour. We discuss variation in family and social relations and the effects of this variation on aging and lifespan evolution in long-lived mammals, and the proximate role of oxidative stress in mediating these costs.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i059-E*

General sessions

Adaptive genetic differentiation in a predominantly selfing species analyzed by transplanting into natural environment, crossbreeding and QST-FST test

Volis S[1]
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Summary statement:

Home advantage test, QST-FST comparison and crossbreeding are complementary rather than alternative approaches for local adaptation testing

Abstract:

I analyzed the role of local adaptation in genetic differentiation of populations of the annual grass Hordeum spontaneum sampled along an aridity gradient using three approaches: home advantage test; QST-FST comparison and crossbreeding.
The study included introduction of plants having desert vs. non-desert origin into natural (desert) environment, analysis of population differentiation in allozymes and RAPDs vs. phenotypic traits, and planting interpopulation hybrids under simulated desert conditions in a greenhouse.
The results of all three approaches were consistent with local adaptation and each method provided additional otherwise unavailable information, which means that they should be viewed as complementary rather than alternative approaches.
I found that differentiation of the desert plants from plants of non-desert origin in phenotypic traits was adaptive, giving them home advantage. Gene exchange between adjacent populations (i.e. populations experiencing desert environment) had positive effect on fitness via enhancing natural selection and counteracting drift. At the same time effect of genes from the species distributional core (non-desert plants) had negative fitness effect despite its enriching effect on neutral diversity. Pattern of outbreeding depression observed in interpopulation hybrids (F1) and their segregating progeny (F2) was inconsistent with underdominance, but indicated presence of both, additive and epistatic effects.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i060-E*

General sessions

Mounting of new immunity in birds under conditions of physiological stress

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Summary statement:

Cell- and antibody-based immunity are competing systems in a wintering bird.

Abstract:

Costs of immunological defense under conditions of limited resources may be sufficiently large to affect fitness (reproductive output, growth, survival). Costs of mounting the immune response, whether to a benign or potentially deadly infection, may push the animal beyond the minimal levels of energy reserves which may affect survival. Recent evidence suggests a trade-off between different arms of immune system. We challenged immunity of wintering great tits in Latvia with Brucella abortus antigen to test whether birds with the activated cell-based immunity associated with inflammatory response would have produce less antibodies against B.abortus antigen. We tested whether there is a trade-off between humoral responses to B.abortus antigen and cellular response, belonging to different arms of immune system. Immune challenge with B.abortus antigen changed concentration of heterophils and lymphocytes in peripheral blood. There was an increase of the H/L ratio of immune challenged birds indicating that mounting immune response increases physiological stress level. Birds with higher stress at the time of capture had lower immune responsivenesss against B.abortus antigen under extreme environmental conditions of cold winters, confirming the expected trade off, which might be rooted in the basis of cross-regulation between humoral and cell-mediated immune responses of birds. Only birds in good health condition were able to acquire new immunity by producing more antibodies against B.abortus. These results suggest a link between physiological stress and winter survival, indicating that H/L ratio may serve a reliable indicator of birds' abilities to adapt to their environment.

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SUN 21 AUG at 1120 - Room N6
Oral presentation *A2-Ge05-1120-O*

General sessions
Disease and immunity

From QTL to SNP: A single mutation effects sex-specific transmission of the parasitic rhabdovirus sigma in Drosophila melanogaster.

Waldron FM[1], Bangham J[2], Carpenter J[3], Magwire MM[4], Jiggins FM[1]
[1]University of Cambridge, Department of Genetics, Cambridge, United Kingdom, [2]University of Cambridge, Department of History and Philosophy of Science, Cambridge, United Kingdom, [3]University of Edinburgh, Institute of Evolutionary Biology, Edinburgh, United Kingdom, [4]North Carolina State University, Department of Genetics, Raleigh, United States

Summary statement:

A combination of mapping approaches identifies major-effect loci affecting different aspects of host defence in the sigma virus-Drosophila melanogaster model of coevolution.

Abstract:

The sigma virus is a naturally occurring vertically transmitted parasite of Drosophila melanogaster. This system provides us with a powerful, tractable model of host-parasite coevolution and molecular arms races. Transmission of sigma through female fruit flies is a Mendelian trait controlled by the ref(2)P locus, but considerable variation exists in paternal transmission. We have identified two major effect QTL which together explain over 40% of the variation underlying male transmission. A candidate gene approach revealed a previously unannotated gene, CG13127, containing a single A-G base change, which was significantly associated with a decrease in paternal transmission. This SNP was also found to confer reduced male transmission of three other strains of sigma from separate European populations. Experiments showed that the SNP effects the transmission of sigma through sperm, but has no effect on viral replication following injection - indicating that different mechanisms underlie these two aspects of host defence. Population genetic analyses in wild samples, suggest that this polymorphism may be under balancing selection. This study demonstrates how a large scale mapping approach can be used to identify single mutations affecting phenotypes, including the transmission of multiple viral strains, and their replication after infection. Our work also shows how model systems can be used to reveal the dynamics of viral infection at the genome level.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i129-R*

General sessions

Condition-dependent usage of alternative double-strand DNA break repair pathways in Drosophila melanogaster

Wang AD[1], Agrawal AF[1]
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Summary statement:

Individual condition (HIGH or LOW) leads to differences in the relative frequencies at which alternative DNA double-strand break repair pathways are used in D. melanogaster.

Abstract:

Although both theoretical and empirical literature suggest that mutation rates are evolvable, a comprehensive understanding of the factors causing mutation rate variation is lacking. One possibility is that variation amongst individuals in condition, caused by either environmental or genetic differences, leads to differentiation in their mutation rates. A plausible mechanism by which differences in condition can lead to differences in DNA repair abilities is if condition effects an individual's usage of alternative DNA repair pathways. Multiple pathways exist for DNA damage repair that confer varying levels of risk for causing mutations. Some pathways are more conservative and can repair DNA without introducing mutations while others are more error prone. We have conducted an empirical study using a system in Drosophila melanogaster that measures how the relative usage of alternative DNA double-strand break repair pathways changes in response to condition. Male D. melanogaster were manipulated to be in either HIGH or LOW condition through manipulation of their larval diet. Individuals were then sampled at separate time points, for up to 5 weeks through their fertile lifetime, to measure the frequency of use of different DNA double-strand break repair pathways in their germ-line cells. Our results show that HIGH and LOW condition males differ not only in the overall relative frequencies at which they use alternative DNA repair pathways, but also in the rate and level of change in repair pathway use as they age.

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WED 24 AUG at 1500 - Room N2
Oral presentation *D3-Ge08-1500-O*

General sessions
Human impact

Reconstructing the origin and spread of horse domestication in the Eurasian steppes

Warmuth V[1], Anders E[1], Manica A[1]
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Summary statement:

We use a spatially explicit model, parameterised with genotyping data from more than 300 horses to reconstruct the origin and spread of horses domestication in the Eurasian steppes.

Abstract:

Despite decades of research across multiple disciplines, the early history of horse domestication remains poorly understood. Some authors have proposed scenarios which involve a spread of domestic horses out of a primary area of domestication; others have suggested that numerous distinct wild horse populations were involved in the domestication process, possibly as a result of the spread of technique. Here we investigate the origin and spread of horse domestication in the Eurasian steppe by fitting a spatially explicit (stepping stone) model to genotype data from more than 300 horses sampled across Northern Eurasia. Because the wild progenitor of domestic horses, Equus ferus, is no longer extant, we first reconstruct the population genetic structure of E. ferus, and then explore several scenarios of horse domestication. We find strong evidence for an expansion of E. ferus out of East Asia about 160 kya, likely reflecting the colonisation of Eurasia by this species. Our best-fitting scenario further suggests that horse domestication originated in a geographically restricted area in the western steppe, and that the spread of domestication involved both a movement of domestic horses and a recruitment of wild animals from across the steppes, thus consolidating key aspects of previously contradictory hypotheses.

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SUN 21 AUG at 1120 - Room N2
Oral presentation *A2-Ge01-1120-O*

General sessions
Behaviour

Dominance and aggression in greylag geese: the complex roles of life history, environment and genetics

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Summary statement:

We show that aggressive behaviour in geese is influenced by life history, social environment and genetics in an age- and sex-dependent fashion.

Abstract:

Knowledge of the genetic and environmental influences on a character is pivotal for understanding evolutionary changes in quantitative traits in natural populations. Dominance and aggression are ubiquitous traits that can be selectively advantageous in many animal societies and have the potential to impact the evolutionary trajectory of animal populations. Here we present data from a long-term study on dominance and aggression in free-living greylag geese (Anser anser). Our analyses showed that a number of factors related to individual life histories, season and the social environment affected goose dominance and aggressive behaviour. Parental effects and the sexratio of the flock were among the strongest determinants and the importance of parental effects, season, sexratio and individual raising history differed considerably between life history stages. Incorporating a multi-generational pedigree into the analyses further showed that parental effects on dominance rank could be partitioned into heritable and direct parental effects, while parental effects on aggression could mainly be attributed to heritability. Heritability was stronger in juveniles than in adults. Furthermore, aggression rate, but not dominance rank, was genetically correlated between the sexes. Our results thus show that dominance rank and aggression in geese result from a complex interplay between life history, the social environment and parental effects, including a heritable component.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i130-R*

General sessions

Variation in founder groups promotes establishment success in pygmy grasshoppers, Tetrix subulata

Wennersten L[1], Karlsson M[2], Caesar S[1], Forsman A[1]
[1]Linnaeus University, School of Natural Sciences, Kalmar, Sweden, [2]The Swedish Board of Agriculture, Jönköping, Sweden

Summary statement:

We report higher establishment success in variable founder groups when small groups of pygmy grasshoppers were introduced into new sites under natural conditions.

Abstract:

Re-introductions and re-stocking of locally extinct or endangered populations may be used to protect biodiversity. It is recognized that establishment success increases with increasing number of individuals per introduction. It has also been hypothesized that more variable founder groups should have higher establishment prospects, but this prediction has rarely been evaluated.
We tested whether diversity enhances establishment success by releasing small founder groups of the colour polymorphic pygmy grasshopper Tetrix subulata into the field under natural conditions. T. subulata colour morphs represent integrated phenotypes that utilize different niches. We constructed founder groups of varying diversity by combining individuals belonging to the same or to alternative morphs and released them in spring.
Establishment success, measured as number of descendants found at the release sites the subsequent year, increased with variation in the founder group. Colour morph diversity in the established populations also increased with variation in the founder group, pointing to a possible evolutionary rescue effect on population persistence.
This influence of variation on establishment has important implications for conservation projects of threatened species when the number of individuals available for re-introductions is limited. Our findings may also be used to identify potential invading species before they become invasive.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i131-R*

General sessions

Natural hybridization in the annual plant genus Rhinanthus: from populations to species

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[1]Louvain University, Biodiversity Research Centre, Louvain-la-Neuve, Belgium

Summary statement:

cpDNA introgression from R. minor into R. angustifolius

Abstract:

Natural hybridization can have important consequences in populations, but also at larger temporal and spatial scales, for the evolution of species. Here we present data on hybridization between two annual hemiparasitic plants, Rhinanthus minor and R. angustifolius (Orobanchaceae). We show that in naturally mixed populations, introgression occurs most often towards R. angustifolius, regardless of the abundance of the parental species. We then proceed to demonstrate the effects hybridization can have on the species scale, by comparing the European phylogeographies of the two species. Whereas R. minor shows a clear geographical structure in both nuclear and chloroplast DNA, the latter has no detectable geographical patterns in R. angustifolius. We discuss explanations for the asymmetrical hybridization patterns at both the local and continental scale.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i132-R*

General sessions

To resist or suppress an infection; a framework and a case study on MHC-based resistance to avian malaria in wild birds

Westerdahl H[1], Ashgar M[1], Hasselquist D[1], Bensch S[1]
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Summary statement:

Measures of both prevalence of infection and infection intensity are needed to understand if an MHC allele is a disease resistance or susceptibility allele.

Abstract:

We outline a framework for how candidate alleles of the immune system associate with infectious diseases in natural populations. Three types of alleles can be separated when both prevalence of infection (a qualitative measure) and infection intensity (a quantitative measure) are included in the model; two disease ‘resistance’ alleles and one ‘susceptibility’ allele. Then we present a case study from a natural bird population of great reed warblers testing our framework on Major Histocompatibility Complex class I (MHC-I) alleles in relation to avian malaria. We have previously reported that one particular MHC-I allele (B4b) was positively related to prevalence of a severe form of avian malaria (Plasmodium ashfordi; lineage GRW2). Here we show that birds carrying the B4b allele have lower GRW2 infection intensities than individuals without this allele, hence B4b is a resistance allele and not a susceptibility allele. A likely explanation for this pattern is that birds carrying the B4b allele can mount an immune response that suppresses the acute phase GRW2 infection.

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SUN 21 AUG at 1120 - Room N7
Oral presentation *A2-Ge04-1120-O*

General sessions
Evolutionary genetics

Same look, different story: Two cryptic species of freshwater invertebrates differ substantially in the degree of population genetic structure

Westram AM[1,2], Jokela J[1,2], Keller I[1]
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Summary statement:

We find very different population genetic patterns between two cryptic species, suggesting large differences in biology and population history, hidden by morphological stasis.

Abstract:

Cryptic species are morphologically indistinguishable, but genetically and often ecologically distinct. Recognizing cryptic species and the differences between them is crucial for correct biodiversity estimates and successful conservation strategies. We compared the population genetic structure between two cryptic species (types A and B) of the common and ecologically important freshwater invertebrate Gammarus fossarum. We genotyped individuals from 36 populations mainly in Switzerland (Rhine and Rhone drainage) using nine polymorphic microsatellite markers amplifying in both species. Type A was found only in the Rhine drainage, while type B occurred in both drainages. We found that, in both species, genetic diversity was geographically structured with different subdrainages often harbouring different genetic clusters. For type A in the Rhine drainage and type B in the Rhone drainage, an isolation by distance pattern indicated a non-recent colonization of these areas. However, genetic differentiation was much lower in type B than type A, suggesting substantial interspecific differences in dispersal and / or population sizes. In the Rhine drainage, type B did not show evidence of isolation by distance, and population differentiation was low even at a scale of several hundred kilometres. Together with the signals of recent bottlenecks observed in multiple populations, this result suggests a recent expansion of type B into the Rhine drainage.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i133-R*

General sessions

Sexual conflict in viscous populations

Wild G[1], Pizzari T[2], West S[3]
[1]The University of Western Ontario, Applied Mathematics, London, Canada, [2]Oxford University, Zoology and Edward Grey Institute, Oxford, United Kingdom, [3]Oxford University, Zoology, Oxford, United Kingdom

Summary statement:

This work was carried out by myself, Tom Pizzari (Oxford), and Stuart West (Oxford). We study sexual conflict with inclusive fitness. We use mathematical models and simulation.

Abstract:

There has been increasing theoretical and empirical examination of how sexual conflict can arise between males and females. However, this work has generally assumed that interactions take place in panmictic populations with complete dispersal, where interactions are between unrelated individuals. Here, we examine the consequences of limited dispersal and population structure for the evolution of a male phenotype that is associated with the male's pre- and post-copulatory reproductive success, using an inclusive-fitness based analysis of a group-structured model. We show that: (i) the sex-specific timing of the dispersal phase of the life cycle can drive the evolution of sexual conflict; (ii) the inclusive fitness of a female in this conflict is determined solely by direct (i.e. personal) effects on its own competitive ability. Our analysis is supported by results from individual-based simulations of multi-level selection. Our results support the suggestion that kin selection can influence the evolution of sexual conflict, but reveal that such role might be more complex than previously appreciated when sex-specific life histories are taken into consideration. More generally, comparison of our analytical results with those from multi-level simulations, illustrates how the inclusive-fitness approach facilitates both theoretical tractability and empirical testability.

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MON 22 AUG at 1200 - Room N2
Oral presentation *B2-Ge01-1200-O*

General sessions
Behaviour

Historical contingency affects signaling strategies and competitive abilities in evolving populations of robots

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[1]EPFL Lausanne, Laboratory of Intelligent Systems, Lausanne, Switzerland, [2]University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland

Summary statement:

Divergent signaling can evolve without sexual selection and in uniform habitats and this has major consequences on the outcome of competition between distinct lineages.

Abstract:

Initially identical populations may subsequently diverge from one another as a result of random variation in the occurrence order of beneficial mutations. Such contingency effects should be important for the evolution of social traits such as communication and competitive behavior. However, because of the difficulty to experimentally follow the evolution of social interactions over many generations, there exists almost no experimental evidence for the effect of historical contingencies on the evolution of communication. Here we examine the evolution of signaling strategies in 20 populations of genetically related robots foraging under identical environmental conditions. We found that historical contingency caused by mutational stochasticity during the evolution of signaling led to the emergence of two divergent communication strategies. About half of the populations relied on one communication channel, whereas the other half developed a more complex strategy using two communication channels. Importantly, the more complex strategy led to less efficient foraging than the simpler strategy. However, when in competition with independently evolving lineages, the populations using the single communication channel experienced a greater performance decrease than those using the more complex communication strategy. Hence, there was a trade-off between efficiency and robustness with the simpler and more efficient communication strategy being more vulnerable to competition. These results reveal that historical contingency can influence the evolution of divergent communication which can also have important consequences on the outcome of competition between distinct lineages.

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MON 22 AUG at 1120 - Room N3
Oral presentation *B2-Ge02-1120-O*

General sessions
Life-history

Longevity does not always come at a reproductive cost

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Summary statement:

Flies selected for increased life span do not show a reproductive trade-off associated with longevity. Longevity females even appear to have increased fecundity throughout life.

Abstract:

The disposable soma theory by Kirkwood (1977) implies that energy allocation for maintenance of the body comes at a cost of reproduction, and vice versa. Long lived individuals are therefore expected to have a lower life time reproduction, with studies demonstrating that long term selection on life span leads to a decrease in life time reproductive output. Here we investigate the evolution of reproductive trade-offs in longevity selected and control Drosophila melanogaster lines examining female life-time fecundity and male life-time reproduction. In contrast to previous studies demonstrating reproductive trade-offs in longevity selected lines we find that increased longevity leads to increased fecundity throughout life. However, fecundity onset in longevity lines was delayed by an average of three hours. To further explore this reproductive delay we examined developmental time and time to first mating. Previous studies have linked increased developmental time to increased longevity, leading to the hypothesis that overall development is slower in comparison to control lines. However, no association between development and longevity was found in this study. Rather, our data suggests that the delayed onset of oviposition in females could be the result of a prolonged period of sexual maturation. Preliminary analysis on life-time reproduction in males suggests a tendency for increased reproductive output in longevity lines and potential limits in male fertility period regardless of selection regime. Our results are in contrast to previous studies which suggest reproductive trade-offs are associated with increased longevity.

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MON 22 AUG at 1200 - Room N6
Oral presentation *B2-Ge05-1200-O*

General sessions
Disease and immunity

Predator-induced defence makes Daphnia more vulnerable to parasites

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[1]Ludwig-Maximilians-Universität München, Biologie II, Planegg-Martinsried, Germany, [2]Université de Fribourg, Département de Biologie, Fribourg, Switzerland

Summary statement:

We show a previously unknown cost to inducible defenses: the defended morphs are more vulnerable to infection by a virulent yeast parasite than undefended morphs.

Abstract:

Inducible defensive traits against herbivores or predators are widespread in plants and animals. Theory predicts that defended morphs have greater fitness in the presence of predators, but lower fitness than undefended morphs in the absence of predators. If such costs did not exist, then a constitutively defended morph would be favored by natural selection; yet, evidence for such costs has been elusive. Our current work reveals a significant cost to inducible defenses. Using the waterflea (Daphnia) model system, we show that induced defended morphs are significantly more vulnerable to infection by a virulent yeast parasite than undefended morphs. In two independent experiments, the proportion of successful infections and the number of parasite spores were higher among defended versus undefended Daphnia. Thus, by demonstrating a previously unknown and environmentally relevant cost to inducible defenses, this study enhances our understanding of adaptive phenotypic plasticity and its evolution.

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Ground floor lecture hall centre *HZ*
Essence poster *E-Ge-i061-E*

General sessions

Phylogeography of circumpolar Chamaedaphne calyculata revealed by chloroplast and nuclear markers

Wróblewska A[1]
[1]University of Białystok, Institute of Biology, Department of Botany, Białystok, Poland

Summary statement:

My specific area of research is the ecology, phylogeography and evolutionary history of vascular plant species.

Abstract:

During last decade, a number of studies have illustrated both 'deep' (older processes) and 'shallow' divergence (recent processes) within circumpolar plant species as well as different phylogeographic patterns among them. Here I focus on the circumpolar plant species Chamaedaphne calyculata (Ericaceae), to unravel its phylogeographic history and patterns of genetic diversity across its geographic range. A survey of 347 samples from 29 populations and a combined analysis of chloroplast DNA, ITS and AFLPs revealed a genetic structuring comprising two groups: Eurasian/northwestern North American and northeastern North American. This can be explained in terms of two glacial refugia: Beringia and SE North America. The variation of cpDNA and ITS strongly indicated the evolutionary history of the NE North American populations to be older than of Eurasia/NW North American populations and rather independent due to different time and development of Sphagnum-dominated peatlands between NE and NW North America until the end of 12,000 BP. Mismatch analysis using ITS confirmed that the present-day population structure is the result of rapid expansion since the last glacial maximum. AFLP data revealed low genetic diversity of C. calyculata ($H = 0.085$) over its geographic range and confirmed high genetic differentiation among populations between groups ($\Phi_{ST} = 0.467$, $p < 0.001$). Drift rather than gene flow, appeared to be the dominant force structuring genetic variation in the Eurasia/NW North American than in NE North American populations. This conclusion is also supported by lack of isolation by distance in the Eurasian/NW North American group albeit not in the NE North America.

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TUE 23 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *C5-Ge-i134-R*

General sessions

Gene duplication in the evolution of sexual dimorphism

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Summary statement:

Gene duplication generates redundancy in the genome. Additional gene copies may permit sex-specific patterns of expression divergence, allowing the evolution of sexual dimorphism.

Abstract:

Males and females share most of the same genes, so selection in one sex will typically produce a correlated response in the other sex. Yet the sexes have evolved to differ in a multitude of traits. How did this sexual dimorphism evolve despite the presence of a common genome? We investigated the potential role of gene duplication in the evolution of sexual dimorphism. Because duplication events provide extra genetic material, the sexes each might use this redundancy to facilitate sex-specific gene expression, permitting the evolution of dimorphism. We investigated this hypothesis at the genome-wide level in Drosophila melanogaster, using the presence of sex-biased expression status as a proxy for the sex-specific specialization of gene expression. If sexually antagonistic selection is a potent force acting upon individual genes, duplication will result in paralog families whose members differ in sex-biased expression. We confirmed that gene members of the same duplicate family can have different expression patterns in males versus females. In particular, duplicate pairs containing one male-biased and one unbiased gene occur more frequently than expected. In addition, whereas the singleton ortholog remains unbiased, duplication appears to allow one of the paralog copies to acquire male-biased expression. Interestingly, female-biased expression is not common among duplicates. As expected, expression divergence occurs more in older than in younger duplicates. We conclude that the data are consistent with a role of gene duplication in fostering male-biased, but not female-biased, gene expression, thereby aiding the evolution of sexual dimorphism.

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SUN 21 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *A5-Ge-i135-R*

General sessions

Evolution of genetic robustness in response to migration load

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Summary statement:

Evolution of genetic robustness in response to migration load

Abstract:

Gene flow between ecologically divergent populations has been thought to strengthen reproductive isolation, but it also might lead to the evolution of genetic robustness, so that the resident genomes are able to accommodate foreign elements without much altering the locally adapted phenotype. I briefly outline invasion dynamics of the genetic systems that increase robustness to migration:
(i) invasion is possible only when the population is already at some form stable polymorphism, such as migration-selection balance;
(ii) the net selection on the modifier of robustness should be at its maximum when selection against immigrants is intermediate, because then the number of available heterozygotes is highest;
(iii) although strong selection tends to eliminate immigrant genotypes before they contribute anything to the local gene pool, this impediment may be resolved by changing the order of events in the life cycle, such as when maternal selection is considered; and
(iv) recombination within the modifier-target system breaks down the most favorable combinations and therefore slows down the invasion.
I then focus on two particular genetic mechanisms that may lead to genetic robustness: dominance and gene duplication.

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MON 22 AUG at 1730 - ground floor campus canteen *Mensa*
Regular poster *B5-Ge-i136-R*

General sessions

Fine-scale temporal and spatial variation of taxon and clonal structure in the Daphnia longispina hybrid complex in heterogeneous environments

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Summary statement:

Our work highlights detailed changes in the clonal structure of the D. longispina hybrid system.

Abstract:

Cyclically parthenogenetic animals are important components of freshwater zooplankton. In particular, water fleas of the genus Daphnia often play key role in pelagic environments. In this study, we analysed 10 microsatellite loci to explore changes in taxon and clonal composition of the Daphnia longispina complex and traced the abundance of the most common clones in two European reservoirs. We focused on temporal changes at the end of the growing season, and on horizontal spatial variation within the heterogeneous reservoir environment. One reservoir was inhabited by a single species (D. galeata), whereas the other was inhabited by two parental species (D. galeata and D. longispina) and their interspecific hybrids; the clonal diversity of the hybrids was significantly lower than that in the coexisting parental species. We hypothesized that clonal diversity should decrease with time as a result of clonal selection. However, the clonal diversity of D. galeata increased with time in the single-species reservoir, as a few dominant clones were replaced by a higher number of less common clones. A loss of selective advantage of the dominant clones may be either due to gradual seasonal changes in environmental conditions or due to selection acting in a negative frequency-dependent manner. Most of the genotypic variance could be explained by within-sample variation; however, both temporal and spatial components also had significant, though low, explanatory power. Our study, the first to traced real clonal lineages in the Daphnia hybrid complex, contributes to understanding how clonal reproduction impacts population structure in cyclically parthenogenetic organisms.

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