

with diminished thyroid colloid area and disrupted thyroid development, while perchlorate-exposed stickleback, but not zebrafish, developed steatosis, indicating both general and species-specific responses to perchlorate exposure. Because of these differences, we exposed developing mice (*Mus musculus*) to perchlorate to determine if the effects observed in fishes are consistent in mice. Male and female mice were exposed to either a control (0ppm), 10ppm, or 100ppm perchlorate solution (based on other studies) for 49 days after weaning. Mice were then euthanized and organs including the liver and thyroid gland were dissected. Livers were weighed, then both organs were paraffin embedded and stained using H&E. Statistics indicated no difference in hepatosomatic index or overall body weight between the control and treatment groups. Thyroid gland histology revealed diminished colloid area and abnormal thyrocyte appearance, however there was no significant alterations to hepatic cell morphology or gross appearance. We conclude that perchlorate affects thyroid gland development, but not liver, in mice exposed post-weaning. Future work should include exposure of pregnant mice to perchlorate to examine potential effects on embryonic development. Future work should also examine mechanisms of action to understand disparate results across vertebrates.

P2-32 Pierce, E.*; Frederich, M.; University of New England, Biddeford, ME, University of New England, Biddeford, ME & University of Maine, Orono, ME; mfrederich@une.edu

Environmental DNA to Detect Invasive Invertebrates; Case Study in a Tide Pool

Environmental DNA (eDNA) monitoring techniques can be applied in marine ecosystems to detect invasive invertebrates quickly and efficiently. Invasive invertebrates threaten natural biodiversity and some of the most valuable fisheries in the world. Visual surveys for these invasive species, the usual monitoring technique, can be inefficient and costly, and often detect invasions only once the species has already established a population. Once established, these invaders can out-compete native biodiversity, so detecting the invasion early is crucial to preventing environmental harm. We tested whether eDNA methods are comparable to visual surveys for detecting and quantifying invasive invertebrates in a tidepool in Maine. Quantitative PCR assays were compiled or designed for green crab, *Carcinus maenas*, Asian shore crab, *Hemigrapsus sanguineus*, European oyster, *Ostrea edulis*, and chain tunicate, *Botrylloides violaceus*-. Environmental DNA sampling and a visual survey were performed collected monthly. The visual survey was completed using the Marine Invader

Monitoring Information Collaborative (MIMIC) survey methods. Preliminary results suggest that eDNA is able to detect some of the invasive species that were found in the visual survey, and that concentration correlates with abundance of some species but not all. Physiology and morphology likely play a role in eDNA shedding rates, affecting detection probability. This suggests that careful testing is required to confirm and field test that eDNA abundance is associated with the biomass of each species. Environmental DNA can be used to detect invasive invertebrates with accuracy, but these methods need refinement for management of invasive invertebrates. Funded by NSF EPSCoR grant# OIA-1,849,227

S11-9 Pinseel, E; Nakov, T; Van den Berge, K; Downey, KM; Judy, KJ; Kourtchenko, O; Krempf, A; Ruck, EC; Sjöqvist, C; Töpel, M; Godhe, A; Alverson, AJ*; University of Arkansas, Fayetteville, USA, Ghent University, Ghent, Belgium and University of California, Berkeley, USA, University of Gothenburg, Gothenburg, Sweden, Leibniz-Institute for Baltic Sea Research, Rostock, Germany, Åbo Akademi University, Turku, Finland; epinsee@uark.edu

Unravelling a natural evolutionary experiment: The colonization of low-salinity habitats in the Baltic Sea by the marine diatom *Skeletonema marinoi*

The salinity gradient separating marine and freshwater environments represents one of the major ecological divides for prokaryotic and eukaryotic microbes. Yet, the mechanisms by which marine diatoms adapt to, and ultimately diversify in, freshwater environments are poorly understood. Here, we take advantage of a natural evolutionary experiment that has played out over the past 9,000 years in one of the world's largest brackish water bodies: the colonization of the Baltic Sea by the marine diatom *Skeletonema marinoi*. We collected eight genotypes of *S. marinoi* from across the Baltic Sea salinity gradient, exposed these to different salinities that mimicked the Baltic Sea salinity cline, and used RNA-seq to compare patterns of gene expression between low and high salinity treatments. Inclusion of multiple genotypes allowed us to characterize a shared response to low salinity among all genotypes as well as highlight intraspecific variation in the response to low salinity. We found that *S. marinoi* cells in low salinities have altered general energy metabolism, experienced increased oxidative stress and higher nutrient demands, and produced more storage compounds and fewer osmolytes. Inclusion of strains from eight different localities revealed that different genotypes differ significantly in their response to low salinity, both in the direction and magnitude of gene expression. These differences

include fundamental cellular processes such as cell division, regulation of transcription and translation, and aerobic respiration. Altogether, our results reveal substantial variation in the response of different genotypes, highlighting an important source of biological variation associated with how diatoms respond and adapt to environmental change.

77-5 Pirani, RM*; Curlis, JD; Arias, C; McMilian, O; Cox, C; Logan, ML; University of Nevada Reno, Reno, NV, University of Michigan, Ann Arbor, MI, Smithsonian Tropical Research Institute, Panama, Smithsonian Tropical Research Institute, Panama, Florida International University, Miami, FL; renatampirani@gmail.com
Uncovering the ecological and genetic basis of a sexual signal: the dewlap of the Panamanian slender anole (*Anolis apletophallus*)

Sexual signals are thought to play an important role in speciation and macroevolutionary trends, yet the genetic basis, microevolutionary processes, and agents of selection that shape sexual signal variation are poorly known. Lizards in the genus *Anolis* have an extendible throat fan called a dewlap which they use for intra and inter-specific signaling, although debate continues over the precise agents of selection that drive dewlap evolution. One major hypothesis is that dewlap coloration should be associated with the light environment in such a way that signal transmission is optimized, namely, that dark colored dewlaps should evolve in bright environments whereas light colored dewlaps should evolve in darker environments. We studied the Panamanian slender anole (*Anolis apletophallus*) which has a dewlap polymorphism; males either have a solid orange dewlap (solid morph) or a white dewlap with an orange spot (bicolor morph). Further, the frequencies of these morphs change continuously across space. First, we examined the relationship between light environment and morph frequency in a single mainland population of the slender anole that was distributed across a canopy cover gradient. Next, we investigated the genetic basis of this polymorphism by assembling the full slender anole genome which we then used as a reference for a pooled population sequencing (Pool-Seq) approach to identify the genomic region underlying this dewlap polymorphism. These data will form the basis for a transplant experiment aimed at identifying the specific agents of selection that maintain this polymorphism in nature.

S9-3 Plum, F*; Labonte, D; Department of Bioengineering, Imperial College London, London, UK; fabian.plum18@imperial.ac.uk

scAnt—an open-source platform for the creation of 3D models of arthropods (and other small objects)

We present *scAnt*, an open-source platform for creating digital 3D models of arthropods and other small objects. *scAnt* consists of a scanner as well as a Graphical User Interface (GUI) and enables the automated generation of multi-view Extended Depth Of Field (EDOF) images. These images are then masked with a novel automated routine which combines random forest-based edge detection, adaptive thresholding, and connected component labelling. The masked images can then be processed further with a photogrammetry software package of choice, including open-source options such as Meshroom, to create high-quality, fully textured 3D models. Due to the exclusive reliance on generic hardware components, rapid prototyping, and open-source software, *scAnt* costs only a fraction of comparable systems. To maximise utility, we provide extensive and free documentation of the manufacturing and assembly process, as well as detailed guidance on software setup and use of the platform. The resulting accessibility of *scAnt* will (i) drive the development of novel and powerful methods for machine learning-driven behavioural studies, leveraging synthetic data; (ii) increase accuracy in comparative morphometric studies as well as extend the available parameter space with area and volume measurements; (iii) inspire novel forms of outreach; and (iv) aid in the digitisation efforts currently underway in several major natural history collections.

P1-3 Plum, F*; Bulla, R; Imirzian, N; Labonte, D; Department of Bioengineering, Imperial College London, London, UK, The Pocket Dimension, Munich, Germany; fabian.plum18@imperial.ac.uk

Synthetic datasets based on photogrammetry models power robust deep neural networks for behavioural analyses in social insects

State-of-the-art machine learning methods promise to transform behavioural research by allowing researchers to gather data at an unprecedented scale. Applying transfer learning strategies to Deep Neural Networks (DNNs)—i.e., pre-training DNNs on highly variable datasets such as ImageNet—has made it possible to achieve human-level performance with minimum hand-labelled training data under well-defined conditions. However, porting these methods to variable and uncontrollable field conditions still poses a major challenge, because their robustness and versatility is limited by the variability and quantity of the supplied training data. Here, we aim to overcome this limitation by training DNNs on extensive synthetic datasets based on quasi-photorealistic computer-generated images. We developed an open-source photogrammetry