

**P3-226** PAPERETTI, C\*: BABBUCCI, M; HARMS, L; LUCASSEN, M; DETTAI, A; AUVINET, J; HEINDLER, FM; PATARNELLO, T; NEGRISOLO, E; University of Padova, Padova, Italy, Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research, Bremerhaven, Germany, Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research, Bremerhaven, Germany, Institut de Systematique, Evolution, Biodiversité, Paris Cedex, France, Université Paris 6, Sorbonne Universités Cassan, Paris Cedex, France, KU Leuven, Laboratory of Biodiversity and Evolutionary Genomics, Leuven, Belgium; *chiara.papetti@unipd.it*

**The Evolution of Mitochondrial Genomes of Notothenioid Fish**

There is much evolutionary and biological interest in the processes that shaped Antarctic notothenioid fish's adaptations via molecular changes. We investigated the evolutionary pathways that produced the diversity of gene orders observed in the mitochondrial genomes (mtDNAs) of these organisms. Antarctic notothenioids exhibit translocations of *nad6* and *trnE* genes in different positions with respect to the standard vertebrate gene order. We sequenced the mtDNAs of 14 Antarctic notothenioids and 1 species with sub-Antarctic distribution. We analysed a big dataset including notothenioid mtDNAs already available in public databases and a broad set of outgroups, encompassing several mtDNAs of other Perciform species. A molecular phylogenetic analysis, based on Bayesian and maximum-likelihood methods, provided a strongly supported notothenioid tree used to map the evolution of gene order in these peculiar fishes. The analysis was completed with the study of the molecular evolution of single mitochondrial genes. In a modern era, when sequencing of large genomes has become a state-of-the-art, this study demonstrates that small compact mitochondrial genomes still embed a large amount of information that advanced analytical approaches can bring to light.

**P1-42** PATEL, T\*: RIMKUS, B; KONOW, N; UMass Lowell; *trushiti\_patel@student.uml.edu*

**Influence of Recruitment Level on Jaw Muscle Operating Lengths During Chewing**

For feeding muscles, our understanding of the operating length-ranges with respect to optimal length ( $L_0$ , where isometric peak force is generated) are based on twitch contraction studies of whole jaw muscles. These studies suggest that jaw muscles operate at short lengths on their length-tension (LT) curve. However, muscles are rarely twitch recruited *in vivo*, and in pennate muscle, fiber contractile behavior may differ from whole muscle behavior. Recent limb muscle data reveal variations in  $L_0$  with recruitment level, but the effect of recruitment on *in vivo* operating length of feeding muscle remains unknown. We measured fiber length change, muscle activation, and muscle force from rat deep masseter, a key jaw elevator, during food processing. An *in situ* approach was then used to construct LT curves for twitch (minimal), sub-maximal (intermediate), and tetanic (maximum) stimulation conditions. This combined approach revealed how *in vivo* fiber operating lengths are shaped by recruitment level and LT effects. Based on recent limb muscle data, we predicted  $L_0$  to be shortest for tetanic, intermediate for sub-maximal, and longest for twitch contractions. In line with our prediction, tetanic  $L_0$  was approx. 17% shorter than twitch  $L_0$ . The LT curve for skeletal muscle describes a trade-off between weak but stable contractions at short lengths, peak force production at intermediate lengths, and weak as well as unstable contractions at long lengths. In contrast to twitch data from earlier jaw muscle studies, our data suggest that chewing at wide gape on hard food may render jaw muscles vulnerable to sarcomere instabilities as they are forced to operate at long, weak, and unstable lengths. These results have implications for determining potential causes of oral physiological dysfunctions.

**P3-85** PARKINSON, KJL\*: HENNIN, HL; JANSSEN, MH; GILCHRIST, HG; LOVE, OP; University of Windsor, Ontario, Environment and Climate Change Canada, Ontario, Environment and Climate Change Canada, Ontario; *parkin11@uwindsor.ca*

**Does environmental variation influence incubation patterns in an Arctic seabird?**

Climate change may limit the ability of individuals to reproduce successfully, with downstream impacts on population demography. Polar species are now faced with rates of warming much higher relative to other ecosystems, potentially placing them at even greater risk than previously expected. Unfortunately, it is unclear whether mechanisms at the heart of key reproductive decisions have the inherent flexibility that will enable individuals (and hence populations) to stay ahead of this rapid change. In waterfowl, ambient temperature can influence a mother's incubation behavior, which in turn can affect the post-hatch success of offspring. Here we test links between environmental variation and incubation parameters in Arctic-breeding common eiders, a species which faces multiple constraints during incubation. Females live in a highly stochastic environment, fast during the entirety of incubation, and yet must control the incubation period carefully so that duckling hatching matches the timing of sea ice break-up. From 2014-2016, we collected local climate data (i.e., ambient temperature, humidity, etc.) and paired this with data loggers to monitor the incubation temperatures of eider hens at East Bay Island, Nunavut, Canada. We aim to relate inter- and intra-individual variability in incubation temperatures to environmental parameters to examine whether and when hens adjust incubation decisions and their body temperature in response to fluctuating ambient temperatures. Determining the capacity of individuals to flexibly adjust reproductive decisions in response to changing environmental conditions further allows us to predict whether certain populations (and hence a given species) have the capacity to persist in response to climate change.

**P2-84** PATTON, ST\*: CLAY, DY; JACOBS, EP; MARIAS, M; GIBBS, AG; Nevada State College, UNLV, SUNY Fredonia, Georgetown Univ; *allen.gibbs@unlv.edu*

**Effects of Diet on Genetically Obese Drosophila**

Over 90 generations of selection for starvation resistance in outbred populations of *Drosophila melanogaster* have resulted in flies that are extremely obese, even when fed a standard *Drosophila* diet. Obesity can also be induced in normally lean flies by rearing them on a low-protein, high-sugar diet. We investigated whether starvation-selected flies respond differently to dietary changes than controls. Have starvation-selected populations reached their maximum lipid content, or can they be made even more obese through dietary manipulations? We reared starvation-selected and unselected lean control larvae on diets containing 5 yeast:sucrose ratios, ranging from 90% yeast:10% sugar (Atkins diet) to 10% yeast:90% sugar (American diet), as well as 3 different caloric concentrations. Starvation-selected and control flies had similar responses to rearing diet: development to adulthood was delayed on high sugar diets, and flies reared on high sugar diets enclosed with significantly greater lipid stores. Total protein levels were not affected, indicating that these flies were fatter, not simply larger due to extended larval feeding. To determine whether lack of micronutrients contained in yeast could have affected these results, we reared flies on high-sugar media containing vitamins, trace metals, cholesterol or RNA, as well as a combination of all of these. Lipid content did not differ from that of flies reared on un-supplemented media. We conclude that starvation-selected flies have not become as obese as possible, despite long-term directional selection favoring lipid storage. Supported by IOS-1355210 and DBI REU 1358896 from NSF and R15-GM100395 from NIGMS.