

59.6 POLLOCK, H/S*; CHEVIRON, Z/A; BRAWN, J/D; University of Illinois at Urbana-Champaign; hpollock@illinois.edu

TESTING JANZEN'S HYPOTHESIS: VARIATION IN AVIAN THERMAL TOLERANCES ACROSS LATITUDE

Understanding the influence of abiotic environments on physiological traits has been a long-standing goal in evolutionary physiology. Janzen's hypothesis predicts that organisms from relatively seasonal environments (e.g. temperate latitudes) will evolve comparatively broad thermal tolerances to cope with greater environmental variation. In contrast, organisms from less seasonal environments (e.g. tropical latitudes) are expected to have narrower thermal tolerances, which may make less tolerant of environmental variation. Understanding how thermal tolerances vary across latitude is crucial in predicting whether tropical organisms have narrower tolerances and thus, greater susceptibility to climate change than their temperate-zone counterparts. We used the breadth of the thermoneutral zone (TNZ) to assay thermal tolerances in suites of tropical and temperate-zone resident bird species using flow-through respirometry. Temperate-zone species had significantly broader thermal tolerances than their tropical counterparts. Latitudinal patterns in thermal tolerance breadth were driven by variation at the lower end of the TNZ (Lower Critical Temperature: LCT), which was significantly lower in temperate-zone species. The upper end of the TNZ (Upper Critical Temperature: UCT) was not significantly different between tropical and temperate-zone species. Both UCT and LCT values were independent of body size and were consistent among individuals of the same species. Thermal tolerance (i.e. TNZ breadth) thus varies predictably with latitude and appears to be driven by exposure to cold temperatures. Our data confirm Janzen's hypothesis and suggest that environmental variation (i.e. past selective regimes and/or current environmental conditions) influences avian thermal tolerances.

65.4 PORTER, M/M*; ADRIAENS, D; MCKITTRICK, J; MEYERS, M/A; Clemson University, Ghent University, University of California, San Diego, University of California, San Diego; mmporte@clemson.edu

Bioexploration: How engineering designs help elucidate the evolution of seahorse tails

In most engineering disciplines, biomimicry often refers to the design process where engineers mimic or gain inspiration from biological systems to develop new technologies. Common examples include robots inspired by snakes or elephant trunks, adhesives inspired by gecko toes or mollusk byssus, and tough ceramics inspired by bone or abalone nacre. However, research in biomimicry can not only inspire new engineering technologies – i.e., *bioinspiration*, but also be used to further explore biological systems – i.e., *bioexploration*. Here, we introduce the first generation of artificial exoskeletons inspired by the prehensile seahorse tail. Mimicking the skeletal structure and function of the seahorse tail, we fabricated two prototypes of articulating structures with different cross-sectional profiles (i.e., square and circular). After exploring the mechanics of the two geometries, we learned that the square exoskeleton has several mechanical advantages over its circular counterpart. Linking that back to the biological system, this discovery helps explain the adaptive nature of the architecture of the bony-plated armor and the tail composed of square segments in relation to its protective and grasping capacities.

84.3 PORATH-KRAUSE, AJ*; PAIRETT, AN; FAGGIONATO, D; SERB, JM; Iowa State University; ajkrause@iastate.edu

Structure and spatial expression differences among duplicated rhabdomeric opsins indicate functional change in photoreception of the scallop

Duplication of the photosensitive protein, opsin, is important for expanding visual and photosensory systems as it can provide the genetic foundation for adaptation. From our transcriptome data, we discovered four rhabdomeric (Gq-protein coupled or Gq-opsins) opsins expressed in the scallop, *Argopecten irradians*. Two of these were previously unrecognized. The four opsins appear to be the result of a series of gene duplication events in Bivalvia. We hypothesize that the four Gq-opsins have diverged since duplicating, and we test this hypothesis using genomic, bioinformatics, and protein-modeling approaches. We provide evidence that the four Gq-opsins 1) have dissimilar amino acid sequences, 2) differ in tertiary structure, and 3) vary in their spatial expression across tissues. Amino acid sequence comparisons between Gq-opsins showed overall percent identity values ranged from 41.3 to 64.6%, and key structural motifs differed in sequence composition. Protein homology modeling predicted four unique tertiary structures, with different amino acid residues interacting with the light-sensitive chromophore. Finally, gene expression data determined that Gq-opsins differ in spatial pattern and relative levels across photosensitive tissues, including the mantle and the eye.

82.6 POWDER, KE*; ALBERTSON, RC; UMass Amherst; kepowder@bio.umass.edu

Evaluation of species-specific ontogenetic trajectories for craniofacial morphologies in Lake Malawi cichlids

East African cichlids exhibit one of the most impressive adaptive radiations, and pivotal to this are species-specific craniofacial structures that allow ecological specialization. In order to understand the developmental origins for this morphological variation, we examined the growth trajectory for three aspects of craniofacial shape from the onset of osteogenesis through juvenile stages using geometric morphometrics. Specifically, we assessed variation in lateral, ventral, and lower jaw shape in six species (n>350 individuals) of Lake Malawi cichlids that span a major ecomorphological axis that distinguishes species that forage from the water column (pelagic) and those that feed from the rocky substrate (benthic). We find that, despite drastic differences in adult craniofacial morphologies, there is striking conservation in the direction of craniofacial ontogeny, suggesting that natural selection is working within a conserved developmental program. However, we also note species-specific differences in the timing and/or duration of particular trajectories (e.g., paedomorphism). Previous work in cichlids and other systems suggests that species-specific differences in adult morphology are due to changes in molecular signaling pathways that regulate early craniofacial development. In support of this, we demonstrate that modulation of Wnt signaling at early stages has discrete effects over extended periods of development, and can shift a developmental trajectory into morphospace normally occupied by another species. However, craniofacial shape recovers by juvenile stages, which underscores the idea that craniofacial development is robust and that adult head shapes are the product of many molecular changes acting over extended periods of development.