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Evolving Systems in Biology: From Molecules to Marsupials

Session Moderator: Billie J. Swalla, Biology
022 JHN
3:45 PM to 5:15 PM

* Note: Titles in order of presentation.

Experimental Evolution of Phenotypic Plasticity

Samuel Evans (Sam) Reed, Senior, Biology (Ecology, Evolution & Conservation)
Mary Gates Scholar
Joseph Henry (Joe) Marcus, Senior, Biology (General)
Mary Gates Scholar
Mentor: Benjamin Kerr, Biology
Mentor: Peter Conlin, Biology

Darwinian natural selection produces an organism that is adapted to its environment, an organism whose traits (phenotype) are tuned in critical ways to its habitat. If organisms and their phenotypes are so finely tuned to their environment, how can they deal with changes to that environment? One strategy is to evolve the ability to change phenotype in response to a change in the environment, or phenotypic plasticity. Theory predicts phenotypic plasticity to be adaptive when (1) organisms experience different environments either spatially or temporally and (2) different environments favor different phenotypes. In some cases, changes may be accompanied by cues that provide reliable information about future selection. Previous studies modeling adaptive plasticity suggest plasticity to be favored when the environmental cue always predicts the correct selection and not when the environmental cue is unreliable. We experimentally tested theoretical predictions about the de novo evolution of adaptive phenotypic plasticity with a clustering phenotype of baker's yeast by selecting alternately for large or small clusters. Selection for size was cued by alternate forms of growth media and this cue was either a reliable predictor of future selection or an unreliable predictor. After a preliminary run of the experiment, we have found indications of an emergent plastic response in one of our replicates from the reliable cue treatment. This provides a biological example that is consistent with accepted theoretical predictions.

Gone with the *Wnts*...The Wnt Signaling Pathway in *Pleurobrachia bachei*

Rebecca Lynn (Rebecca) Bruders, Recent Graduate,
Mary Gates Scholar
Mentor: Billie J. Swalla, Biology

Wnt signaling is known to be critical for proper embryonic development in most animals studied to date. But key evolutionary questions on the origin and evolution of this pathway in the metazoan common ancestor are still unresolved. Recently, the genome of *Pleurobrachia bachei*, a member of the early branching metazoan linage ctenophora, has been sequenced. Insights into the function of the Wnt pathway in *P. bachei* will provide information on early evolution of this key pathway. Three *Wnt* ligand genes were identified in *P. bachei* and cloned for in situ hybridization. These genes showed expression in the combs, tentacles, mouth, ciliated grooves and polar fields of the adult *P. bachei*. In a genomic search for other members of the canonical Wnt pathway, components of the destruction complex and antagonists were incomplete or missing from the genome. High levels of Wnt expression in the adult *P. bachei* indicates that *Wnt* could also be playing a role in signaling in the adult.

Genetic Differentiation Among Color Morphs of the Brain Coral *Lobophyllia spp.* from the Indo-Pacific Ocean

Katrina Jane (Katrina) Herlambang, Senior, Aquatic & Fishery Sciences
Mary Gates Scholar
Mentor: Lorenz Hauser, School of Aquatic and Fishery Sciences
Mentor: Shannon O'Brien, Aquatic and Fishery Sciences
Mentor: Isadora Jimenez, Aquatic & Fishery Science

Corals are important marine animals that provide significant habitats for thousands of marine teleost and invertebrate species, natural barriers to protect coastal communities,

and sources of income for people in more than 100 countries around the world. Despite their vital importance, however, little is known about their taxonomy. Currently, they are classified based on their calcium-based skeleton morphology and coloration, which often causes problems because of high phenotypic variability within species. Thus, I used DNA sequencing in my research to identify species of the genus Lobophyllia from the Indo-Pacific Ocean. Specifically, I tested whether color morphs from different areas in Indonesia actually represent different species or mere color variations. For that purpose, I conducted PCR amplification of the mitochondrial DNA cytochrome oxidase gene and two nuclear genes in 42 colonies of 14 color morphs of Lobophyllia sp. The PCR products were sequenced in both directions at the High Throughput Sequencing Center of the University of Washington, and phylogenetic trees including known species were used to determine the species identities. I expected that color morphs would be genetically differentiated and therefore might represent different species. Regardless of the outcome, this project has helped to understand the biodiversity in coral reefs better, and is also useful to identify appropriate units for coral management and conservation.

Early Activation of Metamorphosis in Tailless Ascidians: Heterochrony Affecting Body Plan

Ceri Joanna (Ceri) Weber, Senior, Biology (Molecular, Cellular & Developmental)
Mentor: Billie J. Swalla, Biology

In typical ascidian development, a tailed larva hatches, swims, becomes competent, and then responds to settlement cues, that initiates metamorphosis. Metamorphosis triggers apoptosis, which is required for tail loss. At this time, the notochord is lost as the tail reabsorbs and the juvenile settles to a substrate. In the ascidian family Molgulidae, species have evolved tailless larval development at least four times independently from a tailed ancestor. We hypothesized that a heterochrony in metamorphosis is responsible for the evolution of tail loss in the tailless ascidian larvae. We show that there is early expression of metamorphosis genes in Molgulidae, including genes involved in the Mannose Binding Lectin (MBL) Complement pathway of innate immunity. We hypothesize that the maturation of the immune system early in tailless larvae could be a progression to competency and trigger to metamorphosis. Jeffery (2002) showed programmed cell death happens in cells that form a tail early in development. We further hypothesize that a heterochrony in metamorphosis promotes the early activation of programmed cell death in the tailless ascidian larvae. Using next generation sequencing techniques, we sequenced transcriptomes of a tailed and tailless species and their hybrid through development. We examined genes that have been shown to be expressed during metamorphosis in other ascidians and saw earlier expression of genes critical for metamorphosis in both species. Our ultimate goal is to elucidate the ascidian molecular trigger for metamorphosis and uncover whether heterochrony of metamorphosis leads to tailless ascidians.

Finite Element Analysis of Teeth and Alveolar Bone, Linking Mammal Chewing Patterns to the Form and Function of the Periodontal Ligament

Becca Anderson, Senior, Biology (Physiology)
Mentor: Susan Herring, Orthodontics
Mentor: Casey Self, Biology

Relatively little is known about the periodontal ligament (PDL), a fibrous collagen structure which anchors teeth to the jaws and is thought to be a key factor in redistributing stress from teeth during mastication. However, to date the nature of this redistribution has not been established, hampering efforts to understand how best to regenerate a PDL that has been damaged. The goal of this project was to determine whether chewing patterns in mammals are correlated with the arrangement and direction of collagen fibers in the periodontal ligament. Specifically, I hypothesized that carnivorans, which chew in an up-down motion with high force, should maximize fiber number. In order to do this, fibers should be arranged radially at an average angle of 90 to the root. Stress should be greatest at the apex of the root. I embedded and sectioned mandible (lower jaw) samples from American mink (*Mustela vison*) into 7-micrometer slices, and examined the stained slides under a microscope to determine fiber angles. Samples were sliced in both horizontal and coronal planes. To assess stress, I created a finite element analysis (FEA) model of a single-rooted tooth using MSC Patran and Nastran, to which I can apply loads in various strengths and directions to simulate the response of the PDL under many different conditions. Due to lack of studies on the PDL in general, this is an isotropic model using material properties from the literature. Although this model is based on idealized geometry it should still show the correlation between stress and fiber angle for a given chewing direction. Preliminary results confirm the expectation of 90 fibers in carnivorans (86 ± 5). These data can now be incorporated into the FEA model. Future work will examine mammals with different chewing directions, such as rabbit (sideways motion) and mouse (forward motion).

Convergent Evolution of Blade-Like Teeth in Mammals

Abby Renee Vander Linden, Senior, Biology (Ecology, Evolution & Conservation)
Mentor: Gregory Wilson Mantilla, Biology

In evolutionary history, distantly related taxa have often independently evolved the same or similar complex structure as a solution to a common problem presented by their environment. One such example is the plagiaulacoid tooth—a laterally compressed shearing blade that convergently evolved in four clades of mammals, some extant and others extinct. To better understand the selective forces that led to the convergent evolution of this specialized trait in multiple lineages, I investigated how this tooth form correlates with diet in a sample of extant taxa. Specifically, I measured complexity of lower cheek tooth rows of 15 species from five families of extant marsupials with plagiaulacoid teeth. To quantify dental complexity I created digital 3-D models from microCT scans of these specimens and used GIS software to generate orientation maps of the tooth surfaces. Contiguous pixels with the same orientation are considered a patch on the tooth surface, and the number of patches approximates the number of shearing surfaces available to mechanically process food. Previous studies of placental mammals have shown that increases in Orientation Patch Count(OPC) (i.e., increases in tooth surface complexity) correlate with increased consumption of plant material. However, I found no correlation between OPC value and diet as recorded in the literature for these taxa. I then compared complexity of the blade to complexity of the molars to investigate the functional contribution of the plagiaulacoid tooth and again found no correlation with diet. Broader sampling will help determine the pattern of tooth complexity and diet in marsupials, but the range of OPC values generated in this study suggests that the convergent evolution of the plagiaulacoid phenotype is not a simple case of one morphological adaptation to a particular environmental problem.

Where Have All the Koalas Gone? A Survey of Arboreal Marsupials and Vegetation in Post-Disturbance Habitat in Springsure, Central Queensland, Australia

Clara Elaine (Clara) Summers, Junior, Eastern European Languages, Literature & Culture, Anthropology
Mentor: Alistair Melzer, Koala Research Centre of Central Queensland, Central Queensland University
Mentor: Tony Cummings

A trend of severe drought and bushfires due to climate change has led to extensive tree death and declines in arboreal marsupial populations at two sites, Minerva Hills and Wallalee, near Springsure, central Queensland, Australia, over the past decade. Researcher observations that the population dynamics may have shifted to domination by common brushtail possums (*Trichosurus vulpecula*) were the impetus for this study, which set out to establish baseline data for future monitoring. This study investigated how the vegetation and populations of koalas (*Phascolarctos cinereus*), greater gliders (*Petauroides volans*), and common brushtail possums have changed since the last studies, and what may have caused the changes. Spotlighting and listening surveys were conducted at each site, and a vegetation survey was also carried out using the point-quarter nearest neighbour method. At Minerva Hills, the greater glider population has declined and the koala population has almost fallen below detectable levels. Common brushtail possums, on the other hand, have had a population boom. The decline of greater gliders and koalas and subsequent increase of common brushtail possums was attributed to a recent bushfire, though previous droughts may also have had an effect. The Wallalee site was almost empty of arboreal marsupials and the vegetation reflected recent floods and previous clearing for agriculture. Recommendations for conservation included management of bushfires and connecting habitat fragments. It was concluded that the best method to protect the populations in these areas would be to combat climate change, and thus lessen the severity of drought, bushfires, and flooding.