

Michael J. Sheehan and Elizabeth A. Tibbetts**Frequency-dependent selection imposed by social interactions**

Identifying broad-scale evolutionary processes that promote and maintain phenotypic and genetic polymorphisms in natural populations has been a major goal of modern evolutionary biology. Here, we present the first experimental evidence that social interactions impose frequency-dependent selection by favoring individuals with distinctive, easily recognizable phenotypes. We show that paper wasps are favored to actively advertise their identities by having unique visual features. Given that recognition is an essential component of social interactions in many taxa, selection for distinctive identity signals may be an underappreciated and widespread mechanism underlying the evolution of phenotypic polymorphism.

Ryan Bebej**Inferring Swimming Mode from Skeletal Proportions in Early Pinnipeds (Mammalia, Carnivora)**

Pinnipeds are semiaquatic carnivores that have a fossil record dating back to the late Oligocene. While the Otariidae (sea lions and fur seals), Phocidae (true or earless seals), and Odobenidae (walruses) are almost certainly members of a monophyletic group, they differ from one another in their primary modes of aquatic locomotion. Otariids swim by oscillating their forelimbs, while phocids and odobenids swim typically by laterally oscillating their lumbus and hind limbs. Assessing the evolution of these derived swimming modes involves reconstructing the locomotor modes of fossil taxa and identifying when changes in swimming style occurred during the group's phylogenetic history. Previous studies of pinniped locomotor evolution suggested that there were only two major locomotor transitions in the history of the group; however, their interpretations of swimming mode in some key fossil taxa have been questioned by other analyses. The fossil pinnipeds *Enaliarctos mealsi* and *Allodesmus kelloggi* are known from virtually complete skeletons and can be quantitatively compared with modern semiaquatic mammals. A principal components analysis of trunk and limb measurements from 58 modern semiaquatic mammals (including 24 pinnipeds) separates the taxa on three primary axes: a size axis (PC-I), a relative aquatic adaptation axis (PC-II), and a swimming mode axis (PC-III). The analysis demonstrates that *Enaliarctos* has post-cranial proportions most similar to modern phocids, implying that it swam using primarily hind limb-dominated locomotion. *Allodesmus*, on the other hand, has proportions more similar to modern otariids, suggesting that it swam using primarily its forelimbs for propulsion. Both of these interpretations are counter to the swimming modes suggested for these animals in previous studies of pinniped locomotor evolution, and these results suggest that the evolution of swimming modes in pinnipeds may not have been as simple or straightforward as it has been portrayed.

Sarah Cobey

Ecological and evolutionary dynamics driving the emergence of influenza viruses in new species of hosts

The evolution of host range is shaped by host ecology and the physiological traits that determine host specificity. In many traits there is a tradeoff: a phenotype suitable for infecting one set of hosts poorly infects another. The focus of this work is how such a tradeoff could affect the evolution of influenza viruses¹ host ranges. We choose one trait underlying host range, the virus's preference for certain conformations of sialic acid receptors, and consider how this preference evolves in a minimal network of host species that differ in their life history and physiology. Using the approach of adaptive dynamics, we find thresholds in interspecific contact rates and host population sizes that allow the emergence of human-adapted viruses. These thresholds are largely robust to the strength of the tradeoff. However, the ability of human-adapted viruses to coexist indefinitely with avian-adapted viruses is quite sensitive to tradeoff strength. Since there is evidence suggesting that tradeoff strength differs between subtypes, our results indicate that their equilibrium host ranges may differ. Furthermore, interventions directed at changing host ecology, such as the contact rates between species, will have a nonlinear effect on viral diversity before evolutionary end points are reached.

Rachel Vannette

Relative impacts of plant genotype, mycorrhizal fungi, and elevated carbon dioxide on the defensive phenotype of *Asclepias syriaca*

Jessica Middlemis

Larval stressors and their post-metamorphic consequences in the wood frog (*Rana sylvatica*)

Measures of physiological stress are being increasingly used by ecologists to determine the sub-lethal impacts of environmental conditions on wild populations. However, current conditions are not the only factors that may influence stress physiology: studies using laboratory animals have shown that early-life experiences may impact an organism's response to stressors through adulthood. I present a three-part study that combines work in the field and lab to show that larval stressors experienced in the aquatic stage may subsequently affect fitness in the terrestrial juvenile and adult stages of the wood frog, *Rana sylvatica*. Specifically, I found that variation in stress hormone production among tadpoles in 10 different ponds corresponds to variation in their aquatic communities. I also show that one of these stressors, predator presence, not only affects tadpole physiology but goes on to change the activity and reactivity of the stress axis even after metamorphosis. Finally, I found that individuals that experienced predation cues as tadpoles are subsequently less able to resist desiccation as juveniles, an effect that is likely tied to survival in the terrestrial environment. Together these results demonstrate

the need to consider the long-term consequences of early experiences in relation to environmental stressors.

Zach Miller

Effects of a Plant Pathogen, *Puccinia podophylli*, on Host Abundance and Plant Community Composition in Eastern Deciduous Forests

Katie Goodall

Intensification and Infestation: agricultural management and avian ectoparasites in Chiapas, México

This study investigates the relationship between coffee agricultural management and avian ectoparasite load in an attempt to better understand how management decisions may ultimately play a role in the extent to which parasitism impacts the survivorship of birds inhabiting coffee systems. During the rainy season of 2006 (May to July) passerine birds were captured by mist-netting in habitats of a coffee agroecosystem in the Soconusco Region of Chiapas, Mexico. The four habitats represent agricultural intensification: shaded monoculture, commercial polyculture, traditional polyculture, and forest fragment (Moguel and Toledo 1999). Standard morphometric and status measurements were collected, including three indices of body condition. After measurement, ectoparasites were removed from birds using standard feather dusting methodology (Clayton and Walther 1997; Lindell, Gavin et al. 2002) and later quantified, identified and analyzed in the laboratory. Different patterns were observed for different parasite groups. While mite prevalence was positively related to agricultural intensification, lice prevalence was not. On the other hand, the intensity of lice infestation on bird hosts was positively related to agricultural intensification. These results suggest that agricultural management may play an important role in avian ectoparasite loads across an agroecosystem.

Mandy Izzo, Michael Wells, Zachary Huang, and Elizabeth Tibbetts

Support for the Fertility-Signaling Hypothesis by the Cuticular Hydrocarbon Profile in the Paper Wasp, *Polistes dominulus*

Cooperatively breeding animal societies are characterized by having dominant individuals that monopolize reproduction, and workers that forgo reproduction. In social insects, dominance hierarchies are typically used to determine reproductive rank, but the nature of signals that initiate and maintain the reproductive primacy of social insect queens are poorly understood. Aggression can be used to initiate and maintain the hierarchy by intimidating rivals or workers into helping, and signals of dominance may be used to maintain the hierarchy after physical aggression ceases. Conversely, signals of

fertility may be used to indicate the potential indirect benefits related helpers will gain by working for a particular queen; this is especially important as workers gain no direct benefits. It has been shown in paper wasps that ranks within a nest are chemically distinguishable by cuticular hydrocarbon profiles and that ovarian development correlates with these ranks. Consequently, a debate over whether social insect queens signal their dominance versus fertility status through their cuticular hydrocarbon profile remains unsolved. Here we show that paper wasp queens are likely utilizing chemical signals of fertility and not dominance. We conducted our study before nests were initiated, and as a result this is the first study to examine the potential signaling roles of the cuticular hydrocarbon (CHC) profile when dominance and fertility were not confounded by rank. We found no relationship between cuticular hydrocarbon profiles and the ability to dominate rivals through aggression. We did however find a strong and significant relationship between ovarian development and the CHC profile, which is expected and necessary if CHCs act as signals of fertility. Finally, we discovered a link between endogenous juvenile hormone (JH) titer, degree of ovarian development, and CHCs. JH may act as the mechanism by which social insects can signal fertility. Fertility signaling by queens offers an evolutionarily stable strategy for gaining and maintaining cooperation within a nest.

Doug Jackson

Indirect influence of an entomopathogenic fungus on the spatial distribution of ant nests in a tropical agroecosystem

A recent study has shown that the spatial distribution of nests of an arboreal-dwelling ant, *Azteca instabilis* (Formica, Hymenoptera), in a tropical coffee agroecosystem may emerge through self-organization. The proposed self-organization process involves both local expansion and density-dependent mortality of the ant colonies. We explored a possible mechanism for the density-dependent mortality involving the entomopathogenic fungus *Verticillium lecanii*. *V. lecanii* attacks a scale insect, *Coccus viridis* (Coccidae, Hemiptera), which is tended by *A. instabilis* in a mutualistic association. By attacking *C. viridis*, *V. lecanii* may have an indirect, negative effect on ant colony survival. To explore this hypothesis, investigations into the mechanisms of fungal spore dispersal and the spread of the fungus at multiple spatial scales were conducted. The hypothesis that *V. lecanii* spores are transported by *A. instabilis* was tested in field and laboratory ant exclusion experiments. The ant exclusion experiments suggest that *A. instabilis* is capable of transporting *V. lecanii* spores, but that other transport mechanisms dominate in the field. In addition, a spatially-explicit computer model of the self-organization process was developed incorporating field survey and photographic data of the spread of the fungus at multiple spatial scales.

Zhi Wang**Abundant indispensable redundancies in cellular metabolic networks**

Cellular life is a highly redundant complex system, yet the evolutionary maintenance of the redundancy remains unexplained. We infer that 37-47% of metabolic reactions in *E. coli* and yeast can be individually removed without blocking the production of any biomass component under any nutritional condition. However, the majority of these redundant reactions are preserved, because they have differential maximal efficiencies at different conditions or their loss causes a fitness reduction that can only be recovered via evolution. The remaining redundancies are attributable to pleiotropic effects or recent horizontal gene transfers. Thus, redundant reactions need not be kept as backups and the genetic robustness of metabolic networks is likely an evolutionary byproduct.

Akane Uesugi**Enemy-free Space in temporally and spatially heterogeneous environment: the leafminer escapes parasitism by using ephemeral host plant species****Diego Alvarado-Serrano****Evaluating the relative importance of environmental variables in the distribution of genetic variants: a preliminary assessment in the Soft Grass Mouse (*Akodon mollis*)**

Despite growing interest in modeling geographic ranges of species and populations, relatively few analytical tools exist to evaluate the relative importance of different environmental predictors in driving patterns of genetic differentiation. The set of variables employed in analyzing geographic structure in populations have traditionally been subjectively chosen given the general lack of systematic procedures to estimate their significance. Yet, the set of predictors employed strongly determine the outcome and accuracy of models. This work is a preliminary exploration of the possibility of using landscape-resistance models as an indirect approach to assess the role of different environmental variables in shaping the spatial distribution of intra-specific genetic variation. I generated landscape-resistance grids for Ecuadorian populations of the Soft Grass Mouse (*Akodon mollis*) based on mean annual temperature, mean annual precipitation, vegetation type, elevation and slope. From these grids, I extracted the resistance values corresponding to the geographic location of genetically distinctive populations of *A. mollis*, and conducted simple and multiple linear regressions of these values on the inter-population genetic distance. The results indicate a high degree of correlation between all variables which hinders the utility of landscape-resistance models in understanding the importance of the different variables. Only the regression between genetic distance and the resistance values based on annual mean precipitation was statistically significant. Yet, this result should be interpreted with caution given the

preliminary nature of the analysis. Further investigation is needed based on a greater population sample and under a historical perspective.

Wenfeng Qian and Jianzhi Zhang

Is protein subcellular relocalization important in the functional divergence of the duplicate genes?

Gene duplication is the primary source of new genes and is important in the evolution of novelty. But, how duplicated genes become fixed and retained in the genome is still an open question. Ashley and Geeta (2007 TREE) proposed protein subcellular relocalization as a means of functional divergence between duplicate genes. To test this hypothesis, we compared the subcellular relocalization rate of duplicate genes generated from the whole-genome duplication that occurred in an ancestor of the yeast *S. cerevisiae* with that of singleton genes. We found that duplicates do NOT have higher subcellular relocalization rates, and thus cannot be an important mechanism during functional divergence of duplicate genes.

Ben-Yang Liao

Co-expression of Linked Genes in Mammalian Genomes is Generally Disadvantageous

Understanding how genes are arranged in a genome and are co-regulated is an important task of genome biology. Similarity in gene expression pattern between linked genes is known in several eukaryotes. Two models have been proposed to explain the presence of such co-expression patterns. The adaptive model assumes that co-expression is advantageous and is established by relocation of initially unlinked but co-expressed genes, whereas the neutral model asserts that co-expression is a type of leaky expression due to similar expressional environments of linked genes, but is neither advantageous nor detrimental. However, these models are incompatible with several empirical observations. Here we propose that co-expression of linked genes is a form of transcriptional interference that is disadvantageous to the organism. We show that even distantly linked genes that are tens of megabases away exhibit significant co-expression in the human genome. However, the linkage is more likely to be broken during evolution between genes of high co-expression than those of low co-expression and the breakage of linkage reduces gene co-expression. These results support our hypothesis that co-expression of linked genes in mammalian genomes is generally disadvantageous, implying that many mammalian genes may never reach their optimal expression pattern due to the interference of their genomic environment and that such transcriptional interference may be a force promoting recurrent relocation of genes in the genome.

Dan Chang

Size and Evolution of Conotoxin Gene Families of Predatory Cone Snails

Celia K. Christianson

Historical Ecology of the Neuston

Huateng Huang

The effect of mutation variance in reconstructing the divergent history of closely related species

Timothy Connallon

Sex-linked inheritance, genic capture, and the lek paradox

Heather E. Adams, B.C. Crump*, and G.W. Kling

Bacterial Community Composition and DOM Control Downstream Processing in Arctic Lakes and Streams

Sarah Barbrow, Heather Adams, Byron Crump, John Hobbie, and George Kling

Kinetics of Substrate Uptake and Activity of Bacteria in Arctic Lakes

Susanna Messinger

The Effects of Spatial Structure on the Evolution of Predator-Prey Interactions

The interaction between two species is shaped by numerous abiotic and biotic factors. Within predator-prey interactions there is growing evidence that spatial structure can significantly influence the strength of the interaction. Evolutionary simulations of predator-prey dynamics where the predator is a pathogen and the prey its host suggest that spatial structure can constrain the evolution of the predators proficiency at exploiting the prey. When the predator-prey dynamics are localized in space, the predator experiences a tradeoff between its predatory proficiency and its persistence in the population. This tradeoff leads to selection for predators of intermediate proficiency. To date, the effect of spatial structure on the evolution of predator proficiency has been done using individual based models (IBMs). While

realistic for pathogen-host interactions, many other predator-prey interactions are more aptly modeled using a metapopulation framework. In IBMs the predator-prey dynamics are localized by 1) restricting colonization distance and 2) limiting predators to adjacent prey. In metapopulation models where each site is occupied by entire predator and prey populations instead of individuals, there is an additional component: the rate of movement between adjacent sites. The goal of this research is to determine how migration rates affect the evolution of predator proficiency.

Kerry Kim**Simulation of evolution in the Drosophila Segment Polarity Network**

The Drosophila segment polarity genes constitute a regulatory network that maintains the boundaries between parasegments during development. A computer model that reconstitutes this network is astonishingly robust to parameter variation (von Dassow et al. 2000. Nature 406:188-192). Here we investigate how diploidy and sex affect robustness in this network using an extension to our model that allows it to bridge genotype to phenotype and simulate evolution of the segment polarity network. We compared the robustness of diploid and haploid networks and found diploidy conferred greater robustness to simulated mutations by allowing a working allele to mask the effect of a deleterious mutation. However, it remains unclear whether diploidy confers an evolutionary advantage because beneficial mutations should be similarly masked. We then simulated evolution of diploid and haploid populations that reproduced either sexually (with random mating & recombination) or asexually (clonally). Sexual populations rapidly evolved increased robustness to both mutations and environmental variation (simulated as noise in the prepattern or variation in all model parameters), with the highest robustness attained in sexual diploid populations. Thus, diploidy, especially in conjunction with sexual reproduction, can confer a robustness advantage at the level of gene networks.