Melissa M. Mark

The effects of nest parasitism by *Tapera naevia* on two species of wren, *Thryothorus rufalbus* and *Thryothorus modestus*, in a modified landscape in Nicaragua

Abstract
We examined the impacts of nest parasitism by the Striped Cuckoo, *Tapera naevia* on nest success in two of its documented host species, *Thryothorus modestus* and *Throythorus rufalbus*. These two species differ in their distribution in forest vs. human-altered habitats and so provide an instructive comparison of habitat use patterns and rates of nest parasitism in a modified landscape. Recent studies have shown that the relationship between forest fragmentation and nest success in temperate birds may be scale dependent. In this study, nest parasitism across habitat types was compared at three scales: nest site, territory site, and local landscape. Nest parasitism on *T. rufalbus* was significantly greater than that on *T. modestus* across all scales. Nest parasitism had the greatest negative impact on *T. rufalbus* on nest site located in coffee and in territory sites neighboring coffee or agricultural fields. The rate of nest parasitism on *T. rufalbus* decreased as distance of the territory from agricultural fields increased. At the local landscape level, the proportion of agricultural fields was positively correlated with higher rates of nest parasitism. A more complicated relationship emerged between the proportion and distribution of shade coffee and rates of nest parasitism.

Adam Ehmer

Herbivory impacts inherited variation in herbivore performance via induced changes to plant quality

Abstract
Niche construction occurs when organisms modify their environment in a way that changes natural selection on themselves. Multivoltine herbivorous insects in temperate climates are particularly susceptible to niche construction because they affect their resource base quantitatively and qualitatively over the course of their growing season. Specifically, the act of herbivory can induce changes in plant quality that impact the performance of subsequent herbivores. Niche construction can be an important evolutionary force if the traits that contribute to niche construction and the traits that respond to niche construction are genetically variable and under selection. The Colorado potato beetle, *Leptinotarsa decemlineata*, is a multivoltine herbivore that feeds on crops and weeds in the genus *Solanum*. The effects of prior beetle herbivory, through changes in plant quality, on the performance of a later generation of beetles were examined in a quantitative genetic framework. Beetles that fed on foliage from previously damaged plants gained less weight as larvae, took longer to develop, and eclosed at lighter weights compared to beetles that fed on undamaged control plants. There was no significant additive genetic variation for any trait measured, but maternal effects were significant for most traits. The magnitude of maternal effects were greater for beetles that fed on foliage from previously damaged plants, suggesting that niche construction could affect evolutionary responses both by altering natural selection and the expression of inherited variation. Genetic correlations suggest that traits contributing to niche construction are positively correlated with those that are sensitive to niche construction.

Sarah M. Gray

Not just an ant trap anymore: using a model system to examine the effect of perturbations on community dynamics.

Abstract
The aquatic community found within the leaves of the carnivorous pitcher plant *Sarracenia purpurea* has been used for decades as an ideal model system for addressing fundamental questions in community ecology. In the experiment I present here, I used this system to test the affect of both biotic and abiotic perturbations on community dynamics. Experimental perturbations include: 1) introduction of a competitively superior intermediate trophic level species, 2) introduction of a competitively superior bottom trophic level species, and 3) a low pH (acid rain) physiological disturbance. All three treatments were added in a full factorial design to replicated communities to test the implication that all possible combinations of these disturbances would have on food web dynamics. I found that the community was dramatically affected by a combination of a low pH disturbance and the introduction of a competitively dominate intermediate trophic level species. This combination caused a reduction in abundance of the other species at the intermediate trophic level. The bottom trophic level species, however, were unaffected by the introduction of either of the competitively dominate species or the low pH treatment. The competitively dominate bottom trophic level species was never able to become completely established in the community, suggesting that there must be a trade-off with its competitive ability, making it more vulnerable to predators and disturbances. This experiment suggests the importance of examining all trophic levels in a system to gain a better understanding of the interactions occurring within an entire community in the face of both biotic and abiotic disturbances.

Sam Amell

Individual recognition and "eavesdropping" during dominance contests in Nile tilapia (*Oreochromis niloticus*)

Abstract
The social intelligence hypothesis states that organisms living in complex social groups can be expected to evolve cognitive abilities commensurate with group living, such as the ability to recognize individuals, track their social interactions, and make inferences about relationships (Humphrey 1976). This hypothesis was originally proposed to explain the evolution of intelligence and large brain size in primates but is now being applied to other taxonomic groups including corvids (Bond et al. 2003) and cichlid fish (Grosenick et al. 2007). We tested the ability of males of a lek-breeding species of cichlid fish, *Oreochromis niloticus*, to recognize individual group members with which they had previously interacted. We also tested the behavioral response of males that were allowed to 'eavesdrop' on dominance contests involving known group members. We hypothesized that Nile tilapia are capable of recognizing group members and would respond differently when observing a dominance contest involving at least one known individual versus observing a contest between two strangers. Males (eavesdroppers)

were allowed to view two fish (demonstrators) interacting in a central compartment from behind one-way mirrors. Using a matched pairs design, we found that eavesdroppers watching known individuals scored higher in two separate behavioral measurements than eavesdroppers watching strangers: the number of charges against the partition divider, and the average proximity to the demonstrators. In a separate experiment, we found that male tilapia respond differently to a stranger if they have just observed that individual defeat their dominant. This could constitute evidence for the use of social transitive inference in this species, and has several implications for the formation of dominance hierarchies in social groups.

Shu-Dan Yeh and John R True

Mapping the genetic region for the loss of two functionally-related trait, wing spots and wing display, in *Drosophila gunungcola*

Abstract
How traits evolve through time is a fundamental question in developmental evolutionary biology. Using quantitative trait locus (QTL) analysis and gene mapping, many studies have been able to dissect the genetic basis of morphological evolution. However, morphological traits often evolve coordinately with other traits, such as behaviors. The non-independent loss of these traits in phylogenetic tree brings up the question on whether genetic constraints, such as physical linkage and pleiotropy, were built up during the evolution of co-opted traits and lost simultaneously as a consequence. In the oriental *Drosophila melanogaster* species group, the presence of wing spots, black patches on the apical wings of males, co-occurs with the wing display, showing both wings in front of a female, in the phylogeny. We carried out a QTL analysis in the backcross hybrid males of *D. elegans*, which possess both traits, and *D. gunungcola*, which has lost both traits since divergence from their common ancestor. As shown by reciprocal F1 hybrid males, the X chromosome strongly influences the presence of wing spots. Interestingly, the X chromosome also has a large effect on the interspecific difference of courtship. A very strong QTL near the gene yellow, which showed differential expression in wing spot region in previous studies, for both traits suggests that tight linkeage or pleiotropy may be responsible for the simultaneous loss of both traits in *D. gunungcola*. Furthermore, the difference of QTL analysis results in courtship between two backcrosses suggests a more complicated genetic architecture for courtship behavior.

Dianna Padilla

Invaders are not a random selection of species

Abstract
We assembled information on 119 freshwater macroinvertebrate invaders in North America and Europe, and compared them to all native freshwater species in North America and Europe. We tested whether the invaders were a random or selected group among taxa (phylum or class), water quality requirements, and feeding habit. We found that freshwater macroinvertebrate invaders are not a random selection of species, and are over represented by molluscs and

crustaceans, while native communities are dominated by insects. Over 35% of native aquatic invertebrates in North America are only able to live in areas with excellent or very good water quality, and are intolerant of organic pollution. In contrast, all invaders are tolerant of at least moderate amounts of organic pollution. There was a significant difference in the distribution of feeding habits between native species and invaders: collector-filterers (including suspension feeders) were 2.5 - 3 times more abundant, and predators were 3 - 4 times less abundant among invaders than among native invertebrates. The ongoing spread of exotic species affects the biodiversity of selected taxa, shifts communities toward greater tolerance of organic pollution and increases the numbers of suspension feeders, thereby enhancing benthic pelagic coupling in waterbodies with high densities of invaders. Because these processes are very similar in Europe and North America, we suggest that the observed patterns may have a common global effect.

Ramona Walls, R. Geeta

Coordinated variation in *Dioscorea* leaf traits and functions linked to leaf size

Abstract
Well-established, global-scale suites of correlated leaf traits arise from trade-offs between the ability to assimilate carbon and the ability to persist. These global patterns have made a significant contribution to explaining plant diversity, but only include a small set of traits. Because precipitation is one of the major factors associated with plant variation and the major axis of climatic variation in my study system (Mexican *Dioscorea*), I analyzed variation in leaf traits related to water use, in the context of global patterns. My goal was to determine if there were patterns of correlated trait evolution within this group and if there were structural traits that could serve as surrogates for physiological functions. I conducted a common garden comparative study using 20 morphological, anatomical and physiological leaf traits in 12 *Dioscorea* species. The major axis of variation was for traits related to leaf size. All size traits were correlated with the major hydraulic functions of leaves, probably due to the correlation between leaf size and the size of conducting elements. While correlations from global studies (leaf mass per area, photosynthetic rate and N content) were present, they were weak, and independent of correlations related to water use and size. These results suggest that there may be at least two major axes of leaf trait variation, one related to carbon and nitrogen allocation and one related to water use, and that size may be a good indicator of water use strategy, at least among closely related species.

Zhu Lei

Mapping of *Drosophila melanogaster* reproductive diapause

Abstract
As *Drosophila melanogaster*, originated from sub-Sahara Africa, dispersed recently into the rest of the world, overwintering survivorship became critically important. Diapause is one of the most important adaptations to seasonality for *Drosophila melanogaster*. We identified a single

replacement change, which results in a Lys/Ile substitution in the RNA binding protein couch potato (cpo), determining diapause phenotype.

H. Resit Akcakaya

Predicting extinction risks under climate change: coupling stochastic population models with dynamic bioclimatic habitat models

Abstract
Current approaches to predict the impact of global climate change on biodiversity include bioclimatic modeling to predict potential shifts and contractions in species' ranges. In reality, the species response to climate change is likely also involve population processes, species interactions, and interactions between demographic and landscape dynamics. In this study we used a novel mechanistic approach to predict the impacts of climate change on plant population viability in South African fynbos, one of the world's biodiversity hotspots. We linked dynamic habitat suitability models with spatially explicit stochastic population models to determine how variations in plant life history, disturbance regime and distribution patterns influence the viability of populations under stable and changing climate scenarios. Results indicate that complex interactions between life history, disturbance regime and distribution pattern mediate whether particular species will be exposed to increased extinction risks under climate change. Our mechanistic approach allows more realistic prediction of future biotic responses than do static bioclimatic niche modeling approaches, and will ultimately support the development of more effective conservation strategies to mitigate biodiversity losses due to climate change.

Joshua A. Banta, Scott C. Stark, Martin H. H. Stevens, Thomas H. Pendergast IV, Anthony Baumert, and Walter P. Carson

Light reduction predicts widespread patterns of dominance between asters and goldenrods

Abstract
Here we investigate the long cited pattern that throughout the eastern United States, *Solidago* species (goldenrods), and in particular *S. canadensis* displace *Aster* species and dominate old-field communities. Theory predicts that such a ubiquitous pattern of repeated dominance should be linked to competitive ability for a limiting resource. However, no one has investigated this possibility in old-fields, representing a potentially significant gap in our understanding of a common human-altered environment. We tested the hypothesis that *S. canadensis* is the superior competitor for light compared to other common co-occurring goldenrod species, and that the goldenrods in general are the superior competitors for light compared to coexisting aster species, which are typically less abundant. We tested this hypothesis by comparing the light attenuation abilities of four goldenrod species, *S. canadensis, S. rugosa*, *S. gigantea*, and *Euthamia graminifolia*, and three aster species, *Aster novae-angliae*, *A. pilosus*, and *A. prenanthoides*. Consistent with our hypothesis, *S. canadensis* had a greater ability to attenuate light than any of the other goldenrods at higher densities, and the goldenrods overall had a greater ability to attenuate light than the asters. By conducting a census in our study area we verified that *S. canadensis* is locally the most abundant goldenrod and that goldenrods are more locally

abundant than asters. Furthermore, by conducting a literature survey we found evidence that *S. canadensis* replaces *A. pilosus* through time. Thus we found a close correspondence between relative abundance in the field and light attenuation ability in field experiments. These results are consistent with theory predicting that competition for limiting resources, in this case light, explains patterns of dominance and relative abundance in old-field plant communities.

Daniel S. Moen and John J. Wiens

Phylogenetic evidence for competitively-driven divergence: Body-size evolution in Caribbean treefrogs (Hylidae: *Osteopilus*)

Abstract
Understanding the role of competition in evolutionary divergence is a challenging problem, given that species that have diverged the most may no longer compete today. However, phylogenetic analyses that show convergence in body-size extremes across communities (i.e., repeated evolution of large and small species) may offer evidence of competitively driven divergence in the past. For example, most regional assemblages of treefrogs around the world contain similar body-size extremes, which appear to have evolved convergently many times. To better understand this global pattern, we studied body-size diversification within the small, endemic radiation of Caribbean treefrogs (Osteopilus), combining analyses of community assembly models, phylogeny, and rates of body-size evolution. Community assembly models show significant deviations from a random model in Caribbean assemblages. Phylogenetic analysis shows that similar body-size extremes on Jamaica and Hispaniola have originated through parallel evolution on each island, rather than through dispersal. Furthermore, the rate of body-size evolution in Osteopilus is much higher than in mainland South American treefrogs, indicating that body-sizes extremes in Osteopilus evolved through deterministic processes. Together, these results suggest that competition may have rapidly driven the diversification of body sizes in Caribbean treefrogs to the extremes seen in older, more species-rich communities around the world.

Joshua Rest

Evolution of untranslated RNA and transcriptional dark matter

Abstract
Expressed but untranslated regions (UTRs) of genes are now known to participate in gene regulation. Using a tiling microarray assay of genome-wide expression levels, we identify length variation of UTRs among different stress conditions in four yeast strains. We characterize the evolution of these condition-dependent length differences between strains, assess their potential impact on the regulatory evolution of stress response, and look for associations with nucleotide change. It has also been observed that there is widespread transcription in the intergenic regions of eukaryotes, leading to the idea of transcriptional dark matter. We characterize the evolution of condition-specific intergenic expression, and assess the hypothesis that it represents neutral change due to gain and loss of spurious binding sites.