

Adams, H.E., B.C. Crump, and G.W. Kling. Bacterial physiological adaptation versus structural shifts in community composition.

Experiments were performed to determine the effect of community composition on system function (bacterial production) in arctic Alaska. In this system bacterial production is controlled by: community, temperature, nutrients, and carbon source. Lake inlet and outlet communities in these experiments were different in composition, based on PCR-DGGE fingerprinting of 16S rDNA. For both communities, nutrient additions increased bacterial production far more than warmer temperatures. Inlet communities were more responsive to temperature increases, and sustained nutrient-stimulated production rates longer than the outlet communities. It is known that bacterial diversity will shift to an optimal composition for given environmental conditions. During a five-day experiment in which temperature, community, and carbon source were manipulated factorially, the two communities shifted towards compositions distinct from each other. Community composition was influenced by temperature more than the provided carbon source. In addition, community composition shifted in response to the nutrient addition over a two week time period. These results imply that bacterial diversity can control system function by mediating community response to shifting environmental conditions such as temperature and nutrient availability both by physiological response and shifting in predominance of community members.

Chang, Dan. Functional genomics: Evolution of venoms of predatory snails

Members of the predatory marine gastropod genus *Conus* use a venom comprised of potent neurotoxins, termed conotoxins, to paralyze prey. Venom composition differs tremendously among *Conus* species and these differences are presumably related to different feeding specializations that *Conus* species exhibit. Previous studies of conotoxin gene transcripts have demonstrated that conotoxin genes are members of large gene families and differences in venom composition among *Conus* species apparently result from unique conotoxin gene expression profiles. However, nearly all of our understanding of the evolution of *Conus* venoms has relied on analyses of conotoxin expression data (mRNA transcripts and peptides) and very little is known concerning the size, organization, regulation and evolutionary history of conotoxin gene families. I will use several approaches, such as PCR amplification, genome library construction and probing, Southern blots, and FISH (Fluorescent In Situ Hybridization), to investigate the evolution of these gene families. Here I report on the diversity of conotoxins derived from *Conus* species genomes determined from amplification of conotoxin gene sequences from genomic DNA. Such studies will tremendously advance our understanding of expression patterns, selection and evolution of ecologically relevant genes.

Chatfield, Matthew. Hybrid Zone Dynamics between Salamanders in the Genus *Plethodon*

Hybrid zones are active areas of research into the causes of speciation and maintenance of species boundaries. This study examines the pattern of introgression of a quantitative trait under putative positive selection through comparison with mitochondrial and nuclear genetic markers. *Plethodon jordani* and *P. metcalfi* (Plethodontidae) form a narrow hybrid zone in the Southern Appalachians of North Carolina. *Plethodon jordani* possesses aposematically colored red cheek patches while *P. metcalfi* has gray cheeks. Introgression of red cheek pigmentation through the hybrid zone across two transects is assessed. This pattern is then compared to a mitochondrial DNA marker. Data collected to date show differences in introgression between red cheek pigmentation and mitochondrial DNA. These data can be interpreted in one of two ways, either (1) red cheek pigmentation is differentially introgressing into the *P. metcalfi* population or (2) that *P. metcalfi* mtDNA is introgressing into the *P. jordani* population. Additional data from nuclear markers is required to distinguish between these alternatives.

Chaves, Luis Fernando & Cohen, Justin M. Schmalhausen's Law and the spatio-temporal patterns of Cutaneous Leishmaniasis in Costa Rica

Schmalhausen's Law, the prediction that a system at the boundary of its tolerance along any dimension of its existence is more vulnerable to small differences along other such dimensions, is extremely relevant to study the effects of global environmental change. It implies that above certain threshold values, or ecological breakpoints, the way in which populations can respond to changes in endogenous and exogenous factors can be greatly amplified. It also implies that the stress caused by new or unusual environmental conditions can exacerbate the effects of regular changes in others.

Analyses of the incidence for American Cutaneous Leishmaniasis at the county level in Costa Rica from 1996 to 2000 provide clear evidence for these implications. The spatio-temporal distribution of the disease is clustered in counties where the highest levels of social marginalization are also clustered. Further analysis ruled out the possibility that disease clustering is driven by landscape or environmental characteristics.

The differences within the subset of counties where the disease is present are best explained by a linear relationship with minimum county elevation, and articulated (i.e., with breakpoints) relationships with rainfall, proportion of people living close to the forest and social marginalization. These variables explain a large fraction of the variance in a statistical model with very high goodness of fit ($R^2=76$).

To gain insight on the role of climate on the spatio-temporal dynamics of the disease, the impact of the El Niño Southern Oscillation (ENSO) on the annual incidence of the disease was evaluated. Models considering the role of ENSO and the variability due to the geopolitical hierarchies of counties belonging to provinces were fitted. The results showed the hierarchy to be significant, with the highest level of variability at the county level, and without a significant effect of ENSO for the whole country. However, a model ($R^2=85\%$) for the counties where the disease is clustered, showed ENSO to be a significant factor, with counties differing in their response to ENSO, probably because of

differences in forest cover, with incidence decreasing during ENSO events in counties with larger proportions of forest cover ($P < 0.05$).

Our results robustly show the role of social outcasting as a major factor shaping the spatio-temporal distribution of the disease. It also shows, against the common belief, that forest cover and distance of households to the forest decrease the disease risk. This fact may indicate the role of disturbed landscape matrices in promoting the transmission and emergence of this disease. Finally, our study points out the need for an integrated agenda to avoid the emergence and spread of zoonotic diseases, conserve biodiversity and promote ecologically sound social development. It also underscores the necessity to understand the contextual determinants of disease transmission to fully assess the effects of climate change.

Connallon, Tim. Adaptive protein evolution of X-linked and autosomal genes in *Drosophila*: implications for faster-X hypotheses

Evolutionary theory predicts that sex chromosomes can either enhance or inhibit adaptive divergence, but it is not known whether sex chromosomes and autosomes do in fact have different adaptive rates of divergence. Using population genetic and divergence data from *Drosophila melanogaster* and *D. simulans*, I show that X-linked genes exhibit stronger signatures of adaptive divergence than autosomal genes. This pattern is due to a higher rate of recombination on the X, which enhances the efficacy of natural selection and promotes adaptation. This property of sex-linkage results from a widespread pattern found in both plant and animal taxa – recombination rates intrinsically differ between males and females, and in most cases is biased towards the homogametic sex (females in the case of *Drosophila*), the sex in which X-linked genes are more often found (two-thirds of the time for X-linked vs. one-half the time for autosomal genes). These results have important implications for the genomic architecture for quantitative traits and for patterns of speciation caused by postzygotic reproductive isolation.

Crants, James E. & Rathcke, Beverly. When a good flower gets a bad name: facilitation of mayapple (*Podophyllum peltatum* L.) pollination by co-flowering neighbors is not always a case of pollination by deceit.

Pollination by deceit occurs when a plant species' flowers advertise a reward that they do not provide. Mayapple (*Podophyllum peltatum* L., Berberidaceae), a nectarless herb of eastern North American deciduous forests, has been identified as a deceptively pollinated plant. Its major native floral visitors, bumble bee queens (*Bombus* spp.), probe for (absent) nectar but never collect (copious) pollen, though exotic honeybees (*Apis mellifera* L.) do gather pollen. Consistent with a reliance on exploratory visits by naïve pollinators to effect pollination, one study found mayapple to have higher visitation, fruit set, and seed set in proximity to a dense patch of common lousewort (*Pedicularis canadensis* L.), a nectar-rich, co-flowering species.

We set out to address two questions. (1) If a dense patch of highly rewarding flowers can facilitate mayapple pollination, can diffuse patches of less rewarding flowers do the same? (2) Do pollinators in our system visit mayapple for nectar or do they forage on its abundant pollen? We observed too few visits to analyze visitation rate, but based on fruit set, wild geranium (*Geranium maculatum* L., Geraniaceae) and garlic mustard (*Alliaria officinalis* L., Brassicaceae) appear to facilitate mayapple's pollination and compete with it for resources.

However, mayapple shares no pollinators with garlic mustard, and removal of neighboring flowers did not significantly reduce reproductive success. Seed set per fruit, like fruit set, was strongly pollen-limited, but seed set results were otherwise difficult to interpret. *Bombus* queens in our sites gathered pollen from mayapple flowers, but did not probe for nectar. The large number of shriveled pollen grains in mayapple anthers is consistent with its dual role as pollinator reward and male gametophyte.

Evans, Mary Anne, MacIntyre, Sally & Kling, George. Internal wave effects on photosynthesis: surfing phytoplankton produce more

Internal waves are ubiquitous in stratified aquatic environments and impact light and nutrient availability to phytoplankton. In this study we used field experiments and mathematical models to determine the effects of internal waves on phytoplankton light climate and photosynthesis. Phytoplankton were moved across depth to mimicking common internal waves, which resulted in photosynthetic rates up to two-fold higher than static incubations. Experiments and modeling revealed that wave effects on photosynthesis depended strongly on surface light variation due to cloud cover, and how that variation interacted with the relative phase of internal waves. Internal wave fields in a wide variety of aquatic systems show a strong potential for wave-induced enhancement of primary production. The realization of this enhancement is dependent on characteristics of the internal waves, of algal photosynthetic response, and of variable surface light.

García-Villacorta, Roosevelt. Phylogeography of Neotropical Figs and Fig Wasps: Understanding the Role of Pollinator Host Switching in Plant Speciation

Figs (*Ficus*, Moraceae) are among the most diverse group of flowering plants. Globally they are represented by approximately 800 species, of which 132 species occur in the tropics of the New World. Tight co-speciation with wasps of the Agaonidae family, which depend on the unique fig inflorescence (syconia) to complete its life cycle, has been proposed early in the study of this association as the main mechanism underlying the high fig diversity. A recent study in the rainforests of Panama has challenged the idea of tight co-speciation between figs and their pollinating wasps (Machado 2005). Specifically, it has been proposed that hybridization and introgression due to pollinator host switches maybe one of the reasons why figs are so extremely diverse. Thus, within a region a particular species of fig can be pollinated by more than one phylogenetically distant species of wasp, breaking the rule of host specificity. Further, the association of fig-pollinating wasps and their fig hosts may change at different regions of the host geographic range. There is also the possibility that fig-pollinating wasps have speciated independently of their host plant species (without host switching) and both mutualists may reflect a non-parallel cryptic divergence not detected by prevalent morphology-based taxonomy. This project will attempt to answer the following questions: What is the degree of genetic divergence between populations of six species of figs and their pollinating wasps? Are the same species of wasps pollinating the same host figs at different regions? The fieldwork will be conducted at the rainforests of Barro Colorado Island (BCI, Panama), and the Peruvian Amazon. A better understanding of this mutualistic system can provide some clues of how the strength (or lability) of this association has influenced plant speciation via pollinator specialization, host switching, hybridization and/or introgression. A widespread occurrence of hybridization and introgression in different regions would have important consequences for conserving plant diversity. This project will expand our knowledge on pollinator specificity in tropical forests which is more prone to collapse than generalist pollination systems.

Grus, Wendy E. System-specific genes reveal an earlier origin for the vomeronasal system.

The vomeronasal system (VNS) is one of two nasal chemosensory systems found in vertebrates. While the morphological components that define this system (accessory olfactory bulb and vomeronasal organ) are only found in tetrapods (amphibians, reptiles, and mammals), the system-specific genes have also been identified from teleost fish genomes. Additional studies reveal that in teleost fish, the VNS-specific genes are functioning together in a section of the olfactory organ distinct from where the main olfactory system genes are functioning. Thus, the VNS-specific signal transduction pathway predates the morphologically defined VNS. To determine if there is an even earlier origin of the VNS in vertebrates, I computationally and experimentally searched for the VNS-specific genes (V1Rs, V2Rs, and Trpc2) in sea lamprey (*Petromyzon marinus*), representing the earliest diverging lineage of vertebrates. Local BLAST searches of the sea lamprey Trace Archive sequences available through NCBI, identified

sequences with high homology to vertebrate V1Rs. These sequences clustered with teleost V1Rs and frog V1Rs with high bootstrap support when T2R taste receptors are used as an outgroup. Both experimentally and computationally, I identified sea lamprey sequence with high homology to vertebrate Trpc2. In a phylogeny with sea lamprey Trpc2 and other vertebrate Trpc genes, the sea lamprey Trpc2 clusters with high bootstrap support with other vertebrate Trpc2 genes. Also, the Trpc2 sequence was amplified from sea lamprey olfactory cDNA indicating that this gene is functioning in chemosensory tissue in this early diverging vertebrate. Thus, two of the three VNS-specific genes could be found in the sea lamprey genome, and one gene was expressed in the chemosensory organ. While this study suggests that the VNS likely originated in the ancestor of vertebrates, coexpression studies of VNS genes and main olfactory system genes are needed to support this earlier origin.

Izzo, Mandy. The control of dominance signal expression and aggressive behavior by Juvenile Hormone in the paper wasp, *Polistes dominulus*.

In animal societies, the presence of a dominance hierarchy is key for maintaining stability and promoting cooperation. Fighting is a universal mechanism for establishing rank, but is ultimately costly; most animals use honest signals of strength to assess rivals in order to avoid these costs. In the primitively eusocial paper wasp, *Polistes dominulus*, the formation of a stable, linear dominance hierarchy is of great importance for maintenance of the social structure and the function of the nest throughout the nest season. Fights among foundresses may end in death, so it is highly beneficial to utilize honest signals for assessment. However, in paper wasps, the signals used for rival assessment are poorly understood. This experiment examines the role of Juvenile Hormone (JH), a ubiquitous insect hormone with specialized functions in social insects, and its effects on behavioral dominance and chemical signal expression. Results show that both behavior and chemical signals are significantly affected by external addition of JH. Treated wasps are significantly more aggressive than control-treated wasps, and the cuticular hydrocarbon profiles of wasps show significant changes after treatment with JH. Juvenile Hormone may therefore act as a “master control” hormone that influences signaler behavior as well as signal development and expression.

Jackson, Doug. 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.

Lerner, H.R.L., Lindsay, A.R., Johnson, J.A. & Mindell, D.P. Is the Harpy Eagle at risk? Population genetics of a long-lived top predator.

The harpy eagle (*Harpia harpyja*) is a large bird of prey of lowland tropical forests historically ranging from southern Mexico to Argentina and Brazil. Wild harpy eagle populations have apparently been in decline for some time and have been extirpated from much of their historic range, particularly in Central America. Geographic patterns of genetic relatedness in extant and historic populations can provide data critical to conservation efforts that aim to maximize genetic diversity for the health of captive and wild populations. Using mitochondrial control region data from individuals in Central and South America we find lower genetic diversity in Central America. The level of genetic diversity found in the entire population is not as low as that seen in several at-risk species in the same family (i.e. Accipitridae); however, long generation times, evidence of restricted gene flow between Central and South American populations and lower genetic diversity accompanied by greater adverse impacts to habitat in Central America suggest that if current trends continue the entire harpy eagle population could be at risk of extinction.

Middlemis-Brown, Jessica. Density-dependence in the terrestrial stage of the wood frog, *Rana sylvatica*

In organisms with complex life cycles, populations may be regulated and experience selection in one or more stages. Amphibians in particular experience a shift from an aquatic to a terrestrial environment during metamorphosis, which produces substantial changes in population density, individual mobility, and selection regime. Although density-dependent growth and survivorship have been well documented in larval amphibians, effects of post-metamorphic density and individual variation remain largely unexplored. An experimental manipulation of juvenile wood frog (*Rana sylvatica*) density in field enclosures corroborates long-term survey data demonstrating strong density-dependent survivorship immediately following metamorphosis in this species. In addition, morphological growth patterns in surviving juveniles were affected by their plastic responses to the larval environment. These results suggest the potential for strong selection on juvenile phenotypes entering the terrestrial environment, highlighting the need for a broader understanding of consecutive phases within complex life cycles and the importance of selective pressures in post-metamorphic stages.

Miller, Zachariah J. The diversity of fungal pathogens associated with host plant species as a function of plant species' range and morphology: phylogenetic independence and the pace of disease community assembly.

In order to understand the processes which underlie disease emergence, it is important to elucidate the factors that determine the diversity of pathogen species infecting host species. If the theory of island biogeography is applicable to plant host species and their associated fungal pathogens, then plant species that are larger in size and with more extensive geographic ranges would represent larger islands and thus support a higher diversity of pathogenic fungi. Previous work, published 25 years ago, found that the richness of fungal-pathogens associated with a plant species is an increasing function of the plant species' range and varies among plant growth forms. Since that time our knowledge of plant and fungal taxonomy and systematics have increased greatly as has our appreciation for need for phylogenetic-independence of cross-species' comparisons. I tested the hypothesis that plant species' range and morphology determine the richness of fungal pathogen component community. The range and fungal-pathogen species richness was estimated for 419 plant species from the United States using published reports. I found that the richness of the fungal-pathogen community is a positive function of plant species' range and size. These data were also tested for phylogenetic independence using current topologies. I find that the host plant species' geographic range and fungal species richness are phylogenetically independent. The results suggest that number of pathogens found on a plant species changes within ecological timescales, that the use of phylogenetically-based data transformations is misleading, and the use of fungal species richness as a measure of plant species' disease burden is unwarranted without further study.

Montgomery, Benjamin R. Patterns and effects of heterospecific pollen receipt on a prairie invaded by *Euphorbia esula*.

This study tests the hypotheses that receipt of heterospecific pollen decreases pollination success, and that selection for avoidance of heterospecific pollen has contributed to the evolution of floral specialization. To investigate these questions, heterospecific pollen receipt rates were determined for twenty-nine species flowering simultaneously with *Euphorbia esula*, an abundant invasive plant, on an Iowa prairie. Consistent with the hypothesis, flowers with non-restrictive morphologies received more pollen from *Euphorbia*, more total heterospecific pollen, and heterospecific pollen from more species than did flowers with restrictive morphologies. Hand-pollination experiments revealed that receipt of *Euphorbia* pollen significantly decreased fruit or seed set for two of six species tested, and that *Euphorbia* pollen receipt was especially detrimental when received early and in large quantities. These results suggest that selection for avoidance of heterospecific pollen receipt may have contributed to the evolution of floral specialization, but that some species have traits which mitigate detrimental effects.

Oldfield, Ronald G. The effects of behavioral interactions on sex determination in the Midas cichlid.

A period of gonad bisexuality occurs early in development in many fish species that only function as one sex throughout their lifetime. Sequential hermaphroditism is thought to evolve when this critical period of lability extends into adulthood, when development can be influenced by social interactions. Sexual lability at an intermediate life stage has been reported in the Midas cichlid, *Amphilophus citrinellus*, and was considered to represent a mid-point on a developmental continuum, lying between fish that have sex controlled genetically and fish that change sex as adults. At the juvenile stage, relatively large individuals of a group were reported to develop as males and small individuals as females. I employed detailed behavioral analyses in laboratory experiments to determine the effects of behavioral interaction and relative body size on sex determination in the Midas cichlid. Groups of fish from different lineages, containing various numbers of individuals, were grown out over long periods. Social interactions were found not to influence whether an individual differentiated as a female or a male. I histologically examined gonads of wild Midas cichlids in order to describe their pattern of development. Of 25 individuals of various ages from Lake Masaya, Nicaragua (the source of fish in the original reports), none had bisexual gonads, although these are often present in sexually labile species. In Lake Apoyo, Nicaragua, underwater observations revealed Midas cichlids socially assorted by body size. Two shoals of juveniles were captured in deep water. Histological analysis revealed that they were at the onset of sexual differentiation, but sex was not associated with body size in either group. The field observations and laboratory experiments consistently indicate that social conditions do not affect sex in this species and that differences in relative body size in adults are due to greater post-maturation growth in males than in females.

Oneal, Elen. Testing for mechanisms promoting divergence in Caribbean crickets using multi-gene data

The Caribbean has a complex geological history, and multiple biogeographic hypotheses have been proposed to explain patterns of taxa distribution in the region. Recent improvements in our understanding of this geological history allow explicit testing of these hypotheses using estimates of species evolutionary relationships. Simultaneously, developments in molecular techniques have lead to an increase in the amount of DNA sequence data available for constructing phylogenies. Using both mitochondrial and nuclear sequence data, we estimate species relationships in a genus of Caribbean ground crickets to test whether divergence in this group reflects the effects of vicariance or dispersal. Furthermore, we use the geological history of the region as a framework for evaluating the ability of different methods of analyzing multi-gene data to distinguish between these hypotheses. Our work sheds light on the timing and pattern of diversification in this group, and explores the possibilities presented by increased gene sampling for hypothesis testing.

Richards, Corine L. Tests of phenotypic and genetic concordance and their application to the conservation of Panamanian golden frogs.

Evolutionarily significant units were originally intended to diagnose intraspecific groups with sufficient adaptive differentiation so as to merit their separate conservation. However, the majority of these designations are based solely on patterns of neutral genetic variation, which may not capture variation relevant to the species' adaptability to changing environmental conditions or accurately represent the evolutionary history of the species. For highly variable taxa, defining a set of management units which meet these criteria is especially challenging. This study uses multivariate analyses of concordance among phenotypic and genetic variation to provide a framework to test whether evolutionarily significant units for Panamanian golden frogs (*Atelopus varius* and *A. zeteki*) faithfully reflect variation pertinent to the long-term preservation of these highly variable species. Our results indicate that the proposed evolutionarily significant units for *A. varius* are phenotypically and genetically differentiated whereas those for *A. zeteki* differ only in phenotype. The analyses identify variation in two phenotypic characters (body size and the extent of dorsal black patterning) which differ among evolutionary significant units for both species, as putative adaptations to aspects of local climate. The study demonstrates the utility and feasibility of combined analyses of ecological, morphological and genetic variation in diagnosing intraspecific conservation units, especially for highly variable taxa.

Sheehan, Michael. Fluctuating asymmetry quality signals in *Polistes dominulus*.

Fluctuating asymmetry (FA) is a pattern of small, random and independent variation in traits on the right and left side of a bilaterian. While the exact origin of FA in development is unclear, it has become an established measure of quality across a wide range of taxa. In the present study I examine the relationship between FA of structural body parts, color patterns and a known quality signal in *Polistes dominulus*. Additionally, I examine the relationship between FA and quality as assessed through dominance trials.

Shilts, Meghan. Testing models of speciation in the northern pocket gopher, *Thomomys talpoides*, species complex.

The northern pocket gopher, *Thomomys talpoides*, is a high elevation species with a widespread distribution across the western U.S and southern Canada. This species is composed of a number of different subspecies and chromosomal races and the phylogenetic relationships of these different races and subspecies has not been comprehensively studied. In my dissertation research, I plan to construct a phylogeny of the different races and subspecies. As well as addressing taxonomic and systematic questions pertaining to this species complex, a comprehensive phylogeny can also be used to test models of speciation, specifically, a chromosomal model of speciation. One version of a model of chromosomal speciation proposes that chromosomal rearrangements suppress recombination, which prevents gene flow and thereby can result in speciation. This model can be indirectly tested by comparing the number of chromosomal rearrangements in allopatric and sympatric sister races: this chromosomal model of speciation predicts that there should be a greater number of rearrangements between allopatric sister races than sympatric sister races. A second prediction of the chromosomal model of speciation is that there should be a proportionally greater number of rearrangements between recently separated sister races than races that have diverged less recently. Both of these predictions can be tested using the *T. talpoides* species complex once the phylogenetic relationships of the races are known.

Uesugi, Akane. Evolution of Beet Avoidance in a Leafmining Fly (*Amauromyza flavifrons*)

What do herbivores do when they encounter a new potential host plant? While theoretical models predict both physiological and behavioral adaptation to occur, examples of behavioral adaptation (i.e. avoidance of the plant) is rare. We asked whether avoidance evolves in a leafmining fly (*Amauromyza flavifrons*) in environments where it is exposed to a low quality host: sugar beet (*Beta vulgaris*). Females from ‘beet-absent’ populations lay more eggs on beet hosts than females from ‘beet-present’ populations, suggesting that beet avoidance has evolved in response to beet exposure. Behavioral adaptation may commonly evolve from selection against indiscriminate oviposition behavior.

Vannette, Rachel. Multi-Trophic Interactions and Defense in Milkweeds: The Role of Mycorrhizae

Following attack by herbivores, plants can regrow and/or increase production of defensive chemicals, but are limited in both by nutrient availability. Hosting AM fungi may aid plants in recovery from herbivore attack by increasing plant growth, replacing lost nutrients, increasing tolerance to damage, and/or increasing production of defenses. However, AM symbionts require 4-20 % of all photosynthate produced by the host plant in return for increased availability of other nutrients. These complex relationships among mycorrhizal infection, plant allocation to defense and resource availability as well as resource demand due to defensive compound turnover remain largely unexplored. The milkweed family (Asclepiadaceae) has been intensively studied because of its toxic defensive chemicals and charismatic herbivore specialists. Members of the family grow in various habitats including prairies, swamps, and woodlands, providing habitat variation in which to study allocation to defense. Most of the Asclepiadaceae produce cardenolides, defensive chemicals that can be induced by herbivory. Cardenolides are carbon-rich steroids that interfere with the ion channel ATPase in eukaryotes. Using plant species in the genus *Asclepias*, I will address the following general questions: 1) Does the presence or absence of mycorrhizae influence the allocation of resources by plants to defense? 2) How does resource availability (nutrients, light) influence allocation of resources to mycorrhizae and what are the consequences for allocation to defense?

Zellmer, Amanda. Fine-scale genetic differentiation between wood frog populations: testing for evidence of local adaptation.

Studies of fine scale genetic population structure can be useful for estimating levels of genetic differentiation between neighboring populations with potentially high amounts of gene flow. If differential selection within populations is strong enough, it is possible that it could outweigh the homogenizing effects of gene flow and promote local adaptation. In this study, I used microsatellites to estimate the amount of genetic differentiation between wood frog (*Rana sylvatica*) populations in Southeastern Michigan. Samples were collected from ponds within a 1500-acre area, where the distances between each of the ponds are well within the maximum-recorded dispersal range of this species. Studying genetic differentiation at this fine scale reduces the effects of geographical distance on dispersal of individuals. In addition, the ponds sampled represent two different selection regimes, between which individuals show genetically distinct morphological, behavioral, and life-history differences. AMOVA was used to test if gene flow is restricted between these two different habitat types, due to the differences in selection pressures. However, the results show that grouping populations into these two pond-type categories does not explain the variation in genetic differentiation. It is therefore suggested that selection is strong enough to allow for genetic differences, regardless of the high level of gene flow between populations