



Committee on Evolutionary Biology
&
Ecology and Evolution
Annual Retreat

Sunday, April 10th, 2011

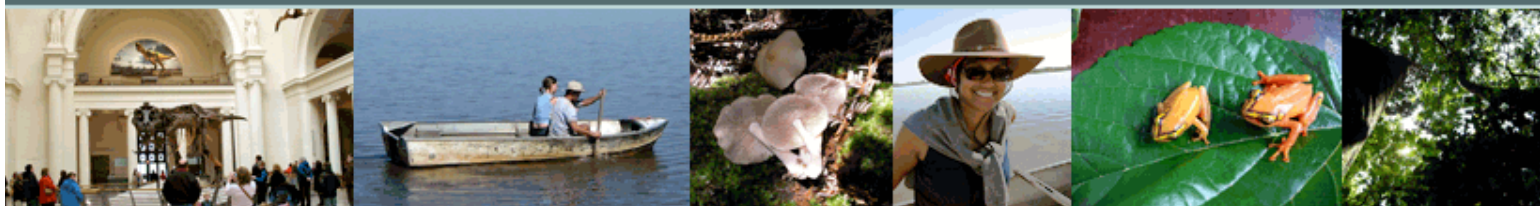
Hosted by the

Chicago Botanic Gardens

<http://www.chicago-botanic.org/>

Glencoe, Illinois USA

Committee on Evolutionary Biology
University of Chicago



Morning Session

- 9:15 Rebecca Dikow " Character optimization across genomes and the distribution of phylogenetic signal"
- 9:30 Matt Heintz " Is Play Training for the Unexpected in Wild Chimpanzees (*Pan troglodytes*)?"
- 9:45 Ben Krinsky " The evolution of a new gene network in *Drosophila*"
- 10:00 Aaron Savit " What drives patterns of intraspecific diversity? Estimating ecological similarity in *Tangara* tanagers."
- 10:15 Natasha Bloch "Molecular genetics and spectral tuning of warbler opsins: a comparative approach to avian color vision"
- 10:30 Will Tyburczy "The interplay of species interactions and environmental stress in an intertidal predator-prey system"
- 10:45 David Bapst "So What Does a Really Big Supertree of Dead Plankton Tell Us About Diversification?"
- 11:00 Kacy Gordon "Distinct functional constraints partition sequence conservation in a cis-regulatory element"
- 11:15 Nick Block "Cryptic species uncovered in a Malagasy passerine, *Bernieria madagascariensis*"
- 11:30 Bin He "Background genetic variations influence phenotype penetrance – using *Drosophila* to study complex human diseases"
- 11:45 Edna Davion "Opsin genes in nocturnal mammals: implications for primate evolution "

Lunch (12:00 – 12:30)

Post-Lunch “Walk & Talks” (12:30-2:00)

M. Coates & M. Webster on “Post doctoral applications & Job Talks”

D. Jablonski, S. Kidwell, M. Long, C. Pfister on “Making the most out of the 1st 2 years of Graduate school”

G. Mueller (Chicago Botanic Garden), R. Ree (FMNH), J. Gilbert (Argonne National Labs) on “Non- University Jobs”. Meet on the trolley at 12:30.

Dr. Laura Katz (guest faculty from Smith College) on “Getting a Job at a small liberal arts College”

Afternoon Session I: Behavior & Evolutionary Ecology

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|------|-----------------|--|
| 2:00 | Chris Schell | "The Influence of Parental Effects on the Ontogeny of Select Phenotypic Traits in Coyotes (<i>Canis latrans</i>)" |
| 2:15 | Colin Kyle | "Mechanistic models to predict the response of an insect fungal pathogen to global climate change" |
| 2:30 | Si Tang | "Persistence and Feasibility of Random Ecosystems" |
| 2:45 | Katie Brooks | "Sociality reduces predation risk in Belding's ground squirrels" |
| 3:00 | Liz Scordato | "Geographical variation in the targets of sexual selection" |
| 3:15 | Aaron Kandur | "Adaptation at a range limit in the mussel <i>Mytilus californianus</i> " |
| 3:30 | Kristen Jenkins | "Variability of marine molluscan community structure over time and space in response to climate and anthropogenic drivers" |

- 3:45 Ben Rubin "The evolution of plant-ant mutualism"
- 4:00 Traci Viinanen "Seed set patterns in the perennial intermediate wheatgrass, *Thinopyrum intermedium*"

Afternoon Session II: Evolution: History & Genetic Mechanisms

- 2:00 Ben Winger "Understanding variability in phenotypic differentiation of birds across a biogeographic barrier in the Andes"
- 2:15 Alice MacQueen "Differential expression of R-genes may mitigate fitness costs of resistance in *Arabidopsis thaliana*"
- 2:30 Laura Merwin "Adaptations of *Arabidopsis thaliana* to a terrestrial near-shore environment"
- 2:45 Deren Eaton "Testing the reticulate history of *Pedicularis* using RAD markers"
- 3:00 Matt Nelson "Phylogenetic relationships of lichen-forming fungi in the class Dothideomycetes"
- 3:15 Nate Upham "Fossils and phylogeny: investigating diversification patterns in a diverse lineage of Neotropical rodents (Caviomorpha: Octodontoidea)"
- 3:30 Paul Grabowski "Genome-wide nucleotide variation and gene flow in switchgrass"
- 3:45 Sophie McCoy "Spatial and temporal trends from the coralline algal isotopic record: Can we reconstruct regional ocean acidification across the Strait of Juan de Fuca?"
- 4:00 Chris Meyer "Detecting Epistasis in Arabidopsis Genome-Wide Data"

2011 GAANN Retreat Abstracts

David Bapst "So What Does a Really Big Supertree of Dead Plankton Tell Us About Diversification?"

The fossil record of marine invertebrates has long been a focus of diversity studies because of its excellent sampling and temporal resolution, but lack the phylogenetic information that allow comparison to phylogenetic studies of extant diversity. The Graptoloidea, an extinct but once diverse clade of zooplankton, provide a opportunity to combine a well-sampled fossil record and relatively detailed phylogenetic relationships. I constructed an inclusive supertree of relationships among 1752 species and sub-species of the Graptoloidea, using a global composite of temporal ranges. The tree is certainly not fully resolved, but the effect of phylogenetic uncertainty on parameter estimates and hypothesis testing can be quantified. Using a novel sampling rate based approach to time-scaling this supertree, diversity histories can be produced that account for anagenesis, budding speciation and range extension. This allows for a new view of the 80 MY of graptoloid evolutionary history and to explore the underlying diversification processes using methods designed for extant phylogenies.

Natasha Bloch "Molecular genetics and spectral tuning of warbler opsins: a comparative approach to avian color vision"

Collaborator: Trevor Price

Understanding the great diversity of color in the animal world requires understanding how animals perceive color, the environmental context, and the extent to which the color vision and color co-evolve. Here, we propose to assess how opsins, and thus color vision, vary in relation to colorful sexual ornaments (plumage color) and the environment, using the New and Old World warblers as a model system.

We obtained complete coding sequences for all opsin genes in more than 15 New World warblers and 7 Old World warblers, and found substantial non-synonymous variation in all cone opsins. The spectral shifts caused by some of these variable sites have already been studied. However, the effects of substitutions at most of these sites remain unknown and we cannot predict their effect on the wavelength of maximum absorbance (λ_{max}) of the corresponding photopigments. To study how the observed variation translates into λ_{max} differences, we used transient transfection of mammalian tissue culture cells to express warbler opsin *in-vitro*. The λ_{max} of purified and reconstituted visual pigments were determined by absorption spectroscopy.

For RH2 we found λ_{max} differences of about 3nm among RH2 in New World warblers and were able to identify C85F as the substitution responsible for this shift. On the other hand, for SWS2 we found differences of 3nm among New World warblers and 5nm among Old world warblers. In addition to within clade variation, SWS2 also differs between New and Old World warblers at 9 residues. Interestingly, the SWS2 consensus of both clades only differs by 1.5nm. According to previous studies and our data it seems S269A could be responsible for a +5nm shift while a S99W substitution compensates this shift, explaining why SWS2 in both clades has similar λ_{max} . In contrast to RH2 and

SWS2, SWS1 and LWS opsins do not differ among warblers.
These data will allow us to study how photopigments evolve in relation to sexual ornaments and the environment.

Nick Block "Cryptic species uncovered in a Malagasy passerine, *Bernieria madagascariensis*"

Collaborators: Marie Jeanne Raheirilalao, Shannon J. Hackett, John M. Bates, and Steven M. Goodman

Long-billed *Bernieria* (*Bernieria madagascariensis*) belongs to an endemic Malagasy passerine family, Bernieridae. It is the only member of the family to inhabit both the western dry forest and eastern humid forest of Madagascar, and its two described subspecies correspond to these habitats. *B. m. madagascariensis* occupies eastern humid forest, and the paler *B. m. inceleber* inhabits the western dry forest. A phylogeographic survey of the species yielded three widely divergent groups, with a 9.3% mean uncorrected pairwise distance between the most distant mitochondrial haplotype clades. Nuclear data are congruent with the mtDNA data. Surprisingly, these clades do not correspond at all to the described subspecies, which cannot be distinguished genetically. One clade is restricted to humid forest in the southeastern part of the island, one is widespread across both subspecies' ranges, and the third is found only in the northeast. No range overlap has been observed, although extensive parapatry is known. Despite plumage differences between the described subspecies, the haplotype clades do not exhibit significant phenotypic differences, including in vocalizations, plumage, or size. Each clade, however, hosts a unique species of *Myrsidea* chewing lice. This level of phenotypical stasis with such significant genetic divergence may be a unique scenario in birds. Further, the data highlight the important role of cryptic species in assessing Malagasy biodiversity.

Katie Brooks "Sociality reduces predation risk in Belding's ground squirrels"

Collaborator: Jill Mateo

Evolutionary theory predicts that group-living, or sociality, will evolve if the fitness benefits outweigh the costs. Species may live in groups to reduce predation risk, increase foraging success or to facilitate mating. Belding's ground squirrels, *Urocitellus beldingi*, live in groups of female kin and unrelated males. Females behave nepotistically towards their female kin by alarm calling to warn relatives of predators and sharing in territory defense, leading many to assume that *U. beldingi* sociality evolved via kin selection. Data from 2009-2010 suggest that predation risk also influenced the evolution of *U. beldingi* group living. Squirrels exhibit reduced vigilance behavior as group size increases, suggesting that group-living decreases predation risk. Reduced vigilance has many benefits, including increased foraging rates, survival and reproductive success.

Edna Davion “Opsin genes in nocturnal mammals: implications for primate evolution “

It has long been accepted that mammals were generally small and nocturnal for the first two thirds of their evolution (210 to 65 mya). It has also been widely accepted that ancestral primates remained nocturnal, with some descendant lineages secondarily developing diurnal behaviour. Early terrestrial vertebrates seemingly had tetrachromatic vision: 4 colour opsin genes corresponded to 4 cone types for photopic vision and a rhodopsin gene corresponded to rods for scotopic vision. Extant mammals, including most primates, are typically dichromatic, having lost 2 ancestral colour opsin genes (SWS2 and RH2) and corresponding cone types. Uniquely among placental mammals, humans, apes and certain diurnal monkeys are truly trichromatic. Nocturnal mammals consistently possess cones, previously thought to serve photopic vision exclusively. Surprisingly, two different cone types (Medium/Long-wave Sensitive M/LWS and Short-wave Sensitive SWS1) are commonly present in the retina of nocturnal mammals. But SWS1 opsins have been suppressed in several lineages, including 3 groups of primates (loris group, dwarf lemurs and owl monkeys). Retention of cone opsins in nocturnal primates led some authors to infer a diurnal ancestry. Here we examine these claims in light of phylogenetic analysis of opsin genes of representative genera of the supraordinal clade Euarchonta: colugos (Dermoptera) and treeshrews (Scandentia). These two taxa have been identified as the closest relatives of primates on morphological and genetic grounds, but relations between them remain unresolved.

Rebecca Dikow " Character optimization across genomes and the distribution of phylogenetic signal"

An analysis of nineteen *Shewanella* (Gammaproteobacteria: Alteromonadales) genomes plus three outgroup species is presented. Primary homologous fragments include 1,559 genes and 1,596,811 unaligned nucleotide base-pairs (bp), 34.3% of the entire genome. A series of phylogenetic analyses were performed: analysis of the concatenated data-set, individual analyses of each homologous fragment, and analyses of random sub-sets of the concatenated data-set. Not a single fragment out of the 243 homologous fragments produced the same topology as the concatenated data-set; in fact, each fragment produced a unique topology. Each randomly sampled sub-set of data, however, produced the same topology as the entire concatenated data-set. These results are put into the context of local vs. global taxonomic signal and gene tree incongruence.

By plotting the distribution of phylogenetic signal across the genome through extensive character optimization, I am finding the regions of phylogenetic incongruence, whether caused by lateral gene transfer or simply character conflict among parts of the genome. A discussion about the boundaries of phylogenetic signal is initiated. The results shown here allow an exploration of whether these boundaries are in line with traditional gene concepts or whether, for phylogenetic pursuits, it is more desirable to recognize some other co-evolving units that contribute to the overall taxonomic signal and to quantify the extent of conflict in our data-sets.

Deren Eaton "Testing the reticulate history of *Pedicularis* using RAD markers"

The plant genus *Pedicularis* has recently experienced a rapid radiation within the mountains of south-central China, causing phylogenetic relationships that remain difficult to resolve. Here, I describe an exploration into the use of high-throughput restriction associated DNA (RAD) markers for phylogenetic reconstruction in this lineage, and test for hybridization as a potential cause of gene tree discordance.

Kacy Gordon "Distinct functional constraints partition sequence conservation in a cis-regulatory element"

Different functional constraints contribute to different evolutionary rates across genomes. To understand why some sequences evolve faster than others in a single *cis*-regulatory locus, we investigated function and evolutionary dynamics of the promoter of the *C. elegans unc-47* gene. We found that this promoter consists of two distinct domains. The proximal promoter is conserved and is largely sufficient to direct appropriate spatial expression. The distal promoter displays little if any conservation between several closely related nematodes. Despite this divergence, sequences from all species confer robustness of expression, arguing that this function does not require substantial sequence conservation. We showed that even unrelated sequences have the ability to promote robust expression. A prominent feature shared by all of these robustness-promoting sequences is an AT-enriched nucleotide composition consistent with nucleosome depletion. Because general sequence composition can be maintained despite sequence turnover, our results explain how different functional constraints can lead to vastly disparate rates of sequence divergence within a promoter.

Paul Grabowski "Genome-wide nucleotide variation and gene flow in switchgrass"

Collaborators: Geoffrey Morris, Justin O. Borevitz

Switchgrass (*Panicum virgatum*) is a wide ranging and widely-adapted warm-season (C4) grass. Geographic patterns of genetic variation can reveal genetic diversity hotspots and identify habitat-specific ecotypes, but patterns of genetic variation in switchgrass are not well characterized in large part due to the constraints of traditional genotyping techniques. Using next-generation sequencing technology, we have identified hundreds of novel candidate SNPs and use them to begin to characterize genetic variation and gene flow at both the landscape and regional level.

Bin He "Background genetic variations influence phenotype penetrance – using *Drosophila* to study complex human diseases"

Background genetic variations have been known to influence the penetrance of many mutant phenotypes, among which human diseases are one of the examples. By crossing a strain of *Drosophila* that expresses a human mutant insulin protein in the eye to a panel of 192 inbred strains representing natural variations, we found a dramatic influence of the background genetic variations on the eye phenotype, ranging from severely reduced eyes to nearly wild-type looking eyes. With whole genome sequences available for a majority of these lines (143 of them were both sequenced and phenotyped at this moment), we did a genome wide association analysis in order to discover contributing genetic loci. Because full genome sequences rather than tag SNPs were used, our analysis can identify Quantitative Trait Nucleotide (QTN). Our preliminary study successfully identified a block of linked, significantly associated polymorphism (smallest p-value = 0.0095 after Bonferroni correction for multiple-testing) inside the second intron of the *sulfateless* gene. Within this 10kb intron also lies a nested protein-coding gene that is about 700bp 3' of the SNP. We re-sequenced a 3kb region surrounding the SNPs both to validate the genome sequences and to discover potential unidentified linked SNPs. The results showed that the most strongly associated loci is a length polymorphism (4bp vs 18bp) rather than single nucleotide polymorphism. We are currently in the process of validating the association and investigating the nature of this polymorphism. We propose that *Drosophila* can be used as an efficient tool to study the problem of background genetic variations influencing complex traits, including complex human diseases, with the advantage of convenient genetic tools and experimentally manipulable system.

Matt Heintz "Is Play Training for the Unexpected in Wild Chimpanzees (*Pan troglodytes*)?"

The training for the unexpected theory suggests that through play, individuals put themselves in situations where they lose control and learn to appropriately regulate their stress response. This theory has gained support over recent years; however there are not any field studies that examine the relationship between play and stress. In order to test how well play regulates the stress response, I compared play rates with fecal glucocorticoid metabolite (FGM) concentrations from wild infant and juvenile chimpanzees. Behavioral observations were collected on infants and juveniles over a 6-month field seasons using instantaneous scan-sampling in Gombe National Park, Tanzania. Fecal samples were collected noninvasively from known individuals and analyzed using a cortisol enzyme immunoassay. Preliminary analyses from 2009 data demonstrate a positive correlation between play rates and both FGM variance ($p < 0.05$) and FGM mean ($p = 0.07$). The majority of play maintained at least one stationary point and energy expenditure is unlikely to influence FGM concentrations. I will also briefly discuss play styles and FGM reactivity; however, initial findings do not support the training for the expected theory for wild infant chimpanzees.

Kristen Jenkins "Variability of marine molluscan community structure over time and space in response to climate and anthropogenic drivers"

Understanding marine community response to climate and anthropogenic changes in the modern is important for developing effective conservation strategies. Although biologists

commonly examine abundance and biomass in living communities, it is important to compare modern observed changes to comprehensive natural baselines using information from past decades, centuries, and millennia. Furthermore, recent advances in understanding population and individual level responses to climate and anthropogenic change are difficult to translate to community level response. I propose using rank abundance distributions (RADs) of molluscan living, death, and fossil assemblages (Pleistocene, 80 kyr ago) to explore variability in the composition and structure of subtidal benthic communities. The U.S. Pacific coast is an ideal system to explore these patterns while building upon knowledge of living communities and expanding that of death assemblages and previously described fossil assemblages from Southern California to Oregon. Applying a comparative analysis of RADs to living, death, and fossil assemblages through these regions would establish a natural baseline of change along a series of spatial and temporal environmental gradients. This comparison would permit the separation of community level impacts due to anthropogenic changes from those due to environmental variability over time. Complementing exploration of these empirical patterns, I propose using multi-species community models to test hypotheses of biological mechanisms through which the RAD pattern can develop. Hypothesis testing is possible through perturbing growth rate and interaction strengths among simulated populations. The changes (or lack thereof) in RAD patterns for perturbed community growth rates and interaction strengths will link community level responses to population level characteristics. Spatial, temporal, and simulated comparisons of RAD pattern will be approached in a similar fashion using nested comparisons of non-linear least squares (nls) models fitted to the data. Goodness-of-fit tests for habitat and regional- specific models relative to non-specific models will be determined using AIC. Ultimately, the synthesis of empirical and model-simulated RAD pattern behavior with theoretical assumptions of community resource distribution reflected by RAD patterns represents critically needed advancement in understanding drivers and inherent variability of community structure.

Aaron Kandur "Adaptation at a range limit in the mussel *Mytilus californianus*"

Range limits are poorly understood ecological and evolutionary phenomena. A primary question related to range limits and their enforcement is whether and how often gene flow induced maladaptation contributes to their determination. Theoreticians have put forth numerous models of range dynamics which include gene flow induced maladaptation, but no empirical examples exist of range limits being set or reinforced by this mechanism. In order to test theory empirically, this project investigates a population likely to be maladapted at a range limit due to gene flow from another part of the range, using the phenotype of thermal tolerance in the species *Mytilus californianus*. The adaptive state of multiple mussel populations along a shallow gradient of thermal change is compared to the adaptive state of a small population at the hot end of a steep thermal gradient which receives immigrants from cold adapted populations. A common garden experiment between the small hot population and the nearby large cold adapted population was used to explore the mechanisms underlying the observed adaptive state of the small population.

Ben Krinsky

" The evolution of a new gene network in *Drosophila*"

Collaborators: Sidi Chen, Xiaochun Ni, Yong Zhang, Maria Vibranovski, Kevin P. White, and Manyuan Long

The study of recently duplicated loci has great potential to shed light on the origins of novel biological functions. Moreover, by concentrating on genes that have a relatively short evolutionary history, it is possible to explore how microevolutionary processes shape genomic evolution. The fruit fly genus *Drosophila*, with its wealth of experimental tools, is an ideal model with which to investigate these phenomena. One recently duplicated gene in *Drosophila*, poetically named *Zeus*, has emerged as a promising candidate for the study of functionally important new genes. Following its origination 4-6 million years ago, the *Zeus* locus underwent a period of very rapid molecular evolution. This gene has acquired a male reproductive system-specific expression pattern, and when expression is silenced via RNAi, male *D. melanogaster* have a ~60% reduction in fertility. On the protein level, both *Zeus* and its parent gene, *Caf40*, have nucleic acid binding domains and are putative *trans*-regulatory molecules. Chromatin-IP followed by microarray (ChIP-chip) analysis in *D. melanogaster* indicates that *Zeus* has acquired over 200 new binding sites relative to *Caf40*. Interestingly, *Zeus* has several lineage specific amino-acid substitutions in each species where it exists (*D. melanogaster*, *D. sechellia*, and *D. simulans*). Thus, in a series of ongoing experiments, transgenic and ChIP-based technologies are being used to investigate the targets of *Zeus* and its parent *Caf40* in species outside of *D. melanogaster*. This work will reveal patterns of lineage specific evolution of a recently duplicated gene, and thus provide key insights into the evolution of gene regulatory networks.

Colin Kyle

"Mechanistic models to predict the response of an insect fungal pathogen to global climate change"

Researchers predict anthropogenic climate change will have important impacts on organisms and ecosystems. Fungal pathogens in particular represent a group of diseases in which climate change is expected to have direct, dramatic effects due to the strong influence of environmental factors on fungal life cycles and ecology. Because fungi naturally help control pest-insects, understanding how these pathogens will respond to climate change will allow us to construct informed long-term pest-control strategies. I therefore plan to construct mechanistic models predicting how one such pathogen, *Entomophaga maimaiga*, which serves as a biocontrol for invasive gypsy moths (*Lymantria dispar*), will respond to different climate change scenarios. To begin parameterizing a climate-sensitive model of disease transmission, I collected observational and experimental data during *E. maimaiga* outbreaks at three different sites along a 395.9 km latitudinal gradient in the summer of 2010. My field sites were located in Michigan's Lower Peninsula and I designed my experiments to quantify the activity of *E. maimaiga*'s two sources of infection. While statistical analyses are still underway, preliminary observations indicate my experiments found differences in the dynamics of the two infection sources which help explain observed epizootic data. Weather and climate also appear to influence fungal dynamics at each of my sites. I have begun

estimating infection parameters from my data but plan to collect more field data and parameterize stochastic epizootic models of differing complexity in the future. Once I have constructed my models, I will simulate the response of the fungus to different climate change scenarios.

Alice MacQueen "Differential expression of *R*-genes may mitigate fitness costs of resistance in *Arabidopsis thaliana*"

Plant *R*-genes are involved in gene-for-gene resistance to pathogens and are typically highly polymorphic, consistent with their important role in the changing landscape of pathogen recognition. However, many features of *R*-genes are not consistent with traditional selective sweep models of pathogen arms races, including the extreme age of most *R*-gene alleles. Interestingly, several *R* loci are segregating for ancient polymorphisms where the *R*-gene is either present or deleted. This polymorphism has been attributed to the large fitness costs of resistance resistant alleles carry in the absence of disease; in light of this cost, one stable evolutionary strategy appears to be losing resistant *R*-genes entirely.

An alternative evolutionary strategy to reduce fitness costs of resistance may be limiting resistant *R*-gene expression to situations when it is of the most benefit to the plant, such as in environments where infection is more probable. *R*-genes may be differentially regulated at the expression level: microarray studies have shown that tissue-specific *R*-gene patterns have no apparent correlation with *R*-gene phylogenetic relationships, and there is significant natural variation in expression levels of most *R*-genes between *Arabidopsis* accessions. I propose to study *R*-gene variation at the expression level to better understand *R*-gene regulation and how it may mitigate fitness costs of resistance. I will use RNA-seq to generate expression data for *Arabidopsis* accessions grown in different environments and mine preexisting data to draw correlations between genome sequence and regulation of *R*-gene expression. I will also alter *R*-gene expression in the field using TILLED alleles to determine whether expression loss mitigates fitness costs.

Sophie McCoy "Spatial and temporal trends from the coralline algal isotopic record: Can we reconstruct regional ocean acidification across the Strait of Juan de Fuca?"

Stable isotopes are a common tool from the geosciences to reconstruct past climate records. Here I explore carbon and oxygen isotopic records of crustose coralline algae to determine whether several species can be used in tandem to identify general trends in ocean chemistry over time.

Laura Merwin "Adaptations of *Arabidopsis thaliana* to a terrestrial near-shore environment"

Adaptation of organisms to new or altered environments is one process that has contributed to global patterns of biodiversity. Understanding adaptation can not only give us insight into evolutionary trajectories of the past, but also into new patterns arising from global change. In its native Swedish range, the model organism *Arabidopsis*

thaliana is largely found in disturbed sites and agricultural areas; however, large persistent populations also exist on beaches throughout southern Sweden. Plants that grow in near-shore terrestrial ecosystems experience environmental stressors that include aridity, saline soils, salt spray, and high winds. Beach *A. thaliana* populations have been observed to exhibit differing morphologies (shorter stature, longer, thicker taproots) as well as higher leaf Na⁺ content. I propose to investigate the genetic basis of these adaptations, determine causal variants, and demonstrate fitness advantages.

Chris Meyer "Detecting Epistasis in Arabidopsis Genome-Wide Data"

Collaborator: Seunghak Lee

The Bergelson lab maintains a genome-wide association (GWA) mapping panel of Arabidopsis accessions genotyped at a density of 250,000 SNPs per genome. This panel now consists of over 1,000 unique genotypes and has been leveraged to map genes associated with hundreds of phenotypes. Since generating glucosinolate profiles for three different plant tissues in this mapping panel (leaves, flowers, and fruits) and identifying SNPs with main effects, we have turned our attention to more sophisticated mapping techniques in collaboration with a statistics group at Carnegie Mellon. Since it has been shown that the generation of fitness-related phenotypes is often achieved via a network of epistatic interactions between genes in addition to typical main effects, this collaboration has focused on a statistical approach for identifying epistatic interactions between SNPs associated with glucosinolate biosynthesis and regulation in these different plant tissues.

Matt Nelson "Phylogenetic relationships of lichen-forming fungi in the class Dothideomycetes"

Collaborators: Robert Lücking, Thorsten Lumbsch, Carrie J. Andrew & Richard Ree

Lichenization has evolved numerous times in both fungi and eukaryotic algae. The fungal class Dothideomycetes (Ascomycota) is primarily composed of saprotrophs and plant pathogens, however, a number of lichen-forming lineages have recently been revealed. Here we discuss the phylogenetic position of these lineages. Additionally, we focus on Trypetheliales, the largest of these lichen-forming lineages, and investigate morphological evolution following the transition to the lichen-forming state.

Ben Rubin "The evolution of plant-ant mutualism"

Obligate plant-ant mutualism has evolved in at least seven genera in four of the 21 ant subfamilies. Within the ant genus *Pseudomyrmex* alone, obligate mutualism has evolved at least three times from a non-mutualist ancestor. Mutualistic ants nest in and feed on their host trees while aggressively protecting them from herbivores, competing plants, and pathogenic fungi. This mutualism represents an extreme change in behavior towards constitutive aggressiveness and dietary specialization. This shift must also require changes in communication strategies between ants and physiological compensation for feeding only on resources derived from a single plant. My PhD research will examine

several aspects of mutualism to better understand the numerous changes that occur during the evolution of behavior. Specifically, I will determine the genes that are differentially expressed in mutualists and non-mutualists, the chemical strategies that mutualists use to effectively communicate and defend their hosts, and the differences in potentially nutrient enriching gut fauna that come with feeding exclusively on host plants.

Aaron Savit "What drives patterns of intraspecific diversity? Estimating ecological similarity in *Tangara* tanagers."

Bioclimatic factors such as precipitation, temperature, and seasonality play an important role in shaping species distributions. I use tanagers of the genus *Tangara* to show how subtle climatic effects can cause unexpected biogeographic distributions. Environmental niche modeling (ENM) can be used to develop and test hypotheses about the influence of climate on species distributions. Using ENM in conjunction with recently developed analytical methods, I test the hypothesis that species turnover is associated with changes in bioclimatic variables. The genus *Tangara* also features many species that are broadly or narrowly sympatric. Similar distributions are likely to be impacted in similar ways by changes in habitat availability and connectivity. I use ENM distribution models of each *Tangara* species to quantify the overlap in preferred habitat among all members of the genus. I present preliminary data illustrating how preference for different climatic regimes can directly affect the evolution of morphological and molecular diversity within species.

Chris Schell "The Influence of Parental Effects on the Ontogeny of Select Phenotypic Traits in Coyotes (*Canis latrans*)"

Experience and response to environmental conditions can structure parental phenotypic traits that directly influence offspring development. These parental effects produce phenotypic variation in progeny, impacting offspring fitness in the process. As a result, parental phenotype can influence evolutionary change of a population through influences on offspring. Parental effects are particularly pronounced in mammals, as parents have extended interactions with offspring through gestation and lactation. Most parental effects research focuses on morphological traits for various mammalian groups, with few studies examining influences on temperamental traits and hormonal profiles. Likewise, few have described this mechanism in a species with biparental care. Coyotes represent a particularly interesting model for parental effects theory, given wide behavioral variation across individuals and biparental care of young. Traits potentially shaped by parental effects such as size and aggression, may determine offspring social status, in turn influencing reproductive success of her progeny (where alpha individuals of a pack sire most of the offspring). Therefore, parental effects in the species may influence the rate of evolutionary change in a population. The goal of this study is to describe the development of behavioral and physiological traits in coyote offspring and examine how parental phenotypic traits influence offspring development. My specific objectives are threefold: (1) determine whether differences in parental traits influence offspring development; (2) describe temperament traits in offspring using natural play behaviors

and response to novelty; and (3) determine the relationship among temperament traits, hormonal profiles, and social rank within the litter.

Liz Scordato "Geographical variation in the targets of sexual selection"

Sexual selection is believed to play an important role in speciation, but the mechanisms by which it acts remain relatively untested. One way sexual selection could contribute to population divergence is if the strength and/or targets of selection vary in different habitats. Shifts in selective pressures may lead to divergence in traits and correlated preferences, ultimately resulting in prezygotic barriers to reproduction. I tested for variation in the strength and direction of sexual selection on song characteristics in two populations of the Greenish warbler ring species (*Phylloscopus trochiloides*). I find that within populations, there is an apparent tradeoff between selection on song due to male-male competition and selection due to female choice. Between populations, the relative strength of female choice vs. male-male competition changes, such that more northern populations are subject to stronger female choice. There is also some evidence for a shift in the targets of female preferences, from large song repertoires to longer songs. These results suggest that changes in the strength and direction of sexual selection have contributed to divergence in sexually selected traits in *P. trochiloides*, and may contribute to reproductive isolating barriers.

Si Tang "Persistence and Feasibility of Random Ecosystems"

Collaborator: Stefano Allesina

The relationship between complexity and stability has been central to theoretical ecology for more than 30 years debate was ignited by Robert May, who showed that large and complex, randomly assembled ecosystems are almost invariably unstable, contrary to previous expectations. He studied a set of "community matrices", which describe the behavior of an ecological system near equilibrium, and found that when the systems are large and highly complex, the probability of finding all species stably coexisting is vanishingly small. Therefore, he suggested that nature should adopt "devious strategies" to support biodiversity. Over the last three decades, ecologists have devised a vast array of stabilizing mechanisms. Subsequent research, however, did not disprove May's findings. Here we take a different approach and show that the May's argument, although valid, is not relevant for food webs. In fact, the vast majority of matrices studied by May cannot represent feasible ecological systems, in which species have positive densities. When we confine the analysis to feasible systems, we find strikingly different results for Random and Predator-Prey networks. In the former, when we assemble very complex networks, dynamics will prune the majority of the species and connections. In the Predator-Prey case, on the other hand, complexity begets persistence. Given the preponderance of consumer-resource relations in natural systems, no devious strategies are required to find persistent food webs as large and complex as those observed in the field. The results presented here are valid for other biological and non-biological networks and lead the way for a general re-thinking of the persistence in complex systems.

Will Tyburczy

"The interplay of species interactions and environmental stress in an intertidal predator-prey system"

While the whelk-barnacle system has historically been known as a strongly interacting predator-prey pair, species density manipulations reveal that for a variety of traits, intraspecific effects are stronger than interspecific ones. High whelk mortality during infrequent climactic events as well as predator feeding patterns may indicate the importance of microhabitat in regulating whelk densities.

Nate Upham

"Fossils and phylogeny: investigating diversification patterns in a diverse lineage of Neotropical rodents (Caviomorpha: Octodontoidea)"

Collaborator: Bruce Patterson

Biodiversity patterns are products of historical processes such as speciation and extinction, but living species preserve only part of this history. Lineages with robust fossil records and diverse ecological and biogeographic radiations offer greater insights. One such lineage is the rodent superfamily Octodontoidea (degus, spiny rats, and their relatives). These rodents are diverse (193 species across six families), found throughout the Neotropics, and their fossil record extends to the Oligocene (78 fossil genera). However, sparse taxon sampling and single-gene analyses currently cloud our understanding of octodontoid phylogenetic relationships. Here we examined sequence variation in 1 mitochondrial (12S rRNA) and 3 nuclear genes (vWF, GHR, and RAG1) across all caviomorph families (including 47 octodontoid taxa), all African phiomorph families, and the sole remaining hystricognath family. Our analyses find that the family Abrocomidae (chinchilla rats) is consistently recovered as the basal element in the Octodontoidea radiation, a finding not previously documented. Divergence time analyses using a conservative placement of five fossil calibrations finds a burst of diversification beginning in the mid-Miocene. Biogeographic analyses robustly recover the Southern Andes-Patagonia complex as ancestral for the Octodontoidea, with subsequent colonization and diversification in the Atlantic Forest, Cerrado and Caatinga, Amazonia, and the Antilles. This reconstruction refutes earlier ideas that the early-appearing, diverse, lowland family Echimyidae gave rise to the Andean lineages of octodonts— instead, the reverse derivation appears true. These results form a wide foundation for continued investigations, with plans for additional taxon and gene sampling as well as fossil-extant morphological analyses. Future work focuses on understanding the ecomorphological context for the Octodontoidea radiation, including the influence of competition from coexisting mammal lineages through time.

Traci Viinanen

"Seed set patterns in the perennial intermediate wheatgrass, *Thinopyrum intermedium*"

Perennial outcrossing species tend to exhibit lower seed set in proportion to the available fertilization sites than self-fertile species. Extensive variation for seed set exists in

perennial intermediate wheatgrass (*Thinopyrum intermedium*), ranging from 0 to 76% in field trials. There are three primary hypotheses to explain reduced seed-setting ability in perennials: low pollen availability, resource limitation, and mutational load. Low pollen availability is not likely in the artificially constructed monocultures of intermediate wheatgrass; however, experiments are underway to test pollen viability. The more likely explanation for reduced seed set is the presence of internal competition for resources between maturing fruits and other plant tissues and/or the build-up of deleterious mutations (mutational load), maintained by an effective outcrossing mechanism. In intermediate wheatgrass, seed abortion has been observed to be specific to floret location, with more distal florets producing less seed, suggesting that abortion is resource-dependent and that the florets closer to nutritional resources are favored. However, seed abortion in approximately half of the plants studied was random and possibly the result of mutational load associated with outbreeding. This is consistent with the generic findings where percentage of ovules developing into seeds in perennial (predominantly outcrossing) species is 50%, compared with 85% in inbreeding species. Greenhouse experiments will be used to determine the relative contribution of resource limitation and mutational load to reduced seed set in intermediate wheatgrass.

Ben Winger

"Understanding variability in phenotypic differentiation of birds across a biogeographic barrier in the Andes"

Despite the intuitive nature of allopatric speciation across a biogeographical barrier, the factors that lead to variability in phenotypic differentiation of species across the same barrier are unknown. I propose to test hypotheses on the determinants of variable phenotypic differentiation using Andean cloud forest bird species that diverge across the Marañón Valley of northern Peru as a model system. This region is a remarkable natural laboratory for testing hypotheses on the factors that control speciation in a comparative framework, due to the variable phenotypic differentiation of co-distributed cloud forest bird species across the arid valley of the Marañón. The results of my research will have implications for questions in evolutionary biology on the influence of time and gene flow on speciation, as well as our understanding of the evolution of the geographic distribution of biodiversity.