



Committee on Evolutionary Biology
&
Ecology and Evolution
Annual GAAN Retreat

April 15th, 2012

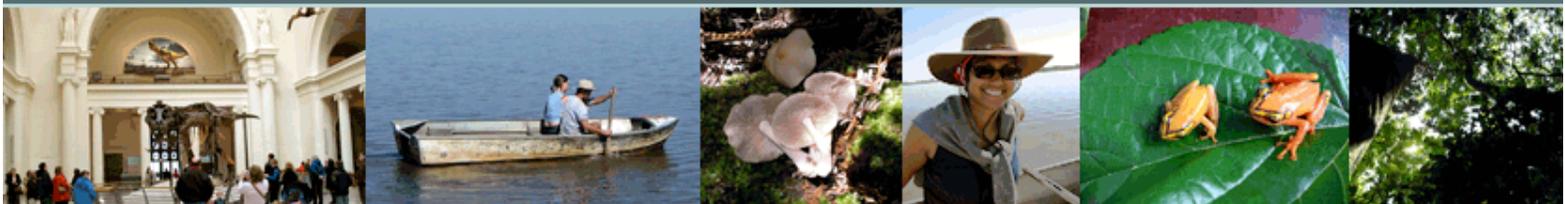
Hosted by the

Chicago Botanical Gardens

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Glencoe, Illinois USA

Committee on Evolutionary Biology
University of Chicago



Morning Session

- 9:15 SophieMcCoy Species interactions among a guild of crustose coralline algae respond to ocean acidification
- 9:30 Traci Viinanen Toward the genetic architecture of domestication: a semi-dwarf, erect-leaf phenotype in the perennial intermediate wheatgrass
- 9:45 Nathan Upham Diversification of a major lineage of Neotropical rodents (Caviomorpha: Octodontoidea): insights from fossil mandibles
- 10:00 Lauren Sallan After the end: how the end-Devonian extinction shaped modern vertebrate biodiversity
- 10:15 Deren Eaton Genomic RAD tags reveal phylogeny and hybridization in a recently diverged clade of *Pedicularis*
- 15 Minute Break
- 10:45 Paul Grabowski Patterns of switchgrass diversity and hybridization revealed by genome-wide genotyping
- 11:00 Christopher Meyer Genome-wide association mapping of defense traits in *Arabidopsis thaliana*
- 11:15 Katherine Brooks Immune function in Belding's ground squirrels
- 11:30 Andrew Dosmann Food, sex, and predators: animal personality persists with multidimensional plasticity across complex environments
- 11:45 Matthew Nelsen Tracing the evolution of lichen associations

Working Lunch (12:00– 2:00)

Jobs at small liberal arts colleges (Elizabeth Davis-Berg, Department of Science and Mathematics, Columbia College Chicago)

Media relations and communicating your science (Rob Mitchum, University of Chicago Medical Center)

Getting a postdoc (Michael Coates, Department of Organismal Biology and Anatomy; Corrie Moreau, Field Museum of Natural History)

Non-university jobs, highlighting NGOs (Andrea Kramer, Botanic Gardens Conservation International, Chicago Botanic Gardens; Melinda Pruett-Jones, Chicago Wilderness)

Afternoon Session I

- 2:00 Will Tyburczy Persistent differences in basic life history across the geographic range of the predatory whelk *Nucella ostrina*
- 2:15 Kristen Voorhies Spatial variation in Oregonian molluscan assemblages
- 2:30 Colin Kyle Mechanistic models to predict the response of an insect fungal pathogen to global climate change
- 2:45 Si Tang Reactivity and stability of large ecosystems
- 3:00 Jonathan Mitchell Ecological controls on North American wood-warbler (Parulidae) diversity
- 3:15 Kathryn Larson Exploring the relationship between form and function in wind-dispersed winged seeds
- 3:30 Aaron Savit The influence of habitat on intraspecific diversification in *Tangara* tanagers
- 3:45 David Bapst Morphological patterns of speciation and the lack of clades in the fossil record

Afternoon Session II

- 2:00 Laura Merwin Coastal stressors and *Arabidopsis*
- 2:15 Alice MacQueen R-gene expression plasticity in *Arabidopsis thaliana*
- 2:30 Talia Karasov Host-pathogen evolution: the maintenance of an ancient balanced resistance polymorphism
- 2:45 Benjamin Krinsky Investigations of young genes in *Drosophila*
- 3:00 Matthew Heintz The stressors related to pregnancy
- 3:15 Benjamin Rubin Mutualistic ants and their bacteria: does dietary specialization affect endosymbiont communities?
- 3:30 Natasha Bloch Molecular genetics and spectral tuning of warbler opsins: a comparative approach to avian color vision
- 3:45 Edna Davion Opsin genes in nocturnal mammals: implications for primate evolution

TALK ABSTRACTS

David Bapst, Department of Geophysical Sciences: Morphological patterns of speciation and the lack of clades in the fossil record

Morphology-based phylogenetic analyses of fossil taxa are often not fully resolved. This has been explained in terms of either methodological difficulties, associated with using morphological data in the fossil record, or as the byproduct of history, such as rapid speciation events. Another historical explanation is possible: morphological 'budding' patterns of speciation and the sampling of ancestor-descendant pairs in the fossil record, issues originally raised by Wagner and Erwin (1995). These phenomena can produce unresolvable polytomies in morphology-based phylogenetics, as they introduce sets of taxa which cannot be resolved into a fully nested (bifurcating) set of relationships. I illustrate these issues using examples from Pokemon species. There is very little work on the relative frequency of such morphological patterns of speciation, making it difficult to measure how resolved trees should be absolutely. Instead, I focus on the question of how unresolved we might expect our cladograms to be under varying sampling rates and mixtures of these morphological patterns. To answer this, I use stochastic birth-death-sampling simulations of the fossil record in the recently released software package *paleotree* for R. In all cases, increased sampling rates decrease the relative proportion of clades present in a set of taxa, as more ancestors and other difficult-to-place taxa are added. I also find that under the patterns of morphological speciation supported by Wagner and Erwin's empirical analyses, even poorly sampled sets of taxa are expected to have only about sixty percent of the possible number of clades on a fully bifurcating tree. This is also an issue for morphological phylogenetics of only extant taxa: some morphological speciation models would be expected to produce fully bifurcating trees while others may have as few as seventy percent of their expected clades. These results suggest that the poor resolution of some morphology-based phylogenies may result from the nature of historical relationships among those morphological taxa.

Natasha Bloch, Department of Ecology and Evolution: Molecular genetics and spectral tuning of warbler opsins: a comparative approach to avian color vision

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.

Katherine Brooks, Committee on Evolutionary Biology: Immune function in Belding's Ground Squirrels

The adaptive value of sociality and social relationships is evident from over 40 years of research. However, the proximate mechanisms of social evolution are relatively unknown. Proximate mechanisms may play a role in the evolution of many traits because physiological changes can lead to fitness changes. For my dissertation, I am studying social benefits and their links to physiology in Belding's ground squirrels (*Urocitellus beldingi*). Belding's ground squirrels live in groups of female kin and unrelated females and males. Females behave nepotistically towards their close female kin by alarm calling to warn relatives of predators and by cooperative territory defense. It is possible that female kin relationships provide fitness benefits, which in turn, are mediated by physiological changes. In this talk, I will discuss my recent work on immune function, as measured by bacteria killing ability (BKA), the ability of plasma proteins to kill bacteria *ex vivo*. Results will be discussed in terms of fitness consequences.

Edna Davion, Committee on Evolutionary Biology: 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). Here we examine claims of a diurnal ancestral primate in light of phylogenetic analysis of SWS1 opsin genes of representative genera of the supraordinal clade Euarchonta.

Andy Dosmann, Committee on Evolutionary Biology: Food, sex, and predators: animal personality persists with multidimensional plasticity across complex environments

The relationship between environmental change and individual's behavior is poorly understood, which undermines efforts to assess behavioral evolution. Studies of behavioral plasticity and animal personality focus on behavioral change across levels of a single environmental variable, overlooking the complexity of natural environments. To address that complexity, we manipulated combinations of foraging, mating, and predation risk variables, measuring their effect on anti-predator behavior of Belding's ground squirrels (*Urocitellus beldingi*). Squirrels exhibited plasticity across predation risk, and plasticity across foraging and mating environments was conditional on predation risk, matching adaptive expectations. Individual differences in plasticity to one variable were consistent across change in the second variable, verifying behavioral plasticity as a target of selection. Still, animal personality persisted across manipulations, implying that temporal aspects of plasticity might produce personality.

Deren Eaton, Committee on Evolutionary Biology: Genomic RAD tags reveal phylogeny and hybridization in a recently diverged clade of *Pedicularis*

The difficulty of resolving species-level relationships is a pervasive problem in phylogenetic systematics. Near the tips of trees, and particularly in rapidly diversified clades, slow evolving markers lack sufficient phylogenetic signal to resolve polytomies, and developing faster markers is costly. Moreover, to account for incomplete lineage sorting, or test hybridization, multiple loci must be sequenced across many species. While formerly unattainable, such data are now generally affordable using multiplexed high-throughput sequencing protocols such as restriction-site associated DNA (RAD). In this case study, we show that genomic RAD markers are capable of resolving phylogenetic relationships in a recently diverged clade of *Pedicularis*, and that such data also allow fine-scale tests for hybridization. We detect hybrid introgression among geographically widespread species of *Pedicularis* at low elevations, and a lack of hybrid introgression among endemic taxa at higher elevations. The high elevation taxa also show greater diversity of floral morphologies. Geography and connectivity thus appear to play a major role in mediating gene flow between species, where isolation may allow differentiation of floral morphologies and the development of species boundaries.

Paul Grabowski, Department of Ecology and Evolution: Patterns of switchgrass diversity and hybridization revealed by genome-wide genotyping

Geographic patterns of genetic variation are generated by a combination of historical and contemporary processes, including migration, genetic drift, and natural selection. Powerful new methods using second-generation sequencing can be applied to non-model organisms to better characterize patterns of variation and start dissecting the causative mechanisms. We use genotyping-by-sequencing to genotype 125 switchgrass (*Panicum virgatum* L.) individuals from across the native range at more than twenty-five thousand loci. Using these data, we identify regional gene pools within both major ecotypes, ecotype-hybrid populations, and find evidence of hybridization of switchgrass with its sister species, *Panicum amarum*.

Matthew Heintz, Committee on Evolutionary Biology: The stressors related to pregnancy

Pregnancy causes a cascade of behavioral changes that influence both hormones and behavior. One of these major changes includes an increase in stress hormones during parturition. Stress hormones inhibit storage of glucose, promote gluconeogenesis and inhibit non-essential functions to enable energy availability for an immediate need. I provide the first evidence of an increase in fecal glucocorticoid metabolites of a wild adult female chimpanzee (*Pan troglodytes*) following parturition. This event is later followed with a severe maternal rejection to her infant offspring, which is also linked to an increase in fecal glucocorticoid metabolites. In addition to hormone changes, differences between behavioral activity budgets prior to and following the pregnancy will be discussed. These data highlight the practical nature of linking hormonal changes with a specific event and also the importance of accounting for reproductive state with behavioral measures.

Talia Karasov, Committee on Genetics, Genomics, and Systems Biology: Host-pathogen evolution: the maintenance of an ancient balanced resistance polymorphism

Resistance (*R*) genes in *Arabidopsis thaliana* frequently exhibit the signature of balancing selection; however, how selection acts to maintain these long-term polymorphisms is unknown. This is due, in large part, to the dearth of *R* gene-effector pairs that are known to interact in nature. Here we clone an *R* gene-effector pair from natural, co-occurring populations of *A. thaliana* and *Pseudomonas syringae*. The *R* gene, *RPS5*, exhibits a balanced polymorphism for the presence or absence of the gene that has been maintained for over 2 million years, and recognizes an *AvrPphB* homolog, which we name *AvrPphB2*. Consistent with the presence of an ancient balanced polymorphism, *RPS5* confers a benefit when plants are infected with an *AvrPphB* homolog but also confers a large (~5-

10%) cost in the absence of infection. Both resistant and susceptible alleles of *RPS5* occur in 90% of surveyed populations globally, suggesting that selection for resistance is frequent and ubiquitous. Curiously, AvrPphB homologs are found at very low frequencies in *P. syringae* populations that infect *A. thaliana* populations. These results suggest that selective forces other than infection with *P. syringae* carrying AvrPphB2 may be involved in the maintenance of the *RPS5* balanced polymorphism. Indeed, we find evidence that AvrPphB(2) has been horizontally transferred, suggesting that it occurs in other pathogen species, and that *RPS5* is capable of recognizing other effectors in *P. syringae*. Our results suggest that the *RPS5* disease polymorphism is stably maintained in *A. thaliana* populations, not through a tight co-evolutionary interaction with one effector, but through complex interactions with many independent selective pressures that favor *RPS5*. We present a simple model to illustrate that long-term polymorphisms are feasible in such uncoupled systems.

Benjamin Krinsky, Committee on Evolutionary Biology: Investigations of young genes in *Drosophila*

The study of recently duplicated genes, also called “new” or “young” genes, provides powerful insights into both molecular evolutionary processes and the origins of novel biological functions and phenotypes. By studying loci that have arisen in the last few million years, we strive to “catch evolution in the act,” as it were, and find interesting phenomena that have not been obscured by the aeonian march of time. The fruit fly genus *Drosophila* provides an ideal system for the study of young genes owing to the wealth of genomic and molecular tools available, and the relatively recent divergence of several closely related species. One particularly interesting young gene candidate is the poetically named *Zeus* locus. This locus arose approximately 5 million years ago in the *Drosophila melanogaster* subgroup, subsequently underwent a period of very rapid molecular evolution, and has also acquired a male-reproductive system specific expression pattern compared to its parental gene, *Caf40*. When *Zeus* expression is knocked-down via RNAi, males exhibit a drastic (~60%) reduction in fertility and a number of reproductive-system phenotypes. On the molecular level, the *Zeus* protein possesses a putative nucleic acid binding domain and has acquired over 200 novel targets genome-wide. Ongoing work seeks to further characterize the functions of this gene as it relates to male reproduction, and understand its molecular role as a newly arisen regulator in multiple species.

Colin Kyle, Department of Ecology and Evolution: Mechanistic models to predict the response of an insect fungal pathogen to global climate change

Global climate change is greatly altering the ecology of some organisms, and scientists are concerned about impacts of changes to the spread of infectious diseases. Fungal pathogens 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 am constructing mechanistic models predicting how one such pathogen, *Entomophaga maimaiga*, which serves as a biological control for the invasive gypsy moth (*Lymantria dispar*), will respond to different climate change scenarios. To investigate how this disease functions under different climate conditions, I collected observational, experimental and weather data during natural *E. maimaiga* outbreaks at three different sites along a 395.9 km latitudinal gradient for two summers. To begin modeling this pathogen, I parameterized and compared different time- and weather-dependent models of fungal spore germination. A delayed, precipitation-dependent model proved to be the current most parsimonious and best fitting model ($\Delta AIC > 3$). This result provides perspective on how weather conditions influence the mechanics of this pathogen. I plan to explore and test other spore germination models in the future and will incorporate my findings into larger models of within- and between-season disease transmission.

Kathryn Larson, Department of Geophysical Sciences: **Exploring the relationship between form and function in wind-dispersed winged seeds**

Since the origin of seed plants, numerous morphological modifications have evolved that increase the success of propagule dispersal away from parent plants. Of these modifications, one of the most frequently evolved structures in wind-dispersed propagules is the wing. Within flowering plants winged fruits have evolved in many lineages and converged on a small number of morphologies. How these repeatedly evolved forms act to influence aerodynamic behaviors of falling seeds has been the subject of much study, but how these forms and behaviors affect dispersal distances during natural dispersal events remains poorly understood. To explore this relationship, wind dispersed fruits from two species of *Carpinus* (Betulaceae) were collected during a natural dispersal event and then subjected to a series morphological and aerodynamic analyses. These analyses demonstrated that wing loading (the mass of the fruit divided by the area of the wing) closely correlated with fruit descent rates when aerodynamic behavior was taken into account, but surprisingly neither wing loading nor descent rates correlated with observed dispersal distances. These results indicate that the high variability of wind speeds experienced in this environment over an entire dispersal season erased any influence intraspecific variation in fruit morphology had on increasing dispersal abilities. This interplay highlights the importance of considering the relative variances of fruit form and wind conditions when studying wind dispersal processes and wind dispersed fruit form evolution as a whole.

Alice MacQueen, Department of Ecology and Evolution: **R-gene expression plasticity 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. Many population-level features of R-genes are not consistent with traditional selective sweep models of pathogen arms races, including the extreme age of some R-gene alleles and presence/absence polymorphisms for entire R-genes. The presence of these features has been attributed to the large fitness costs of resistance (COR) 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 a COR may be to limit resistant R-gene expression to times when it harms plant fitness least, such as in environments where infection is more probable and/or longer growth more favored. R-genes may be differentially regulated at the expression level: there is significant natural variation in expression levels of most R-genes between *Arabidopsis* accessions. However, the extent of R-gene expression plasticity between environments and within-species variation in expression plasticity was unknown. To gauge these qualities, I used qPCR to compare expression levels of 13 R-genes in seven “maximally diverse” accessions of *Arabidopsis thaliana* grown in eight abiotic environments relative to three stably expressed reference genes. R-gene expression was downregulated in hot and dry environments relative to standard greenhouse growth conditions as hypothesized by this alternative strategy. I did not observe similar patterns of expression in an R-gene theorized to follow the strategy of R-gene loss to mitigate COR. These results thus offer a first skein of support for the idea that multiple evolutionary strategies reduce fitness costs of resistance.

Sophie J McCoy, Department of Ecology and Evolution: **Species interactions among a guild of crustose coralline algae respond to ocean acidification**

As the oceans continue to acidify via absorption of carbon dioxide emissions, many consequences are expected for marine organisms and communities. Effects of environmental changes in natural systems can best be detected in areas where species dynamics and interactions have been studied

together with physical and chemical features of seawater. I show changes in species interactions within a well-studied guild of crustose coralline algae over time compared with historical data, and discuss changes in species-specific traits that correspond with observed changes in species ecology in the field and expected responses of coralline algae to acidification.

Laura Merwin, Department of Ecology and Evolution: **Coastal stressors and *Arabidopsis***

Coastal environments encompass a number of unique stressors for terrestrial plant species, including reduced water availability due to the drainage properties of sandy soils. These coastal stressors might lead to genetically-based local adaptation in beach populations. To look for evidence of such adaptation, I compared *Arabidopsis* accessions sampled from beach populations to accessions from inland sites under treatments intended to mimic potential beach water availability and measured fitness (number of seeds). Plants sampled from four source substrates (coarse beach sand, fine beach sand, inland sand, and inland soil) were grown on soil in the greenhouse in control, mild drought, and harsh drought treatment groups. Overall, plants from non-soil substrates, especially coarse sand beaches, produced less seed, but plants from non-soil substrates were less affected by drought treatments. Mild drought treatment reduced seed production in plants from soil sites by about half, but did not reduce (and in some cases increased) seed production in plants from the other three substrate types. Harsh drought treatment reduced seed production in plants from all substrate types, but had the largest effect on plants from soil sites. This treatment by source interaction effect suggests that plants from non-soil substrates may be locally adapted for tolerating reduced water availability.

Christopher Meyer, Department of Ecology and Evolution: **Genome-wide association mapping of defense traits in *Arabidopsis thaliana***

Recent advances in genotyping and sequencing technology have made genome-wide association (GWA) studies an attractive option for studying the genetics underlying natural variation in biological traits. In addition to identifying genes controlling the expression of complex traits, GWA mapping in worldwide natural populations can also reveal the geographical distributions of these traits and their associated alleles. A natural worldwide population of ~200 *Arabidopsis thaliana* accessions genotyped at ~214,000 single nucleotide polymorphisms (SNPs) was used to study the genes controlling plant defense traits and their geographical distribution. The results illustrate that different traits contributing to plant defense against herbivory are correlated and exhibit geographical patterns that may be explained by the distributions of their herbivores.

Jonathan Mitchell, Committee on Evolutionary Biology: **Ecological controls on North American wood-warbler (Parulidae) diversity**

The role of biotic interactions in shaping and controlling clade diversification remains a hotly contested topic in macroevolutionary studies. Evidence based on ecological observations of recent radiations suggests a strong role for biotic interactions, whereas data from phylogenetic and paleontological studies are more ambiguous. North American wood-warblers (Parulidae) have been suggested to have undergone a competition-mediated radiation on the basis of the distribution of cladogenic events in their history (i.e., a strongly negative gamma statistic). However, the number of lineages extant at any given time is an exceptionally crude measure of ecological disparity. Rather than focusing solely on the timing of diversification events, I combine ecological and morphological data derived from modern taxa with a recently published phylogeny to demonstrate how various methods of inferring trait evolution can be extended to elucidate the tempo and mode of ecological change in deep time.

Matthew Nelsen, Committee on Evolutionary Biology: **Tracing the evolution of lichen associations**

The disparity in species richness across fungal lineages is striking. Within the fungal class Lecanoromycetes (Ascomycota), this unevenness is especially pronounced, with the number of species per family ranging from under 15 to nearly 2500. Clade age showed little correlation with clade richness, while a strong correlation was observed between net diversification rate and clade richness. Net diversification rate estimation for families in this class revealed that families such as Parmeliaceae and Cladoniaceae exhibit exceptionally high diversification rates, while a number of families with low species richness, such as Gypsoplacaceae and Miltideaceae, had exceptionally low diversification rates. Finally, an attempt is made to identify potential sources of this variation in diversification rates across Lecanoromycetes.

Benjamin Rubin, Committee on Evolutionary Biology: **Mutualistic ants and their bacteria: does dietary specialization affect endosymbiont communities?**

Several groups of insects are known to depend heavily on endosymbiotic bacteria for nutritional upgrading of an otherwise poor diet. *Pseudomyrmex* acacia-ants feed exclusively on resources derived from their host plants and could potentially benefit from dietary enrichment by such mutualistic bacteria. However, we find that acacia-ants do not host specialized bacterial communities and that *Pseudomyrmex* ants generally have far fewer endosymbionts than many other ants. While the total number of bacteria is small, overall bacterial diversity and the number of bacterial species found exclusively in *Pseudomyrmex* ants are high. Even small numbers of bacteria could have a substantial impact on host nutrition but our findings suggest that acacia-ants do not depend on particular species of bacteria. The dearth of bacteria within *Pseudomyrmex* ants may indicate that these ants possess other adaptations for coping with their extremely limited diets.

Lauren Sallan, Department of Organismal Biology and Anatomy: **After the end: how the end-Devonian extinction shaped modern vertebrate biodiversity**

Modern vertebrate biodiversity is represented by three groups: ray-finned fishes (Actinopterygii; 30,000 species); tetrapods (25,000 species) and sharks (Chondrichthyes; 1,100 species). Investigation of the Devonian-Carboniferous vertebrate record has revealed that a compositionally modern global biota arose abruptly after the Hangenberg event, 359 million years ago. This mass extinction devastated a previously stable fauna armored placoderms and lobe-finned fishes (Sarcopterygii) marked a bottleneck in the evolution of extant vertebrates. Recent biodiversity as a whole is contingent on such historic global events. However, research on the aftermath of the Hangenberg extinction, including a 15 million year period of low tetrapod and fish diversity sometimes called “Romer’s Gap,” has revealed the extent to which aftermath conditions also shaped subsequent diversity. While several vertebrate lineages survived the extinction, nearly half of these were “dead clades walking”: persisting without proliferating for millions of years. Contrary to expectations, the radiations of modern forms, such as actinopterygians, largely failed to converge on lost ecomorphs or recover previous ecosystems. Instead, these radiations produced a wealth of novel body morphologies (e.g. angelfish and eels) and trophic strategies (e.g. crushing predators). The rise of new predators among these previously rare vertebrate clades changed resident ecosystems, impacting the diversity of trophically connected groups, including those spared by the Hangenberg itself. The next challenge is to understand why recovery ecosystems benefited certain groups over others in setting the foundations for modern biodiversity.

Aaron Savit, Committee on Evolutionary Biology: **The influence of habitat on intraspecific diversification in *Tangara* tanagers**

The evolution of intraspecific divergence is integral to the speciation process because it creates standing diversity that can be reinforced by allopatry and secondary contact to eventually yield

different species. Habitats are expected to play a formative role in the evolution of intraspecific diversity as a result of changes in extent and connectivity through time. The geometry of Neotropical habitats varies widely, from scattered archipelagos of high-altitude habitat to thin ribbons of Andean cloud forest to expansive lowland Amazonian ranges. Here I examine the effect of different Neotropical habitats on intraspecific diversification in *Tangara* tanagers. Using molecular data and extensive geographic sampling, I examine the demographic and phylogeographic patterns of each species. I relate the observed patterns to expectations based on the extent and availability of suitable habitat over recent evolutionary history. My results show that different tropical habitats play an important role in shaping patterns of intraspecific diversity, and that different habitats yield consistently different patterns of within-species diversity.

Si Tang, Department of Ecology and Evolution: **Reactivity and stability of large ecosystems**

The study of the local stability of ecological communities has a long tradition. Stability describes whether an ecological system will return to the original steady state eventually after being perturbed.

More recently, the study on the transient dynamics of ecological systems has been recognized as critical, given that continuously disturbed systems might never reach a steady state, and thus the instantaneous response to perturbations alone could determine species persistence. A stable equilibrium can be nonreactive – all perturbations decay monotonically, or reactive -- some perturbations are amplified before eventually decaying. In this talk, I will introduce the classical analysis of stability and reactivity. Then I will show how the stability (long-term response to perturbations) and reactivity (short-term response to perturbations) change with (1) the size of the ecosystem (2) the interaction types, and (3) the interaction strength. A brief summary of the stability and reactivity criteria is included at the end of the talk.

Will Tyburczy, Department of Ecology and Evolution: **Persistent differences in basic life history across the geographic range of the predatory whelk *Nucella ostrina***

Individuals of a single species are generally held to share a common set of fundamental life history traits. This belief may be strengthened by the tendency of individual studies to be conducted at sets of adjacent or nearby sites. However, a species may be confronted with very different sets of ecological challenges across its geographic distribution, creating the potential for a single species to exhibit large variation in its basic life history. Monitoring of both caged and isolated, free-living populations of the predatory whelk, *Nucella ostrina* over several years revealed a consistent geographic pattern of mortality of *N. ostrina*. Mortality was much higher in Washington than Oregon, but per capita egg production was also nominally higher in Washington, suggesting a shift toward semelparity in that region. A literature review of whelk mortality rates across the Northeast Pacific confirmed that the difference in mortality has existed for at least several decades, and suggested a role of barnacle recruitment patterns in driving regional patterns of semelparity and iteroparity.

Nathan Upham, Committee on Evolutionary Biology: **Diversification of a major lineage of Neotropical rodents (Caviomorpha: Octodontoidea): insights from fossil mandibles and DNA**

The Neotropical rodent superfamily Octodontoidea is one of the rare lineages of species that offers both extensive living biodiversity and robust fossil records to assist in the investigation of evolutionary patterns and rates. This research aims to unlock information about this lineage's diversification dynamics – in both time and space – using evidence from their abundant fossils and DNA sequences. Rodents in Octodontoidea comprise 6 living families (38 genera and 193 species), and occupy an array of rodent lifestyles from arboreal spiny rats to fossorial tuco-tucos. Many living species are rare and at least one third are threatened with extinction. Their ecological radiation dates to at least 25 million years ago, with 78 known fossil genera, and they are widespread in their modern distributions across South America, Central America, and the Antilles. This research uses

two discrete steps to investigate Octodontoidea's diversification: 1) construction of a phylogenetic timetree for the superfamily, employing 5 genes and detailed fossil calibrations; and 2) quantifying patterns of mandible shape evolution in both fossil and living members of this radiation. The goal here is to compare evolutionary rates among rodent clades in a rigorous temporal framework, and in relationship to their diverse life history traits. Here I present results from a geometric morphometric analysis of mandible shape variation in fossil taxa from Argentina.

Traci Viinanen, Committee on Evolutionary Biology: **Toward the genetic architecture of domestication: a semi-dwarf, erect-leaf phenotype in the perennial intermediate wheatgrass**

The genetic architecture underlying morphological traits gives insight into how different forms evolve. Major morphological changes arising from few genetic alterations are often involved in the evolution of a domesticated organism from its wild progenitor. I am investigating a semi-dwarf, erect leaf phenotype in intermediate wheatgrass, a perennial grass undergoing the process of domestication for grain and biomass production. Preliminary results suggest there is at least one dominant allele contributing to the phenotype.

Kristen Jenkins Voorhies, Committee on Evolutionary Biology: **Spatial variation in Oregonian molluscan assemblages**

My dissertation research seeks to quantify and evaluate the drivers of change in modern marine molluscan communities: do they presently fall within the realm of natural historical variability (driven by climate and oceanographic stressors) or do they deviate significantly from that baseline (driven by human-related stressors)? My first step to answering this question is to build empirical datasets that include variation in abundance and composition in soft-bottom molluscan assemblages across spatial and environmental gradients in Southern California and Oregon. Additionally, to include historical variation in the data, I evaluate molluscan assemblages of different temporal resolution from an instantaneous snapshot (live-collected data) to a coarser palimpsest (death assemblage data). Currently, I am evaluating environmental drivers of abundance variation in live and dead assemblages collected off of the coast of Newport Bay, Oregon in 2011 in collaboration with Dr. Sarah Henkel (Oregon State University). Variation is mainly driven by location (latitude and longitude), water depth, sample depth (depth of penetration of sampling device), and turbidity among living assemblages. Other environmental variables including temperature, dissolved oxygen, pH, and salinity are not considered here because the effect size of seasonality is larger than the gradients over which the samples are compared. Death assemblages across the same depth gradient do not appear to vary significantly but they do vary with latitude and longitude. These initial results suggest sampling location and size important and future analytical pooling exercises may make patterns more clear. Live and dead data appear positively correlated in site-by-site comparisons but the correlation is only significant in the strongest positive correlation between samples at a deeper site. When all live and all dead data are pooled for bay/habitat level comparison the two are positively and significantly correlated. These initial results support future live-dead comparisons that will be explored using community structure patterns such as rank abundance distributions to gain more insight on the range of variation among assemblages.