



Committee on Evolutionary Biology
&
Ecology and Evolution
Annual GAANN Retreat

April 7th, 2013

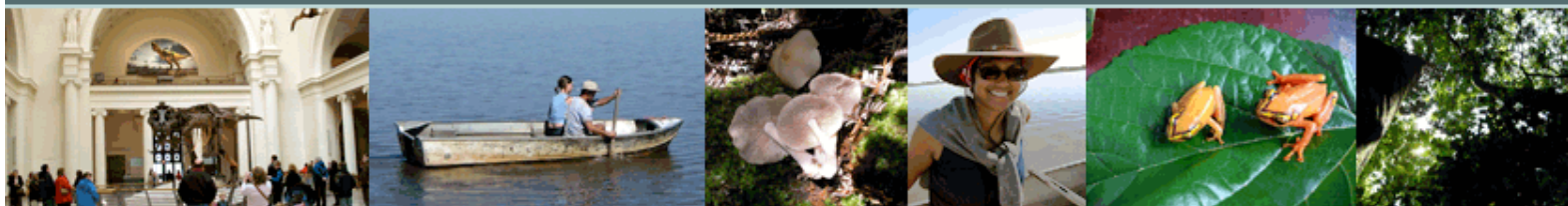
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Glencoe, Illinois USA

Committee on Evolutionary Biology
University of Chicago



Morning Session

Moderator: Sebastian Heilpern

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|-----------------|--------------------|---|
| 9:15 | Talia Karasov | Bacterial gene content variation is only marginally affected by geographic location and host of isolation |
| 9:30 | Christopher Schell | Parents, Pups, and Personality: examining the influence of parental effects in coyotes |
| 9:45 | Laura Merwin | Natural variation in hypocotyl length in Swedish <i>Arabidopsis thaliana</i> associated with SPA2 |
| 10:00 | Ben Rubin | The genome of the arboreal ant <i>Pseudomyrmex gracilis</i> |
| 10:15 | Thomas Stewart | On the origin and evolution of adipose fins |
| 15 Minute Break | | |
| 10:45 | Si Tang | Correlation between interaction strengths drives stability in large ecological networks |
| 11:00 | Colin Kyle | Forecasting the response of an insect fungal pathogen to climate change using mechanistic models |
| 11:15 | Ben Winger | A genomic approach to understanding allopatric speciation in tropical montane birds |
| 11:30 | Alice MacQueen | Fitness of a long-maintained resistance polymorphism in the absence of cognate pathogen |

Lunch Talk (12:00)

Dr. May Berenbaum, University of Illinois at Urbana-Champaign

Dr. Berenbaum's research has focused on the evolution and implications of insect/plant coevolution, particularly the chemical interactions between herbivorous insects and their host plants. She is an experienced (and fantastic) communicator of science to the general public and will talk today about her experience and advice in this area. You can read more about her (and the Insect Fear Film Fest) at <http://www.life.illinois.edu/berenbaum/>

Post-Lunch Walk and Break (reconvene at 2:00)

Afternoon Session I

Moderator: Shane Dubay

2:00	Paul Grabowski	Gene flow, admixture, and ploidy shape genetic variation in switchgrass
2:15	Joyce Pieretti	Fin morphogenesis & Sonic Hedgehog (Shh) Regulation
2:30	Pengyao Jiang	A closer look at <i>Drosophila melanogaster</i> <i>Even-skipped</i> gene expression
2:45	Christopher Meyer	Pleiotropic jasmonate-responsive genes regulate the expression of herbivore defenses in natural plant populations
3:00	Deren Eaton	Genomic introgression at the phylogenetic scale
3:15	Nate Upham	Old rats from the Neotropics: using ancient DNA and fossils to study the evolutionary diversification of a major rodent lineage
3:30	Traci Viinanen	Toward genomic selection in intermediate wheatgrass (<i>Thinopyrum intermedium</i>): using genotyping-by-sequencing for simultaneous SNP discovery, genetic map construction, and trait mapping
3:45	Rob Arthur	Strong conservation of H3K27me3 bypassed by gene duplication

Afternoon Session II

Moderator: Alex White

2:00	Sophie McCoy	Physiological changes in crustose coralline algae alter competitive interactions in response to ocean acidification
2:15	Sara Jackrel	Local adaptation in aquatic communities to intraspecific variation in a terrestrial ecosystem subsidy
2:30	Allison Johnson	Differing patterns of evolution in males and females generate dichromatism in fairy-wrens (Maluridae)
2:45	Orissa Moulton	Interactions between intertidal macroalgae and ammonium-oxidizing microbes in the presence of ammonium, a shared resource
3:00	Jonathan Mitchell	Testing food web models on fossil ecosystems
3:15	Tim Sosa	North America's tiny ersatz piranhas: biogeography and morphological evolution
3:30	Courtney Stepien	The roles of evolutionary history and ecological interactions in the maintenance of a high-diversity algal assemblage
3:45	Matthew Nelsen	Elucidating the evolutionary origins and diversity of lichen symbionts

TALK ABSTRACTS

Robert Arthur, Ecology and Evolution: Strong conservation of H3K27me3 bypassed by gene duplication

Epigenetic marks, such as histone modifications, are strongly correlated with nearby gene expression and the deposition of such marks on specific loci has been shown to be important for cell-type specification in development. Despite these facts, relatively little is known about the evolution of epigenetic marks. We performed ChIP-seq against the repressive mark histone 3 lysine 27 trimethylation (H3K27me3) in four species of *Drosophila*. We found strong conservation of H3K27me3 signal over orthologous genes in all tested species. Areas outside of genes experience more divergence in H3K27me3 signal, and greater divergence is associated with more DNA sequence change. Surprisingly, genic H3K27me3 signal conservation extends even to orthologs in *Caenorhabditis elegans*. However, duplicated genes are consistently less conserved with regards to H3K27me3 signal, and such changes are associated with concomitant changes in gene expression. We discovered that different kinds of duplication events lead to different magnitudes of change in H3K27me3 signal, consistent with the spatial nature of epigenetic regulation. Our findings underscore both the strong conservation of genomic architecture governed by an epigenetic mark across distantly related species and the importance of gene duplication as a mechanism for generating novel H3K27me3 profiles.

Deren Eaton, Committee on Evolutionary Biology: Genomic introgression at the phylogenetic scale

Using simulated and empirical data I show how recently developed methods of testing genomic introgression across shallow phylogenetic scales can be misleading when applied to more distantly diverged taxa, especially within diverse clades where multiple distinct species may have hybridized. To overcome this problem, I developed a new extension to the D-statistic test which more accurately distinguishes shared ancestry from introgression, and can better detect the direction of gene flow.

Paul Grabowski, Committee on Evolutionary Biology: Gene flow, admixture, and ploidy shape genetic variation in switchgrass

Switchgrass, a North American warm-season (C4) grass, is an important component of ecosystems ranging from tall grass prairies to coastal sand dunes. Additionally, switchgrass is an emerging bioenergy crop due to its high productivity on marginal lands. Despite the ecological and economic importance of switchgrass and 50+ years of agronomic research, patterns of genetic variation in switchgrass are still poorly understood. We use next-generation sequencing-based methods to genotype switchgrass from across the United States to evaluate the relationship of populations from across the range. The genotyping results identify several genetically-distinct regional gene pools and indicate that several of the gene pools originated from recent admixture events. The admixed gene pools contain many populations with higher ploidy levels, suggesting that admixture leads to ploidy differences and therefore contributes to the formation of major barriers to gene flow in switchgrass.

Sara Jackrel, Ecology and Evolution: Local adaptation in aquatic communities to intraspecific variation in a terrestrial ecosystem subsidy

Cross-ecosystem fluxes can intertwine otherwise disparate food webs, but the effects that biodiversity at the genotypic level can have on fluxes across ecosystems boundaries is not known. Fresh leaves, which vary in traits such as defensive compounds against terrestrial herbivores, drop off trees and enter streams, providing a vital resource for riverine organisms during their growing season. We demonstrate substantial variation in decomposition rates among individual trees in four

different rivers in the Olympic Peninsula of Washington state, USA. Over time, aquatic decomposer communities have locally adapted to the specific trees supplying the riparian subsidies. We demonstrate experimentally that locally derived red alder leaf litter decomposes on average 24% more quickly than red alder leaf litter introduced from other riparian zones. In energy-limited environments, such as small shaded streams, consumers must be efficient foragers. Our results indicate that this pressure for efficiency has led to adaptation at a particularly fine scale. Further results show that two driving factors of these intraspecific differences are leaf nutrient quality and induced plant defenses caused by terrestrial herbivory. More broadly, these results illustrate how intraspecific diversity and the effects of selection in one ecosystem can indirectly shape the structure of other ecosystems through ecological fluxes across boundaries.

Pengyao Jiang, Ecology and Evolution: A closer look at *Drosophila melanogaster* Even-skipped gene expression

Seven stripe even-skipped gene expression is known to be conserved across long evolutionary distance. However, to what extent the conservation is within species is not known. Previous study shows the relative seven-stripe positions are maintained within species, but we don't know the difference or conservation on expression levels. Here I show some preliminary data of even-skipped for several *Drosophila melanogaster* polymorphic lines. Further analysis is needed to explain this differences. This posts question on what is the functional constraint on developmentally important even-skipped gene expression.

Allison Johnson, Ecology and Evolution: Differing patterns of evolution in males and females generate dichromatism in fairy-wrens (Maluridae)

Sexual dichromatism in birds is often attributed to selection for elaboration in males. Yet evolutionary changes in either sex can result in plumage differences that lead to either gains or losses of dimorphism. We reconstructed the evolution of plumage colors in both males and females of species in Maluridae, a family comprising the fairy-wrens (*Malurus*, *Clytomias*, *Sipodotus*), emu-wrens (*Stipiturus*), and grasswrens (*Amytornis*). Our results show that, across species, males and females differ in their general patterns of color evolution. Male plumage colors have diverged at relatively steady rates, whereas female colors have changed dramatically in some lineages and little in others. Accordingly, in comparisons against evolutionary models, plumage changes in males best fit a Brownian motion (BM) model, whereas plumage changes in females fit an Ornstein Uhlenbeck (OU) multi-peak model indicating natural selection, with different adaptive peaks corresponding to Australia and New Guinea. Levels of dichromatism were significantly associated with latitude, with greater dichromatism in more southerly taxa. Our results suggest that current patterns of plumage diversity in fairy-wrens are a product of evolutionary changes in both sexes, driven in part by environmental differences across the distribution of the family.

Talia Karasov, Genetics, Genomics and Systems Biology: Bacterial gene content variation is only marginally affected by geographic location and host of isolation

Strains of a single bacterial species isolated from different environments can differ extensively in gene content. While these differences may be the basis of adaptation to specific environments, variation in gene content may also result from other molecular, demographic and selective processes. We sequenced the genomes of 18 strains of the plant pathogen *Pseudomonas syringae* extracted from a single host-environment. We find that gene content variation among these strains is nearly as extensive as variation among strains collected from different host species in divergent geographic locations. We identify an ecologically important genomic island enriched in the single-host environment, but overall find that the majority of variation in gene content is uninfluenced by large-scale differences in environment of isolation instead being much more influenced by phylogeny.

These results suggest that extensive variation in gene content, even within largely similar environments, is a common feature of natural microbial populations.

Colin Kyle, Ecology and Evolution: Forecasting the response of an insect fungal pathogen to climate change using mechanistic models

Fungal pathogens represent a group of diseases in which climate change is expected to have direct, dramatic impacts due to the strong influence of environmental factors on fungal life cycles and ecology. However, it is currently unclear whether climate change will cause epizootics of fungal pathogens to be more or less frequent. Therefore, we are constructing mechanistic models predicting how one such pathogen, *Entomophaga maimaiga*, which serves as a biological control for invasive gypsy moth caterpillars (*Lymantria dispar*), will respond to different climate change scenarios. To investigate how this disease functions under different climate conditions, we collected epizootic, experimental and weather data during natural *E. maimaiga* outbreaks at four different sites along a 395.9 km latitudinal gradient weekly for three summers. We experimentally measured fungal force of infection by placing cages of healthy insects at each site for 24 hours each week. Using these data, we fit and compared weather-dependent epidemiological models with different functional responses to weather. We tested universal and site-specific models and estimated parameter values using maximum likelihood calculations. After comparing models using AICc, a site-specific model in which fungal infection rate depended on total accumulated rainfall over the previous 4 to 9 days was the current best-fitting model. A universal model in which infection rates depended on accumulated rainfall over the previous 5 days received the next highest ranking ($\Delta\text{AICc} = 58.9$). Because of the tight, non-linear relationship with rainfall, we therefore predict that the anticipated increase of variance in rainfall due to climate change will lead to more severe, but less frequent, pathogen epizootics.

Alice MacQueen, Ecology and Evolution: Fitness of a long-maintained resistance polymorphism in the absence of cognate pathogen

Plant disease resistance (*R*-) genes confer gene-for-gene resistance to pathogens and are highly polymorphic within *Arabidopsis thaliana*. Balancing selection on *R*-gene presence/absence polymorphism (*R*-P/A) is thought to play an important role in the molecular evolution of *R*-genes. Fitness costs of resistance of six to ten percent have been demonstrated in the field for plants with two *R*-P/A polymorphic genes in the absence of the pathogen they detect. Balancing selection has also been documented for *R*-genes without *R*-P/A, such as *RPS2*. *RPS2* is present in every accession surveyed thus far; however, the *RPS2* gene tree has an ancient bifurcation separating major resistance and susceptibility clades of alleles. We used Cre-lox mediated recombination to insert seven alleles of *RPS2* – four resistant and three partially resistant or susceptible – at three different genomic locations on an isogenic background. We then grew these lines in the field in the absence of the *RPS2*-mediated pathogen resistance and in the greenhouse under stressful abiotic conditions and measured plant seed set and dry weight to determine fitness differences between these lines. We predicted that the four resistant lines would be less fit in the absence of pathogen if *RPS2* had a cost of resistance. Linear models of the fitness data indicate significant fitness differences exist between lines both in the field and growth chamber. In the field, the results were consistent with any *RPS2* allele conferring a fitness benefit to the plant. We speculate that these plants were not grown in the absence of the pathogen they detect. In the greenhouse, the results were generally consistent with a cost of resistance for resistant alleles, although this result did not adhere strictly to the resistance and susceptibility clade division of *RPS2*. On average in the greenhouse, the four resistance alleles were 5% less fit than control plants lacking *RPS2*; the three susceptible alleles were not significantly different than controls. High costs of resistance may thus be a feature of *R*-genes under balancing selection.

Sophie McCoy, Ecology and Evolution: Physiological changes in crustose coralline algae alter competitive interactions in response to ocean acidification

The effects of environmental changes in natural ocean ecosystems can best be detected at locales where species dynamics and interactions have been studied concomitant with physical and chemical features of coastal seawater. To identify ecological changes in response to this temporal gradient in acidity, I repeated competition experiments identical to those performed 1981-1984 among crustose coralline red algae at a site with rapid decline of seawater pH documented over the last 13 years.

These experiments quantify overgrowth competition hierarchies between coralline algal crusts and determine the strength of competitive interactions as a function of herbivory pressure. Large changes are found in the competitive interactions of all species over time when compared between 2010-2012 and 1981-1984. Changes in morphological traits correspond to observed changes in species interaction strengths in the field and hypothesized physiological responses of coralline algae to acidification. This work demonstrates community-level responses to acidification in a natural system.

Laura Merwin, Ecology and Evolution: Natural variation in hypocotyl length in Swedish *Arabidopsis thaliana* associated with SPA2

Arabidopsis thaliana populations found on beaches in southern Sweden exhibit a number of genetically based phenotypes that distinguish them from inland conspecifics. These phenotypes include altered phenology, short stature, high trichome number, large seeds, and long hypocotyls (embryonic stems). Long hypocotyls are thought to be associated with burial of seeds and seedlings in coastal plant populations. I used genome wide association mapping in a panel of 300 Swedish *A. thaliana* accessions from both coastal and inland sites to look for loci associated with natural variation in hypocotyl length. I found a peak in chromosome 4 located over a gene that acts as a suppressor of phytochrome A (SPA2). SPA2 is part of a gene family regulating photomorphogenesis in seedlings, and is thought to primarily regulate growth in darkness, potentially offering support for the hypothesis that seed burial may be a selection pressure influencing this phenotype.

Christopher Meyer, Ecology and Evolution: Pleiotropic jasmonate-responsive genes regulate the expression of herbivore defenses in natural plant populations

Plants in the wild must protect themselves from a myriad of herbivores and microbial pathogens with a correspondingly diverse system of defenses. While much is known about the genetic architecture of many individual defense traits, how these defenses vary and correlate in natural populations is not well understood. In order to begin to address plant defense as a system, two mechanistically-distinct defense phenotypes involved in herbivore resistance were measured simultaneously in a genome-wide association mapping panel of *Arabidopsis thaliana* accessions with a continental-scale distribution. The results indicate that natural variation in trichome density and glucosinolate content is controlled by a few independent loci with major effects and several pleiotropic jasmonate/ethylene-responsive genes. Furthermore, these loci and the phenotypes themselves are correlated and exhibit steep allelic clines that track climatic variables at the continental-scale. These results have implications for fine-tuning crop defenses for different habitats and for understanding how plant defense might evolve in the face of climate change.

Jonathan Mitchell, Committee on Evolutionary Biology: Testing food web models with fossil ecosystems

Perhaps the primary academic goal of conservation biology is to construct a framework for predicting extinction probabilities for various species, to help inform management policy. Food web models have been increasingly used to assess the impact of selective extinction events, but as conservation biologists are unwilling to allow species extinction for model testing purposes, their

accuracy is unknown. To circumvent this, I have applied a basic model of cascading extinctions to tens of thousands of stochastically reconstructed fossil food webs in an attempt to quantify the model's accuracy. Preliminary results show a median 79% agreement between predicted and observed extinctions of vertebrates in fossil ecosystems (range across stochastic webs: 62-96%). By compiling an extensive database on predator-prey interactions in North American vertebrates and using them to better constrain stochastic food web generation, I intend to improve overall accuracy.

Orissa Moulton, Ecology and Evolution: Interactions between intertidal macroalgae and ammonium-oxidizing microbes in the presence of ammonium, a shared resource

Marine macroalgae are often nitrogen-limited, and as a consequence exhibit increased growth rates following nitrogen enhancement by adjacent animals; additionally, an abundant nitrogen-based marine microbial assemblage is associated with nitrogen-excreting animals. North America's Pacific Northwest intertidal and shallow subtidal zones with high animal biomass show increased regenerated nitrogen, ammonium (versus upwelled nitrate). If animals play a quantitative role as nitrogen recyclers in shallow marine systems, then algal and microbial communities dependent upon ammonium excretion are intimately linked to animal community abundance. Microbial nitrification could pose a competitive force on algae via removal of ammonium from the water column. By utilizing ammonium, nitrifying microbes could facilitate algal productivity via retention of nitrogen onshore as nitrate and nitrite in high-energy areas where advection is expected. We query the range of possible interactions between microbial activities on intertidal algae in elevated and ambient levels of ammonium, a shared resource, in laboratory mesocosm experiments, field experiments, and field surveys. Results from 2011 and 2012 indicate that microbial nitrification is increased in high ammonium conditions, microbial communities differ with ammonium availability, and that microbial processes alter water chemistry and thus nitrogen availability to algae. Primary productivity (total *chl*) is highest in high nitrogen conditions, and there is some evidence for positive effect of microbes on productivity in high ammonium. This work reveals linkages between algal growth and microbial activity that could play a key role in broader patterns of coastal productivity.

Matthew Nelsen, Committee on Evolutionary Biology: Elucidating the evolutionary origins and diversity of lichen symbionts

Symbiotic associations are widespread in fungi and algae, yet our understanding of their diversity and evolution remains obscured. Here I clarify the higher-level phylogenetic position of several clades of lichen-forming fungi and algae, and discuss these findings in the context of the evolution of symbiotic associations. Transitions to the lichen-forming state are suggested to be more common than once believed, and lineages previously overlooked are found to play important roles in the evolution of the lichen symbiosis. Finally, a synthesis of available sequence data suggests the diversity of lichen-associated algae is far greater than previously supposed.

Joyce Pieretti, Organismal Biology and Anatomy: Fin Morphogenesis & *Sonic Hedgehog* (*Shh*) Regulation

The vertebrate body plan is the product of a complex array of interactive gene regulatory networks that exhibit both robustness and plasticity. Genes involved in these networks are often regulated by modular transcriptional elements leading to localized patterns of gene expression. This genetic organization allows for the operation of evolutionary processes including heterochrony, co-option, duplication and functional diversification. As part of my dissertation work, I am studying the evolution of a regulatory network incorporating the limb-specific enhancer of *Sonic Hedgehog* (*Shh*) and how these aforementioned evolutionary processes influenced the evolution of a major morphological structure—fins. In developing limbs and fins, *Shh* originates from the zone of polarizing activity, located at the posterior margin of the limb/fin mesenchyme and this domain is responsible for demarcating the anteroposterior (AP) axis of the vertebrate appendage. Here, I will

present some preliminary data testing whether the limb-specific enhancer of *Shh* is unique to paired appendages or if it is also responsible for *Shh* regulation in median fins by way of *Danio rerio* (zebrafish) transgenesis. I will also present some results from *Leucoraja erinacea* (skate) in situ hybridizations to determine the expression patterns of *Shh* and several transcriptional factors in order to draw associations between *Shh* activation and the unique fin morphology of the skate. The goals of this research are to shed light on the origin of a key regulatory element that established AP polarity in limbs and fins as well as assessing comparative differences of spatial and temporal patterns of gene expression and how they may have shaped the skate fin.

Benjamin Rubin, Committee on Evolutionary Biology: The genome of the arboreal ant *Pseudomyrmex gracilis*

The obligate mutualism between ants in the New World genus *Pseudomyrmex* and acacia trees was first characterized nearly half a century ago and is the best known of any ant-plant relationship. In this particular mutualism, ants nest in and feed on the hollow thorns, protein rich Beltian bodies, and extra-floral nectar provided by the acacia. In exchange for these resources, resident ants aggressively protect their hosts by attacking herbivores, trimming encroaching plants, and removing pathogenic fungi. This ant defense is incredibly effective and their absence inevitably leads to plant death. Nearly identical mutualistic behavior has evolved convergently at least two other times within the genus *Pseudomyrmex*. The draft genome sequence of *Pseudomyrmex gracilis* presented here is highly repetitive, but the assembled sequence does, nevertheless, include almost the entire complement of genes present in this species. Although *P. gracilis* is not itself a mutualist, the genome and gene annotations of this species will be used as a reference to examine genomes of representatives from each mutualistic clade to determine the genomic features associated with mutualistic behaviors.

Christopher Schell, Committee on Evolutionary Biology: Parents, Pups, and Personality: examining the influence of parental effects in coyotes

Parental traits such as the prenatal environment, milk yield, and parenting style can play a significant role in shaping offspring traits independent of inherited genes. Offspring fitness is therefore strongly linked to these non-genetic influences from parents. In addition, parental response to ecological stressors during pregnancy may produce changes to parental traits that have direct effects on offspring development. These parental effects are theorized to shape the evolutionary process of a population. Coyotes (*Canis latrans*) provide an intriguing model for parental effects research, given the species' ability to persist long-term in non-native habitats. Flexibility in landscape use, diet, and behavior are often credited for coyote success in urbanized areas. The proximate mechanisms that influence that flexibility, however, are not known. Coyote parents have extended interactions with offspring into adulthood that influence survival. As a result, extended parental care may likely impact behavioral flexibility in offspring. Working at the National Wildlife Research Center (NWRC) in Millville, UT, I investigate parental trait influence on pups through an integrative analysis of temperament and hormonal traits for several captive coyote families. Preliminary offspring results suggest repeated stimulation to mothers during pregnancy has a noticeable influence on pup boldness. In addition, differential parental effects between mothers and fathers may explain variance within litters. Interestingly, offspring data from the 2011 field season demonstrate some influences of paternal behavior on pups not modulated by responses of the mother. This system, therefore, may lend itself to intriguing results that can be used to determine the differential effect of paternal and maternal effects on offspring.

Timothy Sosa, Committee on Evolutionary Biology: North America's tiny ersatz piranhas: biogeography and morphological evolution

The rise of the Isthmus of Panama during the Pliocene mixed the biotas of North and South America. The evolutionary dynamics of terrestrial and aquatic realms differed in both direction and

volume. I am gathering molecular and morphological clues to describe the invasion of North America by the Characiformes, a diverse clade of freshwater fishes with Gondwanan origins. Here I present preliminary results, including evidence that most recognized species are nonmonophyletic, and that some clades may have undergone morphological diversification as they colonized a new continent.

Courtney Stepien, Committee on Evolutionary Biology: The roles of evolutionary history and ecological interactions in the maintenance of a high-diversity algal assemblage

Northeast Pacific intertidal macroalgal assemblages exhibit high trait diversity, high phylogenetic diversity and undergo varying levels of disturbance from biotic and abiotic processes at a small spatial scale, making them an ideal system to evaluate community phylogenetic and functional diversity responses to disturbance. Here, I explore the establishment of distinct successional macroalgal assemblages under varying disturbance regimes to determine how these metrics change during community recovery.

Tom Stewart, Organismal Biology and Anatomy: On the origin and evolution of adipose fins

Adipose fins are appendages found between the dorsal and caudal fins of some teleost fishes. Their evolutionary history is poorly understood, and they are generally regarded as non-functional structures. For example, the literature still regards them as ‘vestigial’, and adipose fins are clipped off by the millions by fishery agencies as a means of tracking salmon. I show that adipose fins have independently evolved three times. Thus, as convergent de-novo appendages, I argue for their functionality and explore the diversity of adipose fin anatomies that have evolved within these two groups. Comparisons are made of their variation in shape and composition. Additionally, I identify muscles that insert upon the adipose fins of several families of catfishes (Siluriformes), which suggests the repeated innovation of musculoskeletal linkage systems among adipose fins. Finally, I explore hypotheses of their developmental origin. This study highlights adipose fins as an emerging model by which to study the evolution of anatomy and function in primitive vertebrate appendages.

Si Tang, Ecology and Evolution: Correlation between interaction strengths drives stability in large ecological networks

Feeding interactions between species are described by food webs, which show markedly non-random structure. Ecologists maintain that this non-random structure is key for community stability, as large random ecological networks would invariably be unstable and thus should not be observed empirically. In this talk, I will present that a largely overlooked feature, the correlation between the effects of consumers on resources and those of resources on consumers, substantially accounts for the stability of natural communities. Remarkably, random food webs built by preserving just the distribution of interaction strengths are as stable as their empirical counterpart. We derive general analytical stability criteria for food webs to show how the distribution of interaction strengths characterizes stability of whole ecological communities.

Nathan Upham, Committee on Evolutionary Biology: Old rats from the Neotropics: using ancient DNA and fossils to study the evolutionary diversification of a major rodent lineage

The Neotropical rodent superfamily Octodontoidea is an informative test case for studying evolutionary patterns and rates because it encompasses both extensive living biodiversity (38 genera, 193 species) and fossil records from numerous time periods over c. 25 million years. Rodents in Octodontoidea occupy arboreal, fossorial, and semi-aquatic niches and are distributed across South America, Central America, and the Antillean Islands. To reconstruct diversification dynamics and character evolution across this lineage, I examined DNA sequence variation in conjunction with fossil ages and species traits. Analysis of five genes (cyt-b, 12S rRNA, GHR, vWF, and RAG1) from 124 octodontoid species reveals that Abrocomidae is consistently recovered as the basal element in

the superfamily radiation. Thirteen genera sequenced here for the first time, several from the dried tissue of museum skins (e.g., the echimyid *Olallamys*, and the capromyid *Geocapromys*), provide phylogenetic support for several inter-generic groupings and suggest a repeated biogeographic polarity from Andean to Amazonian habitats.

Traci Viinanen, Committee on Evolutionary Biology: Toward Genomic Selection in Intermediate Wheatgrass (*Thinopyrum intermedium*): Using Genotyping-by-Sequencing for simultaneous SNP discovery, genetic map construction, and trait mapping

Genotyping-by-sequencing (GBS) combines molecular marker discovery and genotyping and has been successfully utilized in species with large, complex genomes, such as barley and wheat. Intermediate wheatgrass (*Thinopyrum intermedium*) is a perennial species that shows great promise as a dual grain and biofuel crop and is an important source of disease resistance genes for wheat. Intermediate wheatgrass, however, is an allohexaploid with an estimated 14 GB genome, no reference, and minimal marker development. The combination of a large and understudied genome makes genetic studies and genomic assisted breeding for intermediate wheatgrass intractable. To address these constraints, the objectives of this project are to discover SNPs, generate a genetic map, and map important agronomic traits. From several full-sib families and breeding populations, 380 individuals were genotyped with GBS. Additionally, one individual with free-threshing, large seed was selfed and produced 180 progeny; this family was also genotyped with GBS. Thousands of high-quality SNPs were discovered and used to confirm known relationships and reveal new pedigree information. Preliminary analysis suggests that GBS can be utilized in *Thinopyrum intermedium* for de novo genotyping to develop high-density genetic maps and genomic selection models for crop improvement.

Benjamin Winger, Committee on Evolutionary Biology: A genomic approach to understanding allopatric speciation in tropical montane birds

The differentiation of populations in allopatry is widely recognized as the most common pathway to speciation and a driving force in the generation of biodiversity. However, there have been few empirical studies on the factors that control genetic or phenotypic differentiation in allopatry. My research asks the question: why do some species show phenotypic differentiation across a single barrier to dispersal, whereas other species do not? I address this question by integrating genomic methods with a natural experiment comprised of replicates of Andean cloud forest bird species that show variable levels of phenotypic differentiation across the Marañón River valley in northern Peru. I examine the relationship between genetic and phenotypic differentiation in this system, and test whether the phenotypic patterns observed are driven by time spent in allopatric isolation or rates of gene flow (secondary admixture) experienced between populations.