

## TALKS

### SESSION 1: GENETIC UNDERPINNINGS OF EVOLUTION

#### **Experimental evidence for variation in mutation rate due to condition-dependent DNA repair**

Nathaniel Sharp\*, Aneil F. Agrawal

##### Abstract:

The rate at which new mutations arise is typically assumed to be constant among individuals within a population. However, individuals in poor condition may be less able to allocate resources to genome maintenance, leading to an elevated germline mutation rate. I tested this idea by conducting a mutation accumulation experiment in 11 *Drosophila melanogaster* genotypes, which shared an initially-identical “focal” copy of the second chromosome, but varied in the genetic quality of the third chromosome, due to the presence of deleterious “treatment” alleles. After many generations of mutation accumulation I measured the viability of focal chromosomes on a standard genetic background. Focal chromosomes that accumulated new mutations in the presence of treatment alleles declined in fitness much more rapidly. Furthermore, the rate of fitness decline was strongly correlated with the body mass of each genotype, indicating that the effect of the treatment alleles was mediated by condition. I obtained genome sequences from these lines and identified >1000 spontaneous mutations. The rates of point mutation and transposon insertion did not vary among genotypes, but I observed more indel mutations in low-quality genotypes and more gene conversion events (using the homologous chromosome as a template) in high-quality genotypes. These are the expected outcomes of low- and high-fidelity DNA double-strand break repair, respectively. Across genotypes, the rate of indels relative to gene conversion events was correlated with body mass, and with the rate of fitness decline. This is strong evidence that low-condition individuals employed a fast, low-fidelity DNA repair pathway, leading to an increased rate of deleterious indel mutations. This pattern is expected to increase the risk of rapid mutational meltdown in asexual populations, but could also accelerate adaptation to new environments. My findings may also be relevant to human health, given the role played by mutations in cancer and other genetic disorders.

#### **Genetic basis of an evolved acute stress response in the nematode *Caenorhabditis remanei***

Christine H. O'Connor\*, Kristin L. Sikkink, Janna Fierst, John Willis, Patrick C. Phillips

##### Abstract:

Stress response is a functionally important trait whose genetic basis is thought to be conserved throughout animals. Single gene knockout studies and gene expression

analysis of the classic model nematode *Caenorhabditis elegans* have identified gene pathways thought to be important the response to heat, oxidative and other abiotic stresses, but the genetic basis of heat stress and oxidative stress response has yet to be examined within an experimental evolution framework. We are investigating the genetic basis of acute heat stress and acute oxidative stress response in a set of experimentally evolved populations of the polymorphic nematode *C. remanei*. Both heat and oxidative stress are thought to cause an accumulation of misfolded proteins and activation of the insulin-like signaling stress response pathway. However, phenotypic data from experimentally evolved populations shows that adaptation to heat stress does not have a pleiotropic effect on oxidative stress resistance and vice-versa. We use whole genome sequencing and classic population genetics statistics to locate signatures of selection in the genome, comparing the ancestral population with the evolved and lab adapted populations to test whether the lack of phenotypic pleiotropy to stress response is reflected at a the genotypic level. This extensive set of genomic data, coupled with a fully annotated reference genome, helps to specify the size, location and number of regions under selection, allowing us to identify genomic patterns of selection for a multifactorial trait, and information about the genetic basis of heat stress and oxidative stress response. In addition, analysis of transcriptome data from the same set of populations allows us to correlate regions of putative selection with gene expression data, and identify genes whose expression changes are affected by cis or trans-factor mutations.

### **The relationship between plasticity of robustness**

Remi Matthey-Doret\*, Jeremy A. Draghi, Michael C. Whitlock

#### **Abstract:**

Several authors have argued that plastic organisms are developmentally instable. This lack of robustness is seen as a cost of plasticity. While it may seem intuitive that an organism cannot be both plastic and robust, this relationship is currently nothing more than guesswork. We developed a numerical model that brings together gene network dynamics and population genetics. This model allows to simulate the developmental process of each individual within an evolving population and to study the evolution of plasticity, developmental robustness and mutational robustness. We show that plastic organisms have both a low developmental robustness and a low mutational robustness. We show also that the magnitude of the loss of robustness caused by plasticity depends on the developmental pathway by which plasticity is implemented by the organism. Typically, we found that the presence of performance feedback allows an organism to be plastic while retaining a relatively high robustness. We also show that there is an intrinsic relationship between developmental robustness and mutational robustness answering a long-standing question in the literature on the evolution of robustness.

## **Plasmid persistence in *Acinetobacter baumannii* in biofilms and liquid cultures**

Genevieve Metzger\*, Ben Ridenhour, Thibault Stalder, Matthew Settles, Jack Millstein, Karol Gliniewicz, Michael France, Larry Forney, Eva Top

### **Abstract:**

The Center for Disease Control and Prevention has declared antibiotic resistance to be a top health threat. One of the ways in which bacteria gain antibiotic resistance is through plasmids. Plasmids are circular, extrachromosomal pieces of DNA that often encode genes conferring antibiotic or heavy metal resistance to their hosts. There are different mechanisms by which plasmids can persist in their host. We hypothesized that in the presence of selection, plasmid persistence is higher in biofilms than in liquid cultures. For this project, we used the gram negative, opportunistic pathogen *Acinetobacter baumannii* because it is important in nosocomial and wound infections because it rapidly acquires antibiotic resistance. The Inc-P plasmid pB10 does not persist in this host. To test our hypothesis, we cultured *A. baumannii* with pB10 with antibiotic selection in liquid cultures and biofilms grown in flow cells. To assess the evolution of plasmid persistence, we conducted plasmid persistence assays. Our results indicated some biofilm clones were substantially poorer persisters than the ancestor, while others showed better persistence. All liquid clones exhibited better plasmid persistence than the ancestor. In addition, we also discovered the presence of a truncated plasmid that exhibited better plasmid persistence in the biofilm clones. Our results have led us to conclude that there are multiple strategies of plasmid persistence in biofilms, whether through retention of the full-length plasmid or through the plasmid truncation. There seems to be a single strategy of persistence in liquid cultures through the plasmid truncation. By determining the actual mechanisms by which plasmid persistence evolves in biofilm and liquid cultures, we may be able to better understand the spread of antibiotic resistance.

## **Genetic interactions between beneficial mutations in *Saccharomyces cerevisiae***

Jasmine Ono\*, Aleeza C. Gerstein, Sarah P. Otto

### **Abstract:**

Independently evolving populations may adapt to similar selection pressures via different genetic changes. The interactions between such changes can then inform us about how adaptation may proceed and allow us to determine whether gene flow would be facilitated or hampered following secondary contact. We used *Saccharomyces cerevisiae* to measure the genetic interactions between independently evolved first-step mutations to the fungicide nystatin. We found that genetic interactions are prevalent, even among the first adaptive mutations. In some of the cases, one mutation masks the other, often the more beneficial mutation masking the less beneficial one. In other cases, often involving mutations with a large effect on fitness, we found evidence of incompatibility between adaptive solutions. These epistatic relationships depended upon

the environment in which they were measured. The prevalence of sign epistasis is surprising given the small number of mutations combined and the relative simplicity of the adaptive environment.

## SESSION 2: EVOLUTION AND MATING SYSTEMS

### **Plant dispersal in fragmented landscapes: from pollen flow in a tropical tree to seed dispersal in Pacific Northwest prairies**

Pamela G. Thompson\*

#### Abstract:

Forest fragmentation is considered a pervasive threat to the maintenance of plant-pollinator interactions in tropical forests because of its potential to disrupt the foraging of pollinators, and the subsequent impact on their pollen delivery. Here we examine pollinator abundance and gene flow in the bat-pollinated tree, *Crescentia alata*, located in continuous forest (CF) and fragmented forest (FF) sites in seasonally dry tropical forest near Chamela, Mexico. We assessed nectar bat abundance next to flowering *C. alata* trees in CF and FF sites, as well as looked at fruit set in these focal trees. We also sampled adult trees and genotyped 273 seedlings from 17 maternal trees in CF, and 249 seedlings from 17 maternal trees in FF, using 7 microsatellite markers. Landscape type was not a significant factor in nectar bat abundance, only floral display. Fruit set was higher in fragmented forest sites, and lower in trees with higher numbers of *Glossophaga soricina* bats. We found unexpectedly high genetic structure of the pollen pools, and higher structure from CF maternal trees ( $\Phi_{ST} \text{ cont} = 0.164$  vs.  $\Phi_{ST} \text{ frag} = 0.140$ ) suggesting more restricted pollen movement in continuous forest landscapes. However, we also found high connectivity among all trees and sites, and the diversity in pollen gametes was similar among seedlings from continuous and fragmented forest sites. We conclude that forest fragmentation does not negatively impact bat pollinators or pollen delivery in this study system, possibly due to the massive synchronicity of the *C. alata* floral display, which attracts pollinators despite the intervening landscape. We conclude the talk with a discussion of ongoing projects in the Cruzan lab which use similar methodologies to look at seed dispersal among fragmented Pacific Northwest prairie populations, using whole chloroplast genome sequencing and landscape genetics analyses.

### **Male fruit flies use redundant female cues to make rational mate choices**

Devin Arbuthnott\*, Daniel Promislow

#### Abstract:

According to rational choice theory, beneficial preferences should lead individuals to sort available options into linear hierarchies, though the extent to which non-human animals behave rationally is unclear. In an evolutionary sense, no choice has a greater impact for an individual than the choice of whom to mate, making patterns of decision-making in mate choice especially important to understand. We demonstrate that male *Drosophila melanogaster* are able to sort a set of diverse isogenic female lines linearly during mate choice, unambiguously displaying the hallmark of rational behavior, transitivity. By quantifying the number of offspring produced by each tested female genotype, we show that these rational choices are associated with direct benefits, enabling males to maximize offspring production. Furthermore, we demonstrate that female signals act redundantly to signal quality, as males are capable of making rational mate choices when visual or chemical sensory modalities are impaired, but not when both are impaired, which allows males to make advantageous mate choices even with imperfect information. Transitive mate choice among repeatable genotypes reveals that the quality of potential mates varies continuously, and that individuals can detect and evaluate such variation, which has important implications for the evolution of sexual traits, the evaluation of such traits, and the maintenance of genetic variation.

### **Plant mating system influences island biogeography and range size**

Dena Grossenbacher\*, Jeremiah Busch

Abstract:

Key life history traits, such as shifts from outcrossing to selfing, can have major impacts on the geographic properties of species. The reproductive assurance provided by selfing may allow selfers to successfully establish after long distance dispersal events (e.g., to oceanic islands), and to rapidly expand their ranges. Using phylogenies, geographic occurrence and mating system data, we conduct a large-scale test of this hypothesis in flowering plants. We find that 1) self-compatible species are significantly enriched on oceanic islands relative to self-incompatible species and 2) automatically selfing species tend to have larger geographic ranges than their outcrossing relatives, and that this tendency increases with time since a selfing species diverged from its outcrossing relative. Thus, traits that improve mating success may be at least as important as other traits, such as dispersal ability and environmental tolerance, in helping plants to establish new populations and increase their range size.

### **Inbreeding Depression and the Spread of Selfing in Polyploids**

Nathan Layman\*, Jeremiah Busch

Abstract:

Inbreeding Depression and the Spread of Selfing in Polyploids

Things to consider: Two of the most common transitions in angiosperm evolution are the loss of self-incompatibility (SI) and polyploidization. Additionally, these two trends often co-occur in nature. The traditional explanation for this association depends on the fertility advantages of self-fertilization. However, an alternative to this idea is that changes in the genetic cost of selfing following polyploidization drive this pattern as well. Previous theoretical work in this area has generally ignored the dynamic interaction between selfing and its cost in polyploids or has neglected to include the impact of drift. To test the validity of this alternative, an individual based model was created to circumvent these limitations. A simulated diploid population was allowed to reach equilibrium and founders were then drawn to make new sub-populations. Average inbreeding depression and the frequency of a selfing modifier were tracked across these bottleneck events both in the presence and absence of a ploidy shift. Using this approach, we identified conditions that result in the preferential spread of selfing in new polyploids. This work tests the hypothesis that declines in inbreeding depression in polyploids provide more permissive conditions for the evolution of selfing. It also provides an alternative to the commonly held belief that the association between ploidy and selfing is based on fertility. Further, outlining this process sets the groundwork for future investigation into the relationship between these two alternatives.

### SESSION 3: FROM POPULATION GENETICS TO POPULATION GENOMICS

#### **Source-sink dynamics in naturally re-established Pacific Northwest wolves**

Sarah Hendricks\*, Rena Schweizer, Robert Wayne, Paul Hohenlohe

##### **Abstract:**

Contrary to field observations, preliminary genetic results suggest that the naturally reintroduced wolves of the Pacific Northwest (PNW), specifically Washington (WA) and Oregon (OR), have mixed maternal ancestry from the coastal British Columbia (cBC) wolf populations and from the inland wolves of Idaho (ID), Montana (MT), and Wyoming (WY). The presence of diagnostic haplotype lu68 in several WA wolves, which is only found in cBC populations, suggests that the individuals with this haplotype may be offspring of a female from cBC or migrants directly from that population. To determine the nuclear lineage of individuals from the PNW populations, DNA samples were tested with a panel of 24 microsatellite markers that were applied to the characterization of gray wolf samples from the ID, MT, and WY. Using this genetic panel proved to be an insufficient method for determining source populations of the PNW wolves as STRUCTURE was unable to distinguish the ID and WY populations from the cBC population. We plan to test the hypothesis that PNW wolves have multiple genetic sources as well as assess the degree of admixture within this population by using additional genetic data generated from a custom capture array. Continued migration from cBC to the naturally reestablished PNW wolf populations will preserve unique wolf

haplotypes in efforts to increase genetic diversity and possibly decrease inbreeding given that inbreeding depression will likely occur without connectivity. These findings need to be considered when designing accurate conservation and management plans for wolves naturally re-colonizing the Pacific Northwest.

### **Clinal analysis of morphological and genetic variation in a Joshua tree hybrid zone**

Anne M. Royer\*, Sean Stankowski, Christopher I. Smith

#### **Abstract:**

Hybrid zones can offer unique insights into the complex process of speciation. Two species of Joshua tree (*Yucca brevifolia* and *Y. jaegeriana*) have reciprocally obligate relationships with their pollinators, two sister species of yucca moth (*Tegeticula synthetica* and *T. antithetica*). The plant-pollinator pairs exhibit trait matching suggestive of coevolution in key characters involved in the interaction – style length in the trees, and ovipositor length in the moths. Although the moths do not interbreed, the trees hybridize in a narrow contact zone in southern Nevada. Previous work has suggested that selection on phenotype matching may be a major driver of reproductive isolation in this system. Comparing geographic clines of traits and genetic markers can help test such hypotheses about the forces shaping gene flow in hybrid zones. For example, if pollinator-mediated selection on floral features is more important in reproductive isolation in Joshua trees than selection on other traits, we would expect steeper, narrower geographic clines for style length than other traits or random markers. We collected phenotypic data on nearly 3000 Joshua trees, with microsatellite data from 1398 of the trees. We genotyped 308 trees using RADseq, and identified 9516 SNPs in the genome. Next, we identified SNPs associated with phenotypic variation and SNPs that were strongly differentiated across species. We mapped and compared geographic clines in traits and SNPs across the hybrid zone. We found the phenotypic clines were generally wider than genetic clines, consistent with selection against hybrids broadly rather than selection focused on a particular trait. However, the most diverged traits and the majority of SNPs were best fit by clines with tails, supporting previous findings of gene flow between species in spite of likely strong selection against hybrids. Together, these analyses suggest that maintenance of species differences in Joshua trees is more complex than previously believed.

### **RAD genealogies highlight the role of ancient genomic variation during rapid adaptation in threespine stickleback**

Thomas C. Nelson\*, William A. Cresko

#### **Abstract:**

Present genetic diversity, from the level of individual genes to genomic regions and whole chromosomes, is the product of the entire evolutionary history of a species. This deep history influences future adaptive potential. Recent advances in sequencing technologies have provided unprecedented views into patterns of genetic variation and spurred the field of population genomics, which aims to understand the distribution of genetic variation within and among genomes. While short sequence reads have greatly facilitated our understanding of genomic patterns of SNP variation, inference of deeper patterns of sequence evolution has been elusive — a shortcoming especially evident in the majority of taxa for which there are limited genomic resources. To facilitate genomic studies of haplotype evolution, we have used restriction site-associated DNA sequencing (RADseq) to generate phased sequence of length and quality comparable to Sanger reads — and thus amenable to genealogical analysis — at thousands of genomic loci. By comparing two populations of threespine stickleback (*Gasterosteus aculeatus*) to a sister species, the ninespine stickleback (*Pungitius pungitius*), we show that adaptive divergence in a freshwater pond population occurred primarily from standing genetic variation that originated long before the population was founded. Furthermore, we demonstrate that a chromosomal inversion under divergent selection and linked to phenotypic variation is harboring a pair of anciently-evolved haplotypes. Combined, these data highlight the feasibility of sampling gene trees at thousands of sites across the genome and help advance the field of population genomics towards a deeper understanding of the genealogical structure of standing genetic variation and its importance to adaptation in the wild.

## **Hox Cluster Variation and Axial Elongation of the Gulf Pipefish**

Allison Fuiten\*, Susan Bassham, Emily Beck, Julian Catchen, Clayton Small, Adam Jones, William Cresko

### **Abstract:**

The remarkable level of morphological diversity in Syngnathidae (pipefish, pipehorses, seahorses, and seadragons) makes this clade of fish an excellent resource to explore developmental genetic processes underlying extreme morphological diversification. Syngnathid fish have highly derived heads and jaws, and exhibit true male pregnancy. The elongated body axis in particular is a striking novelty, particularly in the pipefish. The deeply conserved hox cluster genes are responsible for positional information in many early developmental processes of all vertebrates, including specification of the anterior-posterior body axis in metazoans. Despite the significant amount of hox gene conservation throughout the animal kingdom in terms of DNA sequence, clustering in the genome, and patterns of expression, changes in these genes may underlie a significant amount of animal body plan diversity. We hypothesize that changes in hox genes content, regulation or sequence in the syngnathid lineage may have contributed to the evolution of their elongated body axis. To test this hypothesis we sequenced, annotated and confirmed the orthology of 45 hox genes in the Gulf pipefish genome – the first syngnathid reference genome. We searched for cis-regulatory elements and miRNAs co-localized near hox genes, and we tested for signatures of positive selection among the hox genes. Our results indicate that Gulf pipefish have the typical number of hox



genes and hox intergenic noncoding elements for teleost fish, with a few key losses potentially related to axial elongation. HoxA7a, which has been hypothesized to be associated with absence of ribs when lost, appears to have deteriorated independently in the tetraodontid pufferfish lineage and the pipefish lineage. Surprisingly, we found that a large number of the hox genes appears to be under positive selection. We conclude that a subset of pipefish hox genes may be involved with the body axis diversification through differential regulation and modification to the coding regions.

### **Rapid evolutionary response to a transmissible cancer**

Brendan Epstein\*, Rodrigo Hamede, Sarah Hendricks, Menna Jones, Hamish McCallum, Elizabeth P. Murchison, Barbara Schönfeld, Cody Wiench, Paul Hohenlohe, Andrew Storfer

#### **Abstract:**

Although cancer rarely acts as an infectious disease, in Tasmanian devils (*Sarcophilus harrisii*) a recently emerged transmissible cancer is nearly 100% fatal and nearly all populations are infected. Devil facial tumor disease (DFTD) has swept across nearly the entire species' range, resulting in localized declines exceeding 90% and an overall species decline of more than 80% in less than 20 years. Using RAD-seq, we found genomic evidence of a rapid evolutionary response to strong selection imposed by DFTD. Specifically, we identified two genomic regions that exhibit concordant signatures of selection across three populations and contain genes related to immune function or cancer risk in other mammals. There is evidence that DFTD spreads between hosts by suppressing or evading the immune system, and our results suggest that hosts are also evolving immune-modulated resistance that could aid in species persistence in the face of this devastating disease.

### **The genomic response to adaptation from standing genetic variation in experimental yeast populations**

Tyler D Hether\*, Amanda Stahlke, Paul Hohenlohe

#### **Abstract:**

The recent flood of population genomic data has provided exciting new insights and challenged our understanding of how evolution structures genomes. Rather than simply "population genetics with more markers", population genomics promises a transformative shift in our understanding of real-time evolution. For example, markers exhibiting elevated genetic differentiation between populations have traditionally been used to detect loci under divergent selection and genomic data reveal that regions of elevated differentiation often extend across large, physically linked regions of chromosomes. These "genomic islands of divergence" are not simply the predictable

result of divergent selection -- rather they reflect complex interactions among selection, epistasis, demography, migration, and recombination. Comparative population genomic data exhibit wide diversity in the number, size, nature, and dynamic behavior of islands, presumably reflecting differences in underlying evolutionary processes. Beyond simply detecting such regions, the volume of data produced by next-generation sequencing has the potential to provide the statistical power necessary to test specific hypotheses about how interacting evolutionary forces structure genomic variation. Herein we use experimental evolution to test the overall hypothesis that such genomic islands of divergence can manifest from divergent selection on standing genetic variation. We test this hypothesis by crossing two haploid strains of budding yeast to generate an admixed polymorphic population from their F2 offspring. We then evolved replicate populations in two different stress environments -- sodium dodecyl sulfate and sodium chloride -- for 12 days and looked for genomic regions that differentially responded to these environments. We found that genomic islands can readily evolve after an episode of introgression, without further gene flow or new mutations, which may broadly explain the prevalence of genomic islands seen in nature.

#### SESSION 4: EVOLUTION IN THE TANGLED BANK

##### **In stressful times, make new friends: Nutrient limitation drives the evolution of metabolic dependencies**

Robin Green\*, Hanbing Mi, Wenying Shou

##### **Abstract:**

Metabolic dependence (auxotrophy) is frequently observed in nature. For example, endosymbionts have lost the ability to synthesize many essential metabolites because they are provided by host cells. This relaxed selection for autonomy coupled with reduced population size allows auxotrophy to sweep via genetic drift. However, metabolic dependence is frequently observed in large populations where selection is the dominant factor shaping population structure. However, auxotrophs are frequently found in stressful, nutrient-poor environments where population growth and yield are attenuated. Given that nutrients are limited and selection should remove unfit genotypes, how can auxotrophs survive? Using experimental evolution of *S. cerevisiae*, we demonstrate that amino acid auxotrophs can rapidly emerge to high frequencies across a repertoire of nutrient-limited environments, even without an exogenous supply of the required amino acids. We demonstrate that niche construction can generate new interactions between subpopulations. Interestingly, we find that the strength of the interaction to be mediated by the degree of nutrient stress the population is under. We show that auxotrophy for a subset of amino acids can provide a strong frequency dependent advantage. Finally, we show that the benefit of auxotrophy may not be explained by energy/resource savings, but possibly through differential physiological

responses to stress. This work provides a potential explanation for the dominance of auxotrophs in nutrient-poor ecosystems.

## **Sanctions, partner recognition, and variation in mutualistic symbiosis**

Jeremy B. Yoder\*

### **Abstract:**

Most mechanisms proposed to protect mutualistic species interactions against invasion by non-cooperative individuals imply that cooperative, well-matched individuals should be fixed; yet empirical studies find that genetic variation in mutualist quality is widespread. A possible explanation for this paradox is that mutualistic interactions are mediated not only by assessment of partner quality, but by recognition of partner signals that are genetically independent of quality. Here, I build and evaluate a model of host-symbiont coevolution in which hosts recognize compatible symbionts via alleles at one locus, and sanction uncooperative symbionts if they carry the correct allele at a second. Symbionts' expression of host recognition factors and cooperation in mutualism are similarly determined by separate loci. In contrast to simpler models that fail to maintain either variation in symbiosis outcomes or long-term persistence of cooperative symbionts, this model can maintain variation in both species while cooperation remains common. Individual-based simulations conducted over a range of reasonable parameter values and starting conditions show that the dual-system model is as likely to maintain mutualism as simpler models, more likely to maintain variation in host loci, and able to promote greater among-site variation in symbiont quality. The dual genetic systems of sanctions and host-symbiont recognition also converge toward conditions similar to one recently-developed model of symbiosis, in which hosts offering the right incentives to potential symbionts can initiate symbiosis without prior screening for partner quality.

## **Even Evolution Gets the Blues**

Brian D. Connelly\*, Sarah P. Hammarlund, Katherine J. Dickinson, and Benjamin Kerr

### **Abstract:**

By benefitting others at a cost to themselves, cooperators are continually threatened by cheaters—individuals that avail themselves of the cooperative benefit without contributing. Evolutionary biologists have long been challenged to understand explain the many instances of cooperation that nevertheless exist throughout the tree of life. We have recently demonstrated how the presence of environmental stress can allow cooperation to flourish. When adaptations to stress compensate for the costs of cooperation, cooperators can rise to dominance through hitchhiking. In spatially-structured environments, populations of cooperators commonly reach higher densities and are therefore more likely to gain these adaptations via mutation. However, this ride

can only continue as long as there are opportunities for adaptation. We show that environmental change, brought about either exogenously or endogenously through niche construction, can allow cooperation to be maintained indefinitely and even invade.

### **Cooperation between distinct viral variants promotes growth of H3N2 influenza in cell culture**

Katherine S. Xue\*, Kathryn A. Hooper, Anja R. Ollodart, Adam Dingens, Jesse D. Bloom

#### **Abstract:**

RNA viruses rapidly diversify into quasispecies of related genotypes. This genetic diversity has long been known to facilitate adaptation, but recent studies have suggested that cooperation between variants might also increase population fitness. Here, we demonstrate strong cooperation between two H3N2 influenza variants that differ by a single mutation at residue 151 in neuraminidase, which normally mediates viral exit from host cells. Residue 151 is often annotated as an ambiguous amino acid in sequenced isolates, indicating mixed viral populations. We show that mixed populations grow better than either variant alone in cell culture. Pure populations of either variant generate the other through mutation and then stably maintain a mix of the two genotypes. We suggest that cooperation arises because mixed populations combine one variant's proficiency at cell entry with the other's proficiency at cell exit. Our work demonstrates a specific cooperative interaction between defined variants in a viral quasispecies.

### **Disentangling Darwin's Tangled Bank with Computational and Microbial Evolution Experiments**

Luis Zaman\*, Ben Kerr

#### **Abstract:**

Darwinian evolution is often thought of as a population adapting towards some optimal "fittest" state. While this idealized concept holds true in many simulations and mathematical models, living systems are embedded within complex ecological networks where adaptations in one species can have resounding effects on what is adaptive to the rest. In other words, each organism within a community makes up parts of the environment for all of the others. At the very end of *The Origin of Species*, Charles Darwin highlighted this mutual dependence by inviting his reader to imagine a "tangled bank," chocked full of interacting plants and animals. How then does evolution proceed in such a tangled bank? In the first part of my talk I will discuss how host-parasite coevolution in populations of self-replicating computer programs shapes what is adaptive for the hosts and ultimately drives the evolution of biological complexity. Biotic factors like host-parasite interactions are also thought to favor higher rates of diversification compared to abiotic factors like climate. However, testing this hypothesis has remained

elusive without careful control over the strength of selective pressures. In the second part of my talk, I will turn to microbial populations and show how new technologies (in this case, continuous culture devices similar to turbidostats) are allowing us to decisively address this central evolutionary question.

### **The role of ploidy in host resistance**

Christina Jenkins\*, Scott Nuismer and Mark Dybdahl

#### **Abstract:**

Polyploidy is common across a wide variety of taxa, which is striking given the many barriers to polyploid establishment. A number of hypotheses compete to explain its prevalence but one intriguing possibility is that an increase in ploidy results in increased resistance to parasitic infection. However, when this hypothesis has been tested in plant populations, the results have been mixed. Sometimes polyploid plants are more resistant, sometimes polyploids are less resistant, and sometimes an increase in ploidy results in no difference in resistance. While the role of polyploidy in parasite resistance has been well tested in plants, it remains largely unaddressed in animal polyploids. We tested whether an increase in ploidy is associated with increased resistance using the freshwater snail system *Potamopyrgus antipodarum* and its trematode parasite *Microphallus* sp. Using experimental inoculations, we found that ploidy had no overall effect on infection rates, indicating that polyploids are not consistently more or less resistant to parasites. Instead, our results demonstrated a significant interaction between parasite source population and snail ploidy suggesting that higher ploidy increases snail resistance to parasites from some lakes but decreases snail resistance to parasites from other lakes.

### **When predators help prey persist: the evolutionary hydra effect**

Matthew Osmond\*, Christopher Klausmeier

#### **Abstract:**

To persist in a changing world, populations must adapt. The ability to adapt is influenced by interactions with other species. One ubiquitous interaction that can impose strong demographic and selective effects is predation. Recent theory suggests that the selective pressures arising from predation may help prey adapt to changing environments, but how this influences persistence remains unclear. In particular, it has not been shown, empirically or theoretically, if predators can cause prey to persist where they would go extinct without predators. Here we examine how predation affects the ability of a prey to adapt and persist in an environment undergoing gradual, directional change. To do so we extend a single-species quantitative-genetics framework to predict population densities and mean trait values, as well as critical rates of environmental

change beyond which a population is certain to go extinct. Assuming consumption of the prey by predators decreases prey density, predators can only help prey persist if they increase prey adaptedness, a phenomenon we call the 'evolutionary hydra effect'. With negative density-dependence we find that this requires both selection and density-dependence to act on prey birth rate. Interestingly, predators do not have to exert a selective pressure to help prey adapt and persist as long as they shorten the time between selective events. We then derive the necessary and sufficient conditions for increasing consumption of prey to help prey persist and present an example with a generalist predator where this is satisfied. Specialist predators, however, cannot affect prey persistence because they always precede the prey in going extinct, but we show with an example how coevolution between a specialist predator and their prey can cause prey to evolve in advance of the changing environment.

## SESSION 5: FACULTY MINI-SYMPOSIUM

### **Reconstructing the ancestral role of a key transcription factor involved in flowering**

Verónica S. Di Stilio\*, Kristen Hewett Hazelton and Melissa J. Wong

#### **Abstract:**

Flowers are the key innovation that propelled angiosperms into one of the most notable adaptive radiations of all times. While much is known about the developmental process for transforming leaves into floral organs in angiosperms, it is unclear how this mechanism evolved. LEAFY (LFY) encodes a transcriptional regulator that induces flower formation in the mature angiosperms sporophyte; it is also present in mosses, where it governs early cell divisions of the zygote (the unicellular sporophyte stage). Here, we examine LFY function in ferns, the sister lineage to seed plants and a class of vascular plants that lies midway in the evolutionary tree between mosses and flowering plants. The overarching biological questions we address are: What was the ancestral role of this key flowering gene prior to the evolution of seed plants? Were flowering functions co-opted from more general reproductive roles, or did they evolve *de novo*? Recent advances in stable transgenic techniques in the emerging model fern *Ceratopteris richardii* present a golden opportunity to address these questions. We first looked at gene expression ontogenetically in wildtype and found no expression in spores, low levels in reproductive gametophytes before fertilization and a peak in young sporophyte tissue, followed by a decline to a steady state as the sporophyte aged. A loss-of-function approach using RNA interference lines allowed us to identify mutant lines with highly altered phenotypes and down-regulation of the target genes. They exhibited decreased fertilization efficiency and persisting, long-lived gametophytes. Taken together, our preliminary results suggest an early role of CrLFY in initial sporophyte development, similar to moss. Therefore, it appears that this transcription factor may have maintained its broader function in early sporophyte development

throughout at least 50 million years of land plant evolution, before being recruited into flower meristem identity with the rise of the angiosperms.

## **Dissecting the causes of natural variation in protein expression dynamics**

Dan Pollard\*, Ciara Asamoto, Austin Abendroth

### **Abstract:**

Yeast cells respond to their environment by coordinating the expression of thousands of genes to produce a specific complement of millions of protein molecules. Natural genetic variation has the potential to impact protein expression dynamics by acting at different levels, including transcription, mRNA stability, translation, and protein stability. The link between genetic variation and mRNA expression divergence is well established, however, the importance of genetic variation acting on protein translation and degradation rates is poorly resolved. To distinguish genetic variation acting directly on mRNA levels from genetic variation acting directly on protein levels, and to dissect how these two types of variation affect different phases of a dynamic cellular response, we measured both mRNA and protein expression dynamics in the *Saccharomyces cerevisiae* laboratory strain S288c and the clinical strain YJM145. We focused on genes in the mating pheromone response network, which is known to harbor heritable variation in gene expression between these strains. We sampled cells from alpha factor treated cultures at time points over the course of eight hours and then measured mRNA levels using qPCR and protein levels using fluorescence microscopy. The majority of genes examined have divergence in protein expression responses that cannot be explained by their mRNA expression responses, suggesting genetic variation is acting on protein translation and/or degradation rates. Decay rate assays and modeling revealed the level of divergence in translation rates and decay rates between the strains for each gene. Allele-specific measurements revealed the level of cis-acting and trans-acting variation on protein levels. Our results suggest that genetic variation commonly acts on protein translation and degradation rates, independently of mRNA levels. We will discuss our ongoing efforts to dissect this new class of genetic variants, including whole proteome analysis, mapping causative variants, and characterizing molecular mechanisms.

## **Genome-Wide Patterns of Genetic Polymorphism and Signatures of Selection in *Plasmodium vivax***

Omar E. Cornejo\*, David Fisher, Ananias A. Escalante

### **Abstract:**

*Plasmodium vivax* is the most prevalent human malaria parasite outside of Africa. Yet, studies aimed to identify genes with signatures consistent with natural selection are rare. Here, we present a comparative analysis of the pattern of genetic variation of five

sequenced isolates of *P. vivax* and its divergence with two closely related species, *Plasmodium cynomolgi* and *Plasmodium knowlesi*, using a set of orthologous genes. In contrast to *Plasmodium falciparum*, the parasite that causes the most lethal form of human malaria, we did not find significant constraints on the evolution of synonymous sites genome wide in *P. vivax*. The comparative analysis of polymorphism and divergence across loci allowed us to identify 87 genes with patterns consistent with positive selection, including genes involved in the “exportome” of *P. vivax*, which are potentially involved in evasion of the host immune system. Nevertheless, we have found a pattern of polymorphism genome wide that is consistent with a significant amount of constraint on the replacement changes and prevalent negative selection. Our analyses also show that silent polymorphism tends to be larger toward the ends of the chromosomes, where many genes involved in antigenicity are located, suggesting that natural selection acts not only by shaping the patterns of variation within the genes but it also affects genome organization.

### **Bet hedging in yeast responses to osmotic stress**

Yoshikazu Hirate, Samuel Bottani and Suzannah Rutherford\*

#### **Abstract:**

Rapid reproduction contributes to evolutionary fitness but can be lethal under stress. Microbes are thought to limit risk in clonal populations by bet hedging; the stochastic expression of a low frequency of slow growing cells constitutively resistant to unpredictable environmental stresses including antibiotics. However fitness depends on rapid recovery and resumption of growth in potentially lethal environments whose severity and duration are also unpredictable. Here we describe trade-offs between osmotic stress-responsive signaling, survival and proliferation in 50 ecologically distinct strains of budding yeast. By contrast with prior examples, programmed bet hedging responses were heritable, specific to osmotic stress and varied continuously in our population. During rapid growth strong osmotic stress signaling promoted survival. Weak signaling predicted lower viability, intense rebound signaling, and robust recovery. Older cultures survived and adapted to unprecedented stress with fitness depending on reproducible, strain-specific proportions of cells with divergent strategies. The most ‘cautious’ cells survive extreme stress without dividing; the most ‘reckless’ cells attempt to divide too soon and fail, killing both mother and daughter. Heritable proportions of cautious and reckless cells generate a tunable, rapidly diversifying model of bet hedging that resembles natural variation and would evolve in different patterns of osmotic stress.

### **Runaway nuclear-mitochondrial coadaptation leaves behind a residue of genomic conflict**

Devin Drown\* and Michael Wade



**Abstract:**

Two alternative evolutionary paradigms are competing to explain the coordinated gene expression patterns of the mutualism between the eukaryotic nucleus and the mitochondrial genome. I use population genetic models to show that adaptation can occur by either conflict or cooperation, but evolutionary conflict occupies a narrower region on the adaptive landscape and occurs more slowly. My results suggest a fundamental difference in the evolutionary response to cooperative gene interactions versus genetic conflict. Where coadaptation is a self-accelerating runaway process, genetic conflict is a decelerating, self-limiting process. This work provides a mechanistic understanding of how the genomic architecture and underlying population structure of genome interactions influences the evolutionary dynamics of adaptation. As an example of the potential of my theory research, I applied the theory of cotransmission of genomes to understanding the distribution of genes within genomes. Mitochondria, being vertically transmitted, serve as an excellent case study. I discovered that nuclear genes which interact with the mitochondrion are significantly under-represented on the X-chromosome in mammals. This study links evolutionary theory of sexual conflict and genomic conflict to explain a highly significant and broad scale genomic pattern.

**Experimental evolution of incipient cooperation provides direct support for social evolution theory**

Chichun Chen, Sam Hart, Jose Pineda, Wenying Shou\*

**Abstract:**

Social evolution theory predicts that when members of a cooperative community evolve in a well-mixed environment, only self-serving changes would be selected for. To test this theory, we engineered a cooperative community where two *S. cerevisiae* strains each paid a cost to overproduce a metabolite essential for its partner. When we propagated this yeast cooperative community lacking prior evolutionary history in a well-mixed environment, all tested cells had indeed evolved self-benefiting phenotypes by improving metabolite uptake. Surprisingly, some evolved cells not only improved metabolite uptake, but also released metabolites at an increased rate. This seemingly “win-win” phenotype was caused by Chromosome 14 duplication. The duplication of a metabolite permease on Chromosome 14 increased metabolite uptake and conferred cells with the selective advantage. As a byproduct of selection, a cell cycle inhibitor was also duplicated, and it increased the cell size and metabolite release rate. Because cells of a larger size required proportionally more partner-supplied metabolites for reproduction, this increased metabolite release rate appeared not to be partner-serving after all. Thus, all phenotypes we have observed so far, including those that initially appeared to be win-win, are strictly self-benefiting.

## POSTERS

### Poster 1

Dissecting the causes of natural variation in protein expression dynamics

Daniel Pollard, Ciara Asamoto, Austin Abendroth\*

#### Abstract:

Yeast cells respond to their environment by coordinating the expression of thousands of genes to produce a specific complement of millions of protein molecules. Natural genetic variation has the potential to impact protein expression dynamics by acting at different levels, including transcription, mRNA stability, translation, and protein stability. The link between genetic variation and mRNA expression divergence is well established, however, the importance of genetic variation acting on protein translation and degradation rates is poorly resolved. To distinguish genetic variation acting directly on mRNA levels from genetic variation acting directly on protein levels, and to dissect how these two types of variation affect different phases of a dynamic cellular response, we measured both mRNA and protein expression dynamics in the *Saccharomyces cerevisiae* laboratory strain S288c and the clinical strain YJM145. We focused on genes in the mating pheromone response network, which is known to harbor heritable variation in gene expression between these strains. We sampled cells from alpha factor treated cultures at time points over the course of eight hours and then measured mRNA levels using qPCR and protein levels using fluorescence microscopy. The majority of genes examined have divergence in protein expression responses that cannot be explained by their mRNA expression responses, suggesting genetic variation is acting on protein translation and/or degradation rates. Decay rate assays and modeling revealed the level of divergence in translation rates and decay rates between the strains for each gene. Allele-specific measurements revealed the level of cis-acting and trans-acting variation on protein levels. Our results suggest that genetic variation commonly acts on protein translation and degradation rates, independently of mRNA levels. We will discuss our ongoing efforts to dissect this new class of genetic variants, including whole proteome analysis, mapping causative variants, and characterizing molecular mechanisms.

### Poster 2

Linking Phenotypic and Genomic Evolution in Stickleback and the Problem of Selection-Mediated Population Structure

Kristin Alligood\*, Emily Lescak, Susan Bassham, Julian Catchen, Frank von Hippel, William Cresko

#### Abstract:

Rapid changes in head and body shape have been documented during the repeated and independent invasion of oceanic threespine stickleback into freshwater habitats in regions deglaciated approximately 13,000 years ago. However, recent research has made clear that similar phenotypic and genetic divergence can occur in decades. A remaining challenge is to link stickleback population genomic variation to causal genes that underlie shape evolution. To address this we used natural populations of stickleback that colonized freshwater ponds created by the 1964 Alaska earthquake on islands in the Gulf of Alaska and Prince William Sound. These very young populations already show phenotypic and genotypic divergence from their marine ancestors. We used a large dataset of single nucleotide polymorphisms (SNPs) generated via RAD-seq to determine genome wide patterns of linkage disequilibrium (LD) and relatedness among individuals, and to use Genome Wide Association Study (GWAS) approaches to link genotype with phenotype. We find evidence for extensive population structure, but primarily in regions that also show signatures of divergent natural selection. Additionally, many genomic regions associated with phenotypic variation are also genomic regions that covary because of LD. However, because we can account for population structure by capturing the relatedness among individuals we expect that the genomic regions identified through GWAS represent the loci that underlie rapid phenotypic evolution and are not heavily influenced by population structure. The LD patterns help to interpret our GWAS findings and suggest that rapid phenotypic evolution may be underlain by many loci across the genome, but that these loci significantly covary because of the history of selection. These young stickleback populations present a rare opportunity to link rapid phenotypic evolution and the genetic and genomic architecture that shapes it in a natural context.

### **Poster 3**

*Drosophila* speciation: All roads lead to Cid

Emily A. Beck\*, William A. Cresko

#### **Abstract:**

Chromosomes contain regions of repetitive DNA, primarily clustered in centromeres and telomeres, involved in a wide range of essential cell processes. Rapid evolution of these satellite repeats contributes to species divergence by accumulating changes, and driving divergence of interacting proteins. This has previously been demonstrated in the essential kinetochore protein Cid (Cenp-A in humans), known to physically interact with rapidly evolving centromeric satellite repeats. Cid is unique in that it localizes exclusively to the centromere during the cell cycle. Additionally, through interactions with many protein complexes, Cid aids in the assembly and function of the centromere, and regulates several stages of the cell cycle. Previously, it has been demonstrated that signatures of positive selection, indicative of rapid evolution, are present not only in Cid, but proteins encompassing the Condensin I Complex; one of many complexes physically

associated with Cid, suggesting possible cascades of positive selection radiating from centromeric satellite repeats. Here we present a comprehensive study of all Cid-associated protein complexes in *Drosophila* for evidence of positive selection. We report widespread positive selection in many interacting protein complexes involved in cell cycle regulation and progression. Interestingly, these protein complexes also include all previously identified *Drosophila* speciation genes with known protein interaction networks including Hmr, Lhr, Gfzf, and Nup98-96. These data indicate the Cid interactome is central to species divergence and *Drosophila* speciation.

#### **Poster 4**

##### **A comparison of ungulate and sciurid paleoecologies**

Eva M Biedron\*, Samantha S. B. Hopkins

##### **Abstract:**

Relationships between mammal species and their preferred habitats are often used to reconstruct past ecology in fossil ecosystems. Ungulate herbivores, whose dental morphology reflects food preferences, are the most common terrestrial mammal group used in habitat reconstruction. Small mammals sample over a narrower geographic range and may offer a more sensitive habitat proxy. Modern ground squirrels favor open environments that facilitate burrowing (although a few taxa may tolerate intermediate habitats) while tree and flying squirrels favor closed habitats. Terrestrial squirrels (like chipmunks) may occupy intermediate or closed areas. If large and small mammals are consistent in paleoecological signal, small mammals would provide alternate habitat indicators, facilitating habitat reconstruction in a greater variety of fossil ecosystems. We hypothesized that sciurid taxa with open-habitat ecologies would be found in assemblages dominated by grazing ungulates rather than browsing or mixed-feeding ungulates. Similarly, assemblages containing sciurid taxa with closed-habitat ecologies would be dominated by browsing ungulates. An occurrence-based dataset of twenty-five Oregon localities ranging in age from the middle Miocene to Recent was compiled using the MioMap database. Ecological data was gathered from the literature and the Fossilworks Paleobiology database. We analyzed this data set using chord distance analysis, a method that quantifies the differences in relative abundance between two sites. We have found that ungulate ecologies are inconsistent with sciurid ecologies in this data set. The chord distance values of sciurids form three distinct clusters, while ungulate chord distance values do not cluster. We interpret this inconsistency as an indication of differences between sciurid and ungulate as habitat indicators. The differences between these large and small herbivores in home range size may yield different habitat information in a heterogeneous landscape. If so, these results suggest sciurids and ungulates are both useful as paleoecological indicators, but that they function on different spatial scales.

## Poster 5

### Should I Lay or Should I Go? Examining Reproductive Patterning in *C. elegans* with Microfluidics

Benjamin W. Blue\*, Stephen A. Banse, Patrick C. Phillips

#### Abstract:

As a hermaphrodite, *C. elegans* can self-regulate both fertilization and egg-laying rates to correspond with food availability. In the extreme, the complete absence of food results in adult reproductive diapause, which extends reproductive span by up to 15-fold, or “bagging”, in which progeny hatch internally and subsist upon the body of the parent. While these drastic cases of starvation have been investigated previously, the effects of smaller dietary differences remain unknown. This is in part due to the experimental difficulty controlling the food density of a bacterial lawn. Additionally, our preliminary data suggests that the complex environment of an agar plate provides confounding mechanical and chemical sensory cues that disallow easy linkage of behavior to dietary input. We will present two novel microfluidic devices that eliminate these confounds while enabling tight control of food density. The first is a microfluidic arena where food preference indices are measured as relative residency time in regions of differing food availability. Using this approach, we demonstrate that *C. elegans* can perceive a range of food concentrations spanning 0 to  $1 \times 10^{10}$  cfu/ml. We additionally determine that while *C. elegans* is able to detect the presence of very small concentrations of food, they do not differentiate between variable concentrations beneath a threshold of  $1 \times 10^6$  cfu/ml. The second microfluidic device contains an array of single-worm arenas that allow recording of reproductive output in real time. Using this device, we evaluate how individuals change their egg-laying as a function of food. This allows us to investigate the patterning of reproduction as a direct response to changes in the quantity or quality of an individual's diet.

## Poster 6

### Effects of gene flow on performance at the northern range margin of *Clarkia pulchella*

Megan Bontrager\* and Amy Angert

#### Abstract:

A persistent question in the fields of biogeography and evolution is what processes limit species' adaptation to conditions beyond their geographic distribution. Both theoretical and empirical studies suggest that asymmetric gene flow between populations may disrupt local adaptation and play a role in shaping distribution boundaries. In the context of range limits, models suggest that gene flow from abundant populations near the

center of the range may prevent range-edge populations from adapting to local conditions. However, the predictions of these models are difficult to translate to organisms living on heterogeneous natural landscapes. Species abundance patterns often deviate from those underlying this hypothesis and environmental differences between populations may not correlate precisely with their geographic distance. We are in the midst of an ongoing field transplant experiment to examine the effects of gene flow from different climatic and geographic distances on individual performance at the northern range margin of *Clarkia pulchella*. Germination rates were not correlated with the environmental or geographic distance of source populations. Here, we present some very recent data on winter survival in relation to the geographic and climatic provenances of experimental populations.

### **Poster 7**

An Extendable Software Architecture for Exploring the Effects of Developmental Interactions on Evolutionary Trajectories

Elizabeth Brooks, Alison Scoville, Filip Jagodzinski

#### **Abstract:**

Quantitative genetic models commonly use the additive genetic variance-covariance matrix (G-matrix) of a set of traits to predict evolution in response to selection. However, non-linear interactions between developmental factors underlying the production of traits can result in dramatic changes to the G-matrix. Because of this, models relying on the G-matrix may not accurately predict evolutionary dynamics. To our knowledge, there are no freely available tools for predicting the effect of non-linear interactions on evolutionary dynamics. We have, therefore, developed a code base and built three models for testing hypotheses regarding the effects of specific non-linear developmental interactions on trait (co)variances and ultimate evolutionary trajectories. This software package will allow researchers to determine the extent to which the developmental architecture of traits affects the evolutionary response of a given species.

### **Poster 8**

Distinct pathways to adaptation to extremely sulfidic environments in closely related populations of fish

Anthony P. Brown\*, Lenin Arias-Rodriguez, Muh-Ching Yee, Michael Tobler, Joanna L. Kelley

#### **Abstract:**

Similar environmental conditions often lead to molecular convergence in different populations, but the factors that affect the likelihood of molecular convergence are understudied. In theory, short divergence times and strong selective pressures should each increase the chances of parallel adaptation. It follows that recently diverged populations facing the same strong selective pressure would likely follow the same evolutionary path to adaptation. Populations of freshwater fish (*Poecilia mexicana* and *P. sulphuraria*) have independently colonized several hydrogen sulfide-rich streams. Hydrogen sulfide is extremely toxic to most organisms; it inhibits cellular respiration by interfering with the respiratory complex cytochrome c oxidase. We performed RNA-sequencing on individuals from three population pairs (adjacent freshwater and sulfidic populations) to test whether the same genes were under selection across three independent transitions into hydrogen sulfide-rich springs. We performed a scan to identify highly differentiated and fixed nucleotide polymorphisms between adjacent freshwater and sulfidic populations. We then compared these variants across drainages to identify evidence of molecular convergence. We found evidence for selection on sulfide detoxification genes in all three drainages, but we only found evidence for selection on cellular respiration genes in two out of the three drainages. The two most closely related sulfidic populations appear to have taken different pathways to adaptation. Overall, the results of this study imply that adaptation to this extreme environmental condition is unpredictable, and that parallel adaptation is unlikely even in closely related populations.

## Poster 9

Investigation into the mechanisms of cooperation of H3N2 viral quasispecies

Jolie Carlisle\*, Katherine Xue, Jesse Bloom

### Abstract:

Viral adaptation is facilitated by the rapid diversification of viral quasispecies. However, recent work has revealed that cooperation between distinct viral variants can increase the fitness of viral populations. Previous work in our lab has shown that two distinct variants of H3N2 influenza grow better in mixed populations than they do alone, thereby suggesting that the variants cooperate with each other to promote viral fitness in cell culture. Epistasis between the hemagglutinin (HA) and neuraminidase (NA) proteins is responsible for promoting this cooperation: cooperation occurs in some HA backgrounds but not others. By comparing the HA sequences between cooperating and non-cooperating strains, we have identified ten nonsynonymous changes as candidates for promoting cooperation. Using site-directed mutagenesis, we are attempting to pin down the HA mutations responsible for cooperation. Once these mutations are identified, we will investigate how selection can act upon this cooperation by testing whether different backgrounds are favored under various conditions.

## Poster 10

Analysis of genome-wide variation reveals evolutionary relationships and resolves longstanding taxonomic controversy in a radiation of monkeyflowers (*Mimulus*)

Madeline Chase\* Sean Stankowski Matt Streisfeld

### Abstract:

Resolving evolutionary relationships within recent radiations is notoriously difficult because the prevalence of incomplete lineage sorting and introgressive hybridization can obscure the species branching order. Additionally, rapid phenotypic divergence, coupled with frequent convergent evolution of taxa occupying similar ecological niches, makes morphological analyses of relationships unreliable. These difficulties have created a controversy in the taxonomic history of a radiation of California monkeyflowers. The *Mimulus aurantiacus* species complex has been described as containing between 2 and 13 distinct species, with previous studies relying only on morphological characters or a handful of genes for determining relationships. Here we use genome-wide data to determine evolutionary relationships of previously described taxa using a combination of phylogenetic and population genomic analyses. We find four highly supported clades, all of which show some degree of mixed ancestry. Existing morphological data fail to group individuals by clade, indicating that convergent phenotypic evolution among the clades confounds the ability to infer evolutionary history from phenotypic variation. Most of the controversy appears to arise from one clade containing the majority of the described species. This work resolves longstanding controversies and will help to inform future studies on the origin and spread of adaptive variation within this radiation.

## Poster 11

Natural variation of longevity and the response to lifespan extending intervention in *Caenorhabditis*

Michelle Chen\*, Christine Sedore\*, Mark Lucanic, W. Todd Plummer, Esteban Chen, Jailynn Harke, Dipa Bhaumik, Brian Onken, Anna L. Coleman-Hulbert, Kathleen J. Dumas, Suzhen Guo, Erik Johnson, Anna C. Foulger, Christina Chang, Anna B. Crist, Michael P. Presley, Jian Xue, Manish Chamoli, Girish Harinath, Suzanne Angeli, Mary Anne Royal, John H. Willis, Daniel Edgar, Shobhna Patel, Elizabeth A. Chao, Shaunak Kamat, June Hope, Carolina Ibznez-Ventoso, Jason L. Kish, Max Guo, Gordon J. Lithgow, Monica Driscoll, and Patrick Phillips

### Abstract:



There is widespread concern regarding the accuracy and reproducibility of results in scientific literature. Potential barriers to reproducibility were addressed in a joint project focused on the identification of potent anti-aging interventions. Natural variation in longevity and other life history traits was assessed for 66,000 individuals from 22 genetically distinct *Caenorhabditis* nematode strains across three laboratories. The primary source of variation was within-lab repeatability, with some strains displaying two distinct modes of aging from trial-to-trial. Bioactive compounds were then screened for their ability to extend lifespan in hermaphroditic species *C. elegans*, *C. briggsae* and *C. tropicalis*, identifying potential genotype-by-environment interactions. We found that some compounds robustly extended lifespan while others generated distinct strain-specific outcomes. Understanding the sources of experimental variation is essential to identifying natural genetic variation in longevity and aging, as well as significant effects of compounds on these traits.

## Poster 12

Beneficial mutations improve fitness in a *Caenorhabditis elegans* mutation-accumulation line

Stephen F. Christy\*, Suzanne Estes

### Abstract:

Most newly arising mutations are deleterious for organismal fitness, yet can readily propagate within populations under a broad range of conditions. Evolutionary genetic processes able to counteract deleterious mutation accumulation include: a) generally beneficial mutations that improve organismal fitness irrespective of genetic background, b) compensatory mutations that specifically mitigate the effects of previously-acquired deleterious mutations through epistasis, and c) reversion mutations back to wildtype. The potential for spontaneous mutations to mitigate the effects of deleterious mutations alters our expectations for the population-level impact of deleterious mutation. However, the capacity of spontaneous mutations to restore ancestral phenotype and the molecular genetic patterns of compensation are still poorly understood in eukaryotic systems. We performed a mutation accumulation (MA) experiment—where mutations are allowed to accumulate in replicate lineages evolving in population sizes of one (i.e., extreme genetic drift)—using a mitochondrial-deficient mutant strain of *Caenorhabditis elegans* nematode, *gas-1*. This strain has lower levels of fitness compared to wildtype. Mutation accumulation is expected to result in further fitness decline due to accumulated deleterious mutations. However, the lines experienced partial phenotypic recovery back to wildtype levels. Next-generation sequencing and bioinformatic analyses revealed several candidate single nucleotide polymorphisms (SNPs) responsible for this recovery. The purpose of this study was to determine the capacity of SNPs to restore fitness in *gas-1*. We introgressed the SNPs onto wildtype and *gas-1* backgrounds, then performed life-history assays to compare the introgressed strains with wildtype and *gas-1* strains.

We discovered that the introgressed strains experience a shift to earlier reproduction compared to wildtype and gas-1 strains and conclude that the SNPs are generally beneficial for fitness. This finding indicates that beneficial mutations are able to accumulate under extremely unfavorable population genetic conditions.

### **Poster 13**

Interaction of gene flow, selection, and genomic architecture on the genetics of heat stress adaptation in *Caenorhabditis remanei*

Sally Claridge\*, Christine O'Connor, Patrick Phillips

#### **Abstract:**

The interplay of gene flow and selection is an important component of how populations diverge and speciate in natural populations. Recent work has shown that, contrary to earlier theory and expectation, two populations can still experience significant genetic and phenotypic divergence even when there is continuous gene flow between them. These dynamics have been studied in a variety of species in the wild and with models and simulations *in silico*. However, they have yet to be studied in an experimental system. We experimentally evolved an outbred population of *Caenorhabditis remanei* in a chronic heat stress environment to test the effects of gene flow on (1) the patterns of neutral divergence between two populations connected by varying levels of gene flow and (2) the genetic architecture of heat stress resistance. Organisms experience a wide range of stressful environments throughout their lifetime. Understanding the genetic architecture of stress response is important because it helps researchers evaluate how a phenotype of interest may respond to selection. Obtaining a better understanding of how the genetics of a complex trait evolve under not only environmental stress but also with gene flow could help elucidate how these gene regulation networks function as a whole and how their interactions over time affect the phenotype in question. Survival and fecundity data from control and heat stress evolved populations at each level of migration tested will be collected to estimate the extent and strength of selection in the heat stress population. Whole genome sequencing data from the ancestral and descendant populations will be compared to identify the number, location, and size of regions under selection and to test the hypothesis that gene flow affects the genetic architecture of adaption.

### **Poster 14**

Characterization of recombination patterns in an F1 hybrid stickleback

Johnathan G Crandall\*, Thomas C Nelson, William Cresko

#### Abstract:

Divergent natural selection generates and maintains biological diversity. Hybridization between divergently-adapted populations, however, has the potential to homogenize genetic variation and eliminate divergence. When hybridization is frequent, therefore, mechanisms may evolve to suppress recombination between divergent genomes. To investigate mechanisms maintaining adaptive divergence, we used the threespine stickleback (*Gasterosteus aculeatus*), a model for the study of adaptation in the wild. Freshwater and oceanic populations of stickleback remain genetically distinct across large genomic regions despite their ability to hybridize, indicating that mechanisms exist to maintain adaptive haplotypes. Previously, chromosomal inversions have been shown to promote divergence by blocking recombination. In this study, we investigate suppression of recombination using restriction site-associated DNA sequencing (RADseq) to create high-density genetic linkage maps. Maps were constructed from freshwater and oceanic lines of stickleback, and from an interpopulation F1 hybrid, to investigate the question: when freshwater and oceanic genomes are combined in a hybrid, do they recombine freely, or is recombination reduced, including in areas of known chromosomal inversion? We report large blocks of substantial recombination reduction across several chromosomes in the F1 hybrid; these blocks overlapped with regions of high genetic differentiation between freshwater and oceanic populations. Interestingly, this general pattern of recombination suppression was conserved in the freshwater and oceanic fish. The hybrid also displayed unique patterns of recombination, including complete suppression across a known chromosomal inversion on chromosome 21, while recombination events occurred in the freshwater and oceanic lines. By characterizing the recombination patterns between divergent genomes, we hope to gain insight into the mechanisms maintaining biological diversity.

#### Poster 15

The discovery and description of a phenotypic and genetic cline in threespine stickleback populations that inhabit the McKenzie River

Mark Currey\*, Susie Bassham, Julian Catchen, Eric Parker, and William Cresko

#### Abstract:

Threespine stickleback fish are widely distributed throughout Oregon's massive south to north drainage, the Willamette Basin. Freshwater ecotypes, characterized by a suite of traits including small body size, reduced bony armor and cryptic pigmentation, predominate in the basin's diverse array of aquatic habitats. Using RAD-seq, we performed population genetic analysis and an in-depth phenotypic analysis of stickleback collected along the McKenzie River. This river hosts a wide range of habitats as it flows west from high elevation in the Cascade Mountains to merge with the Willamette River on the basin floor. We report the surprising discovery of phenotypically oceanic stickleback - typified by large, silvery bodies and armor plating - high in the

McKenzie River watershed more than 300 miles from the ocean. Interestingly, these populations appear to have formed a phenotypic and genetic cline with freshwater ecotype fish residing lower in the watershed. We are using admixed populations within the cline, and populations at its extremes, to perform genome-wide association studies and cline analysis to identify genomic regions associated with phenotypic traits and habitat variables.

## **Poster 16**

Is specialization a typical outcome of 1000 generations of evolution in mutualism?

Yemesrach Demissie\*, Irina Stroynyy\*

### **Abstract:**

When isolated subpopulations adapt to the particular features of the predators, prey, or cooperative partners that are specific to their local environment, populations may become specialized to their local partner and less able to interact with other populations. To what extent might this hypothesis explain the diversification of microbial species, which cooperate or compete with each other in complex communities? For example, when an interaction is based on the cooperative exchange of hydrogen, specialization occurs. We tested whether specialization was a common outcome of evolution between the bacterium *Desulfovibrio vulgaris* and the archaeon *Methanococcus maripaludis* after they evolved together for 1000 generations. To test if *D. vulgaris* populations tended to become specialized for the *M. maripaludis* populations they evolved with (and vice versa), we revived 12 independently-evolved communities, separated the *D. vulgaris* and *M. maripaludis* populations from one another, and then paired each population back up with their sympatric partner (same community) or with 5 allopatrically-evolved partners (isolated community). We used microscopy to quantify the density of *D. vulgaris* and *M. maripaludis* to test whether the absolute fitness of either species was higher in sympatric versus allopatric pairings. We also competed allopatrically-evolved and sympatrically-evolved *D. vulgaris* against one another. We predict that some *D. vulgaris* or *M. maripaludis* populations will have higher absolute fitness on average across all 6 partners, but not specifically with sympatric partners.

## **Poster 17**

Testing the Effects of the Alaskan Microbiome on a Model Organism: *Arabidopsis thaliana*

Jackson W. Drew\* and Devin M. Drown

### **Abstract:**

Climate warming is inducing rapid large-scale changes in the boreal biome due to permafrost thaw. Soil nutrients and microbial processes could mediate the effect of permafrost thaw on plant community dynamics. Most plant species associate with soil microbes. These plant associated microbes facilitate resource uptake and may be a key indicator of climate feedback. The plant hosts are also known to influence their microbes in a variety of ways. During the crop domestication process, we often select upon the ability to provide high yield across varying environments. This also includes the hidden soil microbial environments below the surface. When comparing a domesticated line to one of wild ancestry, the domesticated plants may have lost a certain degree of host control and symbiont choice to shape their microbiomes. Wild type hosts could be more successful than their domesticated counterparts when selecting on environmentally obtained microbiomes, implying that wild lines are potentially better suited for microbiome engineering. This unexplored area of microbiome engineering research has tremendous implications on the implementation and interpretation of future experiments investigating the impact of soil microbes on plant fitness. Here, we compared measures of plant fitness among both an inbred and a natural ecotype of *Arabidopsis thaliana* inoculated with Alaskan microbial communities from a permafrost thaw gradient. We contrast the differences in the host's capacity to incorporate the soil microbes as well as how the soil community differs across the treatments. Understanding the natural diversity of soil microbes within a landscape and how they change across plant history and genetics will help us better utilize and plan for future crops. Future microbiome evolution experiments will shed light on how we can best manipulate the extremely complex relationships plants have with soil microbes.

## **Poster 18**

Is it what you say or how you say it? Looking for expression differences between two apparently identical proteins.

Allison Eggert\*, Kimmy Stanton, Arielle Cooley

### **Abstract:**

The evolution of organisms and their genomes often occurs through gene duplication. Consequently, coding-sequence divergence of duplicate genes has been a prominent study of focus in plant evolutionary genetics over the past two decades. Recently, several species of previously yellow Chilean monkeyflowers have seen the evolutionary gain of red or purple pigmentation in their floral tissue. The gene thought to be responsible in regulating their floral pigment pathway resulting in the purple coloration was gained following multiple duplication events. My research used quantitative RT-PCR to investigate expression differences of the gene duplicates thought to be involved in the gain of anthocyanin floral pigmentation in recently tetraploid *Mimulus luteus* var. *variegatus*, one of three Chilean species *Mimulus* to independently gain red or purple pigmentation. My results suggest that the anthocyanin-activating R2R3 MYB protein

Myb5a is most likely responsible for the evolutionary purple pigment gain in *M. luteus* var. *variegatus*, based on its pattern of high expression in *M. l. variegatus* petals and low expression in other species and tissues. Other copies of Myb5a, created through gene duplication, show different patterns of expression that were not consistent with the activation of petal pigmentation in *M. l. variegatus*. These results help us further understand the genetic mechanisms involved in evolution, and point to the importance of regulatory changes that affect gene expression rather than protein sequence.

## Poster 19

Understanding microevolution in an expanding conifer species using genomics and demography

Joane S. Elleouet\*, Sally N. Aitken

### Abstract:

The level of local adaptation in widely distributed temperate tree species is remarkably high, and so is gene flow. These observations prompt questions about the mechanisms that allow tree species to quickly respond to selection pressures when establishing into new areas. Previous findings have linked life history traits of trees such as long juvenile phase and longevity to a reduced bottleneck effect along colonization routes. It is also hypothesized that infrequent long-distance (or frequent medium-range) dispersal events allowed temperate tree species to quickly track the receding Pleistocene ice sheet into newly available habitat. Our research uses *Picea sitchensis* (Sitka spruce) to empirically test these hypotheses. *Picea sitchensis* shows strong genetic clines of local adaptation across 22 degrees of latitude along the North-American Pacific coast, and its Northern range is still expanding into South-central Alaska. One way to characterize the speed of postglacial colonization and bottleneck severity is to use the Approximate Bayesian Computation framework. The expansion models we developed integrate influential tree life-history traits and were tested using an array of genomic markers developed from sequence capture. During this proposed talk I will present our latest results which used key model parameters to date successive population establishment events and to quantify bottleneck severity in the northern Sitka spruce range. I will then present the link between these findings and a different approach to the same question, in which we focused on the front of colonization on Kodiak Island, Alaska. *Picea sitchensis* reached Kodiak Island about 500 years ago. By sampling trees from 2 to 500 years old and associating tree ages and ring patterns with genotypes (developed from Genotype-by-Sequencing), we can directly monitor the evolution of genetic diversity and structure of the newly established forest. This direct approach complements larger scale statistical inference about population evolution during range expansion.

## Poster 20

## The origins of microbial interdependencies

Sylvie Estrela\* and Ben Kerr

### Abstract:

Microbes perform many costly biological functions that benefit themselves, and may as a consequence also benefit neighboring cells. Losing the ability to perform such functions can be advantageous due to cost savings, but when these functions are essential for growth, organisms become functionally dependent on ecological partners to compensate for the loss of these functions. When multiple functions may be lost, the outcomes of interaction are potentially diverse, including free-living (autonomous) organisms only; one-way dependency where one partner performs all functions and others none (exploitation); or mutual interdependency where partners perform complementary essential functions (mutualism). But what factors drive these different outcomes? I explore this question using a computational model where microbes perform multiple leaky functions that help in detoxifying their environment. Here, I will discuss how the cost of performing the function, the degree of essentiality and spatial structure combine to drive the dynamics and outcome of microbial interdependencies.

## Poster 21

### Eat, Weigh, Love: Diet and body mass drive reproductive strategies in mammals

Nicholas A. Famoso\*, Samantha S. B. Hopkins, Edward Byrd Davis

### Abstract:

Mammalian reproductive strategies evolve in response to a complex combination of physiological constraints and ecological pressures. Reproductive strategies vary from K-selected (producing few offspring with intensive parental care) to r-selected (producing many offspring with little parental care). Here, we investigate how diet and body size impact the reproductive strategies of mammals within a phylogenetic framework. We calculated the number of offspring per year, the percentage of the year dedicated to parental care, and the sexual lifespan for 560 mammal species from the information in the PanTHERIA life history database. A PCA on these reproductive strategy data showed that PC1 accounts for 64.1% of the variance, producing a novel index of reproductive strategy, with low values indicating a predominantly K-selected strategy and high values an r-selected strategy. Using this index, we were able to implement a phylogenetically-informed Analysis of Covariance (ANCOVA) testing the relative effects of body mass and diet on reproductive strategy. We removed marine mammals and chiropterans because their divergent life histories in relation to non-volant terrestrial mammals made their distributions follow distinctly different trajectories. Reproductive strategy is highly phylogenetically conserved ( $\lambda=0.995$ ). There is a negative, significant

relationship between index of reproductive strategy and body mass overall ( $p < 0.001$ ) as well as for herbivores ( $p < 0.0001$ ) and omnivores ( $p = 0.0323$ ). A non-significant relationship exists between the index of reproductive strategy and body mass for organisms with a carnivorous diet ( $p = 0.5217$ ); however, the effect size for this group is comparable to that for the others. In all three dietary categories, the larger the organism the more K-selected they are. The relationship in carnivores is not strictly linear, and may be a consequence of the differences between insectivore and vertebrate carnivores.

## **Poster 22**

### **Evaluating Concordance Between Mechanistic and Correlative Methods of Species Distribution and Performance**

J. Arthur Finger\*, Mark Dybdahl, Robert O. Hall

#### **Abstract:**

Species distribution models are routinely used to make informed decisions about invasive, endangered, and critical species' distributions. Ecological niche theory views a species distribution as the range of geographic space where populations can persist given the underlying environmental conditions. While surveying large swaths of land to determine the extent of a species' range was successful in the past, using a habitat suitability model, a model that predicts the likelihood of species occurrence given environmental parameters, are used in proxy. However, the use of habitat suitability as an accurate proxy for fitness is untested and how the two relate to each other is unknown. Here, we test the relationship between habitat suitability scores and individual field measures of growth and reproduction across wild populations of the invasive New Zealand mud snail, *Potamopyrgus antipodarum*, in the Greater Yellowstone National Park Area (GYA). We show cumulative habitat suitability correlates with growth and reproduction across small geographic scales. Additionally, our results confirm the assumption of a strong link between fitness, habitat suitability, and occurrence that has been assumed across the fields of ecology, conservation, and invasion biology.

## **Poster 23**

### **Investigating Barriers to Gene Flow in the Endangered American Badger to Inform Conservation Action**

Brett Ford\*, Richard Weir, Karl Larsen, and Michael Russello

#### **Abstract:**



Natural geographic features such as mountains, deserts, and rivers have long been perceived as physical barriers preventing gene flow. Recently however, human disturbances have been recognized as other major barriers to gene flow. Urban development, road networks, and pollution may directly decrease population numbers and prevent individuals from effectively dispersing, thereby causing isolation and inbreeding. One such species facing the harmful effects of human disturbance is the American badger (*Taxidea taxus jeffersonii*) of British Columbia (BC). Human development and forest encroachment, sustained by fire suppression, are two predominant threats hindering the badger population. Badgers are currently divided into two designatable units within the province, but there are four population units recognized by the BC Ministry of Environment; levels of genetic variation within and connectivity among these finer-scale units are currently unknown. Using two different molecular markers, mitochondrial DNA (mtDNA) control sequences and microsatellites, we aim to investigate fine-scale genetic structure of badger populations in British Columbia and infer barriers to gene flow across the landscape. We will also compare mtDNA variation detected in BC relative to range-wide estimates, and assess connectivity with badger populations in Washington, USA, which may constitute source populations in the future. The results of this study will directly inform provincial management and conservation strategies.

## Poster 24

Characterization of the adaptive genomic variation in Tasmanian devils *Sarcophilus harrisii* across their geographic range

Alexandra Fraik\*, Brendan Epstein, Joanna L. Kelley, Andrew Storfer

### Abstract:

The world's largest extant carnivorous marsupial, the Tasmanian devil (*Sarcophilus harrisii*), is threatened with extinction by devil facial tumor disease (DFTD). This contagious cancer has spread ~95% of the way across Tasmania, causing ~80% declines in overall devil population size. Despite epidemiological model predictions of species' extinction, devils persist in regions with long-term infection. Inconsistencies between model-based extinction predictions and observed persistence necessitate further research characterizing the adaptive potential of devil populations across Tasmania. We genotyped 360 individuals collected from three populations both pre and post disease arrival using 60,000 SNPs generated from restriction associated DNA sequencing (RAD-seq). From these data, we designed a RAD capture array (Rapture) and genotyped 16,000 SNPs from an additional 3500 individuals. Genome-scan methods and statistical outlier tests will identify candidate loci with outlier  $F_{ST}$  values, indicative of positive selection among populations. Genetic-environment association studies will test for correlations between environmental variables and allelic frequencies to characterize candidate loci under selection across the landscape. To parse out the

selective pressures of disease from environmental association analyses, pre- and post-disease subsets will be compared. Using these data, we test for large differences in allele frequencies in pre- and post-disease subsets to identify candidates signifying adaptation to DTFD.

## **Poster 25**

### **Hybridization and Gene Flow Between Migratory and Non-Migratory Avian Species**

Cooper French\*

#### **Abstract:**

We utilize ddRADSeq-derived loci to ascertain the relationships and continued genetic flow amongst a North American bird genus, *Pipilo*. Investigations include hybridization between migratory and non-migratory species (*P. ocai* & *P. maculatus*) and the restriction of gene flow between morphologically distinct populations in an Eastern US specie (*P. erythrophthalmus*).

## **Poster 26**

### **The interaction of migration load and expansion load during species range expansions**

Kimberly J. Gilbert\*, Nathaniel Sharp, Jeremy Draghi, Frédéric Guillaume, Rémi Matthey-Doret, Gina Conte, Anna Hargreaves, Amy Angert, Michael C. Whitlock

#### **Abstract:**

Species range expansions are unique evolutionary and demographic scenarios. As a species range expands, populations at the expanding front are subject to repeated founder effects and continued small effective population sizes as they continue to colonize new habitat. This reduces the strength of selection and increases random genetic drift in these edge population and results in a process termed gene surfing, where deleterious mutations which would otherwise be selected against and removed from the population are able to persist and rise in frequency at edge populations, causing expansion load. Simulation studies have investigated expansion load and there are controversial studies on human populations positing this as the cause for detrimental genetic diseases after the species expansion out of Africa. Our study addresses a novel factor in this process by introducing an environmental gradient over which range expansion occurs. We compare the presence or absence of this environmental gradient with the presence or absence of deleterious mutations through individual-based simulations on a spatially explicit landscape. We find that the environmental gradient interacts with the load due to deleterious mutations and impacts expansion load accumulated at the range edge. While a steeper gradient increases migration load and

slows range expansion, this decreases the amount of expansion load accumulated because populations have better ability to recover during a slower expansion. Increased deleterious mutations decrease fitness overall, but this effect is alleviated by a steeper environmental gradient. We further explore the details of deleterious loci contributing to expansion load and their effect sizes and frequencies across the landscape with the aim of informing studies on human and other populations likely to be impacted by shifting ranges due to climate change.

## **Poster 27**

The effect of landscape features on fine-scale seed dispersal in upland prairie plants

Monica Grasty\*, Mitch Cruzan, Pamela Thompson, Brendan Kohn

### **Abstract:**

Seed dispersal is a crucial factor in many ecological contexts, especially when considering range expansion, colonization of new habitats, and gene flow among populations. Rare long-distance dispersal events play a disproportionately important role in colonization and gene flow among populations, even at relatively small scales. Unfortunately, long-distance dispersal events are difficult to directly observe. Asking questions about how seed dispersal contributes to genetic differences will help expand general understanding of how plants move. My research employs upland prairie plants of the Pacific Northwest (PNW) as model organisms, specifically in a 400x400 meter prairie of the Whetstone Savanna Preserve of Medford, Oregon. This prairie is a mosaic of habitat types, characterized by vernal pools, large *Ceanothus* bushes, and hummock areas. I hypothesize that on a fine-scale of a few meters, these different landscape features will confer different resistances to gene flow, i.e. isolation by resistance will be a better predictor of gene flow than isolation by distance. There will be lower resistance to gene flow within one habitat than between habitat types. To test this hypothesis, aerial surveys of the prairie were used to generate an aerial orthomosaic and DEM. Using GIS, the landscape features will be classified to create a habitat map to feed into Circuitscape. Circuitscape uses circuit theory to predict gene flow based on resistance values assigned to different landscape features. These resistance values will be generated from genetic distance. I will perform a cpDNA capture to be used for Illumina sequencing to generate estimates of gene flow, and in turn, seed dispersal. *Plagiobothrys nothofulvus*, a PNW prairie native, is specific to the hummock areas of this prairie. Sampling *Plagiobothrys* sites separated by specific landscape features will reveal how these features influence seed dispersal.

## **Poster 28**

Species delimitation in *Castilleja*

Sarah J. Jacobs\*, Samuel Torpey, Maribeth Latvis, and David C. Tank

**Abstract:**

Here we present the current results of ongoing efforts towards species delimitation of several species of *Castilleja* (a genus of plants also known as the “paintbrushes”). Recently, it has become widely acknowledged that multiple lines of evidence may be necessary to delimit species, particularly in young lineages where a given delimitation criteria may or may not be present. However, given multiple lines of evidence, each supporting a different delimitation, the researcher may be forced to resort to a potentially subjective decision as to which delimitation to accept. Here we report on incongruent delimitations of the members of the *Castilleja cusickii* species complex given two separate lines of evidence: coalescent-based, molecular approaches that delimit three distinct lineages, and morphological analyses that delimit two. This study highlights what we expect is a common delimitation obstacle, what to do with conflicting delimitations. Delimitation approaches have been developed that utilize multiple lines of evidence into a single analysis of species limits and may be preferable. Further work will focus on integrated analyses of species boundaries as an opportunity to objectively delimit species boundaries.

**Poster 29**

Use it AND lose it: Alternating selection promotes horizontal gene transfer

Hannah Jordt\*, Eva Top, Wesley Loftie-Eaton, Sylvie Estrela, and Ben Kerr

Unlike eukaryotes, many prokaryotes exchange genes horizontally and can do so at a high frequency. Plasmid transfer via conjugation is a common mechanism of horizontal gene transfer in bacteria. It is still unclear, however, how conjugative plasmids persist in populations given the costs associated with conjugation. And given such costs, why are some genes found on conjugative plasmids rather than the chromosome? Using a mathematical model, we show that conjugative plasmids can be maintained in an environment with alternating selection. This allows the population to be periodically replenished with plasmid-free cells (potential hosts), and ensures that conjugation remains advantageous. I will also test this hypothesis experimentally using a biological system consisting of three players: an *E. coli* strain containing a conjugation-proficient F plasmid, a conjugation-deficient F plasmid, and a plasmid-free strain. I will compete these three strains in an environment that a) constantly selects for the plasmid-encoded gene (antibiotic present), b) constantly selects against the plasmid-encoded gene (antibiotic-free), and c) alternates with periodic switching between the antibiotic-present and antibiotic-free environments. I am currently estimating the parameters of my experimental system (e.g. conjugation rates, segregation rates, plasmid carriage costs, etc.). These will be incorporated into my mathematical model to more accurately

describe the dynamics of my experimental system, and this information will be used to design my final experiment determining whether conjugative plasmids can be maintained experimentally under alternating selection. This project will provide new insights into how and why conjugative plasmids persist. Given the critical role that plasmids play in the spread of antibiotic resistance genes, this work also has wider implications for human health by contributing to our understanding of the impact of antibiotic cycling on antibiotic resistance.

### **Poster 30**

#### Microfluidic Isolation and Evolutionary Analysis of the Nematode Sperm Proteome

Katja Kasimatis\*, John Johnson, Nadine Timmermeyer, Patrick Phillips

##### Abstract:

The reproductive success of a male is determined by his ability to successfully attract mates and out-compete other males for access to females and oocytes. While the winners of pre-mating choices are often assumed to determine paternity, competition among male ejaculates within the female reproductive tract (sperm competition) can have a profound impact on fertilization success. In particular, sperm competition can drive the evolution of seminal fluid proteins involved in modulating female pheromones, stimulating female reproductive physiology, and creating an environment that can be toxic to females. Additionally, seminal fluid proteins have been shown to experience rapid evolution due to positive selection. This study aimed to characterize the male reproductive proteome of *Caenorhabditis* nematodes and to determine if the rate of evolution of these proteins differs by the strength of sexual selection. We used microfluidic technology combined with mass spectrometry to define the reproductive proteomes of *C. elegans* and *C. remanei*. The preliminary data show differences in proteome composition between the species as well as identifying uncharacterized nematode-specific protein domains.

### **Poster 31**

#### Adaptation to an extreme environment through genome reduction in the Antarctic midge, *Belgica antarctica*

Joanna L. Kelley\*, Justin T. Peyton, Anna-Sophie Fiston-Lavier, Nick M. Teets, Muh-Ching Yee, J. Spencer Johnston, Carlos D. Bustamante, Rick E. Lee, Jr. and David L. Denlinger

##### Abstract:

The midge, *Belgica antarctica*, is the only insect endemic to Antarctica; the genome assembly is the first of an extremophile, the first Antarctic eukaryote and at 99 megabases, *B. antarctica* has the smallest known insect genome. With few repeat elements and a reduced intron length, genome architecture changes, not gene content, seem to be contributing to the evolution of the small genome. Genetic diversity is low in the midge, suggesting a small effective population size, implying strong selective pressures have driven the fixation of adaptive alleles in the midge genome.

## Poster 32

The Evolution of Antibiotic Resistance and Collateral Sensitivity in *Escherichia coli*

Homma Khosroyani\*, Elsha Eggink\*

### Abstract:

Antibiotic resistance in bacteria is rapidly rising and our garrison of effective drugs keeps dwindling. As the creation of new antibiotics is incredibly time-consuming and expensive, it's crucial that we slow the rapid evolution of drug resistance to prolong the effectiveness of our current drugs. Recent studies suggest improving current drug cycling practices by exploiting a phenomenon known as collateral sensitivity, where resistance to one drug leaves bacteria more sensitive to a second. By selecting pairs of antibiotics that exhibit collateral sensitivity, this method causes one drug to become more effective at abolishing bacteria after resistance to another drug has occurred. However, it is not known if collateral sensitivity profiles are maintained after further evolution of the bacteria; information that is crucial if we want a long-term method of combating drug resistance. To test the null hypothesis that collateral sensitivity profiles do not change over evolutionary time, we designed an evolution experiment involving Gentamicin-resistant *Escherichia coli* that exhibit collateral sensitivity to Colistin. Here we present preliminary data on collateral sensitivity from a panel of Gentamicin-resistant mutants and describe our experimental design. By comparing the minimum inhibitory concentration (MIC) values before and after our evolution experiment, we can determine if collateral sensitivity changes. This knowledge of how collateral sensitivity patterns change over time will influence the way we treat patients and combat future multidrug-resistant bacteria.

## Poster 33

CallHap: A Pipeline for Population-Level Chloroplast DNA Analysis

Brendan Kohn\*, Mitch Cruzan

### Abstract:

In examining the history of plant population, one important tool is the chloroplast, which is uniparentally inherited in most species and has the potential to show historical long-distance seed dispersal events. However, most studies utilizing chloroplast markers to date have focused on small subregions of the chloroplast and applied standard genetic distance measurements ( $F_{st}$ , etc.) to their frequencies. Since the chloroplast is haploid, genetic distance measurements that depend on heterozygote frequency are inappropriate. However, if the whole chloroplast is considered, the frequency of chloroplast haplotypes in the population can be used for genetic distance measurements. Since sequencing is still fairly expensive, we have developed a protocol which uses pooled chloroplast DNA from a population, along with single-sample sequencing from multiple study populations, to determine the frequency of each haplotype in each population. This process culminates in a bioinformatics pipeline (CallHap) which will call SNPs across populations, define haplotypes, and determine haplotype frequencies. In addition, this pipeline will estimate the identity and frequency of previously unidentified haplotypes that are unique to pooled samples.

## **Poster 34**

The microbial ecology of kelp forests

Matthew Lemay\*, Laura Parfrey

### **Abstract:**

Kelp forest ecosystems are biodiversity hotspots, providing habitat for dense assemblages of marine organisms. They are also an important source of energy and nutrients for marine food webs. Kelp surfaces support diverse communities of microbes that are essential for the development, metabolic functioning, and defense of their hosts, and for facilitating the transfer of carbon from algal primary production to higher trophic levels. Given the ecological and commercial value of kelps, there has been much interest in understanding the co-evolutionary relationships between kelp and their bacterial symbionts, yet multi-species research comparing patterns of bacterial diversity across kelp communities have been lacking. In this study, we quantified the diversity of host-associated bacteria present among eight sympatric species of kelp across four sites. We found that sympatric species of kelp have a high proportion of shared bacteria, yet also show significant differences in the structure of their bacterial communities across host-species and sites. Bacterial community structure does not track host phylogeny, but is significantly influenced by the life-history strategy of the host. Annual and perennial kelp species host bacterial communities consistent with early and late successional stages, respectively. This study provides important base-line data on the structure of bacterial communities associated with kelp forest ecosystems, and suggests a mechanism (life history strategy) that may structure bacterial communities across algal hosts.

## Poster 35

Some like it gradually hot: The evolution of thermostability in changing environments

Cierra Leon Guerrero\*, Sonia Singhal, Stella Wang, Ben Kerr

### Abstract:

As our planet warms, organisms that cannot migrate to more suitable habitats will be forced to adapt to the increasing temperatures or face extinction. An important question to address is how the rate of environmental change affects an organism's chance to adapt. If an environment changes suddenly, then organisms must also adapt rapidly, whereas slower rates of change allow the organism more time to adapt. Microorganisms, such as the virus  $\phi 6$ , can be utilized to answer this question because they evolve rapidly, allowing us to watch evolution in real time. We evolved  $\phi 6$  over 11 weeks to survive high temperatures. In different treatments, the viruses experienced sudden, moderate, or gradual changes in temperature. Sequencing the evolved lineages at two genes revealed multiple mutations. We added the mutations one by one to the ancestor to determine how each mutation affects thermotolerance. We find that each mutation can increase or decrease thermotolerance by a different amount. Interestingly enough, mutations that give the greatest increase in thermotolerance appear in viruses that experienced slower temperature change. Currently, we are working on engineering combinations of mutations to evaluate how the rate of environmental change affects possible pathways to thermostability.

## Poster 36

Looking for Evolution in Wastewater Treatment Plants

Kathleen Luu\*, Stephen Wallen\*, Charlie England, Briar Burgess, Colin Feng, Sujung Lim, Kristina Hilesland, Andy Strehler, Heidi Gough

### Abstract:

Do species evolve in diverse communities, similar to the simple community of our research? We are using the evolution that we've seen in a species of sulfate reducers found in our simple laboratory environment and comparing this evolution to that of a large, more complex anaerobic digester of the wastewater treatment plants. In our 'simple community' a methanogen, *Methanococcus maripaludis* and a sulfate reducer, *Desulfovibrio vulgaris* were paired. When two species are forced to live together over generations we expect to see evolution take place to some extent. It was found that after 1000 generations *D. vulgaris* loses its ability to reduce sulfate in this paired relationship. Using this laboratory pairing as a model, we are looking at the evolution of sulfate reducers in these two different anaerobic digesters, the University of Washington and



Brightwater Municipal Waste Water Treatment Center. Both Digesters have similar conditions, they are both anaerobic with low levels of sulfate present. To test our hypothesis we are currently extracting DNA from weekly samples of both digesters. The *dsrAB* gene is first amplified, as it is a conserved region within sulfate reducers and their relatives. We will then do Illumina sequencing in order to better determine the diversity of sulfate reducers present. Using this information, we will be able to design primers for the *sat*, *apsA* and *apsB* genes. This will show us if any mutations are present among the population of sulfate reducers in both digesters. This will be means for the comparison between real world and experimental conditions. Future work will look for mutations in the *sat*, *apsA* and *apsB* genes. By identifying these loss of function mutations in both the digesters, we will be able to see the impact of evolution on sulfate reducers in complex communities.

### **Poster 37**

Frequency dependence in the evolution of a syntrophic mutualism

Aryanne Macarulay, Samantha Rhothisen, Andrew Tagle\*

#### **Abstract:**

There are many mutualistic interactions that occur naturally in the world. Some of these mutualistic relationships evolve to be obligate, where the presence of one species is dependent on the other for its survival. We study the evolution of an obligate relationship with two model organisms, a sulfate reducer, *Desulfovibrio vulgaris*, and a methanogen, *Methanococcus maripaludis*. These organisms have evolved in an environment that forced their cooperation for 1000 generations, which has shown that 13 out of 22 *D. vulgaris* populations have lost their ability to reduce sulfate. To confirm if these mutations are beneficial or not, we measured the fitness of mutants with knockouts in the sulfate-reducing gene pathway relative to the wild-type strain with either an ancestral or evolved *M. maripaludis* partner. The final population size of each *D. vulgaris* mutant will be measured using *FREQ-Seq*; a technique that quantifies frequencies of various mutations in an amplicon. In previous iterations of this experiment, results presented a discrepancy between replicates (I and II) due to a failed cell lysis technique. We found out that only a small fraction of the cells were lysed. With a better cell lysis protocol, we expect to see an increase in *D. vulgaris* mutant frequencies when paired with either an ancestor or evolved *M. maripaludis* compared to the wild-type. The data collected from these experiments will help us have a better understanding whether losing the ability to reduce sulfate is a beneficial mutation for *D. vulgaris* or not.

### **Poster 38**

Coevolution in an SIRS model

Ailene MacPherson\*, Sally Otto

**Abstract:**

A key tenet of the red queen hypothesis for the evolution of sex is the presence of sustained oscillations in host and pathogen allele frequencies over time. Simple models of coevolution driven by interactions at a single locus are able to produce such stable allele frequency cycles. These models however make several critical assumptions about the demographic dynamics of host pathogen interactions. Similarly, the presence of cycles in epidemiological models are critical for explaining the often cyclic nature of disease outbreaks. These models however, often ignore genetic variation and coevolution between hosts and pathogens. Here we combine a epidemiological SIRS model with a classic single locus coevolution model and analyze the presence of allele frequency and epidemic cycles. In general we find that neither type of cycle is maintained in this more realistic scenario.

**Poster 39**

Genetic diversity in a parthenogenetic invader

Jennifer Madrid Thorson\* and Mark Dybdahl

**Abstract**

Species invasions have been viewed as events inevitably accompanied by genetic bottlenecks, where a very small portion of the ancestral populations' genetic diversity is represented in the invading population. More recently, evidence demonstrating unexpectedly high levels of genetic diversity in invasive populations provides an explanation for invasive success. Propagule pressure, encompassing the size of each introduced population and the number of introduced populations can result in genetically diverse invasive populations. Here we demonstrate an unexpectedly high level of genetic diversity in the invasive range of a parthenogenetic invader, *Potamopyrgus antipodarum*. Without the mechanism of sexual recombination in the invasive range, this species has accumulated genetic diversity through a long time span of invasion. Thus, propagule pressure spread over a long time period can equip invasive populations with high levels of genetic variation, yielding a population capable of responding to environmental heterogeneity in the new range.

**Poster 40**

Riders in the sky (islands): using macro-phylogenetic approaches to understanding species coexistence in the French Alps

Hannah Marx\*, Cédric Dentant, Julien Renaud, David Tank, Sébastien Lavergne

**Abstract:**

Alpine ecosystems are defined by harsh environmental conditions, and species that occur on alpine summits are generally expected to persist due to adaptations to these extreme selective forces. Using species occurrence data collected from floristic surveys within the Écrins National Park, France, along with existing molecular sequence data obtained from GenBank, we used a mega-phylogenetic approach to evaluate phylogenetic alpha and beta diversity patterns given three different hypothetical source pools for species diversity for 15 alpine summits. We used null models to address the importance of species-specific and species-neutral processes to diversity patterns. In addition, we examined environmental, geologic and geographic correlates that might explain phylogenetic diversity patterns. Although we found evidence for strong phylogenetic clustering within alpine summits, we were not able to reject models of species-neutral processes to explain patterns of floristic diversity within and between summits. Our results call into question general assumptions about the importance for adaptation in alpine ecosystems, and may provide evidence in support of the hypothesis that is easier to move than to adapt.

**Poster 41**

**Genome Structure Mediates Introgression in Zebrafish and Related Species**

Braedan M. McCluskey\*, John H. Postlethwait, Peter Batzel

**Abstract:**

Introgression is increasingly appreciated as a major contributor to species diversification. Using exome sequencing for zebrafish and ten related species, we show that introgression played a major role in the diversification of these species. Using the genomic information available for zebrafish, we show that recombination rate variation due to genome structure predicts the frequency of introgressed loci across the genome. Importantly, the evolutionary history inferred using standard methods agnostic to genomic position is at odds with the patterns of introgressed loci, which suggest a different history. Together, these findings demonstrate that frequently used methods for inferring species trees and introgression may be misleading in the presence of high levels of introgression.

**Poster 42**

**Morphological innovation in the sensory system and diversification in Neotropical Leaf-Nosed Bats (Chiroptera: Phyllostomidae)**

Leith B. Leiser-Miller\*, Sharlene Santana

**Abstract:**

The evolution of novel structures or shapes in the sensory system can create new dimensions to ecological niches, allow resource partitioning and potentially spur diversification in bats. Neotropical leaf-nosed bats (Phyllostomidae) are one of the most ecologically diverse groups of mammals. They have a wide range of diets, foraging styles and extreme morphological variation in their sensory structures (i.e. nose leaves and ears). To date, there has been little investigation into how morphological differences of these components of the sensory system evolve and how they functionally affect echolocation parameters in foraging bats. This is an important knowledge gap because morphological differences in the sensory system can directly affect an organism's perception of the environment, such as prey they can detect and potentially spur ecological diversification. We use Phyllostomidae as a model to address an important question about the sensory evolution of bats: how does the morphological diversity of external sensory structures influence ecological diversity? We assess the role of dietary and foraging ecology as a selective force on the morphology of nose leaves and ears, and use these data to illuminate the drivers of ecological diversity in this group. Our analyses investigate how morphological diversity maps onto ecological diversity and how the innovation of new sensory structure shapes open access to new dietary niches and influence changes in diversification rates. This study provides insight into how the morphology of the sensory system could shape bat ecology in an extremely diverse lineage of bats.

**Poster 43**

Reticulate history of the Neotropical plant genus *Lachemilla* (Rosaceae)

Diego F. Morales-Briones\*, David C. Tank

**Abstract:**

Cytosuclear discordance of evolutionary histories is a frequent pattern in plants and is most commonly attributed to hybridization, introgression, and incomplete lineage sorting. Here we explore this issue in the plant genus *Lachemilla*, a group of ca. 80 species distributed in the high mountains of the Neotropics and one of the most important and diverse groups of plants in the Andean páramos. Using multiple different approaches including phylogenies estimated from nuclear ribosomal and plastid DNA sequences, a procrustean approach of cophylogeny, hybridization networks, coalescent simulations, and flow cytometry evidence, we established a reticulate history of *Lachemilla* suggesting it is a product of extensive hybridization and, more specifically, polyploidy among most members of the group. Additionally we establish that the date of origin of *Lachemilla* (~14 MYA) predates the most recent uplifts of the Andes (~5 and ~10 MYA), which has been suggested as the major trigger of the highly diverse and endemic flora of the páramos.

#### **Poster 44**

##### **Genetic Structure of *Camassia* Species in the Snake River Watershed of Northeastern Oregon and adjacent Western Idaho**

Sebastian Mortimer\*, Susan Kephart, Theresa Culley, and Rob Tunison

##### **Abstract:**

The genus *Camassia*, endemic to North America, occurs primarily west of the Rocky Mountains. Totalling six species and ten subspecies the diversity of *Camassia* has been problematic for systematists as many taxa are morphologically, ecologically, and genetically similar. Recent studies have resolved major clades within *Camassia*, but there remain contentious populations within the Snake River drainage. Populations of *C. cusickii*, *C. quamash utahensis*, and *C. quamash* subsp. *breviflora*, whose placement within cpDNA and nrDNA phylogenies is inconsistent, have also been independently identified as different taxa within *Camassia* by their morphological characters. We used 16 microsatellite markers to determine the genetic structure of this taxonomically troublesome subset of the genus *Camassia*. These data complement a morphological analysis to ensure a robust and biologically relevant species delimitation of taxa in the Snake River drainage of northeastern Oregon and western Idaho.

#### **Poster 45**

##### **New micromammals from the Mascall Formation of Oregon's Middle Miocene**

Danielle Oberg\*, Samantha Hopkins

##### **Abstract:**

The Mascall Formation is one of the best-known middle Miocene records in North America; however, it has never been screenwashed, and has a relatively poorly-known microfauna. A new Mascall Formation site in the Crooked River Basin contains productive micromammal horizons which add a diversity of new small mammals to Oregon's Middle Miocene fauna. In particular, eulipotyphlan and marsupial mammals that were not previously known from the Mascall Formation are described here. We collected and heavy-liquid separated anthills at a new site, Cave Basin. We picked, sorted, and identified the fossils, finding occurrences of moles (*Talpinae* & *Proscalopinae*), moon rats (*Galericinae*), and shrews (*Limnoecinae* & *Heterosoricinae*). Moles and shrews were common in throughout the Miocene, but moon rats were previously known only from three localities in Oregon: Quartz Basin, Red Basin, and Round Up Flat. The great diversity of Eulipotyphla in Cave Basin is consistent with Shotwell's suggestion of high levels of habitat diversity in Oregon's Middle Miocene. Along with new occurrences of Eulipotyphla, we found a new specimen of

Herpetotherium at Cave Basin. The tooth, an isolated right M2, has an anteroposterior length of 2.53 mm and a buccolingual length of 2.67 mm, making it larger than almost any other previously described species. Herpetotherium is known from the Late Tiffanian (Middle Eocene) to the Middle Hemingfordian (Middle Miocene) in North America, but the presence of this specimen extends the last occurrence by two million years to the end of the Hemingfordian. Our research continues to shed light on the fauna present during the Middle Miocene of Oregon, demonstrating the diversity of small mammals and the last occurrence of herpetotheriine marsupials in North America.

## **Poster 46**

Diversity within and between Chilean *Mimulus* (Monkeyflower) species

Jessica Palacios\* and Arielle Cooley

### **Abstract:**

The *Mimulus* genus is becoming an increasingly important study species in the biological community, but most studies to date have focused on the North American rather than the South American species complexes. More clarification in taxonomical names can help in unraveling the evolutionary history of a species and add to our understanding of biological diversity. This study sought to look at physiological characteristics that could help determine if the current naming system for three varieties of the *Mimulus* genus from Chile—*M. cupreus*, *M. luteus* var. *luteus*, and *M. luteus* var. *variegatus*—is an accurate representation of their evolutionary relationship. The main research question was whether similarities between the species were influenced by phylogeny or geography. My results show a significant difference between the two varieties of *M. luteus*, which are the most closely related on the phylogenetic tree but *M. l. luteus* is a generalist and *M. l. variegatus* is a specialist. However, there was no significant difference between the two varieties of *M. luteus* in other traits. Instead, there was a trend in similarity. The significant differences in physiological traits between the two varieties of *M. luteus* suggest that the varieties are not as similar as their taxonomy suggests. Mating strategies for *M. cupreus* and *M. l. luteus* were also tested to confirm a previous study's finding that *M. cupreus* is a selfing plant and *M. l. luteus* is an outcrossing plant.

## **Poster 47**

What is the relative importance of genotypic diversity versus phenotypic plasticity on productivity under manipulated drought conditions?

Cynthia Chang, Rebecca Kim\*, Elizabeth Nightingale\*, Erica Qiao\*, Meerit Said\*, Stefany Sideris\*, Nicholas Vradenburg\*

**Abstract:**

Recent research suggests that intraspecific diversity plays important roles in ecosystem function, such as productivity and resilience to climate change. While many studies have shown a positive relationship between genotypic diversity within a single species and productivity, others have shown different direction and strengths in the diversity-productivity relationship depending on the measure and type of genetic diversity. Inherent in the implication of the importance of genotypic diversity on productivity is the idea that diversity at the genetic level translates into phenotypic trait diversity that allows the community to enhance overall productivity. Therefore a genotype's propensity for phenotypic plasticity may be a key driver to increasing community productivity, particularly under varying environmental conditions. We manipulated genotype richness as well as genetic variation for phenotypic plasticity of *Arabidopsis thaliana* grown in combination under drought and non-drought conditions. Each genotype was grown alone and in combination with 6 individuals for each water treatment. Manipulated genotype richness was either 1, 3, or 6 genotypes. Manipulated plasticity was either high or low as determined by phenotypic change (fitness, aboveground biomass) of genotype grown alone under drought and non-drought conditions. Aboveground productivity for each community was measured.

**Poster 48**

Uncovering the genes driving sex determination in *Kryptolebias marmoratus*

Authors: Corey Quackenbush\*, Chris Cornelius, Ryan L. Earley, Joanna L. Kelley

**Abstract:**

The fish, *Kryptolebias marmoratus*, is the only known self-fertilizing vertebrate. Individuals of this species are predominantly hermaphrodites with a small percentage being male. Sex determination in *K. marmoratus* is temperature dependent; the ratio of hermaphrodites to males can be influenced by water temperature. More specifically, water temperatures below 20°C result in a higher percentage of male offspring. These features provide a unique opportunity to study the patterns of gene expression that facilitate developmental sexual plasticity in *K. marmoratus*. To try and understand the gene expression patterns underlying sex determination we performed RNAseq on embryos that have been exposed to cold water temperatures (18-20°C) and embryos that were exposed to warm water temperatures (25-30°C). In addition to sampling based on water temperature we also collected embryos before and after the critical stage in development at which sex is determined. This experimental design allows us to look at gene expression before and after sex has been established. Comparing these differences is an important first step to understanding the genes involved in sex determination in *K. marmoratus*.

## Poster 49

### Morphological evolution of carnivoran milk teeth

Dana M Reuter\*, R. Ben Sulser, Susumu Tomiya

#### Abstract:

Deciduous tooth morphology in mammals has received little attention despite the potential for insight into the ecology and phylogeny of these animals. We investigated the evolution of milk-tooth morphology in carnivorans with two goals: (1) document and quantify ecomorphological variation in deciduous dentition; and (2) assess the morphological integration of deciduous and permanent teeth at macroevolutionary scales. We collected ecomorphological data on milk and adult teeth of 44 extant species from eight families and conducted principal component analysis to identify major variations in the shapes and relative sizes of lower carnassial teeth (dp4/m1) and pre-carnassial premolars (dp3/p4), which are tied to dietary differences in adults. We then conducted phylogenetic regression analyses and fit models of trait evolution to the parallel data sets. Results show complex patterns of morphological variation and integration that depend on the phylogenetic scale. Across the families examined, the basic functional attributes of milk teeth and their adult counterparts are significantly correlated. For example, in canids both milk and adult teeth are conservative compared to other families. Mismatches are observed in some dentally specialized groups: felids and hyaenids have proportionally larger grinding areas in their milk teeth, and ursids have greatly reduced milk teeth. At finer phylogenetic scales (e.g., within families), the correlation between milk- and adult-tooth shapes is generally poor. The limited morphological integration of deciduous and permanent teeth is largely attributed to faster rates of evolution in adult teeth. The limited variation in the shapes of deciduous carnassial teeth may reflect developmental constraint or a homogeneous process of selection in juvenile ecology.

## Poster 50

### The relationship of metabolic rate to shell morphology and environmental differences in endemic land snails of Galapagos

Yannik Roell\*, Jamie Volyes, Christine Parent

#### Abstract:

Adaptive radiation studies mainly focus on morphological characters and often overlook the physiological consequences to these adaptations. The link between morphological and physiological changes with environmental variation would allow for the understanding of why an adaptation would arise and why a lineage has diversified. The



endemic land snails of the genus *Naesiotus* form the most species rich adaptive radiation of the Galapagos islands with over 80 species described. These snails inhabit most islands from low elevations that are hot and arid to higher elevations that are cool and humid. Along this climatic gradient, *Naesiotus* species present a diverse spectrum of shell size, shape, and color. We predict that snails in hot and arid climates have lower basal metabolic rates and smaller shell apertures which would minimize water loss. We quantified the metabolic rate (calculated from oxygen consumption and carbon dioxide production) and water loss of 13 species distributed along two Galapagos elevational transects using a Sable Systems International FoxBox. We measured spatial and temporal variation in temperature and humidity along the transects and tested whether species metabolic rate changes due to morphology or environment or both. This research work will help establish how snail physiology differs along elevational gradients and whether snail shell morphology represents an adaptation to these differences.

## **Poster 51**

### **Predictive Framework to Discover Cryptic Biodiversity using the Pacific Northwest Mesic Forest**

Anahi Espindola, Megan Ruffley\*, Megan Smith, Bryan Carstens, Dave Tank, Jack Sullivan

#### **Abstract:**

With impending threats to earth's biodiversity such as climate change, habitat destruction, and invasive species, it is evident that the characterization of cryptic diversity cannot continue on a species-by-species level. However, if researchers could successfully predict which taxa harbor cryptic diversity in a given ecosystem, those species could be targeted to improve the efficiency by which we discover cryptic species and therefore cryptic biodiversity. The model system used to develop and implement this framework is the disjunct temperate rainforests of the Pacific Northwest (PNW). The PNW mesic forest was once a continuous forest ranging from the Northern Rocky Mountains (NRM) to the Pacific coast. When the Cascades peaked ~5mya, the resulting rain shadow caused the climate east of the Cascades to become arid, forcing the rainforest to retreat to suitable habitat along the NRM. With Pleistocene glaciation, rainforest taxa retreated to small, refugial populations and when the glaciers retreated ~15,000 years ago, previously glaciated areas were either recolonized out of these refugia, or colonized by long-distance dispersal into the newly available habitat. The forests currently contain conspecific populations that may or may not harbor cryptic diversity, depending on each taxon's specific biogeographic history, i.e. how long they have been evolving independently without gene flow. Testing these phylogeographic hypothesis, ancient vicariance and recent dispersal, using divergence time estimation and phylogeographic model selection provides evidence for whether a given species harbors or lacks cryptic diversity. With the classification of species as cryptic or not,

along with ecological variables, a discriminate function is established to characterize the ecological features that each status group share. With this “database” of shared features for both status groups, the discriminant function can be applied to other datasets to ask whether untested taxa share ecological features with taxa harboring cryptic diversity or not.

## **Poster 52**

Seasonal transcriptional changes in brown bears (*Ursus arctos*)

Michael W. Saxton\*, Heiko Jansen, Charles Robbins, Joanna L. Kelley

### **Abstract:**

Brown bears (*Ursus arctos*) are superbly adapted to live in cold, high latitude environments in which they experience an annual winter food shortage. To survive such conditions, they undergo dramatic seasonal shifts in physiology to maximize energy gain and storage in the summer and fall and conserve energy in the winter. During hibernation bears experience a mild decrease in body temperature but up to a 75% reduction in basal metabolic rate, as well as reduced heart rate and cardiac output, reduced respiration rate, and insulin resistance. On arousal from hibernation the bears return to their active season physiology, including a return to insulin sensitivity. Fluctuations in weight and high overall adiposity as seen in bears are contributing factors to cardiovascular disease and diabetes in humans. Using RNA-sequencing, we are examining the transcriptional changes that occur in muscle, liver, and fat tissues of captive brown bears in active, hyperphagic, and hibernation states. Our goal is to identify genes that have significant changes in expression in the three metabolic states that could lead to improved treatment of diabetes and cardiovascular disease. The genetic and biochemical mechanisms underlying these seasonal changes in bears may provide a unique biological model for studying and treating a variety of human diseases.

## **Poster 53**

Landscape Influences on Dispersal of Slender False Brome

Tina Schroyer\*, Mitch Cruzan

### **Abstract:**

Efficacy of dispersal vectors determine a species' ability to migrate over generations. When a seed vector is prone to both directed dispersal and long distance dispersal, it has the potential to drastically increase the migration rates of plants. Invasive species can be used as a model system for studying the effects of dispersal vectors on genetic structure in expanding populations. I propose to investigate the relative contributions of

rural landscape features to dispersal patterns in invasive slender false brome (*Brachypodium sylvaticum*) at its range edge.

## **Poster 54**

Clonal adaptation in *Mimulus guttatus*

Jaime Schwoch\*, Jered Thomas, Mitch Cruzan

It is known that mutations accumulate during vegetative growth but they are often assumed to be deleterious and result in decreased fitness. We propose that the accumulation of beneficial mutations is likely and due to cell lineage selection where deleterious mutations are selected out before the formation of pollen and ovules. The idea of somatic mutation accumulation may provide insight to rapid adaptation in novel environments in plants. Several genets of *Mimulus guttatus*, were pollinated using autogamy (pollen onto same flower) and geitonogamy (pollen onto different stem) in which the progeny were grown and their fitness was quantified. The results of this experiment provided inspiration to our current methods because it suggests that clonal evolution in plants may contribute to their adaptation to novel environments and have implications for the evolutionary advantages of autogamy. Several genets of *M. guttatus* were grown in a saline hydroponics system to impose harsh selection and favor mutation during vegetative growth. Plants were allowed to grow in an incrementally increasing saline environment and later planted into soil where they will be pollinated using autogamous and geitonogamous methods. Selfing increases the rate of homozygosity and therefore increasing the expression of novel somatic mutations. We expect that the surviving clonal progeny of autogamous pollinations will have a higher expression of beneficial mutations making them well adapted to a high saline environment.

## **Poster 55**

Effects of habitat complexity in the rearing environment on adult behavior

Matthew Singer\*, Meghan Bromley, Barrie D. Robison

Abstract:

Wild and captive populations of animals exhibit stark differences in anxiety behaviors where wild populations tend to behave more shy (more anxious) and captive populations tend to behave more bold (less anxious). Previous research has shown these behaviors to have heritability estimates ranging from 0.2 to 0.5, yet phenotypic changes during adaptation to captivity occur more rapidly than evolutionary models would predict. Variation between wild and captive environments might play a role in facilitating behavioral changes during this transition. Spatial complexity has been known to decrease stress and anxiety in captive animals. However, little is known about the

effects of exposure to environmental complexity during critical periods of development. We tested the effects of habitat complexity during juvenile development on behavioral indicators of adult anxiety in a novel open field environment using Zebrafish (*Danio rerio*). We grew 60 fish from 2 days post hatching in environments with and without aquarium plants. At 4 months, the fish were removed from their rearing tanks and placed individually into a novel open field test tank. To account for any effects of novelty in the testing environment, the fish were subjected to a simple or complex open field with a reciprocal cross design. Overall, we found that fish reared with complexity had a reduced anxiety response to the open field, but we observed some patterns that suggest a simple rearing environment enhances behavioral plasticity in response to differing environmental contexts.

## **Poster 56**

Phenotypic variation, epigenetic variation, and local adaptation

Mark Smithson\*, Mark Dybdahl, Michael Skinner, Scott Nusimer, Jennifer Madrid Thorson

### **Abstract:**

Some species are able to occupy diverse environmental conditions with little or no genetic variation as observed most often among some invasive species. A leading hypothesis for such a pattern of phenotypic divergence is variation in gene expression regulation via epigenetic mechanisms. The freshwater snail *Potamopyrgus antipodarum*, which reproduces both sexually and asexually in its native range but only asexually in its invasive range, provides an example. Genetically depauperate asexual populations in their invasive range exhibit adaptive shell shape divergence for different current speeds. Our preliminary data shows that shell-shape polymorphism is associated with epigenetic shifts, measured as DNA methylation. However, what is not known is whether epigenetic shifts are associated with the production of adaptive, maladaptive, or random phenotypic variation. Further, the conditions under which these alternative phenotypic consequences of epigenetic shifts enhance or retard adaptation to local conditions are not clear. In a population genetics model, we confirmed that the adaptive value of epigenetic variation depends critically upon the evolutionary forces acting on the variation. We propose to clarify the role of epigenetic variation in adaptive evolution by (1) comparing the contribution of genetic and epigenetic variation to shell shape divergence in natural sexual and asexual populations that coexist in the same environmental gradient, and (2) developing mathematical models to study the conditions under which alternative phenotypic consequences of epigenetic shifts enhance or retard local adaptation and evolve in sexual versus asexual organisms.

## **Poster 57**

## Geographic cline analysis as a tool for studying genome-wide variation: a case study of pollinator-mediated divergence in a monkeyflower

Sean Stankowski\*, Madeline Chase, Matthew Streisfeld

### Abstract:

A major goal of speciation research is to reveal the genomic signatures that accompany the speciation process. Genome scans are routinely used to explore genome-wide variation and identify highly differentiated loci that may contribute to ecological divergence, but they do not incorporate spatial, phenotypic, or environmental data that might enhance outlier detection. Geographic cline analysis provides a potential framework for integrating diverse forms of data in a spatially-explicit framework, but has not been used to study genome-wide patterns of divergence. Aided by a first-draft genome assembly, we combine an FCT scan and geographic cline analysis to characterize patterns of genome-wide divergence between divergent pollination ecotypes of *Mimulus aurantiacus*. FCT analysis of 58,872 SNPs generated via RADseq revealed little ecotypic differentiation (mean FCT = 0.041), though a small number of loci were moderately to highly diverged. Consistent with our previous results from the gene *MaMyb2*, which contributes to differences in flower color, 130 loci have cline shapes that recapitulate the spatial pattern of trait divergence, suggesting that they may reside in or near the genomic regions that contribute to pollinator isolation. In the narrow hybrid zone between the ecotypes, extensive admixture among individuals and low linkage disequilibrium between markers indicate that most outlier loci are scattered throughout the genome, rather than being restricted to one or a few divergent regions. In addition to revealing the genomic consequences of ecological divergence in this system, we discuss how geographic cline analysis is a powerful but under-utilized framework for studying genome-wide patterns of divergence.

## Poster 58

A one-two punch: combining killing systems within a single cell by going “pro”

Katrina van Raay\*, Benjamin Kerr

### Abstract:

Chemical warfare in the microbial world is ubiquitous. One kind of chemical weapon microbes employ is a proteinaceous toxin called a bacteriocin. The best-studied bacteriocins are the colicins, produced by and active against *Escherichia coli*. Many colicin systems encode suicidal lysis genes, such that the producing cell releases the toxin through cell lysis. Released colicin kills sensitive competing cells allowing immune clones of the producer to capitalize on the liberated resources. However a major group of colicin systems lack this lysis gene, and it has been unclear how such toxins were

released from the producing cell. Here, we explore a newly discovered union between such a colicin system and a prophage (bacterial virus that has been incorporated into the bacterium's genome), where release of the colicin occurs via phage-encoded cell lysis. This union should be detrimental to susceptible cells, which would be hit by a one-two punch: once by the colicin, once by the phage. Preliminary mathematical modeling suggests that the success of this dual killing system depends on the prophage's ability to produce infectious virions. If the prophage is cryptic (encoding lysis, but not producing infectious phage), then this dual system is susceptible to invasion by "cheaters" that only possess the colicin system (and its immunity) but do not lyse. Here, we explore this social dilemma and its potential resolution in detail through a combination of mathematical modeling, microbial evolution experiments, and agent-based simulations.

## **Poster 59**

Evolving a Healthier Worm: Microfluidics, Pharyngeal Pumping, and Experimental Evolution in *C. elegans*

Kelley S. Williams\*, Stephen A. Banse, Ben W. Blue, Patrick C. Phillips

### **Abstract:**

Although *C. elegans* is a popular model for lifespan research, study of genetic and pharmacological interventions that specifically alter healthspan is less thorough. We therefore propose to study nematode healthspan using the decline in rhythmic activity of the feeding organ (pharynx) as a selection metric for experimental evolution. To facilitate this project, we are developing three assay platforms. The first two assay platforms are lower throughput, higher resolution measures of pharyngeal health, while the third is a higher-throughput assay designed for experimental evolution. The first microfluidic device, the "electropharyngeogram chip", allows us to quantify age-related declines in pharyngeal electrical activity. This approach shows the expected changes in pump frequency and prolonged health of known longevity mutants, as well as shows novel changes in pump patterning. The second microfluidic platform, the "feeding chip", is designed to provide tight temporal control of food exposure while imaging feeding animals. This device was designed to enable measurements of grinder (chewing) and peristalsis (swallowing) efficiency. The third device, the higher-throughput "sorter chip", allows automated selection of high performing individuals from ~2000 animals per hour as measured by ingestion rates of a BODIPY-conjugate. We will present the developmental work for all three devices, as well as the intellectual framework in which we are using these devices to evolve a worm that stays healthier, longer.

## **Poster 60**

# Dramatic evolution of body length due to post-embryonic changes in cell size in a newly discovered close relative of *C. elegans*

Gavin C. Woodruff\*, Patrick C. Phillips, Natsumi Kanzaki

## Abstract

Understanding morphological diversity—and morphological constraint—has been a central question in evolutionary biology since its beginning. Nematodes of the genus *Caenorhabditis*, which contains the well-studied model system *C. elegans*, display remarkable morphological consistency in the face of extensive genetic divergence. Here, we provide a description of the broad developmental patterns of a newly discovered species, *C. sp. 34*, which was isolated from fresh figs in Okinawa, Japan and which is among the closest known relatives of *C. elegans*. *C. sp. 34* displays an extremely large body size and can grow to be nearly twice as long as *C. elegans*. Observations of the timing of developmental milestones reveal that *C. sp. 34* develops nearly twice as slowly as *C. elegans*. Measurements of embryo and larval size show that the size difference between *C. sp. 34* and *C. elegans* is largely due to post-embryonic events, particularly during the transition from larval to adult stages. This difference in size is not attributable to differences in germ line chromosome number or the number of somatic cells. The overall difference in body size is therefore largely attributable to changes in cell size via increased cytoplasm. Because of its close relationship to *C. elegans*, one of the most intensively studied animal model systems, the morphological and ecological distinctness of *C. sp. 34* provides an ideal system for the detailed analysis of evolutionary diversification within nematodes.