ECOLOGICAL GENOMICS Symposium

2016 Speaker Abstracts

Causes and consequences of speciation by hybridization in budding yeast

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Hybridization is a powerful mechanism to generate biodiversity, for instance through species formation. However, well-supported cases of hybrid speciation are limited to plants and animals, which indicates that either unicellular eukaryotes have been overlooked or that this mechanism is restricted to multicellular organisms. Experiments in the laboratory have shown that new yeast species can be formed by hybridization, suggesting that this mechanism could be, in principle, observed in nature. Using population genomics, experimental crosses and fitness assays, we show that homoploid hybrid speciation took place recently in natural populations of Saccharomyces paradoxus inhabiting the North American temperate forests. We found (1) evidence of hybridization in the genome, (2) reproductive isolation between hybrid and parental species and (3) a link between hybridization and reproductive isolation. In addition, we found that the hybrid lineage displays specific growth phenotypes that may reflect a new ecological niche. Our results show that hybridization may play a key role in species formation in fungi. Because there is very little opportunity for pre-zygotic isolation among yeast species, this mechanism of speciation could be common in the wild and contribute to fungal biodiversity. Our system will be very insightful for the study of the different roles of hybridization, chromosomal rearrangements and hybrid adaptation during speciation.

Measuring selection and gene flow during reinforcement

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Gene flow can impede the evolution of reproductive isolating barriers between sympatric species. Reinforcement is the process by which pre-zygotic reproductive isolation evolves in sympatry due to selection to decrease costly hybridization. It is known that reinforcement can be prevented by too much gene flow, but it is unknown the extent to which reinforcement has naturally evolved in the presence of gene flow. Theoretical work predicts that strong selection can drive divergence despite gene flow, but it has been difficult to measure the strength of selection causing reinforcement in natural systems. Flower color divergence in the native Texas wildflower, *Phlox drummondii*, is one of the best-studied cases of reinforcement. *P. drummondii* and the closely related species *P. cuspidata* share the same light-blue flower color throughout most of their ranges. But, in sympatric regions, *P. drummondii* has evolved dark-red flowers, which decrease heterospecific matings between these species. We have used common garden field experiments and population genetic modeling to estimate the strength of selection causing reinforcement. Furthermore, we have sequenced transcriptomes from closely related *Phlox* species and used genomic analyses to infer gene flow between *P. drummondii* and *P. cuspidata*. We find evidence of strong selection driving flower color evolution in this system and signatures of gene flow in sympatric populations. We find that gene-flow between these species is asymmetrical, which can explain why reinforcement caused divergence in only one of the sympatric species. We suggest strong selection can explain how reinforcement successfully evolved in this system despite gene flow in sympatry.

Comparative genomics of bees and wasps: insights into the evolution of social behavior

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The evolution of eusociality marks one of the major transitions in evolution and therefore, has been of great interest for understanding the genomic changes that accompany the evolution of complexity. To date, most genomic studies have focused on highly derived eusocial lineages of bees and ants; one of the goals of my work has been to embark on studies of genomics in underrepresented, but highly informative groups such as primitively eusocial wasps. Wasps in the genus *Polistes* are important ecological model systems for understanding the evolution of sociality. In this talk, I will describe genomic, transcriptomic, and epignomic studies on *Polistes*, placed in a comparative context with previous findings from bees and ants. In addition, I will describe the use of field and laboratory experimental manipulations to identify causal genetic and environmental factors underlying paper wasp social organization. These results will be discussed in light of three non-mutually exclusive ideas about genomic mechanisms and their influences on the evolution of sociality. 1) Genetic toolkits: Transcriptomic comparisons across ants, bees, and wasps suggest convergent evolution of castes in different lineages involves similar gene expression patterns in a small set of key pathways (e.g. those related to metabolism, development, and energy balance). 2) Novel genes: The expression of taxonomically restricted genes are often associated with caste differences in wasps and bees. 3) Epigenetics: Genome-wide DNA methylation has been dramatically reduced in *Polistes*, in contrast to other social insects, showing that epigenetic mechanisms are evolutionarily labile and may thus affect social traits in different ways across social insect lineages. Although more data on transitional species are needed, these studies suggest a diversity of genomic mechanisms are involved in evolutionary transitions from solitary to social, and are contributing to a new eco-evo-devo synthetic view of social evolution.

Experimental evidence for eco-evolutionary dynamics in aquatic systems

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There is growing experimental evidence for eco-evolutionary dynamics and feedbacks from laboratory experiments. Similar experimental tests are rarer in more natural settings, where abiotic drivers might strongly influence the outcome of ecological and evolutionary interactions. Here, I present several experimental tests of eco-evolutionary feedbacks in large outdoor mesocosms (~1000L), using stickleback as a model organism. In these experiments I find evidence for key components of Eco-Evo feedbacks: i) stickleback strongly modify their biotic and abiotic environment, ii) heritable trait differences between recently diverged populations likely underlie these effects, iii) ecosystem modifications are persistent over time, and iv) they affect selection pressures and genotype composition in subsequent generations.

Ecological genomics as a tool for breeding climate-resilient crops

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Improving adaptation of crops to environmental stress is critical for ensuring global food security. However, phenotyping plant stress response under field conditions remains a major bottleneck for genetics and breeding. In ecological genomics, associations between natural genetic variants and environmental variables ("genome-environment associations") are often used to identify genome regions underlying adaptation without the use of phenotyping data. Recently we demonstrated that genome-environment associations could be integrated with genomic selection (GS) breeding models to predict environmental adaptation traits in the widely-adapted cereal crop sorghum (*Sorghum bicolor*). We developed genome-wide predictions of environmental adaptation using ~2,000 georeferenced landraces (traditional varieties) genotyped at 400,000 SNPs and validated genomic predictions of drought stress tolerance using common-garden managed-stress experiments in India and Texas. This study suggests a new role for ecological genomics as a tool to support molecular breeding of climate-resilient crops.

Lepidopteran genomics: sex chromosomes and sperm proteomes

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Despite playing a fundamental role in reproductive processes, sperm cells are remarkably diverse in form and function. One example of this diversity is sperm heteromorphism, where distinct types of sperm are produced by a single male. In Lepidopteran insects (moths and butterflies), males produce two sperm types: a “normal”, nucleated sperm morph and a morph that lacks a nucleus or nuclear DNA. Very little is known about the function, molecular composition, or evolutionary significance of these anucleated sperm in Lepidoptera. To investigate this enigmatic cell type, we have developed a novel method for isolating the two sperm morphs and applied shotgun proteomics to comprehensively characterize the proteomes of nucleated versus anucleated sperm proteomes. This work has been replicated in two species, *Manduca sexta* (Carolina sphinx moth) and *Danaus plexippus* (monarch butterfly). The sperm proteomes substantially overlap between the two morphs, with anucleated sperm appearing primarily to contain a subset of nucleated sperm proteome, but also with a few dozen unique proteins absent from nucleated sperm. Comparative analysis indicates a relatively large proportion of lepidopteran-specific genes are found in the sperm proteome relative to the genome as a whole. Sperm proteins are enriched on the Z chromosome relative to autosomes, as predicted by sexual antagonism theory. Preliminary population genomic analysis in Monarch butterflies suggests proteins unique to nucleated sperm are, as a group, evolving adaptively, but that this is not true for anucleated-specific proteins.

An integrative approach to study a behavior-modifying parasite and its fish host

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The cestode *Schistocephalus solidus* is a model parasite with a complex life cycle that successively parasitizes a copepod, a fish – the threespine stickleback, *Gasterosteus aculeatus* – and a piscivorous endotherm, typically a bird. Sticklebacks infected by this parasitic flatworm show large changes in phenotype, including a lack of the typical behavioural response to risky situations. These host changes occur specifically when the parasite is ready to move to its final bird host to reproduce. However, whether this drastic behaviour change is a by-product of facing a parasitic infection, a side effect of infection, or the result of a direct manipulation by the parasite is unknown. Furthermore, parasites with multiple hosts, such as *S. solidus,* undergo dramatic phenotypic transformations and endure major environmental shifts over the course of their life cycle, yet very little are known about how these are orchestrated at the molecular and physiological levels. We used this host-parasite pair as a model to study the mechanisms of behavioural modification by parasites in the host and of host transitions in the parasite. To understand the physiological mechanisms that generate these behavioural changes, we used phenotypic engineering to try to recreate the host behavioural modifications in healthy fish using pharmacological manipulations, and transcriptomics to define a genomic signature of *Schistocephalus* infection in the host brain. In parallel, we examined the transcriptomic response of *S. solidus* over the course of its development in its stickleback host and in the final avian host. Although we were able to change individual behaviours in sticklebacks with certain manipulations, we were not able to replicate the entire behavioural profile of a parasitized fish. Our results suggest that the impact of *S. solidus* on the stickleback might be of a multifactorial nature. Comparing the brain transcriptome of healthy, infected and pharmacologically manipulated sticklebacks that show similar behaviour changes, we find that while some overlap occur, most genes and biological functions differ, although serotonin-manipulated and parasitized sticklebacks show similar behaviours. Finally, we uncovered that major host transitions are modulated through transcriptome-wide reprogramming events in *S. solidus* and that un-annotated and *S. solidus*-specific genes could play a determinant role in host-parasite molecular interactions required to complete the parasite's life cycle. Our results permit future comparative analyses to help disentangle species-specific patterns of infection from conserved mechanisms, ultimately leading to a better understanding of the molecular control and evolution of complex life cycles. Our combined approach to uncover the causes and molecular consequences of behaviour modification by a parasite in a host and the molecular signature of host transitions in the same parasite will contribute to shed new light on parasite-host interactions.

Cyanogenesis and the genetics of local adaptation in white clover

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White clover (*Trifolium repens*) is polymorphic for cyanogenesis, the release of hydrogen cyanide upon tissue damage. First documented more than a century ago, this chemical defense polymorphism has been the subject of dozens of ecological genetic studies examining the environmental factors that maintain it. This work has provided a foundation for our studies examining the molecular basis of the cyanogenesis polymorphism and the population genetic processes that govern its evolution. In the native European range and in introduced populations worldwide, white clover has repeatedly evolved climate-associated cyanogenesis clines; cyanogenic plants predominate in warmer and drier climates. The polymorphism has a simple Mendelian basis, with two independently segregating genes controlling the presence/absence of two required biochemical components: cyanogenic glucosides and their hydrolyzing enzyme. Our work to date has revealed roles for recurrent gene deletions, adaptive gene copy number variation, and a metabolic gene cluster polymorphism. These findings on the molecular basis of the polymorphism are discussed in the context of ongoing work aimed at characterizing the selective factors that maintain this adaptive variation and the relative importance of cyanogenesis loci vs. other genetic factors in white clover's rapid adaptation across climatic gradients.

Blind fish provide big insights

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Cavefish exhibit distinct behavioral (e.g. reduced sleep, reduced aggression), metabolic (e.g. increased fat stores), and phenotypic (e.g. reduced eyes, reduced pigment) traits despite gene flow with surface fish. Mexican tetras have also evolved cave-associated phenotypes multiple times and consist of two major lineages ("new" and "old") that like diverged 1-4 mya. The genetic underpinnings of many cave-associated traits are different among cave populations even within the new and old lineages, and we are examining divergent outlier loci between cave and surface fish within caves among these lineages to infer commonalities about the evolutionary process across multiple origins of the cave phenotype. To address these goals, we generated whole genome resequencing data from three cave populations and two surface populations, including surface and cavefish populations from both the new and old lineages. We also sequenced a closely related congener *A. aeneus* to serve as outgroups for polarizing changes in the *A. mexicanus* cavefish. In total, we have 45 resequenced genomes (7.3x-19x per individual aligned to the reference genome), and have thoroughly explored the relationships between populations, revealing extensive gene flow between new and old cavefish lineages, while the surface fish lineages remain distinct. This gene flow shapes how we interpret adaptation to the cave environment, and the interpretation of outlier loci, and will provide fruitful avenues for future research into gene-flow mediated adaptation.

Genome-scale analyses of individual and species variation in complex behavior phenotypes

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All animals evaluate the salience of external stimuli and integrate them with internal physiological information into adaptive behavior. Natural and sexual selection impinge on these processes, yet our understanding of behavioral decision-making mechanisms and their evolution is still very limited. Social animals in particular possess sophisticated cognitive abilities for assessing, evaluating, and responding to a wide range of social cues. Such social competence allows individuals to optimize their behavior based on the available social information. Despite our detailed understanding of the ultimate (fitness) consequences of social competence in some contexts, surprisingly little is known about its neural and molecular underpinnings. Social competence relies on flexible decision-making processes in the brain. Vertebrates share a Social Decision Making (SDM) Network, an evolutionary conserved network of fore- and midbrain nuclei involved in behavioral regulation and evaluation of stimulus salience. I will present results from several of our studies aimed at identifying the neural circuitry, molecular signaling, and regulatory mechanisms involved in social competence, and how these mechanisms have evolved.