

# Ecological Genomics

# Symposium

## 2015 Speaker Abstracts

(In order of presentation)

### ***Cooperation, exploitation, and discrimination in social amoebae***

**Joan E. Strassmann**  
Washington University in St. Louis



There are advantages to cooperation, but cheaters that enter into an association only to exploit it can foil these advantages. In microbes it is sometimes challenging to see exactly who is doing what, making molecular and genomic tools particularly useful. *Dictyostelium discoideum* amoebae have a social stage in which about 20% of formerly independent cells die to form a stalk, which the others climb and form hardy spores at the top. What keeps some cells from exploiting others? After all, the multicellular body forms from aggregation, so they are not necessarily genetically related. We have approached this question by looking at whether there is sorting into kin groups during aggregation, whether some clones exploit others in aggregations, and whether the multicellular chimeric body functions less well. We have also looked for molecular evidence of rapid evolution of cheater and recognition genes. We have used experimental evolution both to see what kinds of mutations accumulate when the social stage is eliminated and to see what happens to cheaters at very low relatedness. This story is a surprising mix of clarity and puzzles, with many unanswered questions, so it is also good for teaching the process of science, not just the outcomes.

### ***Ecological genomics in a diverse and changing world: Studies in sea urchins and horned beetles***

**Melissa Pespeni**  
University of Vermont



A major goal in evolutionary biology is to reveal the genetic and developmental bases of variation in nature. Arguably, much of this variation is presented by complex traits – that is, traits that are shaped by many genes acting in concert and that may be affected by the environmental conditions in which they are expressed. Research in our lab aims to reveal the molecular bases of these traits in the contexts of their evolution across millions of years or as organisms are faced with geologically unprecedented and accelerating changes in climate conditions. In this talk, I will tell two stories, one about physiological phenotypes important for surviving the rapidly changing ocean chemistry conditions, and one about dramatic morphological phenotypes that vary both within and between species. The specific questions I will address are: Do purple sea urchins have the genetic capacity to respond to ocean acidification? What are the molecular underpinnings of the morphological diversity encompassed in three dramatically different, but closely-related horned beetle species? I address these questions through a combination of lab- and field-based experiments and through the integration of genomics, developmental biology, and ecology.

## ***Finding mechanisms underlying life in extreme environments***

**Michi Tobler**  
**Kansas State University**



Freshwater springs discharging water rich in toxic hydrogen sulfide (H<sub>2</sub>S) belong to the most inhospitable aquatic habitats, and few organisms have been able to persist in these extreme environments. Yet, over a dozen lineages of poeciliid fishes have colonized and thrive in sulfide springs, providing an opportunity to study mechanisms of adaptation and the role of convergent evolution in animal diversification. We used comparative transcriptome analyses in three sulfide spring lineages of *Poecilia mexicana* and matching reference populations from non-sulfidic habitats to test hypotheses about mechanisms mediating tolerance to H<sub>2</sub>S toxicity. Elevated tolerance to environmental H<sub>2</sub>S could be driven by three mechanisms: (1) Modification the integumentary system that reduce the flux of environmental H<sub>2</sub>S into the body. (2) Increased capability to maintain H<sub>2</sub>S homeostasis despite continuous flux from the environment through increased detoxification or decreased endogenous production. (3) Modification of toxicity targets that make individuals more inert to adverse consequences caused by elevated endogenous concentration. Overall, our results from comparisons of gene expression patterns and genetic variation suggest that modification of processes associated with H<sub>2</sub>S detoxification and toxicity likely complement each other to mediate elevated H<sub>2</sub>S tolerance in sulfide spring fishes. Our analyses allow for the development of novel hypotheses about biochemical and physiological mechanisms of adaptation to extreme environments.

## ***The 5000 Daphnia pulex Genomes Project***

**Michael Lynch**  
**Indiana University**



Owing to the pronounced technological achievements in genomics and other derivative “omics” fields, a number of new model systems are emerging in biology. In the fields of ecological and evolutionary genomics, foremost among these is *Daphnia pulex*. We have embarked on a project to sequence the genomes of 96 genotypes from 50 populations in an effort to provide a general service to the research community, as well as to answer several unsolved problems, including: the genomic consequences of the loss of meiosis; the origins of introns; and the impact of long-term population bottlenecks. A broad overview will be given on some of the findings that have begun to emerge from this project. We have also been able to establish a genetic map via the sequencing of single sperm. By revealing the species-wide frequencies of single-nucleotide polymorphisms throughout the entire genome and inferring aspects of selection on individual loci, our work lays the foundations for studies on local environmental adaptation and temporal response to environmental change. To fully capitalize on this project, we encourage collaborative efforts with other researchers working on *D. pulex* or closely related species.

## ***Evolutionary genomics of flower color transitions***

**Stacey D. Smith**  
**University of Colorado at Boulder**



Changes in flower color are among the most common evolutionary transitions in angiosperms and are rapidly becoming among the best understood at the genetic level. Focusing on one class of flower pigments, the anthocyanins, I will discuss the genetic mechanisms that underlie the evolution of novel colors. This growing body of literature suggests that the mutations involved in color transitions are a highly predictable subset of the range of possible mutations. I will describe ongoing work from my lab that aims to formally test this predictability by comparing segregating flower color variation within populations to fixed differences between species. Finally, I will consider the ecological triggers for these flower color shifts and, in particular, evidence from our system for competition among species driving color divergence.

## ***Comparative genomics and the origin of phenotypic novelty in birds***

**Scott V. Edwards**  
**Harvard University**



With the increasing availability of whole genomes of diverse species, phylogeneticists are now able not only to amass hundreds of loci for resolving the history of life, but also attach functions to those loci to better understand links between genotype and phenotype. Here I will present our efforts to understand feedbacks between genome history, genome function and phenotypic evolution using phylogenetics of birds, by identifying genomic regions arising coincidentally with the trait of interest and by exploiting phenotypic convergence. We first use statistical approaches to determine whether genes or gene regulation underlie the origin of feathers. Using over 600,000 non-coding elements variably conserved across vertebrates, we find that highest coincidence with feather origins comes from non-coding regulatory regions, which accumulate at higher-than-expected rates near feather genes in the avian as well as in the amniote ancestor. We then study the genomic basis of flightlessness in birds, using ten new high-quality genomes from ratites and tinamous (Palaeognathae). Analyses so far suggest no role for genome-wide convergence at the proteome level but some signal for adaptive evolution of developmental genes along convergent lineages leading to flightlessness. Together these studies illustrate two ways in which comparative genomics can provide a deeper understanding of evolutionary processes in non-model vertebrates.