

# ECOLOGICAL GENOMICS

# Symposium

## Poster Invited Speaker Abstracts

October 28-30, 2016 · Marriott Country Club Plaza · Kansas City, Missouri

### Genome-scale data reveals that endemic *Poecilia* populations from small sulfidic springs are more diverse and less inbred than populations undergoing range reduction

**Brown, Anthony P.**; Greenway, Ryan; Morgan, Samuel; Quackenbush, Corey R.; Giordani, Luca; Arias-Rodriguez, Lenin; Tobler, Michael; Kelley, Joanna L.

Washington State University, School of Biological Sciences (AB); Kansas State University, Division of Biology (RG); Kansas State University, Division of Biology (SM); Washington State University, School of Biological Sciences (CQ); SAGEA Centro di Saggio S.r.l. Via San Sudario, Italy (LG); División Académica de Ciencias Biológicas, Universidad Juárez Autónoma de Tabasco (UJAT) (LAR); Kansas State University, Division of Biology (MT); Washington State University, School of Biological Sciences (JK)

Populations with limited ranges can be highly vulnerable to changes in their environment and are, thus, of high conservation concern, but it is unclear whether populations with naturally small ranges are more robust to environmental change than populations that have experienced artificial range reductions. Populations that experience human-induced range reductions are often highly inbred and lack genetic diversity, but it is unknown whether this is also the case in populations with naturally small ranges of suitable habitat. The fishes *Poecilia sulphuraria* and *Poecilia thermalis*, which are endemic to small hydrogen sulfide rich springs in southern Mexico, are examples of such populations with inherently small habitats. Land-use in southern Mexico is changing from livestock grazing to palm plantations. As the habitat is increasingly altered, it is important to understand how susceptible and genetically connected these populations are to inform species conservation and land management. We used geometric morphometric and genotyping-by-sequencing approaches to quantify phenotypic and genetic variation within and among two populations of *P. sulphuraria* and one population of *P. thermalis*. Principal component analyses revealed phenotypic and genetic differences among the populations, though the two *P. sulphuraria* populations were more both phenotypically and genetically similar to each other than to the *P. thermalis* population. Analyses of genetic structure as well as a maximum likelihood bifurcating tree also supported this relationship. Evidence for inbreeding was low compared to populations that have undergone habitat reduction. The genotyping-by-sequencing data was also used to infer the demographic history of these populations to obtain estimates for effective population sizes and migration rates. Effective population sizes were generally large given the small habitats these populations reside in. Non-zero migration was inferred in every direction among the populations; the greatest migration rate was from one *P. sulphuraria* population to the downstream population. These migration rates, however, have not prevented the populations from becoming phenotypically and genetically distinct. Overall, our results imply that these three endemic extremophile populations should each be considered a separate conservation unit. Additionally, this study suggests that populations in naturally small habitats generally have lower rates of inbreeding and higher genetic diversity than populations that have undergone a range reduction, and therefore may be better equipped to handle environmental perturbations.

## **Unprecedented Eukaryotic Gut Microbiome Diversity within Long-Tailed Macaques (*Macaca fascicularis*) in Southeast Asia**

Hollocher, Hope and Wilcox, Justin J.S.

University of Notre Dame, Department of Biological Sciences (HH); University of Norte Dame, Department of Biological Sciences (JW).

The majority of eukaryotes have been suggested to live on or in other hosts, but the diversity and ecology of these symbiotic eukaryotes remains consummately uncharacterized, despite unprecedented contemporary interest in prokaryotic microbiomes. Key ecological roles played by eukaryotes in free-living systems and the ubiquity of parasitism, commensalism, and mutualism in eukaryotes suggest that symbiotic eukaryotes may make important contributions to host-associated communities. While previous studies on the host-associated eukaryotic communities of vertebrates have reported low levels of diversity relative to both sympatric prokaryotic and free-living eukaryotic communities, these findings may be more indicative of differences in the methodologies used to characterize these communities than they are of actual ecological differences between these biological systems. To assess the potential for such hidden diversity within guts of non-human primates, we utilize a novel Illumina sequencing approach to characterize eukaryotic diversity within the feces of wild long-tailed macaques (*Macaca fascicularis*) on two islands in southeast Asia: Singapore and Bali, Indonesia. We report substantially higher levels of eukaryotic diversity than previously reported from the feces of primates. All five super-groups of eukaryotic life were represented, and several taxonomic groups were found to be common across all samples, suggesting the existence of a core eukaryotic community with the capacity to perform consistent ecological functions within these macaque hosts. Despite these commonalities, differences in eukaryotic gut assemblages were also detected that could be attributed to differences in host geography and diet. Our results are discussed within the context of how ecological guilds operating in the gut of macaques can drive community assemblage of symbiotic eukaryotes.

## **Coupling transcriptomics with hormone manipulations to discover the molecular mechanisms underlying aphid phenotypic plasticity**

Brisson, Jenn; Vellichirammal, Neetha; Gupta, Purba

University of Rochester, Department of Biology (JB); University of Nebraska (NV); University of Rochester (PG)

Phenotypic plasticity is a key life history strategy used by many plants and animals living in heterogeneous environments. A multitude of studies have investigated the costs and limits of plasticity, as well as the conditions under which it evolves. Much less well understood are the molecular genetic mechanisms that enable an organism to sense its environment and respond in a plastic manner. The pea aphid wing polyphenism is a compelling laboratory model to study these mechanisms. In this polyphenism, environmental stressors like high density cause asexual, viviparous adult female aphids to change the development of their embryos from wingless to winged morphs. Here we describe how analysis of genome-level transcriptome differences between aphids producing winged or wingless offspring implicated the importance of the hormone ecdysone. As predicted by that study, we found that injection of ecdysone or its analog caused a decreased production of winged offspring, while knockdown of the ecdysone receptor using RNAi or treatment with an ecdysone receptor antagonist resulted in an increased production of winged offspring. Our results demonstrate that ecdysone plays a causative role in the regulation of the proportion of winged offspring produced in response to crowding in this polyphenism. Our results also show that an environmentally regulated maternal hormone can mediate phenotype production in the next generation and thus provide significant insight in the molecular mechanisms underlying the functioning of transgenerational phenotypic plasticity.

## **Cavefish evolution as a natural model for insulin resistance**

**Rohner, Nicolas;** Aspiras, Ariel; Tabin, Cliff

Stowers Institute for Medical Research (NR); Harvard Medical School (AA); Harvard Medical School (CT)

Understanding the genetic basis of adaptation has broad implications not only for a basic understanding of evolution, but also for human pathologies given that many human diseases are a consequence of mis-adaptation to modern societies. The emerging model system *Astyanax mexicanus* has become an important fish species to address adaptation to extreme environments due to its unique ecology and the availability of genetic tools and genomic resources.

Cave environments are typically dark and as a consequence nutrient deprived. We have previously shown that cavefish acquired impressive adaptations such as hyperphagia (increased appetite), starvation resistance and altered feeding behaviors to cope with these conditions. Here, we have focused on the fatty livers and symptoms reminiscent of diabetes these fish develop. Interestingly, we detected only very low insulin levels in cavefish (compared to surface fish) partially due to lower numbers of beta-insulin producing cells in the pancreas. In addition, cavefish display strong insulin resistance when administered with ectopic insulin. Despite the consequential elevated and highly fluctuating blood glucose levels, cavefish live long and healthy lives, probing the question whether they have acquired mechanisms allowing them to cope with extreme nutritional levels.

Taking advantage of the newly available genome of *Astyanax mexicanus*, we identified mutations in the Insulin receptor of cavefish most likely responsible for the observed insulin resistant phenotype. Importantly, the same mutations were found in cases of Type-II diabetic patients in human populations. We additionally present strong genetic data that suggest that cavefish are inherently insulin resistant as part of their strategy to acquire starvation resistance. We are currently using genome editing to functionally test these and other candidate mutations in zebrafish and cavefish itself to study in detail the molecular mechanisms underlying the adaptation of cavefish to the extreme and nutrient poor environments, thereby providing potential new insights into human health.