Genetics of Adaptation – From Spiders' Silk to Marathon Mice

Born to Run: Genotype-Phenotype Mapping and the Evolution of Locomotor Activity, **THEODORE GARLAND, JR.** (Department of Biology, University of California, Riverside, Riverside, CA 92521; tgarland@ucr.edu).

Our laboratory uses a replicated artificial selection experiment with laboratory house mice to study the coadaptation of behavior with morphology, physiology, biochemistry, and neurobiology. Beginning from a base population of 220 outbred Hsd:ICR mice, eight separate lines were created. In four lines, designated High Runner or HR, mice are bred for high voluntary wheel running on days 5&6 of a 6-day period of wheel access when young adults. Four additional lines are maintained in identical fashion, except that breeders are chosen without regard to wheel running. Each line has a minimum of 10 breeding pairs per generation, and within-family selection increases the effective population size (Ne) to ~35 per generation. All four HR lines responded to selective breeding with a rapid increase in wheel running, then reached a plateau at generation 16-28, with some variation among lines and between the sexes. Quantitative-genetic analyses using the "animal model" approach through the first 31 generations of selection indicate that additive genetic variance for wheel running remained in at least 3 of the 4 lines when they had reached an apparent selection limit. Simulation results suggest that neither phenotypic epistasis in the components of wheel running (motivation and ability for speed and/or duration) nor genetic dominance is likely to explain the maintenance of additive genetic variance, which suggests that epistatic interactions among alleles at loci that affect wheel running may be important. SNP genotyping and whole-genome sequencing are now being used to identify chromosomal regions that have been important in the response to selection.

How Fast Is Mendelian Adaptation? **MICHAEL R. ROSE[1]*, LARRY G. CABRAL[1], THOMAS T. BARTER[1], GRANT A. RUTLEDGE[1], JAMES N. KEZOS[1], MARK A. PHILLIPS[1], LAURENCE D. MUELLER[1], LEE F. GREER[1], and JOSEPH L. GRAVES, JR[2]** ([1]Department of Ecology and Evolutionary Biology, University of California, Irvine, CA 92697; [2]Joint School of Nanoscience and Nanoengineering, 2907 East Lee Street, Greensboro, North Carolina, 27401; mrrose@uci.edu).

Experimental evolution allows sustained and well-replicated selection, but in Mendelian populations problems of space and time often constrain the magnitude and duration of selection experiments. We have sustained specific selection regimes in our Drosophila laboratories for as many as 1,000 generations, among the longest well-replicated selection experiments in Mendelian evolutionary genetics. We have performed a wide variety of phenotypic assays of these long-evolved populations, covering patterns of life-history, development, phenotypic plasticity, physiological performance, morphology, and so on. Recently, we have started to employ genome-wide sequencing to characterize the genetic effects of such long-sustained selection. Moreover, we have newly imposed three of our long-standing selection regimes, in order to observe the more immediate phenotypic and genetic effects of our selection protocols. We were surprised to find that selection durations of about one-tenth that of our long-standing selection regimes were sufficient to achieve much of the phenotypic and genome-wide differentiation that longer-term selection produced. We will illustrate this pattern using life-history, developmental, and physiological phenotypes as well as genome-wide single-nucleotide polymorphisms.

Molecular Evolution of Spider Silk: Genetics of Functional Repetitive DNA, **CHERYL Y. HAYASHI** (Department of Biology, University of California, Riverside, CA 92521; cheryl.hayashi@ucr.edu).

While silk production has arisen numerous times within Arthropoda, spiders (Araneae) are renowned for their unsurpassed reliance on silk for critical ecological functions, including reproduction, prey capture, predator avoidance, and aerial dispersal. Some of the most spectacular aspects of spider biology are the extensive innovations in silk use that have evolved over the past 300 million years. All spiders possess multiple silk glands, and in the majority of species, the silk glands are differentiated into distinct types, with each type secreting a task-specific fiber or adhesive. Fine-tuned by natural selection, spider silks are remarkable, high performance materials that compare favorably with, and in some cases exceed, the best manmade fibers in terms of strength and toughness. Spider silks are made almost entirely of proteins, with the overwhelming majority of proteins encoded by the spidroin multi-gene family (spidroin is a contraction of "spider fibroin"). Spidroins are enormous molecules (often >250kDa). A spidroin monomer is thousands of amino acids in length, over 90% of which is constructed from tandemly-arranged repeats, and monomers dynamically interconnect to form fibers. Paralogs of the spidroin gene family can dramatically differ from each other in the length and amino acid sequence of their constituent repeat units. Furthermore, attributes of the repeat units are functionally linked to the extraordinary mechanical properties of spider silks. Gene cloning has revealed that spidroin genes contain vast arrays of minisatellite-like nucleotide sequences and insights regarding the molecular evolutionary consequences of functional, highly repetitive DNA will be presented.

Molecular Evolution of Tooth Genes in Toothless Vertebrates: Deciphering Evolutionary History from Pseudogenes, **MARK SPRINGER** (Department of Biology, University of California, Riverside, CA 92521; mark.springer@ucr.edu).

Functional genes are maintained by both positive and negative (purifying) natural selection. In some cases, strong purifying selection has resulted in nearly identical copies of orthologous genes that diverged hundred of millions or billions of years ago. By contrast, inactivated copies of formerly functional genes (pseudogenes) evolve in the absence of purifying selection, rapidly accumulate substitutions and frameshift mutations, and in some cases are excised from the genome. Importantly, pseudogenes retain signatures of their former functional history and inactivation times. Methods based on shared frameshift mutations, rates of frameshift mutation, and dN/dS ratios can be used to reconstruct patterns of evolutionary change, and to predict the occurrence of morphological transitions in the fossil record. Edentulism, or the absence of teeth, has evolved on multiple occasions in vertebrates. Multiple independent iterations of tooth loss, the occurrence of tooth-specific genes, and the hardness of bones and teeth, make edentulism a model system for integrating data from "dead genes" with the fossil record. Here, we employ the pseudogenic remnants of several tooth-specific genes (*ENAM*, *AMEL*, *AMBN*, *MMP20*) with information from the fossil record to reconstruct patterns of

tooth loss in several clades of edentulous vertebrates including baleen whales, pangolins, and the extinct Steller's sea cow, which was extirpated in the 18th century. In every case, molecular and fossil data are concordant, and together combine to yield more synthetic perspectives on macroevolutionary transitions within Vertebrata than would be possible with only genomics or fossil data.

Genomics of Convergently and Experimentally Evolving Populations of Guppies (*Poecilia reticulata*). **BONNIE A. FRASER[1]*, AXEL KUNSTER[1], DAVID N. REZNICK[2], CHRISTINE DREYER[1], and DETLEF WEIGEL[1]** ([1]Department of Molecular Biology, Max Planck Institute for Developmental Biology, Spemannstrasse 37, 72076, Tübingen, Germany; [2]Department of Biology, University of California at Riverside, Riverside, California, 92521, USA; bonnie.fraser@tuebingen.mpg.de).

Convergent evolution represents one of the best lines of evidence for adaptation but there are few cases where we know how convergent evolution of phenotypes is reflected at the genetic level. Guppies inhabiting the northern mountain range of Trinidad are a classic example of convergent evolution, where adaptation to low or high predation environments has been found for a variety of phenotypes. This system offers advantages over other convergently evolving species because their natural history facilitates long-term experimental studies in nature; researchers have transplanted fish from high predation sites, to areas without guppies or predators. We used genome scans of guppies from natural high and low predation populations, and from experimentally established populations to examine whether convergent evolution occurs at the genome level. We used population genetic modeling approaches to reconstruct the demographic history and migration among sampled populations. Surprisingly, we found that naturally colonized low predation populations showed signatures of population growth since colonization, while introduction populations showed signatures of decrease, consistent with recent natural selection. We found only a small number of regions across the genome that showed signatures of selection in all natural populations. However, the two experimental populations shared many genomic regions with signatures of selection, suggesting convergent evolution in these populations. Our results indicate that identifying the signature of convergent evolution at the genome level requires sampling at the appropriate timescale or from populations colonized with high genetic variation; otherwise neutral processes or population-specific selective forces may have a larger effect than convergent evolution.

The Genetics of Floral Adaptation: Flower Color, Shape and Organ Identity, **SCOTT A. HODGES*, NATHAN J. DERIEG, and EVANGELINE S. BALLERINI** (Department of Ecology, Evolution and Marine Biology, University of California, Santa Barbara, CA 93106; hodges@lifesci.ucsb.edu).

The columbine genus, *Aquilegia*, is known for its remarkable diversity of floral forms, with species differing across a suite of traits related to pollinator interactions. Adaptation to major classes of pollinators has generated patterns of phenotypic divergence and convergence. For example, independent shifts from bee to hummingbird, and hummingbird to hawkmoth pollination consistently involve increases in petal nectar-spur length matching the tongue length of the new pollinator. Shifts in flower color are similarly predictable and repeated. We are using whole genome and whole transcriptome sequencing to study the molecular genetic basis of these adaptive shifts. Sequencing of floral transcriptomes from species representing all of the color shifts in North American *Aquilegia* reveals frequent convergence at the gene expression level, even to the level of similar *cis*-regulatory changes, thus indicating that the genetic outcome of natural selection is repeatable. We have also used the fact that species of *Aquilegia* are interfertile to create hybrid populations for studying quantitative trait loci (QTL) underlying phenotypic differences. Because the evolution of nectar spurs appears to have been crucial for pollinator specialization, we have crossed the only spur-less columbine, *A. ecalcarata*, with a spurred species, to fine-map a single QTL of major effect. Lastly we have found a population that has lost petals due to a single gene, which will allow us to further understand how and when petals, and their spurs, are adaptations.