Faculty Search Biology Seminar



Speaker: Nathan Clark

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History repeats itself: Evolutionary convergence reveals the genetic basis of adaptation and genome-wide functional networks



Wednesday, February 07, 2018 | 12:00pm HCK 132 Refreshments at 11:45am

Life is in a constant state of revision in response to evolutionary pressures. The Clark lab identifies and characterizes these adaptive changes by studying evolutionary signatures in genes and regulatory sequences. Driving questions in the lab concern the pace, genetic mechanism, and predictability of adaptive change. Their computational

methods leverage convergent evolution, in which independent phylogenetic lineages evolve the same phenotype, to discover the genetic changes underlying specific adaptations. In marine mammals, the lab identified a large set of genes that responded to the environmental transition from land to water in similar ways for all three unrelated lineages. Evolution in these genes underlies many of the adaptive changes known for marine mammals. They also found convergent loss of function in marine mammal sensory genes and for the PON1 gene, which leaves these species vulnerable to man-made pesticides. Other results demonstrate how studying blind, subterranean mammals yields a wealth of previously unknown vision-related genes and eye-specific cis-regulatory regions, which are proving to be clinically valuable. Finally, a methodological extension, named Evolutionary Rate Covariation (ERC), allows us to infer novel functional relationships between genes and thereby build gene networks. They have applied ERC to discover new, experimentally validated interactions for yeast transport proteins and *Drosophila* reproductive pathways. Overall, molecular patterns left by adaptation and convergence can reveal important phenotypic changes in many biological systems. When examined as a whole, these studies allow us to probe the constraints on genetic networks and the pace of adaptive evolution in general.

Seminar Speaker Hosts: Sharlene Santana