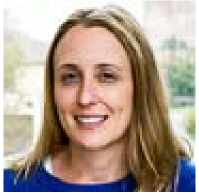
Genome Sciences Seminar

Wednesday, 2.19.20 | 3:30 | Foege Auditorium



Dr. Suzanne McGaugh

Assistant Professor
University of Minnesota

“Little blind cavefish lead to big evolutionary insights”

In the McGaugh Lab, we focus on two main topics. Some of the most fundamental biological questions involve how, why, and how fast organisms can adapt to new environments and whether evolution would proceed down the same path if repeated in an independent event. Cases of repeated evolution offer a window into understanding whether certain types of genetic variants are more likely than others to consistently contribute to evolutionary change. For this work, we interrogate genomes for signatures left by local adaptation in cavefish. Cavefish in northern Mexico have lost their eyes and pigment and experience changes in metabolism and behavior. These changes have occurred independently in multiple cave populations. This repeated evolution offers an opportunity to understand specific characteristics of targets of selection that are repeatedly responsible for phenotypic change.

Another main topic we investigate is how recombination shapes genomes. Variation in recombination rates can produce differences in effective population size experienced by different parts of the genome. In part, this translates to the observation that in regions with high recombination, selection is more efficient than in regions with low recombination. This relationship between recombination and selection shapes nucleotide diversity within species across a wide range of taxa, and recombination can have substantial impacts on genomic features such as GC content and indel distributions. Recombination rate, however, is often measured on a very broad scale across a species’ genome, though this vastly underestimates the variation seen between sexes, between chromosomes, even within chromosomes across several kilobases, and across different environments. Thus, we are uncovering the causes and implications of recombination rate differences in ecological model species.

Lastly, our lab participates in large-scale collaborative projects, mostly investigating population genomics, conservation genetics, and molecular evolution in vertebrates.

https://sites.google.com/view/mcgaughlab/

Refreshments served outside the Auditorium at 3:20pm
Questions? Contact Brian Giebel at bgiebel@uw.edu or visit the Seminar website at http://www.gs.washington.edu/news/seminars.htm