Department of Biological Sciences Seminar Blog

Seminar Date: 2/17/17

Speaker: Dr. Vaughn Cooper, University of Pittsburgh

Title: *"Why mutation rates vary among species and within genomes."*

LOCATION MATTERS: THE PRESERVATION OF IMPORTANT BACTERIAL GENES IN RAPIDLY MUTATING CHROMOSOMES

By: Heather Allen (Biology PhD Student)

Dr. Vaughn Cooper is a relatively recent addition to the University of Pittsburgh, having joined the Department of Microbiology and Molecular Genetics in the fall of 2015 from the University of New Hampshire. His lab studies "evolution in action" by looking at adaptations of different bacterial populations, especially in the formation of biofilms and the development of multicellularity in bacterial communities. Although Dr. Cooper often presents his research in the area of biofilms, he was excited to discuss his work on the differential evolution rate of genome regions instead. The overall goal of studying differential mutation rates is to be able to predict what causes these mutations and how they happen. Understanding this evolution of bacterial genomes will hopefully allow for better treatment of the diseases they cause as well as give us a new angle to understand evolution.

After meeting Dr. Cooper over lunch, it was no surprise that his dynamic personality carried over into his talk. Though I am not usually much of a microbiology person who gets excited about bacteria, it was hard not to get caught up in the excitement he exuded as he discussed the differential mutation rates across species of bacteria and even within bacteria but across chromosomes. His work is centered around performing evolutionary experiments, such as mutation accumulation, in different strains of bacteria with multiple chromosomes and

comparing the mutation rates between strains. Mutation accumulation experiments involve growing bacteria and allowing them to mutate and evolve, selecting the new mutants and transferring them to new media in order to allow them to grow and mutate again. This process is carried out repeatedly until all mutations are exhausted and the bacteria ceases to generate new mutations. Each new mutant can then be sequenced in order to identify the specific mutations gained between each step. I am no stranger to the tedium of bacterial evolution experiments, as I have spent my spring rotation project here at Duquesne doing the exact same thing! Though I haven't *quite* reached the stage where I carry out mutation accumulation experiments for multiple bacterial strains and sequence the genome of every one of the hundreds of mutants I generate and compare them yet, of course.

Although new to me, it is already well known that in bacterial species with multiple chromosomes, the primary chromosome is larger and carries most of the essential genes that are well conserved whereas the secondary one is smaller and contains fewer conserved genes. Additionally, replication is coordinated so that both chromosomes terminate replication at the same time, meaning that replication of the secondary chromosome is initiated after the initiation of the primary chromosome. It turns out that 'late replicated' genes in either chromosome mutate more rapidly, whereas ones closer to the origin of replication are better preserved. It seems that the genes closer to the origin are among the most vital to cell survival and proliferation, perhaps explaining their tendency to be so well conserved. Dr. Cooper's hope was to discover if there were chromosomal biases between primary and secondary chromosomes in mutation rates, and even if there was regional variation of mutation rates within chromosomes.

The mutation accumulation project found that not only do mutation rates vary across the three different species tested (*Burkholderia cenocepacia, Vibrio cholerae, and Vibrio fischeri*), but it also varies

between chromosomes within the same species. Evidence suggested that mutation rates may be periodic- the mutations seemed to happen in the same spots on either side of the bi-directionally replicating circular chromosome. Furthermore, the secondary chromosomes showed the *same* pattern of periodic mutations. What these periodic mutation rates mean, though, is not yet clear. Secondary chromosomes as a whole have a much higher rate of mutation, but yet again the reason is not solidly defined. Perhaps secondary chromosomes are predisposed to evolve more quickly because they contain genes that naturally evolve more quickly (i.e. fewer housekeeping genes). Or maybe they evolve more quickly because simply because there is a fluctuation in either fidelity or repair related to replication timing. Either way, it is obvious that location matters: different genome regions evolve at different rates, and it is likely that genes are competing evolutionarily for optimal regions in order to be highly expressed and avoid mutations.

Mutation rates among chromosomes and adaptations in biofilms are not Dr. Cooper's only scientific interests, though. In speaking to him both at lunch and at the social after seminar, his true passion, it seemed, is his community outreach program, Evolving STEM. The program involves using bacteria to teach evolutionary biology in high schools. In the course of just over a week, high schoolers are able to carry out a bacterial evolution experiment that shows observable evolution happening in real time. Dr. Cooper's program not only introduces high schoolers to performing real science, but it has also been shown to improve test scores assessing their understanding evolution. Doing great science and publishing in high impact journals is all well and good, but I feel like being a good scientist now days requires more. Communicating your science is important, yes, but even more important is using your science to make a difference, whether it's working to educate a scientifically inexperienced public, lobbying to politicians responsible for making laws based on scientific knowledge,

or bringing the excitement of science and discovery to students and encouraging them start thinking scientifically.