Robert May

Laidlaw Scholars Research Project

A microbiome is a community of bacteria, fungi, and other microorganisms that behaves like a miniature ecosystem: each member fills certain ecological niches and interacts with other members in ways that can drive selection and evolution. Microbiomes thrive in all environments that harbor life on Earth, including many of practical interest such as agricultural soils, the sites of wound infections, and the inside of our digestive systems. One diverse genus of bacteria that features prominently in many microbial communities of interest is *Pseudomonas*. Some members of this genus have been found in freshwater and soil, while others form commensal relationships in plant microbiomes, and others still cause infections in insects, animals, and humans[1]. To better understand the roles that *Pseudomonas* species play in these relevant systems, it is essential to study the dynamics of the interactions between the microorganisms that populate these microbiomes.

Most naturally-occurring microbiomes are incredibly complex (the gut microbiome, for example, harbors hundreds of species), making it difficult to study the interactions of select species in their native microbiome or replicate the conditions of the microbiome experimentally[2]. One solution to this obstacle is to study interactions involving fewer, but similar species in easily reproducible model systems[3]. The Wolfe Lab, where I began conducting research in the fall of 2020, uses fermented foods like cheese rinds as such model systems. Considering the ubiquity of the genus *Pseudomonas*, it is unsurprising that several species of these bacteria can grow on cheese rinds, though their role in this environment has yet to be characterized extensively. Previously, I have analyzed the genomes of four strains of *Pseudomonas fluorescens* and two strains of *Pseudomonas fragi* to search for genetic components that could indicate how the strains would interact with other microbes, including bacteria and fungi, in the cheese rind microbiome. The analysis revealed species-level variation in the proportion of genes involved in limiting resource acquisition, antibacterial activity, and antifungal activity in all of the strains.

In my Laidlaw Scholars research project, I will further investigate these results experimentally to answer the following question: How does *Pseudomonas* gene expression change when grown alongside other microbes commonly found in cheese rinds? To address this question, I will use a transcriptomic profiling tool called RNA-sequencing to quantify gene expression levels of *Pseudomonas* species grown alone vs. in pairwise assays with other cheese-residing bacteria and fungi. I will also run physiological assays to identify phenotypic changes experienced by *Pseudomonas* associated with the changes in gene expression. These experiments will show how *Pseudomonas* genetic activity (which represents all of the proteins produced, including those used to interact with the environment) changes in response to neighboring microbes in the cheese rind model, which may shed light on the roles of *Pseudomonas* in other microbiomes as well.

References:

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3. Wolfe BE, Button JE, Santarelli M, Dutton RJ. Cheese rind communities provide tractable systems for in situ and in vitro studies of microbial diversity. Cell. 2014 Jul 17;158(2):422-433. doi: 10.1016/j.cell.2014.05.041.