

Horizontal gene transfer in soil microbial communities

Mentors: Heather Kittredge (PhD student)
Dr. Sarah Evans (Faculty Microbial Ecology Lab)

Project Description:

It is estimated that one gram of soil harbors 10,000 to 50,000 *different species* of microorganisms (i.e., bacteria and fungi), but it is unclear how these different species contribute to ecosystem processes such as plant growth, decomposition or CO₂ emissions. Understanding these processes is especially important as rates of environmental change may exceed the capacity for microbes to adapt. In the face of climate change, many microbial-mediated ecosystem services may be lost, unless microbes can quickly evolve to survive in new environments.

It is common for microbial ecologists (often in the Evans Lab) to study the species of microbes that live in a particular environment, as changes in species composition are often associated with a response to climate change. Microbial genomes are very complex though, and the overall function of a microbe is questionably captured by characterizing it as a particular species. For example, in a comparison of pathogenic and non-pathogenic *Escherichia coli*, only about 40% of protein coding genes are the same. So while many studies show that microbial community composition can be a good predictor of changes in community function, many studies also find that changes in function are not accompanied with changes in species composition. This is in part due to the ability to swap genes between and within different microbial species through a process called horizontal gene transfer (HGT). This unique mechanism is the focus of my research and allows microorganisms to change their functional capabilities without necessarily changing how they are defined as a species. In soil microbial communities a likely mechanism of HGT is transformation, or the uptake of free DNA—called extracellular or eDNA—that is then combined into the bacterial genome. In the face of environmental change, disturbances cause the breakdown of cell membranes which then contributes to pools of eDNA, providing the necessary ingredients for transformation to occur in soils.

My current research focuses on the transformation of genes that give bacteria the ability to fix atmospheric nitrogen (N₂) into ammonia (NH₃). Studying the movement of nitrogen (N) fixation genes has practical applications, in that fixing nitrogen can increase microbial survival when nitrogen is unavailable and offers a valuable ecosystem service as N often limits crop and terrestrial plant productivity. This summer I plan to set up soil mesocosms in order to track the prevalence of gene transfer, and identify the variety of species that have the ability to pick up DNA in the complex soil environment. ***The project will focus primarily on lab work, specifically capitalizing on genomic and molecular techniques to analyze the ecological factors that affect rates of horizontal gene transfer.***