

PROJECT SUMMARY

I mentor undergraduate biology research students in microbial diversity by combining field studies in Yellowstone National Park with methods in molecular biology. The goal of this research is to identify new species of bacteria from hot spring communities using biological molecules. Specifically, we are characterizing what we hypothesize are novel relatives of a known bacterium called Heliothrix. To date, Heliothrix has only been isolated from hot spring communities in Oregon. In 1983, Heliothrix-like bacteria were first discovered in a hot spring community from Yellowstone; as an undergraduate in 1989, I traveled to Yellowstone and characterized the habitat, pigments, cell structure, and metabolism of this novel organism. While its habitat and metabolism were virtually identical to those of Heliothrix, the Yellowstone isolate displayed distinctive pigment chemistry and cell structures. Ultimately, the identification of most new microorganisms relies on DNA sequence analysis, a method that I, as an undergraduate, could not perform due to lack of equipment. After earning my Ph.D. in microbiology, I established my undergraduate laboratory with the intent of training students in molecular methods while maintaining that sense of discovery and connection with the environment in the form of microbial field research in Yellowstone. For two summers, I have had the privilege of leading small groups of undergraduates on field research trips to Yellowstone. The goal of each trip is to thoroughly characterize, document, and map new habitats for Heliothrix-like Yellowstone variants. Teams hike to remote and/or off-trail locations and perform habitat analysis (mapping using global positioning systems, measuring communities with pH and temperature meters, and recording data in formal notebooks). We collect bacterial samples from sites that display Heliothrix-like communities based on the above criteria. To date, we have identified over twelve sites, each harboring what appear to be distinct Heliothrix-like variants. After field trips, I and one or two research students analyze samples using microscopy, pigment chemistry/spectroscopy, and, finally, DNA methods. Students learn how to extract DNA from environmental samples, amplify and clone appropriate identification genes (16S rRNA genes), determine the DNA sequence of these genes, and, finally, submit sequences to national internet-based databases as a means to determine the relationship between each "unknown" isolate and all known DNA sequences. The questions we are addressing in this project are: (1) What is the relationship between each Yellowstone variant and Heliothrix (Are they the same genus? species?); (2) What is the relationship between different Yellowstone variants? (Does each represent a unique genus? species?); and (3) What is the biodiversity and biogeography of Heliothrix-like organisms in Yellowstone.