

NON -TECHNICAL ABSTRACT:

We are currently experiencing incredibly high extinction rates at the hand of human activities. As a result, this decreased biodiversity has profound negative effects on ecosystem functioning and the California Vernal Pool Ecosystem (CPVE) is no exception. Vernal pools are temporary wetlands of great conservation concern because of high habitat loss and their support of high levels of biodiversity, including invertebrates, vertebrates, and plants, many of which are threatened or endangered species. Several studies focus on cataloging and understanding how plants and small invertebrates contribute to the ecology of the pool; however, to date there are no studies which document the bacterial contributions to biodiversity in this system. *Bacteria* are among the oldest life forms and are the most populous organisms on the planet with an estimated population of roughly 4×10^{30} - 6×10^{30} cells. It is estimated that approximately 0.1% of microbes can be grown in the laboratory using standard microbiological methods. It has been only within the last decade that scientists have developed methods, such as metagenomics, to glimpse into the vast diversity of the non-culturable members of the community. Metagenomics allows for the genetic analysis of microbes in an environment without the need to grow microbes on traditional laboratory media. Our goal with this SEED project is to catalog and assess the contribution *Bacteria* have in this understudied ecosystem using both traditional microbiological and metagenomic techniques. Through this study we propose to collect data to count the bacterial populations, determine the identity of *Bacteria* and understand the metabolic contribution of these bacteria to the CPVE. Collectively, data acquired during this project will add to the increasing body of knowledge about the diversity organisms that inhabit this unique ecosystem, and will contribute to the larger understanding of bacterial diversity on the planet.