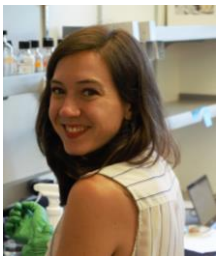
2017 Kathleen L. Miller Fellow

Amelia McKitterick, UC Berkeley PhD Candidate in Plant and Microbial Biology, Seed Lab



Amelia McKitterick is a graduate student in UC Berkeley's Plant and Microbiology program. Amelia received a BA in Biology from Vassar College and an MPH in Hospital and Molecular Epidemiology from the University of Michigan, School of Public Health, where she investigated DNA repair in Acinetobacter baumannii. She is currently investigating the activation of an anti-phage element in epidemic Vibrio cholerae in Professor Kimberley Seed's lab.

Fellowship Proposal

Waterborne bacterial pathogens, such as Vibrio cholerae, the causative agent of the diarrheal disease cholera, are a constant threat to public health, and represent a significant burden on the health systems of countries in which they are endemic. Although cholera is largely absent in developed countries, recent outbreaks in Yemen and Haiti highlight how devastating this disease can be in regions where infrastructure has been compromised and populations have been displaced. Cholera epidemics are hypothesized to be influenced by a variety of factors, including predation of V. cholerae by phages, viruses that prey on bacteria and require bacterial hosts for replication. Phages in aquatic reservoirs are co-ingested with V. cholerae. Once ingested, phages can continue to interact with their bacterial host during intestinal colonization, and they have been shown to drive the evolution of V. cholerae during cholera infection in humans.

Bacteria have evolved many mechanisms to defend against phage predation. One such mechanism in V. cholerae is a chromosomal island (referred to as a PLE) that has anti-phage activity against the predatory cholera phage ICP1. Evidence suggests that ICP1 infection of V. cholerae activates the PLE during cholera infection in humans. Importantly, ICP1 is part of an experimental phage cocktail that is currently being evaluated for prophylactic treatment of household contacts during cholera outbreaks; however, ICP1 predation of epidemic V. cholerae is limited by PLE-mediated anti-phage activity. It is therefore imperative to understand the interaction between ICP1 and PLE in a human host during cholera infection.

In order to understand this interaction, Amelia is investigating the molecular mechanisms by which the PLE is activated upon phage infection. In particular, she will use experimental genetics to identify key phage gene products that are involved in activating the V. cholerae PLE during phage infection. Then, using metagenomic analysis of cholera patient stool samples, she will examine the evolutionary trajectory of these phage gene products both within single patients and between patients during epidemics. By identifying phage genes that contribute to the molecular specificity of the interaction between ICP1 and PLE, Amelia hopes to contribute to our understanding of how phages play a significant role in the evolution of epidemic V. cholerae.