CONSIDER FOR TALK

2021 SEA Symposium Abstract

Western Carolina University

Cullowhee NC

Corresponding Faculty Member: Maria Gainey (mdgainey@email.wcu.edu)

The Search for a Novel Repressor Gene in Cluster M Bacteriophages

Erin Cafferty, Kimberly Gragg, Hannah Miller, Debbie Badillo, Kelly Witzl, Maria D Gainey

Western Carolina University (WCU) joined the SEA-PHAGES program in 2015. Over the past 6 years freshmen students at WCU have isolated and archived 100 Actinobacteriophages. In the Fall of 2016 students at WCU isolated, sequenced, and annotated the genome of a cluster M1 bacteriophage IPhane7. While infection of a bacterial cell by a bacteriophage usually results in bacterial cell death, temperate bacteriophages can enter into a long-term relationship with the bacterial cell. This occurs when the bacteriophage integrates its genome into the genome of the bacterial cell that it has infected. Once integrated into the host’s genome the bacteriophage is called a prophage, and the bacterium that contains the prophage is known as a lysogen. During lysogeny the bacteriophage represses transcription of its own genes by expression of a repressor protein. It has been shown that expression of the repressor protein can also provide the host bacterium with homotypic immunity to closely related bacteriophages. While cluster M bacteriophages have been shown to be temperate, bioinformatics has failed to reveal an obvious repressor candidate. After testing a number of potential repressor gene candidates we have excitingly identified two genes that likely play a role in regulation of cluster M lysogeny. The identity of these genes, and their roles in regulation of lysogeny will be discussed.