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8th Annual SEA-PHAGES Symposium Abstract

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A tale of Three Phages from the WPI Phamily

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Within recent years, researchers have discovered that bacteria are acquiring resistance to antibiotics, thus hindering the efficacy of antibiotic use. Researchers have since begun to shift their focus to the use of bacteriophages, known as one of the most proliferative entities in the world, as a way of defeating these antibiotic resistant species.   
 At Worcester Polytechnic Institute, a two-part exploratory laboratory experience sponsored by the SEA PHAGES initiative was pursued with the intention of aiding researchers in their quest. From the collegians research, numerous bacteriophages were identified, three of which were ultimately selected for analysis: Gompeii16, collected from Amherst Massachusetts, Bircsak, collected from Worcester Massachusetts, and Cocoaberry, collected from Charlton, Massachusetts.   
 The bacteriophage were isolated from soil samples, which were cultured using M. smegmatis bacteria, a non-pathogenic model for M. tuberculosis the pathogenic bacteria causing Tuberculosis. Once the bacteriophage were harvested, the phages were imaged using Transmission Electron Microscopy (TEM). The DNA from the bacteriophages mentioned above, Gompeii16, Bircsak, and Cocoaberry, were sequenced at the Pittsburg Bacteriophage Institute. Once sequenced, the genomes were then analyzed and fully annotated during a second seven week dry lab portion of the research experience.   
 From the annotations, two important findings were made. First, even though Gompeii16 and Bircsak were collected in different locations, these genomes were identical except for a 1 bp insertion/deletion. It was proposed that more research be done to not only confirm the mutation, but also to analyze downstream effects of it on the entire genome. The second finding was in Cocoaberry, as this genome contained a forward coding protein sequence that was observed in a reverse coding section, which was identified as a conserved sequence in the A4 cluster. The three phages and their annotations provide insight into phage function and genetics, and with further research, can aid in the hunt for a novel phage capable of being utilized in the fight against antibiotic resistant bacteria strains.