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10th Annual SEA Symposium Abstract

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Discovery and Annotation of Cluster AN Arthrobacter Phages

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Bacteriophages are viruses that infect a bacteria host, potentially leading to strategies for treating, preventing, or diagnosing bacterial infections such as tuberculosis that are resistant to conventional antibiotics. We have discovered 20 novel phages from the bacterial host *Arthrobacter* sp.ATCC 21022. The phages were collected from soil and water samples by students from various places around South Eastern PA and Southern NJ. and their genomic DNA isolated. After isolating the genomic DNA, they were photographed through the use of an electron microscope and then the DNA was sequenced. The Phages genomes were then annotated using various bioinformatics tools, such as DNA Master; Phamerator; HHpret and GeneMark to determine gene location and function. Using comparative genomics, unique characteristics of the phage’s genome were also explored. This study presents a comparison of seven bacteriophage genomes that were isolated from this research: CGermain, Hunnie, Inspire2; Dewayne; Azathoth; Copper and Ronnie. The genomes of these phages were annotated as a collaborative effort by many students and faculty.