CONSIDER FOR TALK

2022 SEA Symposium Abstract

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Night at the Symposium: The Secret of Jedediah

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Lytic bacteriophages are viruses that infect bacteria, use the bacterium’s cellular machinery to create more phages, then lyse the cell and repeat the process. Jedediah is a C1 phage that was obtained by a park in Philadelphia and was isolated on the host Mycobacterium smegmatis. After purifying the sample through enriched isolation and obtaining a concentrated phage lysate, Jedediah was discovered to be a lytic phage with the morphotype myoviridae. The large genome size contains high potential for unique proteins that can only be applied to phages in this cluster or subcluster, and by annotating the genomic sequence of Jedediah, scientific knowledge of protein functions can increase. By annotating Jedediah, scientists can learn more about C1 subcluster genes and determine the functions of each protein coded. In order to annotate Jedediah, we used the annotation program DNA Master. Data from other softwares including GeneMark, Starterator, Phamerator and BLAST was also used to supplement our annotation of the genome. Several parameters such as coding potential, ribosome binding site, and number of alignments were used to compare the start sites of the genes and to choose the best start. The first 65 genes of Jedediah’s genome were manually annotated. Once this section of Jedediah’s genome has been fully annotated, start site and gene function analysis should indicate a possibility for amino acids sequences resulting in portal proteins, major capsid proteins, acetyltransferase, and more. However, while the putative function of some gene sequences may remain unknown, it provides a potential avenue for further research. Since Jedediah belongs to a cluster with phages that are known to have a large genomic length, there are many opportunities to discover unique functions for a gene. These results are important for finding similarities in C1 phages and what uses they can bring for gene therapy or research.