DO NOT CONSIDER FOR TALK

2025 SEA Symposium Abstract

University of Southern California

Los Angeles CA

Corresponding Faculty Member: Nancy Castro (ncastro@usc.edu)

The Characterization of Phage Ichiang Virion Minor Tail Genes (FF subcluster)

Jazi Aftabi, Shivani Gangireddy, Uttej Kollu, Charli Lu, Calista Ly, Luke Metcalf, Eshaan Patnaik, Dhruv Reddy, Jacob Taylor, Harry Teng, Will Turula, Nalani Wooton, Annie Zhou, Nancy Castro

The SEA-PHAGE program aims to further our understanding of bacteriophages through the utilization of bioinformatics programs to characterize and annotate bacteriophage genes. Bacteriophages, also known simply as phages, are viruses that infect and kill target bacterial cells. These phages will inject their DNA into host bacterial cells, produce replicate phages using the host cell machinery, and finally lyse the bacterium and release the amplified virus copies. Recently, it has been shown that phages can be used in individuals that have developed antibiotic resistance. Since phages do not target human cells, there is a strong implication in using phages as a treatment option for bacterial infections. Thus, there is a significant medical, pharmaceutical, and biotechnology impact in studying phage genes and their function. The University of Southern California students have been investigating the Arthrobacter globiformis B-2979 phage Ichiang, an FF subcluster phage that has a genome length of 41,984 base pairs. The focus of our research was to study and identify the function of all 65 genes within the phage Ichiang genome. With the use of software programs such as HHPRED, NCBI BLAST, and Synteny, we were able to determine the function of most genes. The majority of the genes within the phage Ichiang genome were identiifed as hypothetical proteins. However, with the use of various bioinformatics software programs (ie. DNA Master, Staterator, Phamerator, GeneMark, Glimmer, and BLAST), we were able to predict the open reading frames (ORFs), and assign each gene a start codon. Our study focuses on the annotation of genes 19-26, respectively, which includes the virion minor tail proteins within the phage Ichiang genome. These proteins play an important role in helping to assemble the phage tail and are essential for infection of bacterial cells by allowing the phage to recognize the correct host and inject its DNA into the host cell. Herein, we will describe and show data from our genome annotation process for these minor tail phage proteins.