CONSIDER FOR TALK

8th Annual SEA-PHAGES Symposium Abstract

University of Detroit Mercy

Detroit MI

Corresponding Faculty Member: Jacob Kagey (kageyja@udmercy.edu)

Isolation and characterization of the A3 bacteriophage Kady from the host Mycobacterium smegmatis

John Sherwood, Victoria Torres, Jasmina Cunmulaj, Amber Elinsky, Gabrielle Ford, Emily Gorkiewicz, Christopher Harness, Anthony Huffman, Christina Jones, Anna Julien, Danielle Maxwell, Elizabeth Moak, Payal Patel, Madeleine Reardon, Royce Sherwood, Tamia Waller, Katherine Yacco, Stephanie Conant, Joshua Thomson, Jacob D Cagey

This past fall eight novel bacteriophage were isolated as part of the HHMI SEA-Phages course at the University of Detroit Mercy. Two phages were submitted for sequencing and genomic annotation. Here we present the genomic annotation of the A3 cluster phage, Kady. Kady was isolated from an enriched soil sample from Warren, MI using *Mycobacterium smegmatis* as the host. After isolation, Kady was identified as a lytic phage and purified using a series of streak plates. Once purified, DNA was isolated from Kady and it was sent in for sequencing at Pittsburgh Bacteriophage Institute. In total there are 50,898 base pairs in Kady’s genome. DNA Master was used to auto-annotate the genome. In Silico methods were then used to check all of these predictions as well as look for new genes in the novel genome. The DNA Master program predicted 90 genes in Kady. In total, two protein-coding genes were predicted to be false positives and deleted, and two protein genes were not auto annotated and were added to the genome. We also supported the identification of three *tRNA* genes predicted by DNA Master. After final predictions were made, gene functions were assigned to those genes where function predictions could be made using BLAST data as well as HHPred software. This project is intended to help understand the genetic makeup and evolution of bacteriophages, as well as add to a growing collection of isolated and annotated bacteriophages, especially those who may have the ability to infect Mycobacterium tuberculosis.