CONSIDER FOR TALK

8th Annual SEA-PHAGES Symposium Abstract

Virginia Tech

Blacksburg VA

Corresponding Faculty Member: Stephanie Voshell (svoshell@vt.edu)

Genomic characterization of three novel mycobacteriophages: Florean, Kingsley, and Watson

Steven D Black, Elizabeth L Humes, Allison N Castaneda, Neil T Feste, Natasha N Dziarnowski, Yichen Fu, Chase A Hale, Nicole E Holland, Gabriela I Horn, Carolyn A Mackey, Shannon E Mann, Delaney M Martin, Rebecca L Peterson, Laura C Rodman, Kendall L Schneider, Tetyana F Senchyshyn, Kacy R Thomson, Stephanie L Williams, Dawn A Wright, Faranak Zamani

Three bacteriophages, Florean, Kingsley, and Watson, were isolated and annotated by students during Virginia Tech’s inaugural year (Fall 2015- Spring 2016) in the SEA-PHAGES program. The enrichment method was used to isolate phages capable of infecting *Mycobacterium smegmatis* MC2 155 from soil samples collected in Blacksburg, Virginia. All three phages are members of Siphoviridae and produce clear plaques at 37˚C. Kingsley is a truly novel F cluster (F1 subcluster) phage with 113 putative genes and a mosaic genome matching sections of previously characterized F1 phages Velveteen, Shauna1, and Hamulus. Watson is an A cluster (A3 subcluster) phage found to contain 89 putative genes and 3 tRNAs. Florean is an A cluster (A4 subcluster) phage found to contain 88 putative genes and no tRNAs. A BLASTn search revealed that Watson and Florean are both closely related to other phages in the PhagesDB database, even having identical genome sizes to some of the matches. A closer look revealed missense mutations within some of the putative genes, indicating that Watson and Florean are not completely identical to their nearest relatives. Despite consistently utilizing the lytic cycle when incubated at 37˚C, all three phages possess an integrase gene suggesting they may actually be temperate and utilize the lysogenic cycle under different conditions.