CONSIDER FOR TALK

9th Annual SEA-PHAGES Symposium Abstract

Webster University

Webster Groves MO

Corresponding Faculty Member: Victoria Brown-Kennerly (vbrownkennerly64@webster.edu)

Kalah2: A Novel J-Cluster Actinobacteriophage

Kennedy Killion-Johnson, AbdAllah Mitchell, Jacob Marsh, Shiloh Bradley, Joshua Embry, Mason Justin, Rohan Keenoy, Taylor Kissel, Richard Le, Ryan Glasgow, Kalah Collins, Mary Preuss, Victoria Brown-Kennerly

The world of viruses is still vastly undocumented and even less well understood. Through the SEA-PHAGES program, undergraduate research students discover and characterize novel bacteriophages, which are viruses that infect bacterial cells. Using the *M. smegmatis* host bacterium and a soil sample from Webster University’s campus in St. Louis, MO, we isolated an apparently novel bacteriophage Kalah2 that harbors a 110,713 bp genome and is a J-cluster phage with 61% GC content, encoding 231 verified ORFs and one tRNA gene. We have used the Phamerator program as a starting point for a comparative genomics study. Of all known J phages, the JuicyJay draft genome is most closely related to Kalah2; of fully annotated phages, phage BAKA is the closest published relative via BLASTn comparison, and phage Wanda is most similar via a tBLASTx search. In our preliminary analysis of the first half of the Kalah2 genome, we have found several genomic regions that are rearranged or missing in Kalah2 in comparison to other fully annotated J-cluster phages.