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2021 SEA Symposium Abstract

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Sarge in Charge: A genomic annotation and analysis of FB Arthrobacteriophage Sarge

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In the Investigations and Research course at Virginia State University, senior biology majors are working to annotate the genome of bacteriophage Sarge. Sarge was isolated from host *Arthrobacter globiformis*, a Gram-positive bacterium that grows at 20-30 degrees Celsius and is most commonly found in soil. Sarge was extracted from a clay-like soil sample in 2017 in Pittsburgh, Pennsylvania by University of Pittsburgh student Audrey Jonas. It produces plaques that are small and clear in plaque assays. Sequencing of Sarge’s genome was completed in January 2021 at the Pittsburgh Bacteriophage Institute. Sarge was characterized into the FB cluster, which includes only 3 other members so far: MargaretKali, Kumotta, and Shoya. Sarge has the shortest genome in its cluster at 36,407 base pairs and an estimated 67 genes, with a GC content of 63.5%. Most of its genes are in the forward direction, with 5 in the reverse orientation. It also has 3 potential orpham genes. Like the other FB cluster phage, no tRNAs are predicted in Sarge’s genome. It is predicted that Sarge is a tailed bacteriophage, based on the morphology of other FB phage and the presence of tail genes in the Sarge genome. It is not currently known whether FB phages are generally temperate or lytic for their life cycle. Early genome analysis suggests that Sarge possesses integrase, immunity repressor, and excise genes indicative of a possible temperate lifestyle. Although it is assigned to the FB cluster, Sarge has proven to be very unique, with limited homology to other FB family members as analyzed in Phamerator and BLAST analyses. Similarities between Sarge and genes of Singleton phage and phage of various clusters have also been observed, which is interesting as many of these are viruses that infect species other than *Arthrobacter*. The Sarge genome is being annotated using PECAAN as the primary tool to access PhagesDB, NCBI BLAST, HHPRED, and Conserved Domain Database data. Early class analysis suggests that at least half of Sarge’s genes are of no known function (NKF). With the February 1st start of the spring 2021 semester at VSU, genome annotation for Sarge is on-going and expected to be completed at the end of April.