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2023 SEA Symposium Abstract

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Analysis of StubbySaigey and its Place in the Conserved C1 Cluster

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In the fall semester of 2022, the William and Mary SEAPHAGES program conducted an in-person phage discovery class with 20 freshmen eager to conduct authentic research. Using Mycobacteria smegmatis as the host, each and every student isolated their own phage and was able to carry it through to purification, DNA isolation, gel electrophoresis analysis, and transmission electron microscopy! Of the 20 phages isolated this academic year, electron microscopy revealed that one of our phages, appropriately named StubbySaigey, was a myoviridae. Despite forewarning from the instructor that annotation would be challenging given the length of the genome, the class was eager to discover the genes associated with this relatively unusual morphology (only 8% of phages belong to the C cluster). StubbySaigey is a lytic C1 phage with 266 genes and a genome of 156,308 base pairs. Our bioinformatic and annotation analysis revealed that StubbySaigey is highly conserved with other C1 phages yet shares some very unique differences as well. Bioinformatic analysis will focus on the differences within the highly conserved C cluster and a comparative genomic analysis of the C cluster genes with the genes present in the far more diverse sets of genes present in the siphoviridae.