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2025 SEA Symposium Abstract

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Investigating gene functions in the F1 cluster phage Akhila

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SUNY Old Westbury is a part of the 10th Cohort of the HHMI SEA-PHAGES program, and joined the 3rd cohort of the SEA-GENES project in 2021. The phage Akhila was isolated in Fall 2019 as part of the phage discovery component that was integrated into the honors section of Basic Biosciences I Laboratory (BS2401). As this section was switched to a remote format in Fall 2020, students in this course instead annotated Akhila’s genome as a part of the SEA-PHAGES Bioinformatics project. Akhila has a Siphoviridae morphotype with a temperate life cycle. It was sequenced at the University of Pittsburgh Bacteriophage Institute using Illumina sequencing with a shotgun coverage of 1484. It has 56,251 base pairs and 62.1% GC content. It belongs to the F1 cluster of Mycobacterium smegmatis mc2155 phages. The final annotation of this phage identified 99 genes, 37 with assigned functions, and 62 with no known function. As the GENES program serves to investigate the function of these phage genes, 86 have been amplified from phage DNA, 43 of which have assigned functions, and 53 with no known function. Of these, 68 were chemically transformed into E. coli and confirmed as the correct gene through clone verification PCR. We are currently performing cytotoxicity and defense assays in M. smegmatis to determine the role of these genes in the phage life cycle.