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2025 SEA Symposium Abstract

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Annotation of Subaru, an AZ1 Actinobacteriophage.

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Subaru is a temperate phage isolated during the Fall semester Phage Discovery SEA-PHAGES program as part of the BS2401 Basic Bio Sciences I Lab at SUNY Old Westbury. This phage, part of the AZ1 subcluster, with a Siphoviridae morphotype, was sequenced at the University of Pittsburgh using the Illumina sequencing method, which revealed a 43,471 base pair genome, with an eleven base pair 3’ overhang (CGAAGGGGCAT), 66.6% GC content. Subaru’s closest relative is another AZ1 subcluster phage, Elezi, and it exhibits unique genomic features, such as its 68 putative genes. It was isolated by Alex Thallathukunnel from a soil sample from Captain Tilly Park Playground in Jamaica, Queens, NY. Plaque morphology analysis demonstrated lytic activity, with plaques of 3.6 ± 0.55 mm in diameter and a high titer lysate of 9.8 x 1012 PFU/ml. Subaru was annotated using PECAAN, based on evidence collected by Glimmer, GeneMark, Starterator, PhageSDB, HHPRED, and NCIB. The majority of Subaru’s genes were assigned definitive functions, while approximately 20 remain hypothetical. Some of the gene functions found include portal proteins, capsid maturation protease, scaffolding proteins, major tail proteins, exonucleases, baseplate wedge proteins, and membrane proteins. Annotating phages like Subaru increases the data pool of annotated genes, which facilitates future annotations. Bacteriophage discovery and annotation have the potential to solve a wide variety of problems, from alternatives to antibiotics for treating bacterial infections to applications in food safety and biotechnology.