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2023 SEA Symposium Abstract

Harford Community College

Bel Air MD

Corresponding Faculty Member: Breonna Martin (brmartin@harford.edu)

The speed eater: analysis and genome annotation of bacteriophage Hermeonysus

Jacob Chaney, Nick Bender, Matthew Primus

Our goal in this project is to annotate the genome of the bacteriophage Hermeonysus to update a database of bacteriophages so that they can be studied and used for biotechnology and medical advancements. Phage Hermeonysus was isolated from a grass sample in Bel Air, Maryland. After the amplification of the phage and the extraction of its DNA, the phage’s genome was sequenced by the Pittsburgh Bacteriophage Institute. The phage’s genome was analyzed through DNA Master with the help of various bioinformatics tools such as Phamerator, Starterator, PhagesDB, NCBI, and HHPred. The phage’s predicted genes were compared with the genes of other phages in the cluster and the starts and functions of the genes were analyzed. Hermeonysus displayed a high rate of replication, based on how quickly its plaques cleared the plates. Upon genetic characterization, it was found to be a virulent Siphoviridae phage in the EC cluster. Hermeonysus’s genome is most similar to the genome of the phages Cranjis and Antares. The genome of Hermeonysus has 52,943 base pairs including 89 genes, all of which are forward. This annotation could help add to the SEA-PHAGE database to support advances in phage therapy.