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2024 SEA Symposium Abstract

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Genome Characterization and Annotation of Two Newly Discovered Bacteriophages MakoManhole and Penjamin420

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While many bacteria are beneficial, some can have negative impacts on humans, animals, and the environment. One avenue of exploration to combat these effects is using bacteriophages (phage). Phages are viruses that target and kill specific bacterial host cells. While approximately 1031 bacteriophages exist, 99% of them are undiscovered. In recent years, scientists have utilized phage in real-world applications including fighting antibiotic resistance, food biocontrol, bioremediation, and treating wastewater. Therefore, it is essential to genetically characterize novel bacteriophages for their use in these different bacterial control applications. The aim of this research was to annotate the genomes of newly discovered bacteriophages, MakoManhole and Penjamin420, in Nova Southeastern University’s SEA-PHAGES (Science Education Alliance – Phage Hunters Advancing Genomics and Evolutionary Science) program. Both phages infect the soil bacteria Gordonia rubripertincta NRRL B-16540, which has been known to cause catheter infections in immunocompromised individuals and has the ability to be used in bioremediation of oil spills. Using Illumina Next Generation Sequencing followed by auto-annotation using DNA Master along with manual inspection using Glimmer, GeneMark, BLAST, Starterator, HHPred, and Phamerator, it was determined that MakoManhole was from cluster DR, exhibits a genome length of 61,592 nucleotides, and is composed of ~85 genes. In contrast, Penjamin420 belongs to cluster DV, has a genome length of 67,614 nucleotides and has ~100 genes. Together, these phages are two novel bacteriophages that will be added to the Actinobacteriophage Database (https://phagesdb.org) for their possible use and contribution to various bacterial control applications.