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2025 SEA Symposium Abstract

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Genome Annotation and Bioinformatic Analysis of Mycobacteriophage Kremtemulon

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Bacteriophages are the most abundant organisms in the biosphere, and their genetic diversity is remarkable, with most genes having no known function and lacking recognizable domains. In this research collaboration, a genome annotation and analysis of phage Kremtemulon was conducted. Kremtemulon is a mycobacteriophage classified within Cluster A, Subcluster A4. Kremtemulon was discovered by students at the College of William and Mary in 2022, and genome sequencing was performed by the Pittsburgh Bacteriophage Institute via the Illumina MiSeq platform. Annotation of the sequenced genome revealed 87 genes—many of which encode proteins with no known function (NKF). Over the course of our annotation of the Kremtemulon genome, we identified a few genes that required deep investigation because their classification was not immediately evident. For instance, in the region of the genome, near the immunity repressor Kremtemulon is lacking two genes that are found in other A4 bacteriophages. This can likely be attributed to a recombination event, which results in a deletion of these two genes. Studying bacteriophage's genomes is essential in the process of understanding more of the components that are a part of phage biology. As we continue to understand more about phage biology, we can perform more in depth comparative studies between bacteriophage genomes, which is essential in further developing our understanding of phage biology. Expanding our knowledge of phage biology is crucial for the advancement of many promising developments, such as phage therapy.