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2025 SEA Symposium Abstract

Washington University in St. Louis

St. Louis MO

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Creation of the Streptomyces Bacteriophage Cluster BT: Characterization of Phages Spooks and Bimmel

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As part of the SEA-PHAGES program at Washington University in St. Louis, researchers work to discover novel bacteriophages to further develop phage databases and provide insights about microbial biodiversity. Phages Bimmel, Spooks, and Success, which infect *Streptomyces lividans*, were isolated from soil samples on Washington University’s campus. After enriched isolation and purification, high-quality genomic DNA was obtained from each phage and sent to the McDonnell Genome Institute for sequencing. Novel phages Bimmel and Spooks contain significant genetic similarities with singleton Success, isolated in 2021, resulting in the formation of the new BT cluster. Electron microscopy analysis shows Bimmel and Success having icosahedral heads and long, flexible tails, features characteristic of the Siphoviridae family. The three genomes have an average length of 56,925 bp with 61.4% GC content. Preliminary analysis determined that the phages in this cluster average 82 protein-coding genes and 8 tRNAs. They also have 61 overlapping phamilies and average 10 orphams. Software such as GeneMark, BLAST, and Starterator were used to analyze the cluster’s gene content and start codon positions for the different phages. Functional annotation was performed using HHpred and protein crystal analysis. The cluster averages 48% confirmed functions and 45% NKFs. The team is now finalizing independent studies of the genomes to better characterize these phages, and by extension, the entire BT cluster.