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2025 SEA Symposium Abstract

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Isolation and Annotation of Novel Phage Trackstar

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Bacteriophages are a proliferate group of viruses that target bacteria. Bacteriophage Trackstar was isolated from an enriched soil sample in Miami, Florida using the bacterial host *Microbacterium foliorum*. After isolation, the phage was purified and amplified. Trackstar was visualized by Transmission Electron Microscopy, revealing a siphoviridae morphology. DNA was extracted, sent to the Pittsburgh Bacteriophage Institute and sequenced on the Illumina platform. Bioinformatic analysis of the resulting genome was performed with BLAST, HHPred, and Phamerator. We used tRNAscan and ARAGORN to search for tRNA, as well as Phamerator to identify membrane domains. The goal of our study is to present a full annotation and analysis of Trackstar's minimized gene set. Trackstar’s genome is 17033 base pair long, with 19 of the 24 annotated genes having an assigned function, ranging from structural proteins that construct the viral capsid and tail fibers to regulatory proteins that help replication and host cell lysis. A programmed translational shift at gp10 was found, extending the length of the gene coding for a tail assembly chaperone protein. Additionally, the possibility of a tRNA was rejected after reviewing the evidence from the aforementioned software. Other bacteriophages like those of cluster EK and its subclusters have lengths around 50 genes, many of which have no known function. Unlike phages within other clusters, which possess a high number of hypothetical genes, Trackstar presents a compact genetic blueprint maximized for efficient infection which is an element that may be translated into new host interactions and evolutionary advantages. This compact genome is highly conserved within the EE cluster. The first 19 genes of phages in this cluster are conserved with the exception of gp 13 minor tail protein. Trackstar exhibits a smaller minor tail protein gene when compared to other phages in the same cluster. A smaller minor tail protein gene usually leads to a morphologically smaller protein. Trackstar shares this gene with other closely related phages in the EE cluster which may shed light on how this variation of the protein fits into the broader picture of phage evolution. In conclusion, we believe that Trackstar's minimized genome contains only the basic functions to maintain a stable infection cycle while also exhibiting a gene organization that optimizes its lifestyle. Trackstar supports the idea that larger genomes are not needed to support phage diversity and provides an open model for re-analyzing the minimal requirements of viral existence. Its unique economy in gene content reveals new evolutionary strategies that can help phage-directed therapy and synthetic biology applications. Antibiotic resistant infections are becoming increasingly prevalent, prompting the study of bacteriophages as a tool to fight them. Phage annotation can lead to discoveries of specific functions and proteins that can be used to accomplish this goal.