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Genome Analysis of Multiple Mycobacteriophages

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ABSTRACT

Bacteriophage are viruses that infect and kill bacteria. They can be used as treatments for antibiotic resistant bacterial infections, but more knowledge is needed about phage and how they interact with bacteria in order to develop safe and effective phage therapy treatments. This study examines the genomes of eighteen mycobacteriophage that were isolated from the environment on and surrounding Purdue University. Phage genomes were annotated using several bioinformatics software, including DNA Master, GeneMark, and PECAAN. Evidence was examined to determine the correct location within the genome and the potential function. Approximately two thousand genes were annotated in this study. A variety of functions were predicted that help mediate the interactions with bacteria, such as DNA replication and structural protein. There were also many potential proteins from that phage where the function could not be predicted. Future studies will include other methods beyond annotation to determine the function of the predicted gene products and their impact on bacteria. The outcomes from this research can help provide new knowledge in biotechnology that can ultimately lead to new therapeutic treatments for infectious diseases.

KEYWORDS

Bacteriophage, microbiology, genomics, bioinformatics, genetics