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Decoding the Secrets of Ablatia through Isolation and Characterization

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In an era of antibiotic resistance, bacteriophage research has emerged as a promising solution to this crisis. Mycobacterium smegmatis mc2 155 was the host bacterium used to isolate and characterize Phage Ablatia. During the 2024-2025 academic year, phage Ablatia was collected from an environmental sample near the Howard University campus, then was isolated, purified, and had its’ DNA extracted. Preliminary morphological and genomic analyses were then conducted to better understand Ablatia’s structure and function. Using the MiSeq platform and Illumina at Pittsburg Bacteriophage Institution, Ablatia, a circularly permuted sub cluster C1 phage, was sequenced with a genome length of 155,479 bps, 231 genes, 32 tRNAs, 1 tmRNA and a GC content of 64.7%, which is within 0.3% of the average, and has a Myoviridae morphotype. Currently, Ablatia is being annotated, utilizing programs such as PhagesDB and NCBI BLAST to compare phage sequences; GeneMark, Glimmer, and Starterator to call starts; and HHpred and DeepTMHMM to confirm function. Annotating phages and sequencing genomes assist in scientific advancement and research by identifying specific protein functions and tRNA sequences.

Key words: Mycobacteriophage, Soil, Mycobacterium smegmatis, Myoviridae