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2025 SEA Symposium Abstract

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Unveiling the Viral Mysteries of Phages Iridessa, Jesabah, and Chalmers

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Bacteriophages (phages) are viruses that infect and use the apparatus of their bacterial host to replicate. The SEA-PHAGES program at Howard University seeks to isolate bacteriophages that infect Mycobacterium smegmatis mc2 155, further developing an understanding of phage diversity, evolution, and potential medical applications. The bacteriophages Chalmers, Iridessa and Jesabah were isolated from enriched soil samples that were collected from different locations around the Howard University environment with the following coordinates (38.928472 N, 77.017694 W, 38.902556 N, 77.058333 W and 38.523806 N, 77.13 W respectively). Phages were purified, lysates were collected, and DNA was isolated for sequencing and other required experiments. Upon imaging and sequencing, Iridessa and Jesabah were classified as members of the B1 sub cluster while Chalmers was of the B3 sub cluster. Their genome sizes ranged from 68178 to 69436 bp, with a GC content between 66.4% and 67.5%. Functional annotation is currently being conducted using diverse bioinformatic tools and programs such as PhagesDB BLAST, NCBI BLAST, DeepTMHMM, and HHpred digital with a cutoff E-value of 10-4 to better understand the phage’s gene functions and peculiarities.