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2025 SEA Symposium Abstract

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Discovery and Genomic Characterization of Phages Blessjoy and Temprado.

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The purpose of the SEA-PHAGES program is to isolate a phage that will infect the host cell, Mycobacterium smegmatis mc2 155, to discover an alternative to current antibiotics. By analyzing the morphology and genome of temperate phages Blessjoy and Temprado, both of sub cluster A6, we aim to contribute to the expanding database of characterized bacteriophages. The phages were collected from soil located at the following GPS coordinates: (38.919056 N, 77.023222 W and 38° 55 '13"N 77° 00' 18" W). Phages Blessjoy and Temprado were subsequently isolated following standard protocols, and DNA was sent for sequencing and utilized for other downstream experiments. Sequencing identified both phages as members of sub cluster A6 (temperate) with genome length between 52491 and 52541bp and a GC content of 61.5%, between 99 to 102 genes and 3 tRNAs. Bioinformatic and annotation analysis is revealing that both phages share regions of conservation with other A6 phages yet also display some unique, significant differences. Bioinformatic analysis will focus on a detailed comparative analysis of both phages using the available bioinformatics tools. The information gathered from this study will help further the understanding of phage diversity and their potential applications in bacterial infection treatment.