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2024 SEA Symposium Abstract

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Comparative Genomics of F1 Bacteriophages: Decoding the Genetic information of Jinglebell and PhesterPhotato

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Bacteriophages are viruses that infect bacteria by injecting genetic material into the cell and propagating more phages. With antibiotic resistance on the rise in the past few decades, bacteriophages have become a potential candidate for treating antibiotic-resistant bacterial infections in humans. This study investigated the differences between two distinct bacteriophages in cluster F1, Jinglebell and PhesterPhotato that infect *Mycobacterium smegmatis*, a close relative of *M. tuberculosis*, a bacterium that causes antibiotic-resistant lung infections. Characterizing and understanding the possible applications of these two Mycobacterium phages have therapeutic implications. Phage characterization included isolation and propagation, electron microscopy, and an eventual genomic analysis. During isolation and direct plating, PhesterPhotato yielded significantly larger plaques compared to Jinglebell. By electron microscopy imaging, Jinglebell had distinctly larger capsid heads and longer tail lengths compared to PhesterPhotato. A dot plot analysis between Jinglebell and PhesterPhotato revealed that the beginnings of the genomes are similar in sequence, but the end halves vary greatly. Sequence alignment analysis found that Jinglebell and PhesterPhotato share 65.75% sequence similarity, indicating that these two phages are quite different. The results of this study contribute to the growing diversity of phages, and the comparative analysis sheds light on how each of these phages may have future use in the fields of medicine and biotechnology.