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A Fungi-de to Bacteriophage Strobilo

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Bacteriophages are viruses that infect bacteria and replicate within them to induce bacterial lysis. With an estimated 10E31 phages in the biosphere, they are an abundant biological agent with vast genetic diversity. Discovering and sequencing new phages assists in successfully infecting and eradicating different kinds of antibiotic-resistant bacteria. Phage Strobilo was extracted from an enriched soil sample found in Mays Landing, New Jersey, next to a *Strobilomyces strobilaceus* fungus, also known as the Old Man of the Woods. Eight rounds of purification were conducted using the bacterial host *Mycobacterium smegmatitis*, which displayed the phage’s temperate characteristics. Subsequent to the isolation of Strobilo’s DNA at Saint Joseph’s University, it was confirmed that Strobilo is a temperate phage, and it is in the siphoviridae family assigned to Subcluster K2. The phage was then manually annotated using various bioinformatics tools, including PECAAN, Phamerator, Genemark, BLAST, and The Actinobacteriophage Database, to help identify the function of each gene. Throughout this process, 94 genes were identified, of which 39 with distinct functions, 53 with no known function, and 2 were orphams. Orphams are genes that have unique genetic sequences compared to the genes of all other sequenced phages. Of the ten currently sequenced Cluster K2 phages, TM4 and ZoeJ are the known K2 phages that are able to infect another Mycobacterium—*M. tuberculosis*. Strobiol is 88.52% and 77.77% similar to TM4 and ZoeJ, respectively. If Strobilo is able to infect M. tuberculosis and become lytic, this would make Strobilo another possible candidate for bacteriophage therapy in treating multidrug-resistant tuberculosis.