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Unveiling Megsy: An Exploration of a Novel Phage Genome

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Antibiotic resistant Mycobacterium infections have mortality rates ranging from 10-48% and can be difficult to treat because of increasing antibiotic resistance. Notably, 73.3% of Mycobacterium tuberculosis strains are antibiotic resistant. Bacteriophage (phage) are viruses that can infect and kill bacteria, offering a promising avenue of treating multi-drug resistant infections through phage therapy. However, the lack of knowledge of phage genomes prevents the wide-spread use of phage therapies to treat these Mycobacterial infections. By isolating and annotating the novel phage Megsy, contributions to our understanding of the diversity of phage genomics and potential treatments of antibiotic resistant mycobacterial infections utilizing phage can be made. Megsy is a temperate, siphoviridae, cluster K1 phage that shares genomic similarities with TreyKay and CrimD phages. Megsy was isolated from soil in Orono, Maine through enriched isolation utilizing the host M. smegmatis strain mc2155. Megsy has a genome spanning 60,191 bp with a GC content of 66.8%. Of the 95 putative genes annotated, there are three orphams encoded in the right arm of the genome, which are genes that don’t have any genetic similarities to other genes found in current databases. Megsy is equipped with an HicB-like antitoxin/toxin system that contributes to the host's fitness and a WhiB family transcription factor. With the data that has been charted thus far and further exploration that will be conducted, Megsy presents an intriguing avenue to further our knowledge in phage utilized therapies.