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The Genome of Microbacterium foliorum phage Mandalorian

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Bacteriophages are viruses that infect bacteria. Microbacterium foliorum NRRL B-24224 has commonly been used as a host for bacteriophage discovery due to its relative ease of growth, short doubling time, and natural habitat. We discovered the novel M. foliorum bacteriophage Mandalorian in a compost sample in Provo, Utah, and report its isolation, sequence, and annotation. Phage Mandalorian was isolated using a direct plating method, purified, amplified, and its DNA extracted. The phage’s genome was then sequenced, allowing us to further examine genome structure and identify gene function. DNAMaster was used to annotate the genome, with Glimmer and GeneMark to analyze coding potential. BLASTp and HHPred were used to identify protein function, with Phamerator to compare the genome to other related bacteriophages. Through these methods, it was determined that Mandalorian phage is a siphovirus classified in the EA10 subcluster. Our results show that this is a lytic phage that consists of 40,407 base pairs with 63.8% GC content. Of the 63 predicted protein coding genes, 55% of them have unknown functions. Mandalorian has comparable synteny to EA10 phages Nucci and YuuY. From the data gathered, we conclude that Mandalorian has a novel genome and contributes to the information provided by continued analysis of the EA10 subcluster.