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Isolation and Genomic Summary of Bacillus megaterium phage Brahmus

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Bacteriophages are viruses that specifically target and infect bacterial cells. They have been recognized as a potential alternative to antibiotics for treating bacterial infections, especially in light of the growing problem of antibiotic resistance. In addition, their ability to infect and lyse bacterial cells as well as transfer genetic material make their contributions to bacterial evolution significant. In this study, we report the isolation and genomic characterization of a novel phage, designated as "Brahmus", which was isolated from a sewage sample in Spanish Fork. The phage infects Bacillus megaterium bacteria and was found to belong to the family Myoviridae based on its morphology and genomic features. The genome of phage Brahmus was sequenced using MySeq Illumina sequencing paired end technology and annotated using DNA Master and GeneMark programs. The genome was found to be 155,430 base pairs in length with 261 predicted open reading frames (ORFs). The ORFs encoded various proteins involved in the phage replication cycle, such as capsid and tail proteins, as well as enzymes involved in DNA replication, recombination, and repair. BLASTn analysis of the phage genome indicates 98.26% base pair similarity to another Bacillus phage BSP38, which might suggest similar phage transcriptomes and potential related mechanisms of action. In conclusion, our study provides insights into the genomic features and potential applications of a novel phage, Brahmus, which may have potential as an alternative to antibiotics for treating Bacillus megaterium infections. Further studies are needed to fully understand the mechanism of action of this phage and its potential use in clinical settings.