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Genome annotation of Cluster CS4 phage Teech

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Teech is a lytic phage with a genome size of 75,003 bp and belongs to Cluster CS, Subcluster CS4. While the exact morphotype of TEECH is unknown, Aserprocky, a phage from the same subcluster, is classified as a Siphoviridae phage.
The genome annotation of TEECH was conducted using DNA Master, NCBI BLAST, Phamerator, Starterator, GeneMark, and HHPred. Phamerator identified 97 genes, while DNA Master identified 95 genes. No tRNA genes were found within the genome. Out of the called genes, 30.5% were forward genes, while 69.5% were reverse genes. The predominant start codon was ATG (70.5%), followed by GTG (26.3%) and TTG (3.2%). The longest gene in TEECH’s genome is the tape measure protein at 9,084 bp, while the shortest gene is a membrane protein at 114 bp. No genes were added or deleted manually following BLAST analysis.
Several genes with known functions were identified within Teech, including holin, endonuclease, lysin A, lysin B, DNA polymerase III, DNA binding protein, tape measure protein, and DNA primase. These functional annotations provide insights into the molecular mechanisms underlying Teech’s lytic lifestyle.
Teech shares a high degree of similarity with other phages in Subcluster CS4, most notably Kvothe, Katyusha and Niagara, with Gene Content Similarity (GCS) of 92.87% and is most dissimilar to Vitaenoii, which has a GCS similarity of 68.8%. Teech does not share any phams with phages from different clusters.
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