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Computational Analysis of Microbacterium Phage Kevanna Genome

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Microbacterium phage Kevanna was isolated by the Howard Hughes Medical Institute in the year 2022. The bacteriophage was grown on Microbacterium foliorum NRRL B-24224 isolation host, sequenced using Illumina sequencing and revealed an approximate shotgun coverage of 3693X. It has a genome length of 17441 base pairs, G+C content of 68.4% and a 3’ sticky overhang of 9 bases. Sequence alignment carried out on NCBI BLASTn and phagesdb.org revealed high sequence identity with other phages belonging to cluster EE.  
Auto-annotation of the genome was carried out using Glimmer and GeneMark in-built predictors in DNA Master which predicted 25 protein-coding features, which was also confirmed on the RAST server. Visual inspection of the genome was done using DNA Master and Artemis, while manual inspection for start site refinement was carried out using DNA Master, Starterator, and Pharmerator. Putative functions were assigned on NCBI BLASTp, HHPred databases, and phylogenetic nucleotide identity of the cluster was generated using the Orthologous Average Nucleotide Identity Tool.  
Of the 25 manually validated protein features, 22 are forward oriented genes, while 3 are reversed oriented genes. Putative functional assignment was carried out using NCBI BLASTp and HHPred they successfully assigned putative functions to 68% of the predicted gene features with the forward oriented gene features accounting for 56% and reverse oriented genes accounting for 8% of assigned putative functions. Some of the predicted protein features include terminase, portal protein, major capsid, major tail protein, endolysin and tape measure protein.