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Discovery and Genomic Insights of Bacteriophage JessellCookie

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Bacteriophages infect and replicate within bacteria. They offer insight into novel gene functions and are a gateway to controlling bacterial populations. The study and future application of bacteriophages can improve crop yields, help fight antibiotic-resistant bacteria, and treat waste. JessellCookie is a new bacteriophage discovered in late August of 2023 from a sample in South Florida at a temperature of 30°C. The host Microbacterium foliorum NRRL B-24224 was used to isolate and purify it from an enriched soil sample. Electron Microscopy was used to study its morphology. It shows a Podoviridae morphology, less common than Siphoviridae, and it is characterized by a short non-contractile tail. The phage was sequenced using Illumina NextSeq 1000 at the Pittsburgh Bacteriophage Institute. In this study, we used bioinformatic tools and other resources such as DNA Master, PhagesDB, Phamerator, NCBI Blast, and HHpred to annotate its genome and the corresponding gene functions. Structure prediction programs (AlphaFold, I-TASSER) were used to build 3D structure models based on amino acid sequences to explore the putative function of genes 31-47. Our results show that some hypothetical proteins may encode structural proteins like the barrel, portal, adaptor, tail nozzle, and baseplate proteins. The genome is 53,947 bp long and has a total of 55 genes; 21 of them were assigned a function, while the other 34 have been classified as hypothetical proteins. JessellCookie belongs to the EK1 subcluster. A unique characteristic of JessellCookie is the presence of an orphan gene (gp28). The phage does not seem to contain any slippery sequences. In the EK cluster, a group of minor tail proteins are called consecutively for genes 34, 35, and 36. However, the third minor tail protein (gp36) is only present in ~20% of the phages within the EK1 subcluster. To understand the relationship to other phages in the cluster, a phylogeny tree was created using VICTOR, and Phamerator was used to explore gene synteny. A specific clade of bacteriophages in EK1 contains all 3 genes coding for minor tail proteins. This clade includes the following bacteriophages: JessellCookie, Miami Panther, Wesak, YellowPanda, and TinyTimothy. All phages in cluster EK2 carry three minor tail proteins in their genome but seem to belong to a different Pham than those in EK1. Bacteriophages in other EK1 clades only had two minor tail proteins annotated. This study provides a preliminary overview of some new structural proteins in Podoviridae and possible phylogenetic relations among Podoviridae bacteriophages in cluster EK1.