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2021 SEA Symposium Abstract

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Annotation of the M. foliorum specific EA1 Bacteriophage SJay

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Here we highlight the annotation of the Microbacterium phage SJay, which was discovered from an enriched soil sample in Pittsburgh, Pennsylvania, by Megan Ulbrich. The phage was isolated using the host Microbacterium foliorum. SJay is a member of cluster EA and subcluster EA1, and has a genome length of 41847 base pairs (bp). SJay has a G-C percentage of 63.5%, which is equal to other phages including Teagan, Robinson, and Martin for the12th highest percentage within the subcluster. The bioinformatic tools PECAAN, DNAMaster, Glimmer, Genemark, PhagesDB Blast, NCBI Blast, HHPred, and Phamerator were used in this study. Genome-wide and gene-focused analyses were done to identify gene coordinates and potential functions of encoded proteins. Of the 63 genes identified, 26 had putative functions based on our analysis and included many of the common structural genes. The remaining 37 coding sequences included proteins for which no known function could be determined with the bioinformatics tools used in this study. One interesting feature of SJay that will require further analysis is gene 57; the gene is unrelated to other phages in the EA1 subcluster and more closely aligns with that of five phages in the EC cluster. Another interesting feature of SJay is gene 16, as it has a unique sequence compared to others in the subcluster. We will continue our detailed analysis of these genes.