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Comparing Genomes of Mycobacteriophage Dreamcatcher and Jacksparrow

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The SEA-PHAGES program allows undergraduate students to engage in research by isolating viruses and annotating the genomes of the bacteriophages. Dreamcatcher and Jacksparrow are bacteriophages isolated using the host Mycobacterium smegmatis. These two bacteriophages were annotated during the bioinformatics section of the program during the Spring 2019 semester and were compared to determine similarities and differences between the two mycobacteriophages. Both bacteriophages are classified in the A cluster and A1 subcluster, and both have morphotypes of Siphoviridae. Annotation of Dreamcatcher’s and Jacksparrow’s genome was completed using the computer software DNA Master, Phagesdb.org, BLAST, and HHPred. After completion of the annotation of Dreamcatcher’s genome, the phage contained 97 putative genes. Annotation of Jacksparrow’s genome supported 93 putative genes. Both bacteriophages contained similar genes but each also had some unique properties.