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9th Annual SEA-PHAGES Symposium Abstract

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Isolation and Characterization of the Mycobacterium smegmatis specific, J-Cluster Mosaic Phage ThreeRngTarjay

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In the Fall of 2016 the University of Detroit Mercy SEAPHAGES students isolated 8 unique Mycobacterium smegmatis specific phage. Of these, two were sent for sequence analysis and the genome data was made available for annotation by students in the Winter semester. Here we present the purification process and genome annotation data for our cluster J phage ThreeRngTarjay. ThreeRngTarjay was isolated from a soil sample found on the campus of UDM and was seen to have a unique target-like plaque morphology suggesting alternating lytic and lysogenic life cycles of this phage. It was found that the ThreeRngTarjay genome contains 113,254 base pairs and a predicted 244 genes. T A total of four predicted genes (112, 129, 149, and 201) were identified as false positives based on criteria including contrasting transcription directions, excessive overlap with adjacent genes, a final RBS score highly diverging from zero, and a lack of coding potential delineated by the software Genemark and GLIMMER. One gene was added to the annotation due to coding potential found in gaps between genes 7 and 8 and containing predicted protein functional information. Of note was also a frameshift identified in genes 30 and 31 identified as a tail chaperone protein. After final predictions were made, gene functions were assigned to those genes where function predictions could be made using BLAST data as well as HHPred software. This project is intended to help understand the genetic makeup and evolution of mosaic bacteriophages, as well as add to a growing collection of isolated and annotated bacteriophages, especially those who may have the ability to infect Mycobacterium tuberculosis.