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Genomic Analysis of Mycobacterium phage Jeon

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During the Spring 2017 semester, students at Queensborough Community College annotated analyzed the genome of Mycobacteriophage Jeon. Jeon was discovered in 2013 by a student from Smith College in Northampton, MA. We were very grateful for the opportunity to annotate it. This phage is a member of the family Siphoviridae, and its morphology features large head and a noncontractile tail. Until recently Jeon was considered a singleton, now it is placed in the new Cluster W together with Megabear and Taptic. Megabear is also from Massachusetts and Taptic is from Pennsylvania. Taptic was submitted to the Gene Bank. Jeon has a genome with a length of 60908 bps and 86 predicted genes. 85 are protein coding sequences and one tRNA for Glycine with anti-codon tcc. We used DNA master as the major tool for annotation and performed gene analyses using BLAST, HHpred, GeneMark, Starterator, Phameror and other programs. The genome is very packed, with few long gaps and multiple instances of a few base pair overlap. The first part of the genome contains many genes with well-defined functions like helix-turn-helix DNA binding domanis, terminase, portal protein, major and minor capsids, major and minor tails, tail assembly chaperones, and tapemeasure. In the middle there are LysinA, Holin, DNA recombinase, HNH endonuclease, and WhiB family transcription factor. Towards the end of the genome, there are many very short genes with unknown functions. Another feature of Jeon’s genome is that all of the genes are in forward direction. BLAST of individual genes reviled that of the 85 protein coding regions in the genome, 79 are homologous with genes from Taptic, 4 with phages from Cluster B2, and one each with phages from Clusters F1 and P1. The segment similar to the Cluster B2 is exactly in the middle of the genome. The tRNA sequence is identical to that of Taptic. Megabear and Taptic both share 95% sequence identity with Jeon.