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Genomic Identification of Mycobacterium phage Hope4ever

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During the Spring 2018 semester, students at Queensborough Community College annotated and analyzed the genome of Mycobacterium phage Hope4ever. We were very grateful for the opportunity to adopt Hope4ever. The phage was found in 2012 by Brittany Sklenar, a student from Georgia Gwinnett College, in Lawrenceville, GA. Hope4ever was isolated from Mycobacterium smegmatis mc2155. It has a siphoviridae morphotype, characterized by a large head and a non-contractile tail. It is a temperate phage and forms plaques with bullseye pattern. Hope4ever belongs to the cluster A, subcluster A1. It has a genome with a length of 50455 bps with 86 predicted genes, all of them are protein coding sequences. Hope4ever is shorter and has fewer genes than an average A1 phage. The study of Hope4ever consisted of using bioinformatics programs such as DNA Master, GeneMarkS, HHpred, Blast, TMpred, TMHMM and other to determine homology, coding potential, gene function, open reading frames, length of the genes and possible protein structures. Cluster A is the largest cluster with 556 members, and A1 is its largest subcluster with 141 members. Thus it is not surprising that Hope4ever does not have unique genes and all of Hope4evergenes are homologous to other A1 phages except gp69 which is similar to cluster F. Unfortunately, we could not identify the function of gp69. The phage with highest protein similarity to Hope4ever is U2. On the nucleotide level Hope4ever’s closest relatives are Myorolo and Jasper, both with 97% identity. Just like all other cluster A phages Hpe4ever has first half of the genome in forward direction and the second half reversed. In front of the tapemeasure protein there is a programmed frameshift that results in two different sizes of the tail assembly chaperones. Again a feature common in A phages. We identified functions for many of the genes. Hope4ever has an immunity repressor that is found in C1 phages and some A1 phages. It also has HNH endonuclease, integrase, LysinA, LysinB, terminase, portal, minor and major capsid and many structural proteins.