CONSIDER FOR TALK

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Brown University

Providence RI

Corresponding Faculty Member: Yang Zhou (yang\_zhou@brown.edu)

Characterization of a Novel Mycobacteriophage JuicyJay and Slippery Sequences in its Genome

Hannah Blakely, Emmett  Askira, Micah  Jaffe, Christopher de Graffenried , Sarah Taylor, Yang Zhou

In this study we isolated 19 bacteriophages that infect Mycobacterium smegmatis and analyzed the genome of one of them, the novel cluster J phage JuicyJay. JuicyJay was annotated using the DNA Master Genome Annotation Software, Phamerator, and Starterator. Strong similarities were noted between JuicyJay and the bacteriophage Wanda, but manysections of the genome were more closely related to other cluster J phages. Analysis of JuicyJay's genome lead to further investigation of the J cluster, which is a relatively small and less ­studied cluster.

JuicyJay contains two unusual split genes. They were assigned Pham numbers 17400 and 17701 and are located shortly after the tape measure gene. Pham 17400 is common in all bacteriophage, but the split in the gene is rare, occurring in at least three other J cluster phage and one F1 cluster phage. The second gene is split and has a gene of a different Pham between the two pieces. Of the five phages containing the Pham, only one had the two halves in one piece. Two were missing the first half, and the rest were laid out comparably to JuicyJay. The alignment of the two halves of the gene did not lead to an ordering of the two pieces. Klein was the only other cluster J phage to share both split genes. This raises questions about the functions of the proteins coded for and how that is affected by the splitting of the genes.

Further study was undertaken to explore slippery sequences, short nucleotide sequences that result in ribosomal frameshift, producing a modified protein. This has previously been documented in the tail-assembly chaperone genes of bacteriophage. We analyzed mycobacteriophage genomes for the presence of putative slippery sequences, and determined viability of these sequences in JuicyJay.

We determined the probabilistic frequency of the slippery sequence template XXXXYYYY. This is not the typical XXXYYYZ, but is that present in the tail chaperone genes that undergo ribosomal frameshift in JuicyJay. Within the JuicyJay genome, 20 occurrences of XXXXYYYY were observed. Viability was determined through a series of indicators, including consideration of coding potential, location within ORF, and length of ORF transferred to. Four sequences were determined to have strong potential for functionality.

Through this computational project we aimed to explore slippery sequences in mycobacteriophage by developing scripts that can be utilized and expanded by others in order to do further work. Clusters C1 and D were noted among those analyzed for having far fewer such sequences than anticipated, while others closely resembled the expected rate. This variation in presence between clusters may indicate that slippery sequences take different nucleotide patterns or are employed at differential rates between phage clusters.