CONSIDER FOR TALK

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Annotation of E Cluster Phage Filch, and its Comparison to TB-infecting Singleton Phages

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A bacteriophage is a virus that infects a bacterial host cell by inserting its DNA into the host cell’s cytoplasm. The DNA will multiply within the host cell, along with the capsid and tail of the bacteriophage, killing the host cell once it’s done. Therefore, bacteriophages can be used to treat incurable bacterial infections, causing scientists to annotate bacteriophage genomes in pursuit of medical advances. For example, the bacterial host for bacteriophage Filch is *Mycobacterium smegmatis* which is genetically similar to *Mycobacterium tuberculosis*, the bacteria that causes Tuberculosis. The similarities between the bacterial host of bacteriophage Filch and *Mycobacterium tuberculosis* could lead to the possible treatment for Tuberculosis. However, even though there is a potential treatment for Tuberculosis there are still many unknowns with the bacteriophage, and its functional potential will need to be found through functionally annotating its genome. This work seeks to expand the bacteriophage database collection and increase our overall knowledge of phages and their genomes by contributing to the annotation of Filch’s genome. The phage was run through the DNA Master software when manually annotating the genome, which evaluates coding potential, Starterator information, and BLAST start results to make an informed decision on the annotation of a gene, its start site, while HHPred and Phamerator are used to determine function, by relating the bacteriophage with others in the same pham and cluster. Bacteriophage Filch is in cluster E. Cluster E has distinctive features, such as normally having 2 tRNA and having a temperate life cycle. These features are common within the cluster and within the bacteriophage Filch. The annotation of bacteriophage Filch will enable for more cluster members to be fully annotated - of which 106/130 are fully annotated. After manually annotating 55 genes of the filch genome, 10.9% of the start sites were changed based on evidence that did not support the original start site, and 73% of the 55 genes were determined to not have any known functions. The results after annotating the Filch genome were compared to the singleton mycobacterium, as it is the same cluster for *M. tuberculosis*, to establish whether these genomes present genetic similarities between the two mycobacteria.