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Genome Annotation of Mycobacteriophages ShaboiShabazz and Aubs

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Bacteriophages and bacteriophage diversity are important because of their ability to provide genetic exchange in the environment and be used in medical treatments such as phage therapy to cure (or work to cure) an array of diseases. Mycobacterium smegmatis (mc2155) was the host bacteria for phage discovery and collection of genomic DNA for sequencing. This poster describes the use of bioinformatics databases and tools, such as Pecaan, Blastp, HHpred, and TM-HMM, to annotate the genomes and to determine the protein functions of each gene in Mycobacteriophages ShaboiShabazz and Aubs. Aubs is a cluster F1 phage with a genome length of 58937 basepairs, with 107 open-reading frames, including 1 tRNA gene, and a GC content of 61.4%. ShaboiShabazz is a cluster G1 phage with a genome length of 41901 base pairs, 3’-sticky ends, 61 open-reading frames, no tRNAs, and 66.6% of genomics content. Through genome annotation, students chose the best predicted start positions for genes using the parameters including the longest open-reading frame (ORF), the best ribosome binding site score, a 1:1 BLASTp match, minimal gap/overlap, covered all Genemark-predicted coding potential, and were recommended by Genemark and Glimmer. Through functional annotation, many gene functions were identified through HHPred, BLASTp conserved domains and transmembrane predicting tools. Functional annotations are in the process of being finished, and findings will be shared.