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Genome Annotation of Novel Mycobacterium Phage TomBrady

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A bacteriophage is a virus that infects a specific host bacteria and hijacks its cellular machinery to create more copies of itself. Bacteriophage research drives new advances in molecular biology, especially phage therapy against antibiotic-resistant bacteria. Mycobacterium belongs to the same genus as that of the tuberculosis bacterium and is a gram-positive bacillus/rod shaped bacteria. Phage research also helps provide us with useful information about the structure and diversity of the phage so that we can learn about the evolution of viruses.   
  
During this semester, we annotated the genome of Mycobacterium phage TomBrady using comparison to different databases, such as NCBI, Genbank, HHpred, and TMHMM, to functionally and positionally annotate Mycobacterium phage sequences. Nucleotide and amino acid alignments were used to determine homology and function, along with TMHMM to predict transmembrane proteins. TomBrady has a 41902 genome length. Its end characteristics are 3’ sticky overhang with length 11 base and a sequence of CCCCATGGCAT. TomBrady has 62 open reading frames with 26 functionally annotated ORFs. There are no tRNAs in this phage and TomBrady has a GC content of 66.6%. Based on Blastp conserved domains, HHPRED, and TMHMM, we were able to perform functional annotation for 24 of 62 genes, notably including several structural proteins, lysin and holin, two DNA binding proteins, RecE-like exonuclease, and RuvC-like resolvase with significant similarities to phages in existing databases. Additional areas of coding potential undetected by Glimmer or Genemark within open reading frames were found using the host-trained genemark map. These areas show potential for the annotation of genes. This shows the importance of human involvement in the genome annotation process.