Poster Presentation P38

BACTERIOPHAGE GENOMES ANNOTATION

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This project mainly focuses on analyzing the genomes functions of the bacteriophage Shrimp, which was purified and extracted in last semester. Shrimp is Myoviridae and belongs to the cluster C. After finishing the genome sequencing of Shrimp, we compared the similarity of those sequences to the known sequences by using DNA Master to predict the possible proteins that can be produced by Shrimp's genomes. BLAST and HHpred are used for searching our query protein sequence against all known predicted protein sequences to predict potential gene functions. The coding potential of open reading frames was detected by GeneMark. Aragorn helps to identify the locations and anticodons of tRNA genes in the Shrimp. After the annotation, although the functions of some parts of Shrimp were unknown, we found that Shrimp is very similar to phage Bxz1. The result will help the further identification of Shrimp.