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Exploring the Structures and Functions of Genes and tRNA’s in Phage Jedediah's Genome

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In the advancing scientific environment, more information about gene functions of bacteriophages is needed to understand and explore phage diversity as well as learning about how phages are affected by their genomic functions. By analyzing the genome of the C1 cluster phage Jedediah, this research aims to learn more about phage genomes in the same cluster and to gather insight on its gene functions.

The goal of this study is to discover genes and their gaps or overlap to determine accuracy of auto-annotated start sites of the genes. To accomplish this, DNA-Master was used as it compares how different auto-annotation programs such as Glimmer and GenemarkS annotated Jedediah’s genome. Furthermore, using the Actinobacteriophage Database, Starterator, and Phamerator, these programs compare the genome of C1 phage Jedediah with other phages in and out of the C1 cluster. The aim of this research is to understand the relationships among the genes and their function, and the evolution of the gene size, placement, and functions.

By using DNAMaster alongside other tRNA programs like Aragorn and tRNAscan-Se, the genome of phage Jedediah was annotated to determine its similarity to other phages in its cluster. A cluster refers to phages grouped based upon their amino acid sequence. Jedediah was found to be 156129 base pairs long. In the base pair region of 78682 to 107588, 38 genes were found. This region contained 26 auto annotated tRNA’s and only 24 of those 26 tRNA’s were manually determined to be tRNAs.
Discovering and understanding the structure and functions of the genes in new phages like Jedediah will allow the exploration of phage application involving targeted genomes or newly discovered types of proteins. A potential application includes phage therapy that would be used to treat currently incurable genetic diseases and conditions.