CONSIDER FOR TALK

9th Annual SEA-PHAGES Symposium Abstract

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NoodleTree Myoviridae Bacteriophage Annotation Genomic Annotation and Analysis for Genes Indicating Tuberculosis-Related Activity

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The Mycobacteriophage, NoodleTree, was discovered in 2016 from soil near the main fountain on the Spring Creek Campus of Collin College in Plano, Texas. After isolation, amplification and imaging, it was found to be a unique Myoviridae bacteriophage that infects Mycobacterium smegmatis (mc2155). After DNA extraction, the DNA was sequenced by a team at the Pittsburgh Bacteriophage Institute, and genomic data was made available for annotation. The phage genome has a length of over 150 kbp and is a member of the C1 phage cluster. Upon analysis of the phage genome using DNA Master and its accompanying suite of verifiers, NoodleTree was found to have unique characteristics among viruses that infect M. smegmatis. During annotation, we identified several different genes and gene gaps with unknown/novel function.  
  
Our annotations revealed irregular genomic occurrences including missing and altered genes relative to others in the cluster. A large series of genes present in other C1 clusters is absent from NoodleTree’s genome. The lack of these genes may hold pertinent information as to if the phage has efficacy in its host choice. Gene 26 (Fig. 4) is a divergent pham in comparison to the other C1 Clusters. HHPRED reads this gene as a part of the phasin-phasin protein family, a family of surface binding proteins. This unique gene may allow NoodleTree to recognize and infect bacteria differently than other C1 cluster phages. Gene 61 is also a divergent gene compared to other C1 cluster phages. but the function is currently unknown.  
  
NoodleTree infects the target organism, Mycobacterium smegmatis. M. smegmatis is genetically similar to Mycobacterium tuberculosis. M. smegmatis shares over two thousand homologous genes as well as the same peculiar wall structure found in M. tuberculosis. In analyzing NoodleTree’s genome, genes may be identified that specifically target structural and functional aspects of M. smegmatis and, therefore, M. tuberculosis. In correctly identifying these areas of interest, the overall biological processes of both the phage and target bacteria can be examined for use in several applications including phage therapy, prophylaxis treatment, and oncolytic viral treatments.