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8th Annual SEA-PHAGES Symposium Abstract

Queensborough Community College

Bayside NY

Corresponding Faculty Member: Urszula Golebiewska (ugolebiewska@qcc.cuny.edu)

Genomic Analysis of Mycobacteriophage Tonenili

Mehak Azhar, Elizabeth Acevedo, Denisa Grzywna, Randy Guardiola, Olivia Jackson, Neeraj John, Caroline Kanavatsas, Sana Khan, Julie Leong, Elizabeth Mansilla, Yafit Muladjanov, Joangela Nouel, Swan Oh, Marlina Oppedisano, Ambreen Sajid, Mardee M Samper, Omolegho Ugbeva, Jordy Ramirez, Urszula P Golebiewska

During the Spring 2016 semester, students at Queensborough Community College were very happy to receive for annotation the sequence of Mycobacterium phage Tonenili found by the Xavier University of Louisiana. We used DNA Master, which encapsulates the efforts of other programs such as Glimmer, GeneMark, and BLAST, and web based programs Aragorn, tRNAscan-se, and Sequence Manipulation Suite.

Mycobacterium phage Tonenili belongs to the family Myoviridae, and its morphology features a larger head and a short contractile tail. Tonenili is a member of Cluster C, subcluster C1. On the nucleotide level the closet relatives to Tonenili are Pio and Bxz1 both with 886% coverage and 88% identity.

The genome of Tonenili has 160985 nucleotides and 295 predicted genes, including tRNAs. Of the 263 protein coding genes, 236 genes are homologous with genes from the phage world. 27 of the predicted gene products (10%) don’t have homologous partners in the database. 56 genes or21% of the genes match Bxz1 and 24 or 9%Catera.

One striking feature of Tonenili is that it carries 31 genes for tRNAs and 1 gene for tmRNA. Majority of these tRNA genes are located in one segment from gp 95700 to 102350. This segment is 97% identical to similar tRNA rich segment of Mycobacterium phage ET08. Tonenili has at least one tRNA for every amino acid and stop codon. According to comparisons of synonymous codon usage of Tonenili genes to that of its host M. smegmatis, the Tonenili-specific tRNAs modulate the optimal expression of its proteins during development.