CONSIDER FOR TALK

2025 SEA Symposium Abstract

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Genome sequencing and annotation of mycobacteriophage SilverBell

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Mycobacteriophage SilverBell was discovered by Ryan Nork in 2014 in Philadelphia, PA. We isolated genomic DNA from SilverBell lysates and sequenced the genome using Illumina iSeq 100 at La Salle University, along with four other novel bacteriophages. The sequencing reads were assembled to produce a 68,756 base-pair circularly permeated genome with approximately 190-fold shotgun coverage. SilverBell is a B1 phage with 103 predicted protein coding genes. Genome annotation of SilverBell is being conducted using PECAAN and DNA master software. The genes will be individually assessed for their function. Notably, SilverBell and other B cluster phages contain a gene with similarity to Tail-Assembly Chaperone genes, which is located upstream of the putative Tape Measure Protein gene. However, synteny of this region differs from other Actinobacteriophage genomes, and evidence does not yet exist to confirm if this gene functions as a Tail-Assembly Chaperone. We will discuss how the activity of this gene might be investigated to help assign its function.