The Discovery and Analysis of Mycobacteriophage "LBerry"

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Introduction

Mycobacteriophage "LBerry" was isolated on *Mycobacterium smegmatis* mc^{2}155 from an enriched soil sample from Rochester, New York. LBerry's innate ability to infect *Mycobacterium smegmatis* allows for further studies on the phage to determine its potential as a lysogen for phage therapy in infections caused by pathogenic Mycobacterium, such as *Mycobacterium tuberculosis* and *Mycobacterium abscessus*. An essential part of this determination is the sequence annotation and further experimentation to determine the phage's genomic diversity.

Figure 1: Purification

Mycobacteriophage LBerry was isolated from an enrichment culture and purified by three rounds of purification.

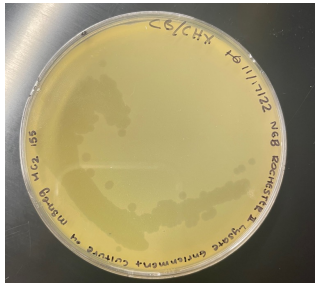

Figure 2: Electron Microscopy

Image of the phage particle shows that LBerry is a Siphoviridae with a contractile tail.

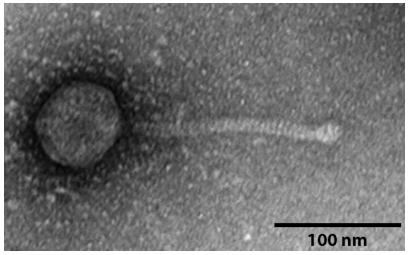

Figure 3: Isolated DNA

Analysis of LBerry DNA, isolated by phenol-chloroform extraction, using a microvolume spectrometer shows that the DNA is of high quality.

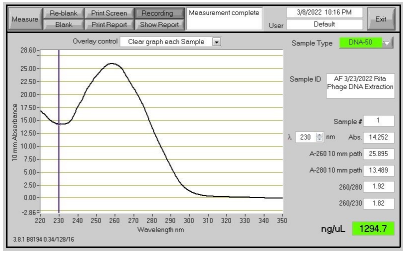

Figure 4: Sequencing

Sequencing confirms assignment to the F1 cluster.

Isolation Temperature	37°C
Genome Length (bp)	50965
Overhang Sequence	CGGGTGGTAA
GC Content	64.0%
Sequencing Facility	Pittsburgh Bacteriophage Institute
Shotgun Sequencing Method	Illumina Sequencing

Figure 5: Immunity Assays

LBerry was determined to be infected by the similar A cluster phages, BXB1 and Sheldon Cooper

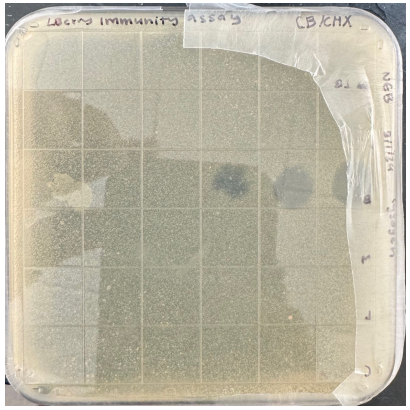

Figure 6: Annotation

Bioinformatics tools DNA Master, PECAAN, Starterator, and Phamerator were utilized to complete a genome annotation. Below is an example annotation for a single gene on DNA Master.

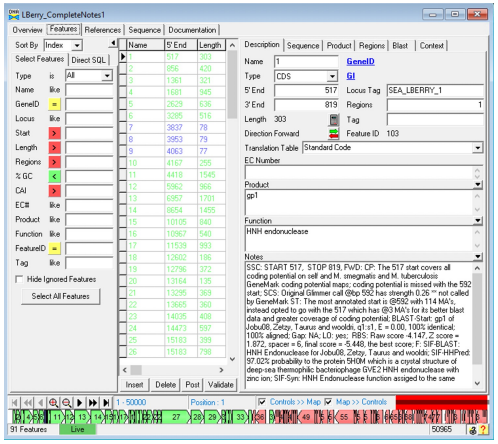

Figure 7: Phamerator Map

Genome map of phage LBerry and similar phages of the same cluster.