

Introduction

Mycobacteriophage Maravista targets host bacterium *Mycobacterium smegmatis* mc²155 and was isolated from this host using an enriched soil sample from Maravista Avenue in Teaticket of Falmouth, Massachusetts, after which the phage is named. As Maravista infects *Mycobacterium smegmatis*, it may have potential in being utilized in phage therapy treatment for infections caused by similar pathogenic mycobacteria, such as *Mycobacterium tuberculosis*, the causative agent of tuberculosis. Bioinformatic analysis of this phage yields insight into Maravista's genomic character and features.

Figure 3: Sequencing

Sequencing confirms assignment to the F1 cluster.

Isolation Temperature	37°C
Genome Length (bp)	60,140
Overhang Sequence	CGGAAGGCGC
GC Content	61.3%
Sequencing Facility	Pittsburgh Bacteriophage Institute
Shotgun Sequencing Method	Illumina Sequencing

Figure 1: Purification

Mycobacteriophage Maravista was isolated from an enrichment culture and purified by four rounds of purification. The phage forms small, clear 1 mm plaques.

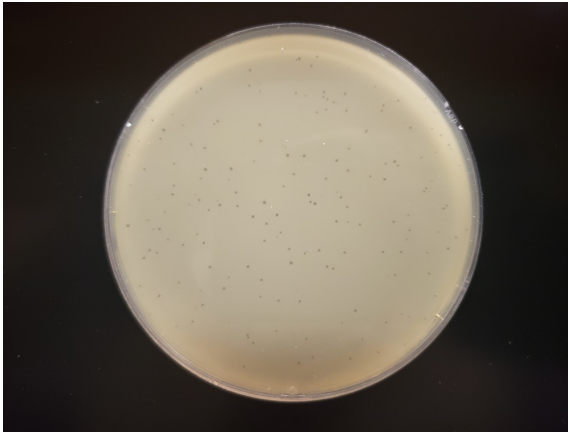


Figure 2: Electron Microscopy

Image of the phage particle shows that Maravista is a Siphoviridae with a long contractile tail (photo by Joseph DeGiorgis).

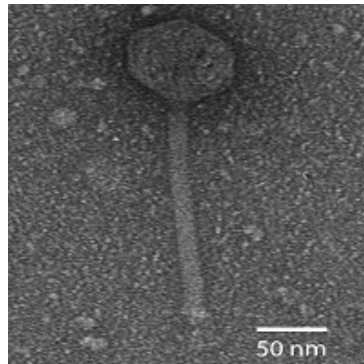


Figure 4: Isolated DNA

Analysis of Maravista DNA, isolated by phenol-chloroform extraction. Depicted on the right is the Nanodrop absorbance spectrum of the DNA. Note the peak at 260 nm, which is the wavelength of light that DNA absorbs, indicating a pure solution of DNA.

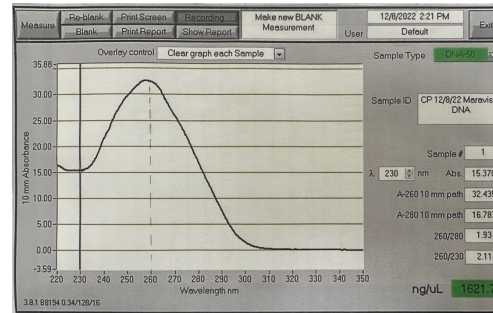


Figure 5: Phamerator Map

This genome map displays the first 15 genes of Maravista and those of the closely related phages PMC and Fruitloop, both part of the same F1 cluster.

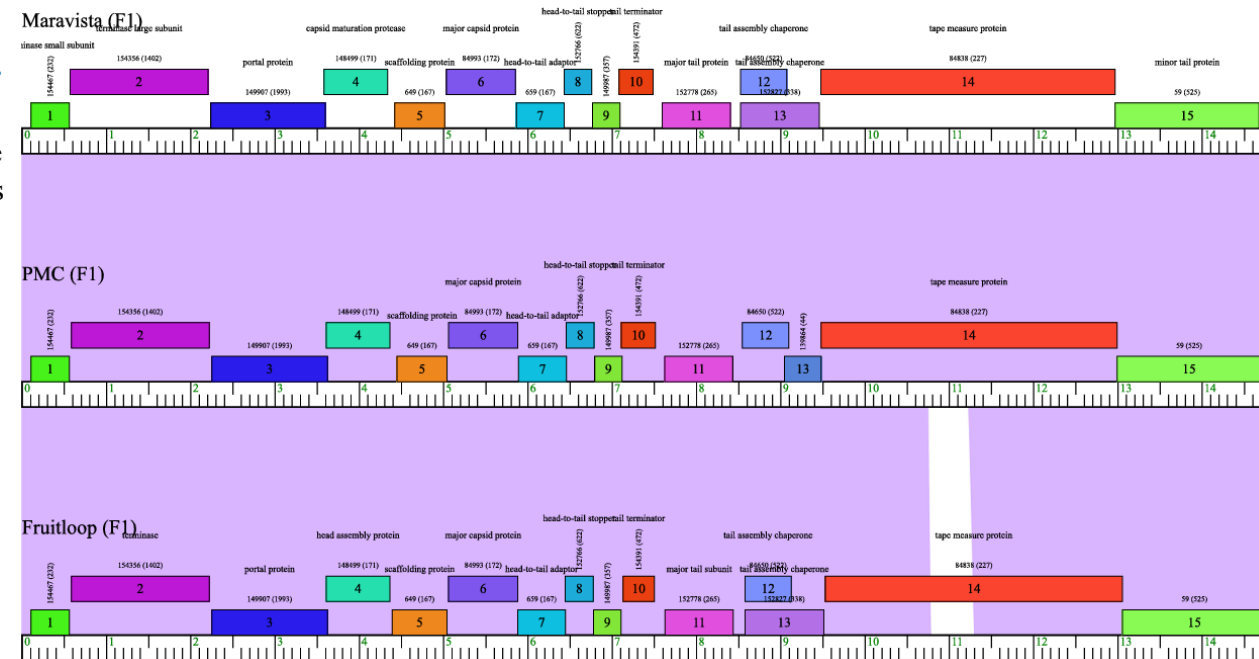


Figure 6: Annotation

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

