Annotation of Bacteriophage Blocker 23 and Discovery of A Novel Actinobacteriophage

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MENTORED BY

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Overview

This researched focus on identifying the genes in the bacteriophage Blocker23 using publicly available software. The wet lab portion focused on identifying a novel bacteriophage which will be characterized in the future.

Introduction

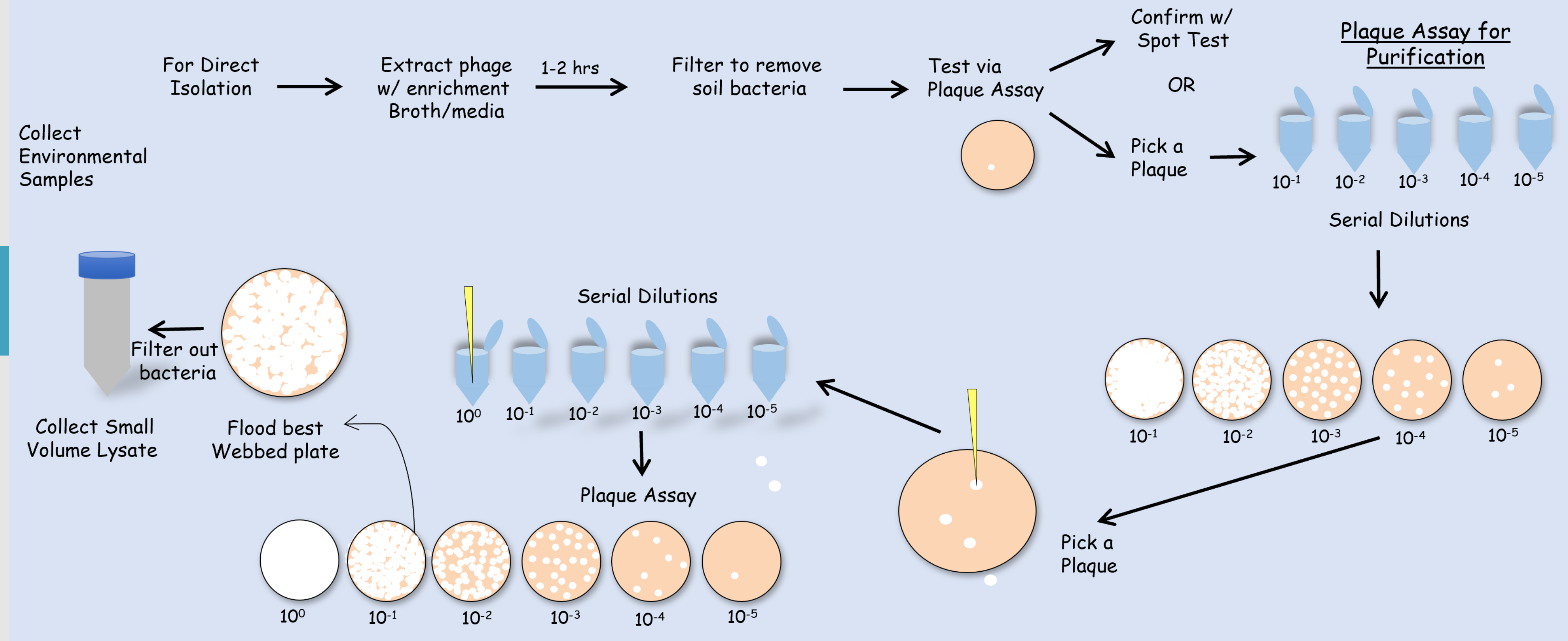
With 10^{23} bacteriophages on Earth, our knowledge is miniscule in comparison to what is out there.
This research aims to add bioinformatic information and discovery of a novel bacteriophage to current research. With bacteriophages' ability to kill bacteria, the annotation of Blocker23 will aid in the research and development for multidrug-resistant bacterial infections. Knowledge of the genes present in bacteriophages can help arm us in the war against antibiotic resistant bacteria by identifying the function of these genes.

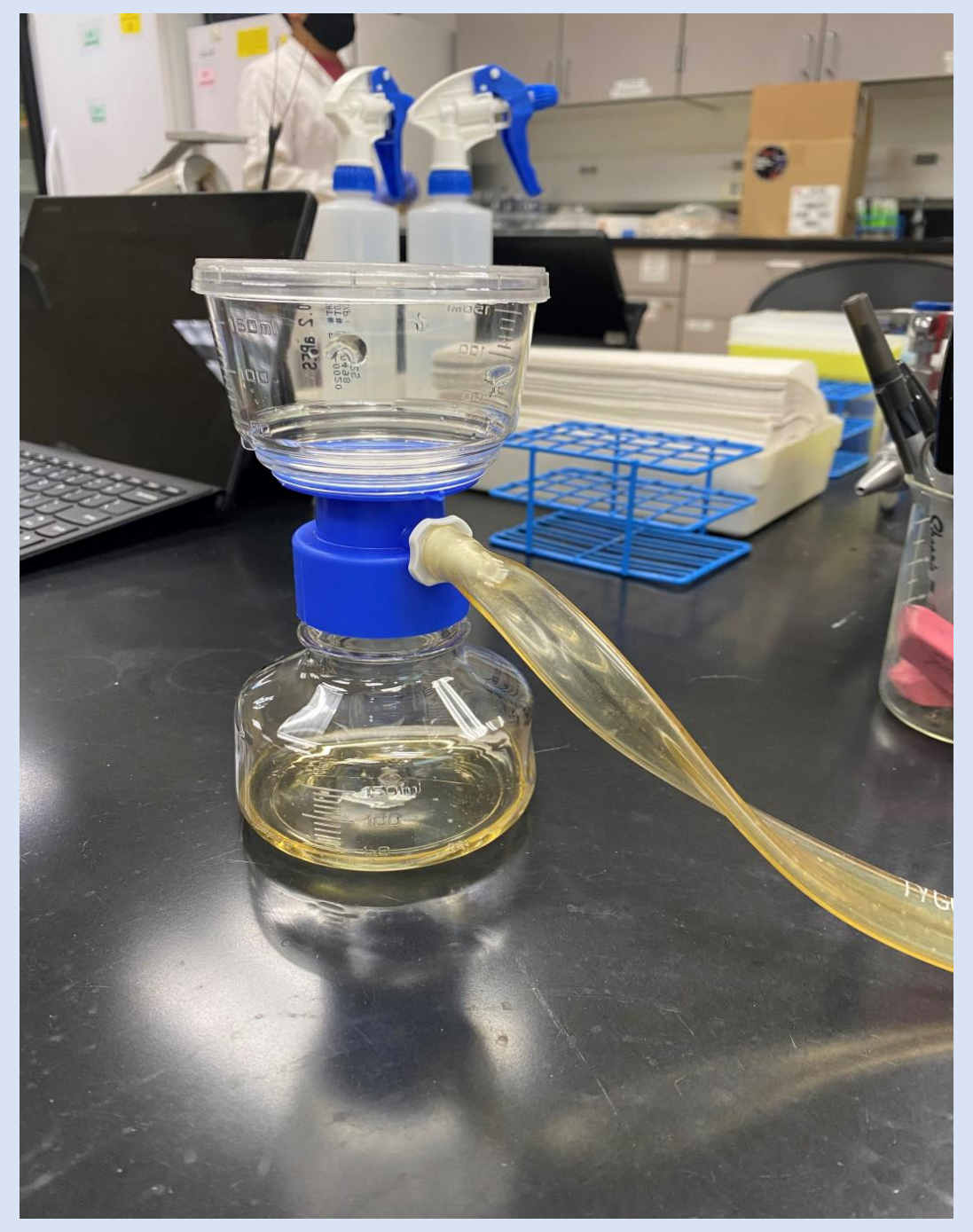
Bioinformatics Methods

Use software DNA Master, gene prediction programs Glimmer/GeneMark, coding potential maps, phamerator, starterator, TMHMM, SOSUI, HHPRED, and BLAST.

Phage Discovery Methods

Soil sample was collected at a duck pond GPS Coordinates 36.1789, -115.186. The below methodology was followed to collect purified bacteriophage lysate.

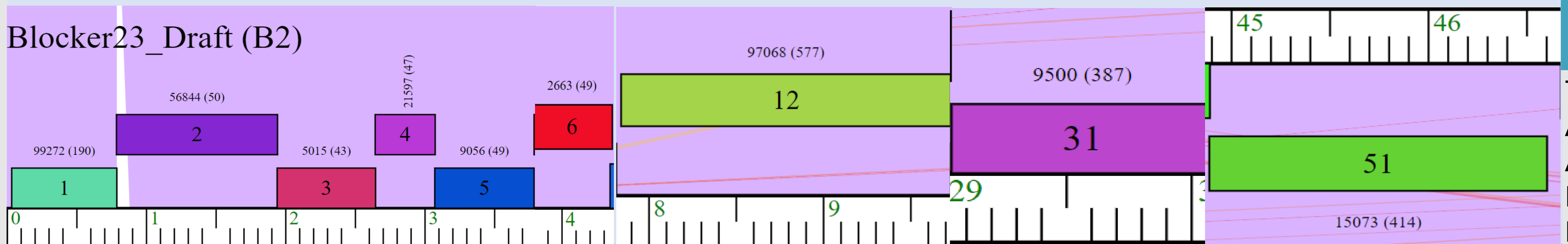




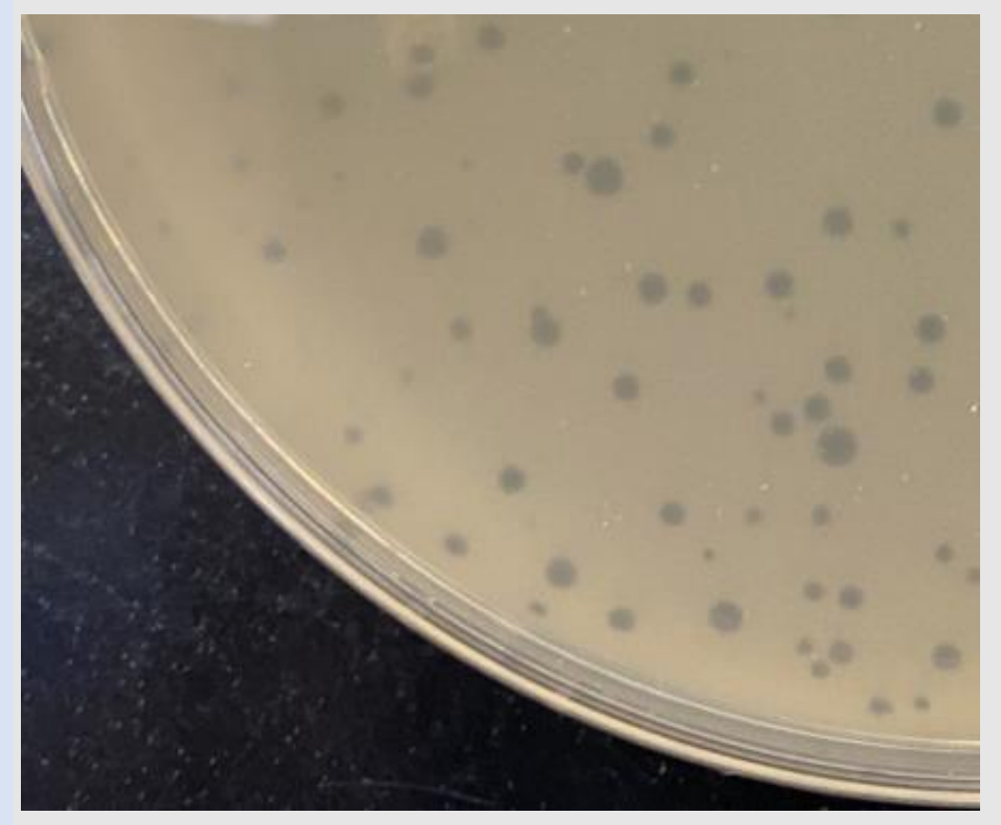
Putative functions of Selected Blocker23 Proteins

Gene No.	Function	Purpose
6	FolE-like GTP cyclohydrolase I	An enzyme that helps create the molecule (BH4) involved in processing amino acids.
12	Portal Protein	Involved in viral replication
31	Minor Tail Protein	Involved in tail formation of bacteriophages
51	DNA Helicase	Enzymes that unwind DNA to aid DNA replication

Graphic Representation of the Length and Locations of the Genes



RESULTS



See table in middle panel for selected genes identified in Blocker23.

Through this research, we identified 92 genes within Blocker 23. Around 41.3% of these identified genes had functions. Paired with the wet lab, a novel bacteriophage was found.

CONCLUSION

The annotation of a genome and discovery of a bacteriophage was accomplished through the findings of gene functions with bioinformatic analysis. The annotation of bacteriophages will aid in research developments against certain bacteria for human health.

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