Discovery of Bacteriophages

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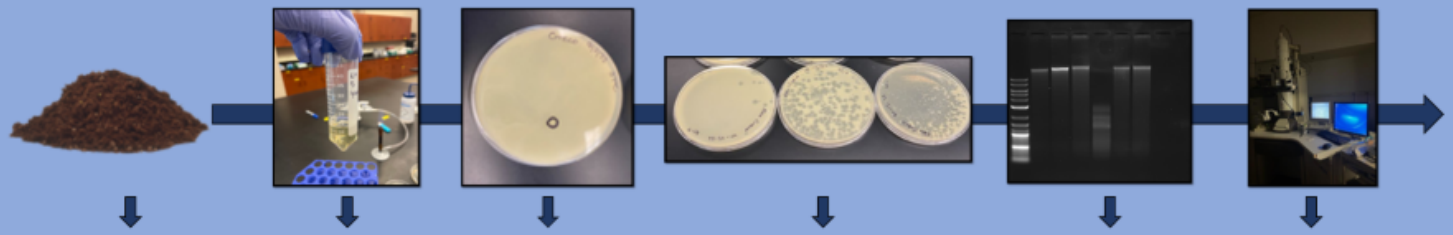
SEA PHAGES



Environment Sample
Taken from soil samples in Conway, SC.

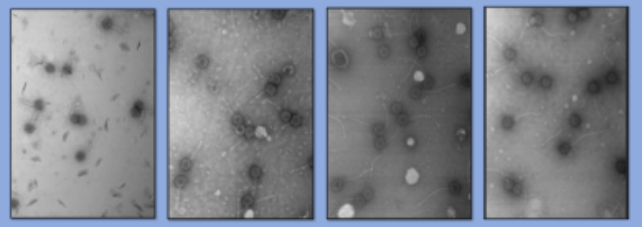
Isolation:
We took our soil samples, added liquid media, and filtered it through a 0.22 µm syringe filter.

Purification:
Filtrates were subjected to plaque assays. Plaques represent single populations of isolated phages.

Amplification:
Purified phages were amplified and then plaque assays of dilutions calculated titers of our samples.

DNA Extraction:
We extracted DNA, analyzed it through gel electrophoresis, and had it sequenced.

Electron Microscope:
We had our phages prepped and taken to Winthrop for imaging.



Our electron microscope pictures from Winthrop University. Clementines (first image) and GrecoEtereo (second image) have similar short tails, while Phayeta, (third image), and CaitheneusMax, (last image), have longer more flexible tails.

Introduction

What is a phage?

Bacteriophages, or phages, are robust, naturally occurring, evolutionary viruses that infect bacteria. The first step of the infection is for phages to bind to the surface of a bacterial cell and inject their DNA into the cell. The phage's DNA then directs synthesis of new phage particles that are released from the cell upon lysis, which kills the host cell.

How do we discover a phage?

Students collected independent soil samples and used SEA-PHAGES protocol, to isolate, purify, amplify, and characterize and four different phages; Phayeta, GrecoEtereo, CaitheneusMax, and Clementines. From there we were able to characterize and sequence these phages using various techniques.

How does this connect to medical field?

Phages can be used as alternatives to antibiotics in order to treat antibiotic resistant viral bacterium. It is our mission to understand the genome characteristics of our phages, and how these phages can be used in phage therapy treatments.

Discussion

What did we find?

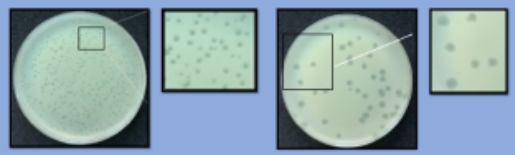
After a semester of trying to discover phages from our soil samples, we eventually discovered four unique phages; Clementines, GrecoEtereo, CaitheneusMax, and Phayeta.

What did we use to continue with sequencing?

Our phages, Phayeta and GrecoEtereo, are currently in the process of being annotated through several bioinformatic techniques and platforms including the Actinobacteriophage Datab ase, GeneMark, DNA master, and Phamerator.

How are we moving forward?

We are currently in the process of concluding the bioinformatic sequencing of Phayeta, and moving forward with sequencing on GrecoEtereo as well. By the end of this semester, we will have two of our phages completely sequenced with all known gene functions.



These are our plaque assays from Phayeta (left) and GrecoEtereo (right). In the inserts individual plaques are shown enlarged.

Acknowledgements

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