

Discovering, Characterizing, and Annotating a Microbacterium Foliorum Phage (Vegas)

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Introduction

Patchy Knowledge

Little is known about phage diversity, whether phage genes truly represent a phage's abilities, interactions between host and phage.

Antibiotic Resistance Crisis

Bacteria are becoming increasingly resistant to antibiotics, but phages can be used as an alternative treatment.

Fundamentals of Molecular Biology

Phages helped with the identification of nucleotides and restriction enzymes. Plus, studying phages helps understand bacterial evolution.

Hypothesis/Objective

Does Vegas identify as a Microbacterium Foliorum Phage?

If so, how much of Vegas's common and unique characteristics be characterized through bioinformatic analyses?

Review of Literature

Bacteriophages (BP) are viruses that can infect and kill bacteria without any negative effect on human or animal cells. For this reason, it is suspected that they can be used, alone or in combination with antibiotics to treat bacterial infections.

(Domingo-Calap & Delgado-Martinez, 2018)

In comparison to antibiotics, BPs are supposed to have several other advantages. It is thought that BPs are significantly safer and better tolerated, as they replicate only in the target bacterium but cannot infect mammalian cells. This conclusion seems supported by all the experiences gathered in the past in Eastern Europe and all the studies carried out more recently in experimental animals and humans, which have not reported significant adverse events following BP administration. (Kakasis & Panitsa, 2018)

Methodology

Summer of 2019 ~ Isolating Vegas

1. Enriched Isolation of Vegas

- Involves amplifying number of phages in environmental sample resulting in exponentially larger concentration of phages specific to host (Microbacterium Foliorum)

2. Spot Test

- Involves screening for the presence of phages and waiting for visible plaques

3. Purification of Vegas

- Involves purifying phages to obtain a clonal phage population

4. Amplification of Vegas

- Involves obtaining high concentration of phage lysate by flooding plates method

Summer of 2020 ~ Genome Annotation

Genome Annotation

Involves predicting gene's functions

Bioinformatic Analyses

Involves using computer programs to determine patterns in sequences and similarities to phage proteins

Predicted gene functions and proteins can provide substantial information about biology and life cycle of the phage

Conclusion

- Going back to the hypothesis/objective of discovering Vegas's characteristics through genome annotation and bioinformatic analyses, this will aid in providing information on bacteriophages and their gene/protein functions.
- In turn, this will help give insights into the future of using bacteriophages as treatment alternatives for bacterial infections and nonetheless give insights into the workings of bacteriophages.

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