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2017

Isolation of a Novel Phage OTooleKemple52

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COMMON WEALTH U IVERSIT N G



Isolation of a Novel Phage OTooleKemple52

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Genes with Predicted

Function

55

Host range testing: Testing was done to determine

whether OTooleKemple52 had a broad or narrow

host range. Clear plaques, suggesting a strong ability

to infect, were only observed on two strains of

thuringiensis. The ability to infect B. cereus T strain

was explored further through additional plating, but

infection was unsuccessful. Below, bacterial growth

is visible where B. cereus and OTooleKemple52 were

Introduction:

A bacteriophage is a virus capable of infecting bacteria like ubiquitous soil-dwelling genus Bacillus. Within the Bacillus genus, there is the "ACT family" made up of B. thuringiensis, B. cereus, and B. anthracis, which are highly related but with different pathogenic characteristics. Because of this, phages isolated using a species in this group may have a broad host range encompassing several species from Bacillus. Since B. cereus and B. anthracis can result in mild to fatal sickness in humans, the non-pathogenic B. thuringiensis kurstaki was used to discover and characterize novel phages.

After isolation, the usage of genomic analysis in phage characterization is key to discovering more about the phage. By looking at predicted proteins and genomes, researchers can further document interrelatedness of the known phages.

Through studying phages we can work to better understand both phage diversity and the interrelatedness of the Bacillus genus. The benefits of studying bacteriophages have reaches from environmental to medical significance because of the ubiquitous and pathogenic characteristics of the host bacteria.

Methods:

Phage Discovery and Characterization

The phage OTooleKemple52 was isolated from a soil sample collected from Chesapeake, VA using "soil enrichment." Soil enrichment involved putting a small amount of soil into a mixture of trypticase soy broth (a growth medium for bacteria) and Bacillus thuringiensis. The goal of enrichment was for the phage to infect bacteria, which would increase phage concentration and thus made infection more likely when plating. A phage plaque was observed from this enrichment infection upon plating.

The phage population was then purified until the morphology of the phage plaques was consistent (3 mm diameter with pinpoint clear centers). A large volume of phage stock (high titer lysate, HTL) was collected and then used to obtain purified DNA for gel electrophoresis and genome sequencing. Additionally, an HTL sample was stained with 1% uranyl acetate and imaged using transmission electron microscopy to determine morphology. The phage was tested for host range by spotting HTL into agar plates with various species of Bacillus.

Phage Genome Sequencing and Bioinformatics:

The sequenced genome was annotated using DNAMaster. GeneMark and Glimmer were used to determine likely reading frames. Predicted proteins were submitted to NCBI's BLAST program to determine if they had segments that were present in conserved protein domains.









Genome

Length (bp)

Bacteria

B. cereus T strain

B. cereus 23857

B. pumilis SAFR32

Plaque Type

clear

clear

turhid

turhid

turbid

turbid

2

Number of

Genes

298

PHAGE GENOME CHARATERIZATION

Number of

tRNA's

7

plated

B. cereus T strai

Terminal

Repeats (bp)

2426

Dotplot phage of genome sequences: The program Gepard was used to produce a dotplot based on the concatenated fasta files from all six of the phages sequenced in the class. This dotplot shows genome similarity between all six of the phages. Darker lines indicate a higher similarity, while a less defined line indicates lower similarity.

Restriction digest of Phage Genomic DNA: The phage DNA was digested using the EcoRI, HindIII, and Clal enzymes and visualized using gel electrophoresis. An undigested DNA sample was included for comparison along with a 1 kb ruler.

Genome map comparison of Bacillus phages OTooleKemple52, PPIsBest, and Janet

Comparisons were done between OTooleKemple52 and two other B. thuringiensis phages, using a comparative genome mapping tool Phamerator. Janet and PPIsBest. Janet is very similar to OTooleKemple52 in its proteins, while PPIsBest has far less similarity. Both phages were isolated by other students in the class. The purple sections on the map indicate regions of high nucleotide sequence similarity. Colored rectangles represent proteins and the color/order of the rectangle represent proteins in the same protein family. Genome similarity between OTooleKemple 52 and Janet is also observed in the dot plot.



Acknowledgements:

VCU Life Sciences and the HHMI SEA-PHAGES program, Sequencing provided by the Pittsburgh Bacteriophage Institute, TEM provided by University of Mary Washington. Additional phages discovered by: Zainab Gbadamosi (Zainny), Brenna Kent (Janet), Rahul Warrier (AaronPhadgers), Erin Cochran (Bubs), and Nashwan Farooque (PPIsBest). If you're interested in bringing this program to your school, information can be found at seaphages.org