A 2024 Report on the Characteristics of Phages Assigned to Cluster DV

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Isolation and Morphological Characteristics

As of June 2024, 35 phages have been assigned to Actinobacteriophage cluster DV (29 annotated, 6 drafts). Cluster DV consists of presumptive lytic phages isolated from environmental samples collected in 11 different US states, with 97.14% using *Gordonia rubripertincta* as the host and 2.86% using *Gordonia terrae* as the host. A sampling of transmission electron micrographs reveals these phages to have siphoviral morphologies, while photographs of plaque assays reveal small- to medium-sized clear plaques. Examples of phages displaying these morphologies include phage BirthdayBoy and OtterstedtS21.

Genometrics

The genomes of phages in this cluster have an average length of 67,261 bp (range: 64,869 bp – 68,848 bp) with an average GC content of 58.2% (range: 57.6% – 58.8%). The genomes have circularly permuted ends.

Gene Content

a. A survey of all manually annotated genomes in this cluster (i.e., excluding draft genomes) reveals the number of genes called per genome to range between 89-102 genes, which represent a total of 210 phamilies (or phams). There is an average number of 97 genes per genome.

b. Of these 210 phams, 58 are fully conserved across the cluster. These phams are assigned putative functions that are involved in structure and assembly (e.g., major capsid proteins, minor capsid proteins, minor tail proteins, tape measure protein, tail assembly chaperones, and a head-to-tail stopper), replication and recombination (e.g., DNA Binding protein and DNA helicase), and lysis (e.g., lysin A and holin). Some other notable putative functions include a metalloprotease. Another 152 phams have varying levels of conservation. There are several phams found only in one phage of the cluster. Examples include an HNH endonuclease and esterase.

c. No tRNA genes have been identified in this cluster. There are also no identifiable integrase or repressor functions, suggesting that phages of this cluster do not form lysogens and are, thus, lytic phages.

d. The genomes are organized with many genes involved in structure and assembly located within the first third of the genome, while those involved in replication and recombination are scattered across the remaining two-thirds of the genome. The Lysin A gene is located at the boundary of these two regions, while the Lysin B is located at the end of the genome. All genes are transcribed in the forward direction.

References

Pollenz RS, Bland J, Pope WH. Bioinformatic characterization of endolysins and holin-like membrane proteins in the lysis cassette of phages that infect Gordonia rubripertincta. PLoS One. 2022 Nov 17;17(11): e0276603. doi: 10.1371/journal.pone.0276603. PMID: 36395171; PMCID: PMC9671378.

Source Data: https://observablehq.com/d/5e5bc78c9b3ae2ed accessed July 2024.

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