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

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Isolation and Morphological Characteristics

As of June 2024, 52 phages have been assigned to Actinobacteriophage cluster DJ. Cluster DJ consists of lytic phages that were isolated from environmental samples collected in 16 different US states, using *Gordonia rubripertincta and Gordonia terrae* as the hosts. A sampling of transmission electron micrographs reveals 100% of 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 FortCran and Secretariat.

Genometrics

The genomes of phages in this cluster have an average length of 60,470 bp (range: 57,731 bp – 62,331 bp) with an average GC content of 51.5% (range: 50.5% – 54%). The genomes have 3' sticky overhang ends.

Gene Content

a. A survey of all genomes in this cluster reveals the number of genes called per genome to range between 84 – 95 genes, which represent a total of 189 gene phamilies (or phams).

b. Of these 189 phams, 45 are fully conserved across the cluster. These phams are assigned putative functions that are involved in structure and assembly (e.g., terminase, portal protein, tape measure, and minor tail proteins), replication and recombination (e.g., DNA primase/polymerase and DNA helicase), and lysis (e.g., lysin A, holin and lysin B). Some other notable putative functions include Cas4 family exonuclease, VRR-NuC domain protein, deoxycytidylate deaminase, and ThyX-like thymidylate synthase.

c. Another 144 phams have varying levels of conservation. Notable here are 30 phams that are each only called once in this cluster.

d. 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.

e. The genomes are organized with genes involved in structure and assembly located within the first third of the genome, while those involved in replication and recombination are in the

center and far right end of the genome. Genes involved in lysis are in the first third of the genome. All genes are transcribed in the forward direction, except Schwartz33, which contains a reverse gene (of unknown function and gene Phamily 167423) adjacent to the highly conserved lysin A gene.

References: No prior publications.

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

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