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

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Isolation and Morphological Characteristics

As of June 2024, 9 phages have been assigned to Actinobacteriophage cluster GA. Cluster GA consists of lytic phages that were isolated from environmental samples collected from 6 different US states (IL, FL, MD, NC, PA, TX) using *Microbacterium foliorum* as the host. A sampling of transmission electron micrographs reveals these phages to have siphoviral morphologies, while photographs of plaque assays reveal little to no consensus on plaque formation or size. Examples of phages displaying these morphologies include phage Warren and Blett.

Genometrics

The genomes of phages in this cluster have an average length of 38,806 bp (range: 38,493bp – 39,364 bp) with an average GC content of 67.9% (range: 67.6% – 68.1%). The genomes have circularly permuted ends.

Gene Content

a. A survey of all manually annotated genomes in this cluster (i.e., excluding draft genomes) reveal the number of genes called per genome to range between 64 – 67 genes, which represent a total of 84 gene phamilies (or phams).

b. Of these 84 phams, 56 are fully conserved across the cluster. These phams are assigned putative functions that are involved in structure and assembly (e.g., terminase, portal protein, major and minor capsid proteins, tape measure, tail assembly chaperones, and minor tail proteins), replication and recombination (e.g., DNA helicase and DNA helicase loader, resolvase, and Rep-A like replication initiator), and lysis (e.g., endolysin and holin).

c. Another 28 phams have varying levels of conservation. Notable here 14 phams are found in only one genome, while two other phams (Pham 34042 and Pham 8617) are found in two genomes (Antuna, and MenE).

d. There is one tRNA gene identified in all phages in the cluster (tRNA-Gly). 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 scattered across the remaining two-thirds of the genome. Genes involved in lysis are located at the boundary of these two regions. All genes are transcribed in the forward direction.

References: No prior publications.

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

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