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

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Isolation and Morphological Characteristics

As of June 2024, 5 phages have been assigned to Actinobacteriophage cluster Y. Cluster Y consists of temperate phages that were isolated from environmental samples collected from 4 different US states (FL, RI, PA, TX), using *Mycobacterium smegmatis* as the host. A sampling of transmission electron micrographs reveals these phages to have siphoviral morphologies, while photographs of Hilltopfarm plaque assays reveal small 1.0-1.5 mm plaques.

Genometrics

The genomes of phages in this cluster have an average length of 76,606 bp (range: 75,686 bp – 77,832 bp) with an average GC content of 66.5% (range: 65.9% – 67.4%). The genomes have 12 bp sticky overhang 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 127 – 135 genes, which represent a total of 188 gene phamilies (or phams).

b. Of these 188 phams, 82 are fully conserved across the cluster. Within these 82 phams, 38 functions were assigned. These phams are assigned putative functions that are involved in structure and assembly (e.g., terminase, portal protein, major capsid protein, tape measure, tail assembly chaperones, and minor tail proteins, major tail subunit, head to tail connector, and capsid maturation protease), replication and recombination (e.g., DNA polymerase, resolvase, and WhiB family transcription factor), and lysis (e.g., lysin A and lysin B). Some other notable putative functions include a BrnT-like toxin, QueE-like queuosine biosynthesis protein, QueD-like queuosine biosynthesis protein, HNH endonuclease, DNAQ-like exonuclease, RecE-like exonuclease, and ATPase.

c. Another 106 phams have varying levels of conservation. Notable here are 18 phams that are only called once in this cluster, while another 83 phams are each only called twice in this cluster. One of these latter phams is assigned as an MPME1 protein (movable element).

d. tRNA genes were identified in the genomes of phages in this cluster. Phages AuntGwenStacy, Typha, and Hilltopfarm each have two tRNAs in their genomes. Phages Typha and Hilltopfarm both have a tRNA-Met and a tRNA-Arg. Phage AuntGwenStacy has two tRNAs although the anticodon of the tRNA was not determined. All phages in this cluster have an identified integrase (with two identified as tyrosine integrases) and an immunity repressor. All phages are reported to be temperate.

e. The genomes are organized with genes involved in structure and assembly located within the first quarter of the genome while those involved in replication and recombination are scattered across the middle of the genome. Genes involved in lysis are located downstream from the structural/assembly genes. Most genes are transcribed in the forward direction, except for most of the lysogeny genes that are transcribed in the reserve direction. The BrnT-like toxin was found to be transcribed in either the forward or reverse direction.

References: No prior publications.

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

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