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

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Isolation and Morphological Characteristics

As of July 2024, 13 phages have been assigned to Actinobacteriophage cluster EH. Cluster EH consists of temperate phages isolated from environmental samples collected in 7 different US states using *Microbacterium* sp. ISAT203, *Microbacterium foliorum*, and *Microbacterium paraoxydans* as the hosts. A sampling of transmission electron micrographs reveals these phages to have siphoviral morphologies, while photographs of plaque assays reveal small- to medium-sized clear or cloudy plaques. Examples of phages displaying these morphologies include phages IAmGroot and SuMoo.

Genometrics

The genomes of phages in this cluster have an average length of 47,802 bp (range: 45,424 bp – 50,154 bp) with an average GC content of 70.0% (range: 69.0% – 71.4%) and are linear.

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 73 - 82 genes, which represent a total of 293 gene phamilies (or phams).

b. Of these 293 phams, 22 are fully conserved across the cluster. These phams are assigned putative functions that are involved in structure and assembly (e.g., head-to-tail adaptor, head-to-tail stopper, terminase large subunit, portal protein, major capsid proteins, tail assembly chaperones, tail terminator and minor tail proteins), replication and recombination (e.g., DNA polymerase I, HNH endonuclease, recombination directionality factor), and lysis (holin). Some other notable putative functions include NrdH-like glutaredoxin, SprT-like protease, exonuclease, and Cas4 family exonuclease.

c. Another 271 phams have varying levels of conservation. Notable here are 130 phams that are each only called once in this cluster, while another 62 phams are each only called twice.

d. Eight phages in the cluster called at least one tRNA gene. Phages Cen1621 (tRNA-Trp), Floof (tRNA-His), Gretchen (tRNA-Lys), Percival (tRNA-Lys), and Zeta1847 (tRNA-Gly) all have one tRNA gene. Phages Caron, Mabodamaca, and SuMoo all have two tRNA genes (tRNA-Trp, tRNA-Asn). GardenState and IAmGroot have serine integrase genes, suggesting that phages of this cluster may form lysogens and be temperate phages.

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 remaining three-quarters of the genome. Genes involved in lysis are located at the boundary of these two regions. All genes are transcribed in the forward direction, except for one gene in the latter half of the genome that is transcribed in the reverse direction in four phages (Percival, Gretchen, IAmGroot, GardenState).

References:

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

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