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

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Isolation and Morphological Characteristics

As of June 2024, 45 phages have been assigned to Actinobacteriophage cluster EC (42 annotated phages, 3 drafts)**.** Cluster EC consists of lytic phages isolated from environmental samples collected in 14 US states, 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 small-to-medium-sized clear plaques. Examples of phages displaying these morphologies include phages Pulchra and Selwyn23.

Genometrics

The genomes of phages in this cluster have an average length of 53442 bp (range: 52,659 bp – 55,431 bp) with an average GC content of 68.8% (range: 67.8% – 69.7%). The percentage of the genomes with circularly permuted ends is 89%. No end type was identified in 11% of annotated genomes.

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 ranges between 89 – 100 genes, which represent a total of 290 gene phamilies (or phams).

b. Of these 290 phams, 29 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 major and minor tail proteins), replication and recombination (e.g., exonuclease, endonuclease, AAA-ATPase), and lysis (e.g., endolysin). Some other notable putative functions include glycosyltransferase and UDP-glucose dehydrogenase.

c. Another 261 phams have varying levels of conservation. Notable here are 61 phams that are each only called once in this cluster, and 89 phams are each only called twice in this cluster. Examples of functions assigned to genes in these phams include deoxycytidylate deaminase and HNH endonuclease. Most genes assigned to these phams are of unknown function.

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 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

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

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