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

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Isolation and Morphological Characteristics

As of July 2024, 67 phages have been assigned to Actinobacteriophage cluster EB. Cluster EB consists of lytic phages that were isolated from environmental samples collected from 22 different states across the United States and 1 from Argentina. 63 phages were found using *Microbacterium foliorum* as the host, and 4 phages were found using *Curtobacterium flaccumfaciens* 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 phage PHISB, Icarian, and Loviatar.

Genometrics

The genomes of phages in this cluster have an average length of 41,014 bp (range: 17,001 bp – 42,655 bp) with an average GC content of 67.3% (range: 65.6% – 69.7%). 95.52% of EB genomes have 3' sticky overhang ends with overhang length of 10 bases (3' - TCTCCCGGCA - '5), 2.9% are circularly permutated, with the remainder having no end type found.

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 63 – 74 genes, which represent a total of 187 gene phamilies (or phams).

b. Of these 187 phams, 34 are fully conserved across the cluster. These phams are assigned putative functions that are involved in structure and assembly (e.g., terminase, portal protein, capsid maturation protein, major capsid protein, head-to-tail adaptor and stopper, tail terminator, tail assembly chaperones, major and minor tail proteins), replication and recombination (e.g., Cas4 family exonuclease, nucleotide pyrophosphohydrolase, thymidylate kinase and synthases, Holiday junction resolvase, recombination directionality factor, DNA primase/polymerase/helicase, DNA polymerase, DNA binding protein/RNA polymerase sigma factor, and resolvase). Some other notable putative functions include a glutaredoxin oxidoreductase.

c. Another 153 phams have varying levels of conservation. Notable proteins that are not conserved include HNH endonuclease, SprT-like protease, and a HicA-like toxin. It appears there are two types of tape measure protein in this cluster, with one group (pham 154727) conserved in 47 of the phages and the other (pham 167111) conserved in 10 of the phages. Two groups of endolysin are also present, with one group (pham 161682) conserved in 30 of the phages and the other (pham 143866) conserved in 17 of the phages.

d. At least one tRNA gene can be identified in all phages in the cluster, and some phages have up to 4 tRNAs. tRNA (Gln) is the most called tRNA in the 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 quarter of the genome, while those involved in lysis are in the second quarter. Genes labeled miscellaneous are dispersed across the remaining half of the genome, with genes of putative proteins of unknown function scattered across the entire genome. Genes transcribed in reverse are scattered in the first two-thirds of the genome, with the only gene of known function being the HicA-like Toxin.

References

Jacobs-Sera D, et al. Genomic diversity of bacteriophages infecting Microbacterium spp. PLoS One. 2020 Jun 18;15(6): e0234636. doi: 10.1371/journal.pone.0234636. PMID: 32555720; PMCID: PMC7302621

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

Acknowledgments: We thank Maddie Bendele, Isobel Cobb, and Steve Cresawn for developing the tools used to generate this report.