A 2024 report on the characteristics of phages assigned to Cluster FE

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Isolation and Morphological Characteristics

As of June 2024, 9 phages have been assigned to Actinobacteriophage cluster FE. Cluster FE consists of lytic phages that were isolated from environmental samples collected in 5 different US states (CA, IL, MA, NH, PA) and Canada (Ottawa, Montreal) using *Arthrobacter globiformis NRRL B-2880, Arthrobacter globiformis B-2979, and Arthrobacter sp. ATCC 21022* as the hosts. A sampling of transmission electron micrographs reveals siphoviral morphology. Examples of phages displaying these morphologies include phage BlueFeather, Corgi, Yavru, Idaho, Noely, and Whytu. Photographs of plaque assays reveal small- to medium-sized clear plaques.

Genometrics

Average length for the genomes is 15,532 bp (range: 15,013 bp - 16,302 bp) with average GC content of 65.5% (range: 63.6% - 68.3%). The ends of the genomes have a 3’ sticky overhang.

Gene Content

a. A survey of all manually genomes in this cluster (i.e., excluding draft genomes) reveals the number of genes called per genome ranges between 22-27 genes, which represent 68 gene phamilies (or phams).

b. Of the 68 phamilies, 8 are conserved across cluster FE. These phams are assigned putative functions that include those involved in structure and assembly (e.g., terminase, portal protein, head-to-tail adaptor, tail terminator, tape measure protein) and lysis (e.g., endolysin and holin). There are no annotated DNA replication or recombination genes. Notable putative functions include DNA methyltransferase, and HNH endonuclease.

c. Another 60 phamilies have varying levels of conservation. 32 phams were called in only one phage while another 7 phams were called in only two phages. Some of the

functions proposed for the putative genes in these phams include helix-turn-helix DNA binding domain protein, endolysin and lysin A.

d. No tRNA genes are identified in this cluster. There are also no identifiable integrase genes or repressor functions, suggesting that phages in this cluster do not form lysogens and are, thus, lytic phages.

e. The genomes are organized with genes involved in structure and assembly located in the left two-thirds of the genome. Genes involved in lysis (e.g., endolysin and holin) are located downstream of the structure and assembly genes. The final third of the genome mostly contains genes with no known function. In all but two genomes (Berka, BlueFeather), all genes are transcribed in the forward direction.

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

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