A 2024 Report on the Characteristics of Phages Assigned to Subcluster AP2

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Isolation and Morphological Characteristics

As of June 2024, 5 phages have been assigned to Actinobacteriophage subcluster AP2. Subcluster AP2 consists of lytic phages isolated from environmental samples collected in four locations (Georgia, Indiana, Pennsylvania, and New York) between 2017 and 2023 using *Arthrobacter globiformis* B-2979 as the host. A sampling of transmission electron micrographs (2 of 5) reveals these phages to have siphoviral morphologies, while photographs of plaque assays reveal small, pinpoint-sized, clear plaques. Examples of phages displaying these morphologies include Beagle and Odyssey395.

Genometrics

The genomes of phages in this subcluster have an average length of 69,741 bp (range: 68,891 bp—70,671 bp) and an average GC content of 65.7% (range: 65.6%—65.8%). The genomes have direct terminal repeat ends with an average length of 588 bp (range: 587-589).

Gene Content

a. A survey of all manually annotated genomes in this subcluster (i.e., excluding draft genomes) reveals that the number of genes called per genome ranges between 123 – 131 genes, representing 145 gene phamilies (or phams). 77% of genes called have unknown functions.

b. Of these 145 phams, 110 are fully conserved across the subcluster. These phams are assigned putative functions that are involved in structure and assembly (e.g., major and minor tail proteins, DNA binding protein, terminase small and large subunits, portal protein, major capsid proteins, head to tail adaptor, tape measure protein, tail assembly chaperone), replication and recombination (e.g., DNA primase/polymerase/helicase, RecA-like DNA recombinase, and RusA-like resolvase). Some other notable putative functions include DNA methyltransferase and deoxyuridine triphosphatase.

c. Another 35 phams have varying levels of conservation. Notable here are 22 phams, each only called once in this subcluster, while another 13 phams are each only called twice. All AP2 phages have an endolysin (or a version of an endolysin called Lysin A) in the center of the genome, in a somewhat non-canonical location (before the tape measure gene rather than after). Two different phams represent the endolysins called before the tape measure gene (Pham 182401 and Pham 87984).

d. No tRNA genes have been identified in this subcluster. There are also no identifiable integrase or repressor functions, suggesting that phages of this subcluster 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 found in the right two-thirds. Genes involved in lysis are located among the genes involved in structure and assembly between the major tail and tail assembly chaperone genes. The first third of genes are transcribed in the forward direction, and the remaining two-thirds are transcribed in the reserve direction.

References: No prior publications.

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

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