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

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Isolation and Morphological Characteristics

As of June 2024, 84 phages have been assigned to Actinobacteriophage cluster AK. Cluster AK consists of lytic phages isolated from environmental samples collected in 10 states (CA, DE, MA, NJ, NY, OH, OK, PA, TX, VA) between 2012 and 2024, using an *Arthrobacter* species (ATCC 21022) as the host. A sampling of transmission electron micrographs reveals these phages to have siphoviral morphologies, while photographs of plaque assays show plaques of variable size (from small to large). Examples of phages displaying these morphologies include phage Carpal and Korra.

Genometrics

The genomes of phages in this cluster have an average length of 43,582 bp (range: 42,561 bp—44,416 bp) and an average GC content of 61.1% (range: 60.6%—61.9%). The genomes have 3' cohesive ends.

Gene Content

a. A survey of all manually annotated genomes (n = 83) in this cluster (i.e., excluding draft genomes) reveals the number of genes called per genome averaged 61.1 and ranged between 57 – 65 genes, which represent a total of 106 gene phamilies (or phams).

b. Of these 106 phams, 35 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 protease, major capsid, head-to-tail adaptor, head-to-tail stopper, tail terminator, major tail, tail assembly chaperones, tape measure, minor tail proteins), lysis (e.g., endolysin, holin) and replication and recombination (e.g., Cas4 exonuclease, ASCE ATPase, DNA primase/polymerase/helicase, DNA polymerase I). Some other fully conserved phams with notable putative functions include PurA-like adenylosuccinate synthetase, dUTPase, and HNH endonuclease.

c. Another 71 phams have varying levels of conservation. In particular, ten phams are each only called once in this cluster, while another seven phams are each only called twice in this cluster. None of these phams have a predicted function. In addition, some of the not highly conserved phams have the following predicted function: DNA helicase (found in 11 phages), a second HNH endonuclease (16 members), tail spike (18 members), three minor tails proteins (38 members), one minor tail protein (44 members). We note that phages that have two minor tail proteins encoded by genes 1 and 2 (the "pyocin knob" proteins) have a shorter minor tail

protein gene after the tape measure gene. In comparison, phages without these early minor tail proteins have a longer minor tail protein gene after the tape measure gene. This arrangement divides the AK phages into two groups.

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. Most genes are transcribed in the forward direction, with the exception of 9 genes transcribed in the reserve direction, 5 of which are highly conserved (found in at least 76 out of 84 phages). These reverse genes are found together, just after the gene encoding the dUTPase, and are located in the last third of the genome.

References: Below are prior publications that include a description of this cluster.

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

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