A 2024 Report on the Characteristics of Phages Assigned to Subcluster AZ2

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Isolation and Morphological Characteristics

As of June 2024, subcluster AZ2 consists of three annotated phages. Phages in subcluster AZ2 are temperate phages that were isolated from environmental samples collected in two different states (New Hampshire and Pennsylvania), using *Arthrobacter globiformis* 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 turbid plaques. Examples of phages displaying these morphologies include phage Maureen, MaGuCo, and Liebe.

Genometrics

The genomes of phages in subcluster AZ2 have an average length of 45,176 bp (range: 43,924 bp – 45,803 bp) with an average GC content of 68.6% (range: 68.2 % – 68.8 %). These linear genomes have 3' sticky overhang ends.

Gene Content

A survey of all manually annotated genomes in this subcluster (i.e., excluding draft genomes) reveals the number of genes called per genome averages 67 genes (range 63 – 69 genes), which represent a total of 75 gene phamilies (or phams). 57 phamilies are fully conserved across the subcluster. The other 18 phamilies have varying levels of conservation.

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 minor tail proteins), replication and recombination (e.g., DNA primase/polymerase, DNA polymerase, DNA helicase, and resolvase), and lysis (e.g., endolysin). Some other notable putative functions include SprT-like protease, serine integrase, and the last gene, predicted to be an HNH endonuclease, which may be involved in genome packaging.

The other 18 phams have varying levels of conservation. Notable here are four phams unique to this subcluster (and only present in MaGuCo), while another 12 phams are each only called twice in this subcluster and have no known function. MaGuCo is the only phage with a DNA methyltransferase in this subcluster.

No tRNA genes were identified in this subcluster.

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, with the exception of a small ~162bp highly conserved gene with no known function that is transcribed in the reverse direction. This gene is located between a Holliday junction resolvase gene and a DNA primase/helicase.

References

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

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