A 2024 Report on the Characteristics of Phages Assigned to Subcluster AS2

Authors: Denise Monti[1], Viknesh Sivanathan[1]

Reviewing Author: Denise Monti[1]

Author Affiliations: [1]Howard Hughes Medical Institute, Chevy Chase, MD

Isolation and Morphological Characteristics

As of November 2024, 11 phages have been assigned to Actinobacteriophage subcluster AS2. Subcluster AS2 consists of temperate phages isolated from environmental samples using *Arthrobacter globiformis* as the host. Samples were collected in six United States locations (California, the District of Columbia, Hawaii, Maryland, New York, and Pennsylvania) between 2017 and 2024. A sampling of transmission electron micrographs reveals that most of these phages (64.29%) have siphoviral morphologies; the remaining 35.71% have no identified morphology. Photographs of plaque assays for phages reveal small (1-3 mm) clear plaques (LittleTokyo) and small (1-3 mm) turbid plaques (Lunar).

Genometrics

The genomes of phages in this cluster have an average length of 38,390 bp (range: 37,967 bp – 39,044 bp) with an average GC content of 66.6% (range: 65.8% – 66.8%). All sequenced genomes have 3’ 12 bp sticky overhangs (overhang sequence GAGTTGCCGGCA).

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 71 – 76 genes, which represent a total of 121 gene phamilies (or phams).

b. Of these 121 phams, 46 are fully conserved across the cluster. These phams are assigned putative functions that include those involved in structure and assembly (e.g., terminase, portal protein, capsid maturation protease, major capsid protein, head-to-tail adaptor, head-to-tail stopper, tail terminator, major tail protein, tail assembly chaperone, tape measure protein, minor tail protein) and replication and recombination (e.g., RecE-like exonuclease, RecT-like DNA pairing protein) and lysogeny (tyrosine integrase, immunity repressor).

c. Another 75 phams have varying levels of conservation. Notable here are multiple helix-turn-helix DNA-binding proteins (Pham 193642, Pham 189138, Pham 111363, Pham 194394, Pham 193749) and HNH endonucleases (Pham Pham193860, Pham 193684, Pham 193637, Pham194619).

d. No tRNA genes are identified in this cluster.

e. The genomes are organized with genes involved in structure and assembly located within the first fifth of the genome, while those involved in replication and recombination are in the center of the genome. Genes in the first fifth of the genome are transcribed in the forward direction, followed by a segment of reverse genes that span to the middle of the genome. Genes in the last half of the genome are all transcribed in the forward direction.

References: No prior publications.

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

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