A 2024 Report on the Characteristics of Phages Assigned to Subcluster AZ3

Authors: Madeline A. Dojs[1], Nicholas P. Edgington[2], Melinda Harrison[3], Adam D. Rudner[4], Sarah J. Swerdlow[5]

Reviewing Author: Véronique Delesalle[6]

Author Affiliations: [1]University of Mary, Bismarck, ND; [2]Southern Connecticut State University, New Haven, CT; [3]Cabrini University, Radnor, PA; [4]University of Ottawa, Ontario, Canada; [5]University of Pittsburgh, Greensburg, Greensburg, PA; [6]Gettysburg College, Gettysburg, PA

Isolation and Morphological Characteristics

As of June 2024, two phages have been assigned to Actinobacteriophage subcluster AZ3. Subcluster AZ3 consists of temperate phages that were isolated from environmental samples collected in two different states (California and Texas), using *Arthrobacter globiformis* as the host. Transmission electron micrographs reveal these phages to have siphoviral morphologies. Phage Snek reports clear plaques approximately 6mm in diameter. Examples of phages displaying these morphologies include phage Snek and Tweety19.

Genometrics

The genomes of phages Snek and Tweety19 in this subcluster have an average length of 40,873 bp with an average GC content of 66.2%. The genomes have 3'sticky overhang ends.

Gene Content

a. A survey of all manually annotated genomes in this subcluster (i.e., excluding draft genomes) reveals the number of genes called per genome to range between 68-69 genes, which represent a total of 68 gene phamilies (or phams).

b. Of these 68 phams, 68 are fully conserved across the subcluster. These phams are assigned putative functions that are involved in structure and assembly (e.g., terminase, portal protein, scaffolding, major capsid proteins, head to tail adaptor, tail terminator, major and minor tail protein, tape measure, tail assembly chaperones, and minor tail proteins), replication and recombination (e.g., endolysin, deoxynucleoside monophosphate kinase, exonuclease, Holliday junction resolvase, DNA primase/polymerase, DNA polymerase I, DNA binding protein, SprT-like protease, and HNH endonuclease), and an endolysin. Some other notable putative functions include serine integrase, NrdH-like glutaredoxin, and metallophosphoesterase.

c. One tRNA gene was identified in Tweety19. There is also one identifiable integrase or repressor function, suggesting that phages of this subcluster do form lysogens and are, thus, temperate phages.

d. 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 one highly conserved gene downstream of the DNA primase/helicase that is transcribed in the reverse direction.

References

1. Klyczek KK, Jacobs-Sera D, Adair TL, Adams SD, Ball SL, Benjamin RC, Bonilla JA, Breitenberger CA, Daniels CJ, Gaffney BL, Harrison M, Hughes LE, King RA, Krukonis GP, Lopez AJ, Monsen-Collar K, Pizzorno MC, Rinehart CA; SEA-PHAGES Program; PHIRE Program; Staples AK, Stowe EL, Garlena RA, Russell DA, Cresawn SG, Pope WH, Hatfull GF. Complete Genome Sequences of 44 *Arthrobacter* Phages. Genome Announc. 2018 Feb 1;6(5): e01474-17. doi: 10.1128/genomeA.01474-17. PMID: 29437090; PMCID: PMC5794937.

2. Kapinos A, Aghamalian P, Capehart E, Alag A, Angel H, Briseno E, Corado Perez B, Farag E, Foster H, Hakim A, Hernandez-Casas D, Huang C, Lam D, Mendez M, Min A, Nguyen N, Omholt AL, Ortiz E, Saldivar LS, Shannon JA, Smith R, Sridhar MV, Ta A, Theophilus MC, Ngo R, Torres C, Reddi K, Freise AC, Moberg Parker J. Novel Cluster AZ Arthrobacter phages Powerpuff, Lego, and YesChef exhibit close functional relationships with Microbacterium phages. PLoS One. 2022 Jan 13;17(1): e0262556. doi: 10.1371/journal.pone.0262556. PMID: 35025964; PMCID: PMC8758107.

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

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