A 2024 report on the characteristics of phages assigned to Cluster AR

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Isolation and Morphological Characteristics

As of June 2024, 21 phages have been assigned to Actinobacteriophage cluster AR. Cluster AR consists of lytic phages isolated from environmental samples collected in 6 different states in the United States, 1 sample from Canada, and 1 sample from Lithuania between 2014 and 2022 using *Arthrobacter sp.* 68b and *Arthrobacter sp.* ATCC 21022 as bacterial hosts. The earliest entry is phage ArV1 from a non-SEA_PHAGES institution isolated in 2014. A sampling of transmission electron micrographs reveals that most phages have myoviral morphology. Examples of phages displaying morphologies include Kabreeze, DrYang, and Linus. Plate images show small- to medium-sized clear plaques.

Genometrics

The genomes of phages in this cluster have an average genome length of 70,132 bp (range: 68,762 bp - 71,200 bp) and an average GC content of 61.7% (range: 61.5 % - 62.6 %). The genome ends are circularly permuted.

Gene content

a. A survey of all manually annotated genomes (n=20) in this cluster revealed the number of genes called per genome averaged 110 genes (range: 101 -114 genes), which represent a total of 188 gene phamilies (or phams).

b. Of these 188 phams, 58 are fully conserved across the cluster. These phams are assigned putative functions that are involved in structure and assembly (e.g., terminase, portal protein, major capsid protein, tail sheath protein, baseplate wedge), recombination/replication (e.g., ssDNA binding protein, helicase, DNA methyltransferase), and lysis (e.g., endolysin and holin).

c. Another 130 phams have varying levels of conservation. In particular, 50 phams appear in only one genome, and 10 phams appear in only two phages. Most of the not highly conserved phams contain genes of unknown function although a few phams include genes with the following predicted functions: endolysin, HNH endonuclease, NUDIX hydrolase.

d. No tRNAs were identified in the genomes. There are also no identified integrase or repressor genes 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. Genes associated with lysis (endolysin and holin) are located after the structure and assembly genes. Following the holin and before the baseplate wedge protein there are approximately 5 genes transcribed in the reverse direction, one of which is often a helix-turn-helix DNA binding domain protein. Replication and recombination genes are located after the reverse genes. Genes in the far left of the genome are mostly of unknown function. Some identified functions in the left hand of the genome include genes related to lysis (endolysin), DNA methylation (DNA methylase), and restriction endonuclease activity (HNH endonuclease).

References

1. Kaliniene L, Šimoliūnas E, Truncaitė L, Zajančkauskaitė A, Nainys J, Kaupinis A, Valius M, Meškys R. 2017. Molecular Analysis of Arthrobacter Myovirus vB_ArtM-ArV1: We Blame It on the Tail. J Virol 91:10.1128/jvi.00023-17. https://doi.org/10.1128/jvi.00023-17
2. 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: https://doi.org/10.1128/genomea.01474-17. PMID: 29437090; PMCID: PMC5794937.
3. Klyczek KK, Bonilla JA, Jacobs-Sera D, Adair TL, Afram P, Allen KG, Archambault ML, Aziz RM, Bagnasco FG, Ball SL, Barrett NA, Benjamin RC, Blasi CJ, Borst K, Braun MA, Broomell H, Brown CB, Brynell ZS, Bue AB, Burke SO, Casazza W, Cautela JA, Chen K, Chimalakonda NS, Chudoff D, Connor JA, Cross TS, Curtis KN, Dahlke JA, Deaton BM, Degroote SJ, DeNigris DM, DeRuff KC, Dolan M, Dunbar D, Egan MS, Evans DR, Fahnestock AK, Farooq A, Finn G, Fratus CR, Gaffney BL, Garlena RA, Garrigan KE, Gibbon BC, Goedde MA, Guerrero Bustamante CA, Harrison M, Hartwell MC, Heckman

EL, Huang J, Hughes LE, Hyduchak KM, Jacob AE, Kaku M, Karstens AW, Kenna MA, Khetarpal S, King RA, Kobokovich AL, Kolev H, Konde SA, Kriese E, Lamey ME, Lantz CN, Lapin JS, Lawson TO, Lee IY, Lee SM, Lee-Soety JY, Lehmann EM, London SC, Lopez AJ, Lynch KC, Mageeney CM, Martynyuk T, Mathew KJ, Mavrich TN, McDaniel CM, McDonald H, McManus CJ, Medrano JE, Mele FE, Menninger JE, Miller SN, Minick JE, Nabua CT, Napoli CK, Nkangabwa M, Oates EA, Ott CT, Pellerino SK, Pinamont WJ, Pirnie RT, Pizzorno MC, Plautz EJ, Pope WH, Pruett KM, Rickstrew G, Rimple PA, Rinehart CA, Robinson KM, Rose VA, Russell DA, Schick AM, Schlossman J, Schneider VM, Sells CA, Sieker JW, Silva MP, Silvi MM, Simon SE, Staples AK, Steed IL, Stowe EL, Stueven NA, Swartz PT, Sweet EA, Sweetman AT, Tender C, Terry K, Thomas C, Thomas DS, Thompson AR, Vanderveen L, Varma R, Vaught HL, Vo QD, Vonberg ZT, Ware VC, Warrad YM, Wathen KE, Weinstein JL, Wyper JF, Yankauskas JR, Zhang C, Hatfull GF. Tales of diversity: Genomic and morphological characteristics of forty-six Arthrobacter phages. PLoS One. 2017 Jul 17;12(7): e0180517. doi: 10.1371/journal.pone.0180517. PMID: 28715480; PMCID: PMC5513430.

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

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