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

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Isolation and Morphological Characteristics

As of October 2024, 22 sequenced phages have been assigned to Actinobacteriophage cluster DR. Cluster DR consists of lytic phages that were isolated from environmental samples collected from 8 different US states, using *Gordonia terrae 3612 and Gordonia rubripincta* as the host. A sampling of transmission electron micrographs reveals these phages to have siphoviral morphologies, while photographs of plaque assays reveal small clear plaques. Examples of phages displaying these morphologies include phage CaiB and Wooper.

Genometrics

The genomes of phages in this cluster have an average length of 61,541 bp (range: 59,580 bp – 63,202 bp) with an average GC content of 69.3% (range: 67.6% – 70.5%). The genomes have circularly permuted ends.

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 ranges between 79-87 genes, which represent a total of 218 gene phamilies (or phams).

b. Of these 218 phams, 36 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 and minor capsid proteins, tape measure, tail assembly chaperones, head-to-tail adaptor, and minor tail proteins), replication and recombination (e.g., DNA primase/polymerase, DNA polymerase alpha subunit, DNA helicase, exonuclease (e.g., Cas4/RecB-like), HNH endonuclease, and RuvC-like resolvase), and lysis (e.g., lysinA and lysinB).

c. Another 182 phams have varying levels of conservation. 77 phams appear only once in the cluster. Functions assigned to some of these phams include HNH endonuclease, GTP cyclohydrolase I, QueE, and QueD-like queosine biosynthesis proteins.

d. Only 1 tRNA gene (tRNA-Arg) is identified in this cluster. This one tRNA gene is found in phage Evaa. No other Cluster DR phage genomes have an identified tRNA gene. 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. The first third of the genome is transcribed in the forward direction (except for a few recombination/replication genes). The remaining two-thirds of the genome contains 2 reverse-transcribed groups of genes with one forward-transcribed group of genes between the reverse-transcribed genes.

References

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

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