CONSIDER FOR TALK

9th Annual SEA-PHAGES Symposium Abstract

University of Pittsburgh

Pittsburgh PA

Corresponding Faculty Member: Marcie Warner (mwarner1@pitt.edu)



Seohyun Im



Allison Schultz

Gordonia phages are highly diverse genetically and exhibit curious patterns in infection of different Gordonia species

Seohyun Im, Allison Schultz, 2016-17 Pitt SEA-PHAGES students, Lyndsay Avery, Rebecca Bortz, Emily Furbee, Sarah Grubb, Debbie Jacobs-Sera, Wynn Meyer, Marcie Warner, Welkin H Pope, Graham F Hatfull

The majority of sequenced bacteriophage isolates infect the same host, *Mycobacterium smegmatis* mc2155. During the 2016-17 academic year, University of Pittsburgh SEA-PHAGES students isolated phages from a related host, *Gordonia terrae* 3612. Like *Mycobacterium* sp., *Gordonia terrae* is of the phylum Actinobacteria. *Gordonia* species have been implicated in foaming of sludge in wastewater treatment plants and human catheter-related infections, suggesting potential industrial and medical applications of this research. SEA-PHAGES students identified 348 *Gordonia* phages of which fifty-two were sequenced. The diversity of these phages is apparent in their variation in G+C content and genome size: G+C content ranges from 50.2% (Ronaldo and Fryberger) to 70% (Yago84) (average 62.8%) and genome size varies nearly 10-fold (smallest = Coeur at 16,223 bp; largest = SCentae at 151,316 bp; average = 66,898 bp). Diversity is also apparent when comparing nucleotide sequences of these phages’ genomes; they span 12 extant clusters (CQ, CR, CS, CU, CV, CX, CZ, DB, DC, DD, DE, and DG), establish 6 new clusters (DH, DI, DK, DN, DO, and DP), and include four new singletons (Angelique, Coeur, Reyja, and Forza).   
Although Reyja is classified as a singleton, a large portion of its genes are conserved and appear to be related to genes from cluster CU and CD *Gordonia* phages as well as cluster F and K mycobacteriophages. In contrast, the 192 genes of the singleton Forza are mostly orphams. The cluster that underwent the greatest expansion due to our discoveries was Cluster CS, which gained 12 additional members (20 total phages). To better characterize this rapidly expanding cluster, we tested the ability of nine CS cluster members (Anamika, BirksAndSocks, Neoevie, Woes, Hotorobo, Chelms, Gorko, Lahirium, and Boneham) to infect four additional *Gordonia* sp. hosts: *G. lacunae*, *G. rubripertincta*, *G. westfalica*, and *G. neofelifaecis*. Six of the cluster CS *Gordonia* phages tested on alternate hosts infect all of them except *G. neofelifaecis*. However, BirksAndSocks infects all of the *Gordonia* strains tested, Lahirium infects only *G. lacunae* and *rupripertincta*, and Woes does not infect any of the alternate *Gordonia* species tested. *Gordonia terrae* phages frequently exhibit promiscuity with regard to infection of alternate *Gordonia* sp, but our results indicate that host range is variable even amongst phage grouped within the same cluster. Although minor tail proteins are frequently involved in host recognition, the only evident difference in minor tail protein pham content amongst this group of phages is the presence of pham 24769 in phages Chelms, Hotorobo, and Gorko in place of pham 20187 in the others. This difference does not correlate with the differences in infection patterns, suggesting that the unique patterns of host range observed with cluster CS phages is due to an as yet undetermined mechanism.