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2021 SEA Symposium Abstract

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The genetic diversity of Gordonia phages may offer insights into the mechanisms that control viral host range

2020-21 Pitt SEA-PHAGES Students, Ping An, Meredith Barbieri, Meghan Bechman, Rebecca Bortz, Kristen Butela, Aimee Danley, Sean Gess, Jennifer Grousd, Brenda Hammer, Nicole McAllister, Aparna Nigam, Ruth Orr, Jessica Robertson, Scott Stuckman, Marcie Warner

The collection of over 18,000 actinobacteriophages, with 3700 of these being sequenced, can reveal insights into phage diversity and evolution. The 2020-2021 student cohort of phagehunters at the University of Pittsburgh isolated 135 phages from environmental samples using the host *Gordonia terrae* 3612, contributing to the overall total of over 2200 phages isolated on *Gordonia* hosts. The genomes of 28 of these phages were sequenced, adding to the existing collection of 548 sequenced *Gordonia* phages. These phage genomes are characteristically mosaic and span considerable genomic diversity, being assigned to 15 extant clusters (A [1], CR [2], CS [2], CT [1], CV [4], CY [3], CZ [6], DA [1], DB [1], DE [3], DG [1], DI [1], DN [1], DY [1]). Phages isolated during the 20-21 academic year differ in genome length ranging from 40,547 bp (Tarzan, Cluster DY) to 75,886 bp (Lizzo, Cluster CS), and G+C% content, ranging from 59% (Lizzo, Cluster CS) to 68.3% (Hans, Cluster DE; *G. terrae* is 67.8%).  
  
In light of the SARS-CoV-2 pandemic, exploration of the mechanisms that control the expansion of viral host range is a critical area of biology that merits further exploration. 20-21 Pitt students sought to address this subject by examining the ability of phages from a variety of clusters to infect several additional *Gordonia* species other than *G. terrae* (in order of nucleotide similarity to *G. terrae*: *G. lacunae*, *G. westfalica*, and *G. rubripertincta*). Phage Leroy (cluster DN) was not able to infect any of the additional *Gordonia sp* hosts. Phages Jalammah (CV) and Floral (CY1) were only able to infect *G. rupripertincta* at a substantially reduced efficiency when compared to infection of *G. terrae*. Two cluster CZ phages (Alum E [CZ1] and Gizermo [CZ2]) were able to infect both *G. rubripertincta* and *G. lacunae*, whereas phage AikoCarson (CT) was able to infect all three alternate *Gordonia sp* hosts at a reduced, but substantial, efficiency when compared to infection of *G. terrae*. This diverse pattern of host infection profiles suggest viral host range is controlled a complex array of factors. Comparison of the genetic content of these phages may shed light on common genetic factors and mutations that influence host range.