CONSIDER FOR TALK

9th Annual SEA-PHAGES Symposium Abstract

Alliance University (formerly Nyack College)

New York NY

Corresponding Faculty Member: Jackie Washington (washjd4@gmail.com)



Maridalia Lillis



Mariana P Moraes

Exploring New Terrae-tories with Gordonia Phages

Maridalia Lillis, Mariana P Moraes, Jellissa Garcia, Rachel Meiners, Jeremiah Sylvain, Peter J Park, Jacqueline M Washington

*Gordonia* sp. are aerobic Gram-positive bacilli that are related to *Mycobacteria* sp. as both are members of the phylum Actinobacteria. Compared to mycobacteriophages, little is known about other actinobacterial phages. Therefore, isolation and characterization of other types of actinobacterial phages will not only increase the diversity of bacteriophages but also give us further insight to phage biology and their evolution. During the 2016-17 academic year, Nyack College isolated bacteriophages using *Gordonia terrae* 3612 as a host and an isolation temperature of 28 degrees. Eight *Gordonia* phages were isolated, five of which were sequenced and identified as members of five different clusters (A15, CV, DN, DD, and DE). The DN cluster phages form a new cluster with six phages first isolated and identified in 2016 from sites in five states across the United States.

The genomes of the sequenced phages range in size from 49,965 bp (Fenry, CV) to 57,555 bp (Ashertheman, DE) with as few as 80 putative genes in Fenry and up to 108 genes in both Phistory (DN) and ShayRa (A15). Similar to other actinobacteria, *Gordonia terrae* has a high GC content of 67.8%. The isolated *Gordonia* phages range from a GC content of 62.1% (ShayRa) to 68.0% (Ashertheman). Interestingly, to date of the nine A15 phages, ShayRa is the smallest primarily due to a 1.3kb deletion in the region where the immunity repressor is typically found. Additional bioinformatic analysis of the phages will be presented.

To further investigate and characterize these phages, wet bench experiments were performed including SDS analysis, temperature sensitivity, determination of host range and immunity assays. SDS analysis of the structural genes revealed unusual results in that although the phages are members of different clusters, the structural genes appear to be of identical sizes. All the phages were able to be grown at temperatures higher than the isolation temperature of 28 degrees, with the exception of Ashertheman (DE). Growth of Ashertheman at 37 degrees results in a several fold loss of viability. Interestingly, these temperature resistant mutants show similar growth profiles at both 28 and 37 degrees. Further experiments to understand the exact mechanism for the acquired temperature resistance are ongoing. To date, host range experiments show that these *Gordonia terrae* phages were unable to infect several strains including *Gordonia amarae*. As several of the phages are able to form lysogens, the results of immunity experiments will also be presented.

Lastly, DNA sequence analysis determined that one of our phages Chazimma was a mixture of DD and DE phages. Indiscernible by plaque morphology, we will present our work on techniques used to separate these phages which proved to be surprisingly challenging.