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9th Annual SEA-PHAGES Symposium Abstract

College of Idaho

Caldwell ID

Corresponding Faculty Member: Ann Koga (akoga@collegeofidaho.edu)



Alyssa Case



Nicole Jordan

Characterization of Gordonia phages asapag and WilliamBoone

Alyssa Case, Nicole Jordan, Nilofar Abdul Shukar, Neal Baronian, Emily Bartlett, Jose Cordova, Kirk Doering, Lauren Downer, Miranda Harrington, Brady Nilsson, Jade Rencher, Daniel Sandoval, Laurel Weiss, Elizabeth West, Ann Koga

In the fall semester we isolated six bacteriophages from *Gordonia terrae* and two phages from *Mycobacterium smegmatis*. We found, through transmission electron microscopy, that the phages all had siphoviral morphology. Because there have been a plethora of mycobacteriophages sequenced, we submitted two *Gordonia* phage DNA samples (WilliamBoone & Asapag) for genome sequencing. WilliamBoone was found to have a genome length of 92,688 bp, and Asapag a much shorter genome length of 55,119 bp. WilliamBoone is a member of Cluster CQ, has a GC content of 61.9%, has eight predicted tRNA genes, and 185 predicted protein-encoding genes, including a programmed frameshift in the tail assembly chaperone protein gene. Although WilliamBoone has a predicted integrase gene, immunity repressor gene and exonuclease gene, we were unable to locate an attB integration site in *Gordonia terrae*. Asapag is a co-founder of a new phage cluster, DN, has a GC content of 63.1%, no predicted tRNA genes, and 101 predicted protein-encoding genes. Five other DN cluster phages were sequenced this year. Asapag has a high degree of nucleotide homology with all five other newly-discovered DN phages. At the right end of the Asapag genome there are several “white” genes. Analysis by HHPred (1) revealed homology of a few of these gene products with previously-described toxin-antitoxin gene products; however the motifs identified are also consistent with transcriptional regulators. More investigation is needed to verify the functions of these genes.  
  
1.Söding J, Biegert A, Lupas AN. 2005. The HHpred interactive server for protein homology detection and structure prediction. Nucleic Acids Res 33:W244–W248.