CONSIDER FOR TALK

11th Annual SEA Symposium Abstract

College of Southern Nevada

Las Vegas NV

Corresponding Faculty Member: James Theoret (james.theoret@csn.edu)



D'Andrew L Harrington

The College of Southern Nevada’s Exploration and Annotation into the DR and CS Clusters throughout the Las Vegas Valley

D'Andrew L Harrington

Throughout the 2018-2019 Fall and Spring semesters, the College of Southern Nevada’s SEA-PHAGES team studied methods of articulation with biological and computational sciences regarding the extraction, annotation, and experimentation of novel *Gordonia*-phages Jellybones and Nhagos. Both phages were discovered within the Las Vegas valley and were identified using the host bacterium *Gordonia rubripertincta*. While sharing the same morphotype, siphoviridae, both phages provided unique overall results. Jellybones exhibited optimal temperatures differing from Nevada’s average soil temperatures.   
  
Jellybones, a CS2 subcluster *Gordonia*-phage, was discovered within the City of Henderson’s Bird Viewing Preserve. Producing plaques ranging from ½ - 1mm, Jellybones has a genomic length of 77,514 base pairs covering 108 encoded genes; 1 transfer RNA was detected with an anti-codon of GTT (Asparagine). A GC percentage of 59.0% was above the 58.9% average for this subcluster. 32.0% of Jellybones was annotated without a classification of NKF. Annotations of *Gordonia*-phage Jellybones was completed with; DNA Master, GeneMark, HHpred, Blast, Starterator, Phamerator, SOSUI, and TMHMM. Experimentation of Jellybones was conducted to determine calcium dependency and temperature ranges for optimal lytic cycles. Results of our temperature assay shows an optimal temperature for the lytic cycle at 20 °C. Results of our calcium assay show plaque growth in the presence of calcium through a lytic cycle. These results can be used for future investigation of *Gordonia*-phages by the College of Southern Nevada’s cohort.  
  
NHagos, a DR cluster *Gordonia*-phage, was discovered within a flamingo exhibit. Producing small, clear and round plaques, Nhagos is a circularly permuted genome sequence with a genomic length of 59,580 base pairs covering 83 encoded genes; no tRNA was detected. A GC of 68.2%, was lower than the 69.2% average for the DR cluster. Annotation and review through Gepard indicate a similar mosaic structure to that of the B (*Mycobacterium*) and W (*Mycobacterium*) clusters. We replicated these findings by providing three separate phages from each cluster; The W cluster consisted of *Mycobacterium*-phages Cepens, GodPhather, and Megabear, while, The B cluster consisted of *Mycobacterium*-phages Cheet0, Apex, and Abinghost. These similarities are measurable within Phamerator throughout each cluster, indicating levels of homology within each cluster. This method of determining homology could, in theory, reduce the amount of NKF proteins found relating to morphotype. The College of Southern Nevada is proud to share its first findings for the SEA-PHAGES symposium and how temperature, calcium, and mosaic patterns could be found in a sea of collaboration.