CONSIDER FOR TALK

2021 SEA Symposium Abstract

La Sierra University

Riverside CA

Corresponding Faculty Member: Arturo Diaz (adiaz@lasierra.edu)

Annotation and Comparative Analysis of Two New Microbacterium foliorum Bacteriophages, Skylord and SBlackberry

Sabrina Benitez, Emily Bouit, Earick J Cagang, Joshua Cantos, Rita Dementyev, Ethan Dewri, Christian Figueroa, Nicole Kim, Rosalia Marenco, Soojeong Moon, Kristen Ngo, Brian Nguyen, Elizabeth Paul, Jennifer Ramon, Joanna Shelim, Jiacheng Zhang, Natasha Dean, Arturo Diaz

Students at La Sierra University discovered 20 novel bacteriophages. Nineteen were isolated from *Microbacterium foliorum* and one from *Gordonia rubripertincta*. Eight phages were obtained through direct plating and 12 through enrichment cultures. These phages exhibit small to medium-sized clear plaque formations. We selected two *M. folioru*m phages, Skylord and SBlackberry, for further analysis.  
  
While Skylord’s tail length is 121.8 nm with a capsid diameter of 65.5 nm, SBlackberry’s capsid morphology is yet to be determined. Using bioinformatic tools such as PECAAN, Phamerator, NCBI Blastp, and HHPred, gene functions were assigned to less than half of the genes for each phage. Skylord’s genome is 39,843 base pairs, with a GC-content of 67.1%. It has 68 genes, of which 33 were assigned functions, and one tRNA. SBlackberry’s genome is 42,048 base pairs, with a GC-content of 66.9%. It has 58 genes, of which 31 were assigned functions. Compared with other phages within Cluster EB, Skylord was found to have a smaller genome length than the average 41,290 base pairs. SBlackberry, classified within Cluster EJ, was found to be smaller than the average genome length of 42,243 base pairs.  
   
While Skylord encodes for a membrane protein and an endolysin, SBlackberry encodes for lysins A and B, holin, and a membrane protein within the same operon. A host range assay performed on various other *Microbacterium* species revealed that these phages could only infect M. foliorum. Investigation of these phages contributes to a greater understanding of phage classification into clusters and phage biology overall.