DO NOT CONSIDER FOR TALK

2021 SEA Symposium Abstract

James Madison University

Harrisonburg VA

Corresponding Faculty Member: Steven Cresawn (cresawsg@jmu.edu)



Elizabeth A Gage



Erica A Glines



Allison N Majors



Samantha T Steigleman-Cox

Genomic characterization of Mycobacteriophages HarveySr and Gravaillia

Alec A Catterton, Elizabeth A Gage, Erica A Glines, Renee C Hartzog, Liana M Jackley-Angulo, Nicholas J Kurdziel, Allison N Majors, Elizabeth H Raterman, Joshua C Sin, Samantha T Steigleman-Cox, Zainab N Alabbasi, Steven G Cresawn

We describe two Mycobacteriophages, HarveySr and Gravaillia, isolated in 2019 from Harrisonburg, Virginia and fully sequenced at the Pittsburgh Bacteriophage Institute using an Illumina MiSeq. Both phages infect *Mycobacterium smegmatis* mc^2 155, a safe and fast growing relative of several human pathogens. Mycobacteriophages have broad genetic diversity and great potential for therapeutic applications in controlling antibiotic-resistant bacterial infections. HarveySr and Gravaillia belong to the family Siphoviridae and are lytic and temperate, respectively. HarveySr is a member of subcluster B3 while Gravaillia belongs to cluster Q. HarveySr has a genome length of 67,773 bp and Gravaillia has a relatively shorter genome length of 53,924 bp. HarveySr contains 100 total protein-coding genes while Gravaillia has 87. Each phage genome has a GC content of 67.6%, which is nearly identical to 67.4% GC content of the M. smegmatis genome. Of the 100 gene products encoded by the HarveySr genome, 11 have matches to the NCBI Conserved Domain Database (CDD) including 9 genes with matches to domains having known functions. There are also 11 genes with functionally annotated homologs in other B3 phages. In the Gravaillia genome, 12 of 87 gene products match conserved domains, 11 of which have known functions. In the temperate phage Gravaillia, gene 50 was identified as the immunity repressor, and the region between 24,863 bp and 24,908 bp was identified as the probable attP site based on its proximity to the predicted Gravaillia integrase, gene 29, and its similarity to a host tRNA gene (a common integration site). Three additional regions in the *M. smegmatis* genome were identified as having equivalent sequence similarity to the putative attP site. Future plans include the isolation and subsequent whole genome sequencing of a Gravaillia lysogen using an Oxford Nanopore MinION to resolve the ambiguity over the specific site of integration.