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Austin Peay State University

Clarksville TN

Corresponding Faculty Member: Sergei Markov (markovs@apsu.edu)

Isolation, characterization and genome annotation of bacteriophage Librie

Nygil L Arms, Kayla J Boyce, Melody R Cardona Pendleton, Angilena M Couch, Leigh E Duncan, Osamiabe I Enodiana, Jaci N Gibson, Kendall J Greer, Claudine M Habib, Ariel A Hensley, Ugonna G Isaac, Tamia C Johnson, Gabriella G Lewis, Summer K Long, Isela A Ogas, Kehinde O Olusoga, Patience O Oni, Kim-Ngan H Victory, Robin J Zimmer, Sergei A Markov

Two new bacteriophages, Librie and CaptainRex, were isolated and characterized from soil samples at Austin Peay State University (APSU) campus using a host bacterium *Microbacterium foliorum* NRRL B-24224. The collected bacteriophages were purified, amplified to high titer lysates, and examined using transmission electron microscopy. All bacteriophages were from the Siphoviridae family with a flexible tail.  
The University of Pittsburgh sequenced bacteriophage Librie' DNA isolated at APSU. The genome of bacteriophage Librie was then manually annotated. It is from the cluster EA and subcluster EA5. Bacteriophage Librie’s DNA size is 39,941 bp with GC content of 65.3%. The bacteriophage had 61 predicted protein-coding genes (of which we assigned predicted function for 30 genes) and 1 gene for tRNA in its sequence. This bacteriophage had predicted programmed translational frameshifts in genes 16 and 17 (tail assembly chaperone genes). Based on Gene Content Similarity tool, this bacteriophage is closely related to the bacteriophage Hasitha (95.19%), which was found in Bowling Green, KY. Currently, subcluster EA5 contains only 8 bacteriophages with an average genome size of 40,634 bp.   
The general genomic architecture of bacteriophage Librie is not canonically organized. The left part of its genome contains genes for structural proteins as in other phages of clusters EN, EC and EE, and the right side of the genome has mainly leftwards-transcribed genes for membrane proteins, DNA replication and metabolism and others genes.