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Isolation and genome annotation of two new bacteriophages, DumpQuist and ChikPic

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Two new bacteriophages, DumpQuist and ChikPik, were isolated and characterized from soil samples at Clarksville, TN 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 and comparative genomics. Bacteriophage DumpQuist is from *Podoviridae* family with a short tail and bacteriophage ChikPic is from the *Siphoviridae* family with a flexible, long tail.
The University of Pittsburgh sequenced bacteriophage DNAs isolated at Austin Peay State University. The genomes of bacteriophages were then manually annotated. Bacteriophage DumpQuist is from the cluster EK and subcluster EK1. Its DNA size is 53,924 bp with GC content of 60.1%. The bacteriophage had 54 predicted protein-coding genes (of which we assigned predicted function for 13 genes). Based on Gene Content Similarity (GCS) tool, this bacteriophage is closely related to the bacteriophage ArMaWen (100%), which was found in Baltimore, MD. Bacteriophage ChikPic (40,333 bp genome size with 62.0% GC content) is from a different cluster EA, subcluster EA2 and has 64 predicted protein-coding genes (of which we assigned predicted function for 25 genes). This bacteriophage had predicted programmed translational frameshifts in genes 13 and 14 (tail assembly chaperone genes). Based on GCS, this bacteriophage is closely related to bacteriophage Eleri (99.22%) found in College Park, MD. Currently, subcluster EA2 contains only 10 bacteriophages with an average genome size of 40,365 bp.