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2025 SEA Symposium Abstract

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Genome Annotation of Cluster A3 Phage Giroux

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Giroux, a mycobacteriophage, was discovered in 2023 by Samuel Burkhimer in Phoenixville, PA, US. It was isolated from a damp garden soil sample collected on a warm October day. Giroux is a temperate Siphoviridae phage with a genome size size of 50,457 bp, and belongs to Cluster A, subcluster A3. Programs used for annotation include DNA Master, NCBI BLAST, Phamerator, Starterator, GeneMark, Gene Content Similarity Tool, and HHPred.
During annotation, DNA Master identified 86 genes, including 2 tRNA genes, while PhagesDB predicted 88 genes, and Phamerator called 93 genes. Out of the 86 Open Reading Frames (ORFs) identified in DNA Master, 63% were reverse genes, and 37% were forward genes. The most frequent start codon (67%), initiating the translation process was ATG, followed by GTG (26%), and TTG (6%). The longest gene, encoding a tape measure protein, was 2190 bp, while the shortest gene encodes a portal protein.
Among the 86 ORFs, 33 genes have known functions, including structural proteins such as the minor tail protein, portal protein, major capsid protein, and tail assembly chaperone. Additionally, DNA processing and replication-associated proteins, including HNH endonuclease, DNA primase, metallophosphatase, Cas4 exonuclease, and immunity repressor, were identified. Host lysis-related proteins such as Lysins A and B were also annotated.
Giroux exhibits strong genetic similarity to other subcluster A3 members, with the highest gene content similarity observed in Puppy (93.7%), followed by Pistachio (93.1%), TNguyen7 (92.7%), Idleandcovert (91.8%), and Heathen (90.8%). When compared to phages previously annotated by Unilag, Giroux shows significantly lower similarity: Peterson (26.3%), Ringer (26.0%), Kenmech (24.8%), and Arcanine (24.5%).