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Genome Analysis of the AN Cluster Bacteriophage Kels

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The goal of this study was to annotate the novel bacteriophage Kels belonging to the AN cluster of Actinobacteriophages. The AN cluster includes 39 phage members, with the average genome size of 15,532bp. Phages in this cluster appear to be lacking the tRNA genes. The genome of phage Kels, discovered in Pittsburgh, PA, is 14830 bp long, has the GC content of 65.4%, and composed of 23 genes. This bacteriophage, isolated on the Arthrobacter globiformis host, utilizes the lytic cycle.
Phage Kels was compared to other members of the corresponding cluster to evaluate the gene content similarity. Comparative genome analysis of all AN cluster phages demonstrated a relatively low variation in GCS, ranging between 69.1% and 65.3%. The highest level of GCS of 65.3% was noted between phage Kels and phage Toulouse, discovered and characterized in Hudson, WI earlier. Genome analysis and annotation were performed using PECAAN, Phamerator, Starterator, as well as run through the DNAmaster annotation software tool. We conclude that in spite of the differences in geographical distribution, AN cluster phage genomes exhibit significant genome and gene function similarities.