CONSIDER FOR TALK

7th Annual SEA-PHAGES Symposium Abstract

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Characterization of Leston, a novel Mycobacteriophage of the subcluster K5

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Studies on the composition and action of bacteriophages can provide insight into the physiology of bacteria and, in the case of pathogenic organisms, suggest mechanisms for their control or elimination. In collaboration with the Science Education Alliance, National Genomic Research Initiative, and Graham Hatfull’s laboratory at the University of Pittsburgh, we are investigating the diversity and genomic strategies of action of bacteriophages that are capable of infecting a laboratory strain of *Mycobacterium smegmatis*.
Investigators collected environmental samples from the El Paso area and assayed them for phage activity. Positive samples were processed to enrich and isolate bacteriophages. Eleven independent phage isolates were purified and characterized by electron microscopy and by DNA restriction analysis. Structural features and DNA fingerprints were compared to mycobacteriophages reported on phagesdb.org. On the basis of its unique characteristics, the bacteriophage Leston was selected for genomic study. Purified DNA was sequenced at Virginia Commonwealth University using 454 technology and assembled to a finished genome of 61,898 bp. Leston was isolated from soil obtained from the Franklin Mountain range, in west El Paso, TX. Its capsid morphology identifies it as a member of the Siphoviridae, and its genome is linear with defined ends and a 3’ overhang. Initial BLAST comparisons to known phage genomes reveal that Leston is a class K5 Mycobacterium phage. Preliminary analysis using Glimmer and GeneMark identified 98 protein coding genes and one tRNA‐Trp gene. We have annotated each of the predicted genes, including phage structural proteins and DNA replication enzymes, and we are investigating additional potential coding regions. Interestingly, scattered along this phage genome we found multiple gap regions between genes, with the longest being 359 bp. The complete annotation of Leston’s genome and its comparison with other mycobacteriophages will provide important insights on the biology and evolution of the most abundant members of Earth’s biome.