CONSIDER FOR TALK

8th Annual SEA-PHAGES Symposium Abstract

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The discovery and annotation of mycobacteriophages HedwigODU and Goldilocks

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As part of the HHMI SEA-PHAGES program, the Old Dominion University Phage Hunters have isolated over a dozen mycobacteriophages. Bacteriophages are ubiquitous in nature and were isolated from soil samples taken from the Tidewater region of Virginia during the first semester of the Phage Discovery and Genomics class. The successful method of isolation was through the use of enrichment (not direct plating) with the host *Mycobacterium smegmatis* mc2155. Many rounds of purification were completed to isolate pure phage using the method of picking a plaque and plating out dilutions as well as using the stick streak method. High titer lysates were produced to isolate viral genomic DNA.   
  
Subsequently, DNA restriction endonuclease mapping revealed unique phages based on the digestion profiles compared to gels submitted to the Actinobacteriophage Database. Transmission electron microscopy revealed that each phage displayed morphological characteristics consistent with a *siphoviridae* morphotype. Two of these newly isolated phages, named HedwigODU and Goldilocks, were chosen for genomic sequencing, analysis and annotation. During the Spring 2016 semester, students in the Phage Discovery and Genomics class annotated and focused on independent projects to understand the genome of these two mycobacteriophage. The genome of HedwigODU consisted of 59,812 bp in length with a nucleotide sequence similar to cluster K (subcluster K1) mycobacteriophages. The genome of Goldilocks comprised of 75,728 bp in length and was characterized as a cluster E mycobacteriophage. HedwigODU and Goldilocks had very few tRNA elements, numerous hypothetical proteins, with synteny among the structural genes and conserved terminase, portal proteins, lysins and both contained a translational frameshift as well as many reverse genes.