CONSIDER FOR TALK

9th Annual SEA-PHAGES Symposium Abstract

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Duke\_13, Passionfruit, and Shiloh(s): Comparative analysis of annotated J-cluster genomes

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Mycobacteriophages in the J-cluster have genomes almost twice the size of the typical myoviridae genome. While the average genome length for phages is around 60,798 base pairs, the J cluster has an average of 110,948 base pairs.
Duke\_13 is a J-cluster phage isolated in 2012 as part of the PHIRE program. Duke\_13 has a typical J-cluster genome size with 111,970 base pairs making up 246 annotated genes. Ninety one genes (~37%) were conserved in all 35 other J-cluster genomes based on analysis in Phamerator. We present core and accessory J-cluster genome and Phams of J-cluster phages were mostly conserved in the E, L, O, X, and Y clusters. None of the J-cluster phams was found in all other clusters.
The annotation of an adopted PHIRE genome came about due to our submission of a genome sample containing two J-cluster genomes, Shiloh-1 and -2. We present work attempting to separate these two from one another and comparing it to Passionfruit, which was isolated from the same original direct isolation plate in fall 2016.
This work adds to our understanding of conservation among these surprisingly long siphoviridae mycobacteriophage genomes and offers guidance for future J-cluster annotation projects.