CONSIDER FOR TALK

7th Annual SEA-PHAGES Symposium Abstract

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Genomic analysis of four mycobacteriophages from Southern Connecticut: Two A3’s, EpicPhail & Veracruz, and two new N cluster phages, Xeno and Phrann.

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SCSU Honors College Freshman isolated 16 new mycobacteriophages that have the ability to infect *M. smeg.* mc2 155 at 42°C. We selected this temperature for several reasons. One reason is that we hoped that the increased temperature would perhaps select for novel cluster members. A second reason is that many other microorganisms cannot grow at 42°C, and thus this temperature would help to reduce contamination problems that could arise. Finally, the higher temperature facilitated a growth rate that allowed plating results to be seen in approximately 24 hours. The sequence was determined for three genomes which revealed their membership in the A11 subcluster (Snape--which we will discuss next year), and the N cluster (Xeno and Phrann). One might predict that phages isolated at 42°C may have a higher genomic GC% than phages isolated at 25°C or 37°C, and indeed the N cluster phages have a relatively high GC% compared to the remaining clusters. Also, Xeno has the highest GC% of all of the sequenced N cluster phages. Notwithstanding the previous two points, in all likelihood there is not a significant correlation between isolation temperature and genomic GC content. Currently, the sample size is too small to make a definitive conclusion. In addition to the phages isolated in the fall of 2014, two A3 phages (EpicPhail & Veracruz) isolated in 2011 were annotated and analyzed using comparative genomics.  
 SCSU isolated half of the new N cluster phages found in 2014, with Phrann being the largest N cluster phage genome sequenced to date. Phrann has a rare orpham (p)ppGpp synthetase/hydrolase (gp30) that is similar to another orpham, Squirty\_gp29 (in the F3 subcluster), as well as a large number of other *Mycobacterium spp.* (p)ppGpp synthetase/hydrolases. We present an analysis of this important gene family. Xeno has many genes that, while present in other sub/clusters, are only present in this one particular N cluster phage. These are discussed in greater detail. The fifty-eight sequenced A3 mycobacteriophages seem to fall into four major groups based on whole genome multiple sequence alignments and phylogenetic tree construction. Interestingly the group to which Veracruz belongs is a very tightly clustered group of eight members, whereas two groups have five members each, and a final large diverse group captures most of the remaining members. Comparative genomics of this subcluster are presented.