CONSIDER FOR TALK

9th Annual SEA-PHAGES Symposium Abstract

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A Bioinformatic Investigation of Gordonia terrae Phage Diversity in Southwest Florida

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Florida Gulf Coast University students isolated fifteen phage using the host *Gordonia terrae* 3612. Of the three phage that were sequenced, two, DatBoi and Mollymur, are cluster DL siphoviridae and one, Skog, a cluster DO myoviridae. Skog is particularly interesting since it has the longest genome of all the sequenced *G. terrae* phage (152,435 bp). We compared our phage genomes to their closest relatives, Pupper and SCentae from cluster DO, found by the University of Pittsburgh, and Bantam from cluster DL, found by University of Wisconsin-River Falls, as well as other more distantly related phage. We analyzed the genomes from all *G. terrae* phage to look for the absence of 6 bp restriction sites. We failed to find any single restriction sites that were missing from all *G. terrae* phage genomes, suggesting that *G. terrae* may not have an active restriction enzyme defense system. This may help explain why *G. terrae* phage are so diverse. To investigate the mosaic nature of phage genomes, a phylogenetic analysis of capsid and immunity repressor genes from all *G. terrae* phage revealed that individual genes do not always evolve similarly, but show evidence of horizontal gene transfer. We discovered that genes with high ratios of amino acid change, quantified by the nonsynonymous to synonymous ratio (Ka/Ks), across the genomes of DL phage Mollymur, DatBoi, and Bantam occurred in clusters towards the 3’ end of the genome. The majority of genes with high Ka/Ks values were DNA binding proteins, suggesting that transcriptional regulation might be under strong evolutionary selective pressure. To study lysogeny in our new DL phage, we identified several potential attP sites upstream of the tyrosine integrase gene. However, further inspection of the *G. terrae* host genome did not reveal any corresponding attB sites. Based on a recent paper describing communication systems in temperate Bacillus phage, we identified possible communication peptides within lytic as well as temperate phage that infect G. terrae and other Actinobacteria hosts. Overall, we found that Southwest Florida has an abundance of *G. terrae* phage with diverse and interesting genomic properties.