CONSIDER FOR TALK

11th Annual SEA Symposium Abstract

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Phylogenetic and genomic characterization of Actinobacteriophages NadineRae and PetterN

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Actinobacteriophages NadineRae and PetterN were isolated on *Gordonia terrae* and *Mycobacterium smegmatis*, respectively, as part of the SEA-PHAGES program at The College of Saint Scholastica. Genomic sequencing of NadineRae revealed a 64,714 bp genome with 66.1% GC content and subcluster CR4 designation. MEGA Phylogenetic analysis indicated *Gordonia* phage Marietta, isolated in 2017 by a St. Scholastica student, was among the closest relatives to NadineRae. Expanded phylogenetic comparisons with both *Gordonia* phages and *Gordonia* bacterial species did not present a clear relationship between Gordonia phage genomes and the particular *Gordonia* species with which they were isolated. Phamerator comparisons with close CR4 relatives indicated several areas of sequence repeats on the right arm of the genome between coordinates 57,000-63,000. When NadineRae’s genome was BLASTed against itself, three distinct sequence repeats were mapped to this region. Within these coordinates, the first repeat with consensus sequence GTAGGGCCCGGCGAGATCTCGCGCCGGGCCCTAC appeared 12 times, the second with consensus sequence GTAGCTCACCCCGTAGGGCCCGGCGAGATCTCGCGC appeared 12 times, and the third with consensus sequence GACGCGCAGCGCGCTGCG---GCCGACGCGGCC appeared 10 times. All three of these repeats appeared elsewhere in the genome, but at lower frequency. The precise function of these repeats was not fully elucidated, but the DNA motif prediction software TomTom identified possible repressor or activator binding activity. In addition, NadineRae protein expression patterns were examined using tandem mass spectrometry. Liquid infections of NadineRae were performed for 4 hours, pelleted and subjected to LC-MS/MS to identify expressed phage proteins. Data is not yet available, but hopefully will be by the symposium. Finally, the lysogeny related genomic sequences of the temperate Mycobacteriophage PetterN were examined. Using the DNA Scan feature in DNA Master 19 stoperator sequences were identified with consensus sequence GTACGATGTCAAG. Most of the genes where these stoperator sequences occurred had no known function, but several played structural or assembly roles.