CONSIDER FOR TALK

8th Annual SEA-PHAGES Symposium Abstract

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Genomic Diversity within Cluster M2 Mycobacteriophages GardenSalsa and GenevaB15

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Cluster M2 Mycobacteriophages GardenSalsa and GenevaB15 were isolated from soil samples collected from a compost pile in Upper St. Clair, PA and dry soil in Freedom, PA, respectively, and characterized by students at Seton Hill University participating in the SEA-PHAGES research program. Both phages were obtained using a modified direct plating method in which phage buffer (1 mM CaCl2) was added to a 15 mL conical tube containing the soil sample. The tube was then shaken at 225 rpm at room temperature for 48 hours before processing liquid through a 0.22 μm filter. Filtrate was added to cultures of *Mycobacterium smegmatis* mc2155, yielding turbid plaques of approximately 1 mm in diameter after 36 h incubation at 30°C. The genomes of GardenSalsa (80.3 kb, 60.9% GC, defined linear ends) and GenevaB15 (80.1 kb, 60.8% GC, defined linear ends) were annotated using DNA Master, HHPred, Phamerator, Starterator, tRNAScan-SE, Aragorn, and the Blast program suite. GardenSalsa and GenevaB15 share 96% nucleotide similarity while respectively sharing 88% and 87% nucleotide similarity with the sequence of the only other published Cluster M2 phage, Rey. GardenSalsa contains 144 predicted protein-coding genes and 22 tRNAs, while GenevaB15 contains 139 predicted protein-coding genes, 1 tmRNA, and 24 tRNAs. GardenSalsa lacks the tmRNA that is common across other Cluster M phages. Four sets of conserved repeats found in other Cluster M phages were identified in both GardenSalsa and GenevaB15. Codon usage was also examined for both phages and analyzed with respect to presence of tRNAs and overall genome location.