CONSIDER FOR TALK

8th Annual SEA-PHAGES Symposium Abstract

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Isolation and Characterization of Mazhar510, Roosevelt and Royals2015

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During the 2015-16 academic year we, the SEA-PHAGES students at North Carolina Agricultural and Technical State University, successfully isolated six bacteriophages using *Mycobacterium smegmatis* mc2155 as the host organism. All six were isolated from soil samples collected in the vicinity of Greensboro, NC via enrichment cultures. Phage isolation and purification followed standard SEA-PHAGES protocols. DNA samples from three bacteriophages, Mazhar510, Roosevelt, and Royals2015, were submitted to the Pittsburgh Bacteriophage Institute for Illumina sequencing. Genomes were annotated and analyzed using DNA Master, as well as associated bioinformatics software programs. Roosevelt and Mazhar510 are in Cluster A, Subcluster A4. They have a GC content of 63.9% and genome lengths of 51,502 base pairs (Roosevelt) and 51,371 base pairs (Mazhar510). Royals2015 is in Cluster F, Subcluster F1. It has a GC content of 61.7% and a genome length of 57,356 base pairs. Roosevelt and Mazhar510 exhibit a high degree of synteny and nucleotide similarity over almost the entire length of their genomes. In contrast, Roosevelt and Mazhar510 show very little similarity to Royals2015. Autoannotation identified 89 open reading frames (ORFs) in Roosevelt and 88 in Mazhar510. In both, approximately 36% of the open reading frames were in the forward direction (32 ORFs), the other 64% in the reverse direction (57 ORFs in Roosevelt, 56 in Mazhar510). Autoannotation identified 108 ORFs in Royals2015; 98 in the forward direction and only 10 in the reverse direction. These comparisons highlight the high level of similarity between members of a subcluster, and the distinctions between members of different clusters.