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10th Annual SEA Symposium Abstract

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Investigating bacteriophage NatB6 and others members in the CR2 cluster that infect Gordonia terrae.

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Gordonia in the Actinomycetes genus consists of a diverse group of bacteria. While some species may cause disease in plants and animals, some are soil dwelling and are able to metabolize environmental pollutants. Studying bacteriophages that infect Gordonia may thus contribute to the pathogenesis of bacterial infections and soil contaminant remediations. We extracted bacteriophages from a soil sample collected from Audubon, PA and enriched specifically for *Gordonia terrae* phages. Bacteriophage NatB6 was purified and characterized; it is a lytic phage producing small clear plaques on bacterial lawns. NatB6 has is the siphoviridae morphology – icosahedral capsid with a long, flexible but non-contractile tail. The completely sequenced (Illumina) genome of NatB6 revealed that it is 67,081bp long, contains approximately 96 protein-coding genes, has 65.7% GC content, and ends with 3’ sticky overhangs. Based on further sequence analysis, NatB6 is sorted in to CR2 cluster. Ten other sequenced phages are in this cluster, with average genome length of 67,311 bp (ranging from 64,124 – 68,626). NatB6 is most similar to Jifall16 (93.25%) and Foxboro (91.79%). We compared all 11 phages in the CR2 subcluster as well as aligned all 24 Gordonia phages in the CR cluster to make evolutionary inferences for phage diversity.