CONSIDER FOR TALK

8th Annual SEA-PHAGES Symposium Abstract

Saint Joseph's University

Philadelphia PA

Corresponding Faculty Member: Julia Lee-Soety (jlee04@sju.edu)



Sarah Muche

Metagenomic analysis of Arthrobacter-specific bacteriophages in the AN cluster

Sarah Muche, Joseph Quinlan, Christina Gareis, Alison Kloiber, Madison Honer, Taylor Nguyen, Haley Patrick, Martin Ryan, Scott Newman, Lakshmi Narayanam, Ashley Frankenfield, Kaleigh Williams, Megan Siwak, Maddison Jeffries, Christina King-Smith, John Braverman, Julia Lee-Soety, Shantanu Bhatt

Phage Safari students at SJU isolated several *Arthrobacter* phages this year. Most were from soil samples collected in students’ hometowns. Phages were enriched in *Arthrobacter sp.* cultures and underwent numerous rounds of purification. Three purified phage DNA were sequenced - Mariposa from Downingtown, PA, Massimo from Camp Hill, PA, and Prospero from Vineland, NJ. These phages yielded clear lytic plaques of varying sizes and shared similar restriction digest patterns. The sequences of the three phages were also highly similar and sorted into cluster AN. During the annotation phase, BLAST analyses through DNA Master showed high identity to another set of AN phages, Decurro, Jessica, and Sandman, all isolated by Bucknell University students. We performed a metagenomic sequence analysis on 6 of these phages plus 19 others that are in the AN cluster. So far, phages in the AN cluster have the shortest genomes, averaging 15,544bp. Full genome alignments showed differences ranging from 1 nucleotide (Yank vs Decurro) to 2182 nucleotides (Taj14 vs Seume). For example, Massimo and Mariposa differed in 3 nucleotides, interestingly located within the genes encoding capsid maturation protease, tape measure protein, and a protein with unknown function. In the gene encoding capsid maturation protease, a single nucleotide mismatch was observed resulting in a conservative amino acid (histidine and arginine) difference. In the gene encoding tape measure protein, the difference was synonymous. A phylogenetic tree was estimated and showed two major groupings. The three genomes processed at SJU are found in the same sub-grouping, thus correlating with common geographic origin. However, in the tree, the entire collection of 25 AN cluster phages did not fall into a perfect correlation with geographic origin. The significance of this research is the combination of genomics analysis and evolutionary inferences.