CONSIDER FOR TALK

11th Annual SEA Symposium Abstract

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Comparative Genomics of EF Cluster Microbacterium foliorum Bacteriophages NarutoRun and Anakin

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At Worcester Polytechnic Institute, two SEA-PHAGES sponsored lab sequences were conducted, resulting in the isolation of two novel EF cluster phages: NarutoRun and Anakin. First, a bacteriophage isolation and amplification lab was conducted in Fall 2018, followed by a bioinformatics lab in which the genetic sequences of the two phages were annotated and compared to each other, other EF cluster bacteriophages, and to bacteriophages of differing clusters. The two sequenced phages were both isolated from Worcester’s Institute Park, with Anakin obtained from a highly trafficked area and NarutoRun from a secluded, grassy location close to the edge of a pond.
Examining the EF cluster bacteriophages, seven genes with known functions were identified to be unique to this cluster. Of these seven two genes are tail-related, two are nondescript membrane proteins, one is the capsid maturation protease, one is an unusual DNA primase, and the last is a RuvC-like resolvase. These seven genes are present in all members of the EF cluster, but no other non-EF bacteriophages.
Upon genetic sequencing, it was discovered that both phages had circularly permuted genomes, and were identical aside from two differing nucleotides, both of which were in coding regions. The first substitution is located in a tail assembly protein, and was ultimately synonymous. The second substitution is located in a RuvC-like resolvase, and was nonsynonymous. This RuvC-like resolvase was of particular interest due to its exclusivity to the EF cluster of bacteriophages, and thus its role in regards to the management of these phages’ circular genomes was investigated. With only a single nonsynomyous difference between the NarutoRun and Anakin bacteriophages, evidence therefore supports the claim that they are functionally identical phages.