CONSIDER FOR TALK

8th Annual SEA-PHAGES Symposium Abstract

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Alternative host range and immunity in mycobacteriophage Clusters A and E

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Mycobacteriophage (phage) are viruses which infect bacteria of the genus Mycobacterium, including M. smegmatis and pathogenic M. tuberculosis. Phage research provides insight into the evolution of bacteriophage and their bacterial hosts. To better understand the diversity of mycobacteriophage, the 2015 HON/BMB150 class used non-pathogenic M. smegmatis as a host to isolate 22 novel phage from soil. Three of the phage sequenced, Acme, Greg and Fajezeel are Cluster A1 phage and a fourth phage, IHOP, is a cluster E phage. Lysogens of all four phage were constructed at the end of the fall semester. These phage expanded the number of phage isolated at UMaine in each of these clusters allowing us to build on the work of previous years into the genetics/genomics of the Cluster A and E phage. The host range for all of the 22 phage isolated was determined in M. smegmatis and in five alternative strains/species of Mycobacterium that are pathogenic in fish. The Cluster A1 phage, Acme was capable of infecting multiple strains of M. chelonae but did not infect M. salminophilum or M. marinum. Fajezeel and Greg, which have 98% sequence identity with Acme, did not infect any of the alternative species. The difference in host range may be due to 2 non-synonymous amino acid changes in a minor tail protein. The lysogen of the Cluster E phage IHOP, along with two other Cluster E phage from previous years, Ukulele and Phaja, were tested for immunity to representative phage from clusters A-X. Cluster E phage have partial to complete immunity to each other. One cluster E lysogen showed partial immunity to A2 and A3 phage. We cannot attribute the partial immunity to the putative immunity repressor since all three phage have identical sequences for this protein. We are also exploring promoter/terminator differences of these phage in light of both the host range and immunity differences.