CONSIDER FOR TALK

7th Annual SEA-PHAGES Symposium Abstract

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OutPHAGEous Discoveries

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Over the course of the year, our class discovered 20 bacteriophages infecting Bacillus thuringiensis subspecies Kurstaki. These phages were purified and tested for their ability to infect and lyse (host range) 16 different strains of Bacillus bacteria. We observed a broad spectrum of host range, with some phages infecting only a few hosts and other phages infecting many host bacteria. We sequenced the genomic DNA of 6 of these novel phages. The genes in each of the genomes were annotated to compare and contrast genome features. We used dot plot and average nucleotide identity analysis to form two groups of myovirus phages in our collection. We completed comparative genomics projects examining both small and large scale genome characteristics. We explored genome features related to host range looking for the long tail fiber and receptor binding proteins. We examined the unique location of endolysin and holin in these genomes compared to a canonical lytic cassette, confirmed each predicted holing has three transmembrane domains, and examined potential promoter elements to explore regulation of expression of these proteins. A DNA Polymerase containing a Bastille-like HNH endonuclease in some phages, and an unrelated HNH endonuclease in other phages highlights a unique recombination event in these phages. Other topics to better understand genomic diversity include analyzing promotor sequences and sigma factor proteins to understand regulation of phage gene expression, and comparison of tape measure proteins. Finally, we’ve characterized one podovirus low sequence similarity to any published phages. Combined, our results show these phages represent a dynamic and and diverse collection of Bacillus phages.