CONSIDER FOR TALK

7th Annual SEA-PHAGES Symposium Abstract

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Isolation and Characterization of Paenibacillus larvae and Brevibacillus laterosporus Bacteriophages to Understand Their Evolutionary Relationships

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Paenibacillus larvae is a spore-forming bacterium that infects honeybees in their larval stages and is a cause of the dwindling honeybee populations worldwide through the devastating diseases American and European foulbrood. A close relative, Brevibacillus laterosporus, is another spore-forming bacterium that causes a secondary gut infection associated with Paenibacillus-inflicted European foulbrood. In an effort to better understand their host and their potential for halting the spread of this infectious disease, six novel Paenibacillus bacteriophages were isolated and three highly-related B. laterosporus bacteriophages were annotated (Xane, Jenst, and Osiris) and compared to the eight that have been previously isolated and sequenced (Abouo, Davies, Jimmer-1, Jimmer-2, Powder, Sundance). To better understand B. laterosporus and its bacteriophages, we clustered phages based on similarity using Gepard dotplots and Mega6 phylogenetic trees, identified and mapped DNA motifs using MIME, FIMO, and DNA Master, identified a transposable region contained in Sundance and Xane but excised from Jenst using HHPred, Phamerator, and DNA Master, and identified repeated genes and compared their predicted tertiary structures using Clustal Omega, RaptorX, and STRAP. From these data, we determined that Powder and Osiris belong in the previously described Jimmer-like cluster, Xane and Jenst form a novel phage cluster, and Sundance is a singleton. A motif repeated throughout Xane and Jenst was frequently located near genes responsible for DNA replication, nucleotide metabolism and transcription suggesting transcriptional co-regulation. In addition, paralogous transcriptional regulator genes were identified in four Brevibacillus phages suggesting conservation of function in the phage lifecycle. Variation at residues predicted to bind specific nucleotides indicates these paralogs likely bind different DNA sequences, exhibiting protein plasticity. Finally, a putative transposable element was identified in Sundance and Xane that carries genes homologous to those found in Brevibacillus hosts. Remnants of this transposable element were also identified in Jenst. Comparing the GC content of this region to the surrounding area indicated that Xane acquired this region more recently than Sundance. These discoveries provide a greater understanding of the unique features of these bacteriophages, their behavior, and their evolutionary relationships to one another.