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Paenibacillus Larvae Phages Contain Regions of Conserved Synteny Despite Large Genomic Differences

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*Paenibacillus larvae* is a species of Firmicute bacteria that causes American Foulbrood, the most widespread brood disease affecting beehives throughout the world. With strains of the bacteria increasing in antibiotic resistance, we posit phage therapy to be a better method of preventing and treating the infection. BYU’s lab has isolated over 40 *P. larvae* phages and sequenced 28 complete genomes. The average genome in our phage library has approximately 43,000 base pairs, 43% GC content, and 75 putative genes. From these fully sequenced and annotated *P. larvae* phages, three new clusters were documented. Through genomic annotation and comparison, we were able to identify individual genes and their products. Although phage DNA has the capacity to adapt rapidly, some essential genes and protein products (especially structural proteins) are highly conserved within each cluster. For example, phages DevRi, PBL1c, and Sitara have synteny across the first 22 genes, with all genes coding for structural proteins located in this region. We suggest transposase activity as a possible mechanism for creating genetic diversity, given that a well-characterized bacterial transposase was found at the site of intergenomic divergence of this group (gp 23). Phages Honeybear and Toothless have 99.9% genetic homology with the exception of two additional genes found in Honeybear (gp 36 and 37). The unrelated Diane family of *P. larvae* phages also contains these two genes. A similar observation was made in phage DevRi: gp 49 codes for an anti-repressor protein present in many otherwise distinct phages. Thus, some gene products are similar across many different phage clusters, suggesting sharing of genes via co-infection. This comparative analysis will contribute to the growing body of research into the diversity of evolution of phages, as well as understanding of *P. larvae* in an aim to prevent and cure American Foulbrood.