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Conservation of Genes in the DNA-Binding Gene Cluster of Phage ShakeItOph

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Grouping bacteriophage (phage) genes into phamilies (phams) based on amino acid similarity is useful for studying their function and evolution. Genome replication and transcription are necessary for proliferation of all phages, suggesting conservation of genes involved in these processes. After isolating and annotating the genome of novel phage ShakeItOph, a duplicated DNA binding protein (DBP) in Pham 137681 was discovered. However, nucleotide and amino acid sequence analysis revealed that the repeated proteins varied from one another, perhaps implying the duplication occurred far back enough to undergo divergent evolution. The DBP was found to only be conserved within subcluster AZ4, but nearby DNA-binding genes appeared conserved in other clusters as well. As such, analysis of this DNA-binding gene cluster was conducted. Examination of the amino acid and nucleotide sequences of the DBP and overall genome structure of AZ4 phages was compared to other subclusters and clusters containing Pham 137681. During analysis, the order of DNA-binding genes became evident: DNA primase/helicase, DNA polymerase I, then DBP(s). Comparison of gene order was extended to other phages containing the genes of interest. Results showed conservation in phages containing the same pham, but not in phages overall, implying gene order conservation may be important for specific methods of replication and transcription, but not in overall ability to carry them out. Analysis of more phages is needed to confirm this conclusion. Understanding these genes allows for better knowledge of bacteriophage replication and transcription, which is in understanding of overall proliferation and phage biology.