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Characterizing Genomic Similarities in Propionibacterium-Infecting Bacteriophages

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*Propionibacterium* is a genus of bacteria that includes the species *P. freudenreichii* (used in cheese production) and *P. acnes* (promotes acne). Like other bacteria, it is infected by bacteriophages, and examination of bacteriophage genomes is crucial for understanding their shared characteristics and behaviors as well as phage-host interactions. Phages in cluster BU infect *P. acnes* and have a lytic life cycle, while phages in cluster BV, BW, and BX infect *P. freudenreichii* and are predicted to have a temperate life cycle. We performed comparative genomic analysis to characterize the similarities and differences in these phages, using various bioinformatic tools such as SplitsTree, Phamerator, Gepard dot plots, and gene content similarity heat maps. Results showed that clusters BV, BX, and BU each had very high average intracluster gene content similarity (95%, 98%, and 99% respectively), while BW was lower (82%). The results from BU were surprising because cluster BU contains almost 50 phages, while the other clusters were much smaller (2-4 phages each). Dot plots of the whole genome nucleotide sequences and amino acid sequences showed that intercluster nucleotide similarity varied among clusters BV, BW, and BX, with no shared nucleotides observed between the lytic cluster BU and the temperate clusters, and only minimal amino acids shared between clusters. Overall, we found different patterns of similarity amongst these clusters, with cluster BU phages being far more similar to each other than phages from BW. This difference could be a result of lytic versus temperate phages populating the cluster, although further exploration would need to be done to confirm this. However, a major limitation was that the temperate clusters were all very small. Insights from this research could influence future clinical therapies for acne, as well as facilitate phage clustering processes.