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Prolate Phages From Specific Hosts Show Conservation of the Major Capsid Protein Gene

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Bacteriophages are one of the most abundant biological entities on earth yet very little is known about them. Phages are diverse, with varying genome lengths, host ranges, life cycle and head morphologies. While most phages have a spherical icosahedral capsid, there are certain phages that have an elongated icosahedral capsid, called a prolate capsid. This study sought to characterize the genomic features of prolate phages infecting different hosts: Gordonia, E. coli, Synechococcus and Lactococcus. It was hypothesized that structural phams may be conserved between prolate phage of different hosts and that phages with a similar head morphology would share genetic features. The hypothesis was answered using gene content tools such as nucleotide dotplots and multiple sequence alignment via COBALT. Bioinformatic analysis revealed that Synecochoccus phages and Gordonia phages shared cross host structural and genomic similarities. It was also found that prolate Siphoviridae phages showed more genomic conservation in their major capsid proteins than their non-prolate counterparts, as evidenced through analysis of Gordonia Cluster CZ phages. Multiple sequence alignment of the major capsid protein gene putatively responsible for head morphology showed that there was variation in the prolate phages infecting the same host, E. coli. Prolate phages display high levels of genetic diversity despite their physical similarities, contributing to further analysis and identification of this unique phage morphology