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Genomic Comparison Reveals Similarities between Low GC% Mycobacteriophages Infecting M.smegmatis

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It is unusual for phages to have a different GC% compared to their hosts and little research on mycobacteriophages in Cluster H, U, R and D has been conducted despite numerous citations of similarity. Uniquely, these four mycobacteriophage clusters are small in size, have a high genomic diversity, and have low guanine-cytosine content (50.4-59.6 GC%) relative to their host, M.smegmatis (67.4 GC%), and other mycobacteriophage clusters. Cluster H, D, U, and R mycobacteriophages were genomically compared using bioinformatic tools in order to gain a better understanding of the similarities and differences between low GC% mycobacteriophages. Nucleotide sequence similarities were found between all clusters except between Clusters D and U; however most notably, average nucleotide identity similarities were the highest between clusters and sub-clusters and the lowest between different clusters. The gene content similarity heat map showed that all clusters shared a range between 16.3-34.9% of similarity and the highest inter-cluster relations observed were between Cluster H and U and Cluster D and R. Tape measure protein (TMP) phylogeny predicted sub-Cluster H1 and H2 TMP in different clades, sub-Cluster H1 with Gordonia Cluster DV and DG, and sub-Cluster H2 with Cluster U. The inter-cluster similarities elucidated relationships between clusters and serves as a foundation to further understand low GC% mycobacteriophage diversity.