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Comparative Genomic Analysis of Mycobacteriophage Cluster W to other Mycobacteriophage Clusters

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Bacteriophages are diverse entities in nature, with mycobacteriophages being of particular interest due to the lethality of Mycobacterium tuberculosis. Cluster W of mycobacteriophages, containing 6 bacteriophages, is relatively understudied and presents a fillable knowledge gap in the genomic characteristics of the phages within Cluster W. Therefore, analyzing Cluster W phages for relationships to more researched mycobacteriophage clusters can provide insights into this understudied cluster. Our genomic analysis approach used BLAST, gene content similarity, nucleotide dotplots, and Phamerator to compare Cluster W phages with other mycobacteriophages, both within and outside the cluster. Cluster W has been shown to have high gene content similarity to Cluster B, specifically Subclusters B2 and B3, along with Singleton Dori. Horizontal gene transfer of Pham (gene family) 51070 between Clusters P1 and W were discovered using Phamerator analysis and analyzed through phylogeny software. Cluster W phages have intercluster similarities to Clusters B2, B3 and P1. The differentiation of at least four Cluster W phages appear to have occured after the horizontal gene transfer of Pham 51070. These similarities were localized and predicted to be a result of inter-cluster gene transfer rather than common ancestry, based on Pham map findings. The inter- and intra- cluster relationships revealed by the bioinformatic analyses provides novel insights on the understudied Cluster W, paving the way for future research applications.