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2021 SEA Symposium Abstract

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Los Angeles CA

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Comparative Genomic Analysis of Cluster H Mycobacteriophages Reveals Conserved Motif and Intra-cluster Variation

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Although bacteriophages are the most abundant organisms in the biosphere, they remain relatively understudied. Recent studies have characterized novel mycobacteriophages isolated from soil samples and grouped them into clusters with high genomic similarity as a means of categorizing phages. Cluster H Mycobacteriophages were among those previously isolated, but no subsequent research has been performed to understand the diversity of this cluster. Cluster H phages are unique based on small cluster size, low GC percentage, and a high number of genes with no known homologues within their genomes, distinguishing Cluster H from related clusters. Intra- and inter-cluster comparisons of phage genomes were performed in an effort to characterize Cluster H. Phamerator maps revealed conserved gene content among Subclusters H1 and H2, which was confirmed through dotplot and gene content similarity analyses. Phamerator maps also showed a variable region within Subcluster H1, and a subsequent MEME analysis of this region identified a repeating sequence motif. Codon usage bias similarity and phylogenetic analyses of the minor tail protein supported previous placement of these phages into Cluster H and Subclusters H1 and H2 and verified phage-to-phage relationships. These findings offered insight into phage evolution and pinpointed genomic characteristics that distinguished these phages from other Mycobacteriophage clusters.