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2021 SEA Symposium Abstract

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Los Angeles CA

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Comparative Genomic Analysis Between Mycobacterium Singletons and Clustered Mycobacteriophages

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Bacteriophages are the most abundant biological entity on the planet and their vast numbers create an immense field to study their genomic diversity. Exploration of bacteriophages infecting numerous hosts such as Mycobacterium has found that singletons, known as bacteriophages that are not clustered due to lower nucleotide similarity, share genomic characteristics with certain mycobacteriophages clusters. However, these relationships have yet to be analyzed further as their explorations can allow for a deeper understanding of the continuum of diversity and how singletons are clustered. This study aimed to uncover the levels of genetic similarity between clustered mycobacteriophages and Mycobacterium singletons to characterize potential patterns of similarity. Since studies have shown that singletons infecting Mycobacterium possess similarity to specific Mycobacterium clusters, if there are singletons sharing genomic features with clustered mycobacteriophages whose relationships can be characterized, then patterns of high genomic similarity between Mycobacterium clusters and singletons will be observed. Gene content similarity (GCS) analysis of all singletons and phages from each mycobacteriophage cluster were compared to look for overall genome similarity. Singletons Kumao, MooMoo, and Dori shared high GCS values with several mycobacteriophage clusters, and Cluster K with multiple singletons. These relationships were further analyzed through Phamerator, Phylogenetic Trees and dotplots. Findings indicated that genome similarities occurred within minor tail proteins. Our hypothesis was supported since singletons shared high genomic similarity with mycobacteriophages. This research allows for better classification of singletons into existing or new mycobacteriophage clusters and provides insights into the genetic characteristics that contribute to phage diversity.