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Singleton Phage Dori Reveals Complex Relationships with Singleton and Clustered Phages

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Bacteriophages are highly diverse and genetically mosaic biological entities with complex relationships which remain understudied. Some phages are grouped into clusters based on genomic similarity, while singletons are phages that lack genomic similarity with any other known phages. Generally, there is a lack of research which investigates singletons in a comprehensive manner. Despite there being an increase in the number of isolated phages within the past decade, mycobacteriophage Dori has continued to be categorized as a singleton since its isolation in 2008. In this study, Gene Content Similarity (GCS) maps of Dori’s genome revealed its strong genomic similarities with already clustered phages, especially Cluster B. In addition, Phamerator maps displayed that specific sections of Dori’s genome shared high similarities with distinct clusters suggesting Dori has a highly mosaic genome. Furthermore, phylogenetic analysis of Dori’s genes revealed strong evolutionary relationships between Dori’s individual genes and various clusters and hosts, which gives insight on where Dori may have acquired a subset of its genome. Altogether these findings revealed that Dori’s genome has a complex relationship with a myriad of clusters, which adds to our understanding of singleton mosaicism. This may provide useful information in future phage research if newly isolated phages are grouped with Dori and other present-day singletons. Overall, the analysis on Dori’s genome supports the current understanding of phages and their extensive interactions, contributing to a continuum of diversity.