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2023 SEA Symposium Abstract

University of California, Los Angeles

Los Angeles CA

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Characterization of Genomic Diversity In Bacteriophages Infecting Rhodococcus

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Bacteriophages are ubiquitous and display pervasive genetic mosaicism and extraordinary diversity. Knowledge of phages that infect Actinobacterial hosts such as *Rhodococcus* is still limited, but the growing number of phages isolated on this host presents an opportunity for analysis and characterization. Here we describe the genomic characteristics of 57 phages isolated on members of genus *Rhodococcus*. These phages were previously isolated at multiple institutions as part of the SEA-PHAGES program using four different species of *Rhodococcus*, specifically: *R. equi, R. erythropolis, R globerulus,* and *R. rhodochrous*. We saw that most *Rhodococcus* phages are grouped together in several distinct clusters, with most phages in Cluster CA; numerous others are classified as singletons being too genetically dissimilar for cluster assignment. The length of *Rhodococcus* phage genomes varies widely, from a minimum of 14,270 bp to a maximum of 142,586 bp. G+C content ranges from 41.2%-68.4%, while the average host G+C content is about 60%. Through the use of comparative genetic tools such as nucleotide and amino acid comparisons, gene content similarity (GCS), Phamerator, and SplitsTree, we found that *Rhodococcus* phages demonstrate high intra-cluster similarity and low inter-cluster similarity, despite being isolated from the same bacterial genus. In contrast, Cluster CA and CC phages, along with several singletons, have higher GCS with phages isolated from bacterial host genera such as *Gordonia, Streptomyces, Mycobacterium,* and *Arthrobacter* than with other *Rhodococcus* phages. Future work will seek to uncover the source of dissimilarities observed in both nucleotide and amino acid content as well as pham assignments to elucidate the genomic regions that lead to such diversity. Additionally, we plan to further explore the relationships these phages have with phages from other host genera.