CONSIDER FOR TALK

7th Annual SEA-PHAGES Symposium Abstract

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Isolation and Analysis of Cluster O Phages Mori and Vorrps and Cluster C Phage Clarice

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Through the Phage Hunters program at Washington University in St. Louis, approximately 120 mycobacteriophages have been isolated, sequenced, and annotated over the last seven years. This year, five new mycobacteriophages have been analyzed: Clarice, Enkatz, Mori, Phlavio, and Vorrps. Four of the phages were isolated from soil samples collected in the St. Louis area. Clarice was isolated from a soil sample collected in front of a restaurant in O’Fallon, Illinois, which is an area that has not often been used as a sampling site for Washington University’s phage hunting initiative. Clarice has an isometric head and a short, stubby tail, which is characteristic of a Cluster C phage. Vincent, another phage that was isolated but not annotated this year, is also a member of the Cluster C group. Only three other Cluster C phages have been isolated by Washington University. They also produce small, clear plaques, suggesting a lytic phage. Phages Mori and Vorrps have very distinct prolate heads, indicating that they are members of the unique Cluster O group. These phages are the first Cluster O phages that have been isolated at Washington University. Both phages were collected on the Washington University campus, but from different locations. They have a 99% sequence similarity, and have the same number and pattern of unique seventeen base pair repeat sequences. The Clarice genome is 154,450 base pairs in length. Overall, 232 genes, all transcribed in the forward direction, were annotated through bioinformatics analysis programs such as DNA Master, BLAST, Phamerator, and GBrowse. The function of 32 of the genes was determined through comparative analysis with other phage proteins. Phamerator was used to generate a map of predicted gene calls, and provided comparisons to two other highly similar phages as well. Detailed analysis of particularly interesting observations will be presented. Some examples include tmRNA comparisons, investigating features of the tapemeasure proteins, the LysM protein, the histidine triad domain, and phosphoesterases. Further analysis will be necessary to understand the evolutionary history of these novel phages.