CONSIDER FOR TALK

8th Annual SEA-PHAGES Symposium Abstract

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Genome Analysis of Mycobacteriophage Nimrod

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Bacteriophages (phages) are viruses that infect bacteria. Nimrod is a recently isolated Mycobacteriophage belonging to cluster E. Nimrod’s genome was annotated and each of its genes were identified and, when possible, the corresponding putative protein’s function was assigned. Nimrod was determined to have a total of 143 genes, 141 of these are protein coding genes, while the remaining two are tRNA genes. Nimrod’s nucleotide sequence was compared to that of all of the annotated phages that were discovered at Montana Tech. Including Nimrod, ten mycobacteriophages from Montana Tech’s programs were compared through analysis of a Dotter plot (Sonnhammer and Durbin, 1995). This comparison revealed that Nimrod is not genetically similar to any of the other Montana Tech phages. Additionally, it was determined that the previously annotated phages from Montana Tech belong to clusters A, B, and F. From each of the ten Montana Tech phages, the lysin A and lysin B amino acid sequences were identified and used for analysis. The lysin A proteins revealed a greater degree of variability than was identified among the lysin B proteins. Generally, the phages that belong to the same cluster had more similar amino acid sequences to each other for both lysin A and B proteins, compared to the lysin A and B of phages from other clusters.