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9th Annual SEA-PHAGES Symposium Abstract

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Host Specificity Testing and Multiple Sequence Alignment Analysis of Bacteriophages Guillsminger and NicoleTera

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The goal of this research was to study host specificity on two mycobacteriophages that were isolated this year, Guillsminger and NicoleTera. Both phages were found in soil in northern Nevada. Unveiling the relationship between how bacteriophages interact with organisms and their environment allows for further insight into their ability to evolve under selective pressure. NicoleTera was found in 2015, sequenced in 2016, and annotated in Spring 2017; it is a subcluster A2 phage with 64% G/C content, containing 91 genes and six tRNAs and is 52,944 base pairs long. Guillsminger was found in 2015, sequenced in December 2016, and annotated in Spring 2017; it is a subcluster K5 with 65% G/C content, containing 94 genes, one tRNA, and is 63,153 base pairs long. Both are of the Siphoviridae morphotype. After soil collection, the bacteriophages were purified and isolated using Mycobacterium smegmatis mc2155 as the host bacteria. High Titer Lysates (HTLs) were prepared for each mycobacteriophage and DNA was isolated for analysis. Both phages were also imaged by transmission electron microscopy at the University of Nevada, Reno and DNA was sent to Pittsburg State University (PSU) for sequencing followed by annotation using PECAAN. Using phamerator, NicoleTera was compared to closely related A2 mycobacteriphages, Echild and ArcherNM while Guillsminger was compared to closely related K5 mycobacteriphages, Gengar and Waterfoul. Preliminary data on host specificity testing suggests that out of 27 bacterial strains Guillsminger can cross infect two, Gordonia terrae and Mycobacterium smegmatis W113. NicoleTera was shown to cross infect Rhodococcus erythropolis and Mycobacterium phlei. Multiple sequence alignment analysis is ongoing, comparing suggested host specificity genes: minor tail proteins, lysin A, lysin B, and holin.