CONSIDER FOR TALK

7th Annual SEA-PHAGES Symposium Abstract

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Identification and Genomic Investigation of the Mycobacteriophage SamScheppers

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In this study we identified and analyzed the novel bacteriophage SamScheppers. SamScheppers was first isolated and identified in 2013 by a group of students from the same institution, and the current cohort followed in 2014 by indentifying seven new phages and annotating the SamScheppers genome. All of the phages were obtained from water and soil samples in the Northeast Missouri region. Enrichment of the bacteriophage samples was performed using Mycobacterium smegmatis mc2 as a bacterial host after which the samples were subjected to several rounds of purification in order to ascertain that only one phage was present. Furthermore, plaque morphology could be observed after purification and SamScheppers created round, clear plaques. Electron microscopy was performed on phage samples, leading to information about the phage characteristics such as size and morphology. SamScheppers was found to possess a Siphoviridae morphotype and approximately 200nm in length. Sequencing of the SamScheppers genome revealed a 58,351bp length and a GC content of 67.6%. The local phage BLAST tool available on phagesdb.org assigned SamScheppers to cluster K, subcluster K4. DNA Master was used to annotate the SamScheppers genome, which was found to contain 94 genes. While a significant number of these genes reported no known function, others were identified with functions including terminase, portal proteins, and exonuclease. One translational frameshift was found, along with a tRNA gene and three genes in reverse sequence. The translational frameshift was located between base pairs 11,957 and 12,837. HHPred, Phamerator, the Hatfull Map and BlastP were used to assign putative protein functions when appropriate.