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9th Annual SEA-PHAGES Symposium Abstract

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Using the DnaB Helicase Gene in the Novel Mycobacteriophage ‘Wyatt2’ to Further Understand M. tuberculosis

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In 2015, it was reported about 1.8 million people died from tuberculosis. Mycobacterium tuberculosis causes infectious tuberculosis. Mycobacteriophages are viruses that infect mycobacterial hosts, such as Mycobacterium tuberculosis (TB) and Mycobacterium smegmatis (M. smeg). In this project we purified, sequenced, and annotated a novel Mycobacteriophage named ‘Wyatt2’. ‘Wyatt2’ is classified as a cluster L, sub cluster L1 with 122 putative genes and 9 putative tRNAs. M. smeg is the host bacteria used to isolate Wyatt2 because it’s closely related to TB. Based on GeneMark coding maps, we found that ‘Wyatt2’ had higher coding potential to TB then M. smeg, which may suggest a closer lineage. We counted 122 genes in total and compared each gene between the M. smeg and TB GeneMark coding maps. In fact, about 96.7% of genes from ‘Wyatt2’s genome had coding potential with M. tuberculosis while about 73.8% of genes with M. smeg. During annotation of Wyatt2’s genome, gene number 68 in the sequence had similar characteristics to DnaB helicase. DnaB functions as a helicase by unwinding DNA. This process starts when DnaA loads a DnaB-DnaC complex onto the DNA. Once the DnaB reaches the replication fork DnaC is released, DnaB then begins to unwind the DNA. The DnaB helicase in Wyatt2’s genome has the potential to give further insight of the function of DnaB in TB. Future studies include the mechanism for DnaB, which could potentially create a drug target to stop or hinder the replication of pathogenic, multi-drug resistant TB.