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7th Annual SEA-PHAGES Symposium Abstract

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An Evolutionary History of A4 Cluster Phage, Skipitt, and the Study of its Infection Potential

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The annotation of the A4 cluster mycobacteriophage, Skipitt, provided a basis for further study of the phage’s evolutionary history and infection potential. Through beginning with the first documented mycobacteriophage, D29, and following its rate of mutation to determine its most recent ancestor, both codon bias and the infection potential of Skipitt were discovered. This also allowed for insight as to how the A4 subcluster is characterized compared to other subclusters. Genome annotation and DNA sequence analysis tools, including DNA Master, NCBI Blast and conserved domain searches, phages.db Blast, Phamerator, and HHPred, were used to determine proper starts and reading frames of Skipitt’s genome and assign gene functions to the reading frames.The same tools were used along with literature research to answer our experimental questions. It was determined that the tape measure protein gene has been used to distinguish phages within their cluster as well as allow for a tracing back of the phage’s history. A 2,649 year period of evolution occurred between Skipitt and its most closely related ancestor, Medusa, since their divergence. Also, Skipitt showed codon bias similar to other A4 cluster phages and although Skipitt showed almost identical codon usage to phage, D29, Skipitt is more closely related to M. tuberculosis. A4 cluster phages are classified in such a way due to various factors including the tape measure protein, but there is no one definitive rule when placing a phage in this subcluster. Skipitt’s relation to other phages within this subcluster was telling of both its history and the evolution of the A4 cluster overall.