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2021 SEA Symposium Abstract

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Gene Function Similarities and Genome Synteny Suggest Evolutionary Relationships Between Bacteriophages

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The genome of a bacteriophage contains genes that code for functional proteins which dictate everything from phage shape to phage function. We annotated Enceladus, a temperate phage belonging to the L1 cluster. This phage was discovered at the University of Colorado at Boulder and is currently being annotated at the same institution. This research attempts to understand similarities in gene function with a focus on phages that possess genes similar to those found in Enceladus. Synteny was used to understand evolutionary relationships between phage genomes. Similarity was found between the genes coding for virion structure and assembly functions in phages belonging to clusters L,M and DU. These results indicate a possible evolutionary connection between the clusters and may be the first step to determining new evolutionary connections between bacteriophages.