CONSIDER FOR TALK

9th Annual SEA-PHAGES Symposium Abstract

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Craff-ting our Phage: Isolation and Annotation of Craff

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Bacteriophages, viruses that infect bacterial cells, are under active investigation because of their diverse potential applications, including as a treatment for antibiotic-resistant bacterial infections. To contribute to advancing the understanding of phage diversity and biology, and as part of our particiation in the HHMI SEA-PHAGES program, we purified the phage Craff from a soil sample in a flowerbed in the Sesquicentennial Oval at the University of Evansville. Craff produces medium-sized, cloudy plaques and has a Siphoviridae morphotype. Sequencing and subsequent sequence analysis show that the Craff genome is 69,263 bp and has 66.4% GC content. Craff is a member of subcluster B1 and has 99% identity to the mycobacteriophage PG1. We auto-annotated Craff with DNA Master, using GeneMark and Glimmer predictions. Then, we compared the nucleotide sequence of all auto-annotated genes to genes in the PhagesDB and NCBI databases with BLAST. Annotations were refined with evidence from Phamerator and Starterator, and HHpred and NCBI BLAST were used to assign functions for the predicted gene products. Our analysis shows that Craff contains 102 genes, 26 of which have known functions. Craff’s annotation will allow for future investigations that may include applications in agriculture, antiseptic techniques, and even medical therapies.