CONSIDER FOR TALK

8th Annual SEA-PHAGES Symposium Abstract

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Functional Genomics of Bacillus Phages

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Over the past three years, VCU students have discovered and characterized the genomes of 12 bacteriophages infecting Bacillus thuringiensis subspecies Kurstaki. These phages can be grouped into several different clusters of genomes and yet these clusters contain a large set of shared proteins, suggesting these phages are both diverse but also contain a core set of functionally important proteins. Many of these proteins are functionally uncharacterized. We are working to apply a variety of functional genomics approaches to predict protein function of this core set of shared proteins, including homology studies, a protein overexpression assay, and computational modeling. This poster will describe some of that work as well as provide examples of Gene Ontology based functional annotations completed through the Spring 2016 “CACAO” (Intercollegiate Annotation Competition) competition.