CONSIDER FOR TALK

7th Annual SEA-PHAGES Symposium Abstract

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Genomic Characterization of 3 Novel Phage Infecting Acinetobacter

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A rise in antimicrobial resistance is a number of bacterial species has led to a resurgence of research to design new therapeutic agents and develop novel strategies for combatting antimicrobial resistant pathogens. The Centers for Disease Control and Prevention has identified 6 ESKAPE pathogens of particular concern: *Enterococcus*, *Staphylococcus*, *Klebsiella*, *Acinetobacter*, *Pseudomonas*, and *Enterobacter* species. Barton, JeffCo, and Effie are novel phage infecting the bacteria host *Acinetobacter* that were isolated from filtered sewage influent samples. Following purification of phage genomic DNA, we sequenced and analyzed each phage’s full-length genome. Freely available bioinformatics software (DNAMaster, Glimmer, GeneMark, Aragorn) and NCBI Blast were used to assist in the identification of putative genes. Phamerator was also used to identify phams and assist in function determination. Our findings show that Barton and JeffCo share a significant number of genes and contain a similar tRNA gene. In contrast, Effie has little gene homology with either Barton or JeffCo. A number of novel genes were also identified in the newly sequenced *Acinetobacter* phage. This work represents the first set of *Acinetobacter* phage analyzed by the UAB Phage Genomics team and expands the pool of available phage infecting *Acinetobacter* for comparative genomics studies.