DO NOT CONSIDER FOR TALK

2023 SEA Symposium Abstract

James Madison University

Harrisonburg VA

Corresponding Faculty Member: Steven Cresawn (cresawsg@jmu.edu)



Isobel Cobb

A Comparative Analysis of Protein and Domain Conservation within Cluster Q Genomes

Isobel Cobb, Rebecca Barklow, Peyton Beasley, Grant Blevins, Will Bowersox, Ria Fisher, Jackie Kossey, Sydney Lee, Noah Liffert, Raymond Martin, Gabby Mendez, Zelda Shifflett, Nehemiah Winesberry, Madison G Bendele, Steven G Cresawn

Bacteriophage genomic data can be assembled into a hierarchy at a variety of levels. Broadly, genomes are grouped into clusters (and optionally subclusters) based on broad patterns of nucleotide sequence similarity. With more granularity, phage proteins are grouped into phamilies based on substantially conserved amino acid sequences. Within the proteins of a given phamily, patterns of conserved amino acid sequences are also detectable as matches to NCBI's database of conserved domains. These conserved domains represent the finest level of granularity in the currently established hierarchy. The conservation of protein phamilies and domains may provide clues as to which elements of a genome are essential to being a functional member of the genome's assigned cluster. Our work analyzes the conservation of phamilies and protein domains in the relatively homogeneous cluster Q with a focus on quantifying conservation. We subsequently hope to apply the metrics to other, more diverse clusters.