CONSIDER FOR TALK

2022 SEA Symposium Abstract

LeTourneau University

Longview TX

Corresponding Faculty Member: Fred Baliraine (fredbaliraine@letu.edu)



Jordan N Angeles



Myah G Beylotte

Remarkable Minor Protein Sequence Diversity Among Subcluster A11 Mycobacteriophages and its Potential Host-Range Implications

Jordan N Angeles, Myah G Beylotte, Christina E Spencer, Angela L Salazar, Frederick N Baliraine

Mycobacteriophages are viruses that infect bacterial hosts of the family *Mycobacteriaceae*. These viruses are grouped in “clusters” based on their overall nucleotide sequence similarity, “subclusters” based on average nucleotide identity values, and “singletons” if there is no significant homology to previous clusters. Currently, there are 717 cluster A members, 22 of which, including phage Gilberta, belong to subcluster A11. While annotating the minor tail protein gene of phage Gilberta, located at 23388-25379 bp, a marked level of sequence diversity was observed on the Phamerator platform among corresponding minor tail proteins (MTPs) of subcluster A11 phages. Minor tail proteins are necessary for host cell recognition and attachment. Thus, MTPs are expected to play a role in determining phage host range, and their sequence diversity could be useful for phage phylogenetic analyses. To examine these possibilities, a comparative analysis of all currently fully annotated MTPs from subcluster A11 was done using PhagesDB, NCBI BLAST, Phamerator, HHPred, MultAlin, GC Content Calculator, and SplitsTree. Members of a subcluster should be expected to have high sequence homology. However, Phamerator and MultAlin analysis of the MTP upstream of the ParA-like dsDNA partitioning protein revealed a remarkable lack of homology in its right arm among various members of subcluster A11. Variations in the MTP sequence length, GC content, and BLAST data were observed. HHPred showed no significant hits to phage or bacterial MTPs, but significant hits to collagen-like proteins in eukaryotic organisms were observed. Notably, SplitsTree data showed sub-clustering within the A11 subcluster. Possible implications of the observed intraspecific MTP sequence diversity on host range and Mycobacteriophage phylogenetics will be discussed.