DO NOT CONSIDER FOR TALK

2021 SEA Symposium Abstract

Brigham Young University

Provo UT

Corresponding Faculty Member: Don Breakwell (breakwell@byu.edu)

Comparative Genomic Analysis of M. foliorum Cluster EE Phages

Jackson Downey, Ben Griffin, Andrew Jensen, Aimee Ludwig, Tiana M Scott, Jacob Spencer, Brianna Thomas, Kevin Vander Werff, Julianne H Grose, Donald P Breakwell

Bacteriophages are grouped into different clusters based on genome synteny and average nucleotide identity (ANI). Analysis using Phamerator and NCBI to compare *Microbacterium foliorum* cluster EE phage genomes revealed that though largely similar, cluster EE phages differ in several ways. Phamerator groups protein coding genes into different “phamilies” or “phams” based on protein similarity. A large portion of all cluster EE genomes are composed of the same phams at their responding loci, suggesting high genome similarity; however, there are certain loci that contain considerable pham variability. Some cluster EE phage proteins even have unique coding sequences that create their own phams. Due to these differences, it is proposed that five subclusters of phages be created within the entire EE cluster. These subclusters were also identified by a phylogenetic tree from NCBI of all cluster EE phages, using the terminase gene for comparison. Finally, phamerator and NCBI tree findings were confirmed using an ANI matrix generated using Clustal2.1 on MAFFT. We propose that cluster EE phages be grouped into five subclusters: EE1, EE2, EE3, EE4, and EE5.