DO NOT CONSIDER FOR TALK

2021 SEA Symposium Abstract

Brigham Young University

Provo UT

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

Characterization of novel Microbacterium foliorum bacteriophage Bri160

Brianna Thomas, Tiana M Scott, Madilynn Moon, Michael Moran, Brandon Wells, Matthew Brown, Samuel Cox, Tristan Packard, Ben Griffin, Jacob Spencer, Andrew Jensen, Kevin Vander Werff, Jackson Downey, Yeiji Lee, Joshua Chamberlain, Emily Doxey, David Eastley, Madeleine Hendricks, Julianne H Grose, Donald P Breakwell

Microbacterium foliorum is a bacterium that has commonly been used in bacteriophage discovery due to its lack of prophage, CRISPR, or restriction-modification systems. We report the isolation, sequence, and annotation of Bri160, a novel M. foliorum EE cluster bacteriophage that was isolated and sequenced in Provo, UT. DNAMaster was used to annotate the genome, with GLIMMER and GeneMark analyzing coding potential. The protein products of the called genes were analyzed using HHPred, NCBI BLAST, phagesdb.org, GenBank. Phamerator maps were constructed to compare the Bri160 genome to other EE cluster phages. Our results show that Bri160 has a 17442-bp double-stranded DNA genome with 68.6% GC content and 25 predicted protein coding genes. Bri160 is closely related to several other bacteriophages in the EE cluster with an average sequence identity of approximately 95% and common synteny especially at the beginning and end of the genome. Our data show that Bri160 has a novel genome and contributes to the information regarding the diversity of cluster EE phages.