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University of Maine, Honors College

Orono ME

Corresponding Faculty Member: Melody Neely (melody.neely@maine.edu)

Applejack, a Novel A1 Mycobacteriophage with Unique Genomic Characteristics

Autumn N Perley, Leah A Cromarty, Emma R Morrison, Grace A Paiement

Bacteriophages are highly diverse viruses that have the ability to lyse and kill bacteria. This capacity can be utilized to treat extremely antibiotic resistant infections in a method known as phage therapy. The novel subcluster A1 phage, Applejack, was isolated through a direct isolation, and characterized from a soil sample located in Orono, Maine (44.704964, 68.91611) using Mycobacterium smegmatis as its host. Applejack is one of 206 phages in its subcluster and has a genome length of 49,791 nucleotides, 93 predicted genes and a GC content of 63.5%. The genome is organized like other cluster A1 phages with forward-transcribed structural genes on the left arm and reverse-transcribed early genes on the right arm. Applejack has distinctive features on its right arm that warrant further research. Temperate phages contain an integrase gene that aids insertion into their bacterial host genomes and an immunity repressor that maintains its presence as a prophage. Applejack is unique in that a large portion of its integrase gene is deleted, causing it to have a lytic phenotype, even though it still encodes an immunity repressor. Another interesting feature in the right arm of the genome is an HNH endonuclease that overlaps completely within a DNA methylase gene, but in a different reading frame, creating rare overlapping transcripts that are conserved in several other cluster A1 phages. Further research into Mycobacterial phages is necessary to provide new knowledge that can be used to create more opportunities for future biomedical applications.