DO NOT CONSIDER FOR TALK

2022 SEA Symposium Abstract

Western Carolina University

Cullowhee NC

Corresponding Faculty Member: Maria Gainey (mdgainey@email.wcu.edu)

The Discovery and Genome Annotation of Gordonia Phages Vardy and Button

Serim Park, Maria Gainey

In the Fall of 2021, Western Carolina University attempted its first isolation of bacteriophages using the host Gordonia rubripertincta. Students sampled various soil types around campus, with many samples being collected from Cullowhee creek. By the end of the semester, 12 new bacteriophages were successfully isolated and archived at the University of Pittsburgh. Two of these bacteriophages, Vardy and Button were selected for whole genome sequencing. Genomic sequencing revealed that bacteriophage Vardy is a member of cluster DJ, and Button is a member of cluster CT. The Vardy genome is 46,090 bp and is predicted to contain 90 genes. While the complete annotation of Vardy is still underway, several features of interest have been noted. Vardy contains four pairs of duplicated genes that are distributed throughout the genome. Phamerator map comparisons of Vardy have also revealed a stretch of the genome (~31,000 to 39,000) that contains many repeat sequences located in intergenic areas. The Button genome is 46,090bp long and is predicted to contain 72 genes. Intriguingly, post sequence comparisons of student restriction enzyme digests to virtual digests revealed that the Button genome, but not the Vardy genome likely contains modified nucleotides. These results and additional genomic features of interest will be discussed.