DO NOT CONSIDER FOR TALK

2024 SEA Symposium Abstract

University of Maine, Honors College

Orono ME

Corresponding Faculty Member: Caitlin Wiafe-Kwakye (caitlin.tetteh@maine.edu)

Trash to Treasure: An Analysis of Cluster B1 Phage, Quisquiliae

Bailey O'Brien, Emma Sammon, Selena Walgreen

Each year, roughly 2 million people are diagnosed with antibiotic resistant bacterial infections, resulting in almost 35,000 deaths. Phage therapy, a medical intervention that uses bacteriophages, has shown promise in treating these multi- or totally drug resistant infections. Bacteriophages (phages) are viruses with a unique structure and genetic makeup that allows them to target and essentially destroy these bacterial cells. Delving into the structure and functions of phage, provides new knowledge about phages and their genetic diversity. Novel bacteriophage, Quisquiliae was directly isolated from a garden soil sample in Old Town, ME using the host Mycobacterium smegmatis. Quisquiliae is a lytic phage with a Siphoviridae morphology that belongs to subcluster B1. Quisquiliae has a tail length of 409.654 ± 8.229 SE nm and an icosahedral head of 90.141 ±1.674 SE nm in diameter. Quisquiliae’s genome has a length of 68,661 bp, a GC content of 66.5%, and codes for 100 putative genes. Researchers have also used mycobacteria phages to study the genetic diversity and evolution of mycobacteria. By analyzing and comparing the genomes of many different phages like Quisquiliae, new information about the genetic variations and adaptations of mycobacteria can be gained and could be used to develop alternative treatments for mycobacterial infections.