CONSIDER FOR TALK

11th Annual SEA Symposium Abstract

University of Mary

Bismarck ND

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Host range infectivity studies of three unique annotated phages, Jiminy (B1), Doug (F1) and Malthus (K4) discovered in water and soil samples near Bismarck, ND

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The students in the Phage Discovery Research Course at the University of Mary discovered in the Fall of 2018, three novel phages using Mycobacterium smegmatis mc2 155 as the host cell. This is the 3rd year of being a part of the SEA Phages Program, which is sponsored by HHMI Science Education Division. The first phage, Jiminy, was isolated from a water sample from the Apple Creek near the University of Mary and is a B1 subcluster phage. The second phage, Doug, was isolated from the garden soil of the University’s President and is an F1 subcluster phage. The third phage, Malthus was isolated from soil near the University and is a K4 subcluster phage. Electron microscopy revealed all three phages to belong to the phage group of siphoviridae. Jiminy had the largest genome with 68777 bp and GC content of 66.4%. Both Doug and Malthus had smaller genomes, 58397 bp and 57802 bp respectively and GC content of 61.1% and 67.9% respectively. Further investigation into the host range infection capabilities using different mycobacterium hosts for these phages revealed interesting results. The three phages, despite being from different subclusters, had varying abilities to infect multiple hosts. Their genomes were annotated in the Phage Genomic Analysis Research Course in the Spring of 2019 and the host range infectivity results as well as the comparison of their genomes will be discussed. These phages were tested using alternative mycobacterium hosts of Mycobacterium smegmatis, Mycobacterium phlei, Mycobacterium nonchromogenicum, Mycobacterium fortuitum, Mycobacterium chelonae and Mycobacterium marinum.