CONSIDER FOR TALK

9th Annual SEA-PHAGES Symposium Abstract

University of Mary

Bismarck ND

Corresponding Faculty Member: Christine Fleischacker (chris@fleischacker.org)



Luke M Keller



Grace P Burns

Isolation and Gene Analysis of North Dakota Phage Old Ben, Maryland Phage Lulumae, and Experiments with Alternative Bacterial Hosts

Luke M Keller, Grace P Burns, Gabriel H Boehne, Veronica R Egging, Miranda M Furchner, Jessica K Gagen, Kathleen A Hecker, Matthew D Heinert, Marriah A Iwuchukwu, Scott M Jennings, Elizabeth B Keller, Micah C Kerney, Matthew A Kuznia, Sandra E Navarrete, Isabel J Stariha, Micah D Zimmerman, Aaron Furchner, David S Ronderos, Margaret Nordlie, Madeline A Dojs, Christine L Fleischacker

Bacteriophages are viruses that infect bacterial cells and are present in many ecosystems, including the soil. During the University of Mary’s inaugural year in the SEA-PHAGE program, two novel bacteriophages were discovered. Both phages were isolated, purified, and amplified, using Mycobacterium smegmatis mc2 155 as the host cell. Lulumae, the first phage discovered, was isolated from Maryland soil and was obtained from direct isolation. Electron microscopy and sequencing revealed Lulumae to be a subcluster B1 bacteriophage of the siphoviridae group of phages. The genome length was 68,056 bp, and the GC content was 66.6%. The second phage, Old Ben, was isolated from soil in Bismarck, ND and was isolated from enriched cultures. Electron Microscopy revealed OldBen to be a subcluster F1 bacteriophage of the siphoviridae group of phages. The genome length was found to be 57,159 bp with a 10 bp overhang, and the GC content was 61.5%. Genome analysis demonstrated that both Lulumae and OldBen have genes similar to other B1 and F1 phages, including the LysA and LysB genes. OldBen also possesses an integrase gene, similar to other F1 phages, that is involved with the lysogenic state. Further experiments were performed to determine the host specificity of these phages. Spot tests, spot titers, and full plate plaque assay with phage titers were performed. The alternative bacterial hosts chosen for these tests were Mycobacterium phlei and Mycobacterium nonchromogenicum. These species were chosen because they fall in the genus mycobacterium, were readily available, and are relatively non-pathogenic. Previous studies have shown that some F1 phages infect M. phlei however it was observed that OldBen, the F1 phage, was not able to infect either of these new bacterial hosts, while Lulumae, the B1 phage, could infect both new species.