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10th Annual SEA Symposium Abstract

Bowling Green State University

Bowling Green OH

Corresponding Faculty Member: Jill Zeilstra (jill.zeilstra@gmail.com)



Eleanor M Behling



Eric M Noss

Mycobacterium smegmatis mc^2 155 bacteriophage of Bowling Green, Ohio

Eleanor M Behling, Eric M Noss, Tessa Alloy, Anisten Aurand, Jocelyn Botta, Lucia Boulos, Susanta Deka, Katelyn Fletcher, Kristina Gara, Megan Gayer, Melanie Heldman, Miranda Jones, Lauren Lukasko, McKenzie Moss, Julia Orshoski, Landon Rohrer, Rachael Sattler, Jenna Sexton, Katherine Sheetz, Kayla Valente, Rowan Wicks, Natalie Wise, Raymond A Larsen, Vipaporn Phuntumart, Zhaohui Xu, Natalie N Stoian, Jill H Zeilstra-Ryalls

Among a total of 23 bacteriophage isolated on the campus of Bowling Green State University during the fall of 2017, five have been sequenced. For three of the phage, plaque and phage (using TEM) morphologies, together with preliminary sequence data, were used to determine their group memberships. The preliminary sequences of PSullivan indicate its genome is composed of 49,990 bp, and the A1 bacteriophage BBPiebs31 (53,171 bp) and Forsytheast (52,695 bp) are its closest relatives. The nearest relatives of Eugenia, whose genome is predicted to be 69,139 bp in size, are the B1 bacteriophage Serpentine (68,884 bp) and Alex (68,910 bp). Preliminary sequence results for Matalotodo, suggest its genome is 69,232 bp in size, and its closest relatives are the B1 phage Vista (68,484 bp) and Murdoc (68,600 bp). Annotation of the other two sequenced bacteriophage was performed during spring 2018. The first of these, Pita2, is a temperate siphoviridae belonging to the A1 group of bacteriophage. Only 3 other A1 phage besides Pita2 encode a tRNA (for tryptophan). The Pita2 genome also includes an ORPHAM (35960). In addition to annotating its genome, immunity and temperature range of infection studies were undertaken to further characterize this phage. The second phage whose genome was annotated is Godphather, a lytic siphoviridae belonging to the uncommon W group. As is true of two other W phage, Taptic and Megabear, the Godphather genome encodes a glycine tRNA gene. Interestingly, Godphather gene 6 is only present in one other W phage, but it is also present in the genome of a singleton phage that was isolated on *Brevibacterium fuscum* NRRL B-14687. Likewise, genes 25 and 26, which encode minor tail proteins, belong to phams that are only represented in one other W phage, but are also represented in phages belonging to clusters B, F, N K, and P as well as cluster EG. The latter cluster comprise phage isolated on *Microbacterium foliorum* NRRL B-24224 SEA. Collectively, these studies of the first Bowling Green phage to be isolated and sequenced suggest that the campus has a diverse phage population. However, since they were all isolated from fertilized soils, the bacteriophage may not be local. Bowling Green is in the region called the Great Black Swamp, which was glacially fed wetland that was drained and settled during the second half of the 18th century. Toward identifying more indigenous phage in future, samples will be taken from areas that are more likely to represent "native" soils.