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Miami University

Oxford OH

Corresponding Faculty Member: Mitchell Balish (balishmf@miamioh.edu)



Jacob W Schlichter

Magnar, a typical subcluster A1 phage with an unusual gene

Jacob W Schlichter, Brendan N Chetty, Susanna D'Silva, Ian G Kausch, Spencer N Kluth, Madelyn K Myers, Garrett M Schilling, Allison M Biedenharn, Amanda C Burgess, Elizabeth Lucas, Mariah S Squire, Kelly Z Abshire, Luis A Actis, Mitchell F Balish

The Miami University Bacteriophage Biology (MBI 223) class of Fall 2017 isolated 17 bacteriophages infecting *Mycobacterium smegmatis* from the soil at various sites in and around Oxford, Ohio. Among these phages, one, designated Magnar, which had been recovered from a trail in a cattle pasture, formed large plaques with distinctively large halos, had typical Siphoviridae virion morphology, and was selected by the class for genome sequencing. The remaining 16 phages were subjected to the DOGEMS protocol, and 12 complete or nearly complete sequences were obtained. Sequencing was performed at the Pittsburgh Bacteriophage Institute using Illumina technology. Of the 12 long sequences obtained by DOGEMS, 8 were cluster A members, and the rest were distributed among clusters B, E, F, and K. Because phages from these clusters are common, no effort was made to identify which genome was associated with which phage isolate. Magnar was revealed to be a member of subcluster A1. Annotation of Magnar by the Bacteriophage Genomics (MBI 224) class of Spring 2018 revealed 91 putative protein coding genes across its 51,428-bp genome, including one encoding an integrase, consistent with Magnar's lysogenic characteristics. Approximately 4% of the reads were from a different phage from subcluster A3. Magnar gene 45, encoding a 78-amino acid protein, was not assigned to a Pham by Phamerator despite being similar in size to genes in syntenic positions in other A1 subcluster phage genomes, immediately upstream of a gene for DNA polymerase I. The encoded protein's only BLAST hit, with an E-value of 1.90 using the default parameters within DNA Master, was to gp48 from A1 subcluster phage KBG, whose coding gene is syntenic with the Magnar gene. BLAST indicated that the predicted proteins share 59% similarity over almost their entire lengths. The KBG protein is a member of Pham 3953, which has 135 members in the Phamerator database as of this writing, none of which are associated with a known function, although the proximity to the DNA polymerase I gene suggests a potential role in DNA synthesis or its regulation. It is tempting to speculate that the unusual plaque morphology of Magnar resulted from contamination with the second phage or, given the absence of a halo in phage KBG plaques, the activity of the highly divergent gene 45.