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2022 SEA Symposium Abstract

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Multiplicity: Gordonia terrae phages from Michigan

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Seven phages were isolated from soil collected in the Grand Rapids, Michigan area using *Gordonia terrae* 3612, an incubation temperature of 30°C, and both direct plating (4 phages) and enrichments (3 phages). Phages Barbochs, Excresco, Gezellig, and Phomeo were chosen for genome sequencing. Phomeo is a Cluster CR2 phage with a genome size of 67,458 bp and contains 94 predicted genes after annotation, including a translational frameshift in the tail assembly chaperone and a HicA-like toxin encoded by most members of the cluster. Phomeo is very similar in length and nucleotide identity to JiFall16, except for a minor tail protein that has been swapped. Gezellig is a Cluster DC1 phage with a genome size of 53,208 bp and differs only by 20 bp to phage Wizard, isolated from Pittsburgh, Pennsylvania. Gezellig and Wizard contain two integrases and one identifiable repressor. Curiously, Excresco (Cluster CV) was found to be a genome duplicate of phage Gambino isolated from Pittsburgh. Noting that a second duplicate of Gambino (MattSquared) was isolated in 2021 from Pittsburgh soil, we also examined the number of duplicates in the Actinobacteriophage database as a percentage of phage genomes sequenced each year for *Gordonia* and other Actinobacteria hosts. The fourth genome, Barbochs, has produced a successful sequencing library and we anticipate annotating the genome this semester.