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2021 SEA Symposium Abstract

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Writing Pages about Phages: A genomic analysis of novel bacteriophages of Microbacterium foliorum and Mycobacterium smegmatis

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During the COVID-19 pandemic, a smaller than usual Miami University Microbiology 223/224 class of 2020-2021 set out to culture, characterize, and annotate genomes of bacteriophages from soil and leaf samples capable of infecting the soil bacterium *Microbacterium foliorum* strain NRRL B-24224. In the fall semester, the work of the eight students, two faculty members, and three graduate assistants resulted in the isolation of six bacteriophages, all of which were lytic. Of these, two, named Josuke and Leafy, were selected for genome sequencing at the Pittsburgh Bacteriophage Institute. Analysis of the resulting genome sequences allowed both bacteriophages to be categorized as belonging to cluster EE, which includes well-conserved actinobacteriophages with the smallest known genomes. Accordingly, the size of the genome of Josuke was 17,453 base pairs, and that of Leafy was 17,407 base pairs. To provide more learning opportunities for the second semester, the class, which now included three additional students, opted to proceed with Leafy but exchange Josuke for a bacteriophage with a larger genome that was available from the Genome Exchange. Zizzle, whose host was *Mycobacterium smegmatis* strain mc2 155, was isolated from soil at a site that had produced three other bacteriophages over the years, each from a different phylogenetic cluster. A member of the more diverse cluster F, subcluster F1, Zizzle had a genome size of 59,381 base pairs. During the Spring 2021 semester, the class intends to use the compact Leafy as a phage on which to be trained in annotation, and then to focus on Zizzle, discerning its genes and their functions.