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Ten New Genomes From the 2021 Illinois Wesleyan SEA Lab: New Cluster GD and EF phages, Big4 and Potty and Eight New Rhodobacter Phages

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Bacteriophages, while relatively common, hold the largest unidentified reservoir of genomic information. This year, we found twelve phages that infect *Microbacterium foliorum* and eight phages that infect *Rhodobacter capsulatus*. Of the *M. foliorum* phages, we found three podoviridae and nine siphoviridae and decided to sequence two of the siphoviridae, Big4 and Potty. These were discovered using soil samples collected from the Illinois Wesleyan campus and a potted plant in a neighborhood in Bloomington, IL, respectively. Both formed small and clear plaques, thereby displaying that they are lytic phages. Based on the capsid diameters and tail lengths from the Transmission Electron Microscopy (TEM) and genome sequencing results, we determined that Big4 is from the GD cluster, a rare cluster with only 5 known members, and that Potty is from the EF cluster, a little more common cluster with 22 known members. The genome of Big4 was found to be significantly larger than that of Potty, and was much less similar to the other members of its cluster.   
In addition to these Microbacterium phages, we also collected water samples in order to isolate phages that infect *Rhodobacter capsulatus* (RC). We used various methods to characterize our RC phages, such as Host-Range, PCR, and TEM analysis and ultimately sequenced all eight of these phages. Of the eight, seven were a part of the RcD cluster and one, RcSwan, was a part of the RcC cluster. Among the RcD cluster phages, one of our phages, RcCWillis, was significantly different from the other phages, as it showed an average nucleotide identity of 77-78% compared to the >90% identity shared by any two other phages in the RcD cluster. Overall, identifying patterns in genomic sequences of phage genomes provided us with an interesting window into understanding phage diversity and evolution.