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Genome Annotation of 3 New *Rhodobacter Capsulatus* Bacteriophages

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Poster Presentation P3

**GENOME ANNOTATION OF 3 NEW *RHODOBACTER*
CAPSULATUS BACTERIOPHAGES**

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In the past several years, bacteriophage research has accelerated. Despite these recent advances, relatively few bacteriophages that infect *Rhodobacter capsulatus* are currently known. Six new phages that infect *R. capsulatus* were discovered and isolated, and three of them (McDreamy, Dormio, and Tiptonus) were classified using information from host-range testing and genomic data. McDreamy and Tiptonus were discovered in the Bloomington-Normal area, and Dormio was found in the Chicago area. Purified DNA of all three phages was sent to the University of Pittsburgh to be sequenced. When the sequence files returned, they were annotated using bioinformatic resources. In order to analyze the genes of the three sequenced phages, their genomic data was compared to past data found for other *R. capsulatus* bacteriophages. The phages currently known to infect this bacterium are grouped into 3 clusters; these clusters have genome sizes averaging 39,072 base pairs. Our research shows that McDreamy and Tiptonus may represent two previously uncharacterized clusters of phages. Both have a genome size significantly greater than any previously discovered *R. capsulatus* phages. Dormio is believed to represent a group that previously had only one member. The annotations of all three genomes will be sent to the GenBank database upon completion.

