Discovery and Genomic Comparison of Bacteriophages BustinJunch and Kimya

Bunch, Justin

Burba, Erin

There are approximately 10^31 phages in the biosphere, making them the most abundant biological entities known to science. They are genetically diverse and play a primary role in bacterial evolution. The purpose of this project was to gain insight into the diversity of the bacteriophage population by isolating and characterizing new bacteriophages from the environment. To complete this task we isolated phages from different environmental samples using Mycobacterium smegmatis as the host. The purified phages were observed using electron microscopy, and their genomes were analyzed by DNA restriction analysis. Although the phages, named “BustinJunch” and “Kimya”, have similar morphologies, the restriction analysis suggests they are unrelated. Our results provide supporting evidence that the global phage population is diverse.

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