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The Isolation, Purification, and Genomic Analysis of Mycobacteriophage BusterBird12 JOSEPH CRAFTON, Department of Biology, Western Kentucky University, Bowling Green, KY, DR. RODNEY KING COLLABORATION[1], DR. CLAIRE RINEHART COLLABORATION[2] — The goal of the Genome Discovery and Exploration Program is to isolate and characterize novel mycobacteriophages from the environment in order to contribute information about their genome structure, geographic distribution, and morphology to the growing mycobacteriophage database. The host bacterium was *Mycobacterium smegmatis*, a nonpathogenic relative of *Mycobacterium tuberculosis*, the causative agent of tuberculosis. A soil sample was collected and enriched to create an environment favoring mycobacteriophage proliferation. Mycobacteriophages were detected by looking for plaque formation, or zones of clearing, on a lawn of host cells. A single plaque was chosen and purified multiple times by a modification of the streak plate technique. The purified phage was named BusterBird12. Electron microscopy revealed that BusterBird12 had an icosahedral capsid and a tail. The average capsid diameter is 52.78 nm, the average tail length is 168.75 nm, and the average tail width is 12.5 nm. Restriction analysis of the purified genomic DNA suggested that BusterBird12 is a member of the K cluster of mycobacteriophages.

[1]Dr. King was an adviser, mentor, and instructor throughout this research.
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