The Discovery, Analysis, and Characterization of Novel Mycobacteriophage PetiteSangsue

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There are approximately 10^31 bacteriophages in the world, but fewer than three thousand have been characterized genomically. Phages have helped in the medical field through phage therapy, but more progress can be made if we have more information. The goal of this study was to expand our knowledge of the phage population. In this study, a novel mycobacteriophage PetiteSangsue was characterized. PetiteSangsue was isolated from a soil sample using Mycobacterium smegmatis as the host. To ensure a pure and homogeneous phage population, four rounds of plaque purification were performed. PetiteSangsue forms turbid plaques, which suggest it is a temperate bacteriophage. Large numbers of the purified phage were grown to facilitate the isolation of the phage genome. The genomic DNA was digested with restriction enzymes, and the products were analyzed using gel electrophoresis. The entire genome of PetiteSangsue was also sequenced using the Illumina Sequencing platform. By comparing the sequence of PetiteSangsue to DNA sequence databases, I concluded it belongs to the A4 subcluster of mycobacteriophages; this group consists of 125 phages. Based on Electron Microscope analysis, I concluded that PetiteSangsue is a siphoviridae bacteriophage with icosahedral, sticky heads, and non-contractile tails. A local blast in PhagesDB found subcluster A4 phage Bumblebee11 to have a similar genome to PetiteSangsue.

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