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Discovery and Genomic Characterization of Bacteriophage BigBubba

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Bacteriophages, viruses that infect and lyse bacteria, are abundant in the biosphere with an estimated population exceeding 10^31 particles. The goal of this study was to characterize the genome of a newly discovered bacteriophage called BigBubba. Phage BigBubba was isolated on the host *Mycobacterium smegmatis* mc²155 by Gabriel Gooden in 2023. BigBubba viral particles have a siphoviridae morphology with an average capsid diameter of 65.5 nm and an average tail length of 263 nm. It produces plaques with clear centers and turbid halos after 48 hours of growth at 30oC. Sequence analysis demonstrated that the genome of BigBubba is 75,006 bp long with a 9 bp 3’ overhang of (CGCTTGTCA). BLAST analysis of the genomic sequence revealed that BigBubba belongs to the E cluster of mycobacteriophages and is most similar to phages Easy2Say, Murphy and Gemini. Cluster E is composed of 127 members, with an average genome containing 75,488 bp, 142.6 genes, and 1.9 tRNAs. E-cluster phages are typically temperate and solely infect Mycobacterium hosts. The Phage Evidence Collection And Annotation Network (PECAAN) program, which compiles data from different bioinformatics databases and algorithms, was used to annotate the genome of BigBubba. The algorithms Glimmer, GeneMark, and Starterator were used to investigate the coding capacity and start site conservation. HHPred, the Conserved Domain Database, and BLAST were used to predict protein functions. The analysis of the BigBubba genome demonstrated variation in gene orientation and many genes with no known function (NKF). Consistent with other members of the E cluster, the genome of BigBubba contains 145 predicted genes and 2 tRNAs. A number of genes were found to contain potential conserved domains such as Helix-turn-Helix DNA binding domains, RecA-like DNA recombinases, and ClpP-like proteases. The presence of a tyrosine integrase supports the classification of BigBubba as temperate and explains the turbid plaque phenotype. This study has extended our knowledge of E cluster phages and provided greater insight into the genetic diversity of the bacteriophage population. A deeper understanding of gene function may allow researchers to utilize individual phage proteins as therapeutics to target antibiotic-resistant bacteria.