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Western Kentucky University

Bowling Green KY

Corresponding Faculty Member: Rodney King (rodney.king@wku.edu)



Katelyn Mattingly



Landon Patton

Genomic Characterization of Mycobacteriophage TinaBug

Katelyn Mattingly, Landon Patton, Billy Goodman, Roby Hardesty, Kaylee Hutchison, Simon Sy, Mateus Vaz, Peicen Yu, Claire A Rinehart, Rodney A King

Bacteriophages are abundant, with an estimated population exceeding 10^31 particles, and represent a largely untapped reservoir of genetic information. The goal of this study was to characterize the genome of a newly discovered bacteriophage called TinaBug. Phage Tinabug was isolated on the host Mycobacterium smegmatis mc²155 in 2024. TinaBug viral particles have a siphoviridae morphology and produce plaques with clear centers and turbid halos after 48 hours of growth at 30oC. Sequence analysis demonstrated that the genome of TinaBug is 42,289 bp long with a 11 bp 3’ overhang of (CCCCATGGCAT). BLAST analysis of the DNA sequence revealed that TinaBug belongs to the G1 subcluster of mycobacteriophages and is most similar to phages Halo, Sweets and BPs. Subcluster G1 is composed of 63 members, with an average genome containing 41,912 bp, 62.6 genes, and 0 tRNAs. Subcluster G1 phages are typically temperate and solely infect Mycobacterium hosts. The Phage Evidence Collection and Annotation Network (PECAAN) program was used to annotate the genome of TinaBug. PECAAN queries algorithms such as Glimmer and GeneMark to investigate coding capacity and identify genes. HHPred, the Conserved Domain Database, and BLAST were used to predict protein functions. Interestingly, most genes in the TinaBug genome are oriented in the same direction and most have no known function (NKF). Consistent with other members of the G1 subcluster, the genome of TinaBug contains 62 predicted genes and 0 tRNAs. A number of genes were found to contain potential conserved domains. The presence of a tyrosine integrase supports the classification of TinaBug as temperate and explains the turbid plaque phenotype. Similar to other members of the G cluster of mycobacteriophages, TinaBug contains a mycobacteriophage mobile element (MPME1). This study extends our understanding of the G1 subcluster of phages. Functional analysis of TinaBug’s genes may allow the identification of proteins that have useful biotechnological applications.