DO NOT CONSIDER FOR TALK

2024 SEA Symposium Abstract

Florida International University

Miami FL

Corresponding Faculty Member: Jaime Mayoral (mayoralj@fiu.edu)

Discovery and Annotation of a New Bacteriophage, Bush, with Potential New Translational Frameshift within its Cluster

Betty Sierra, David Vega, Carlos Rodríguez, Arianna M Ruiz, Nicole Gonzalez Giliberti, Victor A de Melo, Kristen Mclean, Kiryl Yasinski, Gabriela Moyano, Akram Mikhail, Grace Intrator, Alexis Mas, Patricia Waikel, Jaime Mayoral

The discovery and annotation of bacteriophages—viruses that infect bacteria—could help provide a promising treatment against antibiotic resistant bacterial infections when other alternatives have been exhausted. Here, we report on a new bacteriophage, Bush, a siphovirus isolated from soil in Doral, Florida, using the host *Microbacterium foliorum*. Bush belongs to the GA cluster. Bioinformatic tools including DNA Master, Starterator, Glimmer, GeneMark, NCBI, PhagesDB, HHpred, Phamerator, tRNAscan-SE, ARAGORN, and Expasy were used to annotate gene starts and stops, their potential functions, tRNAs, and programmed translational frameshifts. A total of 67 genes were identified in its 38,879 base pairs (bp) long genome, from which 29 were assigned a function. One 74 bp long gly(ccc) tRNA was identified between bp 30,454 and bp 30,528. A translational frameshift was identified in the tail assembly chaperone gene and upstream of the Tape Measure Protein, containing the slippery sequence GGGAAAA at the bp 11,135. Other potential translational frameshifts were explored and a possible one was identified in the terminase small subunit at the 304th bp; this possible frameshift was also found in gene 1 of the genomes of other bacteriophages within this cluster including Appa, Antuna, Blett, Dropshot, and Warren. Bush’s genome annotation and functional assignment offer a template for comparative analysis against current sequenced phages as well as a guide for future annotations of new phages.