DO NOT CONSIDER FOR TALK

2024 SEA Symposium Abstract

Florida International University

Miami FL

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

Discovery and Genome Annotation of the New Phage, Biscayne, discovered in Miami

Jazlyn Appolon, Katherine Artiles, Nicole A Briceno, Pooja Lad, Alexis Mas, Patricia Waikel, Jaime Mayoral

We present here the new bacteriophage Biscayne, isolated from soil next to a pond in Miami, Florida using the bacterial host *Microbacterium foliorum*. The phage was purified and amplified in preparation for DNA extraction, and sequenced at Pittsburgh Bacteriophage Institute using an Illumina platform. Genes were annotated, including their length, start and stop positions using DNA Master, Glimmer, GeneMark, and Starterator. HHpred, BLAST-phagesDB, Phamerator and BLAST-NCBI were used to assign their functions. Transfer RNAs were identified using ARAGORN and tRNAscan-SE. The Biscayne genome is 17,529 base pairs long, with a 68.7% GC content, a 3’ sticky overhanging end and an overhang sequence of 9 bases CCCGCCCCA. It contains 25 genes, three of which were in the 3’ to 5’ direction (genes 20-22). Of the 25 annotated genes, 19 have a known function, while 6 were annotated as hypothetical proteins. Biscayne is a Siphovirus belonging to the EE cluster and has a lytic life cycle. No tRNA was predicted in the Biscayne’s genome. A slippery sequence GGGAAA was identified in the tail assembly chaperone gene at position at bp 7,339.