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2021 SEA Symposium Abstract

University of Massachusetts Amherst

Amherst MA

Corresponding Faculty Member: Jessica Rocheleau (jmrocheleau@umass.edu)

Discovery and gene annotation of Microbacterium foliorum phage Concrete

Angela Zou, Liana Munoz, Shakendine Kelkboom, Jessica Rocheleau

With an estimated population of approximately 10^31, bacteriophages are one of the most abundant and diverse genetic sources in the world. Although abundant, an overwhelming portion of these bacteriophages is still unknown with current databases reporting only 357 sequenced phages that infect Microbacterium foliorum as host bacteria. Microbacterium phage Concrete is a bacteriophage discovered near Hasbrouck Laboratory on the University of Massachusetts Amherst campus. It has become a subject of study following the SEA-PHAGES undergraduate research courses with the purpose of increasing the PhagesDB database and ultimately, understanding genetic diversity in bacteriophages. The research is carried out in two major sections. The first section of the research focused on acquiring an isolated sample of Concrete with a high enough titer for DNA isolation and genome sequencing. Direct isolation, purification, and amplification processes were performed. After sequencing the genome, the second section focused on genome annotation, in which we sought to identify the function of each gene. From these two processes, we found that Concrete is a Siphoviridae bacteriophage belonging to the cluster EE, known for its lytic life cycle. Its plaques are approximately 5mm in diameter with a halo ring surrounding them. With a genome length of 17,432 base pairs, Concrete has a GC content of 68.6% and a total of 25 genes, which does not include a gene we chose to reject during annotation.