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University of Hawaii at Manoa

Honolulu HI

Corresponding Faculty Member: Megan Porter (mlporter@hawaii.edu)



Jennifer Arca



Hailey Hart

Complete Genome Annotation of Actinobacteriophage Casino

Jennifer Arca, Hailey Hart, Raelynn Amasol-Tanoura, Gillian Bradley, Avery Catlin, Saige Edwards, Sophia Faria, Maximiliano Fuentes-Ayala, Lola Gantenbein, Alexis Haiges, Ayden Herrera, Paisley Karlin, Ian Rife, Nana Sannomiya, Landon Schumaker, Katie Thai, Emily Velasquez, Cori Williams, Hannah Moon, Megan L Porter

Bacteriophages are viruses that infect and form parasitic relationships with their bacterial host by lytic or lysogenic methods. Phages play a vital role in the ecosystem by regulating biogeochemical cycles and bacterial populations. In Spring 2024, the SEA-PHAGES Bioinformatics Cohort at the University of Hawai’i at Mānoa annotated the genome of Casino, a bacteriophage within the EM1 subcluster. It was isolated at the University of Connecticut from a soil sample collected in Storrs, Connecticut. Casino is a lytic Actinobacteriophage that infects *Microbacterium foliorum* NRRL B-24224. The genome has a length of 53,667 base pairs and a 64.8% GC content. Of the 48 identified and annotated genes, there were no genes characterized as an orpham. The AAA-ATPase function has been assigned to gene 15, and is involved in cellular processes such as protein folding and cytoskeletal regulation. This genome does not contain any tRNA, and approximately 38% of genes have function assignments, while 62% have been assigned “no known function”. Furthermore, the first 52% of the genes are reverse transcribed, while the remaining 48% are forward transcribed. Within the EM1 subcluster, Casino is most similar to the Hannabella and Gshelby phage genomes. The purpose of this work was to annotate the Casino genome by applying bioinformatic analysis techniques to provide structural and functional details about each identified protein coding gene. Additional studies of the Casino phage genome may provide more details about resistance mechanisms, phage-host interactions, and potential biotechnology applications.