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10th Annual SEA Symposium Abstract

Culver-Stockton College

Canton MO

Corresponding Faculty Member: Esa Seegulam (mseegulam@culver.edu)



Kyle M Strange

Isolation and Characterization of the Bacteriophage Jaykayelowell

Taylor L Barber, Cody A McClain, Dylan J Melton, Cheyenne L Roberts, Kyle M Strange, Muhammad E Seegulam

The goal of this experiment was to isolate and characterize a novel bacteriophage from an environmental soil sample. A soil sample from the Northeast Missouri region containing a putative phage was collected, amplified using the bacterial host M. smegmatis mc2155, and subjected to several rounds of purification in order to identify a novel phage. The formation of plaques on bacterial lawns infected with phage samples indicated the presence of bacteriophage in the sample. Plaque morphology appeared large, circular, and lytic but decreased in size and increased in number with repeated infections and plating. Bacteriophage Jaykayelowell isolated by the 2015 cohort was analyzed. The Jaykayelowell genome was found to be 51,367 base pairs in length and was assigned to cluster A subcluster A4. Among the 85 genes present in the Jaykayelowell genome, several encoded known products including minor tail protein, capsid maturation protease, and membrane domain protein, while 36 of the genes were found to have no known function.The programs used for annotation include DNA Master, Phamerator, Starterator, HHpred, NCBI BLAST and PECAAN.