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2024 SEA Symposium Abstract

University of North Georgia

Dahlonega GA

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Isolation and Genome Characterization of Mycobacteriophage Mao1

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Bacteriophage (phage) are viruses that infect and kill bacteria by injecting their DNA into a host bacterium, producing replicate phages using the bacterium’s machinery, and then lysing the bacterium. In recent years, some bacteria have started developing resistance to antibiotics due to natural selection, which could put the health of humanity at risk since the current medical field is heavily reliant on antibiotics to treat bacterial infections. Phage could reduce or eliminate the need for antibiotics since they are a natural exterminator of bacteria and do not harm humans or cause additional side effects. Phage research also furthers the scientific comprehension of genomics. Genomics can help protect biological ecosystems and describe evolution. Phages are plentiful, impactful, and benign to humans, making them good candidates to study. Researching and annotating the genes of phage like Mao1 broadens the understanding of similar phage and phage as a whole.
Mao1 was discovered in Dahlonega, GA in 2024. It creates cloudy, bullseye plaques that are approximately 3mm in diameter. Mao1 is a siphovirid with a tail of approximately 279 nm and an isometric head of approximately 68 nm. Following DNA extraction and genome sequencing the Mao1 genome was investigated. The genes were annotated using Glimmer, GeneMark, PhagesDB, DNA Master, Starterator, NCBI BLAST, HHPred, Phamerator, and TMHMM. Mao1 is in cluster AD with phages Dori, Sejanus, and Mask. This phage genome consists of 101 predicted genes and is a total of 65,240 base pairs long. One notable gene was Gene 3, which was found to contain a frameshift mutation, disrupting the synteny Mao1 shared with other cluster members Sejanus and Mask. It is an orpham with no predicted function. Also of note was Gene 43, determined to code for tyrosine integrase, which supported that Mao1 was a temperate phage. Mao1 demonstrates continual divergence from other cluster members in the latter half of its genome. Annotating the genes of Mao1 widened the knowledge of cluster AD phages. This will further inform the field of mycobacteriophage genomics and phage biology as a whole.