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2024 SEA Symposium Abstract

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Discovery and Characterization of Gordonia Phage Madvan

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The main goal for this project was to isolate and analyze the bacteriophage, Madvan, and annotate the genome. Madvan was isolated in Bel Air, Maryland from a moist garden soil sample, using the host *Gordonia rubripertincta*. Madvan shows mostly clear medium plaques, and electron microscopy revealed a siphovirus morphology. After DNA extraction and purification, it was sequenced at the Pittsburgh Bacteriophage Institute using Illumina Sequencing with a shotgun coverage of 1240. The genome has a GC content of 51.7% and was assigned to cluster DJ. Madvan is 60,154 base pairs long and has 88 predicted genes. Madvan shares the most genetic similarity with the phages Crocheter (97%), Phepper (96%), and Runhaar (95%). The genome is being annotated using databases like PhagesDB, DNA Master, NCBI, and HHPred. Some of the proteins identified include hydrolase, endonuclease, and portal protein. The genome annotation is ongoing. We aim to investigate the remaining genes and identify additional protein functions. Understanding Madvan’s genome can facilitate its use in future phage therapy applications.