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Discovery, Characterization, and Analysis of Novel Arthrobacter Phage Wildwest

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Bacteriophages are diverse types of viruses that infect and replicate inside of bacterial cells. In this experiment, as part of the SEA-PHAGES (Science Education Alliance - Phage Hunters Advancing Genomics and Evolutionary Science) program, Arthrobacter atrocyaneus was used as the host bacteria to discover, isolate, and characterize a novel Arthrobacter phage. This bacteriophage, named “Wildwest,” was found in a soil sample taken near a lake in St. Charles, Missouri. The isolation process of the bacteriophage was done by washing soil to create lysate. This lysate was used to make plaque assays and spot tests to verify the presence of phage. Then, the phage was characterized through DNA extraction, polymerase chain reaction, gel electrophoresis, and transmission electron microscopy. The extracted DNA was then sent to the Pittsburgh Bacteriophage Institute for Illumina sequencing. Manual annotations were curated using the bioinformatic tools DNA Master, BLASTp from NCBI and PhagesDB, HHPred, Phamerator, and PECAAN. The phage exhibited lytic plaques and is of the Siphoviridae morphotype with a head diameter of 45 nm and a tail length of 100 nm and belongs to the cluster AZ. The genome size of the phage is 43,653 base pairs and has a GC content of 66.9%. Annotations indicate Wildwest has 65 potential genes: 27 genes with no known function and 38 genes with predicted functions. Among these 65 genes, proteins with functions for structure and regulation were found, such as head-to-tail adaptors, stoppers, and endonucleases. Further analysis of the predicted gene functions will contribute to expanding the knowledge of phage structure, function, and diversity. Due to the abundance and adaptability of phages, Wildwest has the potential to be used as a comparative model for future characterization of more Arthrobacter phages and analysis of potential novel genes from its unique genome.