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The Discovery, Isolation, and Characterization of Arthrobacter Phage Sue2

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In an era of antibiotic resistance, bacteriophage research has emerged as a promising solution to this crisis. Bacteriophages are viruses that infect and replicate in their specific host bacteria. Through the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science (SEA-PHAGES) program, a study was conducted to characterize a newly discovered Arthrobacter bacteriophage. The bacteriophage, Sue2, was discovered in the soil in Elmhurst, Illinois. Through soil washing, the sample was isolated and then purified by performing plaque assays with the lysate to confirm the presence of the phage on the host Arthrobacter atrocyaneus. Amplification and characterization were performed through procedures of calculating titer, phage precipitation, DNA purification, polymerase chain reaction, gel electrophoresis, and transmission electron microscopy (TEM). These procedures resulted in a bacteriophage with a high titer of 3.0 x 1010 pfu/mL. The cluster determination was unsuccessful due to available cluster-specific primers for the tape measure protein. The TEM indicated a Siphoviridae morphology with an average head diameter of 48 nm and an average tail length of 108 nm. Sue2 was archived into the SEA-PHAGES database, and its phage genome was sequenced at the Pittsburgh Bacteriophage Institute to compare it to other known bacteriophages. Using bioinformatics tools such as BLAST, HHPred, Glimmer, and GeneMark, annotations of each of the genes from Sue2 were completed. Out of the 67 genes annotated, 29 were found to have no known function. Genome sequencing also revealed that Sue2 is a member of the AZ1 cluster. The knowledge gained from isolating and characterizing Sue2 can be applied to new scientific discoveries and medicinal applications, such as phage therapy.