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The Discovery and Annotation of Gordonia phage OtterstedtS21

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Bacteriophages are a type of virus that infect a host bacteria. By isolating and analyzing individual bacteriophages, scientists can continue to address questions about the viruses’ biological diversity and evolutionary history, as well as make new discoveries in the field of microbiology. *Gordonia rubripertincta* was the host bacteria used for isolation of the novel bacteriophage OtterstedtS21. *G. rubripertincta* is a gram-positive organism commonly used in bioremediation and industrial biotechnology. The objective of this project was to isolate, amplify, and image a bacteriophage that infects the host bacteria using various laboratory techniques. Direct isolation was used to isolate the phage from soil samples. It was then purified using serial dilutions and amplified using a webbed plate method. Genomic DNA was extracted and a restriction enzyme digest was performed. Gel electrophoresis was used to characterize the restriction profile of the phage. A TEM image was obtained, which classified OtterstedtS21 as a siphoviridae phage, which is characterized by a long, non-contractile tail. The DNA of the phage was later sequenced and auto annotated using Glimmer and GeneMark algorithms in the DNA Master software, followed by manual annotation using sources including Starterator, Pharmerator, coding potential data, and NCBI BLASTP. Manual genome annotation resulted in 96 genes, with all 96 being forward genes. Functional annotation then concluded that many of the genes coded for hypothetical proteins, while other functions included capsid proteins, enzymes, structural proteins, and portal proteins. Conducting laboratory research followed by bioinformatic analyses allowed for the discovery and annotation of the OtterstedtS21 phage. The discovery of new phages, as done with OtterstedtS21, can further advancements in the field of science.