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Isolation, Sequencing, and Annotation of Bacteriophage Gilson

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Bacteriophages are one of the most prevalent biological entities in the world, yet only a small fraction of the species in existence have been discovered. Although some phages are used for therapeutic uses, much more research is required before this practice becomes widespread. After directly isolating an environmental soil sample containing Phage Gilson at 38.647 °N, 90.311 °W just off the side of Forsyth Blvd. in St. Louis, MO, we were able to infect bacterial host *Streptomyces griseofuscus* and purify our phage to a high titer of 5.11 x 10^10 and extract its DNA. Through analyzing restriction enzyme digests from gel electrophoresis, we identified that the enzyme *BamHI* did not cut the DNA while enzyme *EcoRI* cut to give an estimated genome of 70,684 base pairs. Using electron microscopy we determined that the phage has an icosahedral head shape with a long, flexible tail. After sending our samples to the Washington University School of Medicine's sequencing facility, we measured a head length of 87 nm, head width of 79 nm, and tail length of 321 nm. After sequencing the genome, Phage Gilson was found to have a genome length of 128,338 base pairs with a fixed, terminally redundant end of 788 base pairs. Several tRNA clusters were also found in Gilson's genome around 5 kbp, and throughout 65 kbp - 105 kbp. Using online tools such as PECAAN (Phage Evidence Collection and Annotation Network), we analyzed coding potential, gap scores, Shine-Dalgarno scores, and DNA BLAST results to determine the presence of 231 genes in the Gilson genome. DNA Master was used to find any gray holes—genes we may have missed in the initial positional annotation. By annotating the positional and functional parts of a novel phage, such as Phage Gilson, we will have a more complete understanding of how to use different bacteriophages' functions in modern science.