Isolation and Characterization of a Novel Bacteriophage from a Local Stream

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ISOLATION AND CHARACTERIZATION OF A NOVEL BACTERIOPHAGE FROM A LOCAL STREAM

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Students collected bacteriophage from the environment, isolated and purified the phage, and then analyzed their genomic properties. A total of sixteen bacteriophages were isolated and purified at Illinois Wesleyan University and may contribute to future scientific research in the field of genomics. Using a phage sample enriched on Mycobacterium smegmatis, each student isolated a single phage population through a series of plating procedures. Once that phage had been purified, students isolated its genomic DNA and analyzed it using gel electrophoresis. Two phages from the class, Morrow and Eidsmoe, were sent to be sequenced. Eidsmoe was sequenced at NC State Genomic Sciences Laboratory. Eidsmoe is highly similar to the other bacteriophage in sub-cluster, A9. Members of this sub-cluster that are the most similar to Eidsmoe are Alma, Catalina, and PackMan with the main deviation in Eidsmoe being the tRNA present. The genome of Eidsmoe is 52,946 bp in length and contains 92 genes. Previously annotated genomes that are most similar to Eidsmoe are Alma and PackMan. The sequenced genomes were annotated and analyzed by students primarily through the programs DNA Master and Phamerator.