

Group 3: Abstract Rough Draft

This research aims to produce an annotated genome of a mycobacteriophage associated with the SEA-PHAGES project. Mycobacteriophage are virions that infect mycobacterial cells for the purpose of utilizing the bacteria's ability to reproduce genetic material. The SEA-PHAGES project is an international effort of undergraduate students to log genomes of mycobacteriophage found in environmental samples in order to discover new genes and their functions to further the field of genetics. Using programs such as DNA Master, GeneMark, BLAST, Starterator, and Phamerator, the genes of this mycobacteriophage were systematically annotated to determine which features were genes and the likely functions of these genes. The predictions from these programs and databases are heavily reliant on historical data from other related mycobacteriophage. After determining start and stop codons of potential genes, BLAST assists in comparing that DNA sequence to known amino acids in order to decide upon the most likely position at which the gene should be called. This annotated genome can now be submitted to the GenBank database where it will be validated through wet lab testing to determine the type and function of the projected proteins. Following validation, the genome can be compared with others from the same cluster to analyze the adaptations and evolution of the phamily. This research ultimately contributes to the knowledge of mycobacteriophages and the mycobacteria they infect and their potential applications in medical and environmental fields.