

Annotation of Bacteriophage Blocker 23 and Discovery of A Novel Actinobacteriophage

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Bacteriophages known as “bacteria eaters” are viruses that infect bacteria through attachment, penetration, and viral replication to kill bacteria. As disease-inducing bacteria can infiltrate human bodies, bacteriophages, viruses relatively harmless to humans, become increasingly important towards developing treatments when antibiotics are no longer an option. This research project focuses on annotating bacteriophage genomes through bioinformatics. Identifying these genes and its purpose helps discern the bacteriophages’ killing cycle allowing this research to become a crucial component towards establishing treatments such as bacteriophage therapy. This research follows the process of identifying genes, identifying the correct start codon for each gene, and assigning putative gene functions. Softwares and resources such as DNA Master, gene prediction programs Glimmer and GeneMark, coding potential maps, phamerator, starterator, TMHMM, SOSUI, HHPRED, BLAST protein homology tools, and google docs were used. As NASA aims to help humanity, this research corresponds with NASA’s mission as it will aid in the fight against bacteria on earth, space, and other origins. Through the annotation of Blocker 23, 92 genes within Blocker 23 were identified with proper starts and 41.3% of these identified genes had putative functions assigned. The annotation of Blocker 23 will help stimulate not only more annotations, but also an incentive to treatments as more knowledge becomes available regarding bacteriophages. The laboratory portion of this project included identifying a novel bacteriophage found in Las Vegas that will be annotated in the future.