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The discovery and genome annotation of Mycobacteriophage CheetoDust

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Bacteriophages or phage are naturally occurring viruses that infect and replicate only in bacterial cells. This, coupled with the wide range of bacteriophage diversity makes for a rich environment that provides seemingly endless opportunities for research and discovery. Application of phage research can be used across several disciplines that could assist in providing potential solutions to issues that arise in biotechnology, agriculture, environment, and medical research, specifically in the development of alternative treatments for drug resistant bacteria. Mycobacterium smegmatis mc2155 is a widely used strain in laboratory experiments, it is nonpathogenic and fast replicating, making it suitable for a host. M. smegmatis mc2155 is also non-pathogenic to humans and in abundance in natural environments. The phage CheetoDust was discovered from a soil sample collected at Virginia Commonwealth University in Richmond, VA. After 6 rounds of phage purification, genomic DNA was isolated at a concentration of 66 ng/μl and submitted for sequencing. This semester, we annotated the genome of phage CheetoDust. The genome of CheetoDust is 59,302 bp, with a 66.5% GC content and codes for a predicted 95 protein codling genes as well as two tRNA genes. We analyzed a variety of computational predictions to determine the best possible start position for each gene. Using comparative annotation tools such as NCBI Blast, HHPRED, and TMHMM we determined the similarities in functional and positional annotation of Mycobacteriophage CheetoDust gene sequences. We then used those tools to compare our genome against previously documented genomes. Several interesting genome features will be shared. Gene product (gp) 30 has 100% query coverage, and 98.97% percent identity with lysin b from several other mycobacteriophages, and functional annotation tools predict enzyme function. The lytic cassette components of mycobacteriophages will be shared. Gp 84 was predicted to be an RNA ligase by functional annotation tools Blastp and HHPred and connections to tRNAs in the genome will be explored. Gene 32 function search using a tool that predicts transmembrane domains (TMHMM) predicts one potential transmembrane area and the sequence features leading to this structure will be shared. Having the opportunity to annotate a phage genome and contributing a piece of information to the overall database of genetic knowledge, is a interesting way to further explore the scientific discovery process.