Introduction

* This research aims to produce an annotated genome of JewelBug, a newly discovered species of mycobacteriophage, for the SEA-PHAGES project.
* Mycobacteriophage are virions that infect mycobacteria in order to replicate.
* The SEA-PHAGES project is an international effort of students characterizing mycobacteriophage found in the environment to discover new genes and their functions.

Relevance

* Viruses are the most genetically diverse group of biological material as well as the least studied. Therefore, they contain the largest number of novel genes.
* The databases provide the groundwork for research into the evolution and adaptation of viruses which in return provides the same groundwork for that of bacteria that the phage infect.
* Mycobacteriophages have specific applications in human medicine since their hosts include M. tuberculosis.

Significant Annotation Adjustments

* Adding a gene between features 72 and 73
  + There was a large 119 bp gap, GeneMark coding potential, and significant blast results once this feature was added
* Deleting features 87 and 89
  + Both features 87 and 89 were in the forward direction, even though all of the other features in this part of the genome were in the reverse direction
  + The features did not have strong BLAST results, if any, and there is not enough space between the surrounding genes to suggest a reversal of direction. Features 86, 88, and 90, on the other hand, have stronger evidence supporting their existence

Noteable Features

* A significant proportion of our features had no known function after thorough analysis of the available evidence.
* The genes in our sections that did have supported putative functions were regulatory proteins (promoters and anti-repressors) or associated with DNA (DNA methylase and a helix-turn-helix domain).
* The majority of our features were similar with to features of other phages found within the A6 cluster with a few exceptions.

Conclusion

* The genome annotation has been improved so that it more likely reflects reality as described by the guiding principles.
* Our section is generally conserved among several other phage in the subcluster. The genes that were not conserved may play a role in the individual characteristics of the phage, such as host range and life-cycle regulation.
* JewelBug’s plaques have halos or cloudy / turbid edges. This suggests that it may be a lysogenic phage. (Many other phages in the subclust also have turbid edges). A lysogenic phage requires more genetic regulation, since it does not automatically complete replication, but integrates itself into the bacteria’s genome for a dormant period instead. This section may contain genes that facilitate this process, since some of the few with identified functions are involved with DNA manipulation and regulation.

Future Work

* JewelBug’s genome annotation will be verified via wet lab testing to determine the accuracy of the gene calls.
* Since many of the genes do not have a known function, these could be determined via wet lab testing. This would also benefit the similar genes from other phages in the subcluster.
* The host range of JewelBug could be found to determine whether or not it is likely to have any application in human medicine.
* A cross comparison with phages in the same cluster and subcluster could provide insight into the evolutionary development of JewelBug and its relatives.