Cover Letter

Annotation: PrincessTrina

November 7, 2015

We reanalyzed our annotation calls using GeneMarkS instead oof GeneMark Mycobacterium smegamatis. We did so because we are finding with Arthrobacter phage genomes that Output GeneMarkS gives coding potential for almost all genes called by Glimmer and GeneMark. There are also several gaps within genes not called by Glimmer and/or GeneMark that had coding potential via GeneMarkS analysis. We included these genes as well in the updated annotation.

There are still some gaps ranging between 100-300bp with no coding potential according to GeneMarkS even if we included the longest open reading frames of annotated genes flanking the gaps.

Another related phage, ArV1, was identified and annotated by a lab outside of the SEA-PHAGES program. Many of the genes annotated as encoding structural proteins we annotated as “Unknown” unless we got confident results via HHPred, BlastP or Phamerator.

Two genes of note are gp5 & gp6 which appear to be part of a toxin-anti-toxin system.

Lastly, we did not detect any tRNA or tmRNA genes via web-based Aragorn or tRNA scan programs.