Cover Letter

Annotation: Sorjuana

September 5, 2015

A tRNA gene (gp14) was added to the annotation. This putative tRNA gene was detected by both Aragorn and tRNA scan. tRNA scan gave a COVE score of 17.37. Both programs could not determine whether the tRNA gene coded for a Gln or a Pro. Perhaps this tRNA gene should be deleted from the final annotation submitted to GenBank.

The genes gp35 & gp36 are annotated as the tail assembly chaperones. They are located adjacent on the left hand side of the TMP. Gp36 is annotated as a minus 1 frameshift protein.

Also of note is that many of the annotated forward genes had at least some GeneMark Smeg coding potential. Many of the reverse genes also had GeneMark Smeg coding potential but the reverse genes detected with GeneMark Smeg were in a different reading frame then noted in DNA Master. For instance, if a reverse gene in DNA Master was in the -2 frame it was in the -3 frame in GeneMark Smeg. When we figured this out we realized that many of the annotated reverse genes had coding potential according to GeneMark Smeg.

One final note is that the phages Sorjuana, Anansi and Gorgeous genomes are VERY similar to one another.

All genes within the annotation with no known function are genes that had less than 95% probability in HHpred or uninformative hits within the function sources of Phamerator, HHpred, and Blastp.