Genome Annotation Submission Cover Sheet

Pre-QC Phage Genome Annotation Checklist

Phage Name:	Rem711
Your Name:	Sharon Isern
Your Institution:	Florida Gulf Coast University
Your email:	sisern@fgcu.edu
Additional emails: (For correspondence)	smgatt9243@eagle.fgcu.edu

Please check each box indicating completion of each task. Annotation Guide section #'s indicated

1. ☑ Does the genome sequence in your final contain the same number of bases and is it the same as the posted sequence on phagesdb.org?
2. ☑ Are all the genes "valid" when you click the "validate" button? *Section 9.3.2*
3. ☑ Have the genes been renumbered such that they go sequentially from 1 to the highest number? *Section 9.3.3*
4. ☑ Have all old BLAST hits been cleared, and all gene features reBLASTed? *Section 9.3.4*
5. ☑ Are the locus tags the phage name? *Section 9.3.3*
6. ☑ Has the Documentation been recreated to match the information in the feature table? *Section 1.4*
7. ☑ Have tRNA ends been adjusted with web-based Aragorn and/or tRNAscan SE? *Section 9.5.3-4*

8. For the items below, generate a genome profile, and review the following. *Section 11.3*

For the YourPhageName_CompleteNotes.dnam5 file:

   a. ☑ Have any duplicate genes (or any with the same stop coordinate?) been removed?
   b. ☑ Does every gene have **one and only one** complete set of Notes (see fig 12.2 in the Annotation Guide)?
   c. ☑ Do the functions in the Notes match the official function list?
   d. ☑ Is the function field EMPTY for all features?
   e. ☑ Do the notes contain the initial Glimmer/GeneMark data from the autoannotation?

For the YourPhageName .dnam5 file:

   a. ☑ Have any duplicate genes (or any with the same stop coordinate?) been removed?
   b. ☑ Is the Notes field empty for all the features with no known function?
   c. ☑ Do the function names in the Notes match the official function list, when applicable?
   d. ☑ Is the function field EMPTY for all features?

9. Describe any issues or specific genes that you were unable to satisfactorily resolve, and warrant further inspection in the Quality Control review.

Rem711 is a Cluster z phage 50,832bp in length. Here's what was found:
1. 85 features were annotated. There were no tRNAs present, thus all were ORFs.
2. Functions were called in roughly 40% of the ORFs whereas the remaining 75% were NKF.
3. Less than 1% of the phams were orphams (1 out of 85).
4. Rem711 was very similar to phage 32HC, thus most genes and their function calls match up with these two phages.
5. ATG (75%) and GTG (24%) were primarily used as start sites. Only one ORF used TTG [gp1_terminase, small subunit] as a start codon
6. Synteny was followed with the structural genes.
7. Interesting features of genes with no known function: