Genome Annotation Submission Cover Sheet

Preliminary Annotation Review Checklist 4-4-2018

Phage Name:	InigoMontoya
Your Name:	Susan Gurney
Your Institution:	Drexel University
Your email:	smg366@drexel.edu
Additional emails: (For correspondence)	rrd62@drexel.edu

Please check each box indicating completion of each task. If you are not sure how to do something, please see the Online Bioinformatics manual page "How to Pass Preliminary Review".

- ☑ 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?
- ☑ 3. Have the genes been renumbered such that they go sequentially from 1 to the highest number?
- ☑ 4. Have all old BLAST hits been cleared, and all gene features reBLASTed?
- ☑ 5. Are the locus tags the"SEA_ PHAGENAME"?
- ☑ 6. Has the Documentation been recreated to match the information in the feature table?
- ☑ 7. Have tRNA ends been adjusted with web-based Aragorn and/or tRNAscan SE?
- ☑ 8. Has the frameshift in the tail assembly chaperone been annotated (where applicable?)

9. For the items below, generate a genome profile, and review the following. 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
- ☑ c. Do the functions in the Notes match the official function list?
- ☑ d. Are all three lines of functional evidence described for EVERY gene?
- ☑ 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 (including hidden marks?
- ☑ c. Do the function names in the Notes match the official function list?
- ☑ d. Is the function field EMPTY for all features?

☑ 10. Did you use PECAAN to annotate your phage?

If, so please describe how in the text field after question 11.

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

The students used PECAAN during the annotation stage. The information was exported from PECAAN and our quality control was performed in DNA Master.

Annotation issues

1. We wanted to insert gene 154646-155217 similar to phage Littleton (but not found in Momo, or Audrick), but couldn't fine the stop site. This suggests the gene is not present in our genome, but we wanted someone else to take a look as well.
2. Gene 118 PhagesDB, HHPRED and CDD suggest N-acetyltransferase, but not supported in similar phages in SYN-FUN and it is not an approved function. So we have listed it as NKF.
3.Gene 185, PhagesDB, HHPRED and CDD all support Homing-endonuclease, but it is not an approved function. So we have listed it as NKF.