Genome Annotation Submission Cover Sheet

Preliminary Annotation Review Checklist 5-15-2018

Phage Name:	Fury
Your Name:	Hui-Min Chung
Your Institution:	University of West Florida
Your email:	hchung@uwf.edu
Additional emails: (For correspondence)	hchung@uwf.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 (including hidden marks?)
- ☑ c. Do the function names in the Product field either match the official function list or say "Hypothetical Protein"?
- ☑ d. Is the Function field empty (including hidden marks?)

☑ 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.

There is no tRNA gene; but I still check the box 7 above.
The tail assembly chaperone genes are gene 46 and gene 47. PECAAN has been really helpful tool for annotating the genome; but I don't know how to change genes with translational frame shift in PECAAN. DNA Master seems still the only one can solve this issue; is it right?
For the head-to-tail connector complex proteins, genes 39-42 did not fit the current criterion, therefore reassign them as "NKF"; this might apply to similar layout in phages Patio and Kabluna.
I practically use PECAAN for assessing the gene calling (SCS), Gap check, Starterator (ST) and SIF-BLAST and SIF-HHPred, but not BLAST-Start check. I notice the Glimmer calling and GeneMark calling in PECAAN are sometimes not identical to those in DNA Master. I used the