Genome Annotation Submission Cover Sheet

Preliminary Annotation Review Checklist 5-15-2018

Phage Name: Twonlo

Your Name: Marie Fogarty

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Additional emails:
(For correspondence)

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".

- [x] 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?
- [x] 2. Are all the genes "valid" when you click the "validate" button?
- [x] 3. Have the genes been renumbered such that they go sequentially from 1 to the highest number?
- [x] 4. Have all old BLAST hits been cleared, and all gene features reBLASTed?
- [x] 5. Are the locus tags the"SEA_ PHAGENAME"?
- [x] 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:

- [x] a. Have any duplicate genes (or any with the same stop coordinate?) been removed?
- [x] b. Does every gene have **one and only one** complete set of Notes
- [x] c. Do the functions in the Notes match the official function list?
- [x] d. Are all three lines of functional evidence described for EVERY gene?
- [x] e. Do the notes contain the initial Glimmer/GeneMark data from the autoannotation?

For the YourPhageName .dnam5 file:

- [x] a. Have any duplicate genes (or any with the same stop coordinate?) been removed?
- [x] b. Is the Notes field empty (including hidden marks?)
- [x] c. Do the function names in the Product field either match the official function list or say "Hypothetical Protein"?
- [x] d. Is the Function field empty (including hidden marks?)

- [x] 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.

Twonlo is a DE3 phage with 56530 bp. All genes are in the forward orientation and there are no gaps of note. Two DE3 phages were used for comparative purposes -Tiamocelo (92.74 % gene content similarity) and Roadkill (96.43 % gene content similarity). PECAAN, alongside with DNA Master, was used for all aspects of annotation and the 'new SEA format' annotation notes were imported to DNA Master. No tRNAs were annotated, one was identified by Aragorn 1.2.38 only, the identified included tRNA included a 131 bp intron, and overlapped with an existing called gene in the minor tail protein area and so was not included.