Genome Annotation Submission Cover Sheet

Preliminary Annotation Review Checklist 5-15-2018

Phage Name: MinionDave

Your Name: Janine LeBlanc-Straceski

Your Institution: Merrimack College

Your email: leblancstraj@merrimack.edu

Additional emails: (For correspondence) berkesc@merrimack.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.

This was an adopted phage discovered by Emily Powell from Jacksonville State University. Students and faculty in Merrimack College Genetics lab course did the first pass, then LeBlanc verified all the genes, added several genes, annotated the frameshift of the tail assembly chaperones, and prepared the files in DNA Master.
During the annotation several small genes were added in the right half of the genome, per the F1 specific annotation notes. The mobile element 1 was identified, and synteny notes were adjusted to the F1 cluster after comparing several annotated genome phamerator maps.
Gene calling at the very end of he genome, which ontains overlapping ORFs in forward and reverse directions, was annotated by comparing Minion Dave to other F1 cluster maps.
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