Genome Annotation Submission Cover Sheet

Preliminary Annotation Review Checklist 5-15-2018

Phage Name: Sephiroth

Your Name: Marie Fogarty

Your Institution: Durham Technical Community College

Your email: fogartym@durhamtech.edu

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".

☑ 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.

Sephiroth is a DU cluster phage with 76058 bp. Two DU phages were used for comparative purposes -Syleon (85.15 % gene content similarity) and Octobien14 (74.9 % gene content similarity, annotated as a singleton by Durham Tech in 2018). PECAAN, alongside with DNA master, was used for all aspects of annotation and the 'new SEA format' annotation notes were imported to DNA Master. Six tRNAs were annotated for Sixama using Aragorn 1.2.38 and tRNAscan-SE. One additional tRNA, identified by Aragorn v 1.2.38 was discarded as it was 95 bp (criteria say < 90 bp) and also contained a 703 bp intron and a low infernal score (17.5). Six gaps were investigated using GenemarkS or Genemark G. terrae 3612, but not found to have supporting evidence for gene addition. In order of gap size: 68672 - 69154 (483 bp), there was moderate coding potential on the reverse strand, but it would have resulted in a