Genome Annotation Submission Cover Sheet

Preliminary Annotation Review Checklist 5-15-2018

Phage Name: Penelope2018

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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".

☑ 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.

PECAAN was used in class for the student to share evidence with one another and to QC each other's assigned genes. phagesdb BLASTp, NCBI BLASTp, and phamerator were checked both on and off PECAAN, and students were required to keep detailed notes regarding why certain choices were made through PECAAN. HH-PRED on PECAAN was used by students, but each gene was checked with HH-PRED independently by the instructor.
RBS scores were retrieved from PECAAN (checked by instructor using DNA Master),.
gene 43 was inserted as there was a large gap between the two other reverse genes (42 and 44).
gene 1 was manually inserted and start and stop determined manually.
This is a D1 phage so no frameshift in tail assembly chaperone could be identified.
original gene 41 was deleted (34878-35708) because of significant overlap with upstream gene (with no solid evidence by CP to support it was true).
original gene 83 (59678-59899) was deleted because it was a reverse gene in midst of all forward and overlap with downstream gene was significant.