Genome Annotation Submission Cover Sheet

Preliminary Annotation Review Checklist 5-15-2018

Phage Name: Anon

Your Name: Dr. Michael R. Rubin

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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?
- [x] 7. Have tRNA ends been adjusted with web-based Aragorn and/or tRNAscan SE?
- [x] 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.

PECAAN was used to verify gene annotations and to generate the DNA Master Complete Notes. Students followed the SEA-PHAGES Online Bioinformatics Guide using DNA Master and Internet Resources for all gene annotations. Students then transferred their traditional annotations to PECAAN for verification and subsequent transfer to DNA Master for SEA-PHAGES submission.

Anon Genome Annotation Submission Cover Sheet Page 2
SEA-PHAGES Program Academic Year 2018 – 2019
Dr. Michael Rubin

Anon Annotation Comments

Note: Genes 18, 20, 21, and 22 all share homology with the head-to-tail adaptor. If only one head-to-tail adaptor function is acceptable, it should be Gene 22 (See notes below for the individual genes).

Gene 18: Possible Function as head-to-tail adaptor (annotated as NKF although has weak homology to Bacteriophage SPP1, gp15)

Gene 20: head-to-tail adaptor weak homology to Bacteriophage SPP1, gp15 (If only one head-to-tail adaptor function is acceptable, then consider changing this function from head-to-tail adaptor to NKF)

Gene 21: Possible Function as head-to-tail adaptor (annotated as NKF)

Gene 22: head-to-tail adaptor significant homology to Bacteriophage SPP1, gp15

Genes 24 and 25: tail assembly chaperone (Frameshift 15604 annotated)

Gene 35: Possible Function as ParB-like dsDNA partitioning protein

Gaps between Genes 33 – 34, Genes 80 – 81, and 102 – 103 annotated as in Rosalind and no genes inserted.

Gene 104: This sequence of DNA provides no viable BLAST results, it is an orpham, and contains no coding potential. This information leads me to believe that perhaps this is not a gene and should be eliminated. It was left in to comply with "better more than less" if justified. Please review.