Genome Annotation Submission Cover Sheet

Pre-QC Phage Genome Annotation Checklist

Phage Name: Barbarian

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Please check each box indicating completion of each task. Annotation Guide section #'s indicated

- ☑ 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? *Section 9.3.2*
- ☑ 3. Have the genes been renumbered such that they go sequentially from 1 to the highest number? *Section 9.3.3*
- ☑ 4. Have all old BLAST hits been cleared, and all gene features reBLASTed? *Section 9.3.4*
- ☑ 5. Are the locus tags the phage name? *Section 9.3.3*
- ☑ 6. Has the Documentation been recreated to match the information in the feature table? *Section 1.4*
- ☑ 7. Have tRNA ends been adjusted with web-based Aragorn and/or tRNAscan SE? *Section 9.5.3-4*

8. For the items below, generate a genome profile, and review the following. *Section 11.3*

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 (see fig 12.2 in the Annotation Guide)?
- ☑ c. Do the functions in the Notes match the official function list?
- ☑ d. Is the function field EMPTY for all features?
- ☑ 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 for all the features with no known function?
- ☑ c. Do the function names in the Notes match the official function list, when applicable?
- ☑ d. Is the function field EMPTY for all features?

9. Describe any issues or specific genes that you were unable to satisfactorily resolve, and warrant further inspection in the Quality Control review.

Barbarian was similar to a few annotated phage, but differed in several regions. The first few genes are different from closely related phage, but the evidence to support these gene calls seemed solid. We could have assigned head-to-tail connector proteins to genes 13 (start 8359) and 14 (start 8550) based on synteny, but did not do so because the HHPred data did not support this. Gene 97 (start 57315) was added because there was a large gap and we got a 1:1 alignment with an endonuclease VII gene. The region represents a difference from other related phage as they have a larger gene there that has been listed as a methyltransferase or a DNA methylase.