Genome Annotation Submission Cover Sheet

Pre-QC Phage Genome Annotation Checklist

Phage Name: Margo

Your Name: Daniel Westholm

Your Institution: The College of St. Scholastica

Your email: dwesthol@css.edu

Additional emails:
(For correspondence)

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

- [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? *Section 9.3.2*
- [x] 3. Have the genes been renumbered such that they go sequentially from 1 to the highest number? *Section 9.3.3*
- [x] 4. Have all old BLAST hits been cleared, and all gene features reBLASTed? *Section 9.3.4*
- [x] 5. Are the locus tags the phage name? *Section 9.3.3*
- [x] 6. Has the Documentation been recreated to match the information in the feature table? *Section 1.4*
- [x] 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:

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

This is the final and fully annotated genome of the Mycobacteriophage Margo from The College of St. Scholastica. We would like you to pay attention to the following genes due to the reasons outlined below. Deleted gene numbers reflect the original auto-annotated position:

• Gene 1 - This gene was deleted due to no blast matches, being called only by GeneMark, containing only 99 bp, and no coding potential shown.
• Gene 7 – This gene was deleted due to it being called only by Glimmer, along with it being a lone reverse gene among many forward genes.
• The second tRNA was trimmed from 78 bp to 74 bp
• Gene 23 – A frameshift was identified at this particular gene. We followed the SEA-Phages