Genome Annotation Submission Cover Sheet

Pre-QC Phage Genome Annotation Checklist

Phage Name: Penny1

Your Name: Kathleen Cornely

Your Institution: Providence College

Your email: kcornely@providence.edu

Additional emails:
(For correspondence)

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.

We feel confident in our annotation of Penny1, an A3 cluster phage, but wish to call the annotation team's attention to the following calls:

Gene 38: Note: A forward gene in the middle of a long stretch of reverse genes seems odd, but the required minimum 50 bp spacing on both sides does exist. SSC: Start 27200 Stop: 27631 (FWD). SCS: Agrees with Glimmer and does not agree with GeneMark. Original Glimmer call @bp 27200 has strength 4.06; GeneMark calls start at 27269. CP: ORF does include all coding potential shown on GeneMark output. SD: -3.899, best score. Gap: 409 bp gap. BLAST: gp35 of Wonder, gp36 of Jobu08, q1:s1 for both; gp37 of Tiffany and putative excisionase of Anubis, q1:s37 for both. LO: 432 bp; not the longest possible ORF. ST: