Genome Annotation Submission Cover Sheet

Pre-QC Phage Genome Annotation Checklist

Phage Name: Updawg

Your Name: Erin Doyle

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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.

Overall I am pretty confident about this annotation. We inserted feature 5 based on Genemark CP and synteny with other A2 phages. We deleted only 1 annotated feature between features 60 and 61. The deleted feature was a relatively short gene (123bp) located on the forward strand (the only forward strand gene in a sea of reverse strand genes).

Things that should be checked closely:
The function assigned to feature 64: the evidence was approximately 50/50 for either hydrolase or esterase

I'm unsure if feature 96 should be retained as a gene or deleted. There is no Genemark