Actinobacteriophage Genome Annotation Submission Cover Sheet

This Cover Sheet will accompany each genome's annotation file(s) submission and succinctly describe the work that your students and you have done. This document ensures that the work done was as complete and thorough as it could be. Most important to the QC reviewer, denote where the trouble spots were in your annotation and how they were resolved.

Phage Name. Destructrice
Your Name. Ann Powell
Your Institution. University of Evansville
Your email. ap96@evansville.edu
Additional emails. (for correspondence).

Describe any issues or specific genes that you would like to highlight for the QC reviewer. This includes any genes that you had questions about or received help with or that warrant further inspection in the QC review process. Include those genes that you deliberated on and/or want to strongly advocate for. If you contacted SMART, workshop facilitator, or a buddy school for help, please document.

The Destructrice genome was very similar to the comparator phage Olicious, Romero, and RetrieverFever. It includes a cassette of 21 tRNAs that matches with the tRNAs of Olicious.

Many of the genes found in most phage genomes were not located in our genome, these include: HNH endonuclease (rank2), Capsid maturation protease (rank 2), Scaffolding protein (rank 2), No minor capsid protein (rank 3), Head to tail adapter (rank3), Head to tail stopper (rank 3), Tail terminator (rank 3), Major tail protein (rank 1) (siphoviridae), Tail assembly chaperones (rank 3) (sipoviridae), Tape measure protein (rank 1) (siphoviridae), Tail fiber or tailspike (rank 3) (siphoviridae), Tail tube protein (rank 1) (podoviridae), and Lower collar protein(podoviridae). Based on phage morphology and cluster (BF), we believe the phage type for this phage may be podoviridae.

We deleted three draft genes: Destructrice_82 (tRNA), _53 and _63 (documented in notes)

We identified a split DNA primase, Destructrice_57, _58 (different reading frames with a large overlap) that was originally noted in Cluster A and BD phages, per Chris Schaeffer's response to our question in the Annotation Forum.

Regions of concern in Destructrice:

SEA_Destructrice_65: We called the Start 34412 which had no MAs, to minimize the gap, Glimmer and GeneMark called 34325.

SEA_Destructrice_67: Glimmer calls 35181 and Genemark calls 35268. We selected Glimmer start 35181to allow a >50 bp gap for a change in direction.

SEA_Destructrice_70: Glimmer predicted start 37042, but this start has no MAs. Gene is also only 114 bp (violation of gulding principles). 37096 (3 MAs) or 37084 (1 MA) may be better start candidates based on Starterator data.

SEA_Destructrice_83: Glimmer calls 43975 and Genemark calls 43993. No starts with MAs. May not be a gene.

We checked all gaps and the only gene added was SEA_Destructrice_58, the second half of the split DNA Primase (see above). These gaps were also present in the comparator phages Immanuel3 and/or RetrieverFever.

Aragorn and tRNAScan SE identified several TRNAs that we not in the autoannotation and we added these. They align with the tRNAs in the comparator phage Olicious.

Please record yes/no for each of the questions below. If further explanation is needed, please add this item to the above box.

In the submitted DNA Master file (Yes/No):

Yes 1. Does the genome sequence in your submitted DNA Master file match the nucleotide fasta file posted on phagesDB (same number of bases, no N bases, etc.)?
Yes 2. Are all the genes 'Valid" when you click the Validation button?
Yes 3. Are the genes (and matching LocusTag numbers) sequential, starting with #1, counting by 1s.
Yes 4. Are the Locus Tags the "SEA_PHAGE NAME" format?
Yes 5. Has the documentation been recreated from the Feature Table to match the latest file version?
Yes 6. Have tRNAs followed the tRNA protocol, **COPYING** tRNA-AMINOACID type (DNA equivalent of the anti-codon) from Aragorn output - tRNA-Gln(ctg) - AND the ends been adjusted to match the Aragorn output?
NA 7. Has the frameshift in the tail assembly chaperone been annotated correctly (if applicable)?
Yes 8. Have you cleared your Draft_Blast data and have you re-Blasted the submitted DNA Master file?
Yes 9. Has every gene been described and supported in your Supporting Data file?
Yes 10. Did you investigate 'gaps'?
Yes 11. Did you delete the genes that you meant to delete?

Now, make a profile of the file you plan to send. (And you can save this file for Review to Improve!)

Yes 1. Have any duplicate genes been deleted?
Yes 2. Has the Notes field been cleared (using the automated buttons)?
Yes 3. Do the gene numbers and locus tags match?
Yes 4. Are the correct Feature_Types correctly selected (most will be ORFs, but check that tRNAs and tmRNAs are correctly labeled)?
Yes 5. Do the function names in the Product field either match the official function list or say "Hypothetical Protein"?
Yes 6. Has the Function field been cleared (using the automated buttons)?

How are you documenting your gene calls in class? Choose any/all that apply:

- PECAAN output
- DNA Master shorthand (previously used format)
- X Spreadsheet
- Powerpoint
- X Word document (must be easily searchable)
- Other: Describe.

What is the file type (sort) submitted for QC to document your gene calls? Choose only one.:

- PECAAN output
- DNA Master shorthand (previously used format)
- X Spreadsheet
- Powerpoint
- Word document (must be easily searchable)
- Other: Describe.