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. Panchaali
Your Name. Francesca De Martini
Your Institution. Mesa Community College
Your email. Francesca.de.martini@mesacc.edu
Additional emails. (for correspondence). N/A

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.

This genome annotation was completed as part of a Course-Based Undergraduate Research Experience (CURE) at Mesa Community College with a class of 21 students. Each student was responsible for the initial annotation of approximately 20 genes using PECAAN.

As a capstone component of the course, each student selected one gene for in-depth investigation, including comparative analyses and phylogenetic approaches, to support or refine functional assignments. Due to time constraints and the structure of the course, this in-depth phylogenetic analysis was completed for a subset of 10 genes rather than the entire genome.

Genes highlighted in yellow in our internal tracking documents represent those for which we encountered the greatest difficulty in assigning functionality. These genes were extensively discussed and reviewed collaboratively, and final calls reflect consensus decisions based on available evidence.

All annotation work was conducted exclusively in PECAAN. DNA Master was not used locally due to hardware limitations common in a community college setting, where not all students had access to computers capable of reliably running DNA Master. A GenBank-formatted export from PECAAN has been provided for downstream processing and QC.

We are confident in the overall quality of the annotation and welcome additional QC review of the highlighted genes.

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): Annotation completed in PECAAN; GenBank-formatted export submitted for QC. DNA Master not used locally.

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.)? N/A – PECAAN-only workflow
2. Are all the genes 'Valid" when you click the Validation button? N/A – PECAAN-only workflow

3. Are the genes (and matching LocusTag numbers) sequential, starting with #1, counting by 1s. N/A – PECAAN-only workflow
4. Are the Locus Tags the "SEA_PHAGE NAME" format? N/A – PECAAN-only workflow
5. Has the documentation been recreated from the Feature Table to match the latest file version? N/A – PECAAN-only workflow
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? N/A – PECAAN-only workflow
7. Has the frameshift in the tail assembly chaperone been annotated correctly (if applicable)? N/A – PECAAN-only workflow
8. Have you cleared your Draft_Blast data and have you re-Blasted the submitted DNA Master file? N/A – PECAAN-only workflow
9. Has every gene been described and supported in your Supporting Data file? Yes– PECAAN-only workflow
10. Did you investigate 'gaps'? yes – PECAAN-only workflow
11. Did you delete the genes that you meant to delete? N/A – PECAAN-only workflow

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

1. Have any duplicate genes been deleted? yes
2. Has the Notes field been cleared (using the automated buttons)? N/A – PECAAN-only workflow
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)? N/A – PECAAN-only workflow

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

X PECAAN output
DNA Master shorthand (previously used format)
X Spreadsheet
Powerpoint
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.:

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