**Annotation: Review to Improve**

Annotating a phage genome well takes tremendous attention to detail combined with an understanding of some of the stranger nuances of phage biology. How do you tell how well you did?

Once your annotation has passed final QC by SM\*ART and been submitted to GenBank, you have one final task: Review to Improve. In order to improve your annotations for the future, compare your annotation to the one approved by SM\*ART . This can be easily accomplished using your initial DNA Master file and submitted DNA Master file, both available on the phage page of phagesdb.org.

Download these files and create Genome Profiles for each file (See the online Bioinformatics Guide).

1. Open these .csv files in Excel and copy the information from one file into the other, such that the annotations are adjacent to each other in the same spreadsheet. Now make a note of where:
2. Genes were added
3. Genes were removed
4. Gene starts were changed
5. Functions were added
6. Functions were removed
7. Do you understand why the change was made? Yes? Great! Can you identify annotation areas you need to focus on? Categorize the types of changes made to see which areas in your understanding are weaker than others. Did you miss a number of genes? Add unsupported functions? Remember to review the cluster specific annotation forums on seaphages.org for those biological nuances that influence annotations, including items such as gene functions and starts that have been confirmed at the bench.

If you are still perplexed, contact the Faculty member who reviewed your file and cc welkin@pitt.edu with specific questions if you do not understand why a change was made.

1. Tally up your changes. In general:

0-3 changes You are likely to be asked to join the Expedited Submitter list if you achieve this for multiple annotations across different clusters.

3-6 changes You are on your way.

6-10 changes This is the average number of changes for a 100 gene annotation for a SEA-PHAGES faculty member in their first two years in the program.

10 or more changes You may not understand some of the annotation concepts well. Keep searching and asking questions on the forums!