New Features to Implement

Last Updated: April 2, 2015

These are more features to implement while I am gone. Push everything to experimental. You are not expected to finish all things on the list while I'm away! You can work on these features in any order.

1. Metadata pop-up will display specific metadata fields only.

Irene and Walter mentioned that they want Curator Comments in the pop-up. You may want to verify if they want any other metadata fields to be displayed in the pop-up.

2. Adjust the first column in Allele Type Query results so that the pop-up doesn't cover any results.

3. Additional features for Disc Diffusion option.

Walter mentioned that clicking on the Disc Diffusion option should hide the MIC fields and set some option to S (Susceptible) or R (Resistant) instead. I don't have full specifications on this feature so you will need to gather more requirements for this feature. They mentioned that this feature was lower priority.

4. Put a header row on top of the CSV file obtained from downloading NG-STAR profiles.

This header file will include the name of the loci for each column. For example, when downloading profiles you will have a file that looks like this (the first column is the NGSTAR type):

st,gyrA,mtrR,parC,penA,ponA,porB
1,0,4,25,1,1,2
2,200,5,72,12,2,3
3,201,6,75,15,5,5

5. Implement feature to View Alleles.

In the Download Alleles page, there is a button to View Alleles. We want the user (everyone, not just the administrator or curator) to be able to view all alleles in a list/table (with columns such as sequence, sequence length, etc). Since there could be thousands of alleles you should use jQuery data tables.

6. Implement feature to View NG-STAR Profiles.

In the Download NG-STAR Profiles page, there is a button to View profiles. We want the user (everyone, not just the administrator or curator) to be able to view all profiles in a list/table. Since there could be thousands of alleles you should use jQuery data tables.

7. Add the full name of NGSTAR on the top panel.

8. Fix Allele Type Query to allow for new lines (\n).

9. Add an entry in the side bar below Download NG-STAR Profiles named Background.

You may want to gather additional requirements on what Irene and Walter want for the Background page.

10. Change the penA allele type to allow decimal places (not just an integer).

This feature is **high priority**. Also, this feature may also be one of the more difficult ones to implement.

You will need to make changes from the front to the back end including the validation as well. You may also need to change the data type in the database. You need to change the data type to a float or decimal for the allele_type column in tbl_Allele.

11. Add indication on batch add profiles example to include what loci each column is.

If you go to Curator Settings, Batch Add New NG-STAR Profiles, and click on "Click here for an example", include in the example what each column is supposed to be. Currently, the order is:

st,gyrA,mtrR,parC,penA,ponA,porB

Give an indication of what the ordering should be **outside** of the textarea.

12. Make error messages more descriptive for adding/editing alleles.

13. Make error messages more descriptive for batch adding alleles.

For 13 and 14, we want to make error messages more descriptive. For example, we may get a message such as "the sequence you have submitted already exists" but in our error message we should also mention which allele type this sequence corresponds to. For example, instead you may have a message that reads: "The sequence you have submitted already exists with allele type X".

14. Change the order of the loci names to this order:

1) penA
2) mtrR
3) porB
4) ponA
5) gyrA
6) parC

You might want to ask if they want this ordering in a specific page (such as in the Allele Type Query page) or if they want this ordering throughout the entire application.

15. Learn how to deploy to CentOS server.

I setup a production server that is accessible from ngstar.corefacility.ca. We are not in production yet, but it may be helpful to learn how to actually deploy to a CentOS server. When we get to production, we would just have to update the application running on the server.

Log into the production server:

ssh myldapusername@ngstar.corefacility.ca

Follow the instructions in Centos_Installation_Guide.md or pdf.
Replace all instances of ngstar-uat with just ngstar

If you have trouble accessing the server please contact Paul Williams.
If there are issues with the installation instuctions, take note of it and send it to me for fixing.

16. 23S Functionality

I would recommend that you leave this feature as the last one to do. 23S is apparently separate from the NGSTAR scheme, so the tables that you need to create in the database should be separate from the tables for NGSTAR.

They want a second form on the Allele Type Query page with 4 textareas and buttons for Submit and Clear.

This is about all the information I was able to record from the past meetings and it seems as though they don't have everything fully (or almost fully) defined yet, so you will need to gather additional requirements for this feature.