

## Welcome to web interface of the Wheat-CAP Database (SGGDM)

This tutorial describes the use of the SGGDM application.

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### **Introduction**

The purpose of the SGGDM database is to manage all the information associated with the submission and data retrieval of DNA or tissue samples for the Wheat-CAP project.

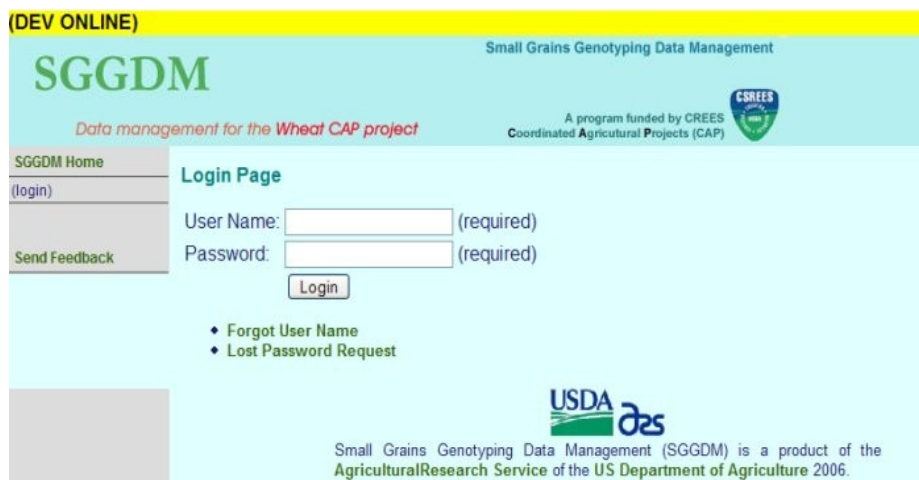
The database is a MySQL based relational database, housed in the server Olin Anderson has in Albany, CA.

### **Accessing the database through the web**

There are two ways to login into the database, both require a user name and a password.

You can either use the direct link to the web interface (<http://rye.pw.usda.gov/sggdm/index.shtml>) or click the link on the main page of the project website (<http://maswheat.ucdavis.edu>).

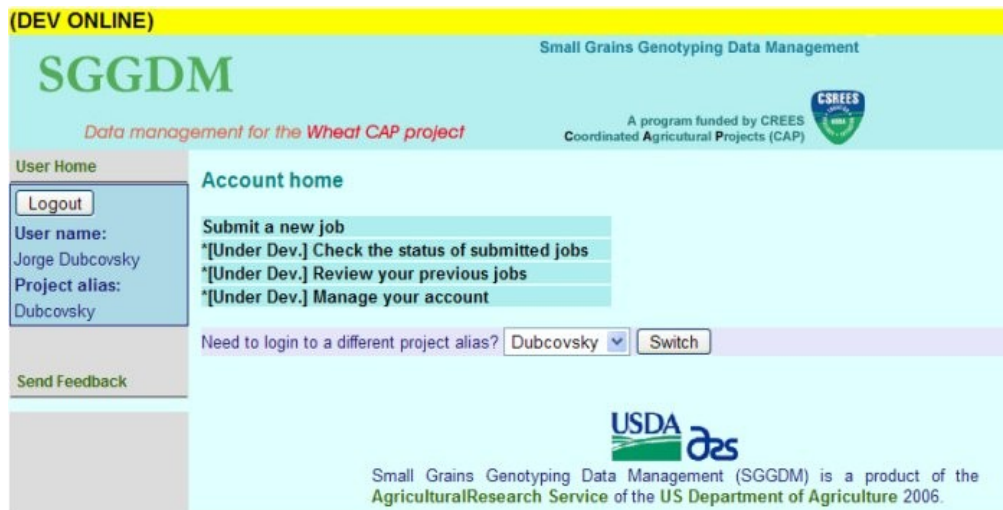
1. Login to the SGGDM database through the web interface of the database, (<http://rye.pw.usda.gov/sggdm/index.shtml>) or click the link on the main page of the project website (<http://maswheat.ucdavis.edu>). If you do not have access to the site, ask your PI to create an account for you.  
There are two links to help you in case you forget your user name or need to reset your password.



The screenshot shows the SGGDM (Small Grains Genotyping Data Management) login page. At the top, there is a yellow banner with the text "(DEV ONLINE)". Below this, the page title is "Small Grains Genotyping Data Management" and the logo "SGGDM" is prominently displayed. Underneath the logo, it says "Data management for the Wheat CAP project". To the right, there is a logo for CSREES (Coordinated Agricultural Projects) and text indicating the program is funded by CREES. On the left side, there is a navigation menu with links for "SGGDM Home", "(login)", and "Send Feedback". The main content area is titled "Login Page" and contains two input fields: "User Name:" and "Password:", both marked as "(required)". Below these fields is a "Login" button. At the bottom of the login area, there are two links: "Forgot User Name" and "Lost Password Request". The footer of the page features the USDA logo and text stating "Small Grains Genotyping Data Management (SGGDM) is a product of the Agricultural Research Service of the US Department of Agriculture 2006."

2. Once you login you will be directed to your account home. From there, you can submit new

jobs, check the status of those already submitted, and retrieve the results once the genotyping analysis is done.



### Submitting a genotyping job

Before you submit any plates or request any job through the database, you have to let know the person responsible for your GL when are you planning to send plates. GLs' supervisors need this information to plan their own activities. Contact your GC to learn how to sign-up in the calendar.

Prior to submitting any plates, you need to request a job through the SGGDM web site.

1. What information you need before you start:
  1. Are you submitting plates for MAS analysis or for map construction?
  2. How many plates are going to submit?
  3. How many markers are you requesting for every sample?

**Note:** Depending on the capabilities and procedures of your GL, you can ask more than one marker for every sample in the plate. If you do so, you have to request the same combination of markers for every well in the plate.

#### Example:

Correct	Wrong
B1: BARC8, BARC101, CFA2028	B1: BARC8, BARC101, CFA2028
...	...
D7: BARC8, BARC101, CFA2028	D7: BARC14, BARC62, BARC101
D8: BARC8, BARC101, CFA2028	BARC14, BARC62, BARC71
...	...
F12: BARC8, BARC101, CFA2028	BARC14, BARC62, BARC71
G12: BARC8, BARC101, CFA2028	BARC14, BARC62, CFA2028

2. To create a new job, click on “submit a new job” on the menu in your home account page.
3. Enter a name for the job and, optionally, comments. Click “Continue”

## Genotyping Job Request Steps

The following process will create a job as a collection of sample plates to submit to a genotyping lab. Note that selection of markers for traits will apply to the entire request. To request another set of markers you must submit another request. The steps for the process are outlined below.

1. **Job Label**
2. Select general plate details
3. Select marker and trait details
4. Generate template for desired number of sample plates
5. Upload sample names
6. Submit Request

### STEP 1: Create a Job Label

Job Label:  (required)

Comments:

**Creating a job label.** The name of the job is a required field, while comments are optional. The next screens have a similar structure. On the upper part you will see highlighted the step you are currently working. On the lower part you have to enter data, select choices or upload files.

4. Specify the details of the plate (a job request can have more than one plate). First, you enter an optional description of the plate, then you select the species, the type of project you are participating (CAP) and the material you will submit (DNA, leaves or seeds). Finally, you have to indicate whether this is a MAS or mapping plate. Your choice for the last point will determine your next screen.

## Genotyping Job Request Steps

The following process will create a job as a collection of sample plates to submit to a genotyping lab. Note that selection of markers for traits will apply to the entire request. To request another set of markers you must submit another request. The steps for the process are outlined below.

1. [\(back to edit\)](#) [DONE] Job Label
2. **Select general plate details**
3. Select marker and trait details
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5. Upload sample names
6. Submit Request

### STEP 2: General plate details

Plate Description

Sample Plant Name

Common Wheat (*Triticum aestivum*)

Project Type

CAP

Sample Material Type

DNA (D)

Job Type

Marker Assisted Selection (MAS)

5. If you selected MAS, at the next screen you will need to indicate what you marker you want to analyze and for what gene. First, you select the category, then the trait. Now, you can choose

one or more among the combinations of genes and markers.

If your option was “mapping”, now you have to choose the SSRs that you want to have analyzed for your plate.

### Example: Submitting a MAS request.

1. First choose the category for your trait, and then the trait.
2. At the next step you can select the marker and gene combination.

Select	Gene/Allele	Marker
(add)	Lr39	GDM35
(add)	Lr47	Lr47-STS

3. You choose markers by clicking on “add”. Depending on your GL you can request more than one marker per well. Your selected markers will appear on the blue box. Click on “remove” if you made a mistake at selecting the marker. Click “Continue”.
4. Indicate how many plates you want to send for analysis with this choice of markers. Click “Continue”.
5. The application will let you download the Excel file you need for submitting your request. You only need to add the samples names, remember to include parental lines for control. Do not indicate any sample for well H12, since it is for internal use at the GL.
6. Once you added the names of your samples, you can upload the file.
7. If there are mistakes on your plates, the application will reply with a message to help you make corrections. Otherwise, you will receive a confirmation e-mail.

### Checking submitted requests

At anytime you can go back to your account home page and click on “View submitted jobs”. Once they were processed, you will see a message offering you to download the file(s) with the results. You can download again your older files by clicking on “Review your previous jobs”.

Job Name	Comments	Status
New Job		Pending
Test3BS	Just testing comments field	Pending
A Job	Job sent by testing.	Pending
Wheat Test		Pending
Test Download	This is a sample genotyping data job.	Results Posted
New Job	This is a new job with some comments.	Active

**The Job Status Panel.** This breeder has requested four jobs, but the GL has not confirmed yet if they were accepted, and their status is “Pending”. The results of another job, named “Test Dowload”, are ready to download.

Finally, “New Job” is a submission currently under processing in the GL.

For different reasons a GL can reject a request or put it on hold. In any case, you will receive an e-mail or a phone call from the person in charge of processing your plates at the GL.

### Genotyping labs interface

Users registered as working in a GL have especial accounts. They can see on their interfaces all the jobs requested to their labs, and can reject or accept them for processing. They cannot submit genotyping request, as a breeder can do.

Note: If the person responsible for the GL decides to reject a job submitted by a breeder, he or she have to contact the breeder by e-mail or phone to explain why the job is not acceptable, and suggest ways to correct that situation.

The screenshot displays the 'Account home' page with two buttons: 'Submit Allele Results for a Job' and 'Manage your account'. Below this is the 'Genotyping Requests' section, which contains three tables: 'Pending Requests', 'Active Requests', and 'Complete Requests'. Each table has columns for 'Breeder', 'Job', and 'Comments'. The 'Pending Requests' table lists four entries with '(view)' links. The 'Active Requests' table lists one entry. The 'Complete Requests' table lists one entry. At the bottom, the 'General database access' section contains two buttons: 'Browse parental screening results' and 'Parental screening batch downloads'.

Pending Requests			
	Breeder	Job	Comments
(view)	TestLastName	: New Job	
(view)	Anderson	: gg	
(view)	TestLastName	: Test3BS	Just testing comments field
(view)	TestLastName	: tsetase	

Active Requests			
	Breeder	Job	Comments
(view)	TestLastName	: New Job	This is a new job with some comments.

Complete Requests			
	Breeder	Job	Comments
(view)	TestLastName	: Test Download	This is a sample genotyping data job

**Genotyping lab interface.** In this example the GL has received four new jobs, they are listed as “Pending Requests”. You can see the details of these jobs and decide if it is acceptable or not by clicking on “view”. Jobs listed as “Active Requests” are submissions that were accepted and are being processed at the GL. When a genotyping job is finished, and the results are ready to release, it will be listed under “Complete Requests”

## Manage your personal data

You can change your personal data and password clicking the “manage your account” link on the menu in the account home page.

**Edit User Account Details**

User Name:   Required

First Name:   Required

Last Name:   Required

Email Address:   Required

Phone:   Optional

**Edit Password**

Old Password  Required

New Password  Required

Confirm New Password  Required

## Add new users

If you are a PI, or you were granted PI privileges, you can create new users for the personnel working in your lab. This users will be able to request jobs and download analysis.

To create a new user, go to the account home page, an click the link labeled “Manage and Add Account Users”.

On the top of the screen there is a table listing all the current users registered for your lab. Below, there is a form to enter the data of the new user. You can ask the new user to enter a new password there, or you can assign one and ask the user to login and change it.

On the drop down box “Access” you define what the new user will be able to do. “Normal Access (Write Ability)” allows the user to submit requests and download data. A “Read only” user can only download the analysis sent by the GL. Finally, a user with “Local Admin” privileges can send requests, download data and create new users. This last option applies mainly for lab managers.

## Using the test database

There is a test site that you can use for exploring the site without risking sending any data to your genotyping lab, or altering the information in the database. This is useful for training people new to the system in your lab. Also, if we need to add new features to the application, or make any many major modification, we will use this site for previewing.

The url of the test site is:

<http://rye.pw.usda.gov/sggdmdev/index.shtml>

You can access the test database with a user name that was previously assigned to every PI and the password “testing”.

Note: it is also possible to access a general account with user: TestUser and password “testing”

If you do not have a user name and password assigned, contact your PI. They can create new accounts for people working in their labs.