BMS V18 Tutorial on Breeding Workflows using rice examples

Contents

Getting started 3

Searching for Germplasm 4

Objectives 4

Searching for germplasm by name 4

Search for germplasm records with names starting with a particular string of characters 6

Search for germplasm records with names containing a particular string of characters 6

To search for a germplasm by Germplasm Identifier (GID) 7

Other filters available in the Germplasm Search App 7

Identify and locate different types of information about a germplasm 8

Importing germplasm and managing lists 13

Objectives 13

Importing a list of germplasm from a template file 13

Exercise – Importing New Germplasm 20

Viewing Lists 22

Adding Inventory for Imported Germplasm 22

Manipulating Germplasm Lists in the List Manager 24

Using Crop Lists to share germplasm between programs 25

Adding Entries from an existing list to another list 27

Adding Entries from the Germplasm Search to a list 28

Exercise on Germplasm Manager 28

Making a Crossing Block 30

Objectives 30

Create a Crossing Block in the Study Manager 30

Use the Crossing Design Tool for Specifying Crosses 35

Using the Crossing Template to make crosses 39

Table 1: BMS Breeding Methods for Self Fertilizing Crops 44

Adding Seed Inventory for a Harvest List 48

Objectives 48

Create pending seed deposits for a harvest list 48

Make labels for the seed packets from a harvest list 50

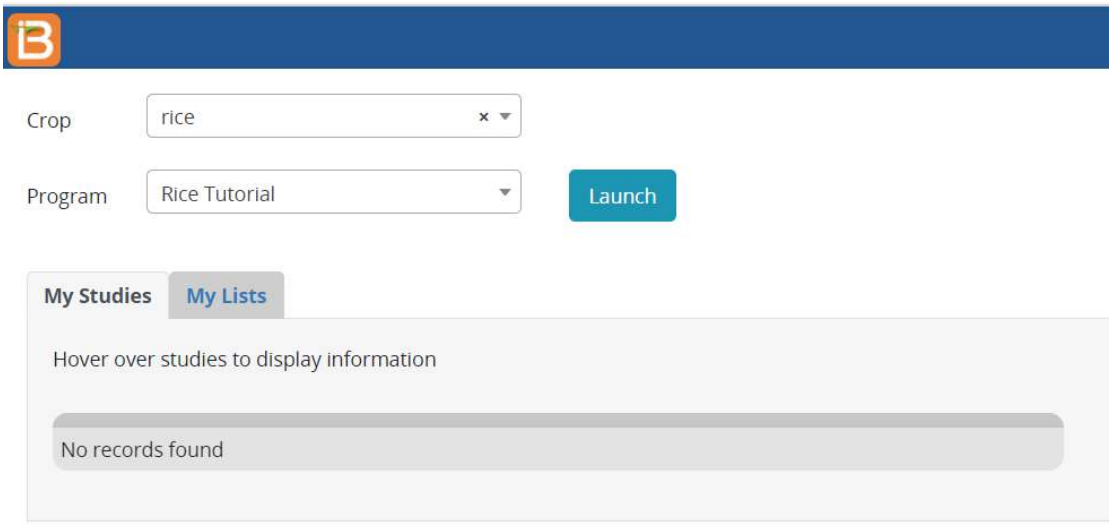
Update pending transactions with weights and package and label seeds 51
Managing Pedigree Nurseries 53
Objectives 53
Create an F1 Nursery 53
Advance the F1 Nursery by bulk selection of all families 54
Create F2 nursery and load some data from a fieldbook 56
Advance some F2 families by single plant selection 58
Save seed inventory for the F3 harvest list 60
Make an F3 Nursery with checks and Prepare seed for planting 61
Managing Evaluation Trials 66
Objectives 66
Create a mulit-location trial 66
Prepare seed and planting labels 71
Set up sub sample units to collect sampling data from plots 74
Export the fieldbook, collect and load plot level data 76
Export a Studybook for the sub sample data and load the values 79
Calculate derived variables 82
Importing existing trial designs and data 85
Objectives 85
Creating a germplasm list for an existing trial 85
Extracting a lay-out file for an existing trial 89
Create the Study for the trial 90
Import the lay-out file 92
Statistical Analysis 95
Objectives 95
Install and License Breeding View 95
Specify single site analysis for a trial in BMS 96
Running Breeding View for Single Site Analysis 99
Saving the means from Single Site Analysis to BMS 102
Specify a multi-site analysis for a trial in BMS 104
Run a multi-site analysis with Breeding View 106

Getting started

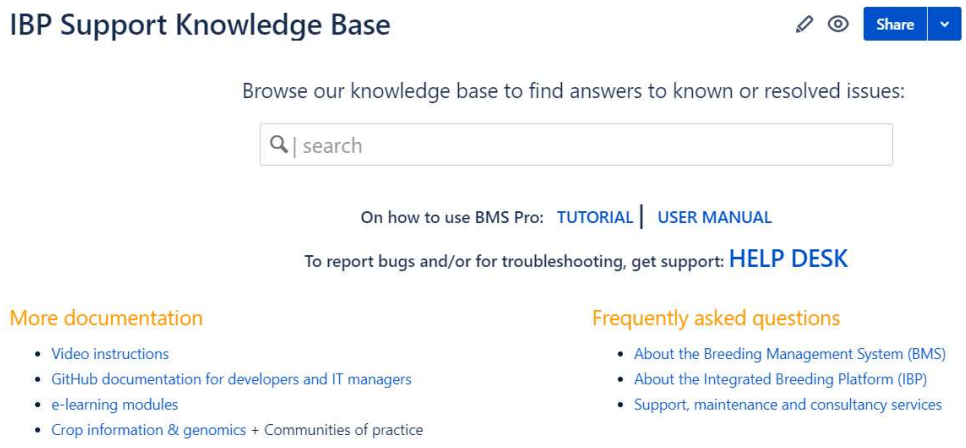
This series of tutorial lessons are designed to show the user the workflows and functionality of the BMS required to follow a pedigree breeding program in an inbreeding crop such as rice.

Assuming you have been given a user account on a server which contains a Rice Tutorial Program and that you have access to that program and that you have set your password and are able to log on to the server then you are ready to start. If any of these conditions are not set there is information in the manual under getting started.

When you log into the system you will arrive at the following workbench screen:



There is a (?) symbol at the top right of the workbench screen which will open the IBP Support Knowledge Base where there are links to the Tutorial Documentation, the User Manuel and many other documents and help tools.



On the Workbench screen, select the crop rice for this tutorial and the program Rice Tutorial. Two tabs appear which would give you quick access to your recent studies (nurseries and trials) and germplasm lists. Since you are starting out you do not have any of these at this stage. Click Launch to open the program in the Germplasm Manager.

Searching for Germplasm

Each BMS crop database preserves a master-list of germplasm in the system which may have multiple names and attributes. There is a powerful search application which allows the user to search this master list in a variety of useful ways.

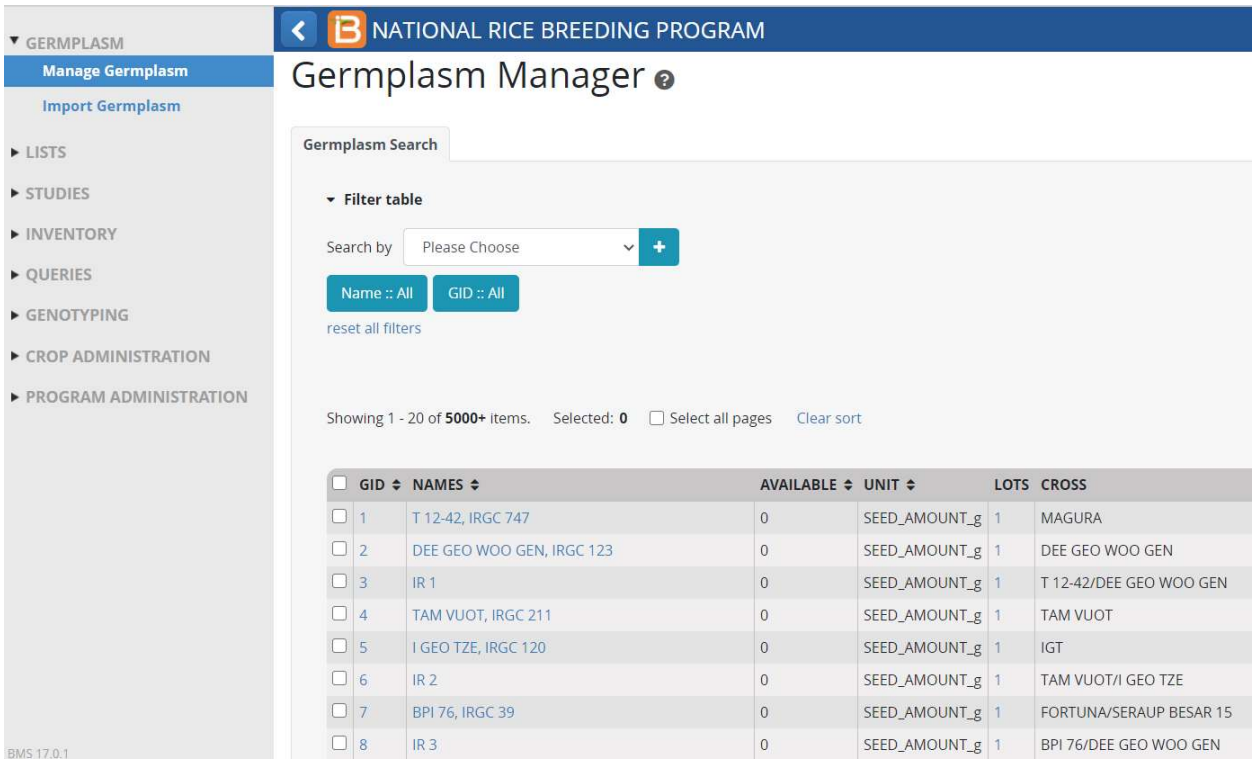
Objectives

At the end of this chapter, the user will be able to:

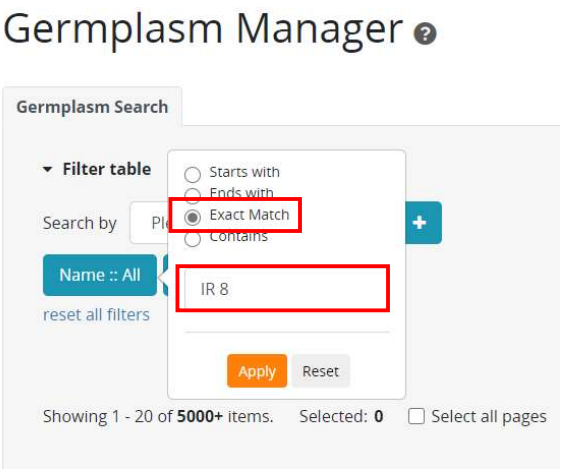
1. Search a particular germplasm by name from the database
2. Search for germplasm records with names containing a particular string of characters
3. Search by Germplasm Identifier (GID) from the database
4. Identify and locate different types of information about a germplasm.

Searching for germplasm by name

Under the **Germplasm** menu, click on **Manage Germplasm**. The Manage Germplasm interface will appear as in the image below:



To search for a **particular** germplasm by name, click on the Name: filter button and enter the search string IR 8 in the text box. Make sure that the "**Exact Match"** radio button is selected. Click on "Apply**".**



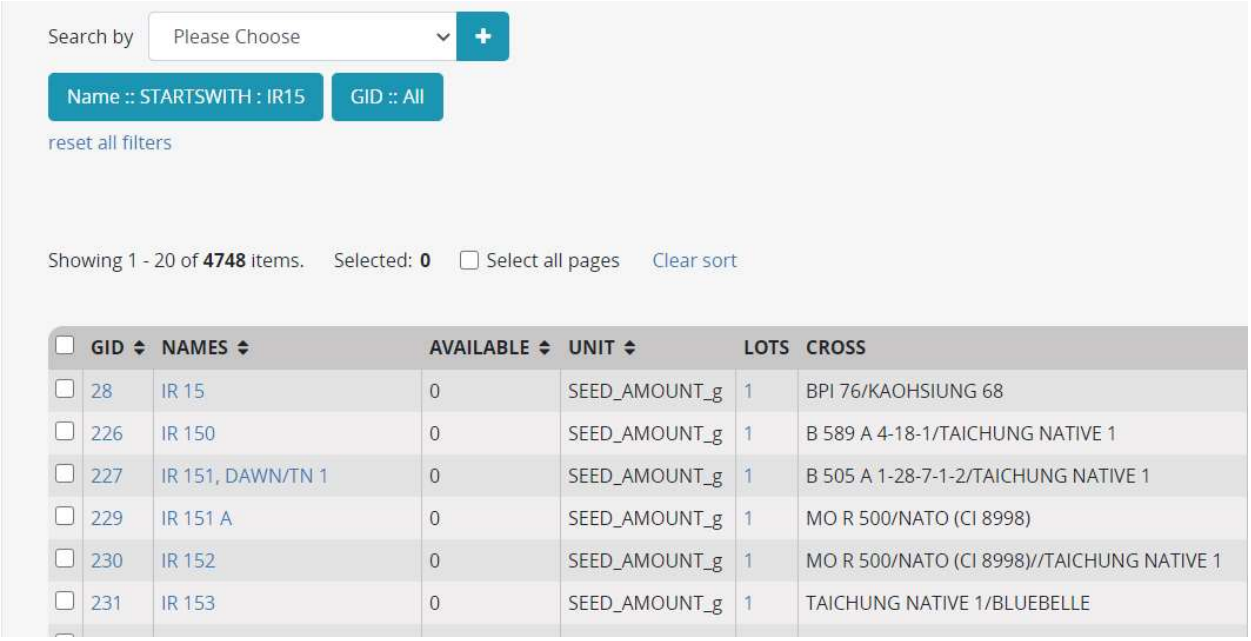
Note that 84 germplasm with name “IR8” or “IR 8”were found and displayed in the result filter box. Most of them have alternative names as well. Searches are not case sensitive.

Showing 1 - 20 of **84** items. Selected: **0** Select all pages Clear sort

GID	NAMES	AVAILABLE	UNIT	LOTS
17	IR 8-CROSS, PETA/DGWG, IR 8	0	SEED_AMOUNT_g	1
715	IR 8, DW 301, IRTP 195, IR 8-288-3	0	SEED_AMOUNT_g	1
351573	IR 8 (ACC 10320), IRTP 16891, IRGC 10320, IR 8	0	SEED_AMOUNT_g	1
366176	IR 8, IRGC 66935, YS 528	0	SEED_AMOUNT_g	1
378514	IR 8	0	SEED_AMOUNT_g	1
432791	IR 8	0	SEED_AMOUNT_g	1
432831	IR 8, JID 3169	0	SEED_AMOUNT_g	1
433736	IR 8	0	SEED_AMOUNT_g	1
433805	IR 8, IET 557	0	SEED_AMOUNT_g	1

Search for germplasm records with names starting with a particular string of characters

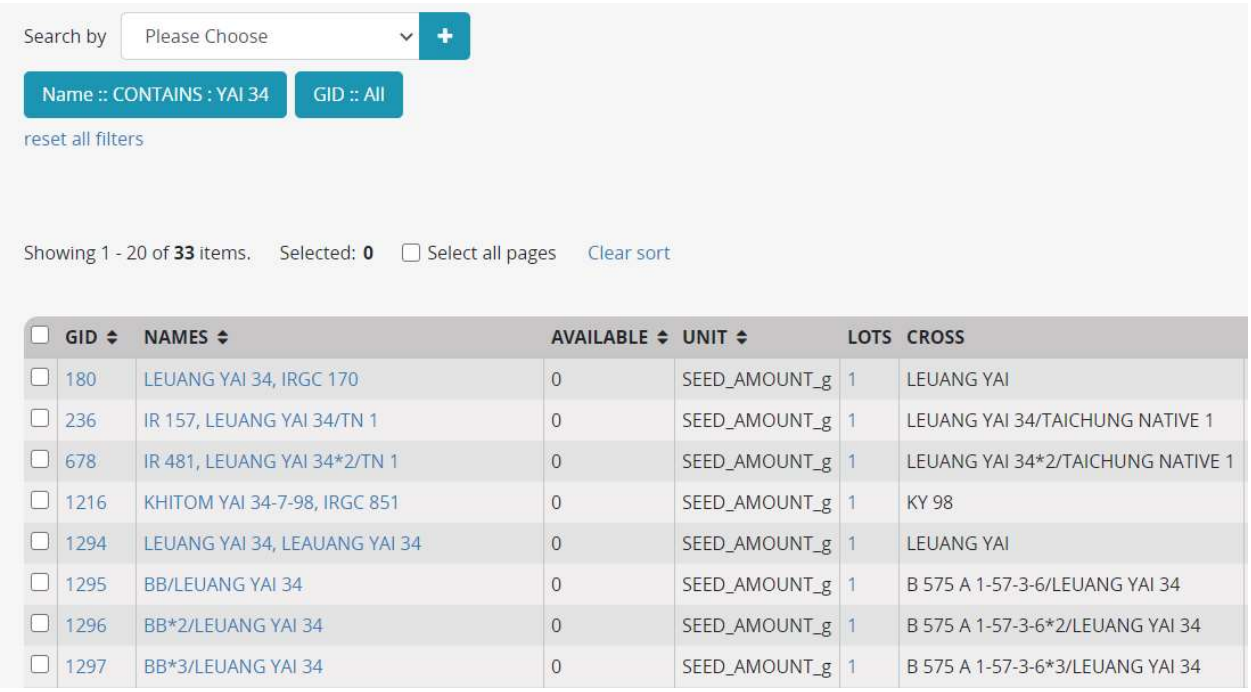
You can search for a germplasm starting with a string of characters by checking the **Starts with** radio button in the Name filter. Enter "IR15" in the text box and click apply. All germplasm with names that start with IR15 or IR 15 will be shown in the filter box.



GID	NAMES	AVAILABLE	UNIT	LOTS	CROSS
28	IR 15	0	SEED_AMOUNT_g	1	BPI 76/KAOHSIUNG 68
226	IR 150	0	SEED_AMOUNT_g	1	B 589 A 4-18-1/TAICHUNG NATIVE 1
227	IR 151, DAWN/TN 1	0	SEED_AMOUNT_g	1	B 505 A 1-28-7-1-2/TAICHUNG NATIVE 1
229	IR 151 A	0	SEED_AMOUNT_g	1	MO R 500/NATO (CI 8998)
230	IR 152	0	SEED_AMOUNT_g	1	MO R 500/NATO (CI 8998)//TAICHUNG NATIVE 1
231	IR 153	0	SEED_AMOUNT_g	1	TAICHUNG NATIVE 1/BLUEBELLE

Search for germplasm records with names containing a particular string of characters

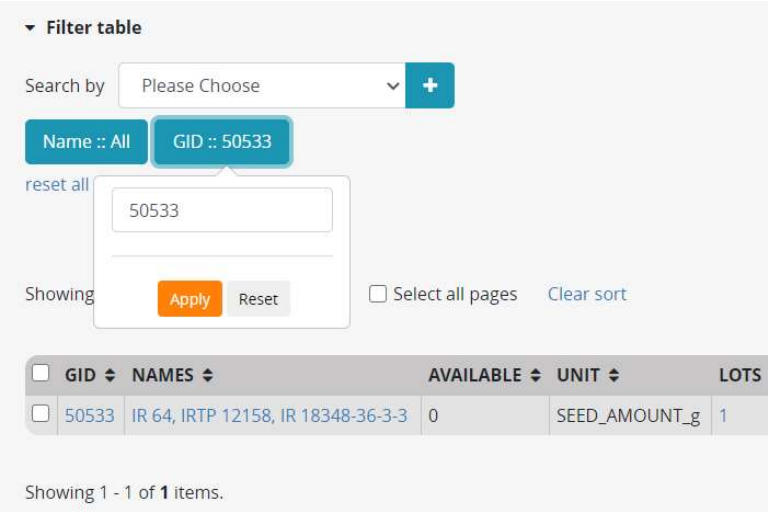
You can search for a germplasm containing a string of characters by checking the **Contains** radio button. Enter "YAI 34" in the text box, check Contains and Clikc Apply. All germplasm with names that contain YAI 34 will be shown in the filter box. This takes a long time for obvious reasons since there are over 4.7 million names in the database, so use this option sparingly.



GID	NAMES	AVAILABLE	UNIT	LOTS	CROSS
180	LEUANG YAI 34, IRGC 170	0	SEED_AMOUNT_g	1	LEUANG YAI
236	IR 157, LEUANG YAI 34/TN 1	0	SEED_AMOUNT_g	1	LEUANG YAI 34/TAICHUNG NATIVE 1
678	IR 481, LEUANG YAI 34*2/TN 1	0	SEED_AMOUNT_g	1	LEUANG YAI 34*2/TAICHUNG NATIVE 1
1216	KHITOM YAI 34-7-98, IRGC 851	0	SEED_AMOUNT_g	1	KY 98
1294	LEUANG YAI 34, LEAUANG YAI 34	0	SEED_AMOUNT_g	1	LEUANG YAI
1295	BB/LEUANG YAI 34	0	SEED_AMOUNT_g	1	B 575 A 1-57-3-6/LEUANG YAI 34
1296	BB*2/LEUANG YAI 34	0	SEED_AMOUNT_g	1	B 575 A 1-57-3-6*2/LEUANG YAI 34
1297	BB*3/LEUANG YAI 34	0	SEED_AMOUNT_g	1	B 575 A 1-57-3-6*3/LEUANG YAI 34

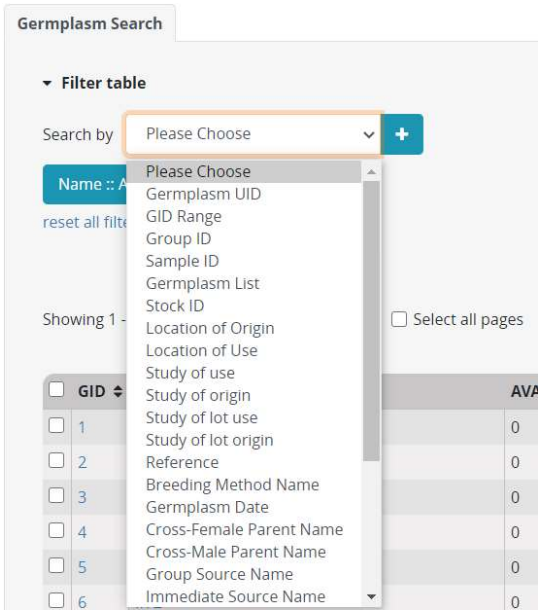
To search for a germplasm by Germplasm Identifier (GID)

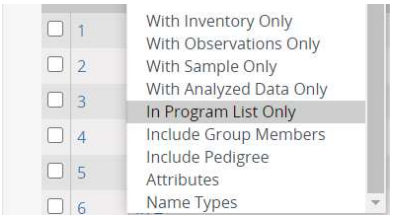
First clear the name Filter by opening the Name Filter button and clicking **Reset**, then click on the **GID** filter button and enter the value 50533 and click **Apply**.



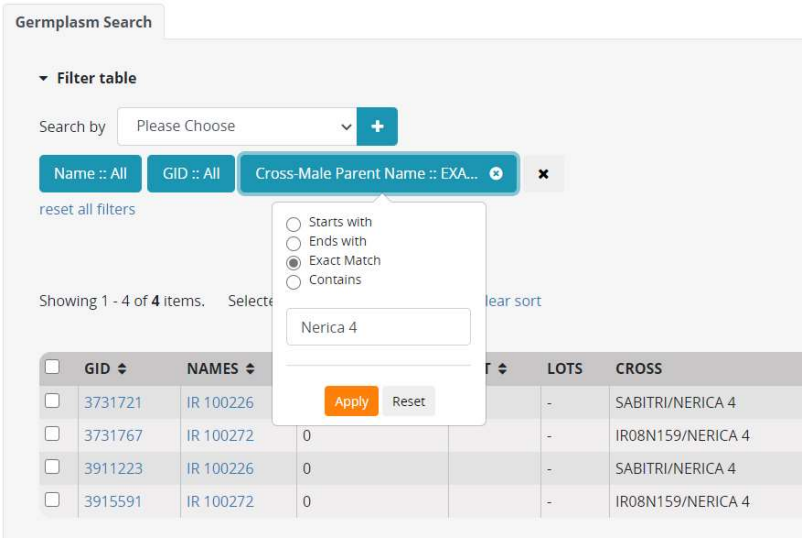
Other filters available in the Germplasm Search App

There are many other filters available in the Germplasm Search App. These are selected from the Search By drop down box:



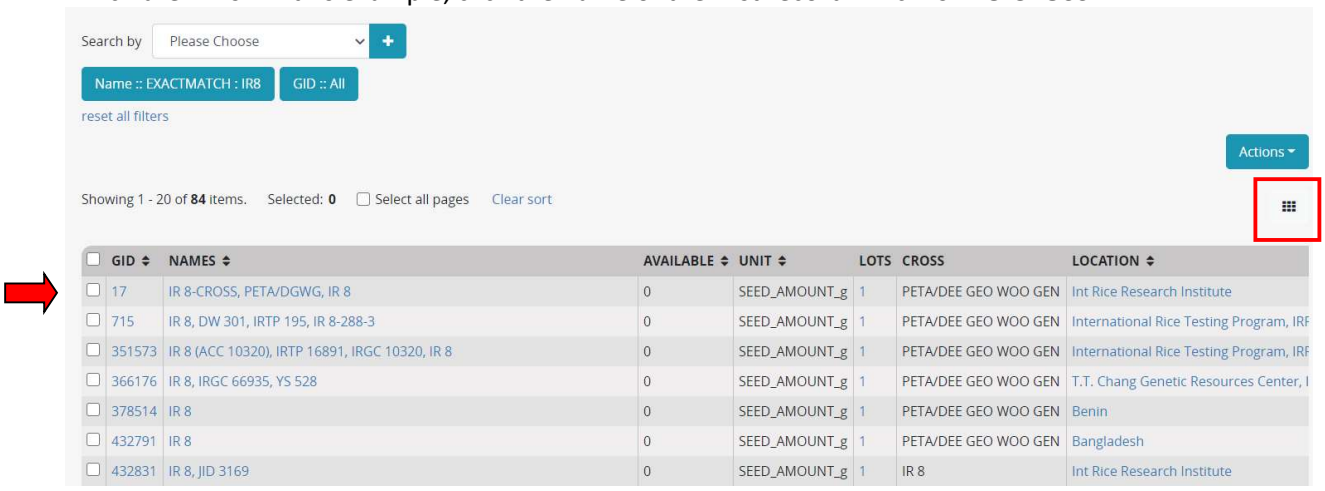


For example if I want to find crosses which have been made with the line Nerica 4 as male parent, I select the filter **Cross-Male Parent Name**, click the + button to the right of the selection box to activate the filter, and enter the name in the text box then click apply. There are four crosses in the database with Nerica 4 as male parent:

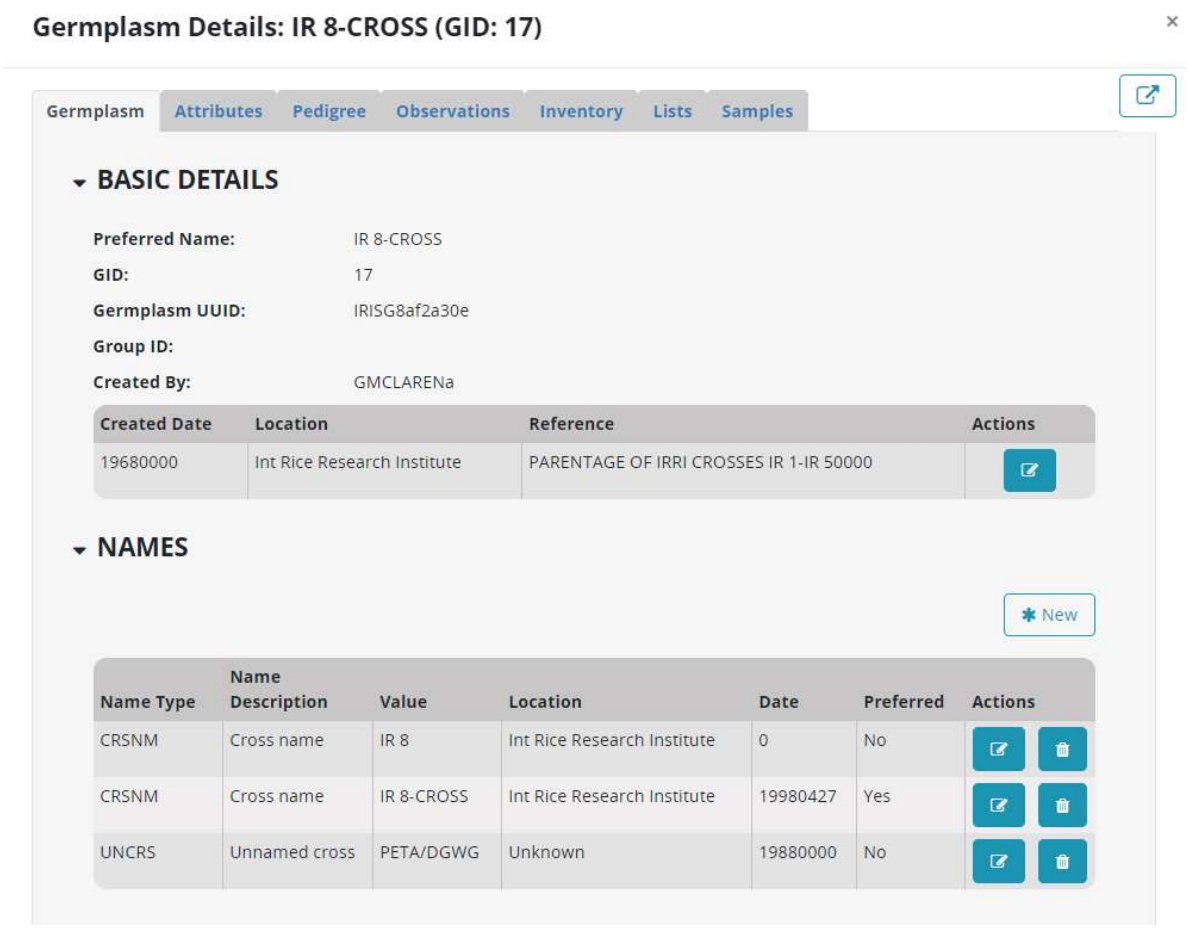


Identify and locate different types of information about a germplasm

Going back to our previous search by name for IR8, some details like cross, location and inventory are shown in the filter table. You can control what columns are shown by clicking the dot icon on the top right of the table (see red box). You can see more details for a particular line by clicking on its name or GID which are links. In this example, click the name of the first record which **is IR 8-CROSS.**



The basic details about the germplasm with name : **IR 8-CROSS** with **GID 17** will be displayed. You will also see the date the germplasm was created, the place where it was developed and a full list of names which have been assigned to the germplasm.



Questions:

a. When was **IR 8-CROSS** developed? _____

b. Where was it developed? _____

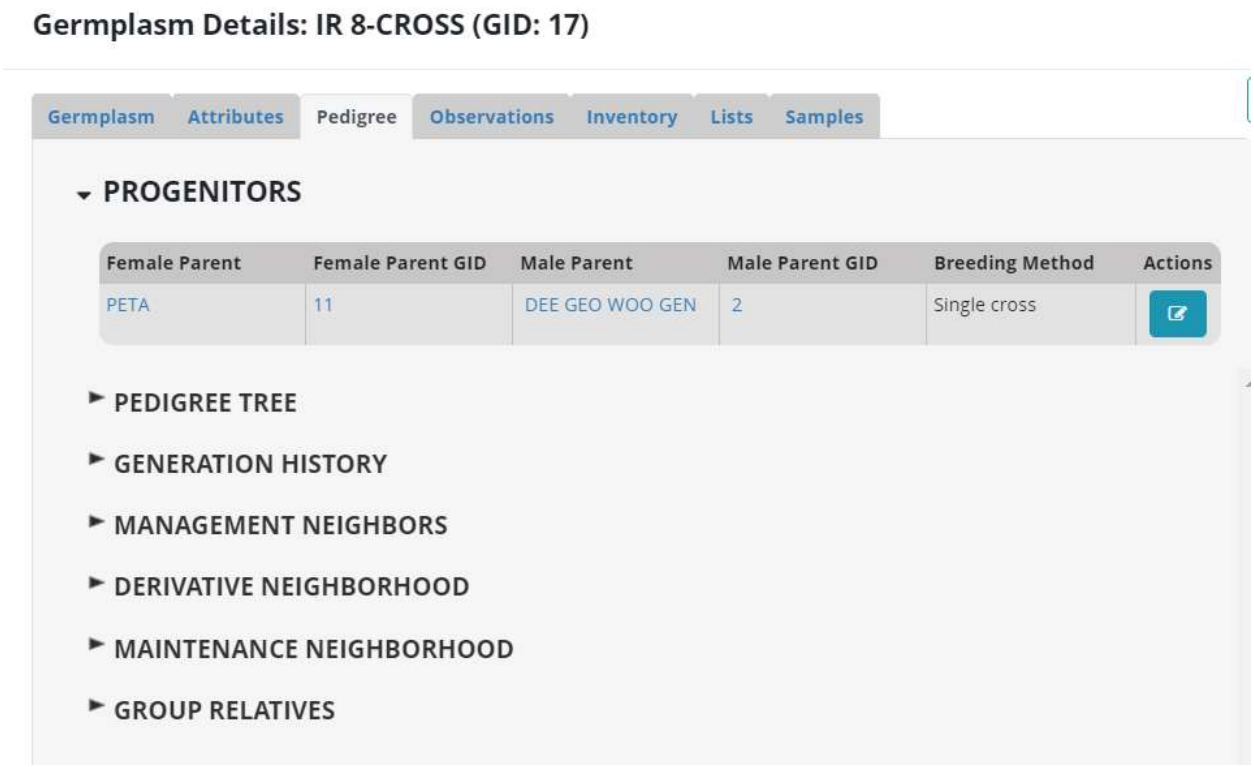
c. What other names does this germplasm have?

If your role has the correct privelages you will see edit and delete buttons next to some of the information you can edit. Those can be explored in a separate tutorial.

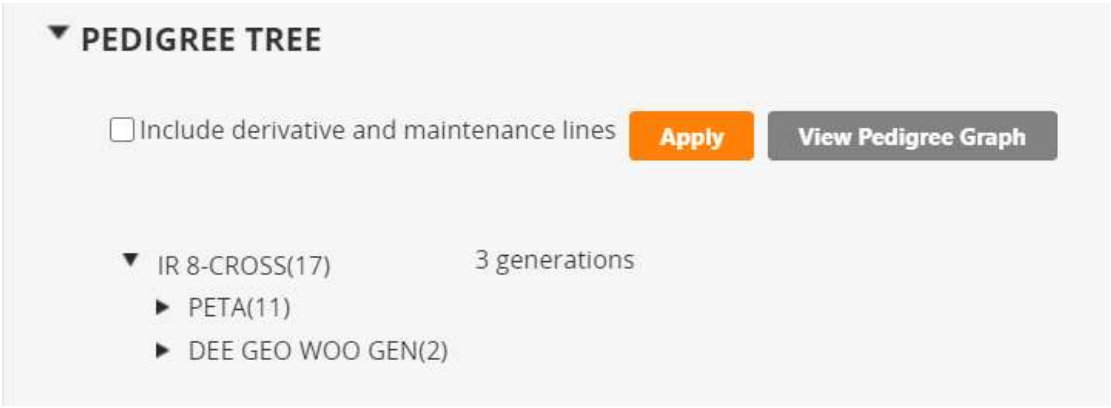
More information is available on other tabs of the Germplasm Details form:

Clicking on the **Attributes** tab will display the germplasm attributes, if any. This germplasm has none.

Click on **Pedigree tab** to display information about the pedigree of the germplasm. In this case IR 8-CROSS was an F1 from a single cross between PETA and DEE GEO WOO GEN so it has no selection history.

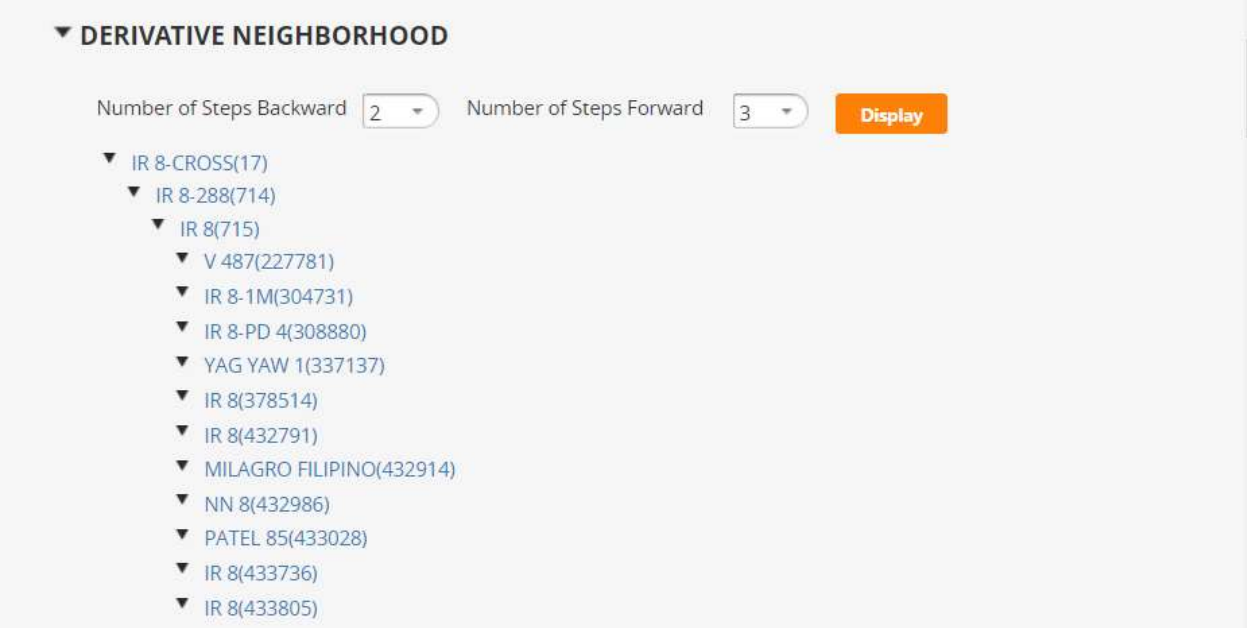


You can click on **Pedigree Tree** and the > symbols to expand the cross history as many generations as you like.

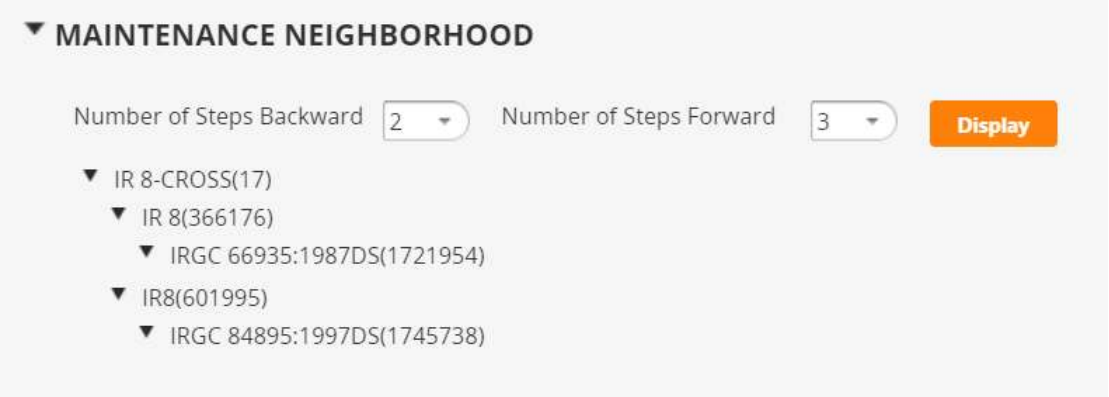


Note: Click on the **View Pedigree Graph** to display a graphical layout of the pedigree.
Generation History shows you all the selection steps leading from the cross to the current germplasm (if they are known). In our case there are no selection steps since IR8-CROSS is an F1
The Derivative Neighborhood will show germplasm which is related to the current germplasm by a specified number of derivative generations (like selections and bulks) or maintenance generations (like seed increase or shipment).

In this example, many lines have been derived from IR 8-CROSS as it is a very good cross developed in IRRI.

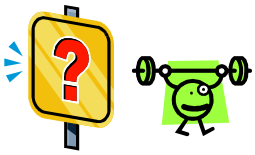


Click on **Maintenance Neighborhood** to get a list of germplasms that were related by maintenance method like Seed Increase.



Group Relatives will show you all the lines from the same cross as the current line.

Other tabs are **Observations, Inventory, Lists and Samples**. They show you the trait data for the current germplasm, the inventory available for the current germplasm, the set of germplasm lists in which the current germplasm appears and the set of sample lists in which the current germplasm appears.



Questions:

1. Search for information on IR 64.

    a. When was IR 64 developed at IRRI?
    b. What was the Derivative Name given by IRRI?
    c. Is PETA or DEE GEO WOO GEN part of its pedigree?

2. Search for information on Nerica 8.

    a. What line did it come from?
    b. What cross did it come from?
    c. What are the female and male parents of its cross?

Lines coming from West Africa have a prefix "WAT" or "WAB". Search for promising lines from Africa by typing WAB 326-B-B-7-H1 in the Name textbox, selecting **Matches starting with** and clicking the **Search** button.

a. Click on different entries to select them. In what country was it developed?

    _____

b. When was it developed? _____

c. Does this line belong to any lists? If yes, what is the name of the list? (Hint: Go to **Lists** tab) What about the entry in the hit list with alternative name IRTP20857?

    _____

Search for a variety name **BASMATI 370**. (If you get too many hits try checking the Exact Matches radio button.)

a. Select the record with Germplasm ID (GID) 1859. What is the preferred name? What are the other names for it?

    _____

b. Does it have any germplasm attributes?

    _____

c. What is the method of development for this record or how is it developed?

    _____

d. Does it occur in any lists?

Importing germplasm and managing lists

One of the key advantages of using the BMS is that it facilitates the unique identification of germplasm and pedigree tracking. To start using the BMS, however, lists of current germplasm from your breeding program should be entered into the database. These lists are ideally imported with complete pedigrees. However, for this exercise, we will consider the simple import of existing lists without pedigrees.

Once germplasm are imported into the database it is often necessary to make lists of germplasm for different purposes such as planting, shipment and testing. These germplasm lists are created by selecting entries from previous lists and adding the imported lines. Other new lists are made from harvest actions from nurseries and trials.

Objectives

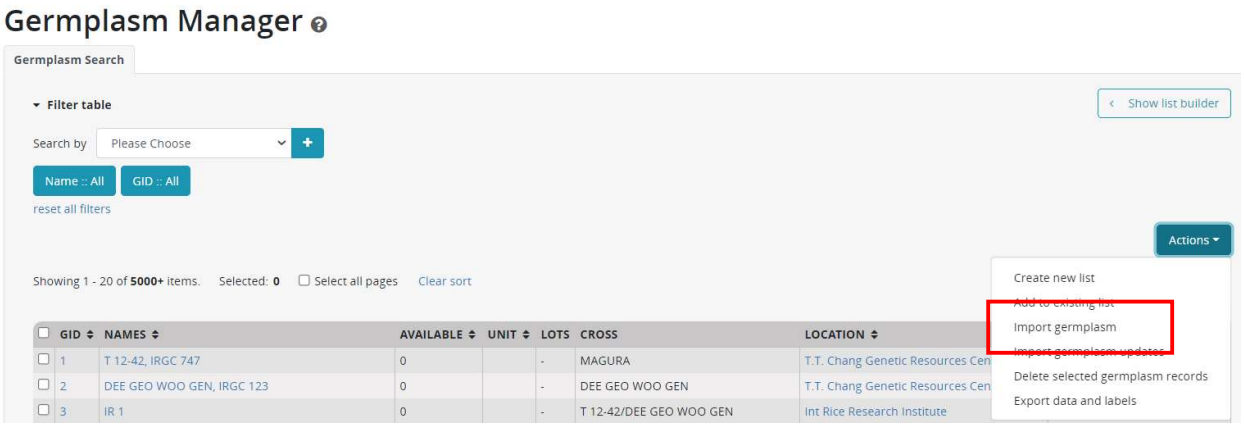
At the end of this chapter, the user should be able to:

1. Complete a template with germplasm names to be imported.
2. Import germplasm into the database from a template (without pedigrees).
3. Add inventory for imported germplasm
4. Select lines from an existing list and add them to a new list of germplasm.

Importing a list of germplasm from a template file.

Creating a basic germplasm list in Excel

Lists of germplasm can be entered into the system using an excel file. This file must follow a specific format so a template has been provided. Users with appropriate permission will see the action **Import Germplasm** on the ACTIONS menu of the **Germplasm Manager** main menu. If you click on this item you will see that you can download a template.



The template has two sheets, an observation sheet where the germplasm details are supplied and a Codes sheet where some metadata codes are available.

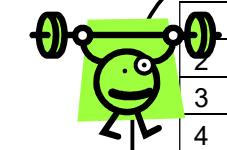
Use Excel to modify the germplasm import template and create a file with the following format and minimum content.

The Observation sheet has a number of proposed columns covering all the characteristics of a germplasm record, but the minimum data required is just a consecutive entry number and a germplasm name. There are still more columns beyond column I which we will ignore for now.

A minimum entry would look as follows:

	A	B	C	D	E	F	G	H	I
1	ENTRY_NO	LNAME	DRVNM	PREFERRED NAME	ENTRY_CODE	LOCATION ABBR	REFERENCE	CREATION DATE	BREEDING METHOD
2	1	IR 72768-12-1-1							
3	2	IR 72768-28-1-1							
4	3	IR 75502-24-1-1-B							
5	4	IR 75516-30-1-1-B							
6	5	IR 75516-56-1-1-B							
7	6	IR 75518-84-1-1-B							
8	7	IR 75531-31-1-2-B							
9	8	IR 76561-AC 8-B							
10	9	CNA 4196							
11	10	IDSA 113							
12	11	FARO 41							
13	12	UPL RI 5							
14	13	WAB 326-B-B-7-H1							
15	14	WAB 534-B-3A 1-1							
16	15	YUNLX NO 28							
17	16	IRRI 132							

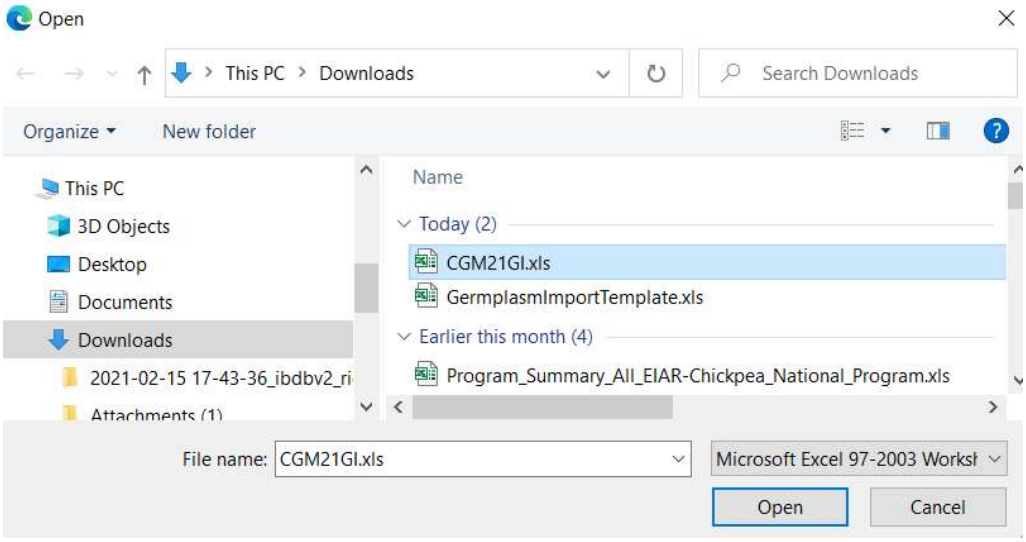
Fill a the first two columns of a template file exactly as shown in the image above and save it as <Your Initials>21GI.xls (CGM21GI.xls for me). The correct germplasm names are given below. Notice the typo in Entry 15 – include that in your file.



	IR 72768-12-1-1
2	IR 72768-28-1-1
3	IR 75502-24-1-1-B
4	IR 75516-30-1-1-B
5	IR 75516-56-1-1-B
6	IR 75518-84-1-1-B
7	IR 75531-31-1-2-B
8	IR 76561-AC 8-B
9	CNA 4196
10	IDSA 113
11	FARO 41
12	UPL RI 5
13	WAB 326-B-B-7-H1
14	WAB 534-B-3A 1-1
15	YUNLU NO 28
16	IRRI 132

To save typing you may be able to copy the names from the above table.

Once the template is completed select **Import Germplasm** form from the Actions Menu of the Germplasm Manager again and browse for the file just created.



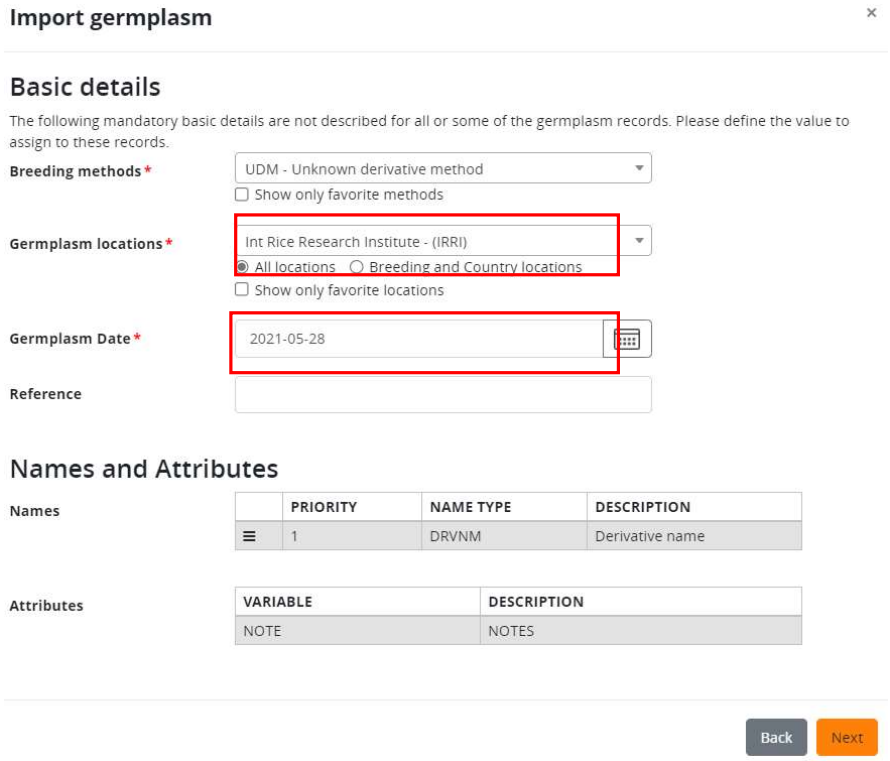
Click Open.

Then click Next.

The Specify Germplasm Details form appears. This form allows you to specify some germplasm information such as the breeding method, the germplasm location, the creation date and preferred name type. These details can also be specified on the Germplasm Import Template, and this allows them to be different for every entry. If they are specified on the Germplasm Details form then the values specified there are used for all cases where they are not specified on the template.
For this exercise we will specify all the items on the form, and leave all the columns for those items blank on the template. On the form:

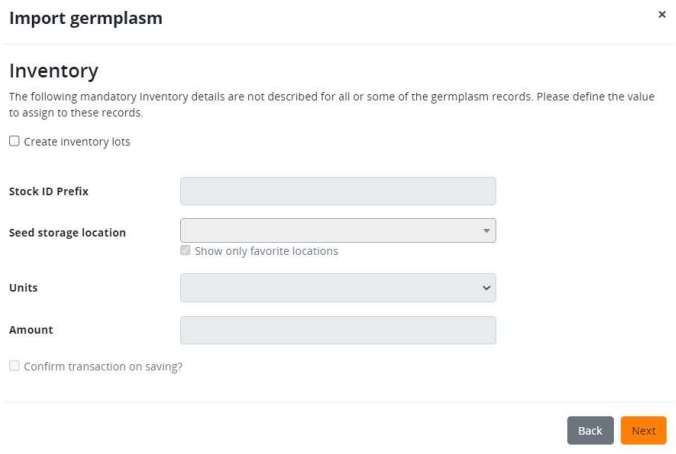
a. The first item is the **method** by which the lines were produced in their last generation. Set this to **Unknown derivative method** by starting to type "unknown " in the box and selecting the result. You will need to uncheck the Show only favorites button.
b. The second is the **location** where the germplasm was obtained or harvested, start to type "Int Rice " and select International Rice Research Institute. You will need to uncheck the Show only favorites button.

c. The third is a **date** that the germplasm was harvested or acquired which you can set to today's date.
d. And finally you can enter a text which will be stored as a **reference** for the germplasm.
e. You will see what columns have been found for alternative names and attributes attributes, in the default case just Derivative name and Notes, but you cannot set values for these on the Basic Details form, they must be supplied via the template.



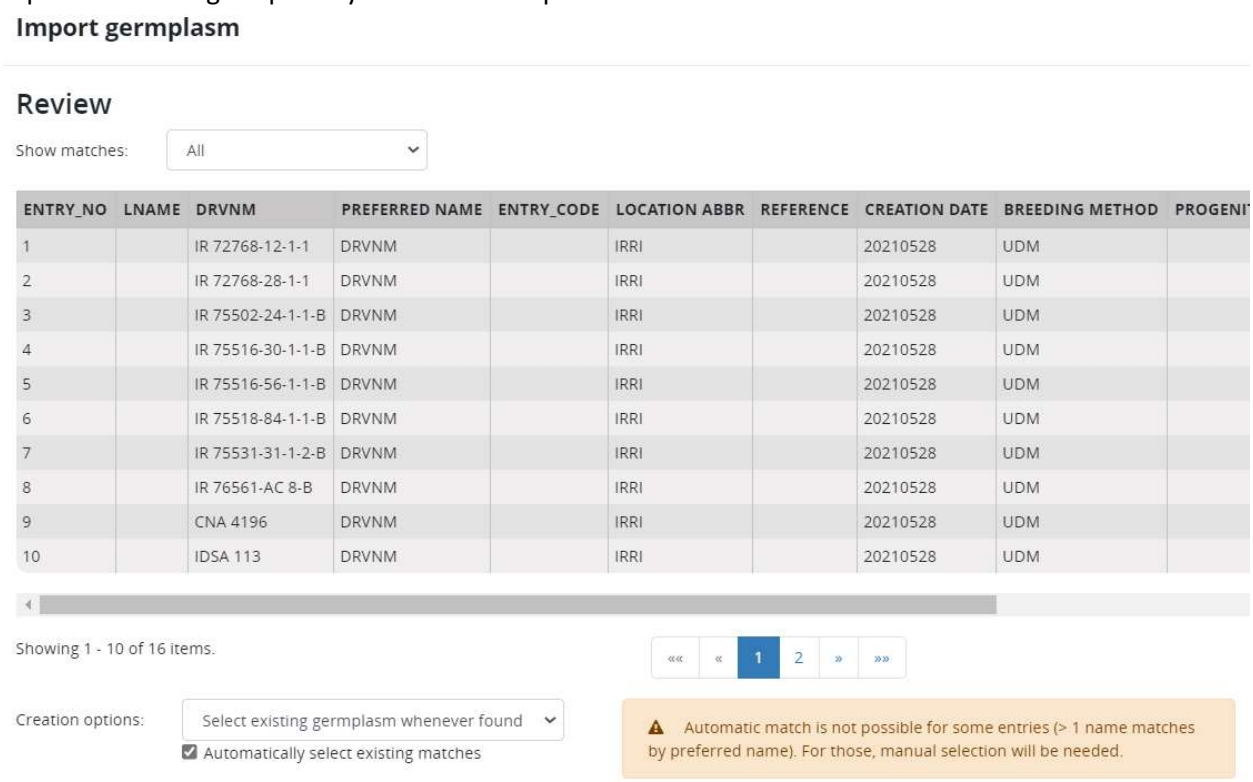
Click Next.

Since the template has columns for inventory and some data has not been entered, you are asked to supply inventory details:

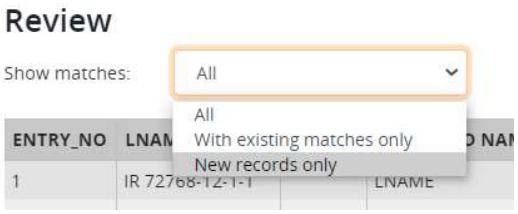


You can just click Next, since we do not want to specify inventory.

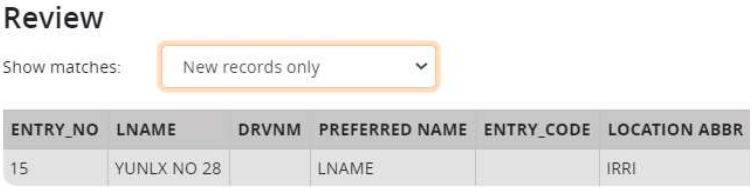
A preview of the germplasm you intend to import follows next:



An important feature of this review form is that it allows you to see which names were found in the database, and which have not been found. Pull down the Show matches pick list and select New records only.

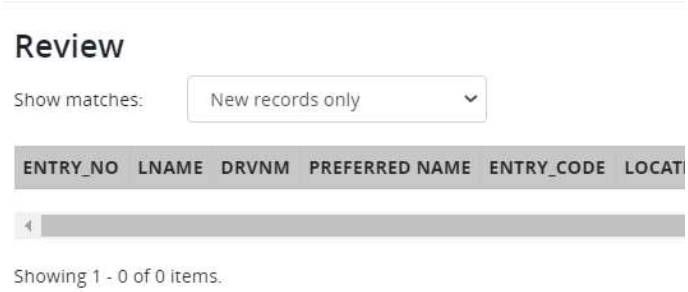


You will see just one entry which corresponds to our typo YINLX NO 28 instead of YUNU NO 28



Since we are expecting all entries to be found we can identify the typo in this way. Click the x at the top right of the Review panel to cancel the import process. Return and edit the template.

Fix the typo – change the X to U for entry 15, save the template again and process from the Import Germplasm item on the actions menu of the Germplasm Manager again. When you get to the review form again you will see there are no New Records.

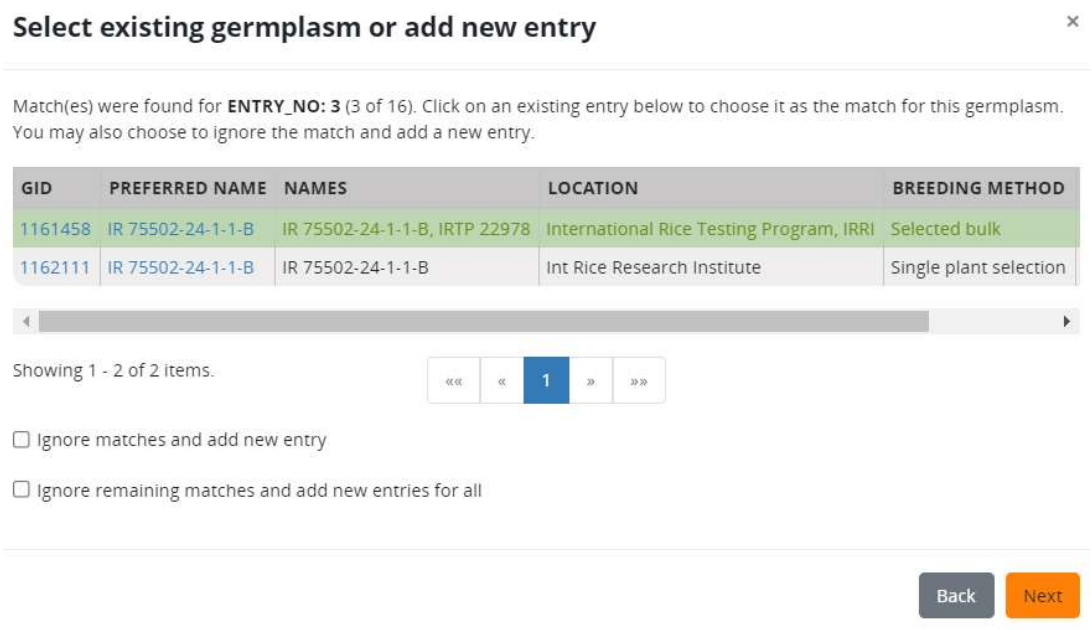


Since we expect the germplasm entries to exist in the database already, and since we want to select those existing entries we select the Creation option “Select existing germplasm whenever found”.

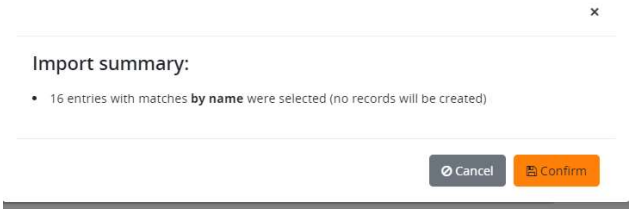
You should almost always choose Select existing germplasm whenever found unless you know the germplasm to be new to the system. Failure to make this selection can result in many duplicate entries being created for a single germplasm and this makes data integration for that line very difficult.

Once you have made this selection, Click **‘Save’**.

There is a checkbox to select single hits whenever found and this is checked by default, all you have to do is click next for each match with a single hit. If there are multiple matches the user must select the most appropriate. For this example select the existing germplasms in the database where the Location is International Rice Testing Program and IRTP {number} as one of its names. Click to highlight the germplasm and click **Next**.

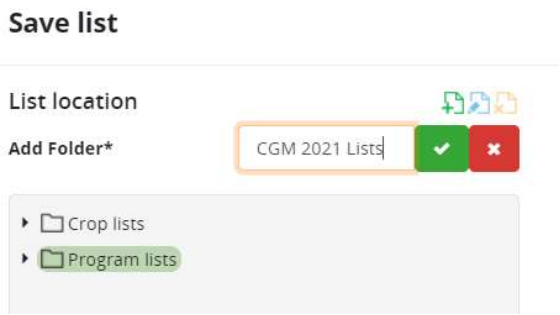


When all the entries have been processed BMS will show you a summary of found and new records. This is a second chance to catch any typos (if there should be no new records) and you can cancel to return to the Review form and see which entries are now with the filter.

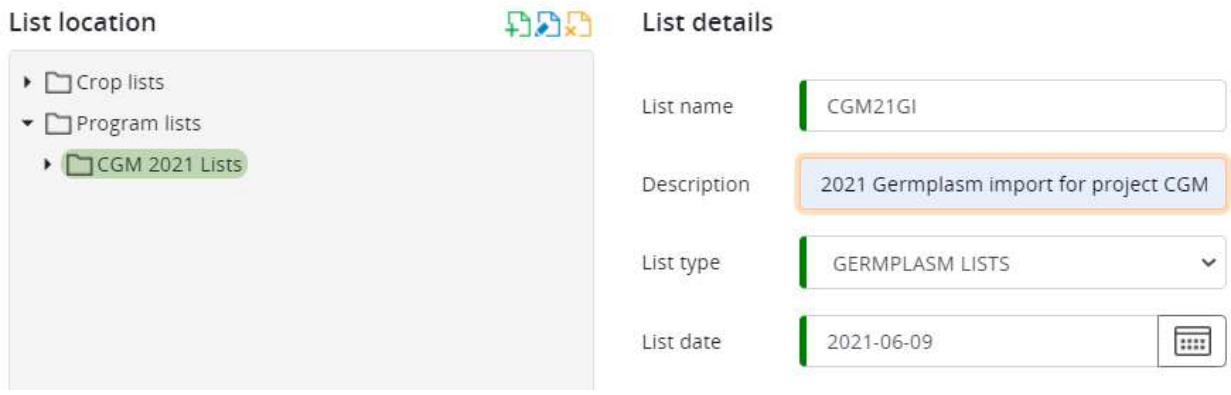


Since we have no new records, which is what we expect, we click Confirm and this opens the Save List page.

You can make a folder for your current lists (if the right one does not exist already) by clicking on the + symbol and enter **<Your initials> 2021 Lists** for example. Again use your initials to keep your lists separate from other students. Then click the tick and the folder will be created.

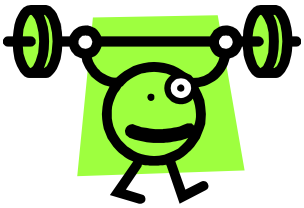


Highlight the newly created folder and fill in the list name and description. The List name should also have your initials so that it is different from list stored by other students.



Then click **Save**.

A message appears that the list has been saved. After which, the newly created list is opened. Click the Germplasm List Data to view the entries.



Exercise – Importing New Germplasm

The Germplasm Import Template is very versitile for supplying a lot of information about new imported germplasm. It is also useful for assembling germplasm, whether new or existing in the database into lists and can be used to add inventory for new or existing entries. However, if the Germplasm exists in the BMS, germplasm information will not be changed. To change or add information about existing germplasm you must use the Germplasm Editing features of the Germplasm Details forms, or the Germplasm Update template from the Germplasm Manager Actions menu.

Use the following example to fill a Germplasm Import template with some germplasm information about some new germplasm that will not be in the database (pick some distinct names with your initials included).

Part 1. - Names and location – will not be modified for existing germplasm records

	A	B	C	D	E	F	G
1	ENTRY_NO	LNAME	DRVNM	PREFERRED NAME	ENTRY_CODE	LOCATION ABBR	REFERENCE
2	1	CGMLine1	CGMx001-B-12-3-4	LNAME	E001	BKE	Tutorial V18
3	2	CGMLine2	CGMx002-B-3-4-5	DRVNM	E002	BKE	Tutorial V19
4							

A. Entry_NO must be filled with a sequential integer 1,2,3 …
B. You can have columns for different name types. By default two name types are listed, LNAME (Line name) and DRVNM (Derivative name) you can add more name types from the Codes sheet (under the heading NAMES). At least one name is required. We will keep the default ones and fill them both with invented names as above. Use your own initials to make you names unique.
C. LNAME is a line name. DRVNM is a derivative name. You must have one name, but can give more. All given names are added for new germplasm but new names are not added for existing germplasm, that must be done with the Germplasm Update template.
D. PREFERRED_NAME enter the name type column heading that you want to be the preferrred name for each new germplasm entry. If this is blank, the first name supplied is preferred.
E. ENTRY_CODE is just a code name for the entry in the list. It is local to the list.
F. LOCATION_ABBR is the abbreviation of the location where the germplasm was produced. You can look up some location abbreviations in the Codes sheet, but this is not a complete list and you can look up others in the BMS Manage Locations page. We will select BKE which is the abbreviation for Africa Rice-Bouake as you can see in the Codes sheet. This may not be available in your Codes sheet so select one that is there.
G. REFERENCE you can provide text which will be added as a reference new germplasm.

Part 2. Pedigree information and attributes – affects new entries only

H	I	J	K	L
CREATION DATE	BREEDING METHOD	PROGENITOR 1	PROGENITOR 2	NOTE
20200609	UDM			Adapted to uplands
20200609	DSP			Susceptable to Blast

H. CREATION_DATE You can enter the date the germplasm was created, collected or received according to your convention.
I. BREEDING_METHOD You can fill the column with the code of the breeding method finally used to produce the entry You can see the codes on the Codes sheet. UDM is Unknown Derivative Method, DSP is Single Plant Selection.
J. PROGENITOR1 and PROGENITOR2 can be used to capture pedigree information for the line. They need to be filled with GIDs of progenitors, the progenitors must already exist in the BMS (You must import the parents first if necessary). If the entry is a cross (an F1) then PROGENITOR1 should contain the GID of the female parent and PROGENITOR2 the GID of the male parent.
K. If the entry is a derived line (not F1) then PROGENITOR2 should contain the GID of the immediate source of the entry. PROGENITOR1 should be set to zero. However if the immediate source is not known, but the cross from which the entry was derived is known then PROGEITOR2 should be zero and PROGENITOR1 should be set to the cross from which the entry was derived.
L. You can add attributes for the entries being imported by adding colums with headings obtained from the Codes sheet. A column for NOTES has be added by default. Add some notes.

Part 3. – Inventory and unique identifiers – inventory can be supplied for new or existing entries

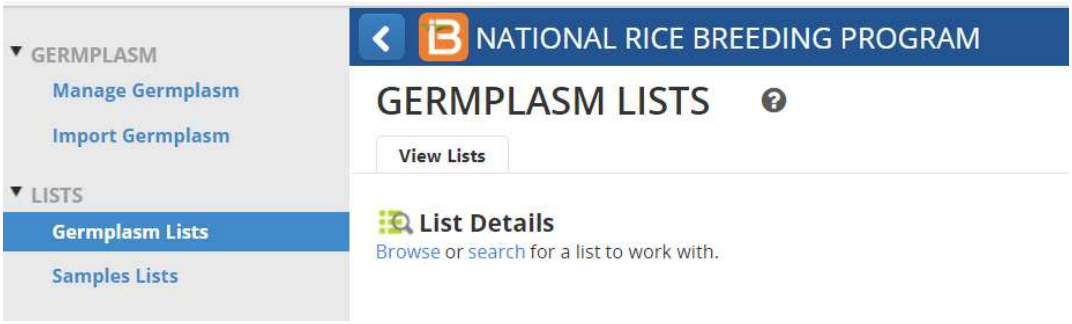
M	N	O	P	Q
STORAGE LOCATION ABBR	UNITS	AMOUNT	STOCK ID	GUID
CR11	SEED_AMOUNT_g	100		XYZ123
CR12	SEED_AMOUNT_kg	2		XWH345

M. STORAGE LOCTION ABBR is for the abbreviation of the seed storage location where you will store the seeds associated with this import list. These seed storage location abbreviations are looked up on the Codes sheet. New ones must be entered through the Location Manager.
N. UNITS contains the name of the storage units for each entry from the list on the Codes sheet.
O. This contains the amount of seed going into storage for new or existing entries.
P. STOCK ID is a short unique ID for the seed lot. It is better to let the BMS assign these codes since they must be unique.
Q. GUID can contain Germplasm Universal Identifies for the entries. If left blank the BMS will assign a unique code, but if a suitable global identifier exists you can enter it here and it will be used for new germplasm. If germplasm exists in BMS with that GUID it will be selected as the imported entry irrespective of any name matching or otherwise.

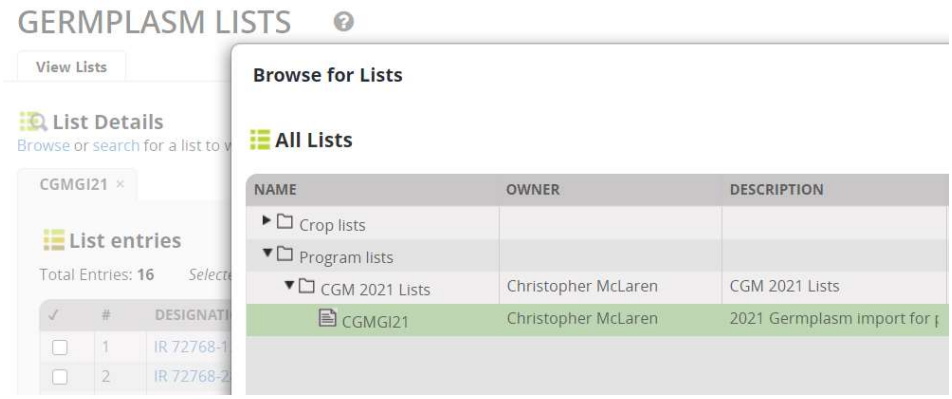
Now select Germplasm Import from the Actions menu of the Germplasm Manager and select the file you have saved to see the effect of the settings.

Viewing Lists

To view any list of germplasm, such as the one just imported, click on **Germplasm Lists** under the **LISTS** main menu.



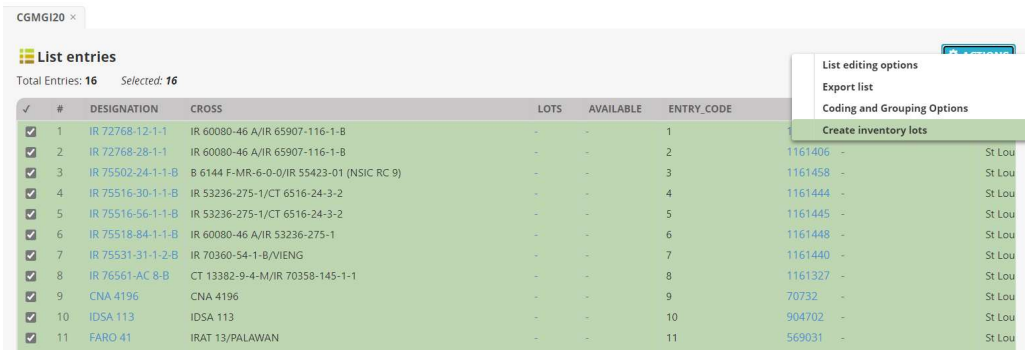
Then click on Browse and navigate to the folder where your list is located and highlight the list you want to view. (You can navigate and highlight several lists). Then click the X at the top right of the navigation box to clear it and you will see the lists you highlightedin separate tabs.



Adding Inventory for Imported Germplasm

Although seed inventory can be added to the seed inventory system by filling the inventory columns on the germplasm import template, it is better to use the inventory functions for the List Manager and the Inventory Manager to do this since this offers more control of how inventory are stored and provides access to a unique LotID which can be used to bar code the seed packets.

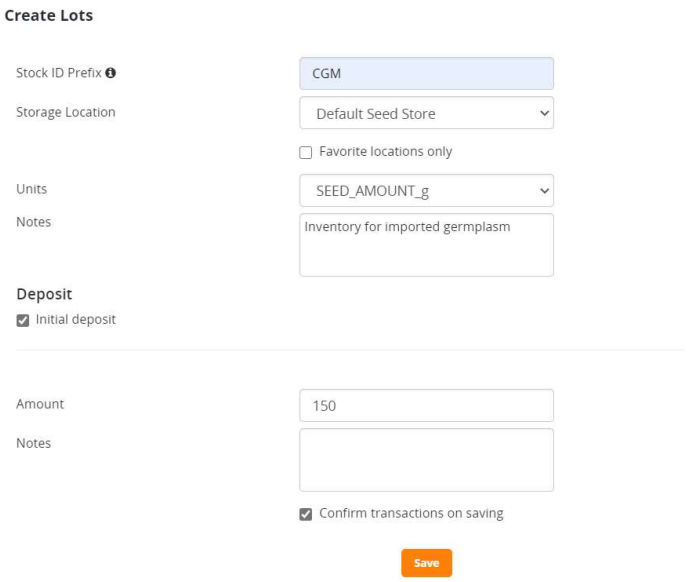
To add inventory for the imported list, open the list in the List manager, select all entries in the list and then select Actions>Create inventory lots:



On the create lots form you must enter a stock ID prefix which should identify the 'owner' or project to which the seed lot belongs. This will be extended by adding a batch number for the seed batch and an entry number for the particular line. It is useful to store the seed packets in order of stockID at the seed storage location for easy retrieval. Enter your initials for this example to keep track of your seed stocks.

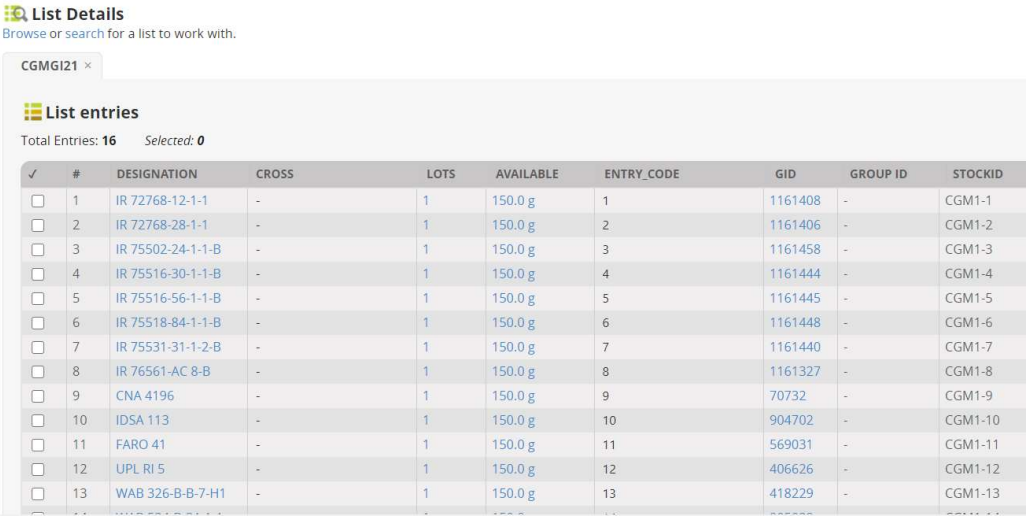
Next select the storage location – we only have a location called the Default Seed Store, but of course other locations can be added as appropriate. Choose the scale in which the seed will be managed and enter a note if desired.

Now we can also add an initial deposit at this time, and if, for example, the sender had sent the same amount of seed for each entry you can enter that here and confirm the transactions directly.



Click save and you will get a message that the lots have been created.

Reload the germplasm list to see the inventory:

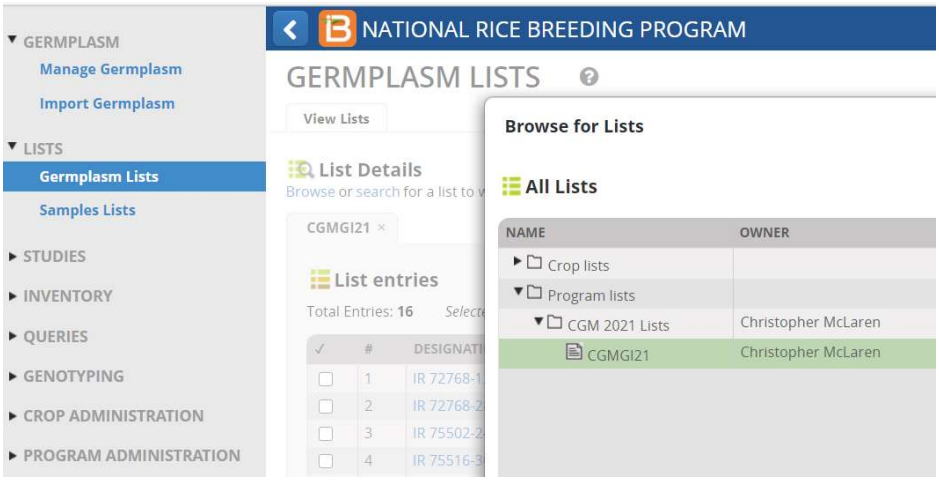


✓	#	DESIGNATION	CROSS	LOTS	AVAILABLE	ENTRY_CODE	GID	GROUP ID	STOCKID
☐	1	IR 72768-12-1-1	-	1	150.0 g	1	1161408	-	CGM1-1
☐	2	IR 72768-28-1-1	-	1	150.0 g	2	1161406	-	CGM1-2
☐	3	IR 75502-24-1-1-B	-	1	150.0 g	3	1161458	-	CGM1-3
☐	4	IR 75516-30-1-1-B	-	1	150.0 g	4	1161444	-	CGM1-4
☐	5	IR 75516-56-1-1-B	-	1	150.0 g	5	1161445	-	CGM1-5
☐	6	IR 75518-84-1-1-B	-	1	150.0 g	6	1161448	-	CGM1-6
☐	7	IR 75531-31-1-2-B	-	1	150.0 g	7	1161440	-	CGM1-7
☐	8	IR 76561-AC 8-B	-	1	150.0 g	8	1161327	-	CGM1-8
☐	9	CNA 4196	-	1	150.0 g	9	70732	-	CGM1-9
☐	10	IDSA 113	-	1	150.0 g	10	904702	-	CGM1-10
☐	11	FARO 41	-	1	150.0 g	11	569031	-	CGM1-11
☐	12	UPL RI 5	-	1	150.0 g	12	406626	-	CGM1-12
☐	13	WAB 326-B-B-7-H1	-	1	150.0 g	13	418229	-	CGM1-13

Manipulating Germplasm Lists in the List Manager

View existing Program Lists

From LISTS go to Germplasm Lists, Browse Program lists><your initials>2021 Lists and highlight the list just entered <your initials>GI21 (CGMGI21 for me).



Clear the Browse for Lists panel by clicking on the x in the upper right corner and you will see the list just entered:

Right click on the header of the Cross column and click Fill with Cross expansion. Select 1 level. Because all the entries were selected from the database, they do have pedigrees which are displayed in the Cross column:

CGMGI21 ×

List entries

Total Entries: **16** *Selected:* ***0***

✓	#	DESIGNATION	CROSS	LOTS	AVAILABLE
☐	1	IR 72768-12-1-1	IR 60080-46 A/IR 65907-116-1-B	1	150.0 g
☐	2	IR 72768-28-1-1	IR 60080-46 A/IR 65907-116-1-B	1	150.0 g
☐	3	IR 75502-24-1-1-B	B 6144 F-MR-6-0-0/IR 55423-01 (NSIC RC 9)	1	150.0 g
☐	4	IR 75516-30-1-1-B	IR 53236-275-1/CT 6516-24-3-2	1	150.0 g
☐	5	IR 75516-56-1-1-B	IR 53236-275-1/CT 6516-24-3-2	1	150.0 g
☐	6	IR 75518-84-1-1-B	IR 60080-46 A/IR 53236-275-1	1	150.0 g
☐	7	IR 75531-31-1-2-B	IR 70360-54-1-B/VIENG	1	150.0 g
☐	8	IR 76561-AC 8-B	CT 13382-9-4-M/IR 70358-145-1-1	1	150.0 g
☐	9	CNA 4196	CNA 4196	1	150.0 g
☐	10	IDSA 113	IDSA 113	1	150.0 g
☐	11	FARO 41	IRAT 13/PALAWAN	1	150.0 g
☐	12	UPL RI 5	SIGADIS (AICRIP)/BPI 76-1	1	150.0 g
☐	13	WAB 326-B-B-7-H1	ITA 235 (TOX 1785-19-18)/WABC 165	1	150.0 g
☐	14	WAB 534-B-3A 1-1	WAB 181-18/DR 2	1	150.0 g
☐	15	YUNLU NO 28	IDSA 6 (IRAT 216)/WUNENGDABAIGU-2-5	1	150.0 g
☐	16	IRRI 132	UPL RI 5/IR 12979-24-1 (BROWN)	1	150.0 g

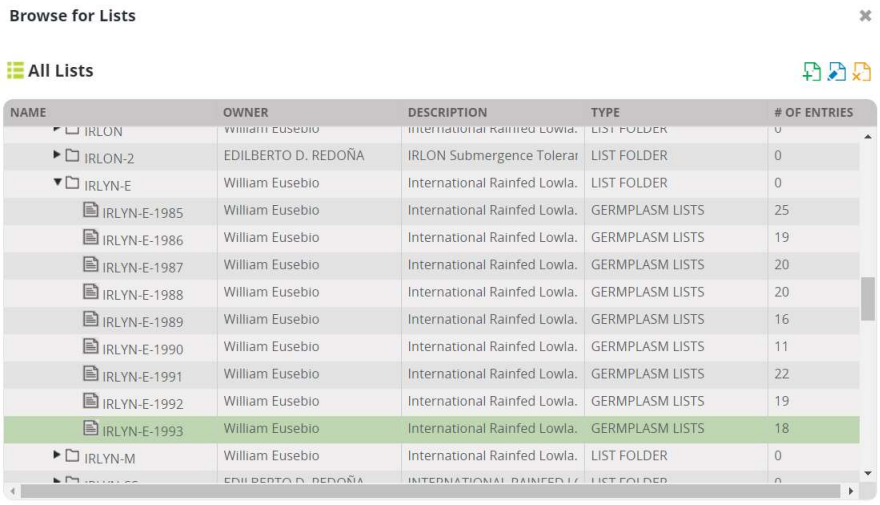
If no cross information is available, the Designation is simply displayed in the cross column.

Click Actions>List Editing Options>Save changes to save the pedigree in the list.

Using Crop Lists to share germplasm between programs

Click on Browse below the heading List Details and expand the Crop Lists section.

Lists saved to or moved to the Crop Lists section are visible to all programs in the crop. Navigate to INGER NURSERIES>IRLYN-E and highlight list IRLYN-E-1993. You can ser this list because it is in the Crop Lists section even though it was nat made in the current program. You cannot do much with this list until you copy it into your Program Lists.

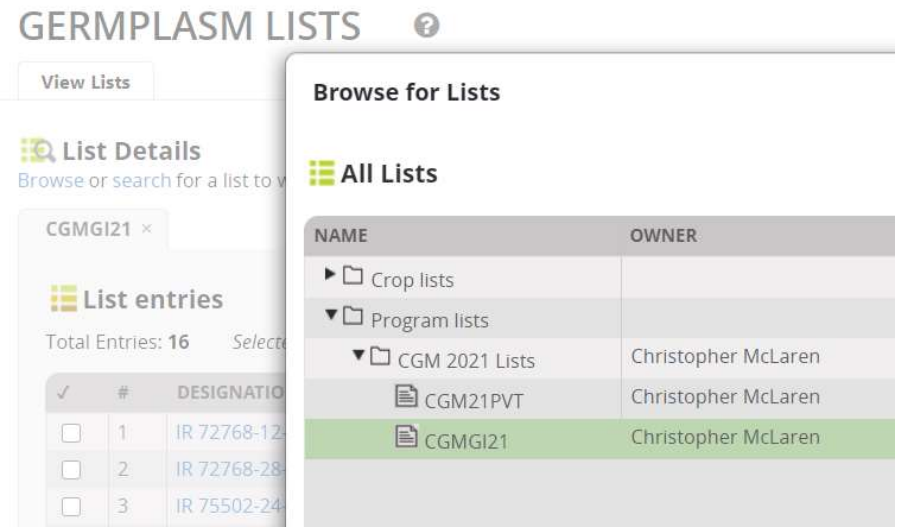


The list contains 18 entries:

Highlight all the entries by clicking on select all at the bottom left of the list. Right click on the green space and click **Add Selected Entries to New List**

The List editor will open with the entries in a new list. Choose Actions>List Editing Options and save the list in the 2020 Lists folder with name :<your initials>21PVT (CGM201PVT for me).

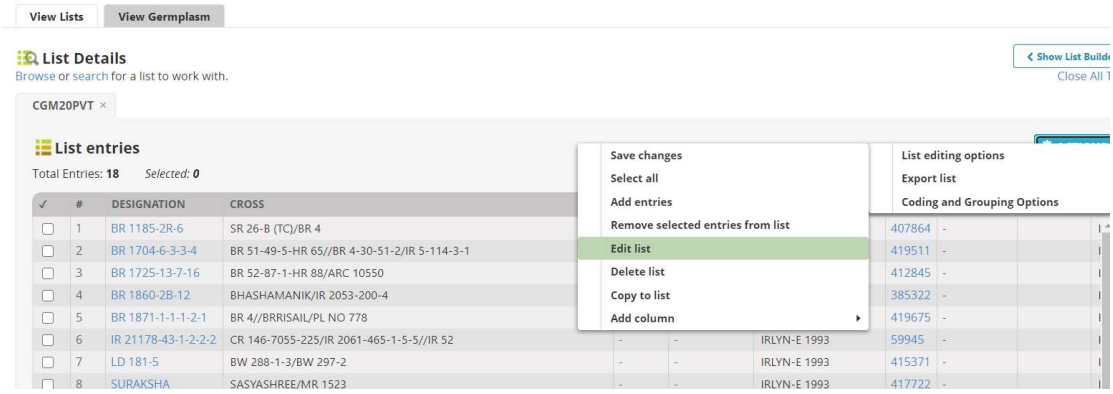
Now in Browse Lists Program Lists> <Your initials>2021 Lists we have a second list:



Adding Entries from an existing list to another list

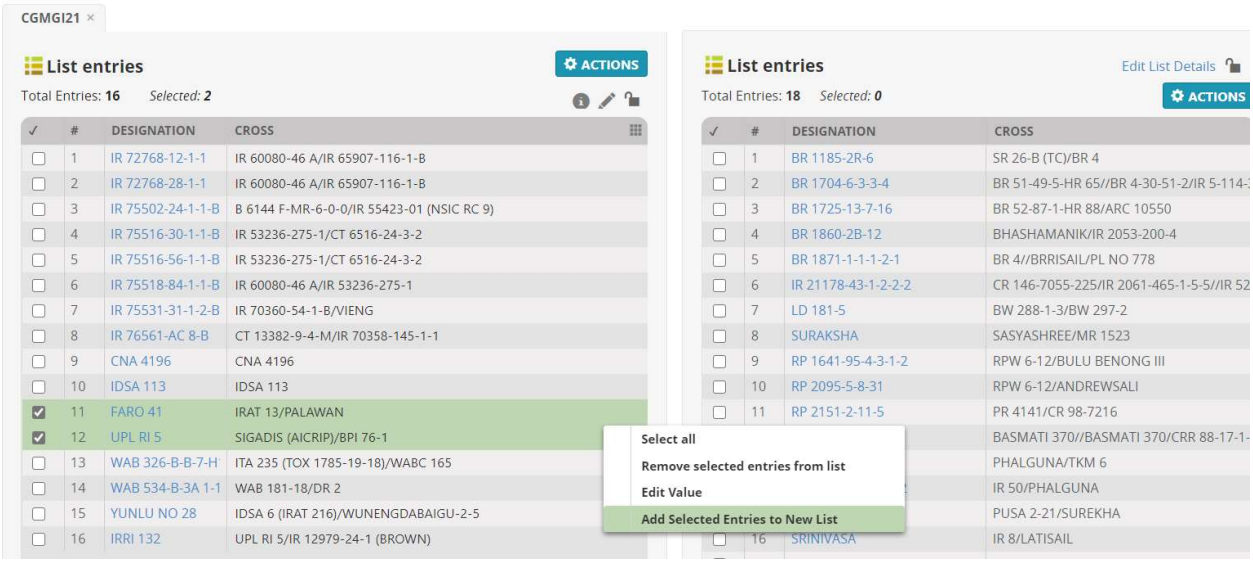
Suppose I wish to add two entries from my import list (<your initials>GI21) to my PVT list to be checks for example.

From Browse Lists open the PVT list and select Actions>List Editing options>Edit list.



The list will open in the Edit list box to the right. Then click Browse again and select the import list (<your initials>GI21). It will open in the Browse list box on the left.

Select two germplasm FARO 41 and UPL RI 5 by checking the tick boxes to the left of the germplasm names. Right click on the green space and select **Add Selected Entries to New List**

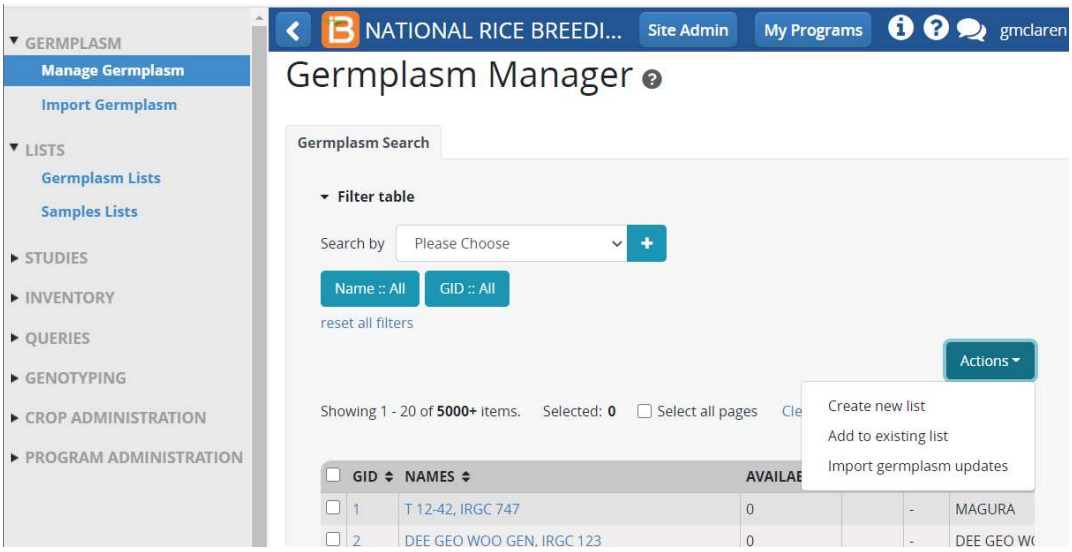


You will see that the selected entries have been added to the end of the list in the Edit Window.

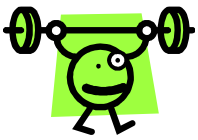
Save the changes.

Adding Entries from the Germplasm Search to a list

You can also add germplasm to lists using the Actions menu items from the Germplasm Search Application:



If you highlight entries in the filter list and click the **Create new list** action item you will be asked to save a new list with those entries added. If you click the Add to existing list item, you will be asked to choose a list and the checked entries will be added to lat list. Try the exercise below.



Exercise on Germplasm Manager

1. Use the Actions Menu on the Germplasm List Browser to try exporting your list to and excel file.
2. Use the Germplasm Search App to search the for the entry of IR 64 with GID 50533. Use the Action menu of the Germplasm Search App to add it to a new list called <your initials>Checks in your 2021 Lists folder, then search for IR 72 (GID 70125) and add that to the same list, finally search for NERICA 4 (GID 765439) and add that to the list. (Note you could search for all three GIDS at the same time and add all three to the new list).
3. In the Germplasm List Browser open your checks list, select all three entries and add inventory lots from the actions menu. Specify location Bulk Seed Store, units KG and add initial deposits of 5 kg for all entries. Confirm the transactions.
4. Use the ? icon on the top right of the workbench to go to the help system. Click on the USER MANUAL section. Click on Germplasm and Genealogy and read about how BMS manages germplasm in a breeding program.

5. Still in the MANUAL, click on BREEDING ACTIVITIES and then MANAGE GERMPLASM and look through the manual section for other things you can do with this application. Can you list some new things?

Making a Crossing Block

A Crossing Block is a nursery planted with parental material for the purpose of making crosses between lines planted in the nursery. In BMS all activities involving planting material are referred to as studies and so nurseries are one kind of study and we use the Study Manager to manage the information for nurseries.

There are two ways a cross list can be formed. Either by making a planned series of crosses by matching parents from a parent list which is planted in a crossing bloc nursery or by recording crosses made in the field in such a nursery using a crossing template. We will demonstrate both options in this tutorial.

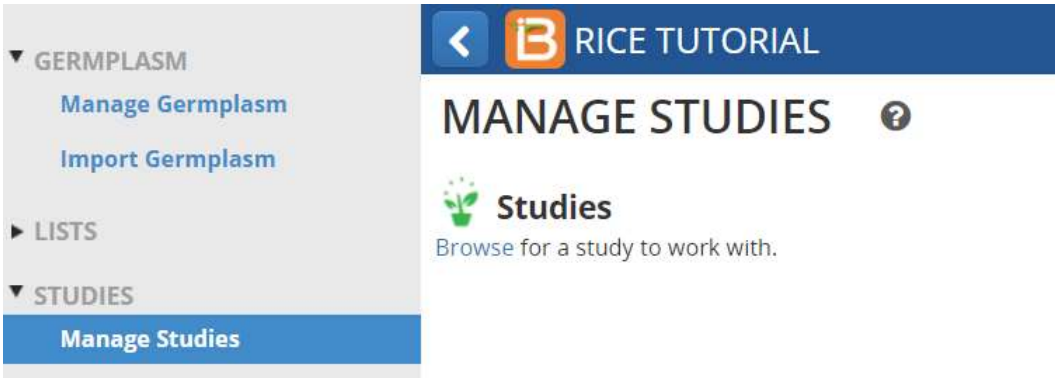
Objectives

At the end of this chapter, the user should be able to:

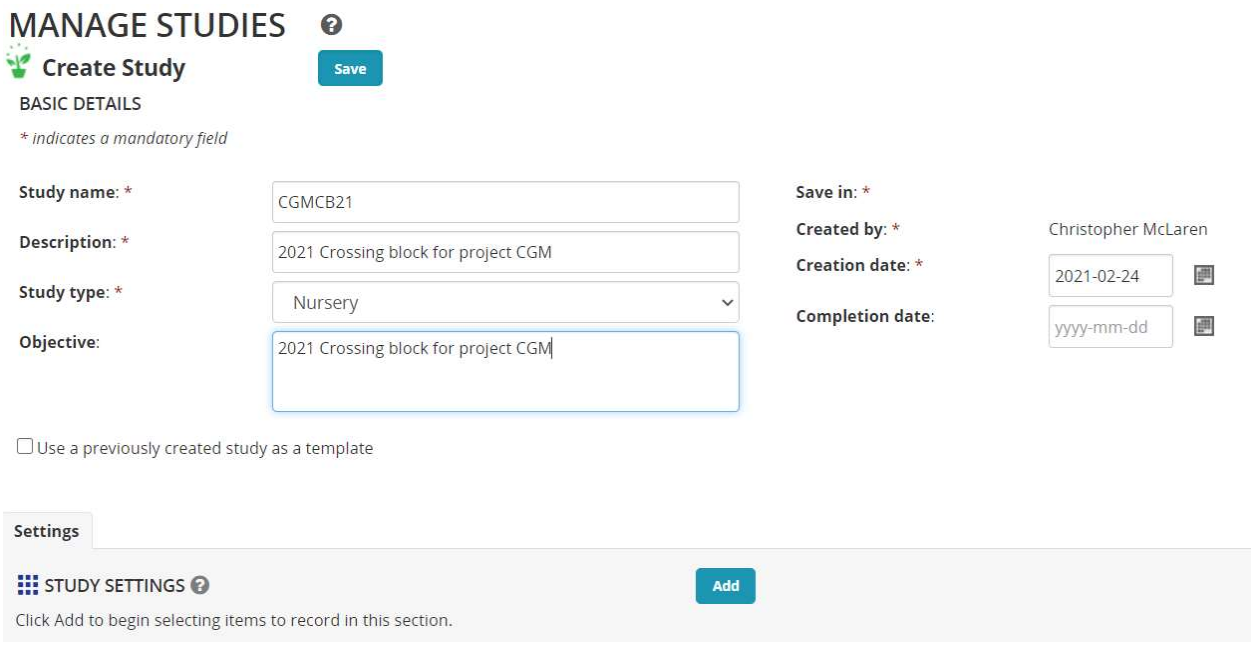
1. Use the Study Manager to create a Nursery, add meta data to the nursery, specify planting material, specify the planting location and create a fieldbook.
2. Use the Crossing Manager to make crosses between matched female and male entries in a crossing block.
3. Specify a naming convention to give the crosses names in a series.
4. Use a crossing template to record crosses made in a crossing block in the field and then load the information into the BMS

Create a Crossing Block in the Study Manager

Click on **Manage Studies** from the STUDIESmenu and then on **Start a new Srudy.**

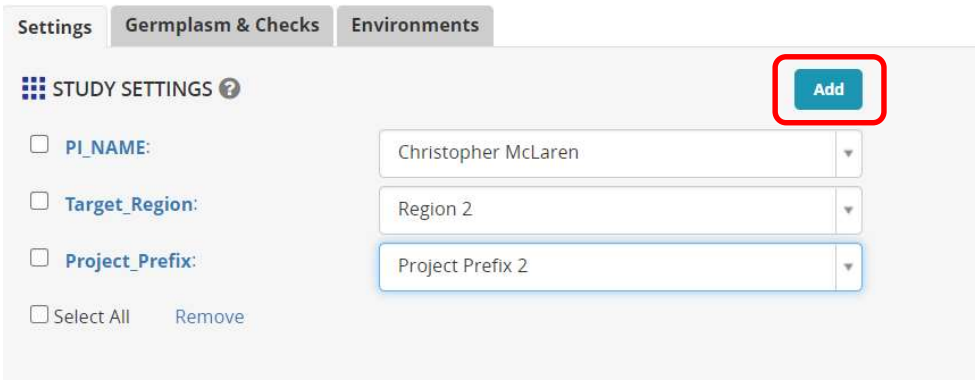


The Create Study form opens. Fill in the basic details with a short Study name (Use your initials in the study name to ensure uniqueness in the class). A description, a study type – Nursery (A nursery is a single location unreplicated trial for population development or germplasm characterization). Give an objective.



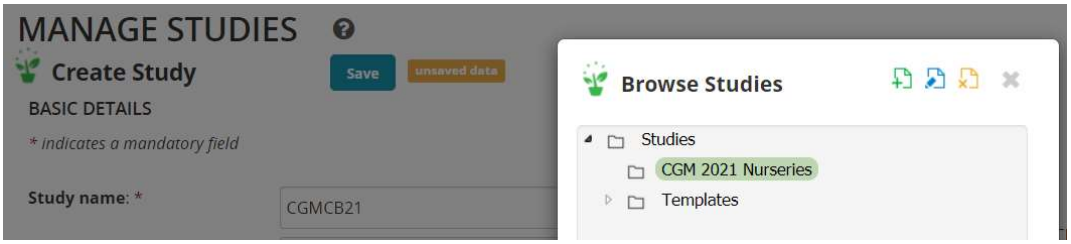
Next click on the Add button next to STUDY SETTINGS. This will open the ontology manager and you may specify variables to be added to the study to record metadata about the study.

In the ontology search box look for PI and add PI Name, look for region and add Target Region and then look for Project and add Project Prefix. These variables can be customized to your particular programs and identify important objectives of the crossing block.



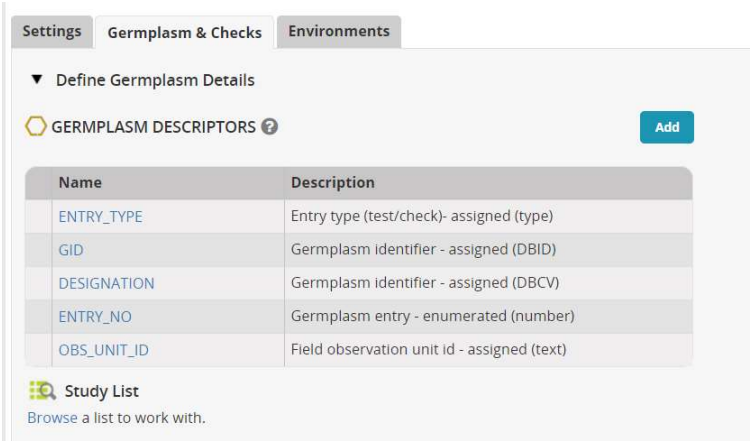
Now save the nursery definition as created so far by clicking on the Save button on the top left of the Study Manager screen.

If there is no folder for <your initials> 2021 Nurseries, create one with your initials to keep your work separate from other students. (To make a folder, click on the + Add folder symbol, Type the name and click the tick symbol)



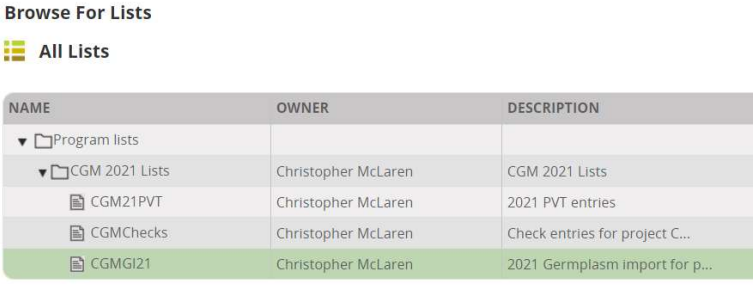
The study will be saved and reloaded with a few new tabs.

Now click on the tab Germplasm and Checks. Click the Add button next to Germplasm Descriptors.

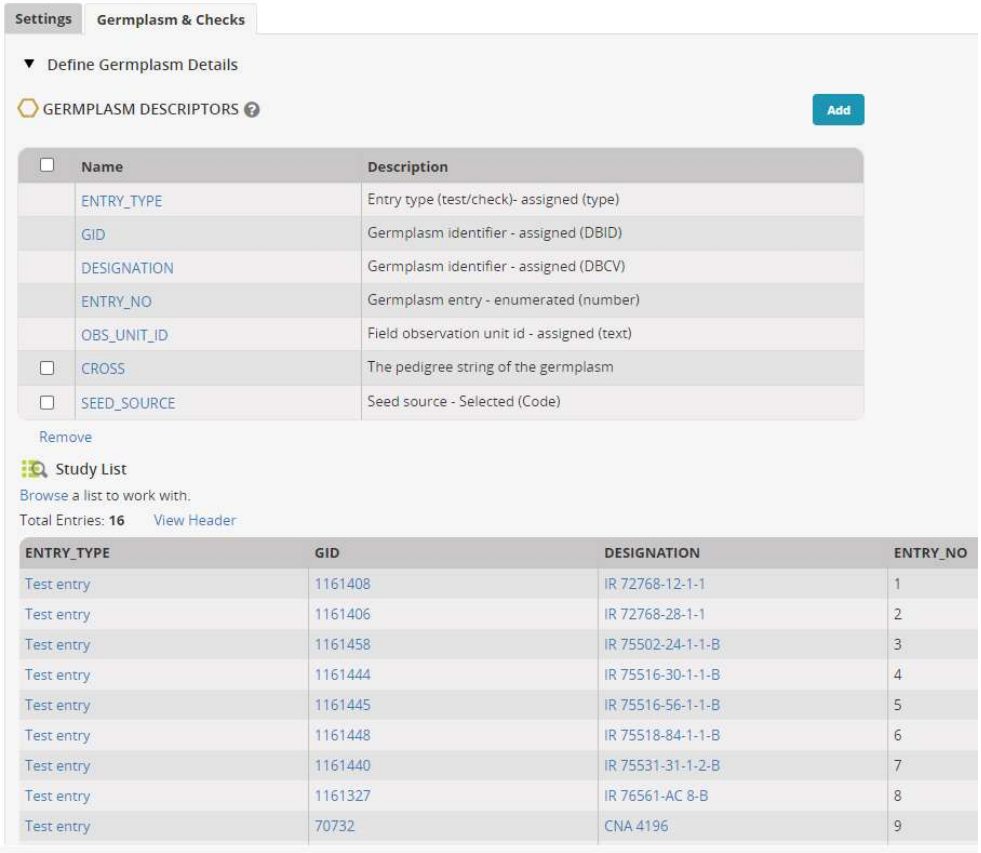


In the Ontology search box look for ‘cross’ and add variable Cross to the descriptors, then search for ‘source’ and add Seed Source to the descriptors.

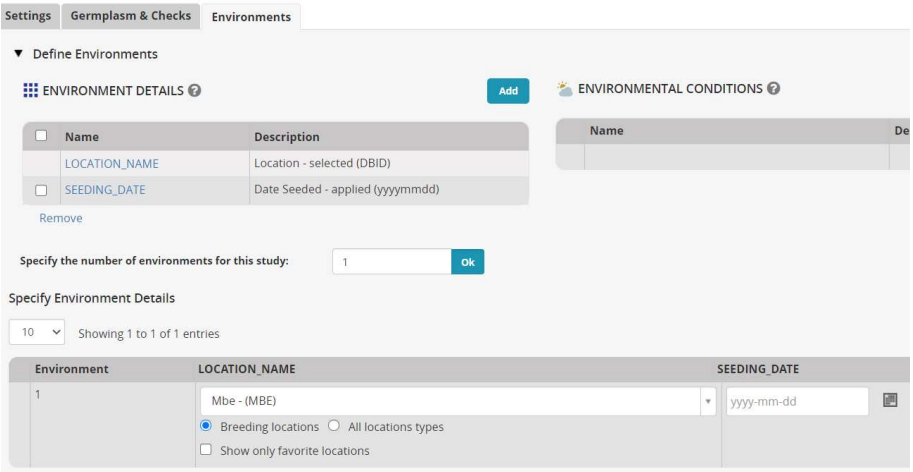
Now click Browse and navigate through the program lists to your imported list and click Select.



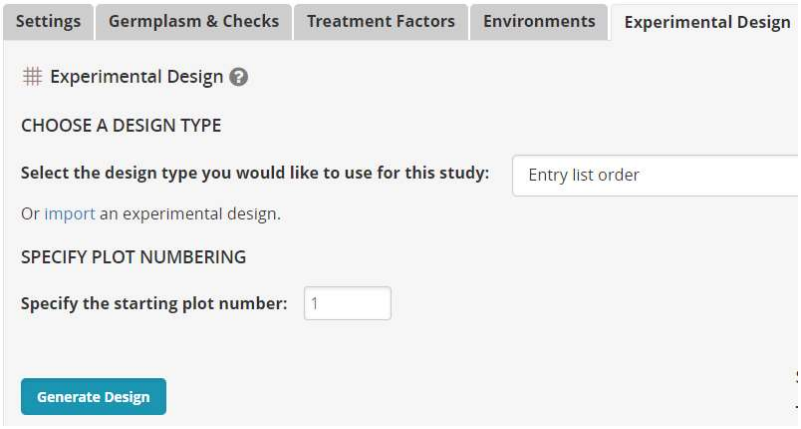
The entries will be imported into the nursery:



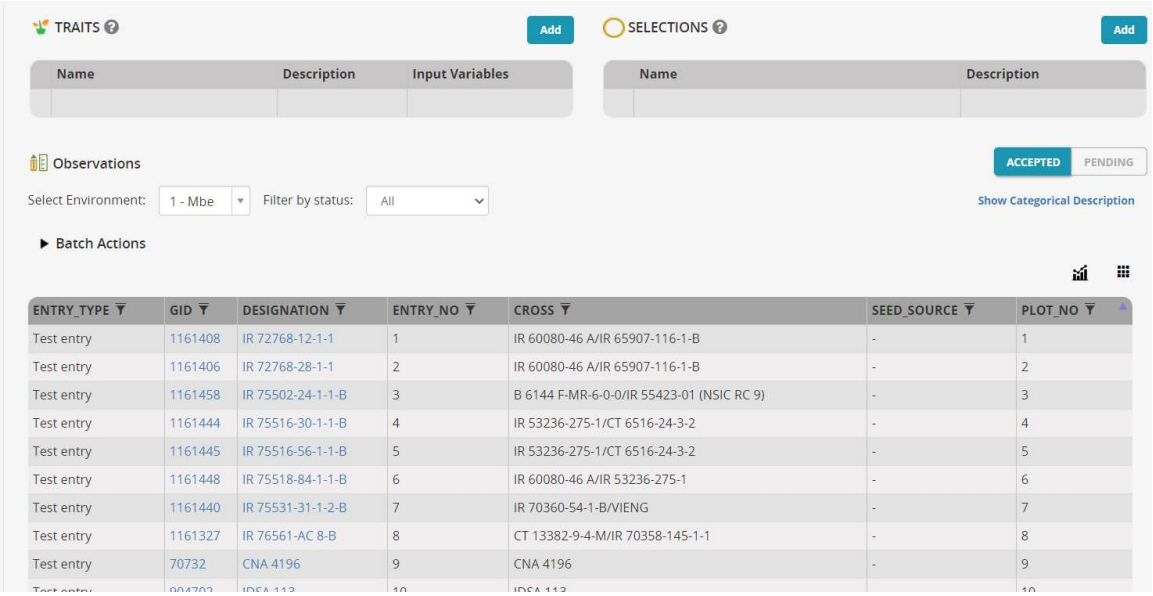
Click on the Environments tab and choose Mbe for the planting location. Click on the Add button next to ENVIRONMENT DETAIL and search for Planting Date in the ontology. You will find SEEDING_DATE – add it to the nursery.



Click on the Experimental Design tab. Select the Design **Entry List Order** and click **Generate Design**.



Select the location (we only have the one) and click **Generate** again. A fieldbook is produced in the observation tab:

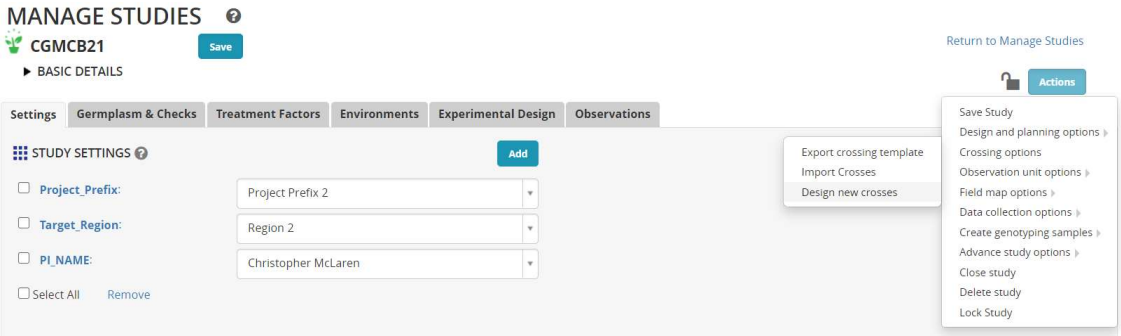


ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	CROSS	SEED_SOURCE	PLOT_NO
Test entry	1161408	IR 72768-12-1-1	1	IR 60080-46 A/IR 65907-116-1-B	-	1
Test entry	1161406	IR 72768-28-1-1	2	IR 60080-46 A/IR 65907-116-1-B	-	2
Test entry	1161458	IR 75502-24-1-1-B	3	B 6144 F-MR-6-0-0/IR 55423-01 (NSIC RC 9)	-	3
Test entry	1161444	IR 75516-30-1-1-B	4	IR 53236-275-1/CT 6516-24-3-2	-	4
Test entry	1161445	IR 75516-56-1-1-B	5	IR 53236-275-1/CT 6516-24-3-2	-	5
Test entry	1161448	IR 75518-84-1-1-B	6	IR 60080-46 A/IR 53236-275-1	-	6
Test entry	1161440	IR 75531-31-1-2-B	7	IR 70360-54-1-B/VIENG	-	7
Test entry	1161327	IR 76561-AC 8-B	8	CT 13382-9-4-M/IR 70358-145-1-1	-	8
Test entry	70732	CNA 4196	9	CNA 4196	-	9

It has 16 plots since there is no replication and the entries are planted in the same order as their entry numbers 1 … 16. This is a reasonable lay-out for a crossing block, and indeed for most nurseries. However absolutely any lay-out can be specified by using the Import design function on the Experimental design tab. We will not use this for this exercise.

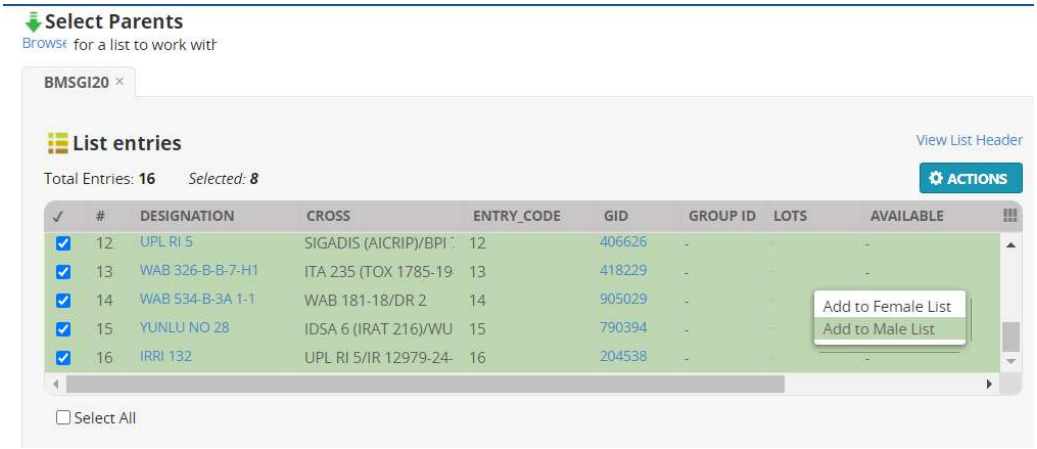
Use the Crossing Design Tool for Specifying Crosses

On the Actions Menu, select Crossing Options and then Design new Crosses.

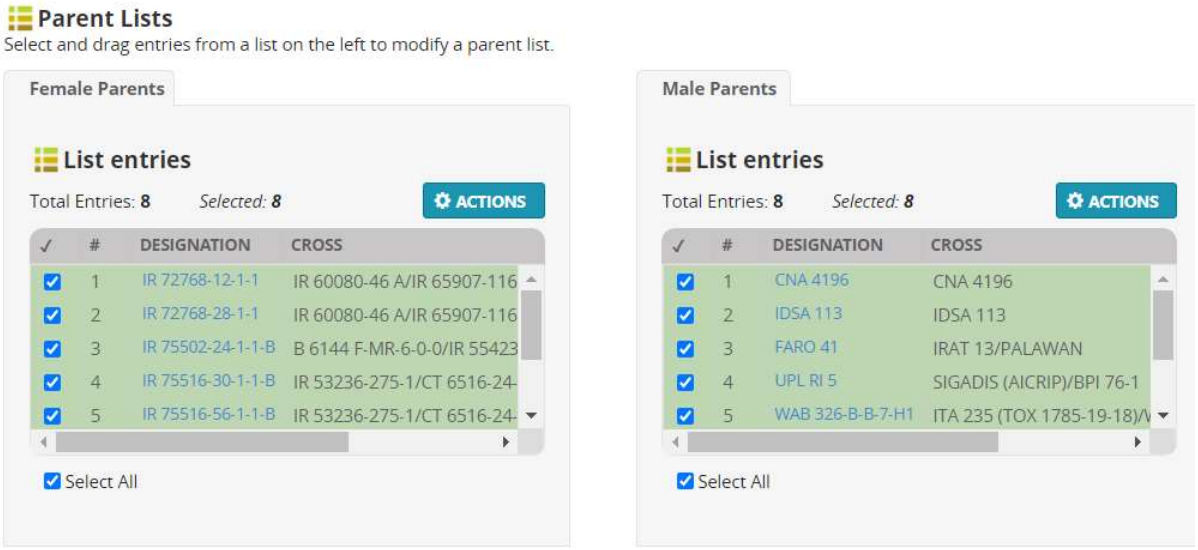


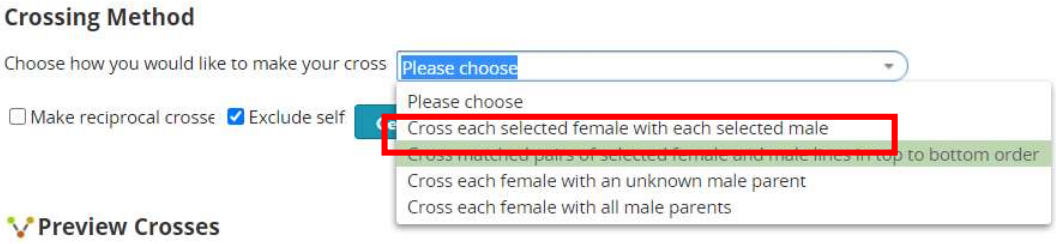
In the Select parents form, highlight the first eight entries (by clicking in the check boxes next to the names) then right click on the green space and select **Add to Female List**:

Uncheck the first eight entries and check the last eight entries and select **Add to Male List:**



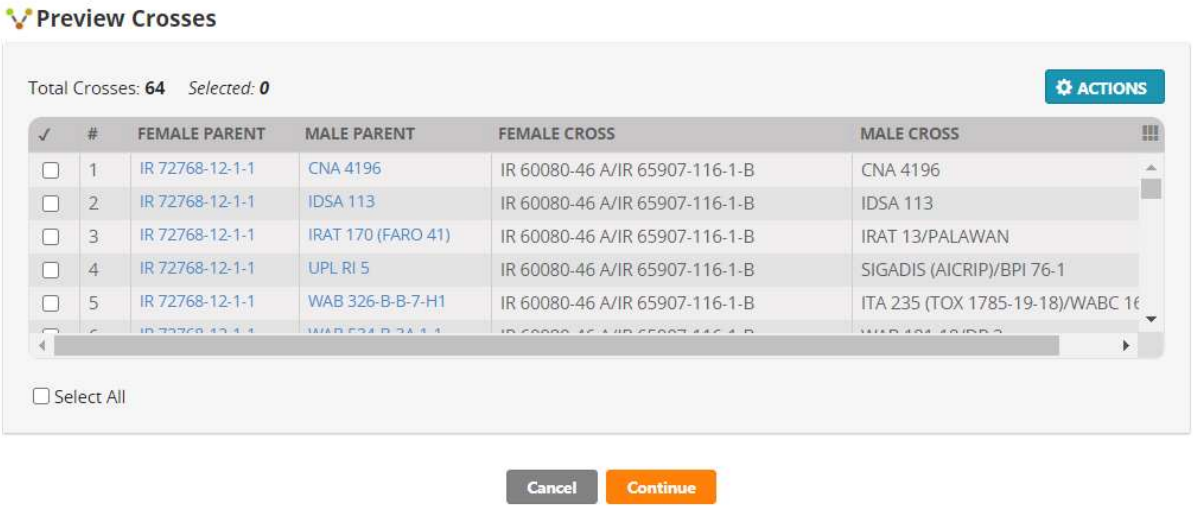
The parent lists now look as follows:



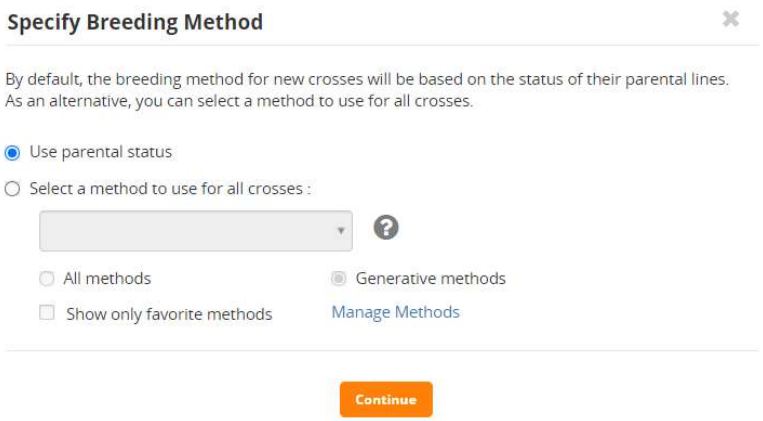


There are several ways to combine parents from the female and male lists. For this exercise we are going to choose **Cross each selected female with each selected male.**

Click Generate Crosses. You will get a preview of 64 crosses:



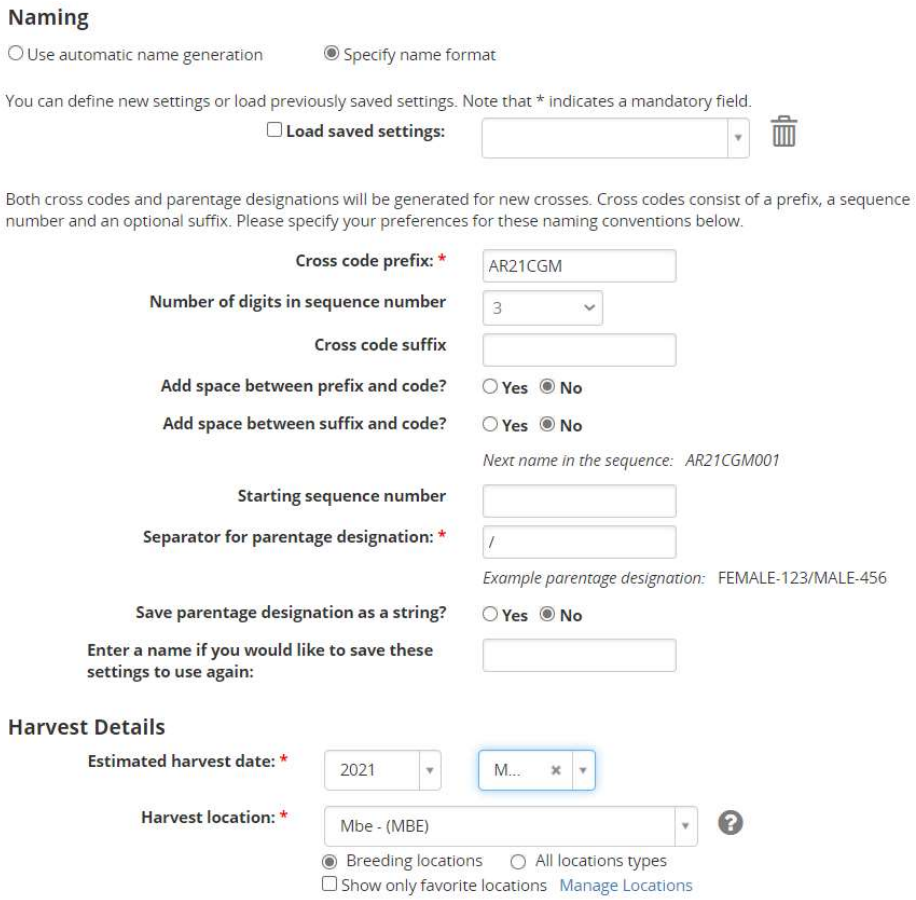
If the crosses are the ones you want to make click Continue. Then you need to specify the method of crossing.



You can select a crossing method for all the crosses from the list at the end of this tutorial by checking the **Select a method to use for all crosses** radio button and then selecting in the box, or you can allow BMS to work out the type of cross being made by using **Use parental status.** We will use the parental status option.

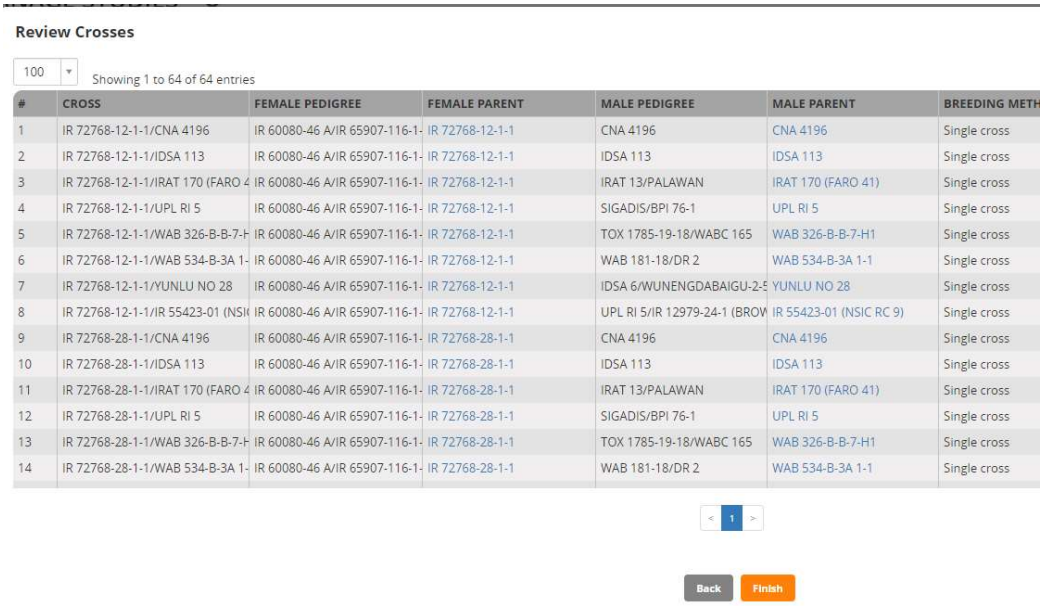
Click **Continue.**

You will be asked to specify Naming and Harvest Details. Click the **Specify name format** radio button.



a. Enter **AR21<your initials>** as prefix of the Cross Code
b. Enter **3** as the number of digits for the sequesnce code.
c. Specify date and location.

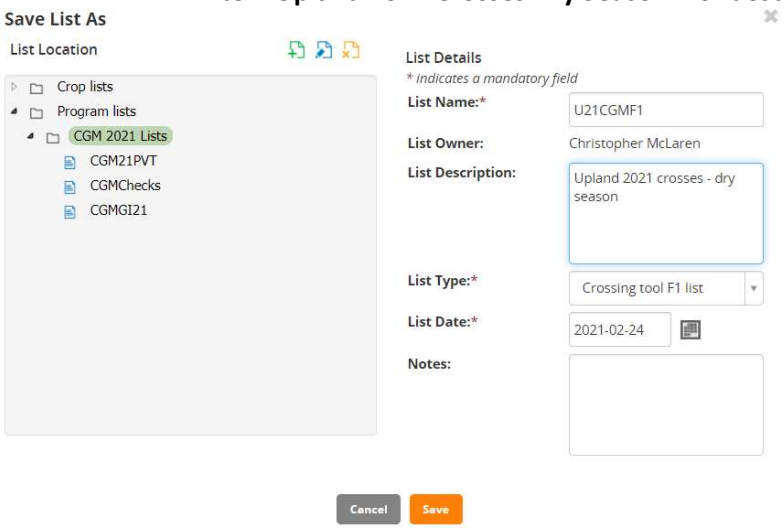
Click **Continue**. You will see a review panel.



Click **Finish.**

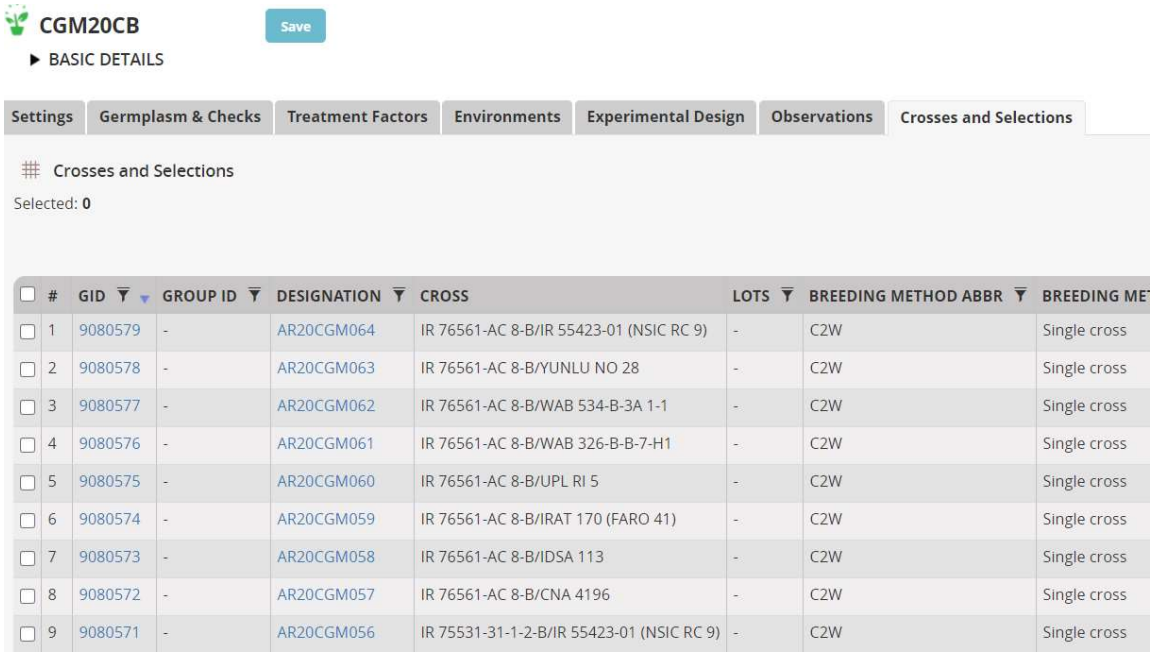
For list details, enter the following

- Enter "**U21<your initials>F1**" as list name
- Enter "**Upland 2021 Crosses Dry Season"** for description



Click **Save**. A message box will be shown about saving the crosses.

The details about the created list will also be shown in the Crosses and Selections Tab.

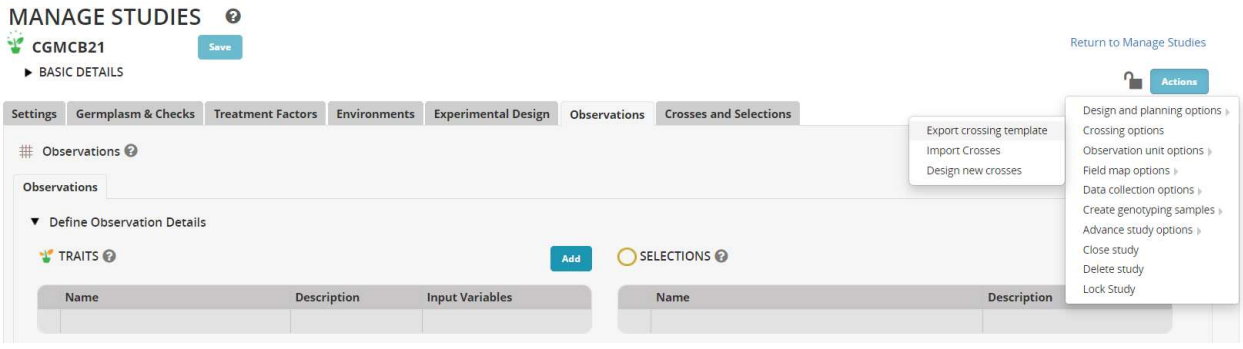


#	GID	GROUP ID	DESIGNATION	CROSS	LOTS	BREEDING METHOD ABBR	BREEDING ME
1	9080579	-	AR20CGM064	IR 76561-AC 8-B/IR 55423-01 (NSIC RC 9)	-	C2W	Single cross
2	9080578	-	AR20CGM063	IR 76561-AC 8-B/YUNLU NO 28	-	C2W	Single cross
3	9080577	-	AR20CGM062	IR 76561-AC 8-B/WAB 534-B-3A 1-1	-	C2W	Single cross
4	9080576	-	AR20CGM061	IR 76561-AC 8-B/WAB 326-B-B-7-H1	-	C2W	Single cross
5	9080575	-	AR20CGM060	IR 76561-AC 8-B/UPL RI 5	-	C2W	Single cross
6	9080574	-	AR20CGM059	IR 76561-AC 8-B/IRAT 170 (FARO 41)	-	C2W	Single cross
7	9080573	-	AR20CGM058	IR 76561-AC 8-B/IDSA 113	-	C2W	Single cross
8	9080572	-	AR20CGM057	IR 76561-AC 8-B/CNA 4196	-	C2W	Single cross
9	9080571	-	AR20CGM056	IR 75531-31-1-2-B/IR 55423-01 (NSIC RC 9)	-	C2W	Single cross

Using the Crossing Template to make crosses

The other method of specifying crosses is to use a crossing template. We will show this option in the same nursery as the one where we demonstrated the Crossing Tool although generally you would use one method or the other but not both in the same nursery.

Open the study you created at the beginning of this tutorial (CGM21CB for me). To obtain a crossing template select Actions>Crossing options>Export crossing template:



The Crossing Template is an excel file with four sheets. The first sheet is the description sheet and you can fill in some metadata about the F1 list you wish to create, such as a list name <your initials>21F1t, a description “2021 F1 list from crossing template” and a date.

	A	B	C	D	E	F	G
1	**LIST NAME**	CGM21F1t		Enter a list name here, or add it when saving in the BMS			
2	**LIST DESCRIPTION**	2021 F1 list from crossing template		Enter a list description here, or add it when saving in the BMS			
3	**LIST DATE**	20210224		Accepted formats: YYYYMMDD or YYYYMM or YYYY or blank			
4							
5	**CONDITION**	**DESCRIPTION**	**PROPERTY**	**SCALE**	**METHOD**	**DATA TYPE**	**VALUE**
6	LIST USER	PERSON WHO MADE THE LIST	PERSON	DBCV	ASSIGNED	C	Christopher McLar
7	FEMALE STUDY	The name of the study of the female parent	STUDY	CODE	ASSIGNED	C	CGMCB21
8							
9	**FACTOR**	**DESCRIPTION**	**PROPERTY**	**SCALE**	**METHOD**	**DATA TYPE**	
10	FEMALE PLOT	Plot No of the Female in the Female Study	PLOT NUMBER	NUMBER	ENUMERATED	N	
11	MALE STUDY	The name of the study of the male parent	STUDY	CODE	ASSIGNED	C	
12	MALE PLOT	Plot No of the Male in the Male Study	PLOT NUMBER	NUMBER	ENUMERATED	N	
13							
14	**VARIATE**	**DESCRIPTION**	**PROPERTY**	**SCALE**	**METHOD**	**DATA TYPE**	
15	BREEDING METHOD	Breeding method applied to each cross event	BREEDING METHOD	BMETH_CODE	OBSERVED	C	
16	CROSSING DATE	Date that the cross was made (YYYYMMDD)	CROSS DATE	DATE	APPLIED	N	
17	NOTES	Technicians notes about the cross	COMMENT	TEXT	OBSERVED	C	

The second sheet is the observation sheet and this is where we will specify the crosses we make.

The third sheet is a Codes sheet where we can look up user names for the description metadata and breeding method codes for the observation sheet. The fourth sheet, Study List is just a fieldbook of the planted material showing you what germplasm was planted on what plot.

On the observation sheet, the important columns are the FEMALE PLOT and the MALE PLOT. These are the plot numbers in the field layout (shown on the Study list sheet) which are crossed. You can either fill these columns as you do the crosses when the plants are flowering, or before you do the crossing as a specification of the crosses you want to make. The column MALE STUDY allows you to specify another study in the field from where pollen was collected. In this case the MALE PLOT is the plot in that study from where the pollen came. IF MALE STUDY is blank it is assumed to be the same study as the FEMALE PLOT.

	A	B	C	D	E	F	G	H
1	**FEMALE PLOT**	**MALE STUDY**	**MALE PLOT**	**BREEDING METHOD**	**CROSSING DATE**	**NOTES**	**FEMALE**	**MALE**
2	1		2	C2W	20210213		IR 72768-12-1-1	IR 72768-28-1-1
3	1		3	C2W	20210213		IR 72768-12-1-1	IR 75502-24-1-1-B
4	1		4	C2W	20210213		IR 72768-12-1-1	IR 75516-30-1-1-B
5	2		5	C2W	20210213		IR 72768-28-1-1	IR 75516-56-1-1-B
6	2		6	C2W	20210213		IR 72768-28-1-1	IR 75518-84-1-1-B
7	2		7	C2W	20210213		IR 72768-28-1-1	IR 75531-31-1-2-B
8	3		8	C2W	20210213		IR 75502-24-1-1-B	IR 76561-AC 8-B
9	3		9	C2W	20210213		IR 75502-24-1-1-B	CNA 4196
10	3		10	C2W	20210213		IR 75502-24-1-1-B	IDSA 113
11								

You can fill in the BREEDING METHOD column with the code for the method of crossing you are doing which you look up in the Codes sheet. C2W is the code for a single cross:

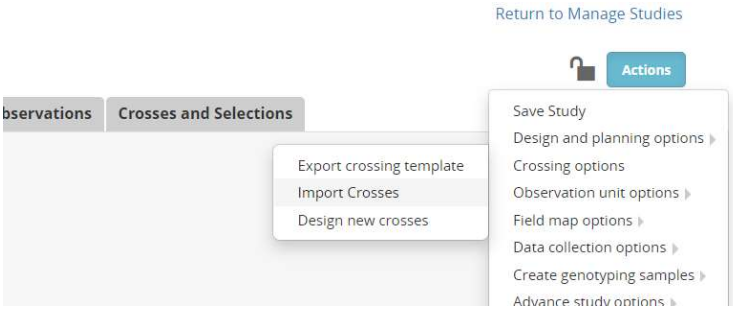
59	VARIATE	BREEDING METHOD	PBR	Recessive population backcross
60	VARIATE	BREEDING METHOD	CSP	Selected pollen cross
61	VARIATE	BREEDING METHOD	PSP	Selected pollen cross pop
62	VARIATE	BREEDING METHOD	C2W	Single cross
63	VARIATE	BREEDING METHOD	P2W	Single cross heterozygotes
64	VARIATE	BREEDING METHOD	SCL	Somoclone

You can leave this column blank if you like and it will be filled by BMS.

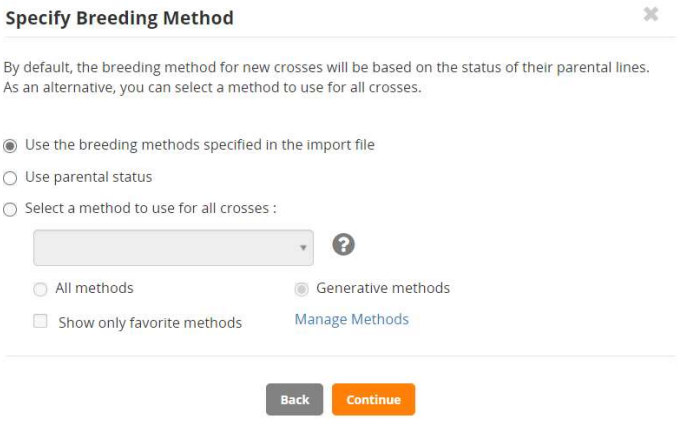
Finally a CROSSING DATE is required, and NOTES may be useful. The two columns Female and Male are not required, they do not come with the template, but have been added here to show what crosses the plot pairs are producing. The have been filled with the excel functions VLOOKUP. (Optional)

=VLOOKUP(A2,'Study List'!$B$2:$F$17,5,FALSE) for Female and =VLOOKUP(C2,'Study List'!$B$2:$F$17,5,FALSE) for Male. Of course, this will not work for the Male if the pollen came from another study.

Once the crossing template is complete (at the end of the crossing cycle) you can import the crosses by selecting Actions>Crossing options>Import crosses.



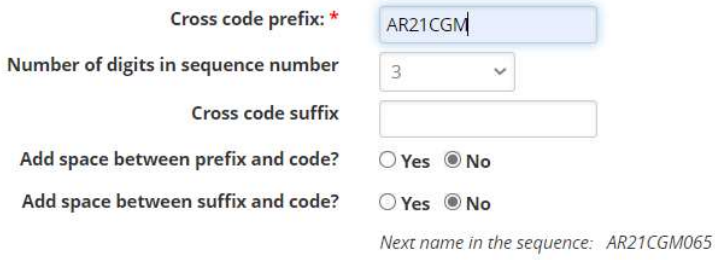
Choose the template file. If you have the Female and Male columns you get a warning that these will be ignored. And then you are asked to specify how the breeding method will be supplied.



You can use the method specified in the template (if you specified it as we have), or you can get BMS to chose the method based on parental status, or you can pick the method for a list.

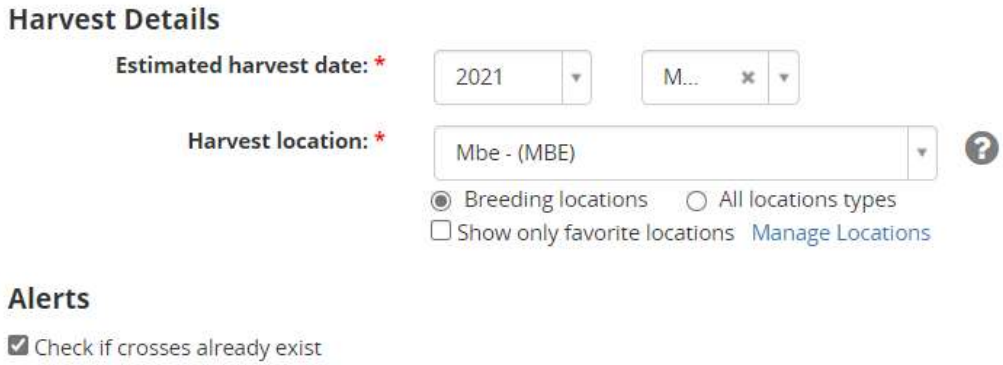
We continue with the default selection.

Now you need to specify a naming convention. We will check the **Specify name format** option. We will use the same format as we used in the last section: prefix AR20<your initials> with three digits for the sequence code:

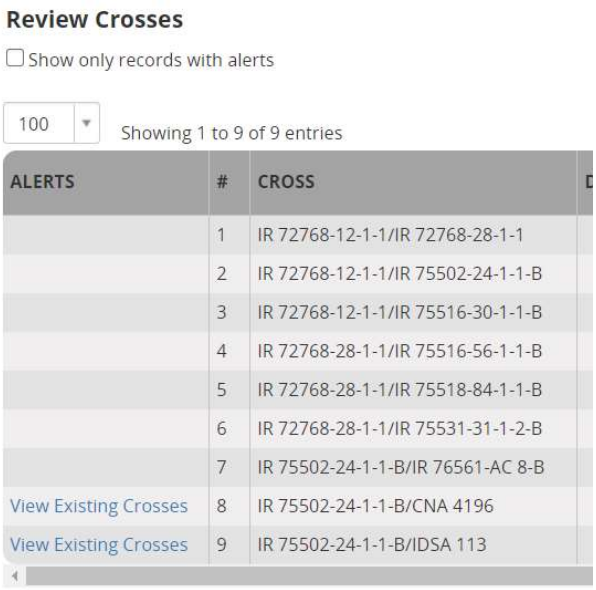


Notice that the next name in the sequence will be AR20CGM065 because we have already made 64 crosses with that naming pattern.

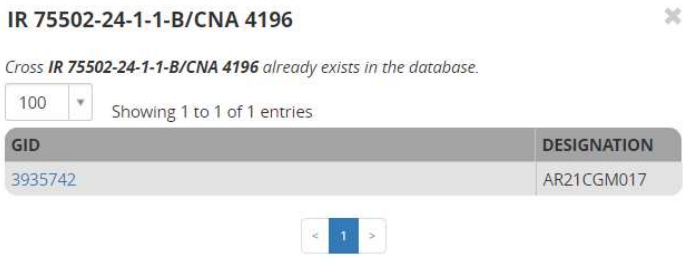
Specify the harvest month and the harvest location and check the box to be warned if the cross already exists (according to parental combination) in the database. Click continue



You will get a list of crosses to review:



You see in the ALERTS column that we are being warned that two of the crosses have been made before. If you click on View Existing Crosses you will see that those duplicates are crosses I made before (in the previous section):



At the moment, the option to remove those crosses would be to cancel and go back to the template and remove them there. I will just keep the duplicates for this exercise (but would only advance one family in the field). Click **Finish** and save the list.

You can also see the results in the Crosses and Selections tab where the 9 new crosses have been added to the previous crosses made.

Table 1: BMS Breeding Methods for Self Fertilizing Crops

METHN	MTYPE	MGRP	MCODE	MNAME	MDESC
Methods for storing historical pedigrees with incomplete information					
1	GEN	S	UGM	UNKNOWN GENERATIVE METHOD SF	Unknown generative method for storing historic pedigrees for self fertilizing species.
4	GEN	S	BDU	F1 BACKCROSS, CYTOPLASM UNKNOWN SF	Cross of F1to recurrent parent when the direction of the cross is unknown for storing historic pedigrees for self fertilizing species.
6	GEN	S	BRU	F2 BACKCROSS, CYTOPLASM UNKNOWN SF	Cross of F2 to recurrent parent when the direction of the cross is unknown for storing historic pedigrees for self fertilizing species.
8	GEN	G	CCU	CROSS, CYTOPLASM UNKNOWN	Cross between two plants, unknown which is female
31	DER	S	UDM	UNKNOWN DERIVATIVE METHOD SF	Unknown derivative method in self-fertilizing species: for storing historic pedigrees
Generic Maintenance Methods					
60	MAN	G	IDN	PLANT IDENTIFICATION	Identifying and naming a plant or population.
61	MAN	G	NSI	SEED INCREASE	Increase seed of a cultivar, line, population or accession.
62	MAN	G	ISE	IMPORT	Import seed, clones or tissue culture of a cultivar, line, population or accession.
63	MAN	G	ESE	EXPORT	Export seed, clones or tissue culture of a cultivar, line, population or accession. This method is not required.
64	MAN	G	SSN	STORE SEED NORMAL	Store seed of a cultivar, line, population or accession in normal method: drift not expected. It is unlikely that this method is needed.
65	MAN	G	SSM	STORE SEED MEDIUM TERM	Store seed of a cultivar, line, population or accession in medium term storage. Some genetic drift is expected. Storage is between 0-4^{O}C and low RH.
66	MAN	G	SSL	STORE SEED LONG TERM	Store seed of a cultivar, line, population or accession. Genetic drift is expected. Storage is about -18^{O}C.
Generative Methods for Inbreeding Crops					
101	GEN	S	C2W	SINGLE CROSS (may consider adding TEST CROSS, for hybrid rice breeding)	Cross between two single plants. If both parents are fixed (pure) inbred lines there will be no segregation for gametes or genotypes and theoretically all crosses will result in the same genetic outcome. In plant breeding practice the theoretical situation is rarely encountered. In spite of this the usual practice is to bulk the seed. However, in genetical studies it is often necessary to keep individual seed separate. When this is done a separate entry in the germplasm table is required for each entity (seed) kept separate.

102	GEN	S	C3W	THREE-WAY CROSS	Cross between two plants, one an inbred line and one a single cross (usually an F1) and thus segregating for gametes. In the theoretical case, rarely achieved, the inbred line would be fixed and the F1 a cross between fixed lines. The segregation for gametes results in different genetic outcomes among different progeny, hence a number of crosses using the same F1 is usually made. Since different F1 s are genetically the same (theoretically) only one F1 is required. In plant breeding programs the different crosses are usually bulked. Again, if individual seeds are kept separate a different entry is required in the germplasm table.
103	GEN	S	CDB	DOUBLE CROSS	Cross between two single crosses (usually two F1s) and hence both segregating for gametes. The comments for method 102 apply but now for both female and male sides of the cross. Again, if individual seeds are kept separate a different entry is required in the germplasm table.
104	GEN	S	CFT	FEMALE COMPLEX TOP CROSS	Cross between a female inbred line and a three-way or more complex cross among inbred lines, thus the male is segregating for genotypes as well as gametes. A consequence of the genotypic segregation is that selection can, and is usually made among the plants used as male parents. A consequence is that there will be genetic variation both within and between each cross. Usually all seed is bulked and selection practiced among the progeny. A different entry is required in the germplasm table for each entity kept separate.
105	GEN	S	CMT	MALE COMPLEX TOP CROSS	Cross between a male inbred line and a three-way or more complex cross among inbred lines, thus the female is segregating for genotypes as well as gametes. The same genetic consequences occur as for the previous complex cross except for the cytoplasm. This method is rarely if ever encountered in practice because of the difficulty of using many females. A different entry is required in the germplasm table for each entity kept separate.
106	GEN	S	CCX	COMPLEX CROSS	Cross between two three-way or more complex crosses among pure lines, thus both sides are segregating for both gametes and genotypes. A different entry is required in the germplasm table for each entity kept separate.
107	GEN	S	BC	BACKCROSS	Backcross to recover a specific gene. The coding in the genealogical table records which parent was used as the female in each cycle. A different entry is required in the germplasm table for each entity kept separate.
108	GEN	S	BCR	BACKCROSS RECESSIVE	Backcross to recover a recessive gene. As this requires a self fertilization (derivative method) in the process some ICIS administrators may distinguish this as a separate method. A different entry is required in the germplasm table for each entity kept separate.
109	GEN	S	CIS	INTERSPECIFIC CROSS	Cross between two species. The problem with making this a separate method is that the species cross could be made by any of the previous (101-108) or following (110-113) methods.
110	GEN	S	CSP	SELECTED POLLEN CROSS SF	A bulk of pollen from a selected set of males used to pollinate a female inbred line.
111	GEN	S	CRP	RANDOM POLLEN CROSS SF	A random bulk of pollen from some population used to pollinate a female pure line. Male is then a population and will be recorded as a single entity.
112	GEN	S	CGO	OPEN POLLENATED SF	Open pollination in a self- fertilized species
151	GEN	S	MUN	NATURAL VARIANT SF	A recognized naturally occurring variant in a self- fertilizing population.
152	GEN	S	MIP	INDUCED MUTATION POPULATION SF	A population derived from inducing mutation in a inbred line.
153	GEN	S	SCL	SOM**A**CLONE SF	Variation induced through tissue culture of a inbred line.

154	GEN	S	ALP	ALLOPOLYPLOID SF	Polyploid formed by doubling the chromosomes of a cross between two or more species. Wheat is an allopolyploid as it contains genomes from three different species.
155	GEN	S	AUP	AUTOPOLYPLOID SF	Polyploid formed by doubling the chromosome number of a species. Lucerne (alfalfa) is an autopolyploid with 4 sets of the same genome.
156	GEN	S	HAP	HAPLOID SF	Individual with chromosome content of reduced gamete. Often formed by female progenitors crossed with a haploid inducer.
157	GEN	S	TRN	TRANSGENIC NUCLEUS SF	Individual derived from genetic transformation of the nucleus in a self fertilizing species.
158	GEN	S	TRC	TRANSGENIC CYTOPLASM SF	Individual derived from genetic transformation of a cytoplasm inclusion (e.g. chloroplast) in a self- fertilizing species.
Derivative Methods for Inbreeding Crops					
201	DER	S	MIL	INDUCED MUTATION LINE	A recognized mutation selected from an induced mutation in a line of a self-fertilized species.
202	DER	S	DDH	DOUBLE HAPLOID LINE	Individual produced by doubling haploid individual usually by anther culture in a self- fertilized crop.
203	DER	S	DPR	PURIFICATION	Selection of one or a few plants from an inbred line or pure line cultivar.
204	DER	S	DRU	ROUGING SF	Eliminating off types from a inbred line or pure line cultivar.
205	DER	S	DSP	SINGLE PLANT SELECTION SF	Derivation through selection of a single plant, inflorescence, fruit or seed from a self-fertilizing population.
206	DER	S	DSB	SELECTED BULK SF	Derivation through bulking seed from a selected set of single plants from a self-fertilizing population.
207	DER	S	DRB	RANDOM BULK SF	Derivation through bulking seed from a random selection of single plants from a self-fertilizing population.
208	DER	S	DSD	SINGLE SEED DESCENT SF	Derived through the production of a single individual without selection from each individual in a segregating population.
209	DER	S	DRS	CMS RESTORER SELECTION	Restorer Lines selected at the end of a program to back cross a gene which restores male fertility to lines carrying a Male Sterile Cytoplasm (CMS) to the male of a commercial hybrid.
210	DER	S	DMS	CMS MAINTAIN ER SELECTION	Maintainer line selected at the end of a program to create the male fertile equivalent of the CMS female parent of a hybrid
251	DER	S	ALP	LANDRACE POPULATION SF	Acquisition only. A Landrace Accession of a self-fertilized species. This population will consist of a heterogenous mixture of homogenous genotypes. This and the following eight methods should be reserved for the acquisition of these types of population to any program when they are first collected. When they are transferred from one collection (germplasm bank, working collection or plant improvement program) to another they should be entered under the IMPORT method.
252	DER	S	ALL	LANDRACE LINE SF	Acquisition only. When the accession derives from a single plant in the Landrace Population.
253	DER	S	ALC	LANDRACE CULTIVAR SF	Acquisition only. A Landrace Cultivar Accession of a self-fertilized species. Accession of a long term cultivar, not bred or maintained by modern breeding methods. This would usually be less heterogenous than a traditional landrace.

254	DER	S	ACP	COLLECTION POPULATION SF	Acquisition only. An accession of a population of a cultivated self -fertilizing species not from farmer's fields.
255	DER	S	ACL	COLLECTION LINE SF	Acquisition only. When the accession derives from a single plant in a Collection Population.
256	DER	S	AWP	COLLECTION WILD SPP POPULATION SF	Acquisition only. An accession of a self-fertilizing species.
257	DER	S	AWL	COLLECTION WILD SPP LINE SF	Acquisition only. When the accession derives from a single plant from a wild collection.
258	DER	S	ADP	COLLECTION WEEDY SPP POPULATION SF	Acquisition only. An accession of a self-fertilizing species which is a weed (because of the result of a hybrid between the cultivated and a wild species of the crop).
259	DER	S	ADL	COLLECTION WEEDY SPP LINE SF	Acquisition only. When the accession derives from a single plant in a collection of weedy species.
Management Methods for Inbreeding Crops					
301	MAN	S	NSP	SEED INCREASE PLANT SF	Seed increase from a single plant in a self-fertilized species.
302	MAN	S	NMX	SEED INCREASE MIXTURE SF	Seed increase from a number of selected plants in a self- fertilized species.
303	MAN	S	NBK	SEED INCREASE BULK SF	Seed increase from an unselected bulk in a self-fertilizing species.
320	MAN	S	VPL	PURE LINE FORMATION	Forming a pure line CV in a self-fertilizing species.
321	MAN	S	VHY	HYBRID FORMATION SF	Forming a hybrid CV in a self-fertilizing crop.
322	MAN	S	VML	MULTI-LINE FORMATION SF	Forming a multi-line CV in a self-fertilizing crop
323	MAN	S	VBS	BREEDERS SEED SF	Producing Breeder's Seed. Pure seed produced by breeder (usually some kept by breeder) in a self-fertilizing crop.
324	MAN	S	VFS	FOUNDATION SEED SF	Producing Foundation Seed. Pure seed derived from Breeders seed (usually kept by seed producing organization) in a self-fertilizing crop.
325	MAN	S	VCS	CERTIFIED SEED	Producing Certified Seed. Pure seed produced under supervision by Government Protocols.
326	MAN	S	VCR	CULTIVAR RELEASE	Release a cultivar

Adding Seed Inventory for a Harvest List

Whenever crosses or advances are made in nurseries and often when trials are harvested, seed from the harvest must be weighed, bagged and labelled and kept in a store for some time. The BMS has features to facilitate this inventory management.

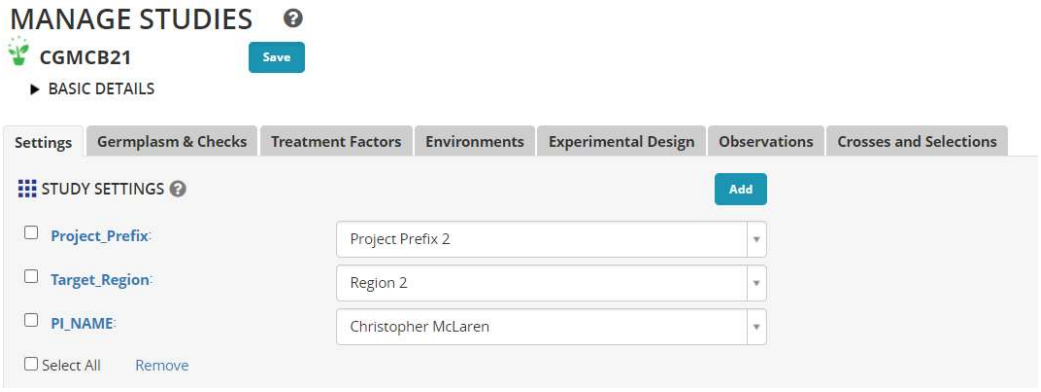
Objectives

At the end of this tutorial, the user should be able to:

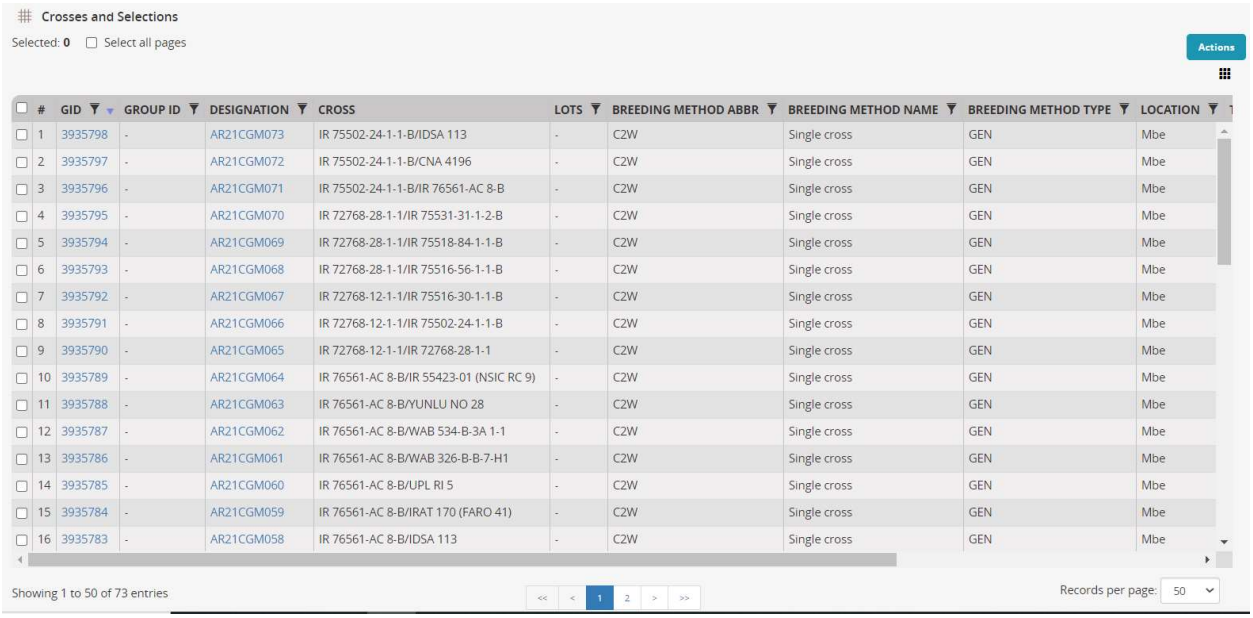
1. Use the Study Manager to create pending seed deposits for any harvest list
2. Produce labels for the seed packets for the harvest
3. Update the inventory system with the amount of seed stored for each entry

Create pending seed deposits for a harvest list

In the study manager, open the crossing block created in the previous tutorial, CGMCB21 in my case:

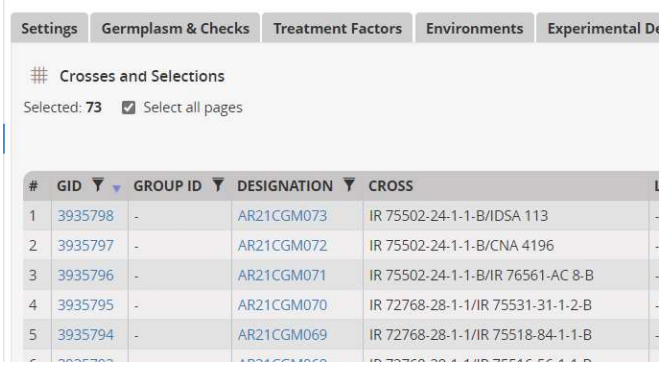


Open the Crosses and Selections tab



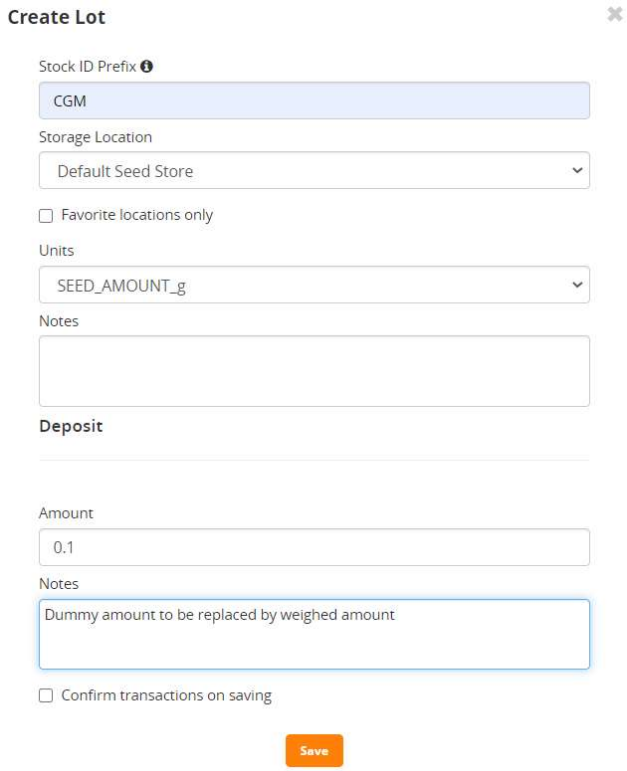
#	GID	GROUP ID	DESIGNATION	CROSS	LOTS	BREEDING METHOD ABBR	BREEDING METHOD NAME	BREEDING METHOD TYPE	LOCATION
1	3935798	-	AR21CGM073	IR 75502-24-1-1-B/IDSA 113	-	C2W	Single cross	GEN	Mbe
2	3935797	-	AR21CGM072	IR 75502-24-1-1-B/CNA 4196	-	C2W	Single cross	GEN	Mbe
3	3935796	-	AR21CGM071	IR 75502-24-1-1-B/IR 76561-AC 8-B	-	C2W	Single cross	GEN	Mbe
4	3935795	-	AR21CGM070	IR 72768-28-1-1/IR 75531-31-1-2-B	-	C2W	Single cross	GEN	Mbe
5	3935794	-	AR21CGM069	IR 72768-28-1-1/IR 75518-84-1-1-B	-	C2W	Single cross	GEN	Mbe
6	3935793	-	AR21CGM068	IR 72768-28-1-1/IR 75516-56-1-1-B	-	C2W	Single cross	GEN	Mbe
7	3935792	-	AR21CGM067	IR 72768-12-1-1/IR 75516-30-1-1-B	-	C2W	Single cross	GEN	Mbe
8	3935791	-	AR21CGM066	IR 72768-12-1-1/IR 75502-24-1-1-B	-	C2W	Single cross	GEN	Mbe
9	3935790	-	AR21CGM065	IR 72768-12-1-1/IR 72768-28-1-1	-	C2W	Single cross	GEN	Mbe
10	3935789	-	AR21CGM064	IR 76561-AC 8-B/IR 55423-01 (NSIC RC 9)	-	C2W	Single cross	GEN	Mbe
11	3935788	-	AR21CGM063	IR 76561-AC 8-B/YUNLU NO 28	-	C2W	Single cross	GEN	Mbe
12	3935787	-	AR21CGM062	IR 76561-AC 8-B/WAB 534-B-3A 1-1	-	C2W	Single cross	GEN	Mbe
13	3935786	-	AR21CGM061	IR 76561-AC 8-B/WAB 326-B-B-7-H1	-	C2W	Single cross	GEN	Mbe
14	3935785	-	AR21CGM060	IR 76561-AC 8-B/UPL RI 5	-	C2W	Single cross	GEN	Mbe
15	3935784	-	AR21CGM059	IR 76561-AC 8-B/IRAT 170 (FARO 41)	-	C2W	Single cross	GEN	Mbe
16	3935783	-	AR21CGM058	IR 76561-AC 8-B/IDSA 113	-	C2W	Single cross	GEN	Mbe

Now we must select the crosses or selections from the Crosses and Selections tab for which we want to save inventory. Since our tab has several pages and we want to add inventory for all the crosses we can just click the select all pages box at the top left of the tab.



On the **Actions** menu of the Crosses and Selections tab click **Creaet lots**.

On the create lots form enter a stock ID prefix which indicates the 'owner' of the seeds, or the 'project' to which they belong, or even 'the storage box' where they will be stored. I specify my initails 'CGM' which indicates 'ownership' and also which section fo the seed store they will be kept in.

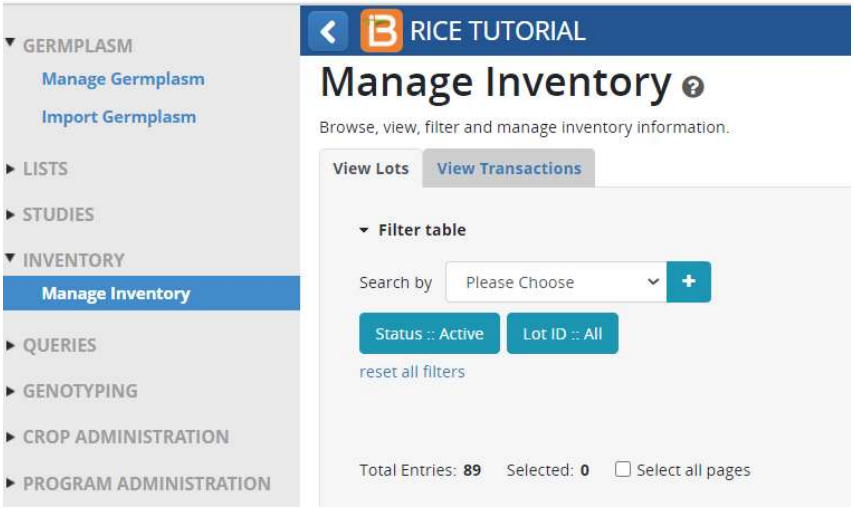


Specify the storage location (which can be a detailed customized list of shelves or boxes or just a room), indicate the units for recording the inventory and then specify a dummy deposit of 0.1g so we can have a pending transaction awaiting the true value when the seeds are weighed.

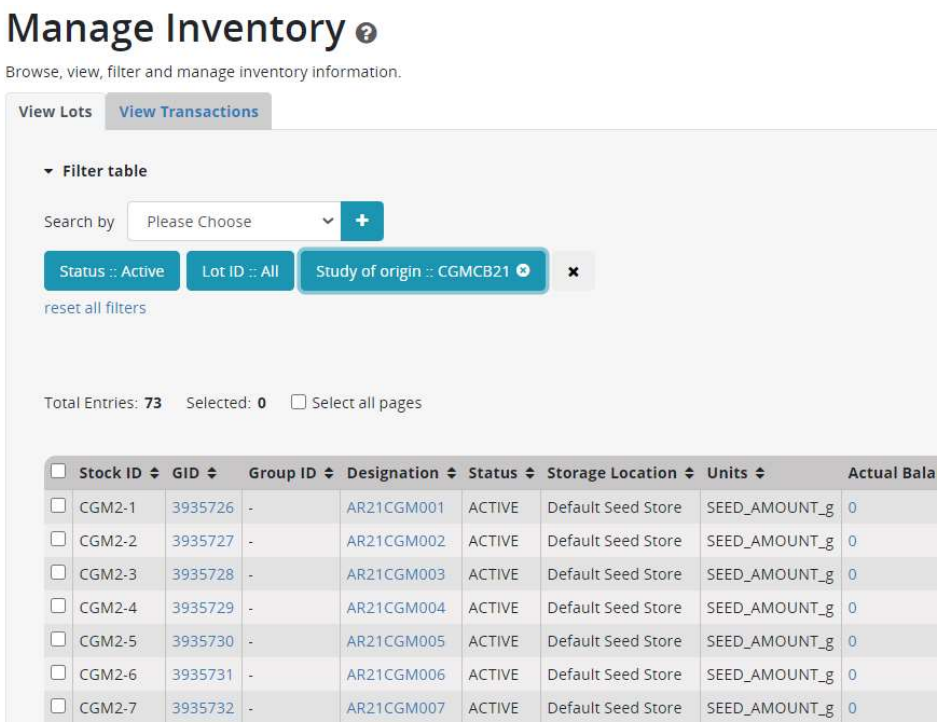
Click save, and then leave the Create lots form by clicking the X and the top right of the form.

Make labels for the seed packets from a harvest list

The user must use the Manage Inventory item from the INVENTORY menu. Note the user must have a Crop role to be able to access the Inventory Module, otherwise it will not be visible.



In the Search by box on the View Lots tab, select 'Study of origin' and click the + symbol. Then crick on the new filter item and select the study where the harvests were made CGM21CB in my case. This filters the lots down to the 73 for the harvest list we are working with:



Stock ID	GID	Group ID	Designation	Status	Storage Location	Units	Actual Bala
CGM2-1	3935726	-	AR21CGM001	ACTIVE	Default Seed Store	SEED_AMOUNT_g	0
CGM2-2	3935727	-	AR21CGM002	ACTIVE	Default Seed Store	SEED_AMOUNT_g	0
CGM2-3	3935728	-	AR21CGM003	ACTIVE	Default Seed Store	SEED_AMOUNT_g	0
CGM2-4	3935729	-	AR21CGM004	ACTIVE	Default Seed Store	SEED_AMOUNT_g	0
CGM2-5	3935730	-	AR21CGM005	ACTIVE	Default Seed Store	SEED_AMOUNT_g	0
CGM2-6	3935731	-	AR21CGM006	ACTIVE	Default Seed Store	SEED_AMOUNT_g	0
CGM2-7	3935732	-	AR21CGM007	ACTIVE	Default Seed Store	SEED_AMOUNT_g	0

From Actions, select **Export data and labels**. From **Output format** select **Formatted PDF label sheets**. Other options are excel file or csv file which can be used with a printing program such as Microsoft Word – Mail Merge to print labels with any desired format.

Select the following fields for the label by dragging the items from the list on the left to the position in the label. Also choose to have an auto generated barcode for each lot:

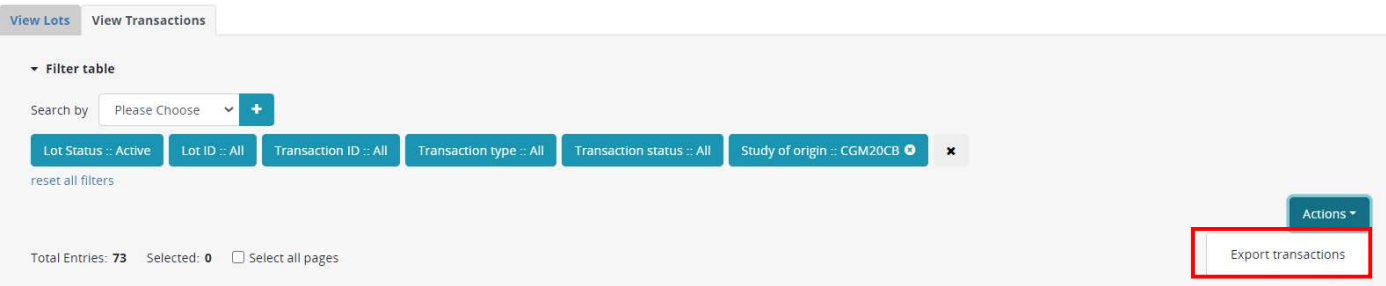
You can save the the settings for future harvest labels and you can print the labels for the present batch by clicking **Export**:

Exit the label printing form by clicking **Cancel**.

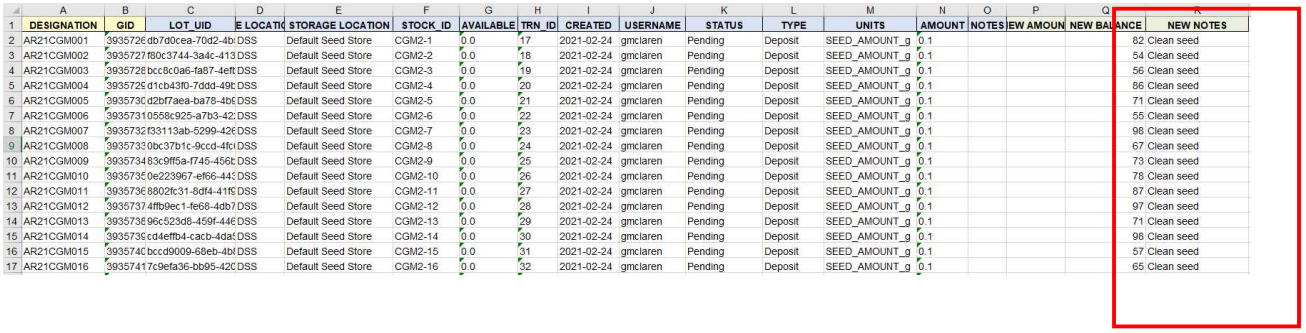
Update pending transactions with weights and package and label seeds

On the Transactions Tab of the Inventory Manager, filter to the transactions for the study of origin – CGM21CB for me, to see the 73 pending transactions.

From **Actions** click **Export transactions** to get a file of transactions to be updated.

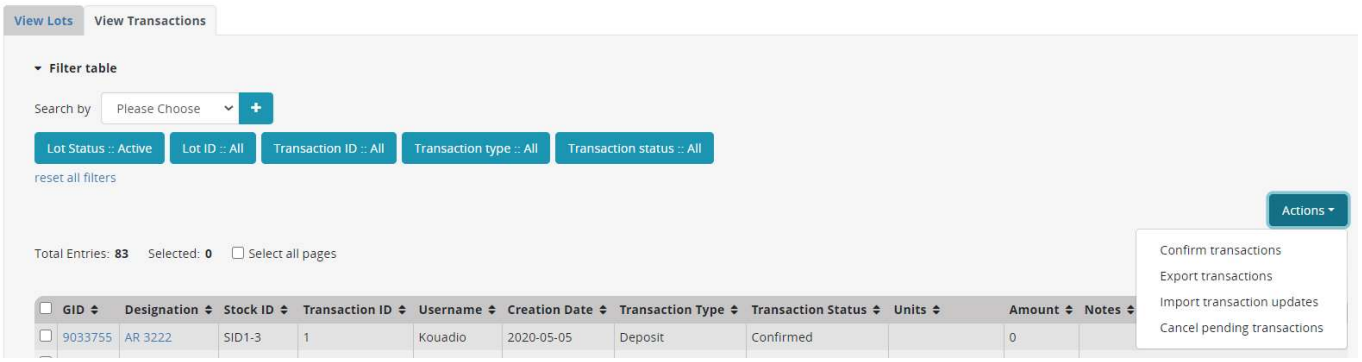


Fill in the NEW BALANCE column with the actual weights and specify a new note to replace the original note:



	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
1	DESIGNATION	GID	LOT_UID	E LOCATIO	STORAGE LOCATION	STOCK_ID	AVAILABLE	TRN_ID	CREATED	USERNAME	STATUS	TYPE	UNITS	AMOUNT	NOTES	EW AMOUN	NEW BALANCE	NEW NOTES
2	AR21CGM001	3935726	db7d0cea-70d2-4b	DSS	Default Seed Store	CGM2-1	0.0	17	2021-02-24	gmclaren	Pending	Deposit	SEED_AMOUNT_g	0.1			82	Clean seed
3	AR21CGM002	3935727	f80c3744-3a4c-413	DSS	Default Seed Store	CGM2-2	0.0	18	2021-02-24	gmclaren	Pending	Deposit	SEED_AMOUNT_g	0.1			54	Clean seed
4	AR21CGM003	3935728	bcc8c0a6-fa87-4ef	DSS	Default Seed Store	CGM2-3	0.0	19	2021-02-24	gmclaren	Pending	Deposit	SEED_AMOUNT_g	0.1			56	Clean seed
5	AR21CGM004	3935729	d1cb43f0-7ddd-49	DSS	Default Seed Store	CGM2-4	0.0	20	2021-02-24	gmclaren	Pending	Deposit	SEED_AMOUNT_g	0.1			86	Clean seed
6	AR21CGM005	3935730	d2bf7aea-ba78-4b	DSS	Default Seed Store	CGM2-5	0.0	21	2021-02-24	gmclaren	Pending	Deposit	SEED_AMOUNT_g	0.1			71	Clean seed
7	AR21CGM006	3935731	0558c925-a7b3-42	DSS	Default Seed Store	CGM2-6	0.0	22	2021-02-24	gmclaren	Pending	Deposit	SEED_AMOUNT_g	0.1			55	Clean seed
8	AR21CGM007	3935732	f33113ab-5299-42	DSS	Default Seed Store	CGM2-7	0.0	23	2021-02-24	gmclaren	Pending	Deposit	SEED_AMOUNT_g	0.1			98	Clean seed
9	AR21CGM008	3935733	0bc37b1c-9ccd-4f	DSS	Default Seed Store	CGM2-8	0.0	24	2021-02-24	gmclaren	Pending	Deposit	SEED_AMOUNT_g	0.1			67	Clean seed
10	AR21CGM009	3935734	83c9ff5a-f745-456	DSS	Default Seed Store	CGM2-9	0.0	25	2021-02-24	gmclaren	Pending	Deposit	SEED_AMOUNT_g	0.1			73	Clean seed
11	AR21CGM010	3935735	0e223967-ef66-44	DSS	Default Seed Store	CGM2-10	0.0	26	2021-02-24	gmclaren	Pending	Deposit	SEED_AMOUNT_g	0.1			78	Clean seed
12	AR21CGM011	3935736	8802fc31-8df4-41f	DSS	Default Seed Store	CGM2-11	0.0	27	2021-02-24	gmclaren	Pending	Deposit	SEED_AMOUNT_g	0.1			87	Clean seed
13	AR21CGM012	3935737	4ffb9ec1-fe68-4db7	DSS	Default Seed Store	CGM2-12	0.0	28	2021-02-24	gmclaren	Pending	Deposit	SEED_AMOUNT_g	0.1			97	Clean seed
14	AR21CGM013	3935738	96c523d8-459f-44	DSS	Default Seed Store	CGM2-13	0.0	29	2021-02-24	gmclaren	Pending	Deposit	SEED_AMOUNT_g	0.1			71	Clean seed
15	AR21CGM014	3935739	cd4effb4-cacb-4da	DSS	Default Seed Store	CGM2-14	0.0	30	2021-02-24	gmclaren	Pending	Deposit	SEED_AMOUNT_g	0.1			98	Clean seed
16	AR21CGM015	3935740	bccd9009-68eb-4b	DSS	Default Seed Store	CGM2-15	0.0	31	2021-02-24	gmclaren	Pending	Deposit	SEED_AMOUNT_g	0.1			57	Clean seed
17	AR21CGM016	3935741	7c9efa36-bb95-42	DSS	Default Seed Store	CGM2-16	0.0	32	2021-02-24	gmclaren	Pending	Deposit	SEED_AMOUNT_g	0.1			65	Clean seed

Now we need to import the transaction updates, but this action is not available unless the user has a Crop role. If I log out and log in with a crop manager account and then go to Manage Inventory on the transactions tab I can see more options and select **Import Transaction Updates:**



Navigate to the completed transactions update template and import the transactiosn:

GID	Designation	Stock ID	Transaction ID	Username	Creation Date	Transaction Type	Transaction Status	Units	Amount	Notes
3935726	AR21CGM001	CGM2-1	17	gmclaren	2021-02-24	Deposit	Confirmed	SEED_AMOUNT_g	82	Clean seed
3935727	AR21CGM002	CGM2-2	18	gmclaren	2021-02-24	Deposit	Confirmed	SEED_AMOUNT_g	54	Clean seed
3935728	AR21CGM003	CGM2-3	19	gmclaren	2021-02-24	Deposit	Confirmed	SEED_AMOUNT_g	56	Clean seed
3935729	AR21CGM004	CGM2-4	20	gmclaren	2021-02-24	Deposit	Confirmed	SEED_AMOUNT_g	86	Clean seed
3935730	AR21CGM005	CGM2-5	21	gmclaren	2021-02-24	Deposit	Confirmed	SEED_AMOUNT_g	71	Clean seed
3935731	AR21CGM006	CGM2-6	22	gmclaren	2021-02-24	Deposit	Confirmed	SEED_AMOUNT_g	55	Clean seed
3935732	AR21CGM007	CGM2-7	23	gmclaren	2021-02-24	Deposit	Confirmed	SEED_AMOUNT_g	98	Clean seed
3935733	AR21CGM008	CGM2-8	24	gmclaren	2021-02-24	Deposit	Confirmed	SEED_AMOUNT_g	67	Clean seed
3935734	AR21CGM009	CGM2-9	25	gmclaren	2021-02-24	Deposit	Confirmed	SEED_AMOUNT_g	73	Clean seed
3935735	AR21CGM010	CGM2-10	26	gmclaren	2021-02-24	Deposit	Confirmed	SEED_AMOUNT_g	78	Clean seed

You now have the correct amount of seed inventory showing in the transaction table.

Managing Pedigree Nurseries

Pedigree nurseries are managed through a series of nurseries facilitated through the Study Manager.

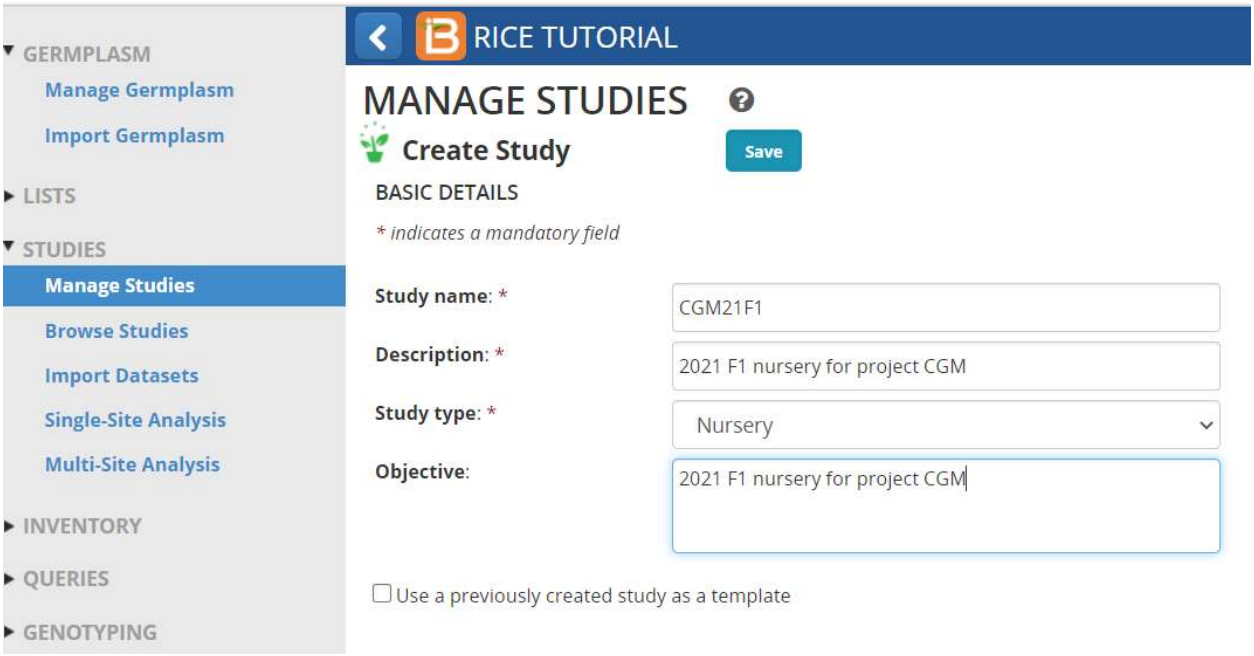
Objectives

At the end of this tutorial, the user should be able to:

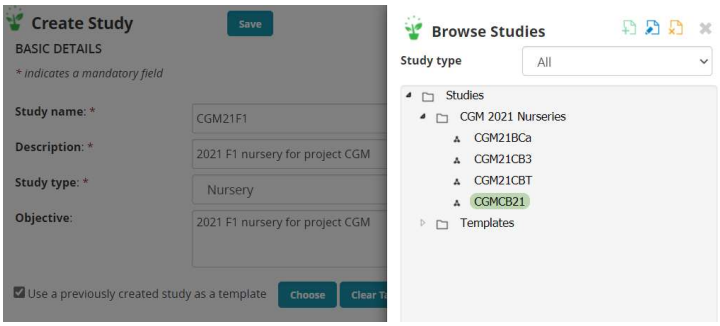
1. Create a nursery study for population development
2. Advance a pedigree nurseries by derivative methods
3. Withdraw seed from inventory and prepare planting labels

Create an F1 Nursery

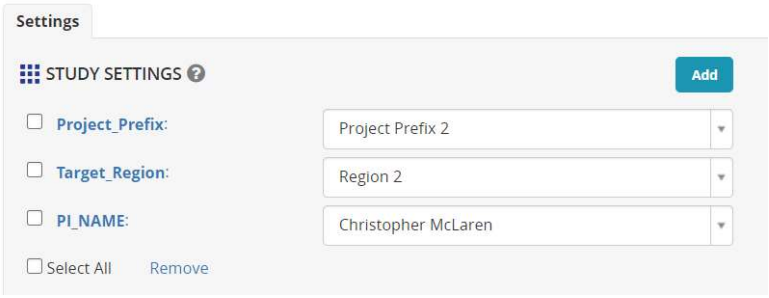
Open the Manage Studies application from the main menu and click on **Start a new study**. Name the nursery <your initials>21F1, CGM21F1 for me, and fill in the basic details of description and objective and select the study type **Nursery**.



You can add variables to the new study directly from the Ontology pick lists as we did for the crossing block in a previous Tutorial, or you can pick up all the variables from any previously used study. To use this option check the **Use a previously created study as a template** check box. Then choose the previous study which is smilar to your current study:



The variables from the template study are imported into the new study. Change the settings if needed.



Save the study in your 2021 Nursery folder.

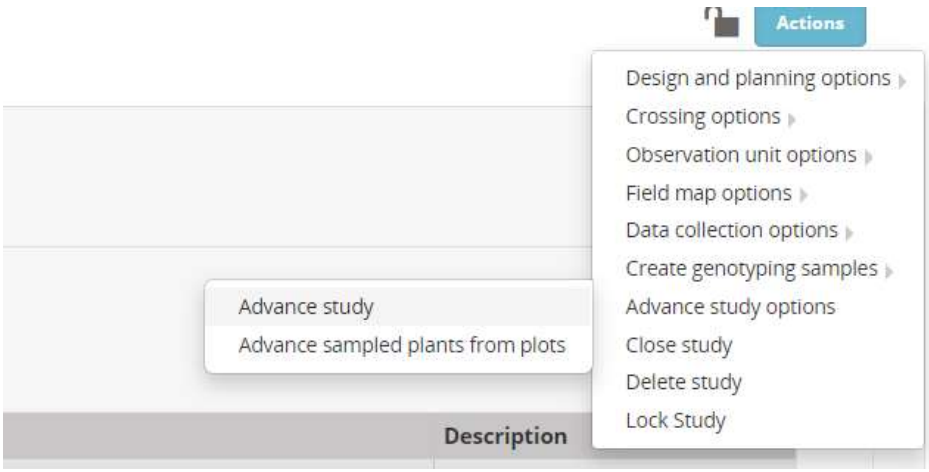
On the Germplasm and Checks tab, the extra variables for Cross and Seed source are also recovered from the template, so you just need to Browse for the list of planting material. The F1 list you made in the crossing Tutorial. **U21CGMF1** in my case.

Mbe has been inherited from the template, and this location is still correct, but a new seeding date should be entered if known.

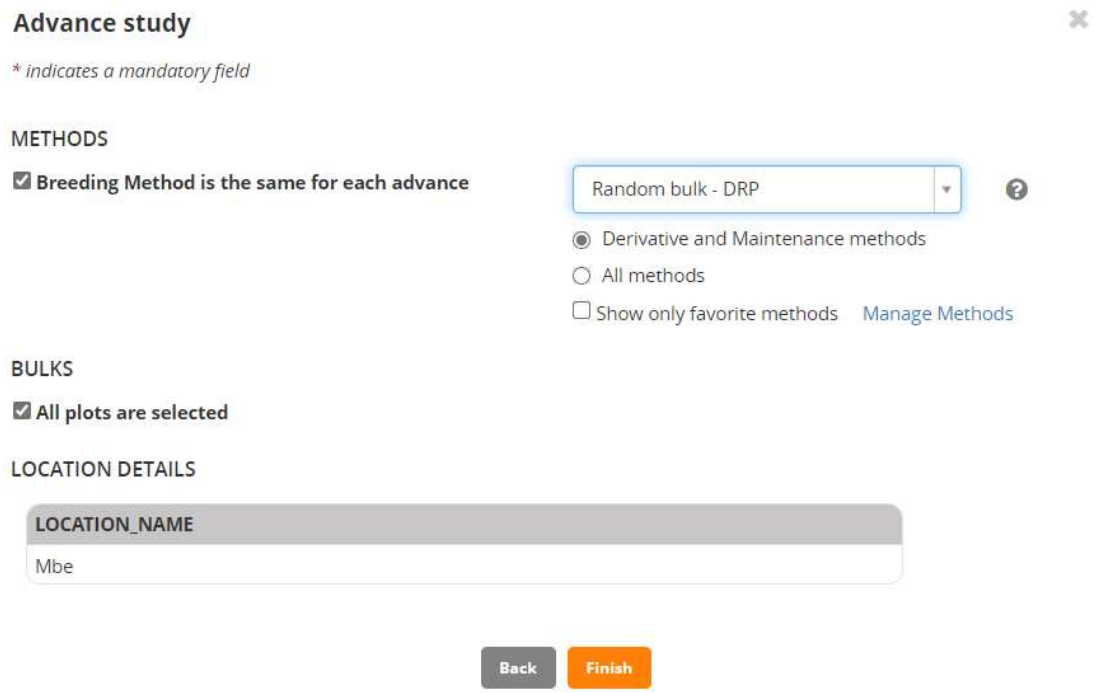
On the Experimental Design tab select **Entry list order** and **Generate** the design.

Advance the F1 Nursery by bulk selection of all families

Once the nursery is planted and harvested we can advance the families to F2 seed by bulking seed from each F1 cross family. Select **Actions>Advance study options>Advance study**:



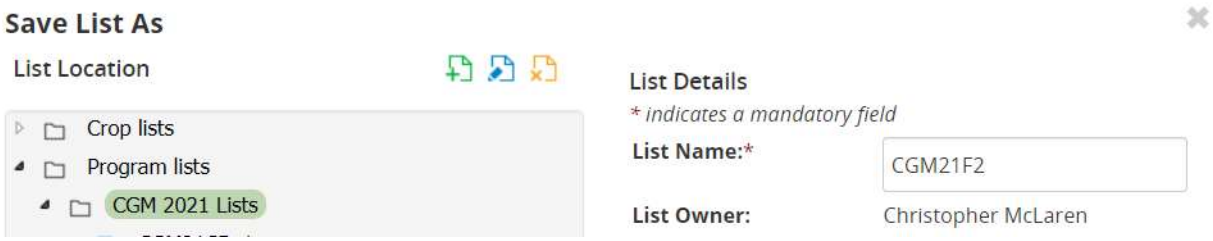
Choose the location to advance (we only have one), then select the advance method for all plots – Random Bulk - DRP. We will advance all plots so leave the **All plots are selected** checkbox ticked.



Click **Finish.**

Review the list of advanced lines, and if it looks correct, click **Finish** again.

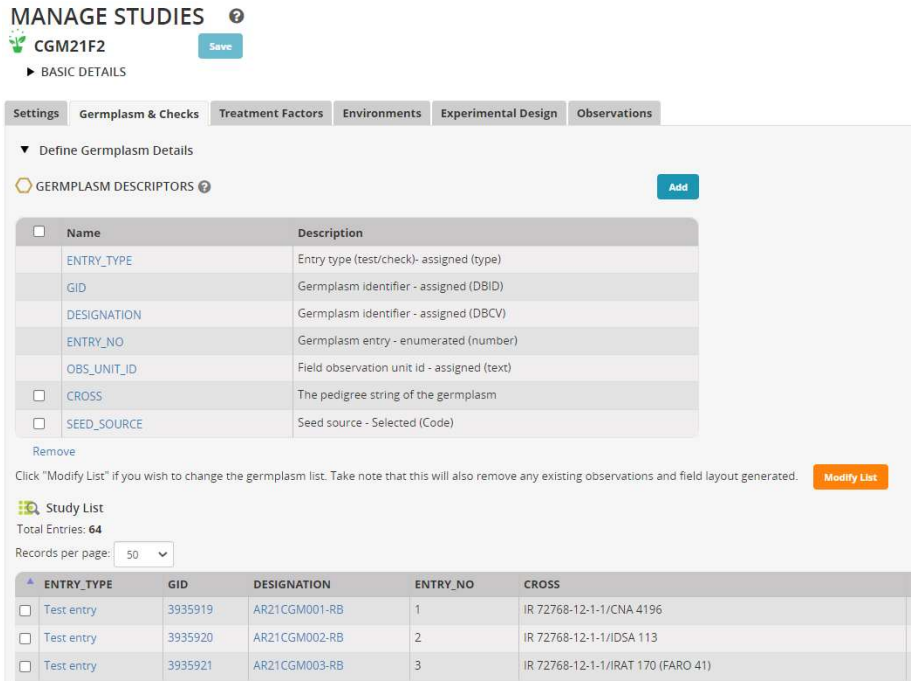
Save the list with name <your initials>21F2 in your 2021 lists folder.



You can follow the steps in the tutorial **Adding Inventory for a Harvest List** to add inventory for the F2 seeds if you would like.

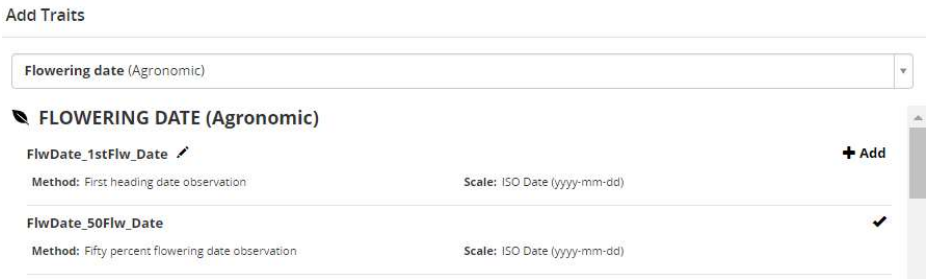
Create F2 nursery and load some data from a fieldbook

Follow the steps to create a new nursery for the F2 seeds. Use the F1 nursery as a template for planting at Mbe in Entry list order. (You can review the steps in the first section above).



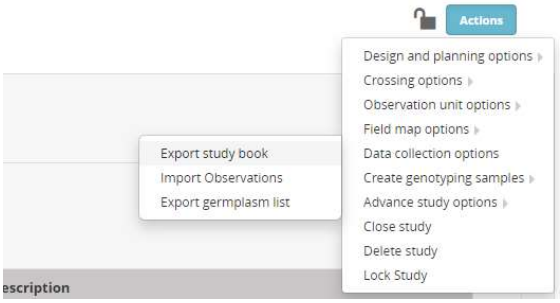
In this nursery we will need to add a variable to record the number of plants selected from each F2 population.

If flowering date is not a column in the Observation sheet, clcik Add opposite Traits and search for flowering and add **FlwDate_50Flw_Date** as a ttrait.



Click the Add button opposite SELECTIONS on the **Observation** tab and look for the variable NPSEL to add to the fieldbook.

Now we can export the fieldbook for data collection. Select **Actions>Data collection options>Export study book**:



Choose Observations and then choose Excel Format.

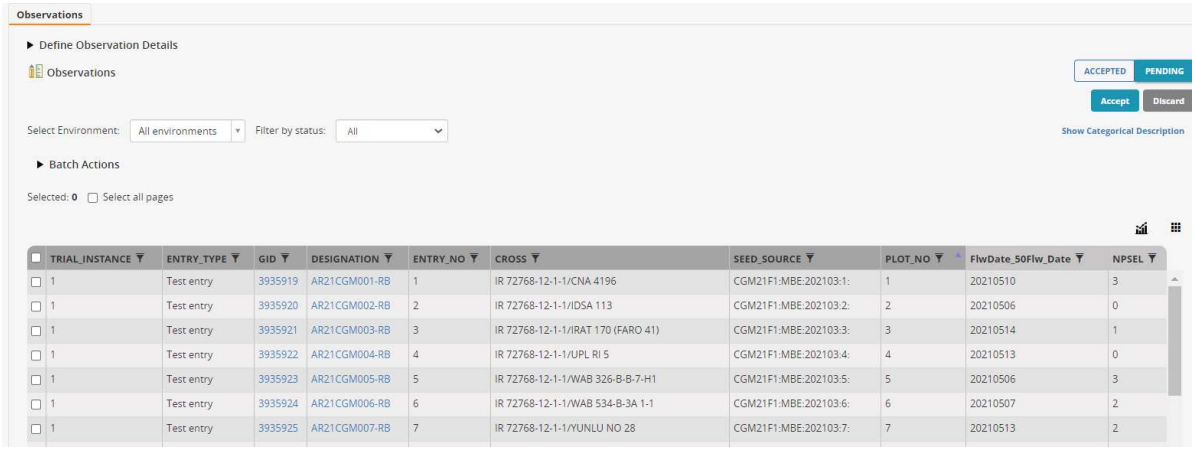
You will download an excel fieldbook with a description sheet:

	A	B	C	D	E	F	G	H	I
1	STUDY	CGM21F2							
2	TITLE	2021 F2 Nursery for project CGM							
3	OBJECTIVE	2021 F2 Nursery for project CGM							
4	START DATE	20210305							
5	END DATE								
6	STUDY TYPE	Nursery							
7									
8	STUDY DETAILS	DESCRIPTION	ONTOLOGY ID	PROPERTY	SCALE	METHOD	DATA TYPE	VALUE	DATASET
9	Project_Prefix	Project Prefix BCID Variable		Breeding Project	Project_Prefix_Scale	Assigned	C	PB	STUDY
10	Target_Region	Target Region Variable		Target Region	Target_Region_Scale	Assigned	C	R2	STUDY
11	PI_NAME_ID	Principal investigator - assigned (DBID)		Person	Person id	Assigned	C	1002	STUDY
12	PI_NAME	Principal investigator - assigned (DBCV)		Person	Person name	Assigned	C	Christopher McLaren	STUDY
13									
14	EXPERIMENTAL DESI	DESCRIPTION	ONTOLOGY ID	PROPERTY	SCALE	METHOD	DATA TYPE	VALUE	DATASET
15	PLOT_NO	Field plot - enumerated (number)		Field plot	Number	Enumerated	N		PLOT
16									
17	ENVIRONMENT DETAI	DESCRIPTION	ONTOLOGY ID	PROPERTY	SCALE	METHOD	DATA TYPE	VALUE	DATASET
18	TRIAL_INSTANCE	Trial instance - enumerated (number)		Trial instance	Number	Enumerated	N	1	ENVIRONMENT
19	LOCATION_ID	Location - selected (DBID)		Location	Location id	Assigned	C	29102	ENVIRONMENT
20	LOCATION_NAME	Location - selected (DBCV)		Location	Location name	Assigned	C	Mbe	ENVIRONMENT
21	EXPT_DESIGN	Experimentaldesign - assigned (type)		Experimental design	Type of EXPT_DESIG	Assigned	C	ELO	ENVIRONMENT
22									
23	ENVIRONMENTAL CO	DESCRIPTION	ONTOLOGY ID	PROPERTY	SCALE	METHOD	DATA TYPE	VALUE	DATASET
24									
25	GERMPLASM DESCR	DESCRIPTION	ONTOLOGY ID	PROPERTY	SCALE	METHOD	DATA TYPE	VALUE	DATASET
26	ENTRY_TYPE	Entry type (test/check)- assigned (type)		Entry type	Type of ENTRY_TYP	Assigned	C		PLOT
27	GID	Germplasm identifier - assigned (DBID)		Germplasm id	Germplasm id	Assigned	C		PLOT
28	DESIGNATION	Germplasm identifier - assigned (DBCV)		Germplasm id	Germplasm name	Assigned	C		PLOT
29	ENTRY_NO	Germplasm entry - enumerated (number)		Germplasm entry	Number	Enumerated	N		PLOT
30	OBS_UNIT_ID	Field observation unit id - assigned (text)		Field plot	Text	Assigned	T		PLOT
31	CROSS	The pedigree string of the germplasm		Cross history	Text	Assigned	T		PLOT
32	SEED_SOURCE	Seed source - Selected (Code)		Seed source	Code of SEED_SOU	Selected	T		PLOT
33									
34	OBSERVATION UNIT	DESCRIPTION	ONTOLOGY ID	PROPERTY	SCALE	METHOD	DATA TYPE	VALUE	DATASET
35									
36	TRAITS	DESCRIPTION	ONTOLOGY ID	PROPERTY	SCALE	METHOD	DATA TYPE	VALUE	DATASET
37									
38	SELECTIONS	DESCRIPTION	ONTOLOGY ID	PROPERTY	SCALE	METHOD	DATA TYPE	VALUE	DATASET
39	NPSEL	Number of plants selected - counted (number)		Selections	Number	Counted	N		PLOT

And an Observation Sheet. Fill in the data for the Flowering Date (dates are entered as numbers in format YYYMMDD) and the number of plants selected from each plot:

	A	B	C	D	E	F	G	H	I	J
1	OBS_UNI	ENTRY_T	GID	DESIGNA	ENTRY_N	CROSS	SEED_SO	PLOT_NO	FlwDate_50	Flw_Date	NPSEL
2	L1DOPAm	T	3935919	AR21CGM	1	IR 72768-1	CGM21F1	1	20210510		3
3	L1DOPME	T	3935920	AR21CGM	2	IR 72768-1	CGM21F1	2	20210506		0
4	L1DOPoZc	T	3935921	AR21CGM	3	IR 72768-1	CGM21F1	3	20210514		1
5	L1DOPJqF	T	3935922	AR21CGM	4	IR 72768-1	CGM21F1	4	20210513		0
6	L1DOP6Zz	T	3935923	AR21CGM	5	IR 72768-1	CGM21F1	5	20210506		3
7	L1DOPCH	T	3935924	AR21CGM	6	IR 72768-1	CGM21F1	6	20210507		2
8	L1DOP8fq	T	3935925	AR21CGM	7	IR 72768-1	CGM21F1	7	20210513		2
9	L1DOP1D	T	3935926	AR21CGM	8	IR 72768-1	CGM21F1	8	20210510		0
10	L1DOPS3	T	3935927	AR21CGM	9	IR 72768-2	CGM21F1	9	20210511		1
11	L1DOPuW	T	3935928	AR21CGM	10	IR 72768-2	CGM21F1	10	20210508		3
12	L1DOPZhc	T	3935929	AR21CGM	11	IR 72768-2	CGM21F1	11	20210512		0

Back in BMS select **Actions>Data collection options>Import observations**. Press **Continue** for the observations sheet, then **browse** to the fieldbook file you just saved. When you have chosen the file click **Import**. The data will be imported into a staging area and the user is required to review it and accept it before it is saved into the study.

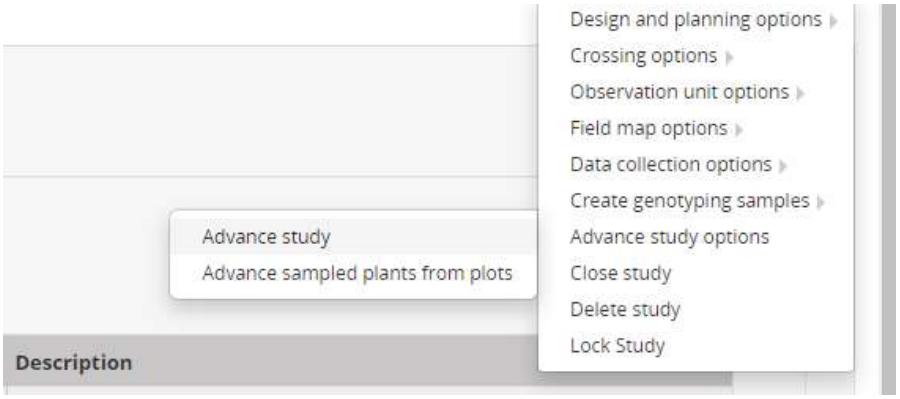


TRIAL_INSTANCE	ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	CROSS	SEED_SOURCE	PLOT_NO	FlwDate_50Flw_Date	NPSEL
1	Test entry	3935919	AR21CGM001-RB	1	IR 72768-12-1-1/CNA 4196	CGM21F1:MBE:202103:1:	1	20210510	3
1	Test entry	3935920	AR21CGM002-RB	2	IR 72768-12-1-1/IDSA 113	CGM21F1:MBE:202103:2:	2	20210506	0
1	Test entry	3935921	AR21CGM003-RB	3	IR 72768-12-1-1/IRAT 170 (FARO 41)	CGM21F1:MBE:202103:3:	3	20210514	1
1	Test entry	3935922	AR21CGM004-RB	4	IR 72768-12-1-1/UPL RI 5	CGM21F1:MBE:202103:4:	4	20210513	0
1	Test entry	3935923	AR21CGM005-RB	5	IR 72768-12-1-1/WAB 326-B-B-7-H1	CGM21F1:MBE:202103:5:	5	20210506	3
1	Test entry	3935924	AR21CGM006-RB	6	IR 72768-12-1-1/WAB 534-B-3A 1-1	CGM21F1:MBE:202103:6:	6	20210507	2
1	Test entry	3935925	AR21CGM007-RB	7	IR 72768-12-1-1/YUNLU NO 28	CGM21F1:MBE:202103:7:	7	20210513	2

If the data looks correct, click Accept on the right of the observation tab. The data will be saved into the database.

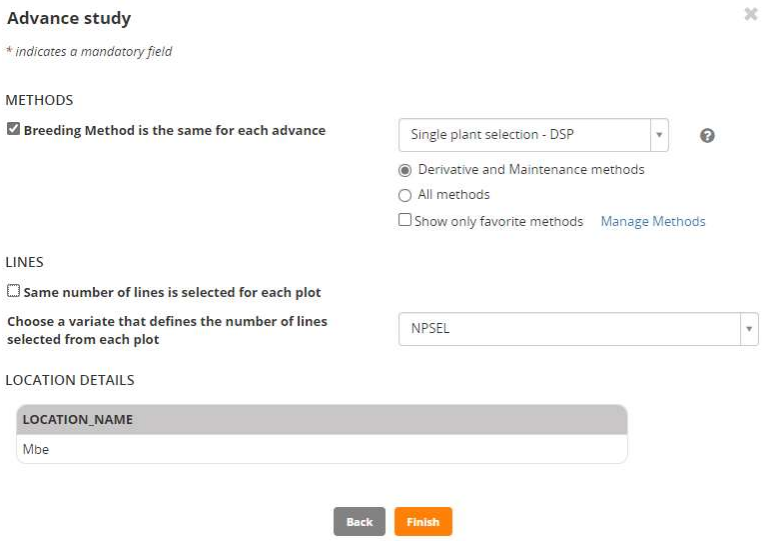
Advance some F2 families by single plant selection

Now select Actions>Advance study options>Advance study:



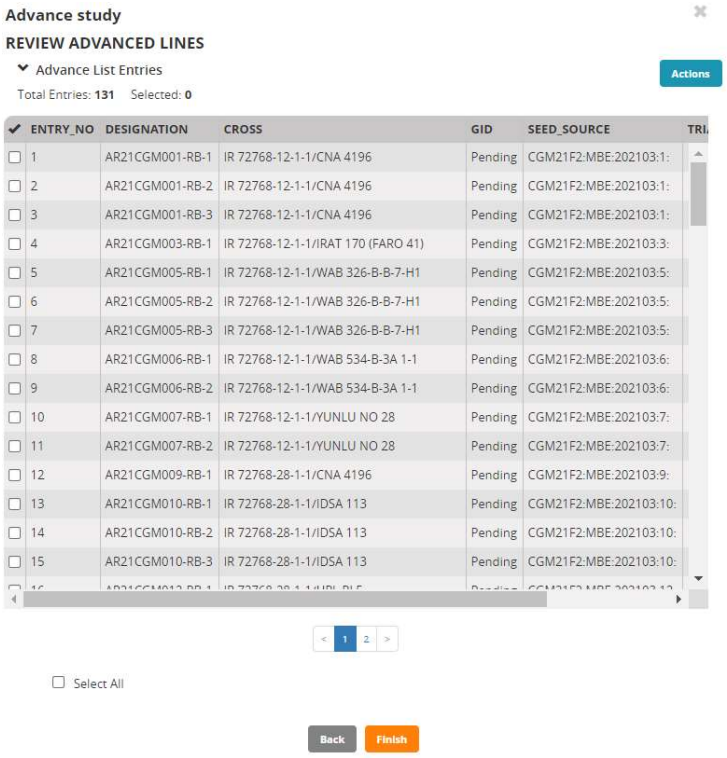
Click Continue to select the location, Mbe.

Choose the method **Single Plant selection** in the drop down box. Now this time we will not select the same number of lines from all plots, so uncheck that tickbox and then make sure that NPSEL is selected as the variable which defines the number of lines selected from each plot.



Click Finish.

Review the F3 lines and click Finish again then save the lines in an F3 list – CGM20F3 for me.



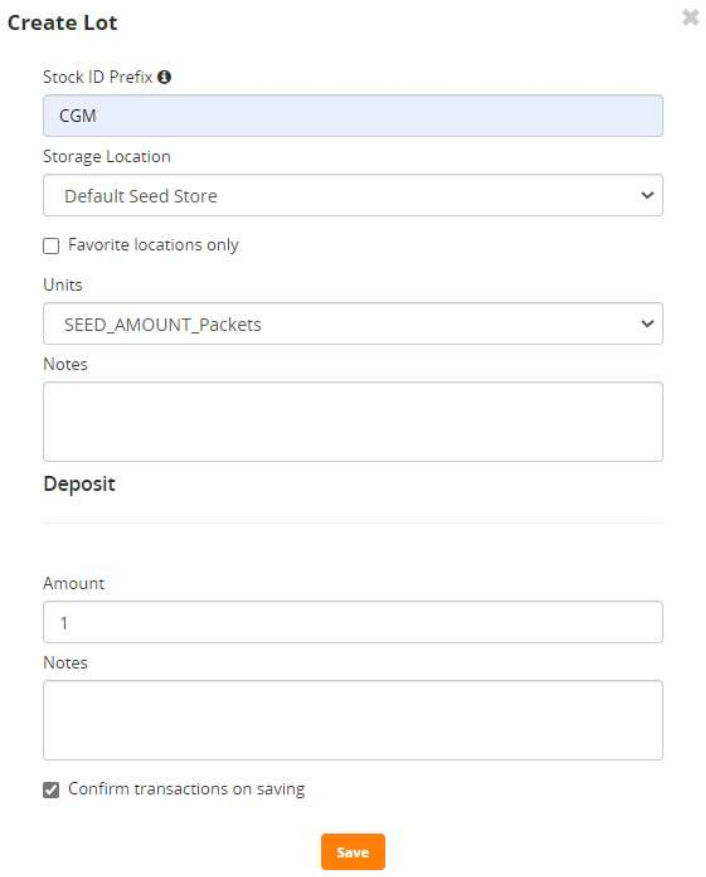
Save seed inventory for the F3 harvest list

We follow the steps in tutorial **Adding Invnetory for a Harvest List** to save inventory for the F3 harvest list.

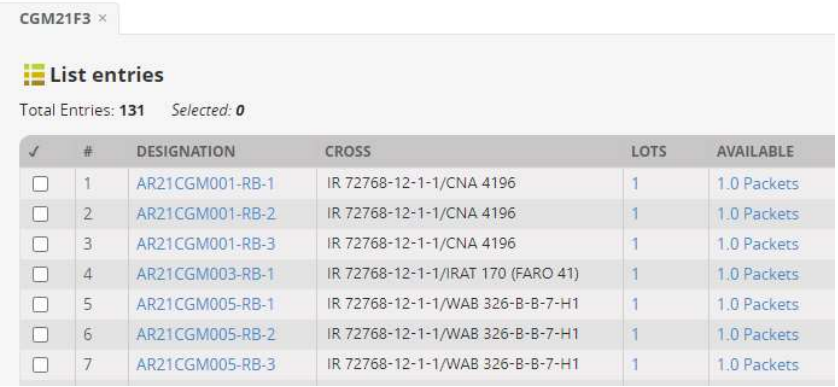
Open the F2 nursery (CGM21F2 for me) and on the **Crosses and Selections** tab select all the entries.

From the **Actions** menu on the **Crosses and Selections** tab choose **Create lots**.

Fill in the Creat Lot form with the Stock ID prefix (CGM for me), the storage location, and choose the units number of packets since we will not weigh the seed for each F3 line in this example. Since we know the number of packets, one for each line, and where they will be stored we can commit the inventory straight away by checking the **Confirm transactions on saving** check box. You can create labels for this inventory by following steps in the in tutorial **Adding Invnetory for a Harvest List.**



If you go to the list manager (LISTS>Germplasm Lists) and open the F3 list you can see the inventry:



✓	#	DESIGNATION	CROSS	LOTS	AVAILABLE
☐	1	AR21CGM001-RB-1	IR 72768-12-1-1/CNA 4196	1	1.0 Packets
☐	2	AR21CGM001-RB-2	IR 72768-12-1-1/CNA 4196	1	1.0 Packets
☐	3	AR21CGM001-RB-3	IR 72768-12-1-1/CNA 4196	1	1.0 Packets
☐	4	AR21CGM003-RB-1	IR 72768-12-1-1/IRAT 170 (FARO 41)	1	1.0 Packets
☐	5	AR21CGM005-RB-1	IR 72768-12-1-1/WAB 326-B-B-7-H1	1	1.0 Packets
☐	6	AR21CGM005-RB-2	IR 72768-12-1-1/WAB 326-B-B-7-H1	1	1.0 Packets
☐	7	AR21CGM005-RB-3	IR 72768-12-1-1/WAB 326-B-B-7-H1	1	1.0 Packets

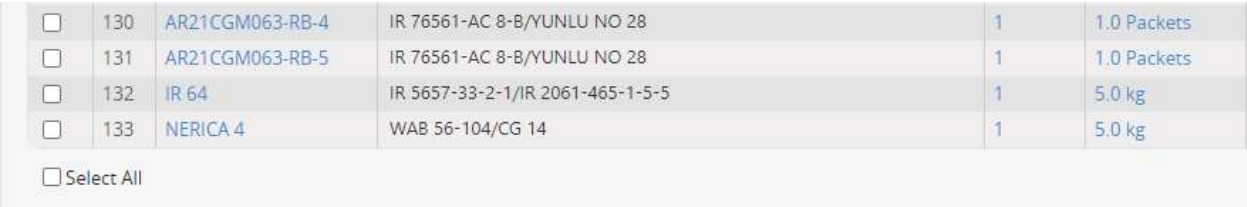
Make an F3 Nursery with checks and Prepare seed for planting

For the F3 nursery we are going to add two check entries to the planting list and plant them alternately every ten plots. To do this we must add two entries to the F3 germplasm list.

In Manage Germplasm, search for exact matches to the name IR 64. Check the box next to the entry with GID 50533 (which should have 5kg of seed available if you did the earlier exercise). From the Actions menu select Add to existing list and select your F3 list (CGM21F3 for me) and click Add.

Do the same for NERICA4 (GID 765439)

Now go to LISTS>Germplasm Lists and browse to your F3 list to verify that the two entries have been added.



☐	130	AR21CGM063-RB-4	IR 76561-AC 8-B/YUNLU NO 28	1	1.0 Packets
☐	131	AR21CGM063-RB-5	IR 76561-AC 8-B/YUNLU NO 28	1	1.0 Packets
☐	132	IR 64	IR 5657-33-2-1/IR 2061-465-1-5-5	1	5.0 kg
☐	133	NERICA 4	WAB 56-104/CG 14	1	5.0 kg

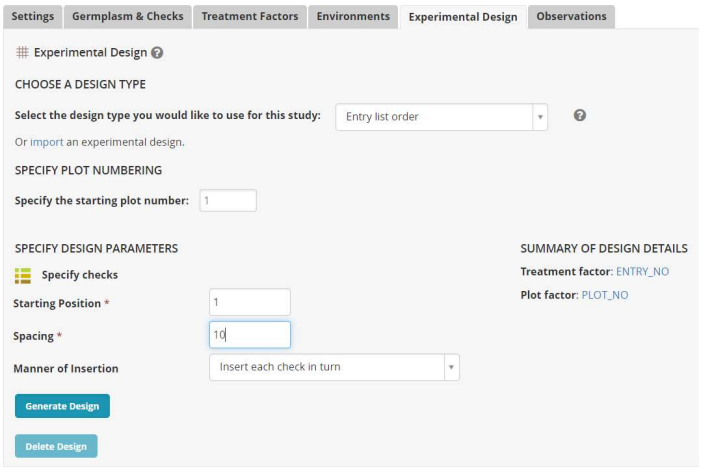
☐ Select All

Now Use the Study manager and follow the steps above to make an F3 nursery. I will call mine CGM21F3. Use the F2 nursery as a template. Load the F3 germplasm list for planting and specify the last two entries NERICA4 and IR64 as check entries. To do this scroll down the entreis on the Germplasm and

Checks tab, click on the Entry Type value for each of these entries, select **Check entry** from the list box and click the tick symbol:

They will both be marked as Check Entries.

Next, click on the Experimental Design tab and select Entry list order. BMS detects that there are checks in the entry list and has added two boxes to the design details form. One asking the spacing between checks (ie how many test entries to place between checks) and the other asking whether all checks should be planted in each check position, or whether they should be plance one at a time in turn. We select 10 for spacing and Insert each check in turn. Click **Generate Design.**



You will see on the observation sheet that every 10 plots is followed by one of the check entries:

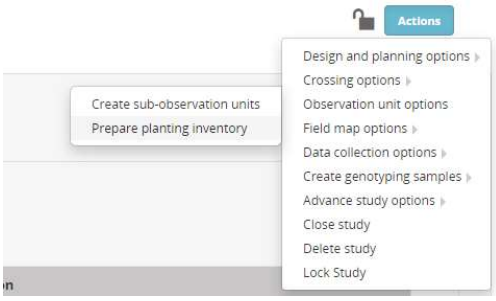
ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	CROSS	SEED_SOURCE	PLOT_N
Check entry	50533	IR 64	132	IR 5657-33-2-1/IR 2061-465-1-5-5	Unknown	1
Test entry	3935983	AR21CGM001-RB-1	1	IR 72768-12-1-1/CNA 4196	CGM21F2:MBE:202103:1:	2
Test entry	3935984	AR21CGM001-RB-2	2	IR 72768-12-1-1/CNA 4196	CGM21F2:MBE:202103:1:	3
Test entry	3935985	AR21CGM001-RB-3	3	IR 72768-12-1-1/CNA 4196	CGM21F2:MBE:202103:1:	4
Test entry	3935986	AR21CGM003-RB-1	4	IR 72768-12-1-1/IRAT 170 (FARO 41)	CGM21F2:MBE:202103:3:	5
Test entry	3935987	AR21CGM005-RB-1	5	IR 72768-12-1-1/WAB 326-B-B-7-H1	CGM21F2:MBE:202103:5:	6
Test entry	3935988	AR21CGM005-RB-2	6	IR 72768-12-1-1/WAB 326-B-B-7-H1	CGM21F2:MBE:202103:5:	7
Test entry	3935989	AR21CGM005-RB-3	7	IR 72768-12-1-1/WAB 326-B-B-7-H1	CGM21F2:MBE:202103:5:	8
Test entry	3935990	AR21CGM006-RB-1	8	IR 72768-12-1-1/WAB 534-B-3A 1-1	CGM21F2:MBE:202103:6:	9
Test entry	3935991	AR21CGM006-RB-2	9	IR 72768-12-1-1/WAB 534-B-3A 1-1	CGM21F2:MBE:202103:6:	10
Test entry	3935992	AR21CGM007-RB-1	10	IR 72768-12-1-1/YUNLU NO 28	CGM21F2:MBE:202103:7:	11
Check entry	765439	NERICA 4	133	WAB 56-104/CG 14	Unknown	12
Test entry	3935993	AR21CGM007-RB-2	11	IR 72768-12-1-1/YUNLU NO 28	CGM21F2:MBE:202103:7:	13
Test entry	3935994	AR21CGM009-RB-1	12	IR 72768-28-1-1/CNA 4196	CGM21F2:MBE:202103:9:	14

On the Observation tab add SELECTION variable NPSEL into the observation sheet. (Somehow it gets left off from the template).

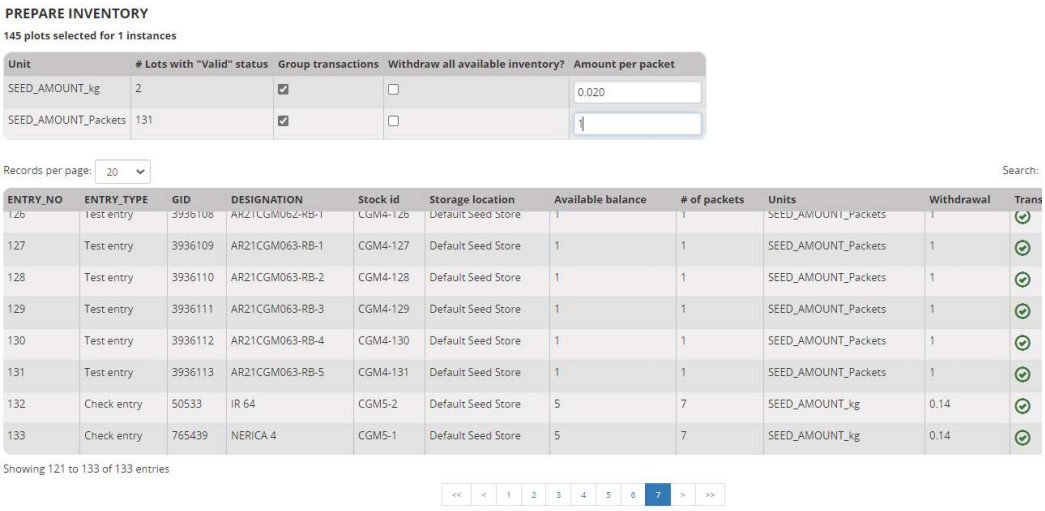
Now to prepare seed for planting you must first specify the plots for which you wish to prepare seed. You do this by selecting observation uints on the Observations tab. Since there is only one environemnt we only need to check the Select all pages check box to select the 145 plots in the nursery (131 test entries and 14 check plots):

ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	CROSS
Check entry	50533	IR 64	132	IR 5657-33-2-1/IR 2061-465-1-5-5
Test entry	3935983	AR21CGM001-RB-1	1	IR 72768-12-1-1/CNA 4196

Next, select Actions>Observation unit options>Prepare planting inventory.

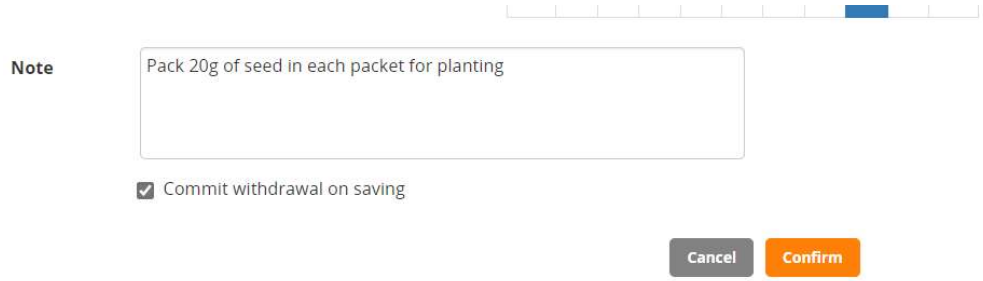


The Prepare inventory tab has a box for you to enter the amount of seed to be packaged for each planting packet and a table showing whether there is enough seed for each entry for all the plots in the trial. In our nursery we have one plot per test entry, and in our inventory we only have 1 bag per test entry, so we need to withdraw one bag for each test entry. We also have some bulk seed stored in kgs for the checks and we need to withdraw 20 g per packet for these entries.

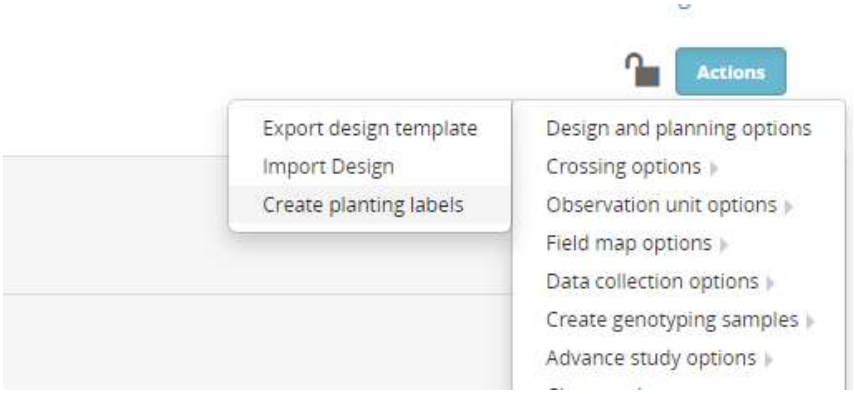


ENTRY_NO	ENTRY_TYPE	GID	DESIGNATION	Stock id	Storage location	Available balance	# of packets	Units	Withdrawal	Trans
126	Test entry	3936108	AR21CGM062-RB-1	CGM4-126	Default Seed Store	1	1	SEED_AMOUNT_Packets	1	
127	Test entry	3936109	AR21CGM063-RB-1	CGM4-127	Default Seed Store	1	1	SEED_AMOUNT_Packets	1	
128	Test entry	3936110	AR21CGM063-RB-2	CGM4-128	Default Seed Store	1	1	SEED_AMOUNT_Packets	1	
129	Test entry	3936111	AR21CGM063-RB-3	CGM4-129	Default Seed Store	1	1	SEED_AMOUNT_Packets	1	
130	Test entry	3936112	AR21CGM063-RB-4	CGM4-130	Default Seed Store	1	1	SEED_AMOUNT_Packets	1	
131	Test entry	3936113	AR21CGM063-RB-5	CGM4-131	Default Seed Store	1	1	SEED_AMOUNT_Packets	1	
132	Check entry	50533	IR 64	CGM5-2	Default Seed Store	5	7	SEED_AMOUNT_kg	0.14	
133	Check entry	765439	NERICA 4	CGM5-1	Default Seed Store	5	7	SEED_AMOUNT_kg	0.14	

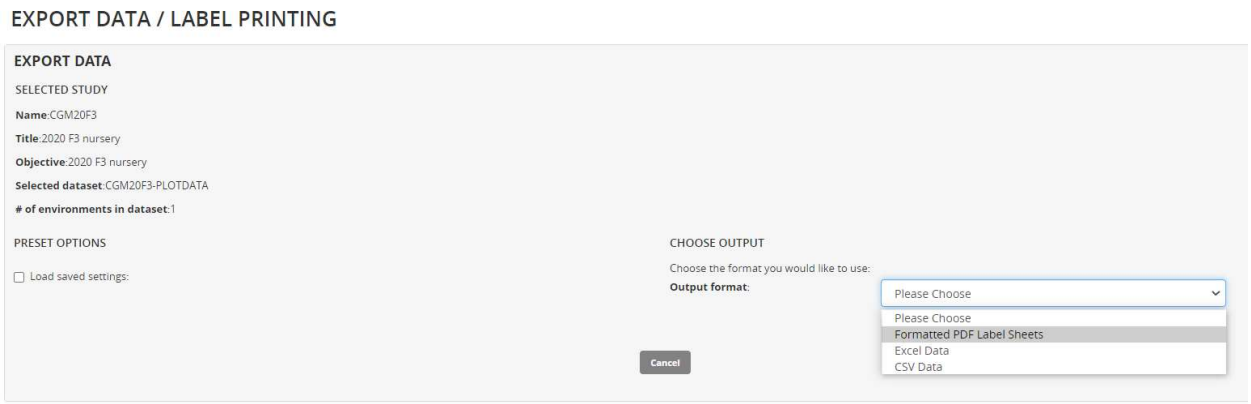
You can add some packing instructions, select Commit withdrawal on saving and click Confirm.



To prepare planting labels select Actions>Design and planning options>Create planting labels:



Select Onservations and then select Formatted PDF label sheets for the output type:



Drag Stock_id, DESIGNATION, Storage location abbr and ENTRY_NO to the left hand part of the label to indicate where to get the seed from, and then drag Study Name, LOCATION_NAME and PLOT_NO to the right hand part of the label to indicate where to plant the seed.

Click **Export** to export the labels in PDF format, and then **Cancel** to leave the label printer.

Stock id : CGM5-2 DESIGNATION : IR 64 Storage location abbr : DSS ENTRY_NO : 132	Study Name : CGM21F3 LOCATION_NAME : Mbe PLOT_NO : 1	Stock id : CGM4-1 DESIGNATION : AR21CGM001-RB-1 Storage location abbr : DSS ENTRY_NO : 1	Study Name : CGM21F3 LOCATION_NAME : Mbe PLOT_NO : 2	Stock id : CGM4-2 DESIGNATION : AR21CGM001-RB-2 Storage location abbr : DSS ENTRY_NO : 2	Study Name : CGM21F3 LOCATION_NAME : Mbe PLOT_NO : 3
Stock id : CGM4-3 DESIGNATION : AR21CGM001-RB-3 Storage location abbr : DSS ENTRY_NO : 3	Study Name : CGM21F3 LOCATION_NAME : Mbe PLOT_NO : 4	Stock id : CGM4-4 DESIGNATION : AR21CGM003-RB-1 Storage location abbr : DSS ENTRY_NO : 4	Study Name : CGM21F3 LOCATION_NAME : Mbe PLOT_NO : 5	Stock id : CGM4-5 DESIGNATION : AR21CGM005-RB-1 Storage location abbr : DSS ENTRY_NO : 5	Study Name : CGM21F3 LOCATION_NAME : Mbe PLOT_NO : 6

When the nursery is planted you can export the fieldbook and collect some data. Again the only trait is Flowering Date, and now the NPSEL column should be filled with 1 for families you want to keep as selected bulk F4 seeds, and 0 for families you want to discard.

Proceed to load the data and advance the nursery with Selected bulk method using the NPSEL variable.

Managing Evaluation Trials

Trials are evaluation experiments managed through the Study Manager. They are generally multi-location, replicated and randomized.

Objectives

At the end of this tutorial, the user should be able to:

1. Create a trial for germplasm evaluation
2. Prepare seed and print lables for a trial
3. Use sub-observation units to collect sub-sample data
4. Export a fieldbook and import collected data
5. Validate collected data and compute calcualted variables.

Create a mulit-location trial

First you need to prepare a germplasm list with test and check entries to be planted in the trial. We are going to use the list of imported germplam we created in the Import Germplasm Tutorial. Probably called <your initials>GI21– CGMGI21 for me. Use LISTS>GermplasmLists>Browse to view it.

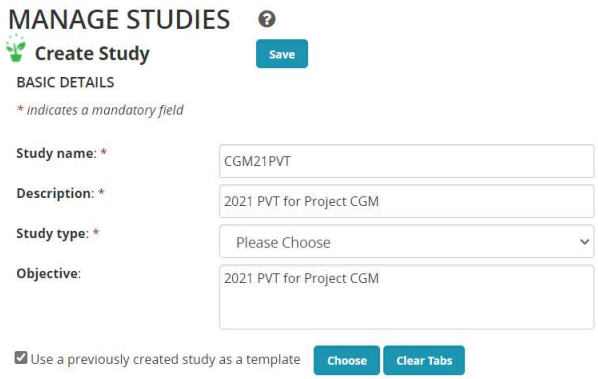
CGMGI21 ×

List entries

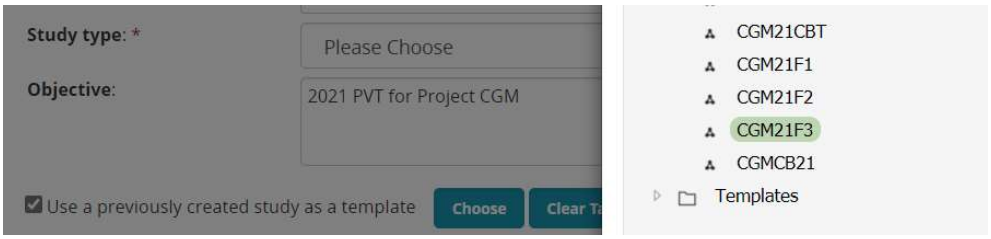
Total Entries: **16** *Selected:* ***0***

✓	#	DESIGNATION	CROSS	LOTS	AVAILABLE
☐	1	IR 72768-12-1-1	IR 60080-46 A/IR 65907-116-1-B	1	150.0 g
☐	2	IR 72768-28-1-1	IR 60080-46 A/IR 65907-116-1-B	1	150.0 g
☐	3	IR 75502-24-1-1-B	B 6144 F-MR-6-0-0/IR 55423-01 (NSIC RC 9)	1	150.0 g
☐	4	IR 75516-30-1-1-B	IR 53236-275-1/CT 6516-24-3-2	1	150.0 g
☐	5	IR 75516-56-1-1-B	IR 53236-275-1/CT 6516-24-3-2	1	150.0 g
☐	6	IR 75518-84-1-1-B	IR 60080-46 A/IR 53236-275-1	1	150.0 g
☐	7	IR 75531-31-1-2-B	IR 70360-54-1-B/VIENG	1	150.0 g
☐	8	IR 76561-AC 8-B	CT 13382-9-4-M/IR 70358-145-1-1	1	150.0 g
☐	9	CNA 4196	CNA 4196	1	150.0 g
☐	10	IDSA 113	IDSA 113	1	150.0 g
☐	11	FARO 41	IRAT 13/PALAWAN	1	150.0 g
☐	12	UPL RI 5	SIGADIS (AICRIP)/BPI 76-1	1	150.0 g
☐	13	WAB 326-B-B-7-H	ITA 235 (TOX 1785-19-18)/WABC 165	1	150.0 g
☐	14	WAB 534-B-3A 1-1	WAB 181-18/DR 2	1	150.0 g
☐	15	YUNLU NO 28	IDSA 6 (IRAT 216)/WUNENGDABAIGU-2-5	1	150.0 g
☐	16	IRRI 132	UPL RI 5/IR 12979-24-1 (BROWN)	1	150.0 g

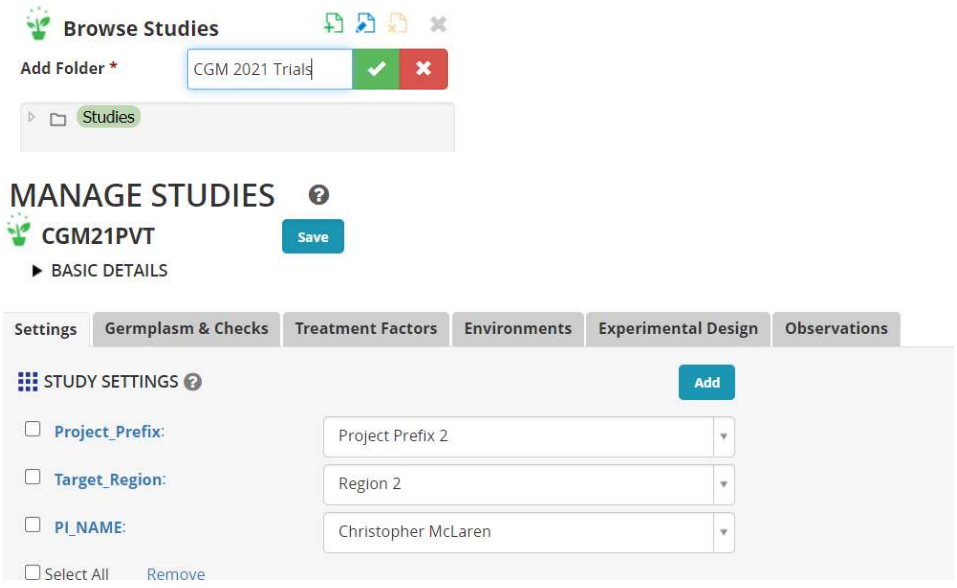
Open the Manage Studies application from the STUDIES menu and click on **Start a new study**. Name the trial <your initials>21PVT, CGM21PVT for me, and fill in the basic details of description and objective and select the study type **Trial**.



You can add variables to the new study directly from the Ontology pick lists as we did for the crossing block, or you can pick up all the variables from any previously used study. To use this option check the **Use a previously created study as a template** check box. Then choose the previous study which is smilar to your current study. We dont have a previous trial yet so we will use a nursery:

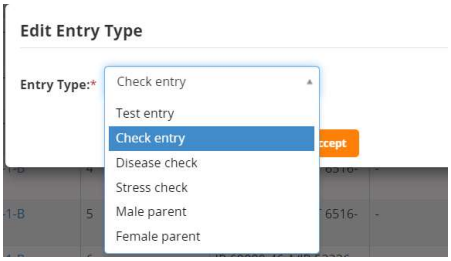


The variables from the template study are imported into the new study. Change the settings if needed and Save the study in a new folder <your initials> 2021 Trials (CGM 2021 Trials for me).



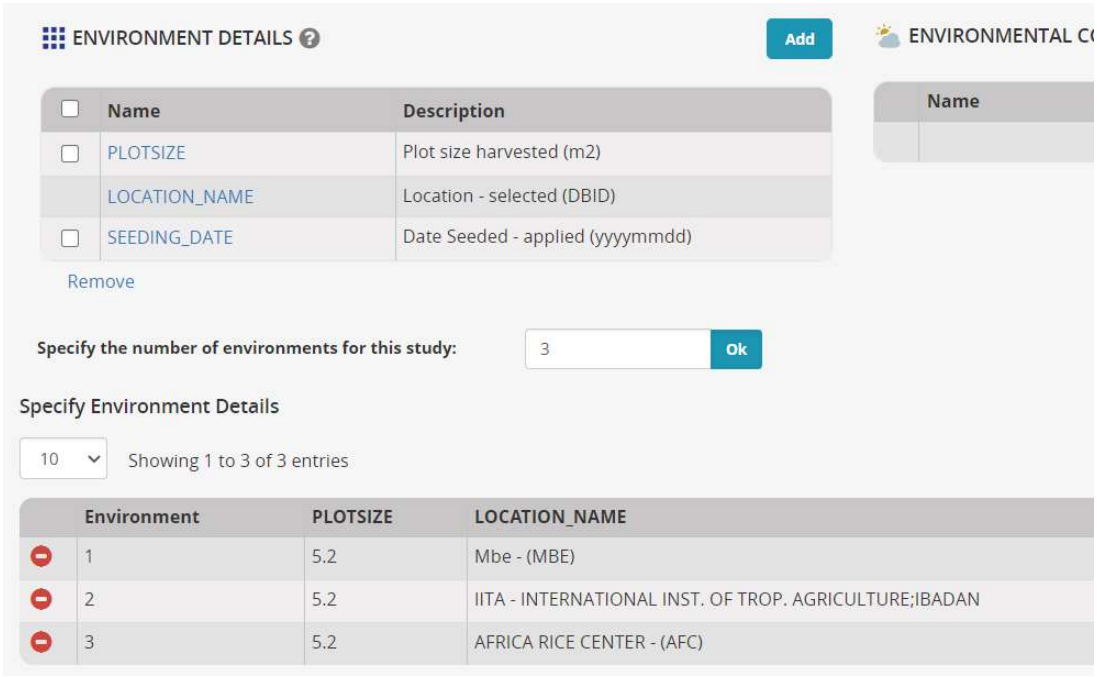
On the Germplasm and Checks tab, the extra variables for Cross and Seed source are also recovered from the template, so you just need to Browse for the list of planting material. The imported germplasm list you made in the Import Germplasm Tutorial. CGM21GI in my case.

You can set the Check entries on the Germplasm Tab. Click on the entry type for the line(s) to be made checks, (we will make IRRI 132 a check entry), choose Check Entry from the list and click accept.

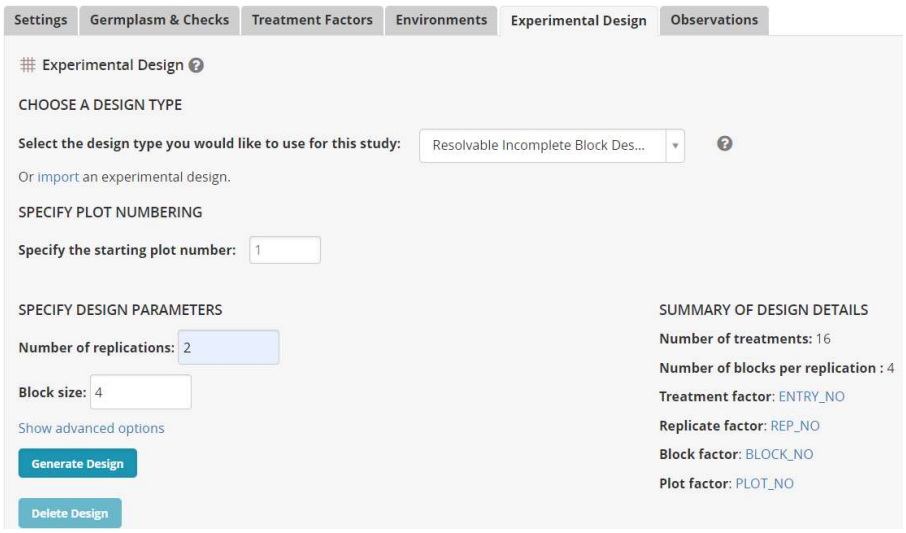


On the **Environments tab** set the number of environments to 3 and click OK.

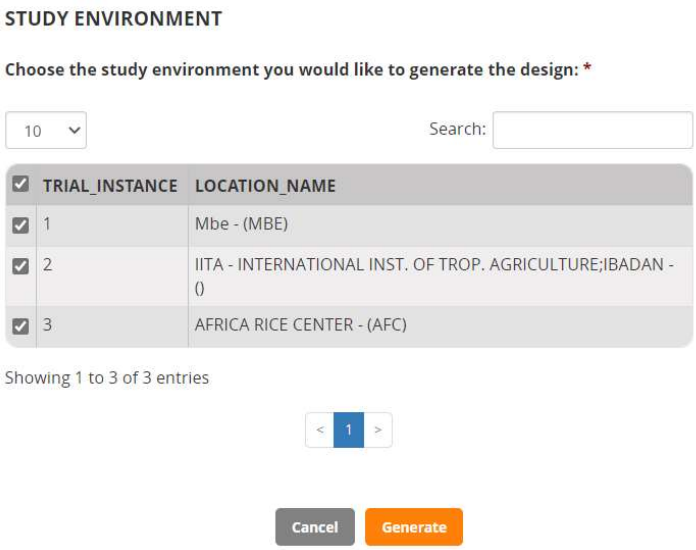
Mbe has been inherited from the template for the first environment, and this location is still correct, select IITA-Ibadan and Africa Rice CENTRE as the other two locations. You will have to uncheck Show Favorite Locations since we have not specfied favorite locations. Click Add next to Environmental Details variable, and and search for Seeding date and Plotsize and add them to the Environment Details section. Enter 5.2 m squared for the plot size at each location. You may not know the Seeding date at this time.



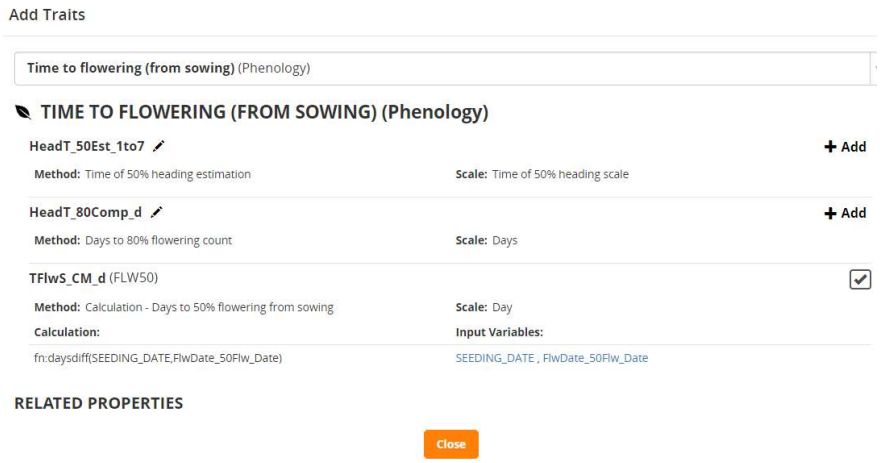
On the **Experimental Design** tab select **Resolveable Incomplete Block Design** (Alpha lattice), enter 2 for number of replications and 6 for block size then click **Generate Design**.



Generate the design for all locations**:**



You will get a success message and now the Observation tab will contain a fieldbook. At the moment the only trait there is the date of 50% flowering inherited from our nursery so we will add some more traits. Click Add next to the traits box. Search for FLW50 and add it to the trial. (If you cant find FLW50 use TFlwS_CM-d).



Notice that trait TFlwS_CM-d has Alias FLW50 and has a computation formula associated so that it can be calculated within BMS.

Add **GrYld_wgh_gplot,** then **GRMOIST,** and finally **GYTHA** which is also a variable which can be calculated in BMS.

The traits box now looks like this:

TRAITS

Add

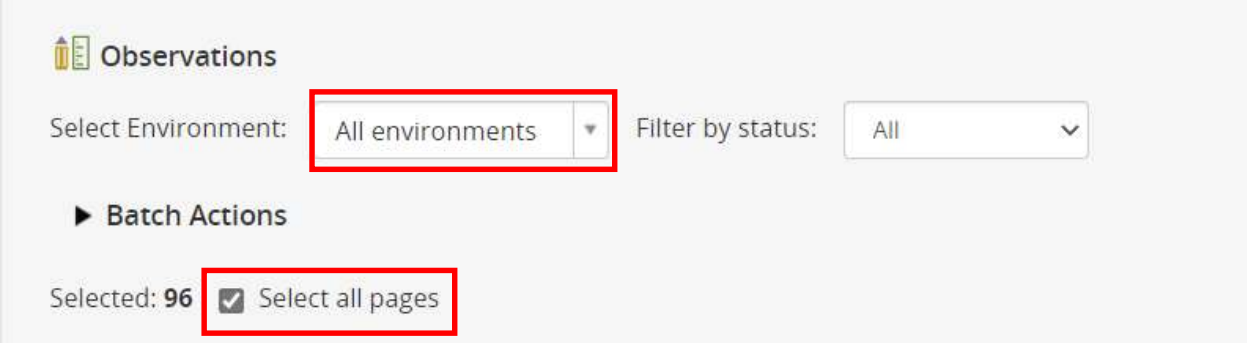
Name	Description	Input Variables
FlwDate_50Flw_Date	Flowering date -BY- Fifty percent flowering date observation-IN- ISO Date (yyyymmdd)	
FLW50	Time to flowering (from sowing) -BY- Calculation - Days to 50% flowering from sowing -IN- Day	SEEDING_DATE , FlwDate_50Flw_Date
GrYld_wgh_gplot	Grain yield -BY- AYLD_CONT method -IN- G per plot	
GRMOIST	Moisture content of grain. Expressed in percentage.	
GYTHA	Grain yield in T per Ha corrected for moisture	GRMOIST , PLOT SIZE , GrYld_wgh_gplot

Remove

Prepare seed and planting labels

To prepare seed for a study you must select the plots for which you wish to prepare the seed.

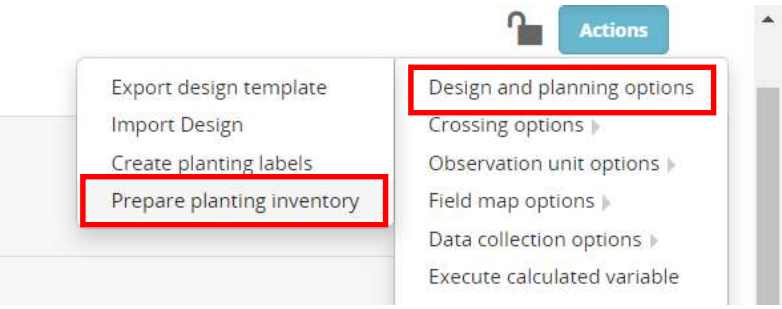
To select all plots, from the Observation sheet you must set the Select Environment box to All environments and check the Select all pages checkbox:



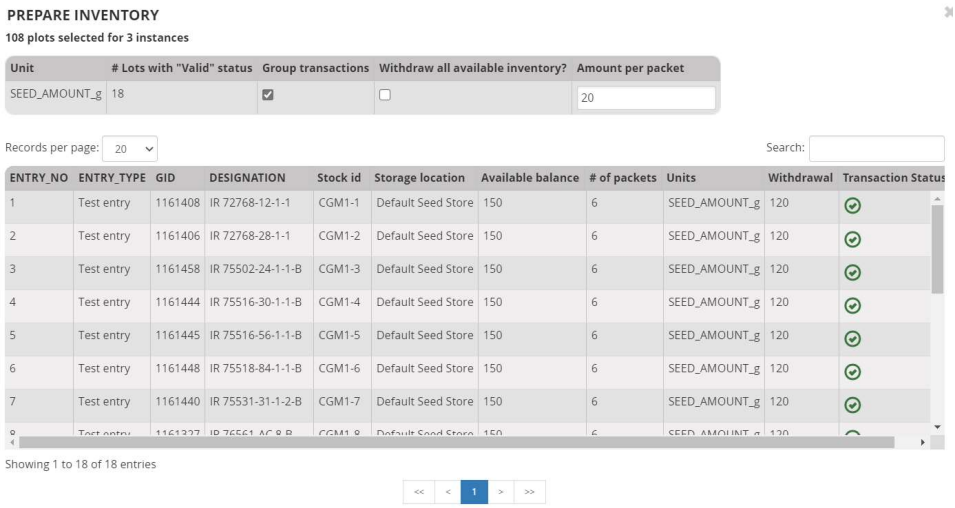
We have 96 plots – 16 entries by 3 location by 2 repliacations.

XXXXXXXXXXXXXX

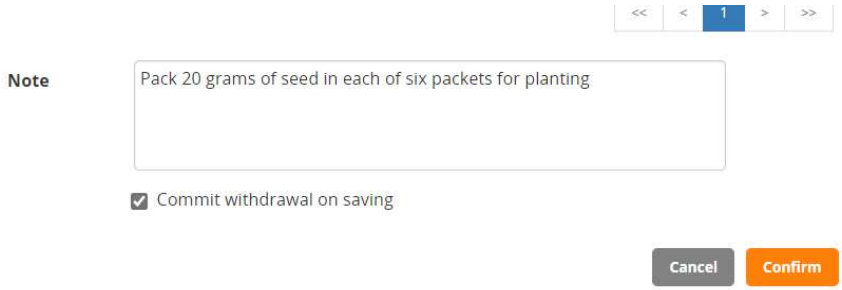
Next select Actions>Design and planning options>Prepare planting inventory:



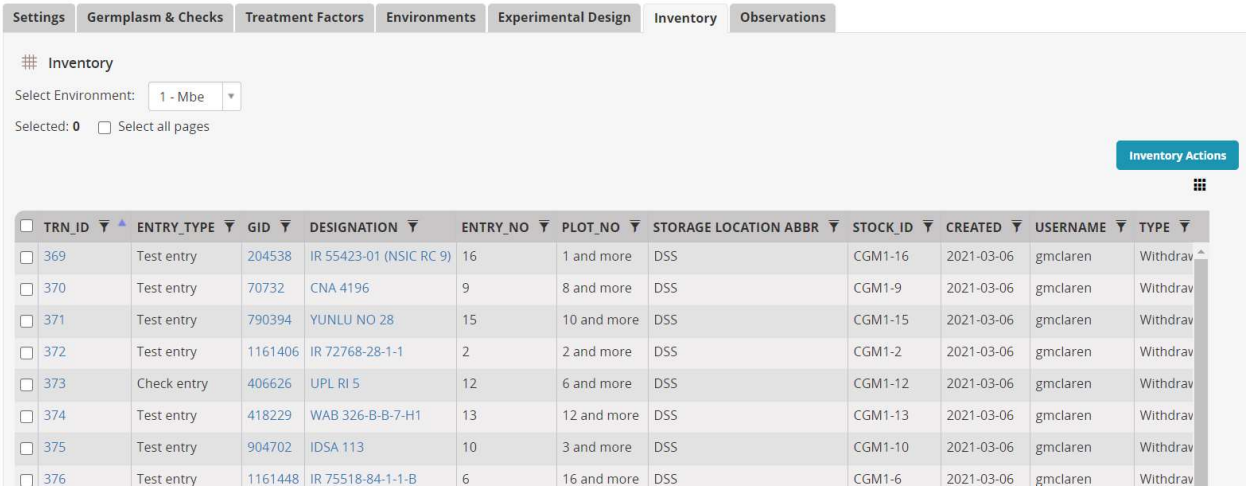
The Prepare inventory form shows a box for specifying the amount of seed to pack per plot (packet) and a table showing the number of packets for each entry and the total seed amount specified for packing.



You can add a note at the bottom of the form and if you are the one to do the packing you can **Commit the withdrawal on saving**. (If a store manager will do the packing you should not check the **Commit withdrawal on saving** checkbox because the store manager will commit the transaction when the packing is complete). Click **Confirm**.

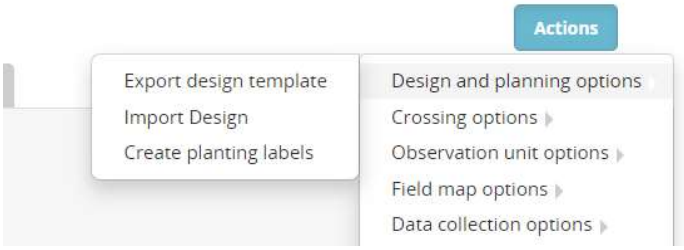


A new tab called inventory has been added to the study showing the seed preparation transactions.

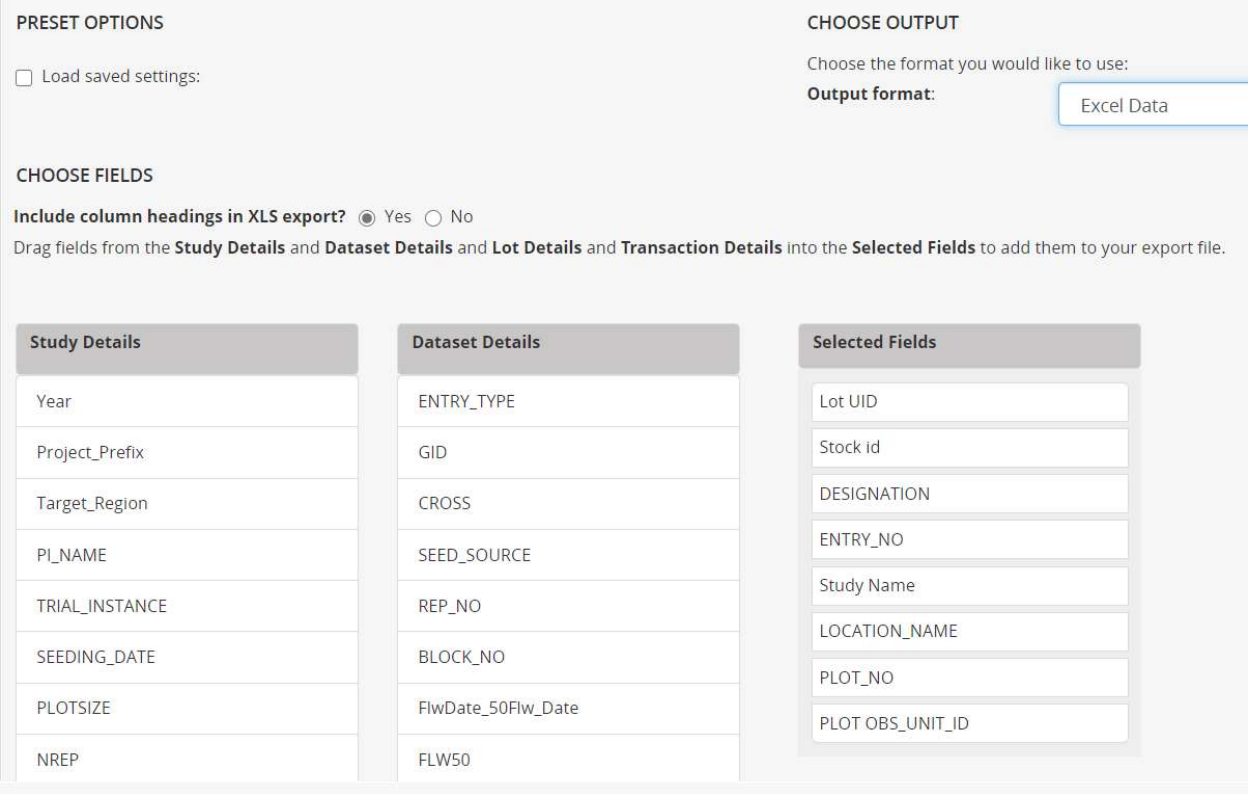


TRN_ID	ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	PLOT_NO	STORAGE LOCATION ABBR	STOCK_ID	CREATED	USERNAME	TYPE
369	Test entry	204538	IR 55423-01 (NSIC RC 9)	16	1 and more	DSS	CGM1-16	2021-03-06	gmclaren	Withdrav
370	Test entry	70732	CNA 4196	9	8 and more	DSS	CGM1-9	2021-03-06	gmclaren	Withdrav
371	Test entry	790394	YUNLU NO 28	15	10 and more	DSS	CGM1-15	2021-03-06	gmclaren	Withdrav
372	Test entry	1161406	IR 72768-28-1-1	2	2 and more	DSS	CGM1-2	2021-03-06	gmclaren	Withdrav
373	Check entry	406626	UPL RI 5	12	6 and more	DSS	CGM1-12	2021-03-06	gmclaren	Withdrav
374	Test entry	418229	WAB 326-B-B-7-H1	13	12 and more	DSS	CGM1-13	2021-03-06	gmclaren	Withdrav
375	Test entry	904702	IDSA 113	10	3 and more	DSS	CGM1-10	2021-03-06	gmclaren	Withdrav
376	Test entry	1161448	IR 75518-84-1-1-B	6	16 and more	DSS	CGM1-6	2021-03-06	gmclaren	Withdrav

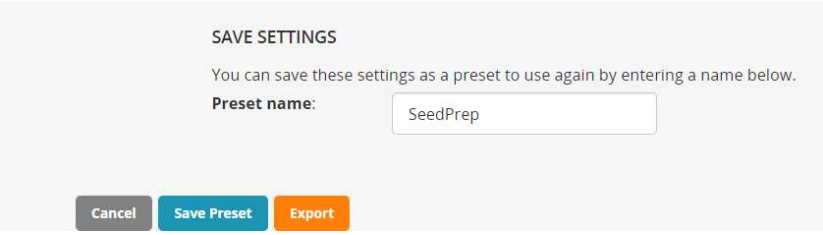
To prepare planting labels select Actions>Design and planning options>Create planting labels:



On the Export Data form, select Excel Data for the Output format and then drag the following variables to the Selected Fields box: Lot UID, Stock id, DESIGNATION, ENTRY_NO (these variables say where the seed is to come from) then add Study Name, LOCATION_NAME, PLOT_NO and PLOT OBS_UNIT_ID (and these variables say where it is going).



You can save the setup for futire use with the name SeedPrep and then click Export to generate the labels file.



Now the labels should be pinted with a label printing software such as Microsoft Word Mail-merge function. However the label records are currently in plot within location order, and for the packing process you want to have all the labels for each entry together. You can achieve this order by sorting the excel sheet on Entry_NO before you print the labels with mail-merge.

The fields Lot UID and/or PLOT OBS_UNIT_ID can be printed as barcodes to facilitate bar code use in packing, sorting and planting.

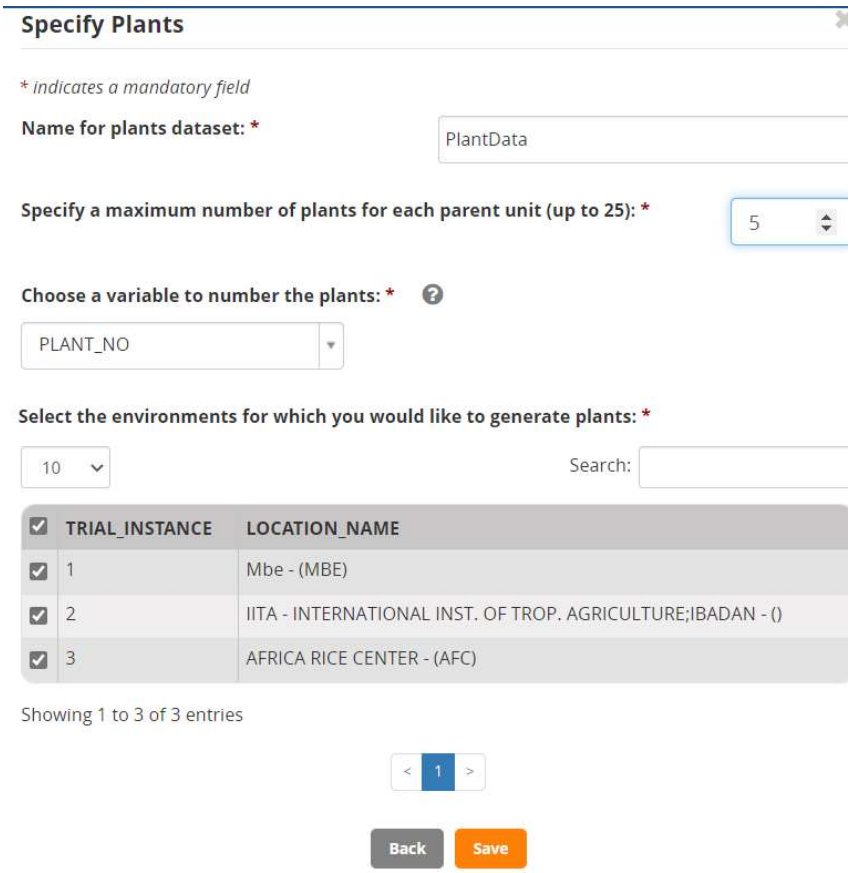
	A	B	C	D	E	F	G	H
1	Lot UID	Stock id	DESIGNATION	ENTRY_NO	Study Name	LOCATION_NAME	PLOT_NO	PLOT OBS_UNIT_ID
2	db764734-4b6c-4709-b286-ec1e964f824e	CGM1-1	IR 72768-12-1-1	1	CGM21PVT	Mbe	5	L1DOPhdQgZRcq
3	db764734-4b6c-4709-b286-ec1e964f824e	CGM1-1	IR 72768-12-1-1	1	CGM21PVT	Mbe	30	L1DOP12nyPeUd
4	db764734-4b6c-4709-b286-ec1e964f824e	CGM1-1	IR 72768-12-1-1	1	CGM21PVT	IITA - INTERNATIONAL INST. OF TROP. AGRICULTURE;IBADAN	12	L1DOPeHeVLm5T
5	db764734-4b6c-4709-b286-ec1e964f824e	CGM1-1	IR 72768-12-1-1	1	CGM21PVT	IITA - INTERNATIONAL INST. OF TROP. AGRICULTURE;IBADAN	17	L1DOPywkzr4Vv
6	db764734-4b6c-4709-b286-ec1e964f824e	CGM1-1	IR 72768-12-1-1	1	CGM21PVT	AFRICA RICE CENTER	6	L1DOP7baj5UEW
7	db764734-4b6c-4709-b286-ec1e964f824e	CGM1-1	IR 72768-12-1-1	1	CGM21PVT	AFRICA RICE CENTER	31	L1DOPZyinsxB2
8	225f90e6-ca9b-48b5-aaec-e7c375d12cca	CGM1-2	IR 72768-28-1-1	2	CGM21PVT	Mbe	2	L1DOPSFWR3Guv
9	225f90e6-ca9b-48b5-aaec-e7c375d12cca	CGM1-2	IR 72768-28-1-1	2	CGM21PVT	Mbe	28	L1DOP4nlOauuz
10	225f90e6-ca9b-48b5-aaec-e7c375d12cca	CGM1-2	IR 72768-28-1-1	2	CGM21PVT	IITA - INTERNATIONAL INST. OF TROP. AGRICULTURE;IBADAN	4	L1DOP7kBLiTyn
11	225f90e6-ca9b-48b5-aaec-e7c375d12cca	CGM1-2	IR 72768-28-1-1	2	CGM21PVT	IITA - INTERNATIONAL INST. OF TROP. AGRICULTURE;IBADAN	25	L1DOPkaljdnXu
12	225f90e6-ca9b-48b5-aaec-e7c375d12cca	CGM1-2	IR 72768-28-1-1	2	CGM21PVT	AFRICA RICE CENTER	16	L1DOPgwZBLhVL
13	225f90e6-ca9b-48b5-aaec-e7c375d12cca	CGM1-2	IR 72768-28-1-1	2	CGM21PVT	AFRICA RICE CENTER	23	L1DOPHn0No3Yn
14	f80e1c2b-a3de-4f6b-98d2-704f6891221e	CGM1-3	IR 75502-24-1-1-B	3	CGM21PVT	Mbe	9	L1DOPts1ARNKs
15	f80e1c2b-a3de-4f6b-98d2-704f6891221e	CGM1-3	IR 75502-24-1-1-B	3	CGM21PVT	Mbe	29	L1DOPQWjU7F52
16	f80e1c2b-a3de-4f6b-98d2-704f6891221e	CGM1-3	IR 75502-24-1-1-B	3	CGM21PVT	IITA - INTERNATIONAL INST. OF TROP. AGRICULTURE;IBADAN	6	L1DOPaN4mQaKY
17	f80e1c2b-a3de-4f6b-98d2-704f6891221e	CGM1-3	IR 75502-24-1-1-B	3	CGM21PVT	IITA - INTERNATIONAL INST. OF TROP. AGRICULTURE;IBADAN	27	L1DOPazwvYMVD
18	f80e1c2b-a3de-4f6b-98d2-704f6891221e	CGM1-3	IR 75502-24-1-1-B	3	CGM21PVT	AFRICA RICE CENTER	9	L1DOPUbtSHufm
19	f80e1c2b-a3de-4f6b-98d2-704f6891221e	CGM1-3	IR 75502-24-1-1-B	3	CGM21PVT	AFRICA RICE CENTER	26	L1DOPzwpjZVou
20	381dae85-c12c-408d-b845-edda799398ef	CGM1-4	IR 75516-30-1-1-B	4	CGM21PVT	Mbe	11	L1DOPFvFDP43y
21	381dae85-c12c-408d-b845-edda799398ef	CGM1-4	IR 75516-30-1-1-B	4	CGM21PVT	Mbe	27	L1DOPpVxyquqk
22	381dae85-c12c-408d-b845-edda799398ef	CGM1-4	IR 75516-30-1-1-B	4	CGM21PVT	IITA - INTERNATIONAL INST. OF TROP. AGRICULTURE;IBADAN	5	L1DOPxOooWB0y
23	381dae85-c12c-408d-b845-edda799398ef	CGM1-4	IR 75516-30-1-1-B	4	CGM21PVT	IITA - INTERNATIONAL INST. OF TROP. AGRICULTURE;IBADAN	31	L1DOPHdU5UbhL
24	381dae85-c12c-408d-b845-edda799398ef	CGM1-4	IR 75516-30-1-1-B	4	CGM21PVT	AFRICA RICE CENTER	10	L1DOPEvTbxe1g
25	381dae85-c12c-408d-b845-edda799398ef	CGM1-4	IR 75516-30-1-1-B	4	CGM21PVT	AFRICA RICE CENTER	18	L1DOPV2zsA8Lx
26	51a2fa9d-31a7-49c2-b493-61c1127b2b94	CGM1-5	IR 75516-56-1-1-B	5	CGM21PVT	Mbe	7	L1DOPR2Wc7O4o

Set up sub sample units to collect sampling data from plots

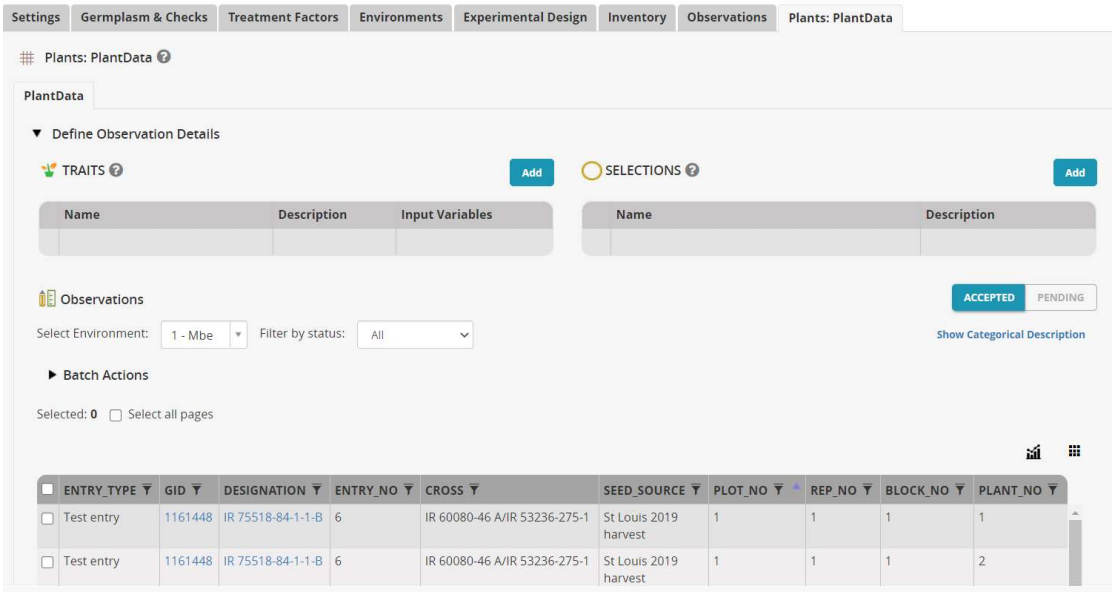
The BMS is able to have sub-sample observations sheets for the collection of data from multiple samples from each plot. To set up a sub-sample observation sheet, open the trial in the trial manager and select Actions>Observation unit options>Create sub-observation units:

Select the type of sub observation units you want. In our case Plants:

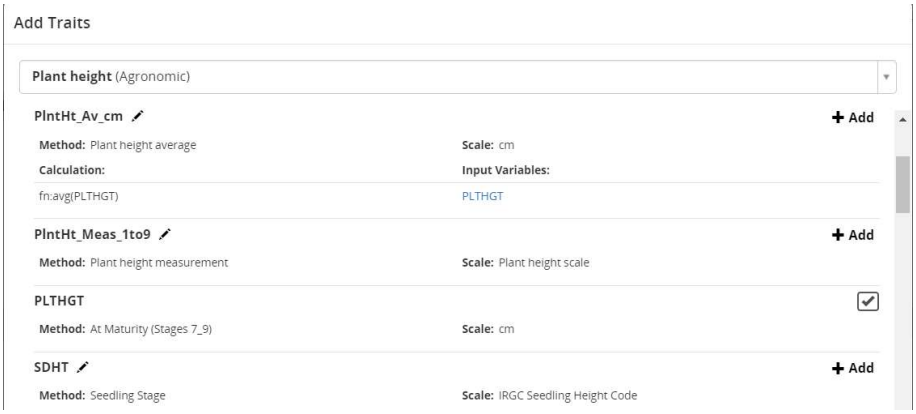
Specify a name for the subsample data sheet – we use PlantData, specify the number of plants to be sampled from each plot – 5 in our case, allow the variable to number the plants to be called PLANT_NO, and select all locations for sub-sampling. Click **Save**.



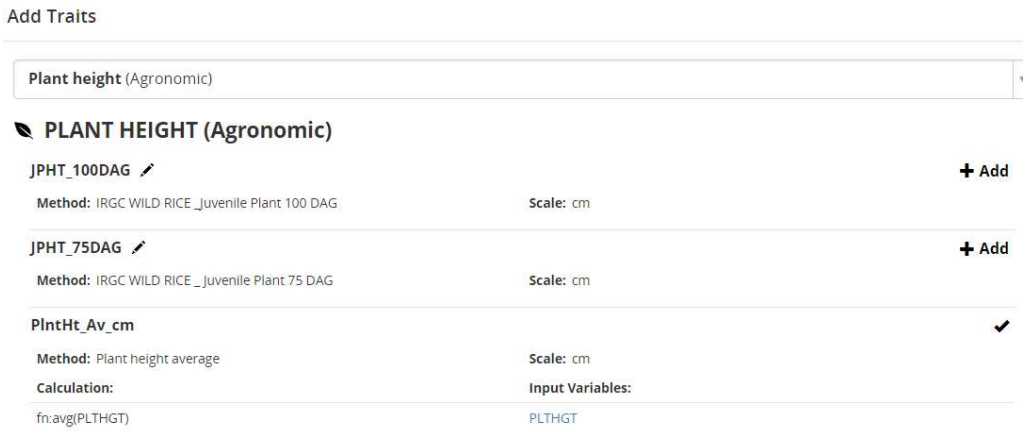
A new tab has been added to the study with one row for each sub-sample unit, indexed by Plant_NO within Plot.



Now we need to add traits to be measured on the sampling units. Click Add opposite the Traits section and search for plant height, choose PLTHGT – Plant height at maturity, cm. This variable will be added to the PlantData observation tab.



Now return to the Observation tab and add a new trait to the plot level observations - PlntHt_Av_cm;



This variable has a formula – avg(PLTHGT) which we can used to average the sample plant values.

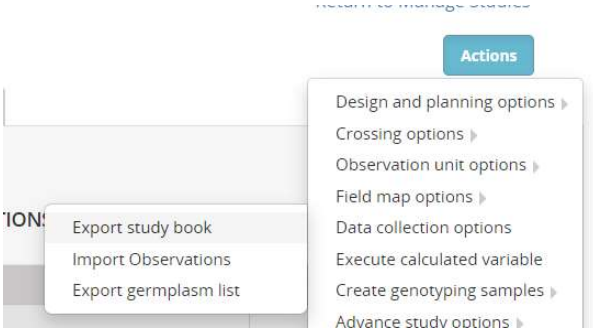
To collect the sub sample data you must export a study book for the sub sample dataset which we will do later.

Export the fieldbook, collect and load plot level data

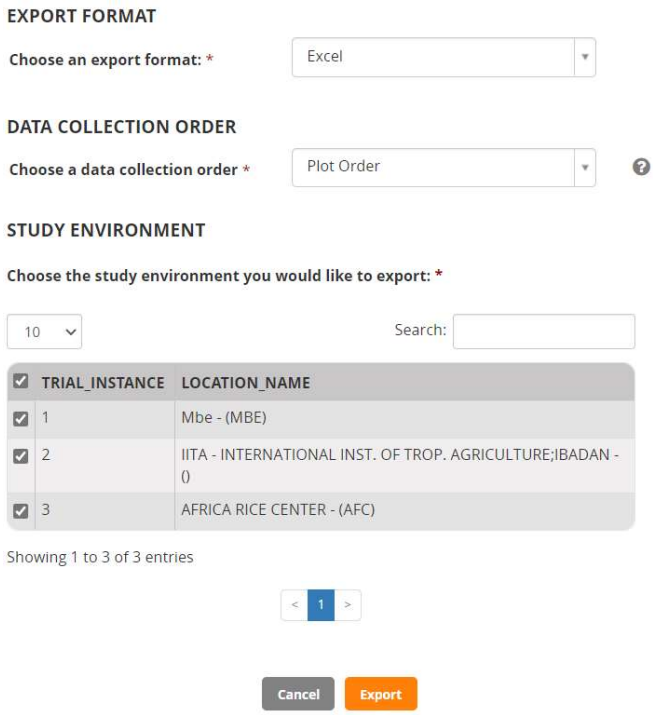
Now we can suppose that the trials are all planted and so we can first fill on the SEEDING_DATE on the environments tab. Lets assume they were all planted around mid July.

	Environment	PLOTSIZE	LOCATION_NAME	SEEDING_DATE
⊖	1	5.2	Mbe - (MBE)	20210714
⊖	2	5.2	IITA - INTERNATIONAL INST. OF TROP. AGRICULTURE;IBADAN	20210715
⊖	3	5.2	AFRICA RICE CENTER - (AFC)	20210713

Now select Actions>Data collection options>Export study book



Select Observations for export, then select **Excel** for the export format and **Plot** Order and choose all environment for export. Click **Export.**



Three fieldbooks will be downloaded into a zip file. Extract the files from the zip and open the fieldbook for Mbe:

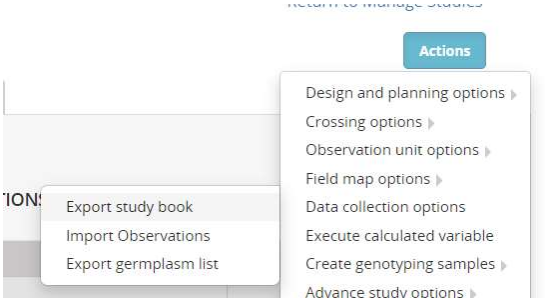
Each fieldbook has two sheeds, a Description sheet which describes what is on the Observation sheet, and the Observation sheet which will contain the data.

Enter some plausable random data into the columns for FlwDate_50Flw_Date, GrYld_wgh_gplot, and GRMOIST. (Leave the other traits since these can be calculated by BMS).

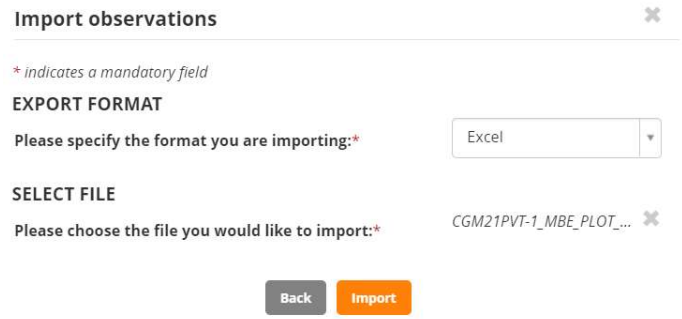
	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	OBS_UNIT	ENTRY_T	GID	DESIGNATION	STOCK_IE	ENTRY_N	CROSS	SEED_SO	PLOT_NO	REP_NO	BLOCK_N	FlwDate_50	Flw_Date	FLW50	GrYld_wgt	GRMOIST	GYTHA	PlntHt_Av
2	L1DOP5F	T	204538	IRRI 132	CGM1-16	16	UPL RI 5/IR 12979-24-1 (BROWN)	-	1	1	1	20211004			2857	11		
3	L1DOPSF	T	1161406	IR 72768-28-1-1	CGM1-2	2	IR 60080-46 A/IR 65907-116-1-B	-	2	1	1	20211001			1726	14		
4	L1DOP1V	T	904702	IDSA 113	CGM1-10	10	IDSA 113	-	3	1	1	20211009			2808	11		
5	L1DOPO0	T	569031	FARO 41	CGM1-11	11	IRAT 13/PALAWAN	-	4	1	1	20211010			2876	16		
6	L1DOPhd	T	1161408	IR 72768-12-1-1	CGM1-1	1	IR 60080-46 A/IR 65907-116-1-B	-	5	1	2	20211004			2696	11		
7	L1DOPx5	C	406626	UPL RI 5	CGM1-12	12	SIGADIS (AICRIP)/BPI 76-1	-	6	1	2	20211003			1556	11		
8	L1DOPR2	T	1161445	IR 75516-56-1-1-B	CGM1-5	5	IR 53236-275-1/CT 6516-24-3-2	-	7	1	2	20211003			1280	13		
9	L1DOP3R	T	70732	CNA 4196	CGM1-9	9	CNA 4196	-	8	1	2	20211011			2055	12		
10	L1DOPts1	T	1161458	IR 75502-24-1-1-B	CGM1-3	3	B 6144 F-MR-6-0-0/IR 55423-01 (NSIC RC 9)	-	9	1	3	20211004			1583	13		
11	L1DOPr0t	T	790394	YUNLU NO 28	CGM1-15	15	IDSA 6 (IRAT 216)/WUNENGDABAIGU-2-5	-	10	1	3	20211005			2642	16		
12	L1DOPFv	T	1161444	IR 75516-30-1-1-B	CGM1-4	4	IR 53236-275-1/CT 6516-24-3-2	-	11	1	3	20211010			2902	16		
13	L1DOPvHr	T	418229	WAB 326-B-B-7-H1	CGM1-13	13	ITA 235 (TOX 1785-19-18)/WABC 165	-	12	1	3	20211012			1961	15		
14	L1DOPcIF	T	1161327	IR 76561-AC 8-B	CGM1-8	8	CT 13382-9-4-M/IR 70358-145-1-1	-	13	1	4	20211002			1667	15		
15	L1DOPsKI	T	1161440	IR 75531-31-1-2-B	CGM1-7	7	IR 70360-54-1-B/VIENG	-	14	1	4	20211007			1404	15		
16	L1DOPy7ε	T	905029	WAB 534-B-3A 1-1	CGM1-14	14	WAB 181-18/DR 2	-	15	1	4	20211009			2539	11		
17	L1DOPZM	T	1161448	IR 75518-84-1-1-B	CGM1-6	6	IR 60080-46 A/IR 53236-275-1	-	16	1	4	20211006			1476	12		
18	L1DOPkm	T	204538	IRRI 132	CGM1-16	16	UPL RI 5/IR 12979-24-1 (BROWN)	-	17	2	1	20211006			2991	11		
19	L1DOPiHE	T	1161448	IR 75518-84-1-1-B	CGM1-6	6	IR 60080-46 A/IR 53236-275-1	-	18	2	1	20211003			1433	15		
20	L1DOPFG	C	406626	UPL RI 5	CGM1-12	12	SIGADIS (AICRIP)/BPI 76-1	-	19	2	1	20211011			2522	14		
21	L1DOPNL	T	418229	WAB 326-B-B-7-H1	CGM1-13	13	ITA 235 (TOX 1785-19-18)/WABC 165	-	20	2	1	20211003			2130	13		
22	L1DOPNX	T	569031	FARO 41	CGM1-11	11	IRAT 13/PALAWAN	-	21	2	2	20211004			1009	14		
23	L1DOPreb	T	790394	YUNLU NO 28	CGM1-15	15	IDSA 6 (IRAT 216)/WUNENGDABAIGU-2-5	-	22	2	2	20211002			1076	16		
24	L1DOP2X	T	1161440	IR 75531-31-1-2-B	CGM1-7	7	IR 70360-54-1-B/VIENG	-	23	2	2	20211002			2437	14		
25	L1DOPFX	T	1161445	IR 75516-56-1-1-B	CGM1-5	5	IR 53236-275-1/CT 6516-24-3-2	-	24	2	2	20211010			1510	16		
26	L1DOPt26	T	70732	CNA 4196	CGM1-9	9	CNA 4196	-	25	2	3	20211004			1489	13		
27	L1DOPMI	T	1161327	IR 76561-AC 8-B	CGM1-8	8	CT 13382-9-4-M/IR 70358-145-1-1	-	26	2	3	20211004			1273	11		
28	L1DOPpV	T	1161444	IR 75516-30-1-1-B	CGM1-4	4	IR 53236-275-1/CT 6516-24-3-2	-	27	2	3	20211007			2922	12		
29	L1DOP4nI	T	1161406	IR 72768-28-1-1	CGM1-2	2	IR 60080-46 A/IR 65907-116-1-B	-	28	2	3	20211011			1547	15		
30	L1DOPQV	T	1161458	IR 75502-24-1-1-B	CGM1-3	3	B 6144 F-MR-6-0-0/IR 55423-01 (NSIC RC 9)	-	29	2	4	20211004			1376	11		

Save the fieldbook.

Select Actions>Data collection options>Import Observations



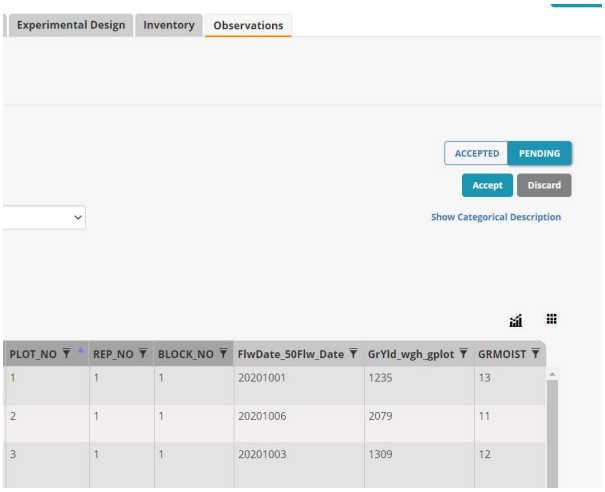
Click continue for Observations and then browse to the file just saved:



Click **Import**

(If you get a warning saying that you are trying to enter data for variables which are not in the dataset. Do you want to add them? Click NO to ignore it).

The data from the fieldbook will be moved into a staging area on the Observation sheet awaiting your approval.

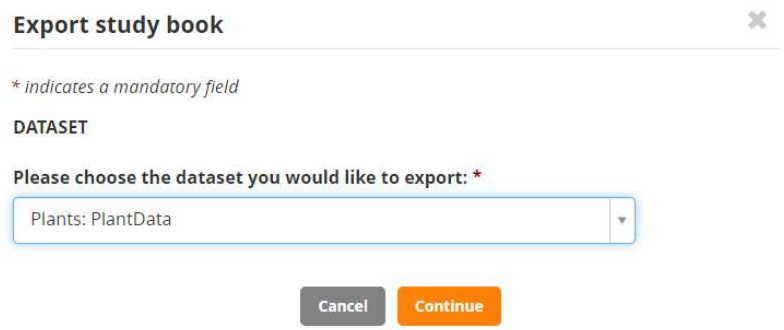


Any out of range data will be flagged and you can discard the whole dataset or correct the flagged entries. But if the data look good you click **Accept** and it is transferred into the study database.

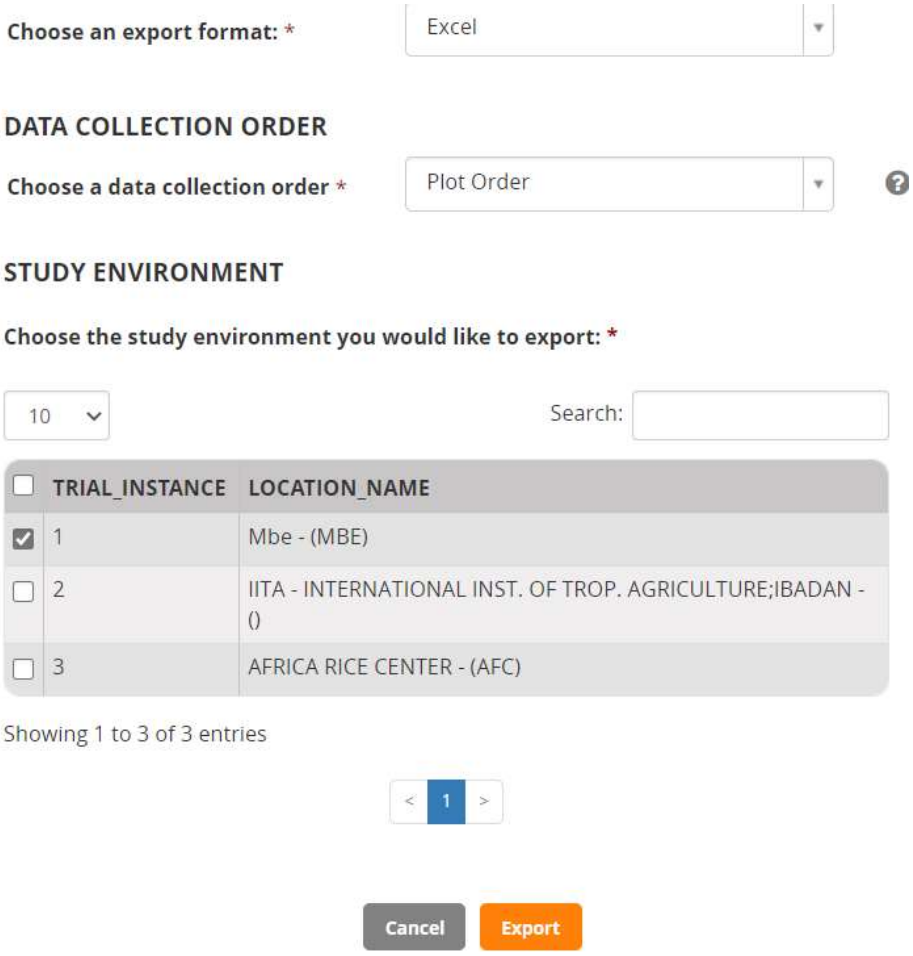
Export a Studybook for the sub sample data and load the values

Since our study has a sub-sample dataset called PlantData we need to export a study book for this dataset and collect that data. Select Actions>Data collection options>Export studybook.

Then select the PlantData observation set for export:



You can export as CSV, Excel or KSU formatted files. We will just export as Excel and just for location Mbe.

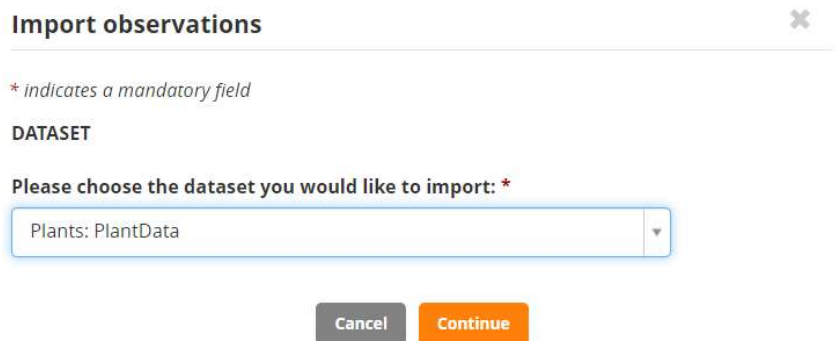


The study book is named with the Study, Location, Dataset- CGM20PVTa-1_MBE_PLANT_PlantData.xls.

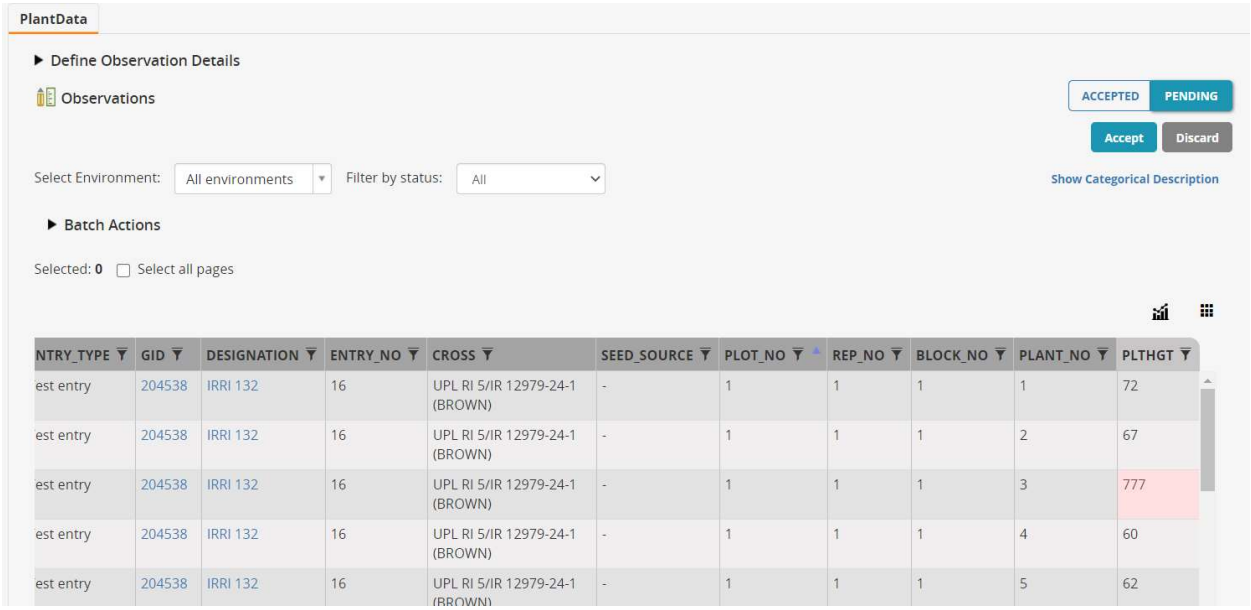
Collect the plant height data:

	A	B	C	D	E	F	G	H	I	J	K	L
1	OBS_UNIT	ENTRY_T	GID	DESIGNATION	ENTRY_N	CROSS	SEED_SO	PLOT_NO	REP_NO	BLOCK_N	PLANT_N	PLTHGT
2	L1DOPeC	T	204538	IRRI 132	16	UPL RI 5/IR 12979-24-1 (BROWN)	-	1	1	1	1	72
3	L1DOPfX	T	204538	IRRI 132	16	UPL RI 5/IR 12979-24-1 (BROWN)	-	1	1	1	2	67
4	L1DOPW	T	204538	IRRI 132	16	UPL RI 5/IR 12979-24-1 (BROWN)	-	1	1	1	3	777
5	L1DOPNl	T	204538	IRRI 132	16	UPL RI 5/IR 12979-24-1 (BROWN)	-	1	1	1	4	60
6	L1DOPFQ	T	204538	IRRI 132	16	UPL RI 5/IR 12979-24-1 (BROWN)	-	1	1	1	5	62
7	L1DOPpaf	T	1161406	IR 72768-28-1-1	2	IR 60080-46 A/IR 65907-116-1-B	-	2	1	1	1	66
8	L1DOPq4	T	1161406	IR 72768-28-1-1	2	IR 60080-46 A/IR 65907-116-1-B	-	2	1	1	2	70
9	L1DOPZjla	T	1161406	IR 72768-28-1-1	2	IR 60080-46 A/IR 65907-116-1-B	-	2	1	1	3	76
10	L1DOP90I	T	1161406	IR 72768-28-1-1	2	IR 60080-46 A/IR 65907-116-1-B	-	2	1	1	4	67
11	L1DOPYP	T	1161406	IR 72768-28-1-1	2	IR 60080-46 A/IR 65907-116-1-B	-	2	1	1	5	65
12	L1DOP6T	T	904702	IDSA 113	10	IDSA 113	-	3	1	1	1	79
13	L1DOPEH	T	904702	IDSA 113	10	IDSA 113	-	3	1	1	2	66
14	L1DOPem	T	904702	IDSA 113	10	IDSA 113	-	3	1	1	3	72
15	L1DOPegl	T	904702	IDSA 113	10	IDSA 113	-	3	1	1	4	80
16	L1DOPvZL	T	904702	IDSA 113	10	IDSA 113	-	3	1	1	5	72
17	L1DOPy2l	T	569031	FARO 41	11	IRAT 13/PALAWAN	-	4	1	1	1	65
18	L1DOPrY9	T	569031	FARO 41	11	IRAT 13/PALAWAN	-	4	1	1	2	65
19	L1DOPjPV	T	569031	FARO 41	11	IRAT 13/PALAWAN	-	4	1	1	3	78
20	L1DOPXk	T	569031	FARO 41	11	IRAT 13/PALAWAN	-	4	1	1	4	71
21	L1DOPYn	T	569031	FARO 41	11	IRAT 13/PALAWAN	-	4	1	1	5	75

Import the data – Actions>Data collection options>Import observations. Then select the PlantData datset.



Browse to the file just saved - CGM21PVT-1_MBE_PLANT_PlantData.xls and click **Import**. The data is entered into a staging aread witing for review and approval. We see already one out of bounds valuse since limits have been set between 40 and 80 cm for PLTHGT.



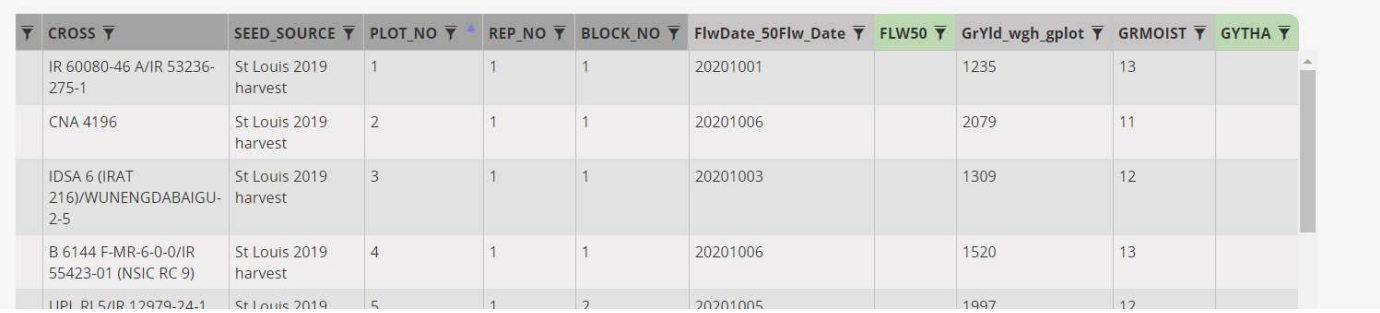
NTRY_TYPE	GID	DESIGNATION	ENTRY_NO	CROSS	SEED_SOURCE	PLOT_NO	REP_NO	BLOCK_NO	PLANT_NO	PLTHGT
est entry	204538	IRRI 132	16	UPL RI 5/IR 12979-24-1 (BROWN)	-	1	1	1	1	72
est entry	204538	IRRI 132	16	UPL RI 5/IR 12979-24-1 (BROWN)	-	1	1	1	2	67
est entry	204538	IRRI 132	16	UPL RI 5/IR 12979-24-1 (BROWN)	-	1	1	1	3	777
est entry	204538	IRRI 132	16	UPL RI 5/IR 12979-24-1 (BROWN)	-	1	1	1	4	60
est entry	204538	IRRI 132	16	UPL RI 5/IR 12979-24-1 (BROWN)	-	1	1	1	5	62

You can use the Filter by status box to filter to all out of bounds values and you will see there is only one in this set.

You can type in the cell with the out of bounds value and make it empty – a missing value. Then Accept the importd data.

Calculate derived variables

Once the data has been accepted you will see it in the full observatuions sheet with some variable headers in Green. These variables have associated formulae, and can be computed from the other data in the study. (Note they can also be read in from the excel spreadsheet if this is more convenient).



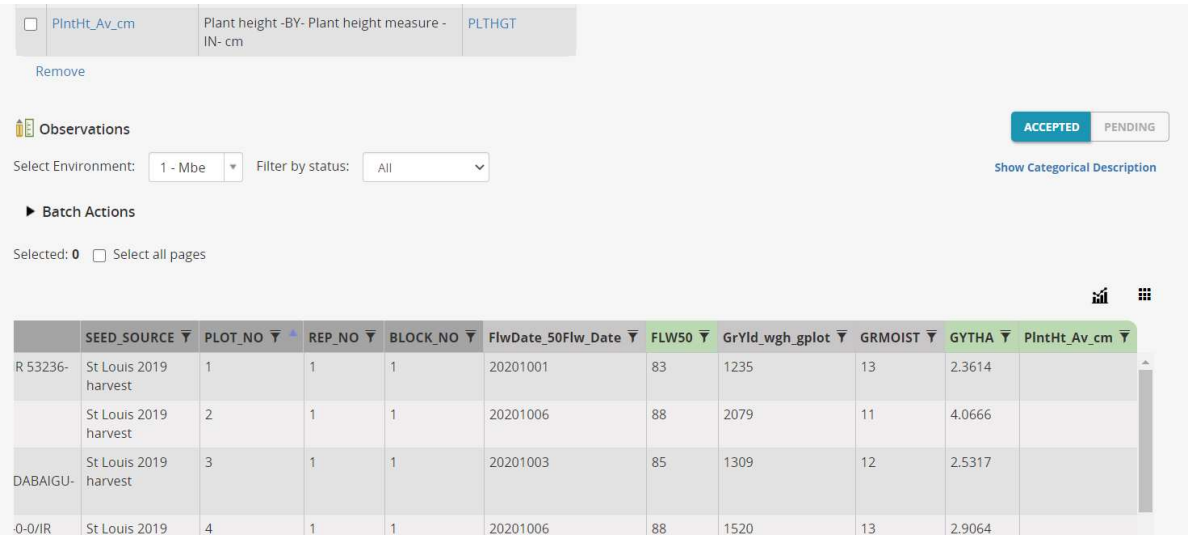
CROSS	SEED_SOURCE	PLOT_NO	REP_NO	BLOCK_NO	FlwDate_50Flw_Date	FLW50	GrYld_wgh_gplot	GRMOIST	GYTHA
IR 60080-46 A/IR 53236-275-1	St Louis 2019 harvest	1	1	1	20201001		1235	13	
CNA 4196	St Louis 2019 harvest	2	1	1	20201006		2079	11	
IDSA 6 (IRAT 216)/WUNENGDABAIGU-2-5	St Louis 2019 harvest	3	1	1	20201003		1309	12	
B 6144 F-MR-6-0-0/IR 55423-01 (NSIC RC 9)	St Louis 2019 harvest	4	1	1	20201006		1520	13	
UPL RI 5/IR 12979-24-1	St Louis 2019	5	1	2	20201005		1997	12	

To calcualte the flowering days, select Actions>Execute calculate variable. Continue with Observations, choose the flowering date variable (it may be called by the original name in the table) and select location Mbe, since this is the only one for which we have entered data. Click **Execute**, You will see that the dycount between SEEDING_DATE and FlwDate_50Flw_Date has been calculated and stored in FLW50.

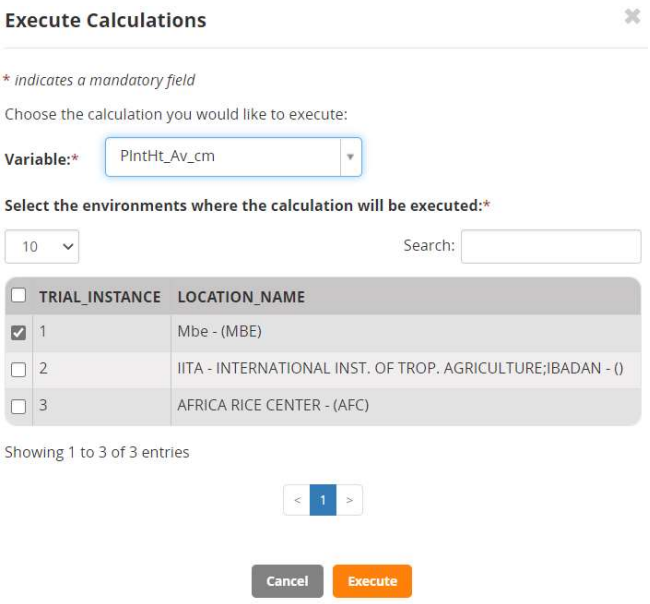
Repeate the calcualtion operation for the derived variable – GYTHA.

PLOT_NO	REP_NO	BLOCK_NO	FlwDate_50Flw_Date	FLW50	GrYld_wgh_gplot	GRMOIST	GYTHA
1	1	1	20211004	82	2857	11	5.5884
2	1	1	20211001	79	1726	14	3.2623
3	1	1	20211009	87	2808	11	5.4926
4	1	1	20211010	88	2876	16	5.3095
5	1	2	20211004	82	2696	11	5.2735
6	1	2	20211003	81	1556	11	3.0436
7	1	2	20211003	81	1280	13	2.4475

Now we also have a calculated variable for Plant height:



Select Actions>Execute calculate variable. Continue with Observations, choose the PlntHt_Av_cm variable and select location Mbe, since this is the only one for which we have entered data.



Click **Execute**.

The plant height averages have been filled in:

PLOT_NO	REP_NO	BLOCK_NO	FlwDate_50Flw_Date	FLW50	GrYld_wgh_gplot	GRMOIST	GYTHA	PlntHt_Av_cm
1	1	1	20211004	82	2857	11	5.5884	65.25
2	1	1	20211001	79	1726	14	3.2623	68.8
3	1	1	20211009	87	2808	11	5.4926	73.8
4	1	1	20211010	88	2876	16	5.3095	70.8
5	1	2	20211004	82	2696	11	5.2735	70.4
6	1	2	20211003	81	1556	11	3.0436	69.4
7	1	2	20211003	81	1280	13	2.4475	66.6
8	1	2	20211011	89	2055	12	3.9745	67

Notice that the first plot value is 65.25 which is the average of the four non-missing plants from that plot so it has been correctly adjusted for the missing plant value.

Return to the fieldbooks for the other two locations. Enter some data and calcualte the computed variables.

Importing existing trial designs and data

Frequently, especially when you start using BMS, you will have an existing trial which has been designed and planted outside BMS. You may or may not already have data collected for this trial but you want to import the trial design and data (if it exists) into BMS and proceed with analysis for BMS.

Actually in BMS there are two ways to perform this operation, one using the Study manager with a feature to **Import your own design**, and another using an Information Management application called **Import Datasets**. We will demonstrate the Study manager approach with Import your own design. For the second method you can look at the How to Article in the Knowledge base on Importing Historical Trial Data.

Objectives

At the end of this tutorial, the user should be able to:

1. Import entries for an existing or historical trial
2. Create a study for an existing or historical trail
3. Import the design of an existing or historical trial
4. Load data for an existing or historical trial.

Creating a germplasm list for an existing trial

Often an existing trial may be available in excel such as the file CGM20AVT.xlsx where the experimental design and the data are stored in a format like the one shown below.

	A	B	C	D	E	F	G	H	I	J	K	L
1	LOCATION_NAME	PLOT_NO	REP_NO	BLOCK_NO	ENTRY_NO	DESIGNATION	PANH	FLW	PlntHt_Av_cm	GY_wgh_gplot	GRMOIST	BLAST
2	Raipur RRS	1	1	1	13	IR 68815-51-PMI 2-UBN 2-5-B	10	81	67.65	1977	16.11	7
3	Raipur RRS	2	1	1	16	IR 68815-51-PMI 2-UBN 4-7-B	7	90	66.63	2030	17.02	1
4	Raipur RRS	3	1	1	3	IR 68823-40-7-B-7-B	10	91	67.65	1981	16.38	2
5	Raipur RRS	4	1	1	1	IR 68835-58-1-1-B	8	77	67.41	1929	16.14	8
6	Raipur RRS	5	1	1	19	IR 68201-21-2-B-4-B-B	7	96	65.31	2026	16.33	7
7	Raipur RRS	6	1	1	6	IR 68853-50-6-B-1-B	11	103	66.5	2026	16.64	1
8	Raipur RRS	7	1	1	15	IR 68815-51-PMI 2-UBN 3-4-B	8	98	64.24	1988	16.77	7
9	Raipur RRS	8	1	1	23	IR 68098-B-10-2-1-3-B	9	100	67.17	1968	16.62	2
10	Raipur RRS	9	1	2	10	IR 68815-25-PMI 3-UBN 6-B-B	8	79	65.79	2029	16.53	0
11	Raipur RRS	10	1	2	25	IR 68098-B-10-2-1-B-B	7	82	69.2	1949	16.14	5
12	Raipur RRS	11	1	2	32	IR 72	11	77	66.14	2029	16.96	6
13	Raipur RRS	12	1	2	8	IR 69513-23-SRN-1-UBN 4-1-B	11	97	66.82	1919	16.33	4
14	Raipur RRS	13	1	2	12	IR 68815-51-PMI 2-UBN 2-4-B	9	85	67.6	1992	16.56	9
15	Raipur RRS	14	1	2	22	IR 67488-B-43-1-1-2-B	9	95	66.19	1976	16.87	6
16	Raipur RRS	15	1	2	29	IR 70182-18-PMI 7-2-B	8	84	66.91	2010	16.42	5
17	Raipur RRS	16	1	2	7	IR 69513-21-SRN 2-UBN 1-7-B	12	103	67.01	1999	16.55	5

There may be data for several sites stacked together as with the file CGM20AVT.xls (4 sites) which you can find in the Sample Files folder, or the data for different sites may come is separate but similar files. We need to load this data into a BMS study for analysis.

The first thing to do is to create a germplasm list for the distinct entries in the trial. This can be done by finding the entries in the BMS and adding them to a list with the List Manager, or it can be done by extracting the distinct entries from the file(s) and importing them with Germplasm Import.

We will use Germplasm Import, but it is important to check that the entry numbers and the designations are consistent across every rep of the trial. When you have checked this you can extract the ENTRY_NO and DESIGNATION for site 1 rep 1 and paste it into a Germplasm Import template:

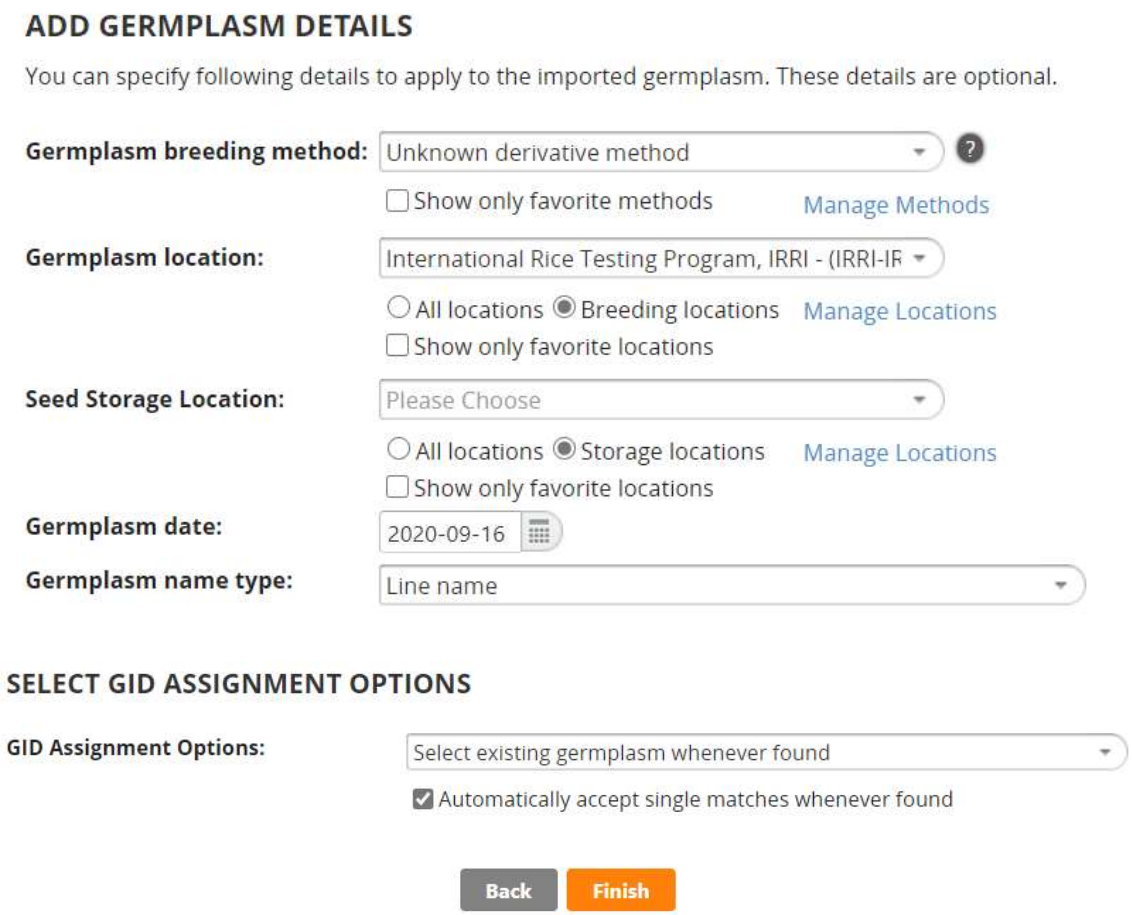
The observation sheet looks like this:

	A	B	C	D	E
1	ENTRY	DESIGNATION	GID	CROSS	SOURCE
2	1	IR 68835-58-1-1-B			
3	2	IR 68821-101-4-B1-1-B			
4	3	IR 68823-40-7-B-7-B			
5	4	IR 68835-88-1-B-2-B			
6	5	IR 68835-91-1-B-4-B			
7	6	IR 68853-50-6-B-1-B			
8	7	IR 69513-21-SRN 2-UBN 1-7-B			
9	8	IR 69513-23-SRN-1-UBN 4-1-B			
10	9	IR 69515-26-KKN 3-UBN 3-4-B			
11	10	IR 68815-25-PMI 3-UBN 6-B-B			
12	11	IR 68815-51-PMI 2-UBN 2-2-B			
13	12	IR 68815-51-PMI 2-UBN 2-4-B			
14	13	IR 68815-51-PMI 2-UBN 2-5-B			
15	14	IR 68815-51-PMI 2-UBN 2-6-B			
16	15	IR 68815-51-PMI 2-UBN 3-4-B			
17	16	IR 68815-51-PMI 2-UBN 4-7-B			
18	17	IR 68815-51-PMI 2-UBN 7-1-B			
19	18	IR 68815-51-PMI 2-UBN 10-1-B			
20	19	IR 68201-21-2-B-4-B-B			
21	20	IR 67632-14-2-5-1-2-B			
22	21	IR 67632-14-2-5-1-3-B			
23	22	IR 67488-B-43-1-1-2-B			
24	23	IR 68098-B-10-2-1-3-B			
25	24	IR 68098-B-10-2-1-6-B			
26	25	IR 68098-B-10-2-1-B-B			
27	26	IR 68098-B-10-2-2-2-B			
28	27	IR 68098-B-78-2-1-6-B			
29	28	IR 68098-B-78-2-1-12-B			
30	29	IR 70182-18-PMI 7-2-B			
31	30	IR 70173-29-SRN 2-1-B			
32	31	IR 64			
33	32	IR 72			

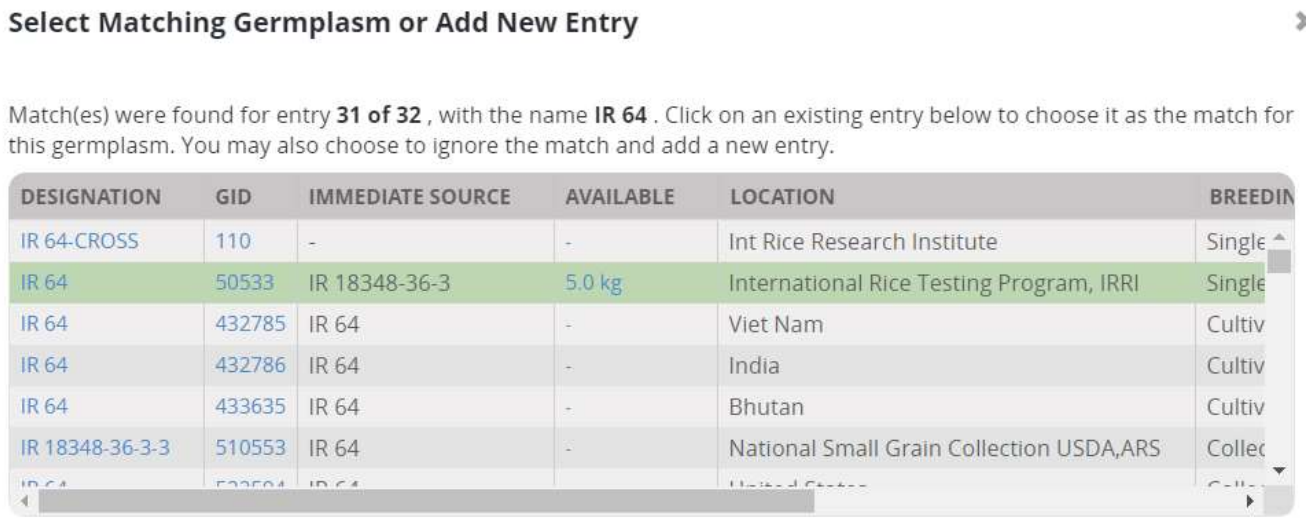
And the description sheet like this:

	A	B	C
1	**LIST NAME**	CGM20AVT	
2	**LIST DESCRIPTION**	2020 AVT for Project CGM	
3	**LIST DATE**	20200101	
4	**LIST TYPE**	LST	
5			
6	**CONDITION**	**DESCRIPTION**	**PROPERTY**
7	LIST OWNER	Name of the Principal Investiga	PERSON
8	ID OF LIST OWNER	ID of the Principal Investigator	PERSON
9			
10	**FACTOR**	**DESCRIPTION**	**PROPERTY**
11	ENTRY	The germplasm entry number	GERMPLASM ENTRY
12	DESIGNATION	The name of the germplasm	GERMPLASM ID
13	GID	The GID of the germplasm	GERMPLASM ID
14	CROSS	The pedigree string of the gerr	CROSS NAME
15	SOURCE	The seed source of the germp	SEED SOURCE
16	ENTRY CODE	Germplasm entry code	GERMPLASM ENTRY
17	DRVNM	Derivative Name	GERMPLASM ID

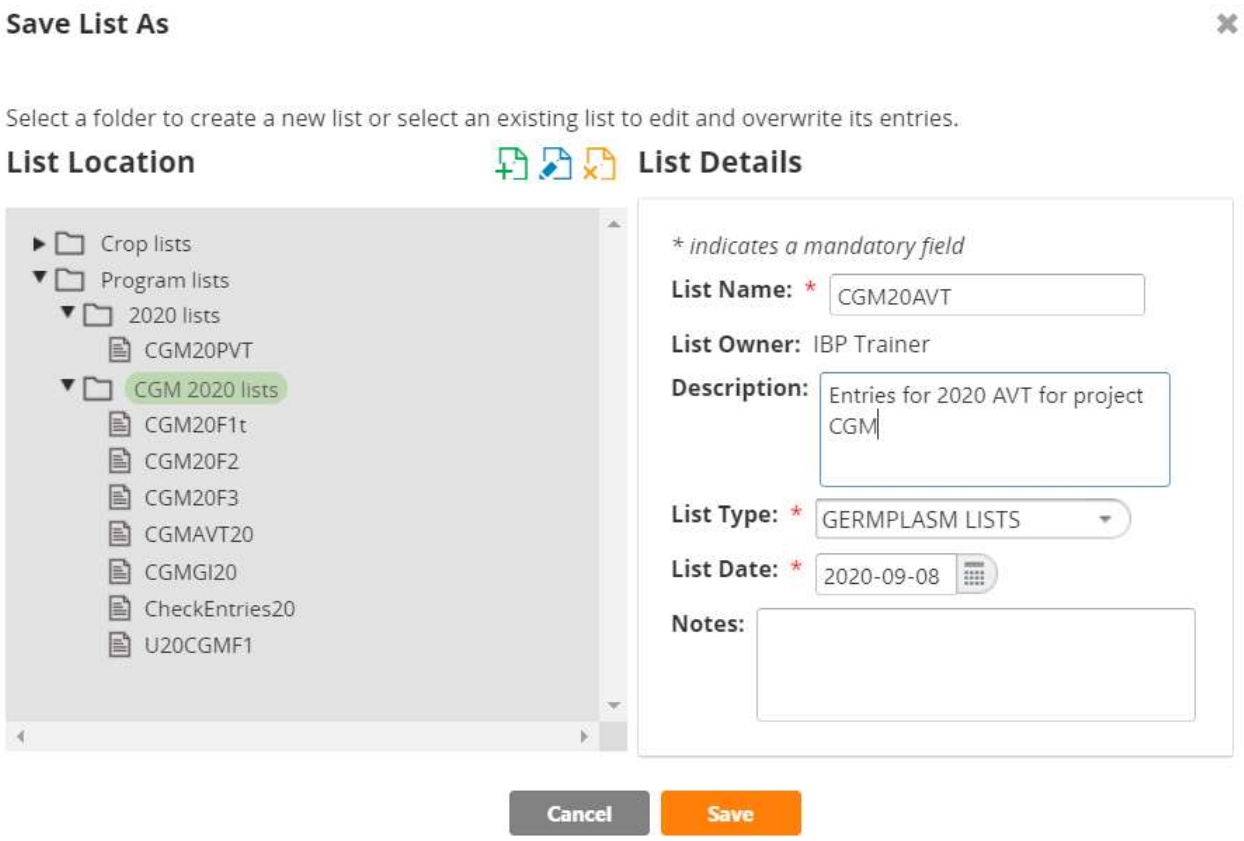
This list is now imported int BMS taking care to select existing enteries wherever appropriate: Go to Import Germplasm, browse for the template file, fill in the import details and click **Finish**.



Select appropriate germplasm when there are multiple hits, such as for the checks IR 64 and IR 72. (Select the ones with seed stock):



Save the list:



Extracting a lay-out file for an existing trial

Since this trial has already been planted, we cannot generate a trial in BMS. Instead we must read in the existing randomization – the lay-out.

A lay-out file is a very simple csv file which contains information about the experimental design and optionally, the trait names and values. It has one row for each plot in the trial and it must have a column called TRIAL_INSTANCE containing an integer number indicating which site the plot comes from, it must have a column called PLOT_NO with a sequence number of 1 to number of plots at each location, it must have a column called ENTRY_NO indicating which entry is planted on the plot. Then it may have columns like REP_NO and BLOCK_NO giving design details, and it can have columns with trait names for headings and these columns may or may not have data. If they have data it will be entered, if they do not, the expectation is that fieldbooks will be exported after the design is completed and the data collected and entered through the fieldbooks in the usual way.

So our lay-out file could look as follows:

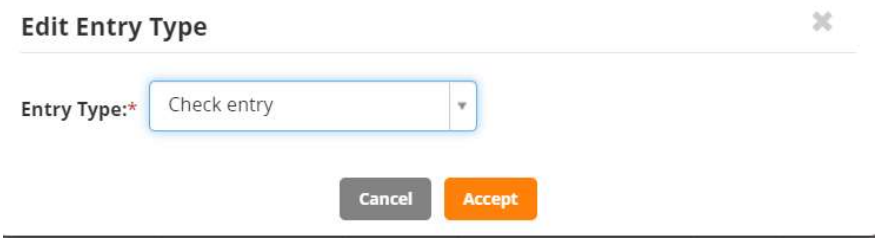
	A	B	C	D	E	F	G	H	I	J	K
1	TRIAL_INSTANCE	PLOT_NO	REP_NO	BLOCK_NO	ENTRY_NO	PANH	FLW	PlntHt_Av_cm	GY_wgh_gplot	GRMOIST	BLAST
2	1	1	1	1	13	10	81	67.65	1977	16.11	7
3	1	2	1	1	16	7	90	66.63	2030	17.02	1
4	1	3	1	1	3	10	91	67.65	1981	16.38	2
5	1	4	1	1	1	8	77	67.41	1929	16.14	8
6	1	5	1	1	19	7	96	65.31	2026	16.33	7
7	1	6	1	1	6	11	103	66.5	2026	16.64	1
8	1	7	1	1	15	8	98	64.24	1988	16.77	7
9	1	8	1	1	23	9	100	67.17	1968	16.62	2
10	1	9	1	2	10	8	79	65.79	2029	16.53	0
11	1	10	1	2	25	7	82	69.2	1949	16.14	5
12	1	11	1	2	32	11	77	66.14	2029	16.96	6
13	1	12	1	2	8	11	97	66.82	1919	16.33	4
14	1	13	1	2	12	9	85	67.6	1992	16.56	9
15	1	14	1	2	22	9	95	66.19	1976	16.87	6
16	1	15	1	2	29	8	84	66.91	2010	16.42	5
17	1	16	1	2	7	12	103	67.01	1999	16.55	5
18	1	17	1	3	28	7	96	67	1989	16.64	0
19	1	18	1	3	18	12	80	67.14	2060	16.69	5
20	1	19	1	3	14	12	96	69.34	2001	16.81	6
21	1	20	1	3	20	11	108	66.39	2001	17	0
22	1	21	1	3	2	12	83	67.96	2026	16.98	6
23	1	22	1	3	4	8	109	65.61	2022	16.97	3

It is best have the data for all the sites stacked together in one file, but not essential, extra sites can be added later.

Create the Study for the trial

From the Study Manager select Start a new study. Enter some metadata, and select use and existing study as a template.

On the Germplasm and Checks tab enter the germplasm list we imported and set the last two entries, IR 64 and IR 72 to be check entries. (click on their Entry Type to change it)



Save the new trial in your 2020 Trials folder, make one if you do not have one (CGM 2020 Trials for me).

On the Environments tab, set the number of environments to 4 and click ok. Then in the location names box look for the sites of the trial - Raipur RRS, Titabar RRS, Pusa RRS and Cuttack RRS. If the locations do not exist in your database they need to be added by a Crop Manager since the function of adding locations is a crop role not a program role.

The Environment numbers and names must match those in the original data file and the lay-out file. If you know the plot size and seeding date, enter them.

Go to the Observations sheet and remove all the traits. Select them and click **Remove**. This is because we will be entering the traits from the lay-out file in this case.

TRAITS

Add

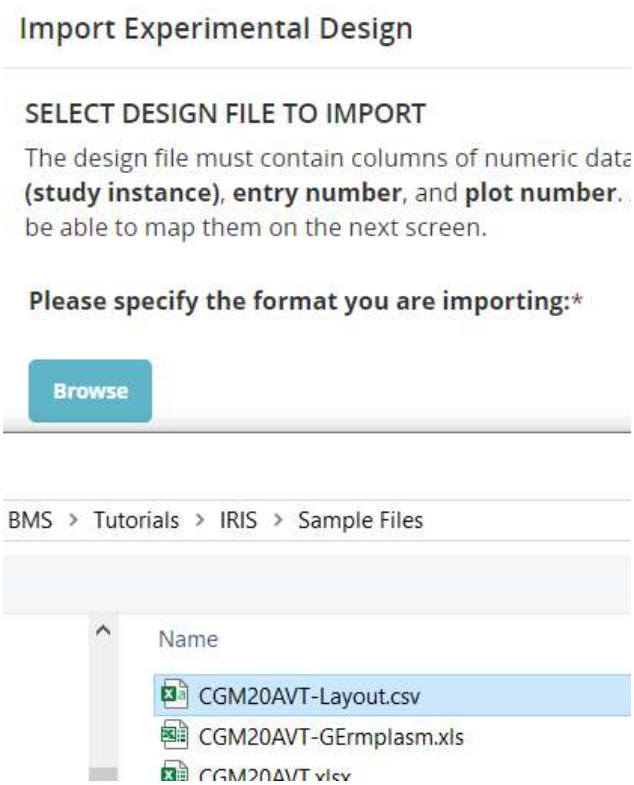
	Name	Description	Input Variables
☑	FlwDate_50Flw_Date	Flowering date -BY- Fifty percent flowering date observation-IN- ISO Date (yyyymmdd)	
☑	FLW50	Time to flowering (from sowing) -BY- Calculation - Days to 50% flowering from sowing -IN- Day	SEEDING_DATE , FlwDate_50Flw_Date
☑	GrYld_wgh_gplot	Grain yield -BY- AYLD_CONT method -IN- G per plot	
☑	GRMOIST	Moisture content of grain. Expressed in percentage.	
☑	GYTHA	Grain yield in T per Ha corrected for moisture	GRMOIST , PLOT SIZE , GrYld_wgh_gplot
☑	PlntHt_Av_cm	Plant height -BY- Plant height measure -IN- cm	PLTHGT

Remove

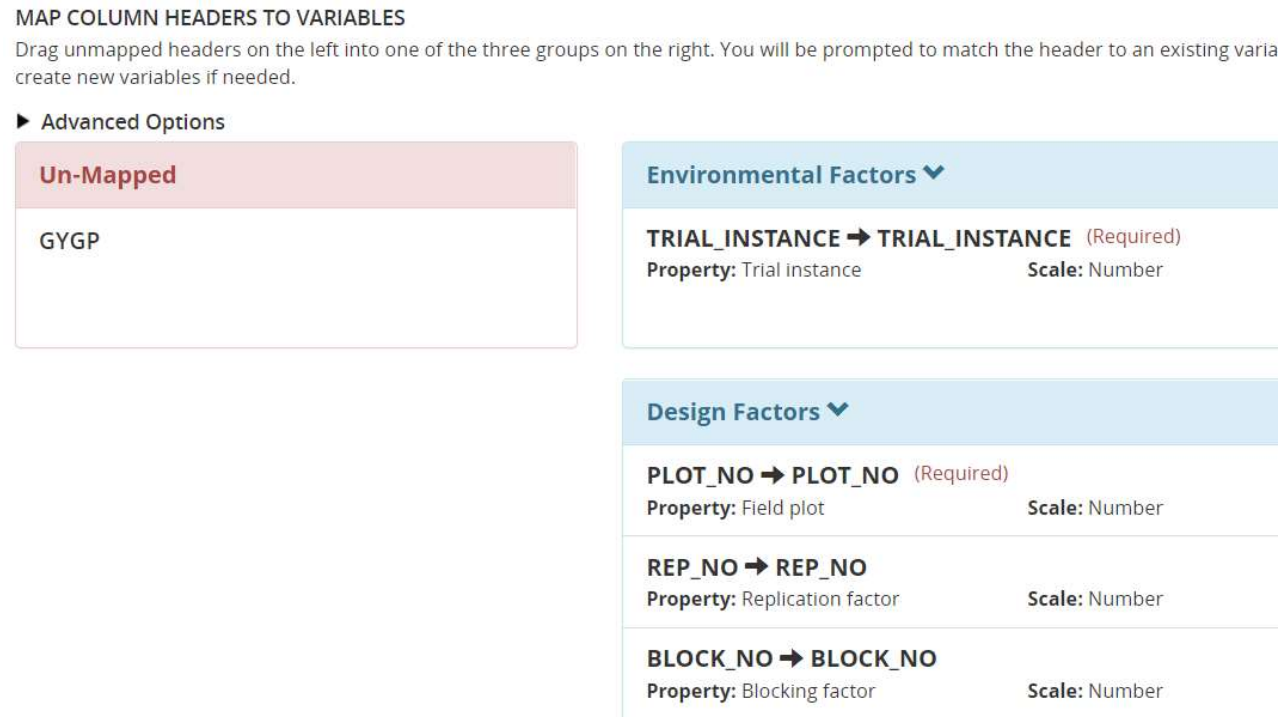
Import the lay-out file

Now open the Experimental Design tab and click **import** an experimental design:

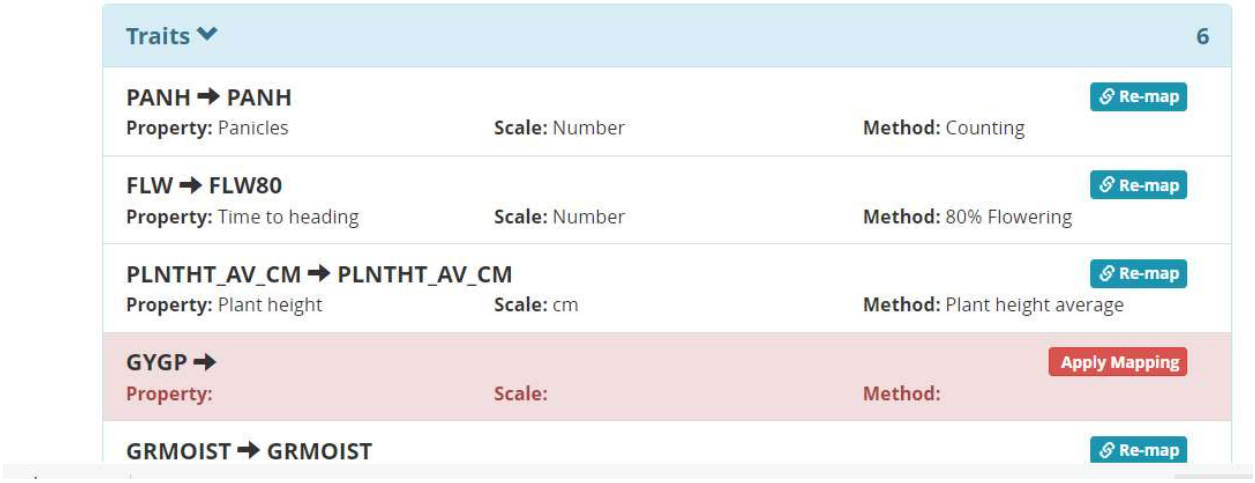
Browse to the layout file and open it:



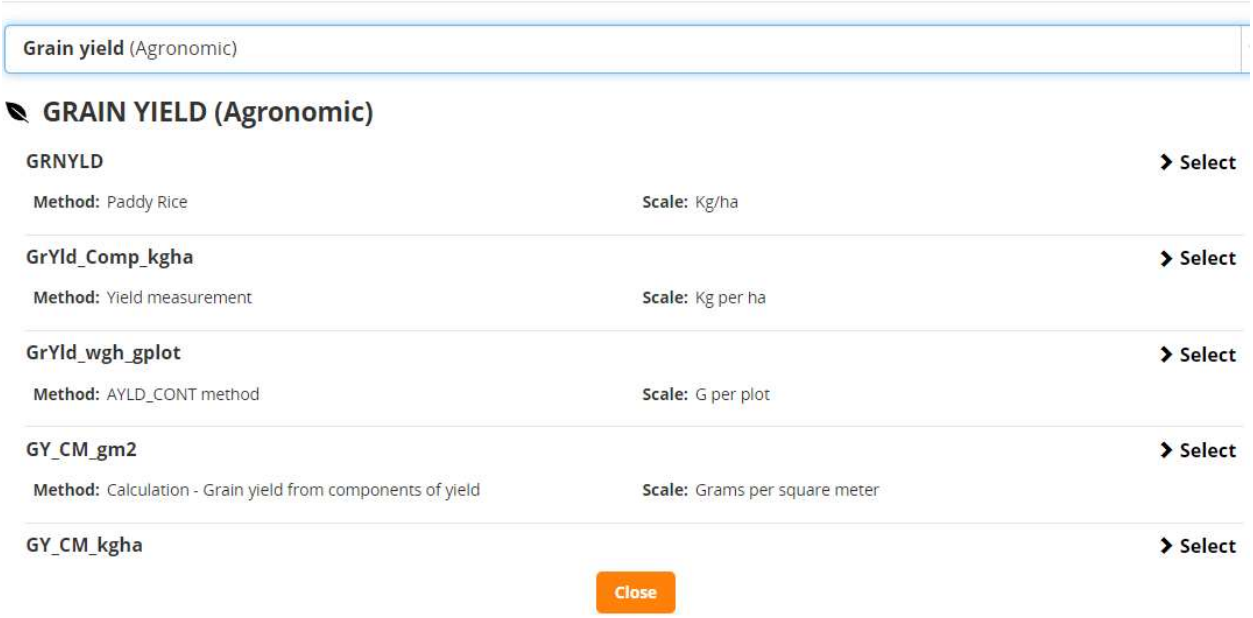
Click Continue to read the layout file and you will open a trait mapping form. Nearly all the traits have been automatically mapped to variables in the ontology because they have exactly the same names. You should check each to be sure the automatic mapping is correct. Any variables which cannot be mapped remail in the Unmapped variables box.



In our case GYGP – grain yield in grams per plot has not been mapped. It should be mapped to the variable GrYld_wgh_gplot. To make this mapping drag the variable down and place it in the Traits section then click Apply Mapping.

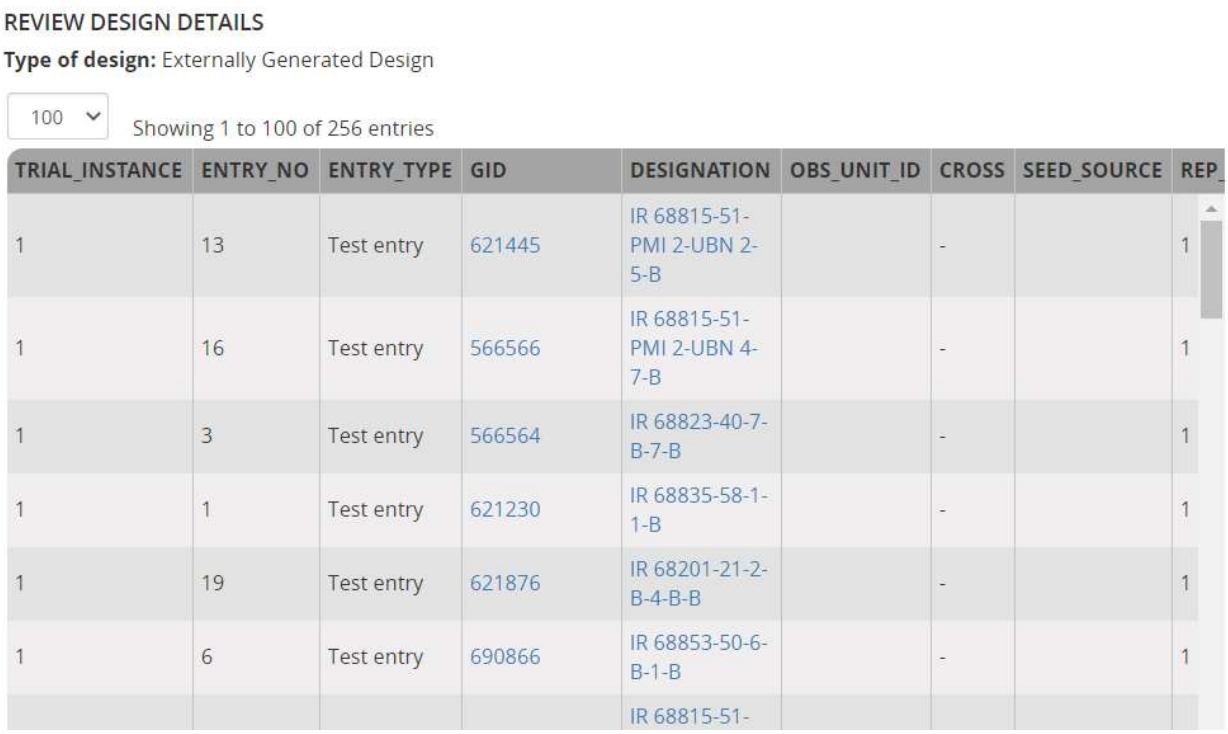


This will open the Ontology search box. Look for grain yield traits and select GrYld_wgh_gplot.



Now the mapping is complete click **Next**.

You will get a review panel to check the import:



TRIAL_INSTANCE	ENTRY_NO	ENTRY_TYPE	GID	DESIGNATION	OBS_UNIT_ID	CROSS	SEED_SOURCE	REP_
1	13	Test entry	621445	IR 68815-51-PMI 2-UBN 2-5-B		-		1
1	16	Test entry	566566	IR 68815-51-PMI 2-UBN 4-7-B		-		1
1	3	Test entry	566564	IR 68823-40-7-B-7-B		-		1
1	1	Test entry	621230	IR 68835-58-1-1-B		-		1
1	19	Test entry	621876	IR 68201-21-2-B-4-B-B		-		1
1	6	Test entry	690866	IR 68853-50-6-B-1-B		-		1
				IR 68815-51-				

Click Finish and the design (and data in our case) will be stored.

Add trait GYTHA if necessary and compute its values for all locations.

Statistical Analysis

BMS links with a Statistical Analysis package called Breeding View. This package is propriety software developed by VSNi and is based on Genstat and uses ASREML for mixed model analysis of plant breeding trials. Breeding View is designed to quickly perfor routine analysis for plant breeding. It is not so versitile as a statistical package, such as the full version of Genstat, which is required for research analysis.

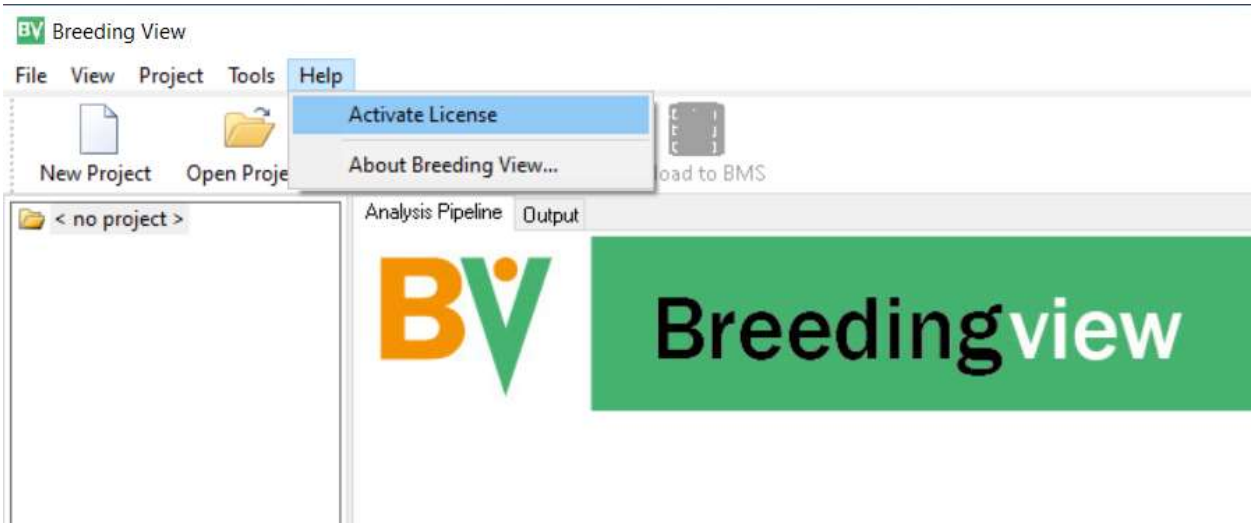
Objectives

At the end of this tutorial, the user should be able to:

1. Specify single site analysis for a trial in BMS
2. Run Single site analysis with Breeding View and save the means back to BMS
3. Specify a GxE analysis for trial means for a study in BMS
4. Run the GxE analysis with Breeding View.

Install and License Breeding View

Breeding View is a stand alone program which must be downloaded to your windows 64 bit computer, and installed. Before you can use it you must sspply a license key by clicking Help>Activate license:

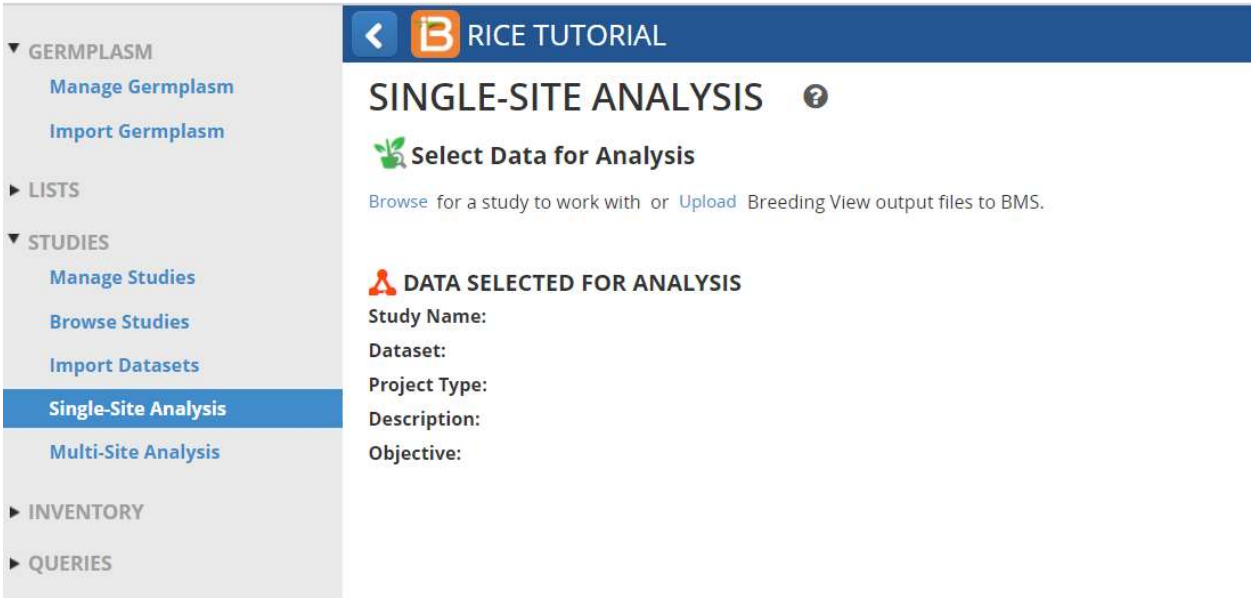


Once the license is activiated you can use Breeding View but it normally requires an internet connection to check the validity of the license before running. There is more informations about installing and licensing Breeding View in the manual.

https://bmspro.io/1937/breeding-management-system-manual-40/install-breeding-view-statistical-application

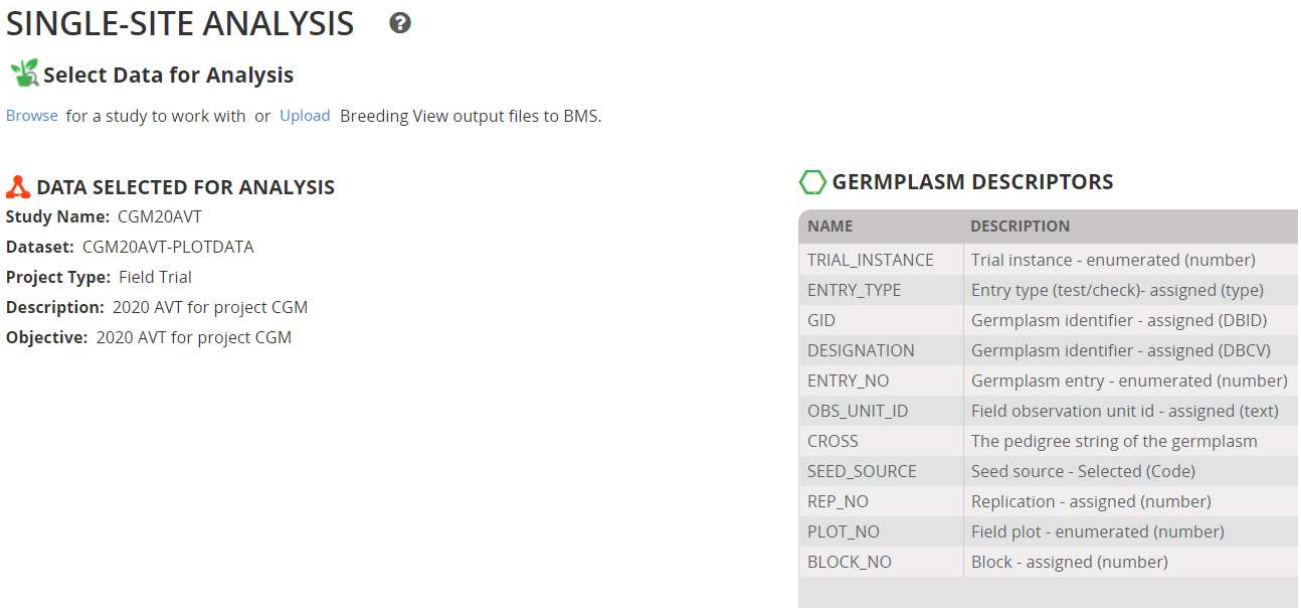
Specify single site analysis for a trial in BMS

From the **STUDIES** menu select **Single-Site Analysis**:

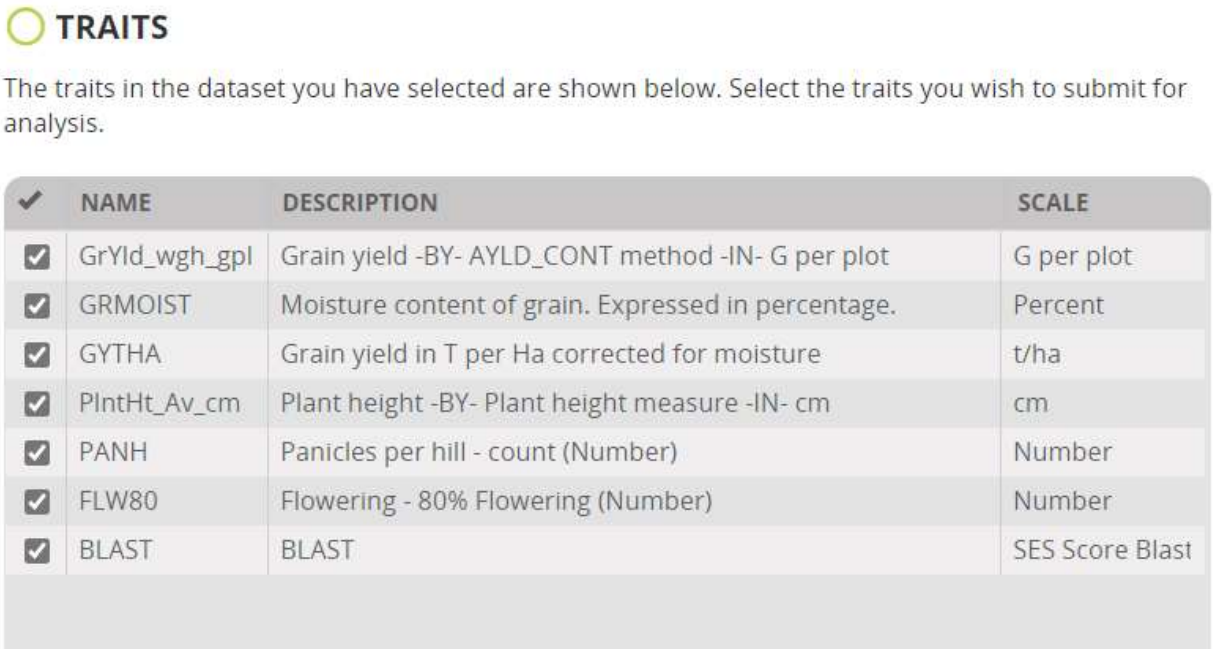


Browse for the study containing the data to be analysed. We will select the trial we created and imported in the previous tutorial – CGM20AVT for me. Highlight the file and click Select.

The Study will open and display the factors it contains:



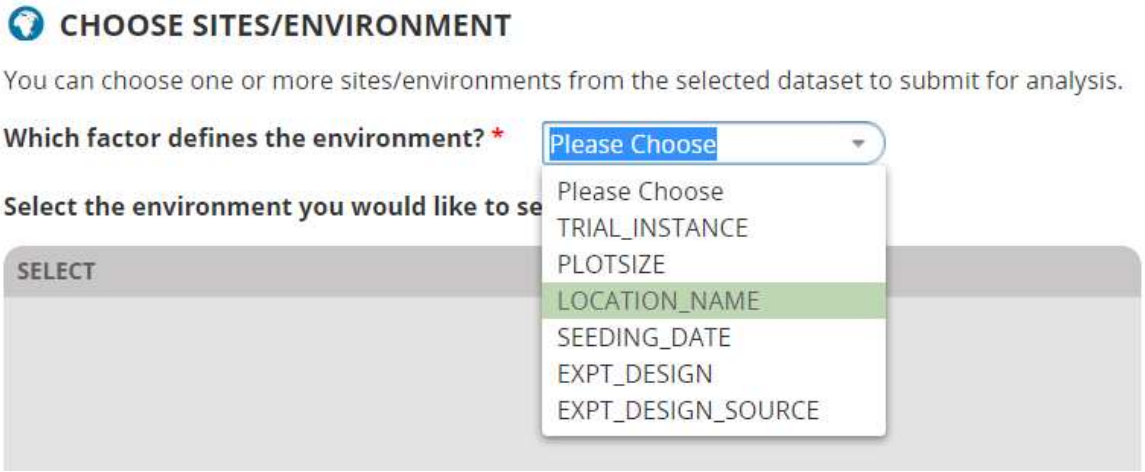
And the traits it contains:



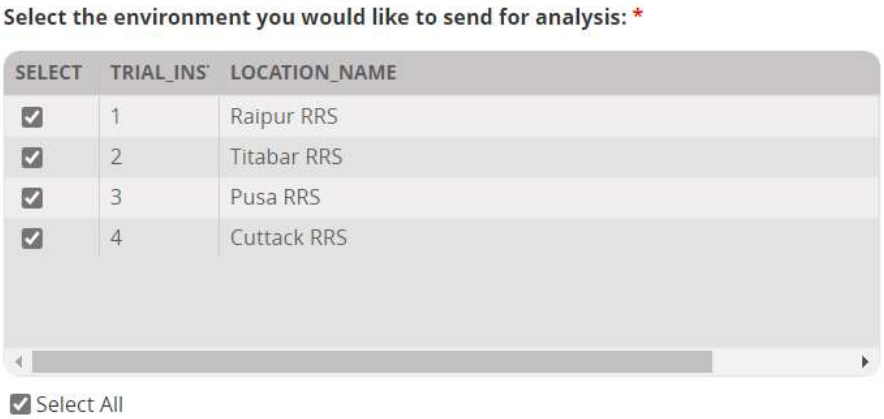
By default all the traits are selected for Analysis. Deselect those which do not require analysis, GrYld_wgh_gplant and GRMOIST in our example do not require analysis. We will analysis the BLAST score even though it is not a continuous variable, it is an ordinal variable with a fair number of classes.

Any of the non-analysed varaibles can be specified to be covariates in an analysis of covariance for the analysed variables. We will not specify any covariates. Click **Next**.

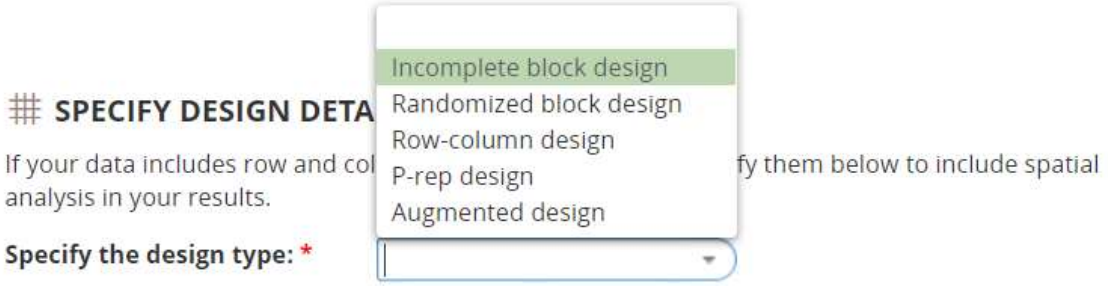
On the form to Specify Options for Breeding View Analysis you must first select the variable which distinguishes between sites. You always have the variable TRIAL_INSTANCE available, but usually the LOCATION_NAME is preferable. We will select LOCATION_NAME.



And we will select all the locations for analysis:

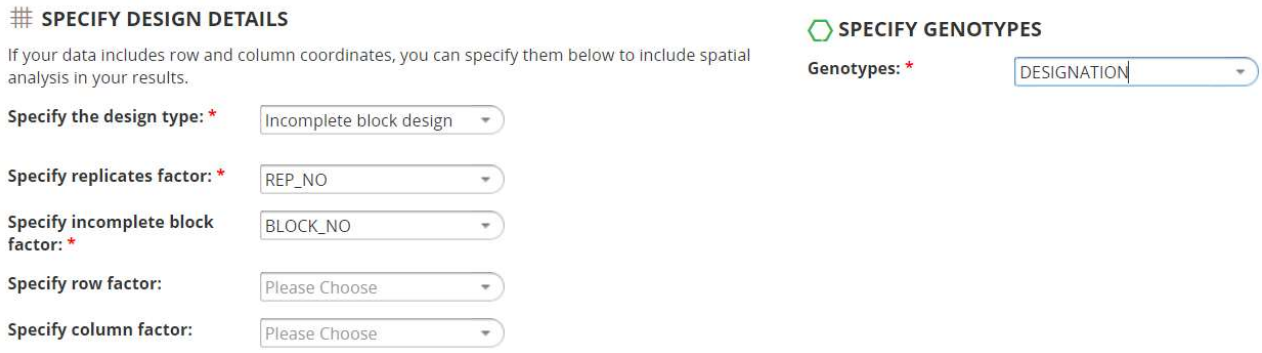


Next you must specify the design type. Since our design was imported the system doesn not know the design type. Select Incomplete block design:



This selection opens a form requesting the design variables – Rep and Block for our design. REP_NO and BLOCK_NO have been selected by default. There are also fields for specifying variables indicating the row and column layout of the trial. These variable are created by the process of making and Field Plan (which you can do in the Study Manager using Actions>Field map options>Make a Fieldmap). If the row and column layout is available then Breeding View will attempt a Spatial Analysis of the trial to reduce the error variability. If they are not available (as in our case) or a spatial analysis is not wanted the variables should not be selected.

Finally you need to specify the variable which deines the entries in the trial. You always have ENTRY_NO available, but usually the DESIGNATION is preferred:



Once the analysis details are specified you must request a Download of the Input Files for Breeding View. Click Download Input Files:

This will download a zip file with the names of the study.zip – CGM20AVT.zip for me.

You need to extract the files from this zip file int a directory where the analysis will be performed. There are two files in the zip, one csv file which contains the data to be analysed and on xml file which contains the instructions for the analysis.

Running Breeding View for Single Site Analysis

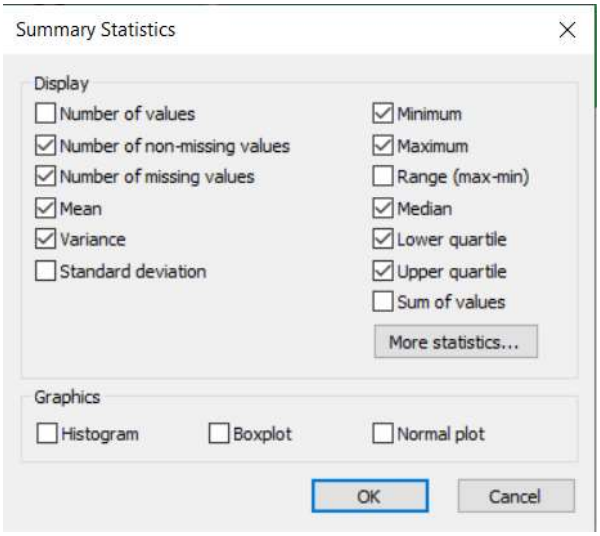
Once the files have been extracted you can run Breeding View and clcik the Open Project icon and navigate to the directory where the files have been extracted. Select the xml file and click Open.

The Single Site Analysis Pipeline will be activiated:

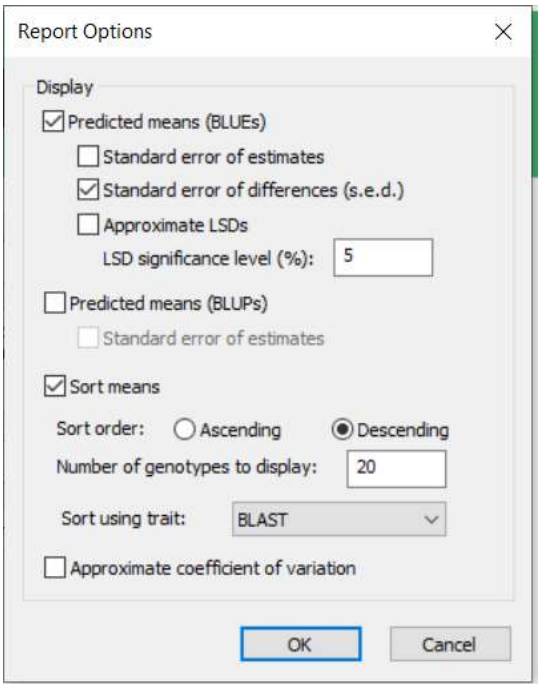
This contains a menu on the left showing the Environments and the Traits which have been specified for analysis. You can select or deselect any and all sites and or traits for analysis. We will leave all the sites and all the variables to be analysed.

The right hand panel shows the pipeline of tasks for single site analysis. Each task has a default configuration, but can also be specially configures by righ-clicking of the task icon and selecting settings and adjusting the menu.

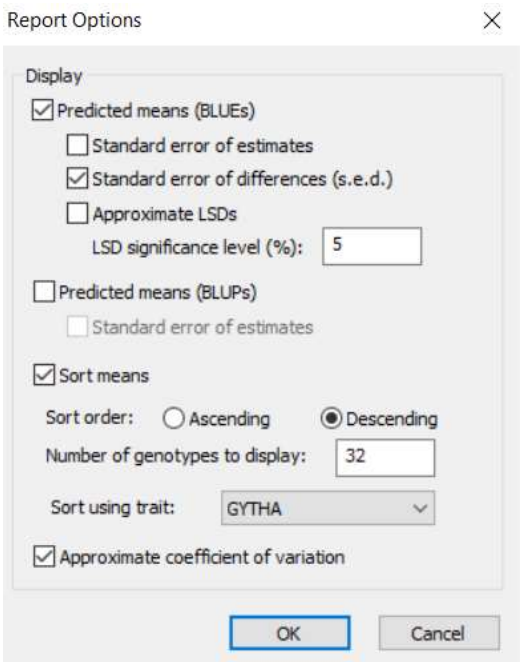
For example right click on **Quality control phenotypes**, click Settings and you will get the following menu:



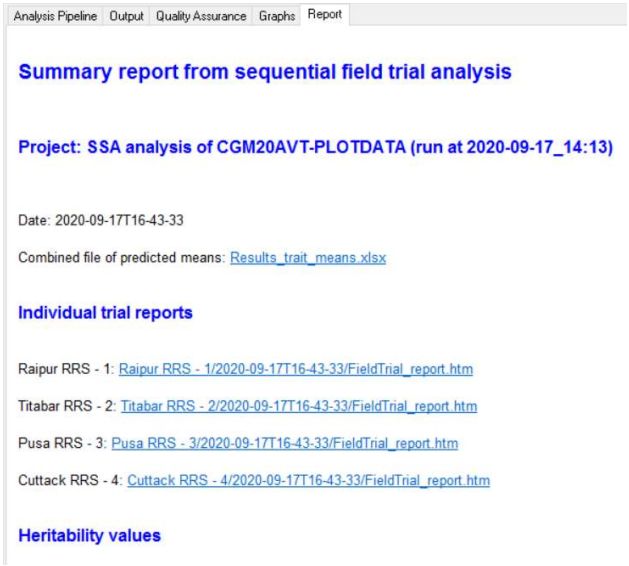
We will accept the default settings for this task. However right click on the icon for Generate Report and select settings:



You will see that the table of means will be sorted on BLAST score in descending order and only the 20 entries with largest BLAST score will be printed in the report. This is clearly not what we want, so you should change the setting to 32 genotypes to be displayed and sort using GYTHA and we would also like to see the Coefficient of Variation so we check that box, then click OK.



To run the analysis right click on the Quality crontol phenotypes icon and select **Run selected envirment pipeline.**

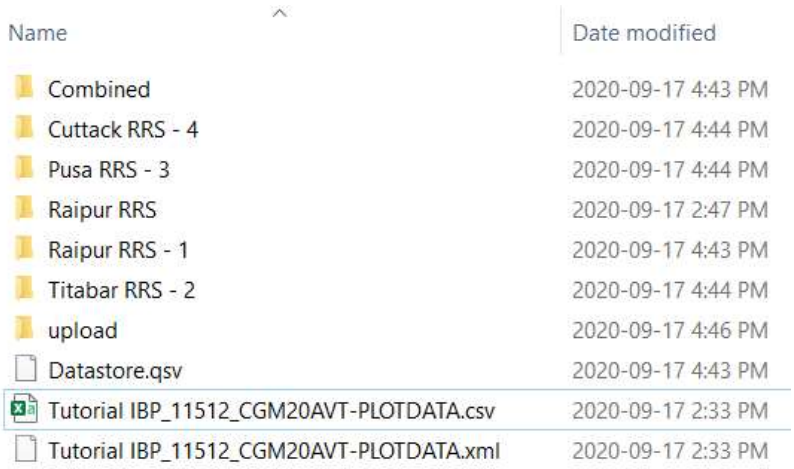


To understand how to interpret the Breeding View output you can colsult the Mamual under the topic Statistical Analysis at this URL

https://bmspro.io/1823/breeding-management-system/tutorials/maize-single-site-analysis-4-location-batch

Saving the means from Single Site Analysis to BMS

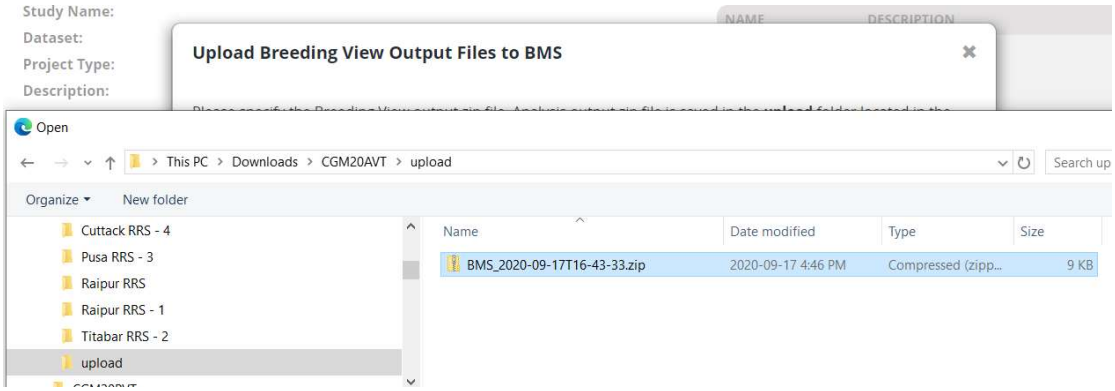
The output from the Single Site Analysis is stored in the folder where the original downloaded files were extracted. A folder has been added with the results for each site, and two other folders are added, one called combined with a table of means over all locations, and another called upload which contains a zip file of means ready for uploading to the BMS.



In the BMS click Single Site ANlsysis for the Statistical Analysis menu, then click **upload** to upload Breeding View output files.

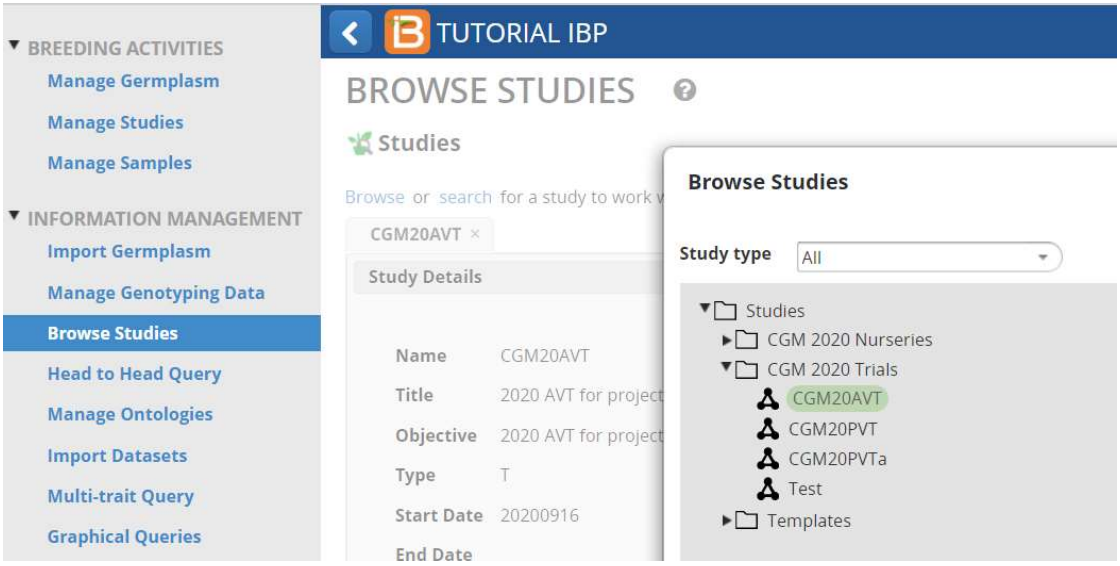
Select the study for which the analysis has been completed – CGM20AVT for me.

Click Browse and navigate to the Upload folder in the Breeding View output directory. Select the zip file from the upload folder.

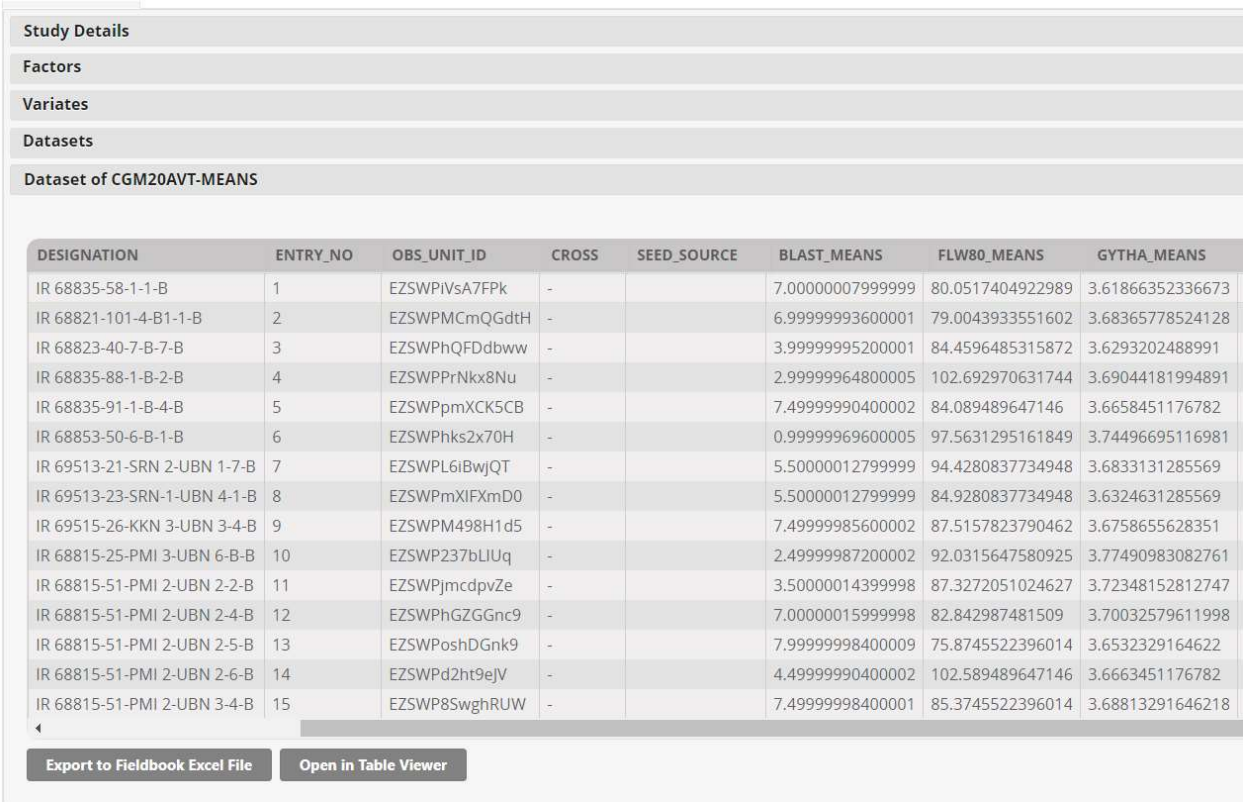


Click open and then upload. The upload will take a few seconds to complete and you should receive a Success notice.

To see the means in BMS you can use the Browse Studies app for the INFORMATION MANAGEMENT menu.



Open the study for which you wish to see the means, click on Datasets and select the means dataset:

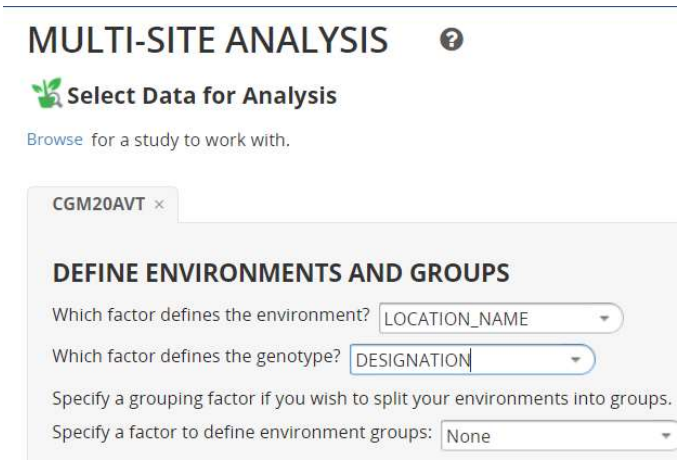


DESIGNATION	ENTRY_NO	OBS_UNIT_ID	CROSS	SEED_SOURCE	BLAST_MEANS	FLW80_MEANS	GYTHA_MEANS
IR 68835-58-1-1-B	1	EZSWPiVsA7FPk	-		7.00000007999999	80.0517404922989	3.61866352336673
IR 68821-101-4-B1-1-B	2	EZSWPMCmQGdtH	-		6.99999993600001	79.0043933551602	3.68365778524128
IR 68823-40-7-B-7-B	3	EZSWPhQFDdbww	-		3.99999995200001	84.4596485315872	3.6293202488991
IR 68835-88-1-B-2-B	4	EZSWPPrNkx8Nu	-		2.99999964800005	102.692970631744	3.69044181994891
IR 68835-91-1-B-4-B	5	EZSWPpmXCK5CB	-		7.49999990400002	84.089489647146	3.6658451176782
IR 68853-50-6-B-1-B	6	EZSWPhks2x70H	-		0.99999969600005	97.5631295161849	3.74496695116981
IR 69513-21-SRN 2-UBN 1-7-B	7	EZSWPL6iBwjQT	-		5.50000012799999	94.4280837734948	3.6833131285569
IR 69513-23-SRN-1-UBN 4-1-B	8	EZSWPmXIFXmD0	-		5.50000012799999	84.9280837734948	3.6324631285569
IR 69515-26-KKN 3-UBN 3-4-B	9	EZSWPM498H1d5	-		7.49999985600002	87.5157823790462	3.6758655628351
IR 68815-25-PMI 3-UBN 6-B-B	10	EZSWP237bLIUq	-		2.49999987200002	92.0315647580925	3.77490983082761
IR 68815-51-PMI 2-UBN 2-2-B	11	EZSWPjmcdpvZe	-		3.50000014399998	87.3272051024627	3.72348152812747
IR 68815-51-PMI 2-UBN 2-4-B	12	EZSWPhGZGGnc9	-		7.00000015999998	82.842987481509	3.70032579611998
IR 68815-51-PMI 2-UBN 2-5-B	13	EZSWPoshDGnk9	-		7.99999998400009	75.8745522396014	3.6532329164622
IR 68815-51-PMI 2-UBN 2-6-B	14	EZSWPd2ht9eJV	-		4.49999990400002	102.589489647146	3.6663451176782
IR 68815-51-PMI 2-UBN 3-4-B	15	EZSWP8SwghRUW	-		7.49999998400001	85.3745522396014	3.68813291646218

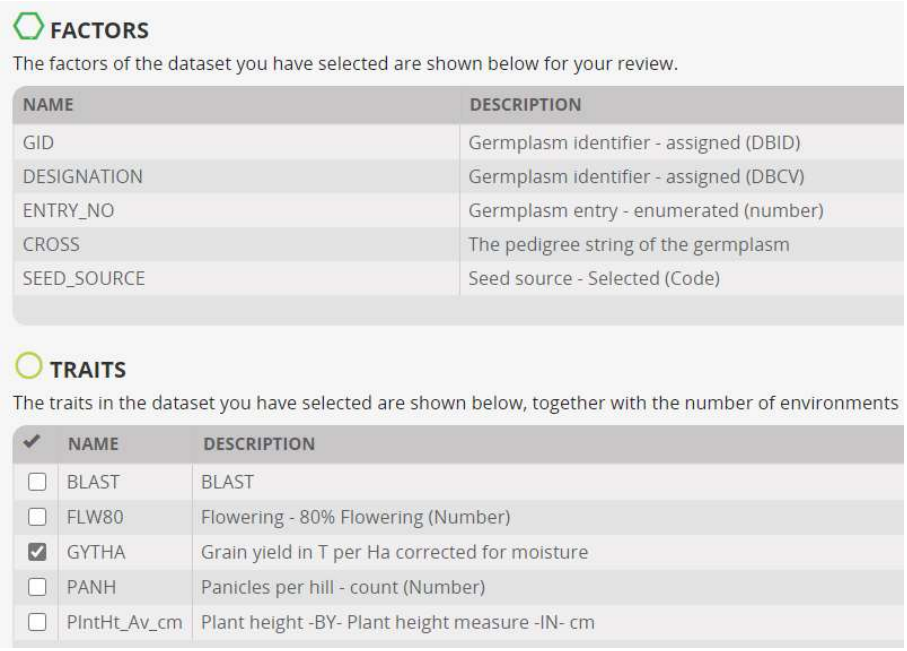
You can export any of the datasets from this application as well.

Specify a multi-site analysis for a trial in BMS

From the **STUDIES** menu select **Multi-Site Analysis** and browse to the study for which you have uploaded means and for which you wish to do a multi-site analysis. You need at least three sites for a GxE analysis and four or more is better. As with the single site anlaysis you are asked to specify the variable defining sites – usually use LOCATION_NAME, and for genotypes – usually DESIGNATION. Next the form asks if your environments are already grouped in some way which would account for significant GxE interactions. Usually we do not know about groupings at the early stage, and mostly do not have enough environments for subsets.



The form also show the variables in the study and asks the user to check the traits for which a GxE analysis is required. We will analysis only GYTHA. Click **Next**.



FACTORS

The factors of the dataset you have selected are shown below for your review.

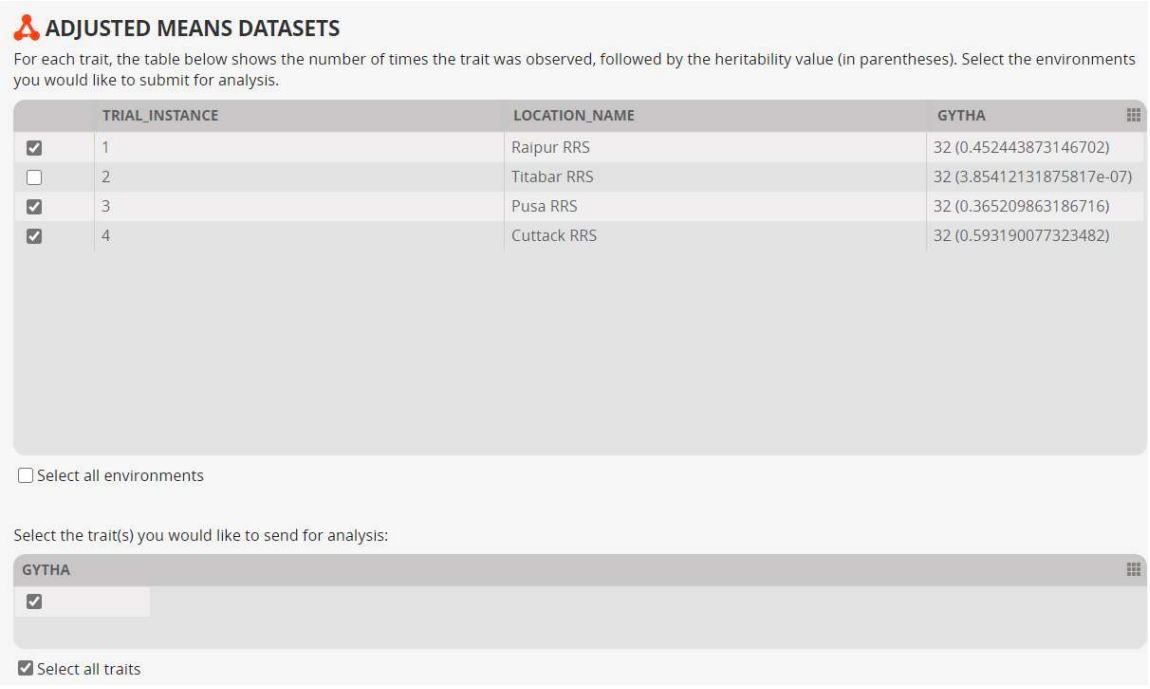
NAME	DESCRIPTION
GID	Germplasm identifier - assigned (DBID)
DESIGNATION	Germplasm identifier - assigned (DBCV)
ENTRY_NO	Germplasm entry - enumerated (number)
CROSS	The pedigree string of the germplasm
SEED_SOURCE	Seed source - Selected (Code)

TRAITS

The traits in the dataset you have selected are shown below, together with the number of environments

	NAME	DESCRIPTION
☐	BLAST	BLAST
☐	FLW80	Flowering - 80% Flowering (Number)
☑	GYTHA	Grain yield in T per Ha corrected for moisture
☐	PANH	Panicles per hill - count (Number)
☐	PlntHt_Av_cm	Plant height -BY- Plant height measure -IN- cm

A form displaying a data summary for the locations and the selected traits is presented. This allows you to eliminate environments for which there is insufficient data of for which the heritability is too low, and similarly at the botton you can eliminate traits. Whe have already limited out traits to one, but we notice that Environment 2 has zero heritability. There would not normally be any reason to include an environment in a GxE alanysis which was showing a very small heritability so we will uncheck environment 2 and continue the analysis with just three environments.



ADJUSTED MEANS DATASETS

For each trait, the table below shows the number of times the trait was observed, followed by the heritability value (in parentheses). Select the environments you would like to submit for analysis.

	TRIAL_INSTANCE	LOCATION_NAME	GYTHA
☑	1	Raipur RRS	32 (0.452443873146702)
☐	2	Titabar RRS	32 (3.85412131875817e-07)
☑	3	Pusa RRS	32 (0.365209863186716)
☑	4	Cuttack RRS	32 (0.593190077323482)

☐ Select all environments

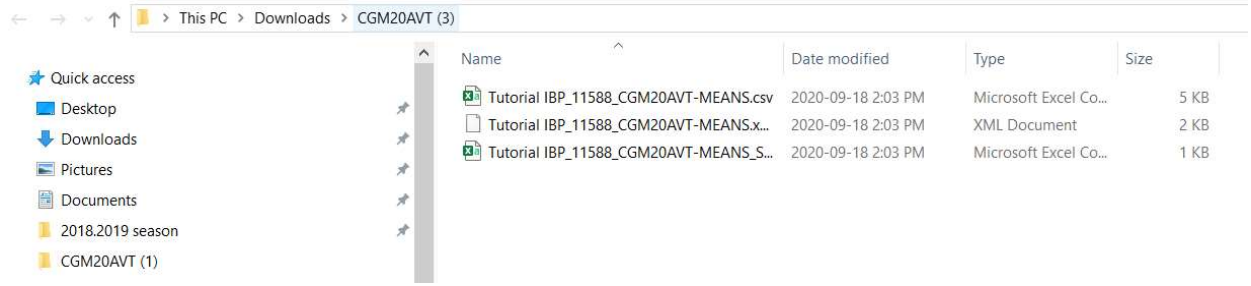
Select the trait(s) you would like to send for analysis:

GYTHA
☑

☑ Select all traits

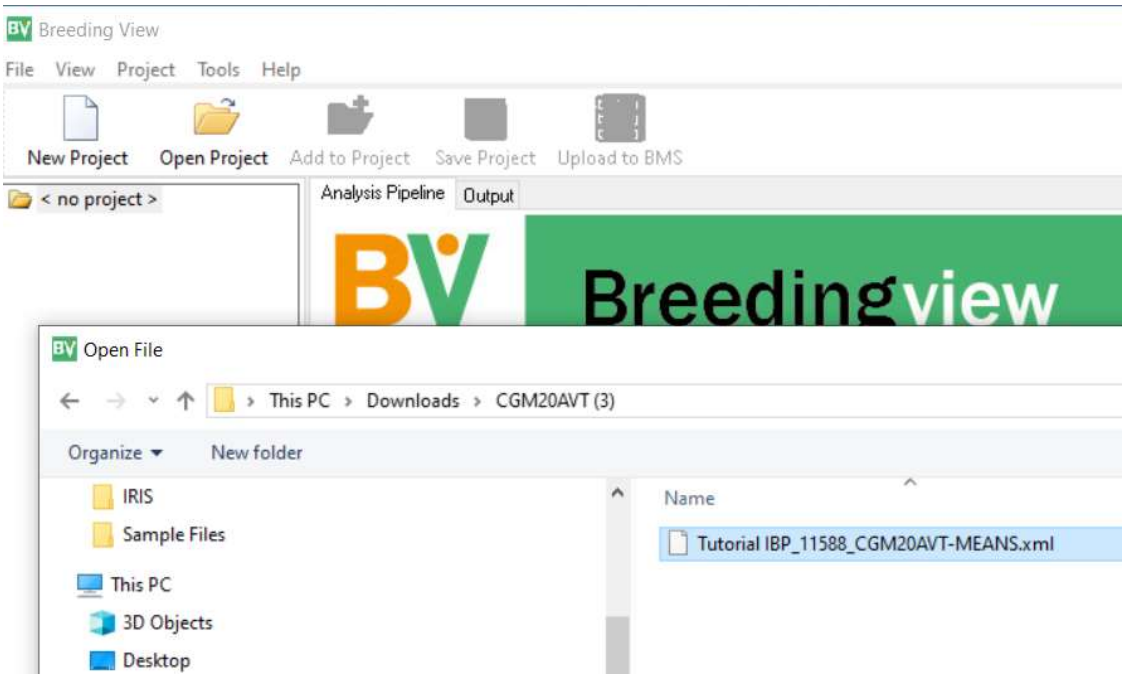
Click Download Input Files at the bottom of the form.

A zip file with the name of the study will be downloaded. You could extract the three files in this zip to a directory for analysis.

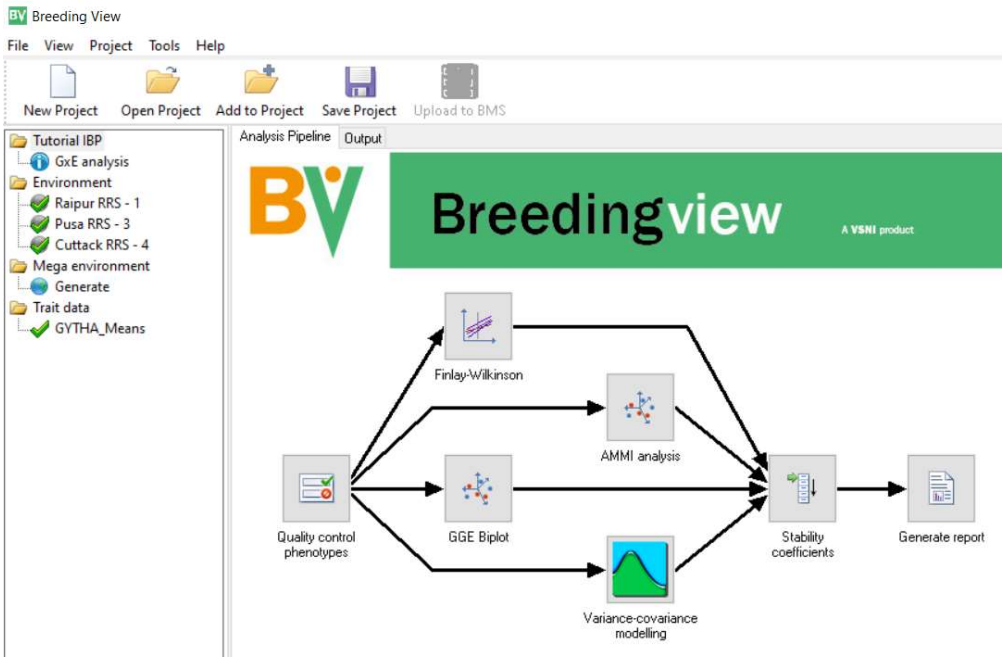


Run a multi-site analysis with Breeding View

Start the Breeding View Application and click on the Open Project icon and navigate to the directory where the files have been extracted. Select the xml file with the analysis specification:

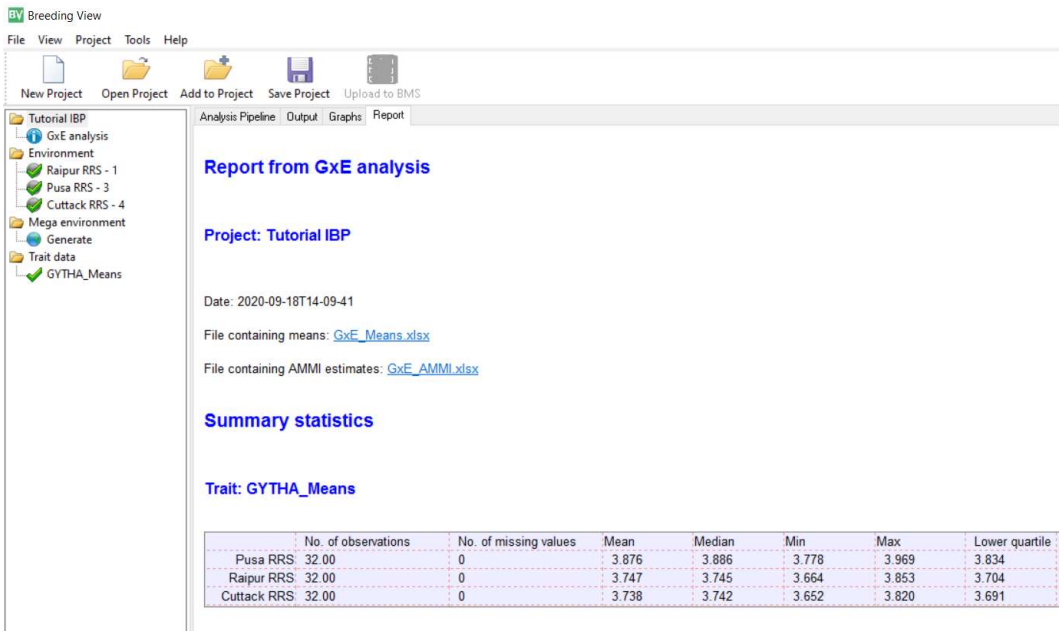


The multi-site analysis workflow will open:



To run the analysis right-click on the Quality control phenotypes icon and select Run pipeline.

The analysis will run, and provided there are no data errors will complete with a report page:



There is a detailed explanation about the report in the manual at:

https://bmspro.io/1949/training/breeding-management-system-manual-50/genotype-by-environment-analysis