

# BMS Tutorial on Breeding Workflows using rice examples and BMS V16

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## Introduction

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.

## 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 mast 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 Germplasm **Management**, click on the **View Germplasm** tab. The View Germplasm interface will appear as in the image below:

The screenshot shows the 'MANAGE GERmplasm' interface. At the top, there are two tabs: 'View Lists' and 'View Germplasm'. Below the tabs is a search section titled 'Search for Germplasm' with a magnifying glass icon. It includes a search input field, a 'Search' button, and a help icon. There are three checkboxes: 'With inventory only', 'Include parents', and 'Include details'. Below these are three radio buttons: 'Matches starting with' (selected), 'Exact matches', and 'Matches containing'. The interface shows 'Total Results: 0' and 'Selected: 0'. Below this is a table with a header row containing a checkmark, 'NAMES', 'CROSS', 'LOTS', 'AVAILABLE', and 'STOCKID'. The table body is currently empty.

To search for a **particular** germplasm by name, make sure that the “Search for: **Exact Matches**” radio button is selected. Type the search string **IR8** on the blank text box beside **Name**. Click on “Search”.

IR8 Search ?  With inventory only  Include parents  Include group members  
 Matches starting with  Exact matches  Matches containing

Note that 84 germplasm with name “IR8” or “IR 8” were found and displayed in the result list box. Most of them have alternative names as well.

Total Results: **84** Selected: **0**

✓	NAMES	CROSS	LOTS	AVAILABLE	STOCKID	GID	GROUP ID	LOCATION
<input type="checkbox"/>	IR 8, IR 8-CROSS, PE...	PETA/DEE GEO WOO GEN	0	-		17	-	Int Rice Research Institute
<input type="checkbox"/>	DW 301, IR 8, IR 8-2...	PETA/DEE GEO WOO GEN	0	-		715	-	International Rice Testing Program, IRRI
<input type="checkbox"/>	IR 8, IR 8 (ACC 1032...	PETA/DEE GEO WOO GEN	0	-		351573	-	International Rice Testing Program, IRRI
<input type="checkbox"/>	IR 8, IRGC 66935, YS...	PETA/DEE GEO WOO GEN	0	-		366176	366176	T.T. Chang Genetic Resources Center, IRRI
<input type="checkbox"/>	IR 8	PETA/DEE GEO WOO GEN	0	-		378514	-	Benin
<input type="checkbox"/>	IR 8	PETA/DEE GEO WOO GEN	0	-		432791	-	Bangladesh
<input type="checkbox"/>	IR 8, JID 3169	IR 8	0	-		432831	-	Int Rice Research Institute
<input type="checkbox"/>	IR 8	PETA/DEE GEO WOO GEN	0	-		433736	-	Nepal
<input type="checkbox"/>	IET 557, IR 8	PETA/DEE GEO WOO GEN	0	-		433805	-	India

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 **Matches starting with** radio button. Enter “IR15” in the text box beside Name. All germplasm with names that start with IR15 or IR 15 will be shown in the list box.

IR15 Search ?  With inventory only  Include parents  Include group members  
 Matches starting with  Exact matches  Matches containing

Total Results: **4748** Selected: **0**

✓	NAMES	CROSS	LOTS	AVAILABLE	STOCKID	GID	GROUP ID	LOCATION
<input type="checkbox"/>	IR 15	BPI 76/KAOHSIUNG 68	0	-		28	-	Int Rice Research Institute
<input type="checkbox"/>	IR 150	B 589 A 4-18-1/TAICHUNG	0	-		226	-	Int Rice Research Institute
<input type="checkbox"/>	DAWN/TN 1, IR 151	B 505 A 1-28-7-1-2/TAICHI	0	-		227	-	Int Rice Research Institute
<input type="checkbox"/>	IR 151 A	MO R 500/NATO (CI 8998)	0	-		229	-	Int Rice Research Institute
<input type="checkbox"/>	IR 152	MO R 500/NATO (CI 8998)	0	-		230	-	Int Rice Research Institute
<input type="checkbox"/>	IR 153	TAICHUNG NATIVE 1/BLU	0	-		231	-	Int Rice Research Institute
<input type="checkbox"/>	IR 154	B 5580 A 1-15/TAICHUNG	0	-		232	-	Int Rice Research Institute



## 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 Matches containing radio button. Enter “YAI 34” in the text box beside Name. All germplasm with names that contain with YAI 34 will be shown in the list 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.

YAI 34  ?  With inventory only  Include parents  Include group members  
 Matches starting with  Exact matches  Matches containing

Total Results: **33** Selected: **0**

✓	NAMES	CROSS	LOTS	AVAILABLE	STOCKID	GID	GROUP ID	LOCATION
<input type="checkbox"/>	IRGC 170, LEUANG YAI...	LEUANG YAI	0	-		180	180	T.T. Chang Genetic Resources Center, IRRI
<input type="checkbox"/>	IR 157, LEUANG YAI 3...	LEUANG YAI 34/TAICHUN	0	-		236	-	Int Rice Research Institute
<input type="checkbox"/>	IR 481, LEUANG YAI 3...	LEUANG YAI 34*2/TAICHL	0	-		678	-	Int Rice Research Institute
<input type="checkbox"/>	IRGC 851, KHITOM YAI...	KY 98	0	-		1216	1216	T.T. Chang Genetic Resources Center, IRRI
<input type="checkbox"/>	LEUANG YAI 34, LEUA...	LEUANG YAI	0	-		1294	-	Thailand
<input type="checkbox"/>	BB/LEUANG YAI 34	B 575 A 1-57-3-6/LEUANG	0	-		1295	-	Int Rice Research Institute
<input type="checkbox"/>	BB*2/LEUANG YAI 34	B 575 A 1-57-3-6*2/LEUA	0	-		1296	-	Int Rice Research Institute
<input type="checkbox"/>	BB*3/LEUANG YAI 34	B 575 A 1-57-3-6*3/LEUA	0	-		1297	-	Int Rice Research Institute
<input type="checkbox"/>	LEUANG YAI 228-2-34,...	LEUANG YAI	0	-		253256	-	Thailand

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

Type the value 50533 into the GID search. Check **Exact matches** for a precise match. Click on “**Search**”. The search for the GID is no different to other strings and so would also pick up germplasm with names containing the string.


50533  ?  With inventory only  Include parents  Include group members  
 Matches starting with  Exact matches  Matches containing

Total Results: **1** Selected: **0**

✓	NAMES	CROSS	LOTS	AVAILABLE	STOCKID	GID	GROUP ID
<input type="checkbox"/>	IR 18348-36-3-3, IR ...	IR 5657-33-2-1/IR 2061-46	0	-		50533	-

## Identify and locate different types of information about a germplasm

Going back to our previous search by name, click on the name “**IR8**” then highlight a germplasm to know its information. In this example, click the name of the first record which is **IR 8-CROSS**.



✓	NAMES	CROSS	LOTS	AVAILABLE	STOCKID	GID	GROUP ID
<input type="checkbox"/>	IR 8, IR 8-CROSS, PE...	PETA/DEE GEO WOO GEN	0	-		17	-
<input type="checkbox"/>	BR 9, C 15, C 180, C...	PETA/DEE GEO WOO GEN	0	-		715	-
<input type="checkbox"/>	IR 8, IR 8 (ACC 1032...	PETA/DEE GEO WOO GEN	0	-		351573	-
<input type="checkbox"/>	IR 8, IR8, IRGC 6693...	PETA/DEE GEO WOO GEN	0	-		366176	366176
<input type="checkbox"/>	IR 8	PETA/DEE GEO WOO GEN	0	-		378514	-
<input type="checkbox"/>	IR 8	PETA/DEE GEO WOO GEN	0	-		432791	-
<input type="checkbox"/>	IR 8, JID 3169	IR 8	0	-		432831	-
<input type="checkbox"/>	IR 8	PETA/DEE GEO WOO GEN	0	-		433736	-
<input type="checkbox"/>	IET 557, IR 8	PETA/DEE GEO WOO GEN	0	-		433805	-
<input type="checkbox"/>	IR 8, PB 8	PETA/DEE GEO WOO GEN	0	-		434397	-
<input type="checkbox"/>	BRRI 2277, IR 8, PI ...	PETA/DEE GEO WOO GEN	0	-		508018	-
<input type="checkbox"/>	IR 8, PI 446915	PETA/DEE GEO WOO GEN	0	-		511274	-

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 the method of development.

### Germplasm Details: IR 8-CROSS (GID: 17)

▼ **BASIC DETAILS**

Preferred Name: IR 8-CROSS      Creation Date: 19680000  
Creation Method: Single cross      Location: Int Rice Research Institute

Grouped Line      Group id (MGID): 0

► **ATTRIBUTES**

► **PEDIGREE TREE**

► **NAMES**

► **INVENTORY INFORMATION**

► **LISTS**

► **SAMPLES**

► **STUDIES**

► **GENERATION HISTORY**



### Questions:

a. When was **IR 8-CROSS** developed? \_\_\_\_\_

b. Where was it developed? \_\_\_\_\_

c. What was the method of development used?

More information is available below the germplasm details.

Germplasm Details: IR 8-CROSS (GID: 17)

▼ **BASIC DETAILS**  
Preferred Name: IR 8-CROSS      Creation Date: 19680000  
Creation Method: Single cross      Location: Int Rice Research Institute  
 Grouped Line      Group Id (MGID): 0

▶ **ATTRIBUTES**  
▶ **PEDIGREE TREE**  
▶ **NAMES**  
▶ **INVENTORY INFORMATION**  
▶ **LISTS**  
▶ **SAMPLES**  
▶ **STUDIES**  
▶ **GENERATION HISTORY**

Clicking on the > next to **Names** will give you information about the other names the germplasm is known by in the database. In this example, IR 8 is its cross name and it is also known as PETA/DGWG.

NAME	DATE	LOCATION
IR 8-CROSS	19980427	Int Rice Research Institute
IR 8	0	Int Rice Research Institute
PETA/DGWG	19880000	Unknown

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

Click on **Generation history** to display information about the selection history of the germplasm. In this case IR 8-CROSS is an F1 so it has no selection history.

GID	PREFERRED NAME
17	IR 8-CROSS

You can click on **Pedigree Tree** and the > symbols to expand the cross history.

▼ **PEDIGREE TREE**

Include derivative and maintenance lines **Apply** **View Pedigree Graph**

▼ IR 8-CROSS(17) 3 generations

- ▶ PETA(11)
- ▶ DEE GEO WOO GEN(2)

Note: Click on the **View Pedigree Graph** to display a graphical layout of the pedigree.

You can click on **List** to view the names of lists containing this germplasm. None in this case.

Click on **Group Relatives** to get a list of relatives within the cross it came from, if any. In this case none, since it is a cross.

Click on **Management Neighbors** to get a list of lines related with it that were produced by management methods like seed increase. In this case none.

Click on **Derivative neighborhood** to get a list of derived lines from this germplasm.

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

▼ **DERIVATIVE NEIGHBORHOOD**

Number of Steps Backward  Number of Steps Forward  **Display**

▼ IR 8-CROSS(17)

- ▼ IR 8-288(714)
  - ▼ IR 8(715)
    - ▼ V 487(227781)
    - ▼ IR 8-1M(304731)
    - ▼ IR 8-PD 4(308880)
    - ▼ YAG YAW 1(337137)
    - ▼ IR 8(378514)
    - ▼ IR 8(432791)
    - ▼ MILAGRO FILIPINO(432914)
    - ▼ NN 8(432986)
    - ▼ PATEL 85(433028)
    - ▼ IR 8(433736)

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

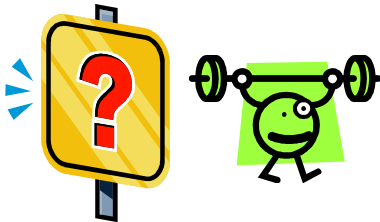
▼ **MAINTENANCE NEIGHBORHOOD**

Number of Steps Backward  Number of Steps Forward  [Display](#)

- ▼ IR 8-CROSS(17)
  - ▼ IR 8(366176)
    - ▼ IRGC 66935:1987DS(1721954)
  - ▼ IR8(601995)
    - ▼ IRGC 84895:1997DS(1745738)

Click on **Inventory information** to get information about the amount of seeds stored in the seed bank, if available. In this case there is none.

Click on **Study Information** to get a list of studies in the database where this germplasm has been used. In this case there are none.



**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? (Hint: Click on the Names/Attributes tab)

\_\_\_\_\_

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

\_\_\_\_\_

- c. 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 INFORMATION MANAGEMENT menu. If you click on this item you will see that you can download a template:



Each template has three sheets, a description sheet where some meta-data can be added, and which describes the columns on the observation sheet where the germplasm details are supplied. There is also 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:

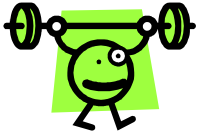
a) the Description sheet should look like this (some details filled in rows 1 to 4). The first row, cell B1 contains a name that will be given to the list. You should customize this by entering <Your initials>GI20 rather than BMSGI20 as in the image because list names must be unique and if several students use the same name there will be a clash.

1	A	B	C	D	E	F	G	I
1	LIST NAME	BMSGI20		Enter a list name here, or add it when saving in the BMS				
2	LIST DESCRIPTION	2020 Germplasm import for BMS		Enter a list description here, or add it when saving in the BMS				
3	LIST DATE	20200907		Accepted formats: YYYYMMDD or blank				
4	LIST TYPE	LST						
5								
6	CONDITION	DESCRIPTION	PROPERTY	SCALE	METHOD	DATA TYPE	VALUE	COMMENTS
7	LIST OWNER	Name of the Principal Investigator	PERSON	DBCV	ASSIGNED	C		
8	ID OF LIST OWNER	ID of the Principal Investigator	PERSON	DBID	ASSIGNED	N		
9								
10	FACTOR	DESCRIPTION	PROPERTY	SCALE	METHOD	DATA TYPE		COMMENTS
11	ENTRY	The germplasm entry number	GERMPLASM ENTRY	NUMBER	ENUMERATED	N		Sequence number - mandatory
12	DESIGNATION	The name of the germplasm	GERMPLASM ID	DBCV	ASSIGNED	C		Germplasm name - mandatory, unless a GID is provided
13	GID	The GID of the germplasm	GERMPLASM ID	DBID	ASSIGNED	N		GID value if known (or leave blank)
14	CROSS	The pedigree string of the germplasm	CROSS NAME	NAME	ASSIGNED	C		Cross string showing parentage - optional
15	SOURCE	The seed source of the germplasm	SEED SOURCE	NAME	Seed Source	C		Text giving seed source - optional
16	ENTRY CODE	Germplasm entry code	GERMPLASM ENTRY	CODE	ASSIGNED	C		Text giving a local entry code - optional
17	DRVNM	Derivative Name	GERMPLASM ID	NAME	ASSIGNED	C		See valid name types on Codes sheet for more options
18								
19	INVENTORY	DESCRIPTION	PROPERTY	SCALE	METHOD	DATA TYPE		COMMENTS
20	SEED_AMOUNT_g	Amount of seed imported	INVENTORY AMOUNT	g	Weighed	N		Weight of seed lot in grams - optional; see Codes sheet
21	STOCKID	ID of an inventory deposit	Germplasm stock ID	DBCV	ASSIGNED	C		Existing StockID value if known (or leave blank)
22								
23	VARIATE	DESCRIPTION	PROPERTY	SCALE	METHOD	DATA TYPE		COMMENTS
24	NOTE	Additional details about germplasm	ATTRIBUTE	Text	Observed	C		Optional

b) The Observation sheet should look like this (minimum requirement – entry no and name):

1	A	B	C	D	E	F	G	H	I	J
1	ENTRY	DESIGNATION	GID	CROSS	SOURCE	ENTRY COD	DRVNM	SEED_AMOUNT_g	STOCKID	NOTE
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	YUNLU NO 28								
17	16	IRRI 132								





Create a file exactly as shown in the image above and save it as *BMSGI20.xls*



1	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.

Importing the list. Once the template is completed open the **Import Germplasm** form.

Click Browse and search for the completed template.

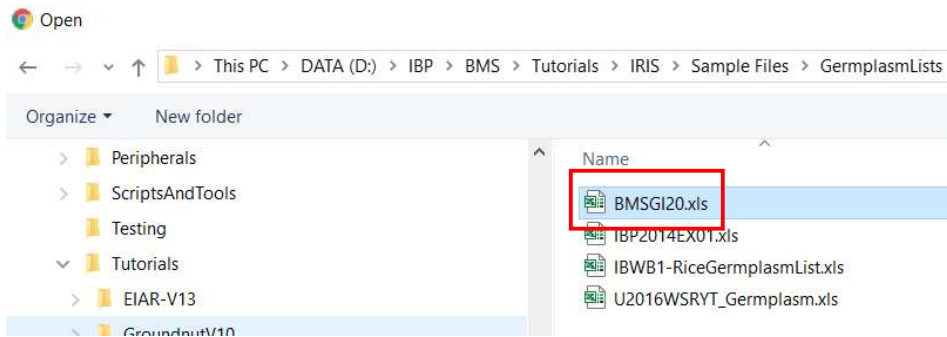
# IMPORT GERMPLASM ?

## Choose Import File

Choose the file you would like to import. You can download a template [here](#).

**Browse**

Browse to the location where you stored the completed template file **BMSGI20.xls**. Click **Open**.



Once you have selected the file, click **Open**.

A message appears indicating a successful upload. Click **Next**.

The Specify the Germplasm Details form appears. This form allows you to specify some information which will be applied to all the unknown entries in the list.

- The first is the **method** by which the lines were produced in their last generation. Set this to **Unknown derivative method** by starting to type un in the box and selecting the result.
- The second is the **location** where the germplasm was obtained or harvested,
- The third is a storage location where seeds will be stored. Since we have not specified any inventory with this list we can leave this blank,
- The fourth is a **date** that the germplasm was harvested or acquired,
- And finally you can specify the **type of name** given in the designation – this is defaulted to **Line name**.

## Specify Germplasm Details

### ADD GERmplasm DETAILS

You can specify following details to apply to the imported germplasm. These details are optional.

**Germplasm breeding method:**  ?  
 Show only favorite methods [Manage Methods](#)

**Germplasm location:**   
 All locations  Breeding locations [Manage Locations](#)  
 Show only favorite locations

**Seed Storage Location:**   
 All locations  Storage locations [Manage Locations](#)  
 Show only favorite locations

**Germplasm date:**  📅

**Germplasm name type:**

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

#### REVIEW IMPORT FILE DETAILS

Please review and confirm the details of your import records.

Total Entries: 16

ENTRY_NO	ENTRY_CODE	DESIGNATION	CROSS	GID	STOCKID	SEED_SOURCE
1		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 75521-24-1-1-B				

If this does not look correct, click **Cancel** and check the template.

Finally you must specify how germplasm identifiers should be assigned to germplasm where the names are found already existing in the database:

#### SELECT GID ASSIGNMENT OPTIONS

GID Assignment Options:

Add all entries with new records connecting to existing sources  
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 **'Next'**.

There is a checkbox to select single hits whenever found and this is checked by default, but if you prefer to check every match you can uncheck this box. 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, select use this match for other instances and click **Continue**.

**Select Matching Germplasm or Add New Entry** ✕

Match(es) were found for entry **3 of 16**, with the name **IR 75502-24-1-1-B**. Click on an existing entry below to choose it as the match for this germplasm. You may also choose to ignore the match and add a new entry.

DESIGNATION	GID	IMMEDIATE SOURCE	AVAILABLE	LOCATION	BREEDING I
IR 75502-24-1-1-B	1161458	IR 75502-24-1-1	-	International Rice Testing Program, IRR	Selected bu
IR 75502-24-1-1-B	1162111	IR 75502-24-1-1	-	Int Rice Research Institute	Single plant

Use this match for other instances of this name in the import list  
 Ignore matches and add a new entry  
 Ignore remaining matches and add new entries for all

Cancel Continue

When all the entries have been processed BMS will open the Save List page. This section has picked up details about the list from the description sheet of the template file which you can change if you like.

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> 2020 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. You can modify the List name by adding your initials so that it is different from list stored by other students. Then click **Save**.

**Save List As** ✕

Select a folder to create a new list or select an existing list to edit and overwrite its entries.

**List Location**

Add Folder \*  ✔ ✕

- ▶ Crop lists
- ▼ Program lists

**List Details**

*\* indicates a mandatory field*

List Name: \*

List Owner: Christopher McLaren

Description:

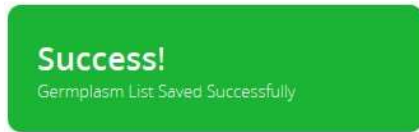
List Type: \*

List Date: \*

Notes:

Cancel 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.



## 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:

The screenshot shows a web application interface for 'List entries'. At the top, it says 'Total Entries: 16 Selected: 16'. Below this is a table with columns: #, DESIGNATION, CROSS, LOTS, AVAILABLE, and ENTRY\_CODE. There are 11 rows of data, each with a checkmark in the first column. A context menu is open over the table, showing options: 'List editing options', 'Export list', 'Coding and Grouping Options', and 'Create inventory lots' (which is highlighted in green).

#	DESIGNATION	CROSS	LOTS	AVAILABLE	ENTRY_CODE
1	IR 72768-12-1-1	IR 60080-46 A/IR 65907-116-1-B	-	-	1
2	IR 72768-28-1-1	IR 60080-46 A/IR 65907-116-1-B	-	-	2
3	IR 75502-24-1-1-B	B 6144 F-MR-6-0-0/IR 55423-01 (NSIC RC 9)	-	-	3
4	IR 75516-30-1-1-B	IR 53236-275-1/CT 6516-24-3-2	-	-	4
5	IR 75516-56-1-1-B	IR 53236-275-1/CT 6516-24-3-2	-	-	5
6	IR 75518-84-1-1-B	IR 60080-46 A/IR 53236-275-1	-	-	6
7	IR 75531-31-1-2-B	IR 70360-54-1-B/VIENG	-	-	7
8	IR 76561-AC 8-B	CT 13382-9-4-M/IR 70358-145-1-1	-	-	8
9	CNA 4196	CNA 4196	-	-	9
10	IDSA 113	IDSA 113	-	-	10
11	FARO 41	IRAT 13/PALAWAN	-	-	11

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.

### Create Lots

Stock ID Prefix **CGM**

Storage Location **Default Seed Store**

Favorite locations only

Units **SEED\_AMOUNT\_g**

Notes **Inventory for imported germplasm**

#### Deposit

Initial deposit

Amount **150**

Notes

Confirm transactions on saving

Save

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

Reload the germplasm list to see the inventory:

CGMG120 x

#### List entries

Total Entries: 16 Selected: 0

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

## Manipulating Germplasm Lists in the List Manager

### View existing Program Lists

From Manage Germplasm go to View Lists, open Program lists>2020 lists and highlight the list just entered BMSGI20

The screenshot shows the 'MANAGE GERMPPLASM' interface. On the left is a navigation menu with categories like 'BREEDING ACTIVITIES', 'INFORMATION MANAGEMENT', 'STATISTICAL ANALYSIS', and 'INVENTORY MANAGER'. The main area has tabs for 'View Lists' and 'View Germplasm'. A 'List Details' panel is open, showing 'BMSGI20' selected. Below it is a table of 'List entries' with columns for selection, ID, and designation. A 'Browse for Lists' panel is also open, showing a tree view of lists under '2020 lists' with 'BMSGI20' highlighted.

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:

The screenshot shows the 'MANAGE GERMPPLASM' interface with the 'View Lists' tab selected. The 'List Details' panel is open, showing 'BMSGI20' selected. Below it is a table of 'List entries' with columns for selection, ID, designation, cross, lots, and availability. The cross column contains pedigree information for each entry.

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

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 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.

**Browse for Lists**

All Lists

NAME	OWNER	DESCRIPTION	TYPE	# OF ENTRIES
IRLON	William Eusebio	International Rainfed Lowla.	LIST FOLDER	0
IRLON-2	EDILBERTO D. REDOÑA	IRLON Submergence Tolerar	LIST FOLDER	0
IRLYN-E	William Eusebio	International Rainfed Lowla.	LIST FOLDER	0
IRLYN-E-1985	William Eusebio	International Rainfed Lowla.	GERMPLASM LISTS	25
IRLYN-E-1986	William Eusebio	International Rainfed Lowla.	GERMPLASM LISTS	19
IRLYN-E-1987	William Eusebio	International Rainfed Lowla.	GERMPLASM LISTS	20
IRLYN-E-1988	William Eusebio	International Rainfed Lowla.	GERMPLASM LISTS	20
IRLYN-E-1989	William Eusebio	International Rainfed Lowla.	GERMPLASM LISTS	16
IRLYN-E-1990	William Eusebio	International Rainfed Lowla.	GERMPLASM LISTS	11
IRLYN-E-1991	William Eusebio	International Rainfed Lowla.	GERMPLASM LISTS	22
IRLYN-E-1992	William Eusebio	International Rainfed Lowla.	GERMPLASM LISTS	19
<b>IRLYN-E-1993</b>	William Eusebio	International Rainfed Lowla.	GERMPLASM LISTS	<b>18</b>
IRLYN-M	William Eusebio	International Rainfed Lowla.	LIST FOLDER	0
IRLYN-S	EDILBERTO D. REDOÑA	INTERNATIONAL RAINFED L	LIST FOLDER	0

The list contains 18 entries:

**List Details**  
Browse or search for a list to work with.

IRLYN-E-1993

List entries

Total Entries: 18 Selected: 0

✓	#	DESIGNATION	CROSS	LOTS	AVAILABLE	ENTRY_CODE
<input type="checkbox"/>	1	BR 1185-2R-6	SR 26-B (TC)/BR 4	-	-	IRLYN-E 1993
<input type="checkbox"/>	2	BR 1704-6-3-3-4	BR 51-49-5-HR 65//BR 4-30-51-2/IR 5-114-3-1	-	-	IRLYN-E 1993
<input type="checkbox"/>	3	BR 1725-13-7-16	BR 52-87-1-HR 88/ARC 10550	-	-	IRLYN-E 1993
<input type="checkbox"/>	4	BR 1860-2B-12	BHASHAMANIK/IR 2053-200-4	-	-	IRLYN-E 1993
<input type="checkbox"/>	5	BR 1871-1-1-1-2-1	BR 4//BRRISAIL/PL NO 778	-	-	IRLYN-E 1993
<input type="checkbox"/>	6	IR 21178-43-1-2-2-2	CR 146-7055-225/IR 2061-465-1-5-5//IR 52	-	-	IRLYN-E 1993
<input type="checkbox"/>	7	LD 181-5	BW 288-1-3/BW 297-2	-	-	IRLYN-E 1993
<input type="checkbox"/>	8	SURAKSHA	SASYASHREE/MR 1523	-	-	IRLYN-E 1993
<input type="checkbox"/>	9	RP 1641-95-4-3-1-2	RPW 6-12/BULU BENONG III	-	-	IRLYN-E 1993
<input type="checkbox"/>	10	RP 2095-5-8-31	RPW 6-12/ANDREWSALI	-	-	IRLYN-E 1993



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**

**List entries**  
Total Entries: 18 Selected: 18

✓	#	DESIGNATION	CROSS	LOTS	AVAILABLE	ENTRY_CODE
<input checked="" type="checkbox"/>	1	BR 1185-2R-6	SR 26-B (TC)/BR 4	-	-	IRLYN-E 1993
<input checked="" type="checkbox"/>	2	BR 1704-6-3-3-4	BR 51-49-5-HR 65//BR 4-30-51-2/IR 5-114-3-1	-	-	IRLYN-E 1993
<input checked="" type="checkbox"/>	3	BR 1725-13-7-16	BR 52-87-1-HR 88/ARC 10550	-	-	IRLYN-E 1993
<input checked="" type="checkbox"/>	4	BR 1860-2B-12	BHASHAMANIK/IR 2053-200-4	-	-	IRLYN-E 1993
<input checked="" type="checkbox"/>	5	BR 1871-1-1-1-2-1	BR 4//BRRISAIL/PL NO 778	-	-	IRLYN-E 1993
<input checked="" type="checkbox"/>	6	IR 21178-43-1-2-2-2	CR 146-7055-225/IR 2061-465-1-5-5//IR 52	-	-	IRLYN-E 1993
<input checked="" type="checkbox"/>	7	LD 181-5	BW 288-1-3/BW 297-2	-	-	IRLYN-E 1993
<input checked="" type="checkbox"/>	8	SURAKSHA	SASYASHREE/MR 1523	-	-	IRLYN-E 1993
<input checked="" type="checkbox"/>	9	RP 1641-95-4-3-1-2	RPW 6-12/BULU BENONG III	-	-	IRLYN-E 1993
<input checked="" type="checkbox"/>	10	RP 2095-5-8-31	RPW 6-12/ANDREWSALI	-	-	IRLYN-E 1993
<input checked="" type="checkbox"/>	11	RP 2151-2-11-5	PR 4141/CR 98-7216	-	-	IRLYN-E 1993
<input checked="" type="checkbox"/>	12	RP 2167-323-1-2	BASMATI 370//BASMATI 370/CRR 88-17-1-5	-	-	IRLYN-E 1993
<input checked="" type="checkbox"/>	13	RP 2199-14-2-6-1	PHALGUNA/TKM 6	-	-	IRLYN-E 1993
<input checked="" type="checkbox"/>	14	RP 2235-200-91-62	IR 50/PHALGUNA	-	-	IRLYN-E 1993
<input checked="" type="checkbox"/>	15	RP 2246-7-2	PUSA 2-21/SUREKHA	-	-	IRLYN-E 1993
<input checked="" type="checkbox"/>	16	SRINIVASA	IR 8/LATISAIL	-	-	IRLYN-E 1993
<input checked="" type="checkbox"/>	17	IR 46	IR 1416-131-5/IR 1364-37-3-1//IR 1366-120-3-1/IR 1539-111	-	-	IRLYN-E 1993

Select All

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>20PVT (CGM20PVT for me).

Now in Browse Lists Program Lists>2020 Lists we have a second list:

**MANAGE GERmplASM** ?

View Lists View Germplasm

**List Details**  
Browse or search for a list to view

CGM20PVT x

**List entries**  
Total Entries: 18 Selected: 18

✓	#	DESIGNATION	CROSS	LOTS	AVAILABLE	ENTRY_CODE
<input type="checkbox"/>	1	BR 1185-2R-6	SR 26-B (TC)/BR 4	-	-	IRLYN-E 1993
<input type="checkbox"/>	2	BR 1704-6-3-3-4	BR 51-49-5-HR 65//BR 4-30-51-2/IR 5-114-3-1	-	-	IRLYN-E 1993

**Browse for Lists**

**All Lists**

NAME	OWNER	DESCRIPTION
▶ Crop lists		
▼ Program lists		
▼ 2020 lists	IBP Trainer	2020 lists
BMSGI20	IBP Trainer	2020 Germplasm inport for B
CGM20PVT	IBP Trainer	2020 PVT for project CGM

## Adding Entries to an existing list

Suppose I wish to add two entries from my import list (BMSGI20) to my PVT list to be checks for example.

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

**List Details**  
Browse or search for a list to work with.

CGM20PVT

**List entries**  
Total Entries: 18 Selected: 0

#	DESIGNATION	CROSS
1	BR 1185-2R-6	SR 26-B (TC)/BR 4
2	BR 1704-6-3-3-4	BR 51-49-5-HR 65//BR 4-30-51-2//IR 5-114-3-1
3	BR 1725-13-7-16	BR 52-87-1-HR 88/ARC 10550
4	BR 1860-2B-12	BHASHAMANIK//IR 2053-200-4
5	BR 1871-1-1-1-2-1	BR 4//BRRISAIL//PL NO 778
6	IR 21178-43-1-2-2-2	CR 146-7055-225//IR 2061-465-1-5-5//IR 52
7	LD 181-5	BW 288-1-3//BW 297-2
8	SURAKSHA	SASYASHREE//MR 1523

**List editing options**  
Export list  
Coding and Grouping Options

The list will open in the Edit list box to the right. Then click Browse again and select the import list (BMSGI20). It will open in the Brows 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**

**List Details**  
Browse or search for a list to work with.

BMSGI20

**List entries**  
Total Entries: 16 Selected: 2

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

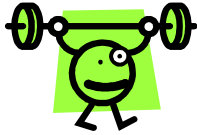
**Edit list**  
Build or revise your list by dragging in entries from the left.

**List entries**  
Total Entries: 18 Selected: 0

#	DESIGNATION	CROSS
1	BR 1185-2R-6	SR 26-B (TC)/BR 4
2	BR 1704-6-3-3-4	BR 51-49-5-HR 65//BR 4
3	BR 1725-13-7-16	BR 52-87-1-HR 88/ARC 1
4	BR 1860-2B-12	BHASHAMANIK//IR 2053
5	BR 1871-1-1-1-2-1	BR 4//BRRISAIL//PL NO 7
6	IR 21178-43-1-2-2-2	CR 146-7055-225//IR 206
7	LD 181-5	BW 288-1-3//BW 297-2
8	SURAKSHA	SASYASHREE//MR 1523
9	RP 1641-95-4-3-1-2	RPW 6-12//BULU BENON
10	RP 2095-5-8-31	RPW 6-12//ANDREWSALI
11	RP 2151-2-11-5	PR 4141//CR 98-7216
12	IR 1167-323-1-2	BASMATI 370//BASMATI
13	IR 1199-14-2-6-1	PHALGUNA//TKM 6
14	IR 1235-200-91-62	IR 50//PHALGUNA
15	IR 1246-7-2	PUSA 2-21//SUREKHA

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

Save the changes.



### Exercise:

1. Use the Actions Menu to try exporting your list to an excel file.
2. Use your list editing skills to search the germplasm for entries IR 64 with GID 50533, add it to a new list, then search for IR 72 (GID 70125) and add that to the new list, finally search for NERICA 4 (GID 765439) and add that to the list. Save the list as <your initials>Checks.
3. In the 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.

**BMS 12.0 Manual**

## User manual

- ▼ GET STARTED
- INTRODUCTION
- GERMPLASM & GENEALOGY**
- ACCESS & USER MANAGEMENT
- FILE DIRECTORIES

- [Germplasm \(GID\)](#)
- [Genealogy Management](#)
  - [Breeding Methods](#)
  - [Pedigrees](#)
- [Related](#)

# Germplasm (GID)

Germplasm is the fundamental unit of plant breeding

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 BREEDING ACTIVITIES menu and then on **Start a new Study**.



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.

# MANAGE STUDIES ?

## Create Study

Save

### BASIC DETAILS

*\* indicates a mandatory field*

Study name: \*

Description: \*

Study type: \*

Objective:

Save in: \*

Created by: \*

Creation date: \*

Completion date:

Use a previously created study as a template

Settings **Germplasm & Checks** Environments

### STUDY SETTINGS ?

Add

Click Add to begin selecting items to record in this section.

Next click on the Add button next to STUDY SETTINGS. This will open the ontology manager and you may specify variable 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 look for Project and add Project Prefix. These variables can be customized to your particular programs and identify important objectives of the crossing block.

Settings **Germplasm & Checks** Environments

STUDY SETTINGS ? **Add**

**PI\_NAME:**

**Target\_Region:**

**Project\_Prefix:**

Select All [Remove](#)

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

Settings | **Germplasm & Checks** | Environments

▼ Define Germplasm Details

GERMPLASM DESCRIPTORS ? Add

Name	Description
ENTRY_TYPE	Entry type (test/check)- assigned (type)
GID	Germplasm identifier - assigned (DBID)
DESIGNATION	Germplasm identifier - assigned (DBCv)
ENTRY_NO	Germplasm entry - enumerated (number)
OBS_UNIT_ID	Field observation unit id - assigned (text)

Study List  
Browse a list to work with.

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.

## Browse For Lists

### All Lists

NAME	OWNER	DESCRIPTION
▼  Program lists		
▼  2020 lists	IBP Trainer	2020 lists
CGM20PVT	IBP Trainer	2020 PVT for project CGM
▼  CGM 2020 lists	IBP Trainer	CGM 2020 lists
CGMAVT20	IBP Trainer	CGM Advanced variety trial ...
CGMGI20	IBP Trainer	2020 Germplasm Import for p...

The entries will be imported into the nursery:

Settings **Germplasm & Checks**

▼ Define Germplasm Details

GERMPLASM DESCRIPTORS Add

<input type="checkbox"/>	Name	Description
<input type="checkbox"/>	ENTRY_TYPE	Entry type (test/check)- assigned (type)
<input type="checkbox"/>	GID	Germplasm identifier - assigned (DBID)
<input type="checkbox"/>	DESIGNATION	Germplasm identifier - assigned (DBC)
<input type="checkbox"/>	ENTRY_NO	Germplasm entry - enumerated (number)
<input type="checkbox"/>	OBS_UNIT_ID	Field observation unit id - assigned (text)
<input type="checkbox"/>	CROSS	The pedigree string of the germplasm
<input type="checkbox"/>	SEED_SOURCE	Seed source - Selected (Code)

Remove

**Study List**  
Browse a list to work with.  
Total Entries: 16 [View Header](#)

ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO
Test entry	1161408	IR 72768-12-1-1	1
Test entry	1161406	IR 72768-28-1-1	2
Test entry	1161458	IR 75502-24-1-1-B	3
Test entry	1161444	IR 75516-30-1-1-B	4
Test entry	1161445	IR 75516-56-1-1-B	5
Test entry	1161448	IR 75518-84-1-1-B	6
Test entry	1161440	IR 75531-31-1-2-B	7
Test entry	1161327	IR 76561-AC 8-B	8
Test entry	70732	CNA 4196	9

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

**MANAGE STUDIES** ?

**Create Study** Save unsaved data

**BASIC DETAILS**

If there is no folder for 2020 Nurseries, create one with your initials to keep your work separate from other students. (Type the name and click the tick symbol)

**MANAGE STUDIES** ?

**Create Study** Save unsaved data

**BASIC DETAILS**  
*\* indicates a mandatory field*

Study name: \*

Description: \*

**Browse Studies** + + + ×

Add Folder \*  ✓ ✗

▸

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

Settings | Germplasm & Checks | Environments

▼ Define Environments

ENVIRONMENT DETAILS ? Add ENVIRONMENTAL CONDITIONS ?

<input type="checkbox"/>	Name	Description
<input type="checkbox"/>	LOCATION_NAME	Location - selected (DBID)
<input type="checkbox"/>	SEEDING_DATE	Date Seeded - applied (yyyymmdd)

Remove

Specify the number of environments for this study:  Ok

Specify Environment Details

10 Showing 1 to 1 of 1 entries

Environment	LOCATION_NAME	SEEDING_DATE
1	Mbe - (MBE) <input checked="" type="radio"/> Breeding locations <input type="radio"/> All locations types <input type="checkbox"/> Show only favorite locations	yyyy-mm-dd

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

Settings | Germplasm & Checks | Treatment Factors | Environments | Experimental Design

Experimental Design ?

CHOOSE A DESIGN TYPE

Select the design type you would like to use for this study:

Or [import](#) an experimental design.

SPECIFY PLOT NUMBERING

Specify the starting plot number:

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**:

**Select Parents**  
Browse for a list to work with

BMSGI20 x

**List entries** View List Header

Total Entries: 16 Selected: 8 ACTIONS

✓	#	DESIGNATION	CROSS	ENTRY_CODE	GID	GROUP ID	LOTS	AVAILABLE	⋮
<input checked="" type="checkbox"/>	5	IR 75516-56-1-1-B	IR 53236-275-1/CT 65	5	1161445	-	-	-	
<input checked="" type="checkbox"/>	6	IR 75518-84-1-1-B	IR 60080-46 A/IR 5323	6	1161448	-	-	-	
<input checked="" type="checkbox"/>	7	IR 75531-31-1-2-B	IR 70360-54-1-B/VIEN	7	1161440	-	-	-	
<input checked="" type="checkbox"/>	8	IR 76561-AC 8-B	CT 13382-9-4-M/IR 70	8	1161327	-	-	-	

Select All

Add to Female List  
Add to Male List

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

**Select Parents**  
Browse for a list to work with

BMSGI20 x

**List entries** View List Header

Total Entries: 16 Selected: 8 ACTIONS

✓	#	DESIGNATION	CROSS	ENTRY_CODE	GID	GROUP ID	LOTS	AVAILABLE	⋮
<input checked="" type="checkbox"/>	12	UPL RI 5	SIGADIS (AICRIP)/BPI	12	406626	-	-	-	
<input checked="" type="checkbox"/>	13	WAB 326-B-B-7-H1	ITA 235 (TOX 1785-19	13	418229	-	-	-	
<input checked="" type="checkbox"/>	14	WAB 534-B-3A 1-1	WAB 181-18/DR 2	14	905029	-	-	-	
<input checked="" type="checkbox"/>	15	YUNLU NO 28	IDSA 6 (IRAT 216)/WU	15	790394	-	-	-	
<input checked="" type="checkbox"/>	16	IRRI 132	UPL RI 5/IR 12979-24	16	204538	-	-	-	

Select All

Add to Female List  
Add to Male List

The parent lists now look as follows:

### Parent Lists

Select and drag entries from a list on the left to modify a parent list.

**Female Parents**

**List entries**

Total Entries: 8 Selected: 8 ACTIONS

✓	#	DESIGNATION	CROSS
<input checked="" type="checkbox"/>	1	IR 72768-12-1-1	IR 60080-46 A/IR 65907-116
<input checked="" type="checkbox"/>	2	IR 72768-28-1-1	IR 60080-46 A/IR 65907-116
<input checked="" type="checkbox"/>	3	IR 75502-24-1-1-B	B 6144 F-MR-6-0-0/IR 55423
<input checked="" type="checkbox"/>	4	IR 75516-30-1-1-B	IR 53236-275-1/CT 6516-24
<input checked="" type="checkbox"/>	5	IR 75516-56-1-1-B	IR 53236-275-1/CT 6516-24

Select All

**Male Parents**

**List entries**

Total Entries: 8 Selected: 8 ACTIONS

✓	#	DESIGNATION	CROSS
<input checked="" type="checkbox"/>	1	CNA 4196	CNA 4196
<input checked="" type="checkbox"/>	2	IDSA 113	IDSA 113
<input checked="" type="checkbox"/>	3	FARO 41	IRAT 13/PALAWAN
<input checked="" type="checkbox"/>	4	UPL RI 5	SIGADIS (AICRIP)/BPI 76-1
<input checked="" type="checkbox"/>	5	WAB 326-B-B-7-H1	ITA 235 (TOX 1785-19-18)/V

Select All

### Crossing Method

Choose how you would like to make your cross

Please choose

Make reciprocal crosses

Exclude self

- Please choose
- Cross each selected female with each selected male
- Cross matched pairs of selected female and male lines in top to bottom order
- Cross each female with an unknown male parent
- Cross each female with all male parents

### Preview Crosses

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:

### Preview Crosses

Total Crosses: 64 Selected: 0 ACTIONS

✓	#	FEMALE PARENT	MALE PARENT	FEMALE CROSS	MALE CROSS
<input type="checkbox"/>	1	IR 72768-12-1-1	CNA 4196	IR 60080-46 A/IR 65907-116-1-B	CNA 4196
<input type="checkbox"/>	2	IR 72768-12-1-1	IDSA 113	IR 60080-46 A/IR 65907-116-1-B	IDSA 113
<input type="checkbox"/>	3	IR 72768-12-1-1	IRAT 170 (FARO 41)	IR 60080-46 A/IR 65907-116-1-B	IRAT 13/PALAWAN
<input type="checkbox"/>	4	IR 72768-12-1-1	UPL RI 5	IR 60080-46 A/IR 65907-116-1-B	SIGADIS (AICRIP)/BPI 76-1
<input type="checkbox"/>	5	IR 72768-12-1-1	WAB 326-B-B-7-H1	IR 60080-46 A/IR 65907-116-1-B	ITA 235 (TOX 1785-19-18)/WABC 16

Select All

Cancel
Continue

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

## Specify Breeding Method ✕

By default, the breeding method for new crosses will be based on the status of their parental lines. As an alternative, you can select a method to use for all crosses.

Use parental status

Select a method to use for all crosses :



All methods

Generative methods

Show only favorite methods

[Manage Methods](#)

**Continue**

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:

- a. Enter **AR20<your initials>** as prefix of the Cross Code
- b. Enter **3** as the number of digits for the sequence code.
- c. Specify date and location.

## Specify Naming and Harvest Details



Choose how you would like the names to be generated for the new crosses. You can use the automatic name generation rules for your program, or specify a name format

### Naming

Use automatic name generation  Specify name format

You can define new settings or load previously saved settings. Note that \* indicates a mandatory field.

Load saved settings:

Both cross codes and parentage designations will be generated for new crosses. Cross codes consist of a prefix, a sequence number and an optional suffix. Please specify your preferences for these naming conventions below.

**Cross code prefix: \***

**Number of digits in sequence number**

**Cross code suffix**

**Add space between prefix and code?**  Yes  No

**Add space between suffix and code?**  Yes  No

*Next name in the sequence: AR20CGM001*

**Starting sequence number**

**Separator for parentage designation: \***

*Example parentage designation: FEMALE:123/MALE:456*

**Save parentage designation as a string?**  Yes  No

**Enter a name if you would like to save these settings to use again:**

### Harvest Details

**Estimated harvest date:**

**Harvest location:**

Breeding locations  All locations types

Show only favorite locations [Manage Locations](#)

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

### Review Crosses

100  Showing 1 to 64 of 64 entries

#	CROSS	FEMALE PEDIGREE	FEMALE PARENT	MALE PEDIGREE	MALE PARENT	BREEDING METH
1	IR 72768-12-1-1/CNA 4196	IR 60080-46 A/IR 65907-116-1-	IR 72768-12-1-1	CNA 4196	CNA 4196	Single cross
2	IR 72768-12-1-1/IDSA 113	IR 60080-46 A/IR 65907-116-1-	IR 72768-12-1-1	IDSA 113	IDSA 113	Single cross
3	IR 72768-12-1-1/IRAT 170 (FARO 4	IR 60080-46 A/IR 65907-116-1-	IR 72768-12-1-1	IRAT 13/PALAWAN	IRAT 170 (FARO 41)	Single cross
4	IR 72768-12-1-1/UPL RI 5	IR 60080-46 A/IR 65907-116-1-	IR 72768-12-1-1	SIGADIS/BPI 76-1	UPL RI 5	Single cross
5	IR 72768-12-1-1/WAB 326-B-B-7-H	IR 60080-46 A/IR 65907-116-1-	IR 72768-12-1-1	TOX 1785-19-18/WABC 165	WAB 326-B-B-7-H1	Single cross
6	IR 72768-12-1-1/WAB 534-B-3A 1-	IR 60080-46 A/IR 65907-116-1-	IR 72768-12-1-1	WAB 181-18/DR 2	WAB 534-B-3A 1-1	Single cross
7	IR 72768-12-1-1/YUNLU NO 28	IR 60080-46 A/IR 65907-116-1-	IR 72768-12-1-1	IDSA 6/WUNENGDABAIGU-2-5	YUNLU NO 28	Single cross
8	IR 72768-12-1-1/IR 55423-01 (NSI	IR 60080-46 A/IR 65907-116-1-	IR 72768-12-1-1	UPL RI 5/IR 12979-24-1 (BROW	IR 55423-01 (NSIC RC 9)	Single cross
9	IR 72768-28-1-1/CNA 4196	IR 60080-46 A/IR 65907-116-1-	IR 72768-28-1-1	CNA 4196	CNA 4196	Single cross
10	IR 72768-28-1-1/IDSA 113	IR 60080-46 A/IR 65907-116-1-	IR 72768-28-1-1	IDSA 113	IDSA 113	Single cross
11	IR 72768-28-1-1/IRAT 170 (FARO 4	IR 60080-46 A/IR 65907-116-1-	IR 72768-28-1-1	IRAT 13/PALAWAN	IRAT 170 (FARO 41)	Single cross
12	IR 72768-28-1-1/UPL RI 5	IR 60080-46 A/IR 65907-116-1-	IR 72768-28-1-1	SIGADIS/BPI 76-1	UPL RI 5	Single cross
13	IR 72768-28-1-1/WAB 326-B-B-7-H	IR 60080-46 A/IR 65907-116-1-	IR 72768-28-1-1	TOX 1785-19-18/WABC 165	WAB 326-B-B-7-H1	Single cross
14	IR 72768-28-1-1/WAB 534-B-3A 1-	IR 60080-46 A/IR 65907-116-1-	IR 72768-28-1-1	WAB 181-18/DR 2	WAB 534-B-3A 1-1	Single cross

< 1 >

Back Finish

Click **Finish**.

For list details, enter the following

- Enter “U20<yourinitials>F1” as list name
- Enter “Upland 2020 Crosses Dry Season” for description
- Select “F1 NURSERY LIST” as list type
- Select “2020-09-08” as list date

**Save List As** ✕

List Location

- └ Crop lists
- └ Program lists
  - └ 2020 lists
    - BMSGI20
    - CGM20PVT

List Details

*\* indicates a mandatory field*

List Name:\*

List Owner: IBP Trainer

List Description:

List Type:\*

List Date:\*

Notes:

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.

**CGM20CB** Save

▶ BASIC DETAILS

Settings
Germplasm & Checks
Treatment Factors
Environments
Experimental Design
Observations
Crosses and Selections

# Crosses and Selections

Selected: 0

#	GID	GROUP ID	DESIGNATION	CROSS	LOTS	BREEDING METHOD ABBR	BREEDING ME	
<input type="checkbox"/>	1	9080579	-	AR20CGM064	IR 76561-AC 8-B/IR 55423-01 (NSIC RC 9)	-	C2W	Single cross
<input type="checkbox"/>	2	9080578	-	AR20CGM063	IR 76561-AC 8-B/YUNLU NO 28	-	C2W	Single cross
<input type="checkbox"/>	3	9080577	-	AR20CGM062	IR 76561-AC 8-B/WAB 534-B-3A 1-1	-	C2W	Single cross
<input type="checkbox"/>	4	9080576	-	AR20CGM061	IR 76561-AC 8-B/WAB 326-B-B-7-H1	-	C2W	Single cross
<input type="checkbox"/>	5	9080575	-	AR20CGM060	IR 76561-AC 8-B/UPL RI 5	-	C2W	Single cross
<input type="checkbox"/>	6	9080574	-	AR20CGM059	IR 76561-AC 8-B/IRAT 170 (FARO 41)	-	C2W	Single cross
<input type="checkbox"/>	7	9080573	-	AR20CGM058	IR 76561-AC 8-B/IDSA 113	-	C2W	Single cross
<input type="checkbox"/>	8	9080572	-	AR20CGM057	IR 76561-AC 8-B/CNA 4196	-	C2W	Single cross
<input type="checkbox"/>	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 (CGM20CB for me). To obtain a crossing template select Actions>Crossing options>Export crossing template:

The screenshot shows the 'MANAGE STUDIES' interface for study 'CGM20CB'. The 'Crosses and Selections' tab is selected. The 'Actions' menu is open, showing options like 'Save Study', 'Design and planning options', 'Crossing options', 'Export crossing template', 'Import Crosses', and 'Design new crosses'. The 'Export crossing template' option is highlighted.

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>20F1t, a description “2020 F1 list from crossing template” and a date.

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

	A	B	C	D	E	F
1	<b>LIST NAME</b>	CGM20F1t		Enter a list name here, or add it when saving in the BMS		
2	<b>LIST DESCRIPTION</b>	2020 F1 list from the crossing template		Enter a list description here, or add it when saving in the BMS		
3	<b>LIST DATE</b>	20200910		Accepted formats: YYYYMMDD or YYYYMM or YYYY		
4						
5	<b>CONDITION</b>	<b>DESCRIPTION</b>	<b>PROPERTY</b>	<b>SCALE</b>	<b>METHOD</b>	<b>DATA TYPE</b>
6	LIST USER	PERSON WHO MADE THE LIST	PERSON	DBC	ASSIGNED	C
7	FEMALE STUDY	The name of the study of the female parent	STUDY	CODE	ASSIGNED	C
8						
9	<b>FACTOR</b>	<b>DESCRIPTION</b>	<b>PROPERTY</b>	<b>SCALE</b>	<b>METHOD</b>	<b>DATA TYPE</b>
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	<b>VARIATE</b>	<b>DESCRIPTION</b>	<b>PROPERTY</b>	<b>SCALE</b>	<b>METHOD</b>	<b>DATA TYPE</b>
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 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.

	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	20200910		IR 72768-12-1-1	IR 72768-28-1-1
3	1		3	C2W	20200910		IR 72768-12-1-1	IR 75502-24-1-1-B
4	1		4	C2W	20200910		IR 72768-12-1-1	IR 75516-30-1-1-B
5	2		5	C2W	20200910		IR 72768-28-1-1	IR 75516-56-1-1-B
6	2		6	C2W	20200910		IR 72768-28-1-1	IR 75518-84-1-1-B
7	2		7	C2W	20200910		IR 72768-28-1-1	IR 75531-31-1-2-B
8	3		8	C2W	20200910		IR 75502-24-1-1-B	IR 76561-AC 8-B
9	3		9	C2W	20200910		IR 75502-24-1-1-B	CNA 4196
10	3		10	C2W	20200910		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	Somoclon

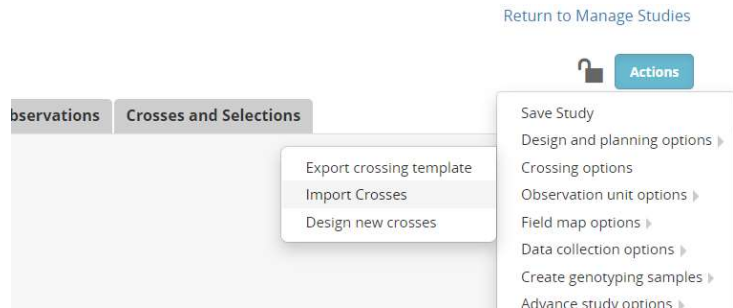
You can leave this column blank if you like and it will be filled by BMS.

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

=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.

### Specify Breeding Method ✕

By default, the breeding method for new crosses will be based on the status of their parental lines. As an alternative, you can select a method to use for all crosses.

Use the breeding methods specified in the import file

Use parental status

Select a method to use for all crosses :

All methods  Generative methods

Show only favorite methods [Manage Methods](#)

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:

Cross code prefix: \*

Number of digits in sequence number

Cross code suffix

Add space between prefix and code?  Yes  No

Add space between suffix and code?  Yes  No

Next name in the sequence: AR20CGM065

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

**Harvest Details**

Estimated harvest date: \*

Harvest location:  ?

Breeding locations  All locations types

Show only favorite locations [Manage Locations](#)

**Alerts**

Check if crosses already exist

[Back](#) [Continue](#)

You will get a list of crosses to review:

**Review Crosses**

Show only records with alerts

Showing 1 to 9 of 9 entries

ALERTS	#	CROSS
	1	IR 72768-12-1-1/IR 72768-28-1-1
	2	IR 72768-12-1-1/IR 75502-24-1-1-B
	3	IR 72768-12-1-1/IR 75516-30-1-1-B
	4	IR 72768-28-1-1/IR 75516-56-1-1-B
	5	IR 72768-28-1-1/IR 75518-84-1-1-B
	6	IR 72768-28-1-1/IR 75531-31-1-2-B
	7	IR 75502-24-1-1-B/IR 76561-AC 8-B
<a href="#">View Existing Crosses</a>	8	IR 75502-24-1-1-B/CNA 4196
<a href="#">View Existing Crosses</a>	9	IR 75502-24-1-1-B/IDSA 113

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):

**IR 75502-24-1-1-B/CNA 4196** ✕

*Cross IR 75502-24-1-1-B/CNA 4196 already exists in the database.*

Showing 1 to 1 of 1 entries

GID	DESIGNATION
9080532	AR20CGM017

[<](#) [1](#) [>](#)

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
<b>Methods for storing historical pedigrees with incomplete information</b>					
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 F1 to 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
<b>Generic Maintenance Methods</b>					
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°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°C.
<b>Generative Methods for Inbreeding Crops</b>					
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	SOMACLONE 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.
<b>Derivative Methods for Inbreeding Crops</b>					
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	ROUING 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.
<b>Management Methods for Inbreeding Crops</b>					
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, CGM20CB in my case:

**MANAGE STUDIES** ?

**CGM20CB** Save

► BASIC DETAILS

Settings **Germplasm & Checks** Treatment Factors Environments Experimental Design Observations **Crosses and Selections**

STUDY SETTINGS Add

Project\_Prefix: Please Choose

Target\_Region: Please Choose

PI\_NAME: Please Choose

Select All Remove

### Open the Crosses and Selections tab

Settings **Germplasm & Checks** Treatment Factors Environments Experimental Design Observations **Crosses and Selections**

Crosses and Selections

Selected: 0 Actions

#	GID	GROUP ID	DESIGNATION	CROSS	LOTS	BREEDING METHOD ABBR	BREEDING METHOD NAME	BREEDING METHOD TYPE	LOCATION
1	9080588	-	AR20CGM073	IR 75502-24-1-1-B/DSA 113	-	C2W	Single cross	GEN	Mbe
2	9080587	-	AR20CGM072	IR 75502-24-1-1-B/CNA 4196	-	C2W	Single cross	GEN	Mbe
3	9080586	-	AR20CGM071	IR 75502-24-1-1-B/IR 76561-AC 8-B	-	C2W	Single cross	GEN	Mbe
4	9080585	-	AR20CGM070	IR 72768-28-1-1/IR 75531-31-1-2-B	-	C2W	Single cross	GEN	Mbe
5	9080584	-	AR20CGM069	IR 72768-28-1-1/IR 75518-84-1-1-B	-	C2W	Single cross	GEN	Mbe
6	9080583	-	AR20CGM068	IR 72768-28-1-1/IR 75516-56-1-1-B	-	C2W	Single cross	GEN	Mbe
7	9080582	-	AR20CGM067	IR 72768-12-1-1/IR 75516-30-1-1-B	-	C2W	Single cross	GEN	Mbe
8	9080581	-	AR20CGM066	IR 72768-12-1-1/IR 75502-24-1-1-B	-	C2W	Single cross	GEN	Mbe
9	9080580	-	AR20CGM065	IR 72768-12-1-1/IR 72768-28-1-1	-	C2W	Single cross	GEN	Mbe
10	9080579	-	AR20CGM064	IR 76561-AC 8-B/IR 55423-01 (NSIC RC 9)	-	C2W	Single cross	GEN	Mbe
11	9080578	-	AR20CGM063	IR 76561-AC 8-B/YUNLU NO 28	-	C2W	Single cross	GEN	Mbe
12	9080577	-	AR20CGM062	IR 76561-AC 8-B/WAB 534-B-3A-1-1	-	C2W	Single cross	GEN	Mbe
13	9080576	-	AR20CGM061	IR 76561-AC 8-B/WAB 326-B-B-7-H1	-	C2W	Single cross	GEN	Mbe
14	9080575	-	AR20CGM060	IR 76561-AC 8-B/UPL RI 5	-	C2W	Single cross	GEN	Mbe
15	9080574	-	AR20CGM059	IR 76561-AC 8-B/IRAT 170 (FARO 41)	-	C2W	Single cross	GEN	Mbe
16	9080573	-	AR20CGM058	IR 76561-AC 8-B/DSA 113	-	C2W	Single cross	GEN	Mbe

Showing 1 to 73 of 73 entries Records per page: 100

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 we can either select each page in turn, or set the Records per page to a high number and then select the single page with 73 records.



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

On the create lot 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 initials 'CGM' which indicates 'ownership' and also which section fo the seed store they will be kept in.

**Create Lot** ✕

Stock ID Prefix ⓘ

Storage Location

Favorite locations only

Units

Notes

**Deposit**

---

Amount

Notes

Confirm transactions on saving

Specify the storage location (which can be a details 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.

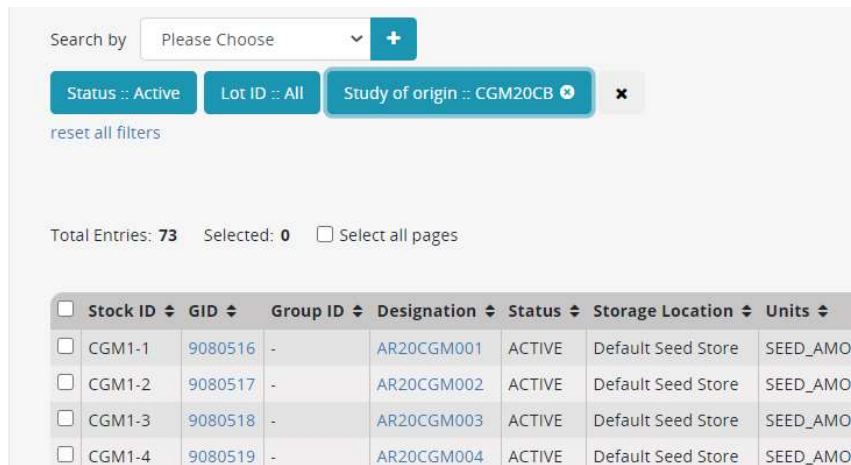


## Make labels for the seed packets from a harvest list

The user must use the Manage Inventory item from the INVENTORY MANAGE menu:

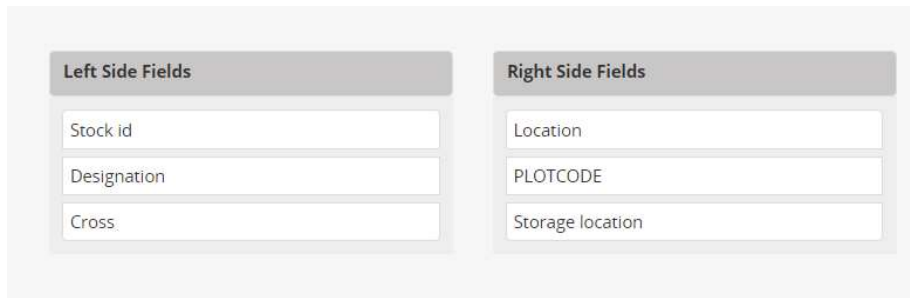


In the Search by box on the View Lots tab, select 'Study of origin' and click the + symbol. Then click on the new filter item and select the study where the harvests were made CGM20CB in my case. This filters the lots down to the 73 for the harvest list we are working with:



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 printing labels with any desired format.

Select the following fields for the label and 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**:



EZSWLbclUAgmlo  
 Stock id : CGM1-1  
 Designation : AR20CGM001  
 Location : Mbe  
 PLOTCODE : CGM20CB:Mbe:202009  
 :1;/CGM20CB:Mbe:202009:9:  
 Storage location : Default Seed Store  
 Cross : IR 72768-12-1-1/CNA 4196



EZSWLECVb0K40  
 Stock id : CGM1-2  
 Designation : AR20CGM002  
 Location : Mbe  
 PLOTCODE : CGM20CB:Mbe:202009  
 :1;/CGM20CB:Mbe:202009:10:  
 Storage location : Default Seed Store  
 Cross : IR 72768-12-1-1/IDSA 113



EZSWLbr0CpCw  
 Stock id : CGM1-3  
 Designation : AR20CGM003  
 Location : Mbe  
 PLOTCODE : CGM20CB:Mbe:202009  
 :1;/CGM20CB:Mbe:202009:11:  
 Storage location : Default Seed Store  
 Cross : IR 72768-12-1-1/IRAT 170 (FARO 41)



EZSWLidiYozh7  
 Stock id : CGM1-4  
 Designation : AR20CGM004  
 Location : Mbe  
 PLOTCODE : CGM20CB:Mbe:202009  
 :1;/CGM20CB:Mbe:202009:12:  
 Storage location : Default Seed Store  
 Cross : IR 72768-12-1-1/UPL RI 5



EZSWLidv6kZy  
 Stock id : CGM1-5  
 Designation : AR20CGM005  
 Location : Mbe  
 PLOTCODE : CGM20CB:Mbe:202009  
 :1;/CGM20CB:Mbe:202009:13:  
 Storage location : Default Seed Store  
 Cross : IR 72768-12-1-1/WAB 326-B-B-7-H1



EZSWLLp01cz1X  
 Stock id : CGM1-6  
 Designation : AR20CGM006  
 Location : Mbe  
 PLOTCODE : CGM20CB:Mbe:202009  
 :1;/CGM20CB:Mbe:202009:14:  
 Storage location : Default Seed Store  
 Cross : IR 72768-12-1-1/WAB 534-B-3A 1-1

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 – CGM20CB for me, to see the 73 pending transactions.

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

View Lots View Transactions

Filter table

Search by

Lot Status : Active Lot ID : All Transaction ID : All Transaction type : All Transaction status : All Study of origin : CGM20CB

reset all filters

Total Entries: 73 Selected: 0  Select all pages

Actions

Export transactions

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	
	DESIGNATION	GID	LOT_UID	LOCA	BE	LG	STOCK_ID	AVAILABLE	TRN_ID	CREATED	USERNAME	STATUS	TYPE	UNITS	AMOUNT	NOTES	NEW AMOUNT	NEW BALANCE	NEW NOTES
2	AR20CGM001	9080516	EZSWLbclUAgmlo	DSS	Defat	CGM1-1	0.0	11	2020-09-10		itrainer	Pending	Deposit	SEED_AMOUNT_g	0.1	Dummy amount to be updated		60	Clean seed
3	AR20CGM002	9080517	EZSWLECVb0K40	DSS	Defat	CGM1-2	0.0	12	2020-09-10		itrainer	Pending	Deposit	SEED_AMOUNT_g	0.1	Dummy amount to be updated		71	Clean seed
4	AR20CGM003	9080518	EZSWLbr0CpCw	DSS	Defat	CGM1-3	0.0	13	2020-09-10		itrainer	Pending	Deposit	SEED_AMOUNT_g	0.1	Dummy amount to be updated		80	Clean seed
5	AR20CGM004	9080519	EZSWLidiYozh7	DSS	Defat	CGM1-4	0.0	14	2020-09-10		itrainer	Pending	Deposit	SEED_AMOUNT_g	0.1	Dummy amount to be updated		51	Clean seed
6	AR20CGM005	9080520	EZSWLidv6kZy	DSS	Defat	CGM1-5	0.0	15	2020-09-10		itrainer	Pending	Deposit	SEED_AMOUNT_g	0.1	Dummy amount to be updated		52	Clean seed
7	AR20CGM006	9080521	EZSWLLp01cz1X	DSS	Defat	CGM1-6	0.0	16	2020-09-10		itrainer	Pending	Deposit	SEED_AMOUNT_g	0.1	Dummy amount to be updated		54	Clean seed
8	AR20CGM007	9080522	EZSWLlubbQFKF	DSS	Defat	CGM1-7	0.0	17	2020-09-10		itrainer	Pending	Deposit	SEED_AMOUNT_g	0.1	Dummy amount to be updated		68	Clean seed
9	AR20CGM008	9080523	EZSWLIWohh3MI	DSS	Defat	CGM1-8	0.0	18	2020-09-10		itrainer	Pending	Deposit	SEED_AMOUNT_g	0.1	Dummy amount to be updated		59	Clean seed
10	AR20CGM009	9080524	EZSWLqj8XH0tb	DSS	Defat	CGM1-9	0.0	19	2020-09-10		itrainer	Pending	Deposit	SEED_AMOUNT_g	0.1	Dummy amount to be updated		78	Clean seed
11	AR20CGM010	9080525	EZSWLZjKc3u0M	DSS	Defat	CGM1-10	0.0	20	2020-09-10		itrainer	Pending	Deposit	SEED_AMOUNT_g	0.1	Dummy amount to be updated		51	Clean seed
12	AR20CGM011	9080526	EZSWLhJzn668S	DSS	Defat	CGM1-11	0.0	21	2020-09-10		itrainer	Pending	Deposit	SEED_AMOUNT_g	0.1	Dummy amount to be updated		55	Clean seed
13	AR20CGM012	9080527	EZSWLTkq4YRDh	DSS	Defat	CGM1-12	0.0	22	2020-09-10		itrainer	Pending	Deposit	SEED_AMOUNT_g	0.1	Dummy amount to be updated		68	Clean seed
14	AR20CGM013	9080528	EZSWL3zh9qaX0	DSS	Defat	CGM1-13	0.0	23	2020-09-10		itrainer	Pending	Deposit	SEED_AMOUNT_g	0.1	Dummy amount to be updated		78	Clean seed
15	AR20CGM014	9080529	EZSWL74zKnUzL	DSS	Defat	CGM1-14	0.0	24	2020-09-10		itrainer	Pending	Deposit	SEED_AMOUNT_g	0.1	Dummy amount to be updated		79	Clean seed
16	AR20CGM015	9080530	EZSWLg0BsoUIM	DSS	Defat	CGM1-15	0.0	25	2020-09-10		itrainer	Pending	Deposit	SEED_AMOUNT_g	0.1	Dummy amount to be updated		54	Clean seed
17	AR20CGM016	9080531	FZSWLlp01cz1X	DSS	Defat	CGM1-16	0.0	26	2020-09-10		itrainer	Pending	Deposit	SEED_AMOUNT_g	0.1	Dummy amount to be updated		77	Clean seed

Now we need to import the transaction updates, but this action is not available to the Breeder 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**:

The screenshot shows the 'View Transactions' interface. At the top, there are tabs for 'View Lots' and 'View Transactions'. Below this is a 'Filter table' section with a search dropdown and several filter buttons: 'Lot Status :: Active', 'Lot ID :: All', 'Transaction ID :: All', 'Transaction type :: All', and 'Transaction status :: All'. There is a 'reset all filters' link. Below the filters, it shows 'Total Entries: 83' and 'Selected: 0' with a 'Select all pages' checkbox. An 'Actions' dropdown menu is open, showing options: 'Confirm transactions', 'Export transactions', 'Import transaction updates', and 'Cancel pending transactions'. The 'Import transaction updates' option is highlighted. Below the menu is a table with columns: GID, Designation, Stock ID, Transaction ID, Username, Creation Date, Transaction Type, Transaction Status, Units, Amount, and Notes. The first row shows: 9033755, AR 3222, SID1-3, 1, Kouadio, 2020-05-05, Deposit, Confirmed, 0.

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

The screenshot shows the 'View Transactions' interface with filters: 'Lot Status :: All', 'Lot ID :: All', 'Transaction ID :: 11,12,13,14,15,...', 'Transaction type :: All', and 'Transaction status :: All'. It shows 'Total Entries: 73' and 'Selected: 0' with a 'Select all pages' checkbox. An 'Actions' dropdown menu is visible. Below is a table with columns: GID, Designation, Stock ID, Transaction ID, Username, Creation Date, Transaction Type, Transaction Status, Units, Amount, and Notes. The table contains 12 rows of data, all with 'Confirmed' status and 'Clean seed' notes.

GID	Designation	Stock ID	Transaction ID	Username	Creation Date	Transaction Type	Transaction Status	Units	Amount	Notes
9080516	AR20CGM001	CGM1-1	11	itrainer	2020-09-10	Deposit	Confirmed	SEED_AMOUNT_g	60	Clean seed
9080517	AR20CGM002	CGM1-2	12	itrainer	2020-09-10	Deposit	Confirmed	SEED_AMOUNT_g	71	Clean seed
9080518	AR20CGM003	CGM1-3	13	itrainer	2020-09-10	Deposit	Confirmed	SEED_AMOUNT_g	80	Clean seed
9080519	AR20CGM004	CGM1-4	14	itrainer	2020-09-10	Deposit	Confirmed	SEED_AMOUNT_g	51	Clean seed
9080520	AR20CGM005	CGM1-5	15	itrainer	2020-09-10	Deposit	Confirmed	SEED_AMOUNT_g	52	Clean seed
9080521	AR20CGM006	CGM1-6	16	itrainer	2020-09-10	Deposit	Confirmed	SEED_AMOUNT_g	54	Clean seed
9080522	AR20CGM007	CGM1-7	17	itrainer	2020-09-10	Deposit	Confirmed	SEED_AMOUNT_g	68	Clean seed
9080523	AR20CGM008	CGM1-8	18	itrainer	2020-09-10	Deposit	Confirmed	SEED_AMOUNT_g	59	Clean seed
9080524	AR20CGM009	CGM1-9	19	itrainer	2020-09-10	Deposit	Confirmed	SEED_AMOUNT_g	78	Clean seed
9080525	AR20CGM010	CGM1-10	20	itrainer	2020-09-10	Deposit	Confirmed	SEED_AMOUNT_g	51	Clean seed
9080526	AR20CGM011	CGM1-11	21	itrainer	2020-09-10	Deposit	Confirmed	SEED_AMOUNT_g	55	Clean seed
9080527	AR20CGM012	CGM1-12	22	itrainer	2020-09-10	Deposit	Confirmed	SEED_AMOUNT_g	68	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.

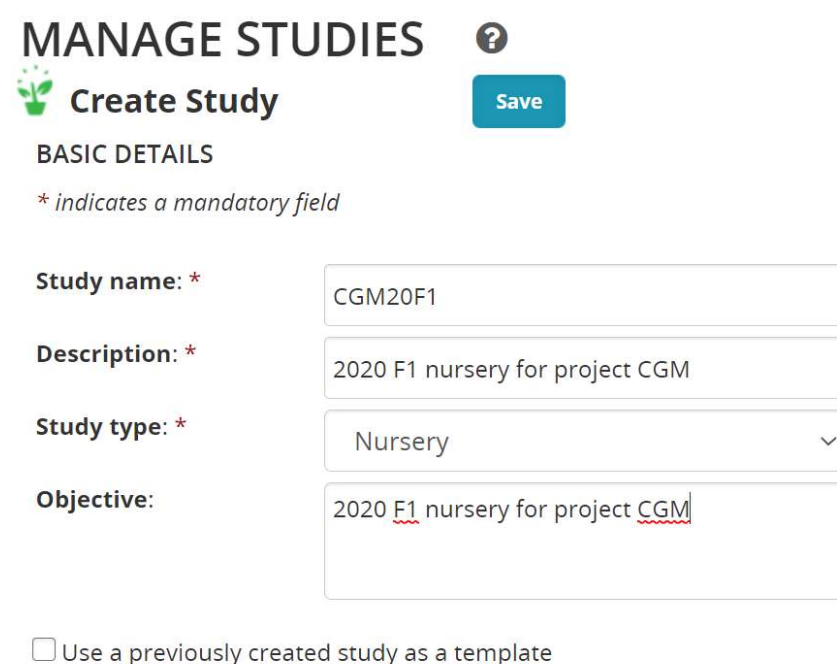
### Objectives

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>20F1, CGM20F1 for me, and fill in the basic details of description and objective and select the study type **Nursery**.



**MANAGE STUDIES** ?

 **Create Study** Save

BASIC DETAILS

*\* indicates a mandatory field*

**Study name: \***

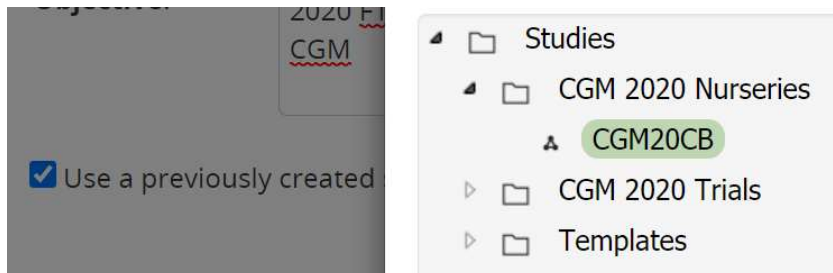
**Description: \***

**Study type: \***

**Objective:**

Use a previously created study as a template

You can add variables to the new study directly from the Ontology pick lists as we did for the crossing block in Tutorial 004, 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 similar to your current study:



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

Settings **Germplasm & Checks**

**STUDY SETTINGS** ? Add

**Project\_Prefix:** Project Prefix 2

**Target\_Region:** Region 3

**PI\_NAME:** Christopher McLaren

Select All Remove

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 Tutorial 004. CGM20F1 in my case.

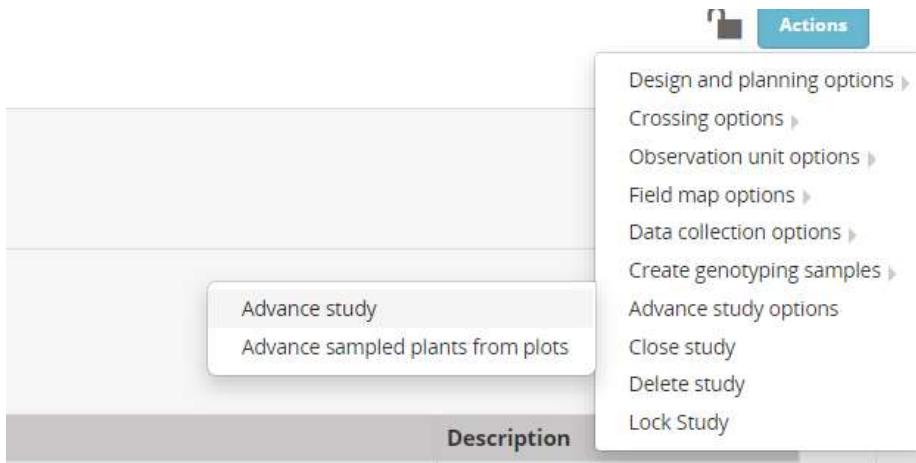
Save the study in your 2020 Nursery folder.

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.

## Advance study



\* indicates a mandatory field

### METHODS

Breeding Method is the same for each advance

Random bulk - DRP

Derivative and Maintenance methods

All methods

Show only favorite methods [Manage Methods](#)

### BULKS

All plots are selected

### LOCATION DETAILS

LOCATION\_NAME

Mbe

Back

Finish

Click **Finish**.

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

Save the list with name <your initials>20F2 in your 2020 lists folder.

## Save List As



### List Location



- Crop lists
- Program lists
  - 2020 lists
    - CGM 2020 lists**
      - CGM20F1t
      - CGMAVT20
      - CGMGI20
      - U20CGMF1

### List Details

\* indicates a mandatory field

List Name:\* CGM20F2

List Owner: IBP Trainer

List Description: F2 seeds harvested from CGM20F1 nursery

List Type:\* HARVEST LIST

List Date:\* 2020-09-11

Notes:

Cancel


Save

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).

**MANAGE STUDIES** 

CGM20F2 Save Return to Manage Stu



▶ BASIC DETAILS Act

Settings **Germplasm & Checks** Treatment Factors Environments Experimental Design **Observations**

Observations 

Observations

▼ Define Observation Details

TRAITS  Add SELECTIONS  Add

Name	Description	Input Variables
<input type="checkbox"/> FlwDate_50Flw_Date	Flowering date -BY- Fifty percent flowering date observation-IN- ISO Date (yyyymmdd)	

Remove

Observations ACCEPTED PENDING Show Categorical Description

Select Environment: 1 - Mbe Filter by status: All

Batch Actions

Selected: 0  Select all pages

ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	CROSS	SEED_SOURCE	PLOT_NO	FlwDate_50Flw_Date
<input type="checkbox"/> Test entry	9080589	AR20CGM001-RB	1	IR 72768-12-1-1/CNA 4196	CGM20F1:Mbe:202009:1:	1	
<input type="checkbox"/> Test entry	9080590	AR20CGM002-RB	2	IR 72768-12-1-1/ISA 113	CGM20F1:Mbe:202009:2:	2	
<input type="checkbox"/> Test entry	9080591	AR20CGM003-RB	3	IR 72768-12-1-1/RAT 170 (FARO 41)	CGM20F1:Mbe:202009:3:	3	

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

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

Add Selections

Selections (Breeding process)

**SELECTIONS (Breeding Process)**

NPSEL

Method: Counted Scale: Number

**RELATED PROPERTIES**

Breeding method

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

**Actions**

- Design and planning options >
- Crossing options >
- Observation unit options >
- Field map options >
- Data collection options
- Create genotyping samples >
- Advance study options >
- Close study
- Delete study
- Lock Study

Export study book

Import Observations

Export germplasm list

escription

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	CGM20F2							
2	TITLE	2020 F2 nursery for population development							
3	OBJECTIVE	Select single plant lines from the F2 populations							
4	START DATE	20200911							
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_Scal	Assigned	C	PA	STUDY
10	Target_Region	Target Region Variable		Target Region	Target_Region_Scal	Assigned	C	R3	STUDY
11	PI_NAME_ID	Principal investigator - assigned (DBID)		Person	Person id	Assigned	C	97	STUDY
12	PI_NAME	Principal investigator - assigned (DBCY)		Person	Person name	Assigned	C	Christopher McLaren	STUDY
13									
14	EXPERIMENTAL DESIG	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 DETAIL	DESCRIPTION	ONTOLOGY ID	PROPERTY	SCALE	METHOD	DATA TYPE	VALUE	DATASET
18	TRIAL_INSTANCE	Trial instance - enumerated (number)		Trial instance	Number	Enumerated	N		ENVIRONMENT
19	LOCATION_ID	Location - selected (DBID)		Location	Location id	Assigned	C	29102	ENVIRONMENT
20	LOCATION_NAME	Location - selected (DBCY)		Location	Location name	Assigned	C	Mbe	ENVIRONMENT
21	SEEDING_DATE	Date Seeded - applied (yyymmdd)		Planting date	Date (yyymmdd) of Applied		D		ENVIRONMENT
22	EXPT_DESIGN	Experimental design - assigned (type)		Experimental design	Type of EXPT_DESIG	Assigned	C	ELO	ENVIRONMENT
23									
24	ENVIRONMENTAL CON	DESCRIPTION	ONTOLOGY ID	PROPERTY	SCALE	METHOD	DATA TYPE	VALUE	DATASET
25									
26	GERMPLASM DESCRIP	DESCRIPTION	ONTOLOGY ID	PROPERTY	SCALE	METHOD	DATA TYPE	VALUE	DATASET
27	ENTRY_TYPE	Entry type (test/check)- assigned (type)		Entry type	Type of ENTRY_TYP	Assigned	C		PLOT
28	GID	Germplasm identifier - assigned (DBID)		Germplasm id	Germplasm id	Assigned	C		PLOT
29	DESIGNATION	Germplasm identifier - assigned (DBCY)		Germplasm id	Germplasm name	Assigned	C		PLOT
30	ENTRY_NO	Germplasm entry - enumerated (number)		Germplasm entry	Number	Enumerated	N		PLOT
31	OBS_UNIT_ID	Field observation unit id - assigned (text)		Field plot	Text	Assigned	T		PLOT
32	CROSS	The pedigree string of the germplasm		Cross history	Text	Assigned	T		PLOT
33	SEED_SOURCE	Seed source - Selected (Code)		Seed source	Code of SEED_SOU	Selected	T		PLOT
34									
35	OBSERVATION UNIT	DESCRIPTION	ONTOLOGY ID	PROPERTY	SCALE	METHOD	DATA TYPE	VALUE	DATASET
36									
37	TRAITS	DESCRIPTION	ONTOLOGY ID	PROPERTY	SCALE	METHOD	DATA TYPE	VALUE	DATASET
38	FlwDate_50Flw_Date	Flowering date -BY- Fifty percent flowering date observation-IN-1		Flowering date	ISO Date (yyyy-mm-d)	Fifty percent flowe	D		PLOT
39									
40	SELECTIONS	DESCRIPTION	ONTOLOGY ID	PROPERTY	SCALE	METHOD	DATA TYPE	VALUE	DATASET
41	NPSEL	Number of plants selected - counted (number)		Selections	Number	Counted	N		PLOT
42									

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

	A	B	C	D	E	F	G	H	I	J
1	OBS_UNIT	ENTRY_T	GID	DESIGNA	ENTRY_N	CROSS	SEED_SO	PLOT_NO	FlwDate_50Flw_Date	NPSEL
2	EZSWPmi	T	9080589	AR20CGM	1	IR 72768-	CGM20F1	1	20200920	0
3	EZSWPC	T	9080590	AR20CGM	2	IR 72768-	CGM20F1	2	20200920	1
4	EZSWPt0	T	9080591	AR20CGM	3	IR 72768-	CGM20F1	3	20200916	5
5	EZSWPZG	T	9080592	AR20CGM	4	IR 72768-	CGM20F1	4	20200912	2
6	EZSWPmi	T	9080593	AR20CGM	5	IR 72768-	CGM20F1	5	20200913	0
7	EZSWPuS	T	9080594	AR20CGM	6	IR 72768-	CGM20F1	6	20200919	2
8	EZSWPT0	T	9080595	AR20CGM	7	IR 72768-	CGM20F1	7	20200914	5
9	EZSWPX&	T	9080596	AR20CGM	8	IR 72768-	CGM20F1	8	20200913	3
10	EZSWPpx	T	9080597	AR20CGM	9	IR 72768-	CGM20F1	9	20200919	1
11	EZSWPbE	T	9080598	AR20CGM	10	IR 72768-	CGM20F1	10	20200911	2
12	EZSWPgE	T	9080599	AR20CGM	11	IR 72768-	CGM20F1	11	20200911	1
13	EZSWPyE	T	9080600	AR20CGM	12	IR 72768-	CGM20F1	12	20200919	0
14	EZSWP08	T	9080601	AR20CGM	13	IR 72768-	CGM20F1	13	20200917	5
15	EZSWPW	T	9080602	AR20CGM	14	IR 72768-	CGM20F1	14	20200914	3
16	EZSWPrjI	T	9080603	AR20CGM	15	IR 72768-	CGM20F1	15	20200913	4
17	EZSWPp5	T	9080604	AR20CGM	16	IR 72768-	CGM20F1	16	20200920	1
18	EZSWP0h	T	9080605	AR20CGM	17	IR 75502-	CGM20F1	17	20200913	0
19	EZSWPQf	T	9080606	AR20CGM	18	IR 75502-	CGM20F1	18	20200918	1
20	EZSWPYi	T	9080607	AR20CGM	19	IR 75502-	CGM20F1	19	20200914	4
21	EZSWP8L	T	9080608	AR20CGM	20	IR 75502-	CGM20F1	20	20200917	1
22	EZSWP80	T	9080609	AR20CGM	21	IR 75502-	CGM20F1	21	20200920	0
23	EZSWPRC	T	9080610	AR20CGM	22	IR 75502-	CGM20F1	22	20200920	0
24	EZSWPiJ	T	9080611	AR20CGM	23	IR 75502-	CGM20F1	23	20200914	1
25	EZSWPkq	T	9080612	AR20CGM	24	IR 75502-	CGM20F1	24	20200918	1
26	FZSWPR&	T	9080613	AR20CGM	25	IR 75516-	CGM20F1	25	20200920	4

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.

Observations

Define Observation Details

Observations

ACCEPTED PENDING

Accept Discard

Show Categorical Description

Select Environment: All environments Filter by status: All

Batch Actions

Selected: 0 Select all pages

TRIAL_INSTANCE	ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	CROSS	SEED_SOURCE	PLOT_NO	FlwDate_50Flw_Date	NPSEL
1	Test entry	9080589	AR20CGM001-RB	1	IR 72768-12-1-1/CNA 4196	CGM20F1:Mbe:202009:1:	1	20200920	0
1	Test entry	9080590	AR20CGM002-RB	2	IR 72768-12-1-1/IDSA 113	CGM20F1:Mbe:202009:2:	2	20200920	1
1	Test entry	9080591	AR20CGM003-RB	3	IR 72768-12-1-1/RAT 170 (FARO 41)	CGM20F1:Mbe:202009:3:	3	20200916	5

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:

- Design and planning options
- Crossing options
- Observation unit options
- Field map options
- Data collection options
- Create genotyping samples
- Advance study options
- Close study
- Delete study
- Lock Study

Advance study

Advance sampled plants from plots

Description

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.

### Advance study ✕

*\* indicates a mandatory field*

#### METHODS

Breeding Method is the same for each advance

Single plant selection - DSP ?

Derivative and Maintenance methods  
 All methods  
 Show only favorite methods [Manage Methods](#)

#### LINES

Same number of lines is selected for each plot

Choose a variate that defines the number of lines selected from each plot

NPSEL

#### LOCATION DETAILS

**LOCATION\_NAME**

Mbe

[Back](#) [Finish](#)

Click Finish.

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

#### REVIEW ADVANCED LINES

▼ Advance List Entries

[Actions](#)

Total Entries: 131 Selected: 0

<input checked="" type="checkbox"/>	ENTRY_NO	DESIGNATION	CROSS	GID	SEED_SOURCE	TR
<input type="checkbox"/>	1	AR20CGM002-RB-1	IR 72768-12-1-1/IDSA 113	Pending	CGM20F2:Mbe:202009:2:	
<input type="checkbox"/>	2	AR20CGM003-RB-1	IR 72768-12-1-1/IRAT 170 (FARO 41)	Pending	CGM20F2:Mbe:202009:3:	
<input type="checkbox"/>	3	AR20CGM003-RB-2	IR 72768-12-1-1/IRAT 170 (FARO 41)	Pending	CGM20F2:Mbe:202009:3:	
<input type="checkbox"/>	4	AR20CGM003-RB-3	IR 72768-12-1-1/IRAT 170 (FARO 41)	Pending	CGM20F2:Mbe:202009:3:	
<input type="checkbox"/>	5	AR20CGM003-RB-4	IR 72768-12-1-1/IRAT 170 (FARO 41)	Pending	CGM20F2:Mbe:202009:3:	
<input type="checkbox"/>	6	AR20CGM003-RB-5	IR 72768-12-1-1/IRAT 170 (FARO 41)	Pending	CGM20F2:Mbe:202009:3:	
<input type="checkbox"/>	7	AR20CGM004-RB-1	IR 72768-12-1-1/UPL RI 5	Pending	CGM20F2:Mbe:202009:4:	
<input type="checkbox"/>	8	AR20CGM004-RB-2	IR 72768-12-1-1/UPL RI 5	Pending	CGM20F2:Mbe:202009:4:	
<input type="checkbox"/>	9	AR20CGM006-RB-1	IR 72768-12-1-1/WAB 534-B-3A 1-1	Pending	CGM20F2:Mbe:202009:6:	
<input type="checkbox"/>	10	AR20CGM006-RB-2	IR 72768-12-1-1/WAB 534-B-3A 1-1	Pending	CGM20F2:Mbe:202009:6:	
<input type="checkbox"/>	11	AR20CGM007-RB-1	IR 72768-12-1-1/YUNLU NO 28	Pending	CGM20F2:Mbe:202009:7:	
<input type="checkbox"/>	12	AR20CGM007-RB-2	IR 72768-12-1-1/YUNLU NO 28	Pending	CGM20F2:Mbe:202009:7:	
<input type="checkbox"/>	13	AR20CGM007-RB-3	IR 72768-12-1-1/YUNLU NO 28	Pending	CGM20F2:Mbe:202009:7:	
<input type="checkbox"/>	14	AR20CGM007-RB-4	IR 72768-12-1-1/YUNLU NO 28	Pending	CGM20F2:Mbe:202009:7:	
<input type="checkbox"/>	15	AR20CGM007-RB-5	IR 72768-12-1-1/YUNLU NO 28	Pending	CGM20F2:Mbe:202009:7:	
<input type="checkbox"/>	16	AR20CGM008-RB-1	IR 72768-12-1-1/IR 55433-01 (WAB 534-B-3A)	Pending	CGM20F2:Mbe:202009:8:	

< 1 2 >

Select All

[Back](#) [Finish](#)

## Save seed inventory for the F3 harvest list

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

Open the F2 nursery (CGM2F2 for me) and on the **Crosses and Selections** tab select all the entries. You may have to step through the pages of selections and select all on each page.

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** checkbox. You can create labels for this inventory by following steps in the in tutorial **IBP2020-DM-005-Adding Inventory for a Harvest List**.

### Create Lot ✕

Stock ID Prefix ⓘ

Storage Location

  
 Favorite locations only

Units

Notes

#### Deposit

---

Amount

Notes

Confirm transactions on saving

If you go to the list manager and open the F3 list you can see the inventory:

## MANAGE GERmplasm ?

View Lists View Germplasm

**List Details**  
Browse or search for a list to work with.

CGM20F3 x

**List entries**  
Total Entries: 131 Selected: 0

✓	#	DESIGNATION	CROSS	LOTS	AVAILABLE
<input type="checkbox"/>	1	AR20CGM002-RB-1	IR 72768-12-1-1/IDSA 113	1	1.0 Packets
<input type="checkbox"/>	2	AR20CGM003-RB-1	IR 72768-12-1-1/IRAT 170 (FARO 41)	1	1.0 Packets
<input type="checkbox"/>	3	AR20CGM003-RB-2	IR 72768-12-1-1/IRAT 170 (FARO 41)	1	1.0 Packets
<input type="checkbox"/>	4	AR20CGM003-RB-3	IR 72768-12-1-1/IRAT 170 (FARO 41)	1	1.0 Packets
<input type="checkbox"/>	5	AR20CGM003-RB-4	IR 72768-12-1-1/IRAT 170 (FARO 41)	1	1.0 Packets
<input type="checkbox"/>	6	AR20CGM003-RB-5	IR 72768-12-1-1/IRAT 170 (FARO 41)	1	1.0 Packets
<input type="checkbox"/>	7	AR20CGM004-RB-1	IR 72768-12-1-1/UPL RI 5	1	1.0 Packets
<input type="checkbox"/>	8	AR20CGM004-RB-2	IR 72768-12-1-1/UPL RI 5	1	1.0 Packets
<input type="checkbox"/>	9	AR20CGM006-RB-1	IR 72768-12-1-1/WAB 534-B-3A 1-1	1	1.0 Packets
<input type="checkbox"/>	10	AR20CGM006-RB-2	IR 72768-12-1-1/WAB 534-B-3A 1-1	1	1.0 Packets
<input type="checkbox"/>	11	AR20CGM007-RB-1	IR 72768-12-1-1/YUNLU NO 28	1	1.0 Packets
<input type="checkbox"/>	12	AR20CGM007-RB-2	IR 72768-12-1-1/YUNLU NO 28	1	1.0 Packets
<input type="checkbox"/>	13	AR20CGM007-RB-3	IR 72768-12-1-1/YUNLU NO 28	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 to entries to the F3 germplasm list. So with the germplasm Manager open the F3 germplasm list (CGM20F3 for me).

Select Actions>List editing options>Edit list

**List Details** Show List Builder  
Browse or search for a list to work with.

CGM20F3 x

**List entries**  
Total Entries: 131 Selected: 0

✓	#	DESIGNATION	CROSS	LOTS	AVAILABLE
<input type="checkbox"/>	1	AR20CGM002-RB-1	IR 72768-12-1-1/IDSA 113	1	
<input type="checkbox"/>	2	AR20CGM003-RB-1	IR 72768-12-1-1/IRAT 170 (FARO 41)	1	
<input type="checkbox"/>	3	AR20CGM003-RB-2	IR 72768-12-1-1/IRAT 170 (FARO 41)	1	
<input type="checkbox"/>	4	AR20CGM003-RB-3	IR 72768-12-1-1/IRAT 170 (FARO 41)	1	
<input type="checkbox"/>	5	AR20CGM003-RB-4	IR 72768-12-1-1/IRAT 170 (FARO 41)	1	
<input type="checkbox"/>	6	AR20CGM003-RB-5	IR 72768-12-1-1/IRAT 170 (FARO 41)	1	0.0 Packets E0006 9080658 -

List editing options

Export list

Coding and Grouping Options

Create inventory lots

Save changes

Select all

Add entries

Remove selected entries from list

**Edit list**

Delete list

Copy to list

Add column

Click on the Germplasm search tab and look for IR64, exact match, with inventory:

## MANAGE GERmplasm ?

View Lists

View Germplasm

### Search for Germplasm

Select germplasm from the results to add to a new list, or click the name to see full details.

[Hide List Builder](#)

### Edit list

Build or revise your list by drag

Search ?

> Hide List Builder

With inventory only
  Include parents
  Include group members  
 Matches starting with
  Exact matches
  Matches containing

Total Results: **1**    Selected: **0** ⚙️ ACTIONS

	NAMES	CROSS	LOTS	AVAILABLE	STOCK
<input type="checkbox"/>	IR 18348-36-3-3, IR ...	IR 5657-33-2-1/IR 2061-465-1-5-5	1	5.0 kg	B20C1-1

#### List entries

Total Entries: **131**    Selected: **0**

	#	DESIGNATION
<input type="checkbox"/>	1	AR20CGM002
<input type="checkbox"/>	2	AR20CGM003
<input type="checkbox"/>	3	AR20CGM003
<input type="checkbox"/>	4	AR20CGM003
<input type="checkbox"/>	5	AR20CGM003
<input type="checkbox"/>	6	AR20CGM003
<input type="checkbox"/>	7	AR20CGM004

Select the hit with inventory and add it to a new list:

Total Results: **1**    Selected: **1** ⚙️ ACTIONS

	NAMES	CROSS	LOTS	AVAILABLE	STOCK
<input checked="" type="checkbox"/>	IR 18348-36-3-3, IR ...	IR 5657-33-2-1/IR 2061-465-1-5-5	1	5.0 kg	B20C1-1

Add Selected Entries to New List

Select All

IR64 will be added to the Edit list. Do the same for check NERICA4.

Search ?

> Hide List Builder

With inventory only
  Include parents
  Include group members  
 Matches starting with
  Exact matches
  Matches containing

Total Results: **1**    Selected: **1** ⚙️ ACTIONS

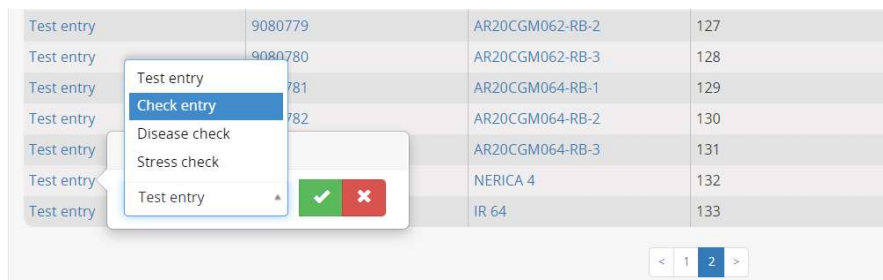
	NAMES	CROSS	LOTS	AVAILABLE	STOCK
<input checked="" type="checkbox"/>	NERICA 4, WAB 450-I	WAB 56-104/CG 14	1	5.0 kg	B20C1-3

The list in the edit box now has two new entries at the bottom:



Click Save to save the changes to this list.

Now Use the Study manager and follow the steps above to make an F3 nursery. I will call mine CGM20F3. 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 entries 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.

Save the study, then 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 planted one at a time in turn. We select 10 for spacing and Insert each check in turn. Click **Generate Design**.

Settings | Germplasm & Checks | Treatment Factors | Environments | Experimental Design | Observations

# Experimental Design

CHOOSE A DESIGN TYPE

Select the design type you would like to use for this study:  ?

Or import an experimental design.

SPECIFY PLOT NUMBERING

Specify the starting plot number:

SPECIFY DESIGN PARAMETERS

Specify checks

Starting Position \*

Spacing \*

Manner of Insertion

Generate Design

Delete Design

SUMMARY OF DESIGN DETAILS

Treatment factor: ENTRY\_NO

Plot factor: PLOT\_NO

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_NO	FlwDate_50Flw_Date
<input type="checkbox"/> Check entry	2264738	NERICA 4	132	WAB 56-104/CG 14	Unknown	1	
<input type="checkbox"/> Test entry	9080653	AR20CGM002-RB-1	1	IR 72768-12-1-1/DSA 113	CGM20F2.Mbe:202009-2:	2	
<input type="checkbox"/> Test entry	9080654	AR20CGM003-RB-1	2	IR 72768-12-1-1/RAT 170 (FARO 41)	CGM20F2.Mbe:202009-3:	3	
<input type="checkbox"/> Test entry	9080655	AR20CGM003-RB-2	3	IR 72768-12-1-1/RAT 170 (FARO 41)	CGM20F2.Mbe:202009-3:	4	
<input type="checkbox"/> Test entry	9080656	AR20CGM003-RB-3	4	IR 72768-12-1-1/RAT 170 (FARO 41)	CGM20F2.Mbe:202009-3:	5	
<input type="checkbox"/> Test entry	9080657	AR20CGM003-RB-4	5	IR 72768-12-1-1/RAT 170 (FARO 41)	CGM20F2.Mbe:202009-3:	6	
<input type="checkbox"/> Test entry	9080658	AR20CGM003-RB-5	6	IR 72768-12-1-1/RAT 170 (FARO 41)	CGM20F2.Mbe:202009-3:	7	
<input type="checkbox"/> Test entry	9080659	AR20CGM004-RB-1	7	IR 72768-12-1-1/UPL RI 5	CGM20F2.Mbe:202009-4:	8	
<input type="checkbox"/> Test entry	9080660	AR20CGM004-RB-2	8	IR 72768-12-1-1/UPL RI 5	CGM20F2.Mbe:202009-4:	9	
<input type="checkbox"/> Test entry	9080661	AR20CGM006-RB-1	9	IR 72768-12-1-1/WAB 534-B-3A 1-1	CGM20F2.Mbe:202009-6:	10	
<input type="checkbox"/> Test entry	9080662	AR20CGM006-RB-2	10	IR 72768-12-1-1/WAB 534-B-3A 1-1	CGM20F2.Mbe:202009-6:	11	
<input type="checkbox"/> Check entry	505533	IR 64	133	IR 5657-33-2-1/IR 2061-465-1-5-	Unknown	12	
<input type="checkbox"/> Test entry	9080663	AR20CGM007-RB-1	11	IR 72768-12-1-1/YUNLU NO 28	CGM20F2.Mbe:202009-7:	13	
<input type="checkbox"/> Test entry	9080664	AR20CGM007-RB-2	12	IR 72768-12-1-1/YUNLU NO 28	CGM20F2.Mbe:202009-7:	14	
<input type="checkbox"/> Test entry	9080665	AR20CGM007-RB-3	13	IR 72768-12-1-1/YUNLU NO 28	CGM20F2.Mbe:202009-7:	15	
<input type="checkbox"/> Test entry	9080666	AR20CGM007-RB-4	14	IR 72768-12-1-1/YUNLU NO 28	CGM20F2.Mbe:202009-7:	16	

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 units on the Observations tab. Since there is only one environment we only need to check the Select all pages check box to select the 131 plots in the nursery:

Observations

Select Environment:  Filter by status:

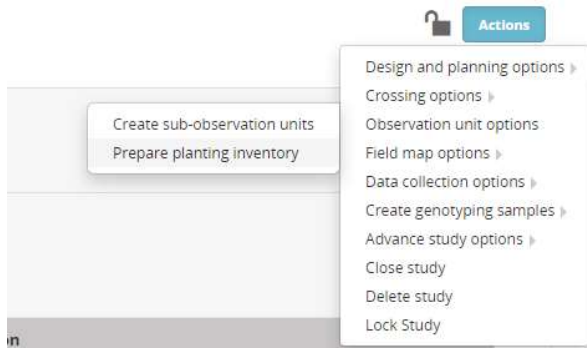
Batch Actions

Selected: 145  Select all pages



There are 145 plots because several plots have been added for check entries.

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.

#### PREPARE INVENTORY

145 plots selected for 1 instances

Unit	# Lots with "Valid" status	Group transactions	Withdraw all available inventory?	Amount per packet
SEED_AMOUNT_kg	2	<input checked="" type="checkbox"/>	<input type="checkbox"/>	0.020
SEED_AMOUNT_Packets	131	<input checked="" type="checkbox"/>	<input type="checkbox"/>	1

Records per page: 20

Search:

ENTRY_NO	ENTRY_TYPE	GID	DESIGNATION	Stock id	Storage location	Available balance	# of packets	Units	Withdrawal	Transaction
127	Test entry	9080779	AR20CGM062-RB-2	CGM2-127	Default Seed Store	1	1	SEED_AMOUNT_Packets	1	<input checked="" type="checkbox"/>
128	Test entry	9080780	AR20CGM062-RB-3	CGM2-128	Default Seed Store	1	1	SEED_AMOUNT_Packets	1	<input checked="" type="checkbox"/>
129	Test entry	9080781	AR20CGM064-RB-1	CGM2-129	Default Seed Store	1	1	SEED_AMOUNT_Packets	1	<input checked="" type="checkbox"/>
130	Test entry	9080782	AR20CGM064-RB-2	CGM2-130	Default Seed Store	1	1	SEED_AMOUNT_Packets	1	<input checked="" type="checkbox"/>
131	Test entry	9080783	AR20CGM064-RB-3	CGM2-131	Default Seed Store	1	1	SEED_AMOUNT_Packets	1	<input checked="" type="checkbox"/>
132	Check entry	2264738	NERICA 4	B20C1-3	Default Seed Store	5	7	SEED_AMOUNT_kg	0.14	<input checked="" type="checkbox"/>
133	Check entry	50533	IR 64	B20C1-1	Default Seed Store	5	7	SEED_AMOUNT_kg	0.14	<input checked="" type="checkbox"/>

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



Note

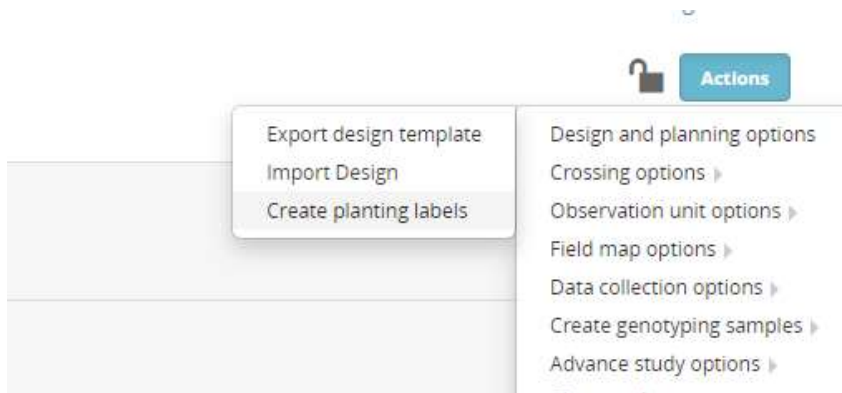
Pack 20g of seed in each packet for planting

Commit withdrawal on saving

Cancel

Confirm

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



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

#### EXPORT DATA / LABEL PRINTING

**EXPORT DATA**

SELECTED STUDY

Name:CGM20F3  
Title:2020 F3 nursery  
Objective:2020 F3 nursery  
Selected dataset:CGM20F3-PLOTDATA  
# of environments in dataset:1

PRESET OPTIONS

Load saved settings:

CHOOSE OUTPUT

Choose the format you would like to use:

Output format:

Please Choose  
Please Choose  
Formatted PDF Label Sheets  
Excel Data  
CSV Data

Cancel

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.

Left Side Fields	Right Side Fields
Stock id	Study Name
DESIGNATION	LOCATION_NAME
Storage location abbr	PLOT_NO
ENTRY_NO	

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

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

Tials 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 labels 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 calculated variables.

### Create a multi-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 germplasm we created in Tutorial 3. Probably called <your initials>GI20 – CGMGI20 for me.

## MANAGE GERmplasm

[View Lists](#)

[View Germplasm](#)

### List Details

Browse or search for a list to work with.

CGMGI20 

### List entries

Total Entries: 16 Selected: 0

✓	#	DESIGNATION	CROSS	LOTS	AVAILABLE
<input type="checkbox"/>	1	IR 72768-12-1-1	IR 60080-46 A/IR 65907-116-1-B	1	150.0 g
<input type="checkbox"/>	2	IR 72768-28-1-1	IR 60080-46 A/IR 65907-116-1-B	1	150.0 g
<input type="checkbox"/>	3	IR 75502-24-1-1-B	B 6144 F-MR-6-0-0/IR 55423-01 (NSIC RC 9)	1	150.0 g
<input type="checkbox"/>	4	IR 75516-30-1-1-B	IR 53236-275-1/CT 6516-24-3-2	1	150.0 g
<input type="checkbox"/>	5	IR 75516-56-1-1-B	IR 53236-275-1/CT 6516-24-3-2	1	150.0 g
<input type="checkbox"/>	6	IR 75518-84-1-1-B	IR 60080-46 A/IR 53236-275-1	1	150.0 g
<input type="checkbox"/>	7	IR 75531-31-1-2-B	IR 70360-54-1-B/VIENG	1	150.0 g
<input type="checkbox"/>	8	IR 76561-AC 8-B	CT 13382-9-4-M/IR 70358-145-1-1	1	150.0 g
<input type="checkbox"/>	9	CNA 4196	CNA 4196	1	150.0 g
<input type="checkbox"/>	10	IDSA 113	IDSA 113	1	150.0 g
<input type="checkbox"/>	11	FARO 41	IRAT 13/PALAWAN	1	150.0 g
<input type="checkbox"/>	12	UPL RI 5	SIGADIS (AICRIP)/BPI 76-1	1	150.0 g
<input type="checkbox"/>	13	WAB 326-B-B-7-H'	ITA 235 (TOX 1785-19-18)/WABC 165	1	150.0 g

Open the Manage Studies application from the main menu and click on **Start a new study**. Name the trial <your initials>20PVT, CGM20PVT for me, and fill in the basic details of description and objective and select the study type **Trial**.

**MANAGE STUDIES** ⓘ

**Create Study** Save

BASIC DETAILS

*\* indicates a mandatory field*

Study name: \* CGM20PVT

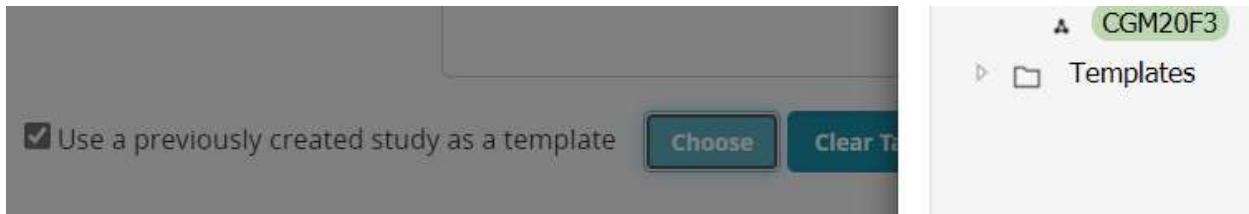
Description: \* 2020 PVT for project CGM

Study type: \* Trial

Objective: 2020 PVT for project CGM

Use a previously created study as a template Choose Clear Tabs

You can add variables to the new study directly from the Ontology pick lists as we did for the crossing block in Tutorial 004, 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 similar to your current study. We don't 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.

Settings Germplasm & Checks

**STUDY SETTINGS** ⓘ Add

Project\_Prefix: Project Prefix 1

Target\_Region: Region 3

PI\_NAME: Christopher McLaren

Select All Remove

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 Tutorial 003. CGM20GI in my case.

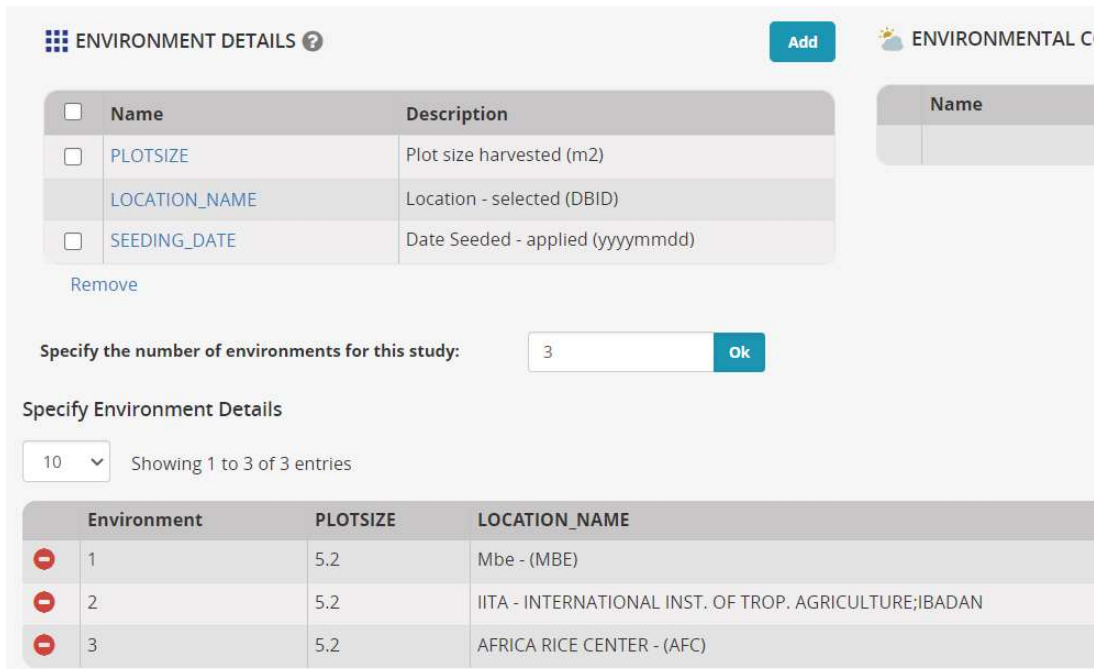
You can set the Check entries on the Germplasm Tab. Click on the entry type for the line(s) to be made checks, (we will make IRRI 132 a check entry), choose Check Entry from the list and click the tick symbol.



Save the study in your 2020 Trials folder. Make one called <your initials> 2020 Trials if it does not exist already.

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 specified favorite locations. We leave seeding date as an Environmental Details variable, and click Add and search for Plotsize and add it 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 4 for block size then click **Generate Design**.

**Generate** the design for all locations:

**STUDY ENVIRONMENT**

Choose the study environment you would like to generate the design: \*

10 ▾ Search:

<input checked="" type="checkbox"/>	TRIAL_INSTANCE	LOCATION_NAME
<input checked="" type="checkbox"/>	1	Mbe - (MBE)
<input checked="" type="checkbox"/>	2	IITA - INTERNATIONAL INST. OF TROP. AGRICULTURE;IBADAN - 0
<input checked="" type="checkbox"/>	3	AFRICA RICE CENTER - (AFC)

Showing 1 to 3 of 3 entries


< 1 >

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 triatis. Click Add next to the traits box. Search for FLW50 and add it to the trial:

Add Traits


Time to flowering (from sowing) (Phenology)

**TIME TO FLOWERING (FROM SOWING) (Phenology)**

HeadT\_50Est\_1to7  + Add

Method: Time of 50% heading estimation      Scale: Time of 50% heading scale

---

HeadT\_80Comp\_d  + Add

Method: Days to 80% flowering count      Scale: Days

---

TFlwS\_CM\_d (FLW50)

Method: Calculation - Days to 50% flowering from sowing      Scale: Day

Calculation:  $f_n: \text{daysdiff}(\text{SEEDING\_DATE}, \text{FlwDate\_50Flw\_Date})$       Input Variables: SEEDING\_DATE , FlwDate\_50Flw\_Date



**RELATED PROPERTIES**

Close

Notice that trait TFlwS\_CM-d has Alias FLW50 and has a computation formula associated so that it can be calculated withing 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

<input type="checkbox"/> Name	Description	Input Variables
<input type="checkbox"/> FlwDate_50Flw_Date	Flowering date -BY- Fifty percent flowering date observation-IN- ISO Date (yyyymmdd)	
<input type="checkbox"/> FLW50	Time to flowering (from sowing) -BY- Calculation - Days to 50% flowering from sowing -IN- Day	SEEDING_DATE , FlwDate_50Flw_Date
<input type="checkbox"/> GrYld_wgh_gplot	Grain yield -BY- AYLD_CONT method -IN- G per plot	
<input type="checkbox"/> GRMOIST	Moisture content of grain. Expressed in percentage.	
<input type="checkbox"/> 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 you must from the Observation sheet you must set the Select Environment box to All environments and check the Select all pages checkbox:

Observations

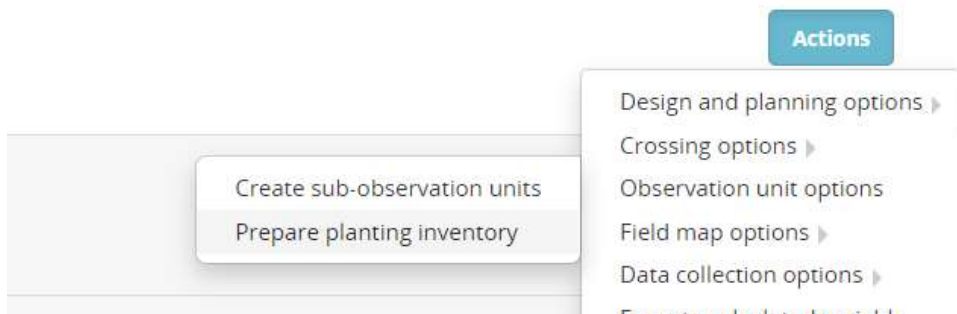
Select Environment: All environments Filter by status: All

► Batch Actions

Selected: 96  Select all pages

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

Next select Actions>Observation unit 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.

**PREPARE INVENTORY** 3

96 plots selected for 3 instances

Unit	# Lots with "Valid" status	Group transactions	Withdraw all available inventory?	Amount per packet
SEED_AMOUNT_g	16	<input checked="" type="checkbox"/>	<input type="checkbox"/>	20

Records per page: 20 Search:

ENTRY_NO	ENTRY_TYPE	GID	DESIGNATION	Stock id	Storage location	Available balance	# of packets	Units	Withdrawal	Transaction Status
1	Test entry	1161408	IR 72768-12-1-1	CGM3-1	Default Seed Store	150	6	SEED_AMOUNT_g	120	<input checked="" type="checkbox"/>
2	Test entry	1161406	IR 72768-28-1-1	CGM3-2	Default Seed Store	150	6	SEED_AMOUNT_g	120	<input checked="" type="checkbox"/>
3	Test entry	1161458	IR 75502-24-1-1-B	CGM3-3	Default Seed Store	150	6	SEED_AMOUNT_g	120	<input checked="" type="checkbox"/>
4	Test entry	1161444	IR 75516-30-1-1-B	CGM3-4	Default Seed Store	150	6	SEED_AMOUNT_g	120	<input checked="" type="checkbox"/>
5	Test entry	1161445	IR 75516-56-1-1-B	CGM3-5	Default Seed Store	150	6	SEED_AMOUNT_g	120	<input checked="" type="checkbox"/>
6	Test entry	1161448	IR 75518-84-1-1-B	CGM3-6	Default Seed Store	150	6	SEED_AMOUNT_g	120	<input checked="" type="checkbox"/>
7	Test entry	1161440	IR 75531-31-1-2-B	CGM3-7	Default Seed Store	150	6	SEED_AMOUNT_g	120	<input checked="" type="checkbox"/>
8	Test entry	1161377	IR 75561-40-2-B	CGM3-8	Default Seed Store	150	6	SEED_AMOUNT_g	120	<input checked="" type="checkbox"/>

Showing 1 to 16 of 16 entries

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**.

**Note**

Pack 20 grams of seed in each of six packets for planting

Commit withdrawal on saving

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

Settings | Germplasm & Checks | Treatment Factors | Environments | Experimental Design | **Inventory** | Observations

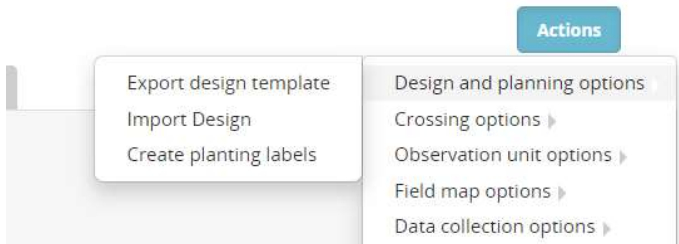
# Inventory

Select Environment: 1 - Mbe

Selected: 0  Select all pages

TRN_ID	ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	PLOT_NO	STORAGE LOCATION ABBR	STOCK_ID	CREATED	USERNAME
362	Test entry	1161448	IR 75518-84-1-1-B	6	1 and more	DSS	CGM3-6	2020-09-14	gmclaren
363	Test entry	569031	IRAT 170 (FARO 41)	11	7 and more	DSS	CGM3-11	2020-09-14	gmclaren
364	Test entry	1161458	IR 75502-24-1-1-B	3	4 and more	DSS	CGM3-3	2020-09-14	gmclaren
365	Test entry	70732	CNA 4196	9	2 and more	DSS	CGM3-9	2020-09-14	gmclaren
366	Test entry	905029	WAB 534-B-3A 1-1	14	13 and more	DSS	CGM3-14	2020-09-14	gmclaren
367	Test entry	1161406	IR 72768-28-1-1	2	11 and more	DSS	CGM3-2	2020-09-14	gmclaren
368	Test entry	790394	YUNLU NO 28	15	3 and more	DSS	CGM3-15	2020-09-14	gmclaren
369	Check entry	204538	IR 55423-01 (NSIC RC 9)	16	5 and more	DSS	CGM3-16	2020-09-14	gmclaren
370	Test entry	1161440	IR 75531-31-1-2-B	7	16 and more	DSS	CGM3-7	2020-09-14	gmclaren

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).

**PRESET OPTIONS**

Load saved settings:

**CHOOSE OUTPUT**

Choose the format you would like to use:

**Output format:**

**CHOOSE FIELDS**

**Include column headings in XLS export?**  Yes  No

Drag fields from the **Study Details** and **Dataset Details** and **Lot Details** and **Transaction Details** into the **Selected Fields** to add them to your export file.

Study Details	Dataset Details	Selected Fields
Year	ENTRY_TYPE	Lot UID
Project_Prefix	GID	Stock Id
Target_Region	CROSS	DESIGNATION
PI_NAME	SEED_SOURCE	ENTRY_NO
TRIAL_INSTANCE	REP_NO	Study Name
SEEDING_DATE	BLOCK_NO	LOCATION_NAME
PLOTSIZE	FlwDate_50Flw_Date	PLOT_NO
NREP	FLW50	PLOT OBS_UNIT_ID

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

**SAVE SETTINGS**

You can save these settings as a preset to use again by entering a name below.

**Preset name:**

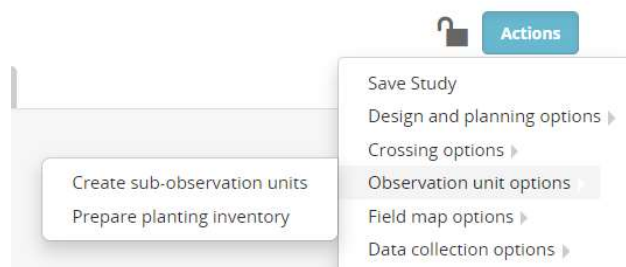
Now the labels should be printed with a label printing software such as Microsoft Word Mail-merge function. However the label records are currently in plot withing location order, and for the packing process you want to have all the labels for each entry together. You can achieve this order by sorting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

The fields Lot UID an/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	EZSWLkkUQkOj7	CGM3-1	IR 72768-12-1-1	1	CGM20PVTa	Mbe	12	EZSWPM24yd9s3
3	EZSWLkkUQkOj7	CGM3-1	IR 72768-12-1-1	1	CGM20PVTa	Mbe	19	EZSWPHgkR8W40
4	EZSWLkkUQkOj7	CGM3-1	IR 72768-12-1-1	1	CGM20PVTa	IITA - INTERNATIONAL	8	EZSWPhEJ69Xd5
5	EZSWLkkUQkOj7	CGM3-1	IR 72768-12-1-1	1	CGM20PVTa	IITA - INTERNATIONAL	19	EZSWPrpJ0CJ15
6	EZSWLkkUQkOj7	CGM3-1	IR 72768-12-1-1	1	CGM20PVTa	AFRICA RICE CENTER	9	EZSWPQerAmLLJ
7	EZSWLkkUQkOj7	CGM3-1	IR 72768-12-1-1	1	CGM20PVTa	AFRICA RICE CENTER	22	EZSWPq4Nr8bjS
8	EZSWLqbgvg1le	CGM3-2	IR 72768-28-1-1	2	CGM20PVTa	Mbe	11	EZSWPHAW7sqB3
9	EZSWLqbgvg1le	CGM3-2	IR 72768-28-1-1	2	CGM20PVTa	Mbe	29	EZSWPwiTVNJTM
10	EZSWLqbgvg1le	CGM3-2	IR 72768-28-1-1	2	CGM20PVTa	IITA - INTERNATIONAL	13	EZSWPYn1gzi4L
11	EZSWLqbgvg1le	CGM3-2	IR 72768-28-1-1	2	CGM20PVTa	IITA - INTERNATIONAL	22	EZSWPshVjVH2Z
12	EZSWLqbgvg1le	CGM3-2	IR 72768-28-1-1	2	CGM20PVTa	AFRICA RICE CENTER	2	EZSWPE1NylLWUy
13	EZSWLqbgvg1le	CGM3-2	IR 72768-28-1-1	2	CGM20PVTa	AFRICA RICE CENTER	21	EZSWPUQJfRYd5
14	EZSWLLIXYN3SK	CGM3-3	IR 75502-24-1-1-B	3	CGM20PVTa	Mbe	4	EZSWPzG3ehxCP
15	EZSWLLIXYN3SK	CGM3-3	IR 75502-24-1-1-B	3	CGM20PVTa	Mbe	32	EZSWPYi0vn01p
16	EZSWLLIXYN3SK	CGM3-3	IR 75502-24-1-1-B	3	CGM20PVTa	IITA - INTERNATIONAL	9	EZSWP1rbTLwfS
17	EZSWLLIXYN3SK	CGM3-3	IR 75502-24-1-1-B	3	CGM20PVTa	IITA - INTERNATIONAL	28	EZSWPizPB5N6D
18	EZSWLLIXYN3SK	CGM3-3	IR 75502-24-1-1-B	3	CGM20PVTa	AFRICA RICE CENTER	1	EZSWPWq5aaaMS
19	EZSWLLIXYN3SK	CGM3-3	IR 75502-24-1-1-B	3	CGM20PVTa	AFRICA RICE CENTER	20	EZSWPkaDILcbG
20	EZSWLSKMM5oga	CGM3-4	IR 75516-30-1-1-B	4	CGM20PVTa	Mbe	9	EZSWP1smLTocS
21	F7SWL SKMM5oga	CGM3-4	IR 75516-30-1-1-B	4	CGM20PVTa	Mbe	23	F7SWPHvmSkaTr

## 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 plots. 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:

### Subdivide Observations

\* indicates a mandatory field

How would you like to define the number of sub-observations per parent unit?\*

- Plants
- Quadrats
- Time Series
- Custom

Cancel Continue

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**.

### Specify Plants

*\* indicates a mandatory field*

Name for plants dataset: \*

Specify a maximum number of plants for each parent unit (up to 25): \*

Choose a variable to number the plants: \*

Select the environments for which you would like to generate plants: \*  Search:

<input checked="" type="checkbox"/>	TRIAL_INSTANCE	LOCATION_NAME
<input checked="" type="checkbox"/>	1	Mbe - (MBE)
<input checked="" type="checkbox"/>	2	IITA - INTERNATIONAL INST. OF TROP. AGRICULTURE;IBADAN - ()
<input checked="" type="checkbox"/>	3	AFRICA RICE CENTER - (AFC)

Showing 1 to 3 of 3 entries

< 1 >

Back Save

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

Settings Germplasm & Checks Treatment Factors Environments Experimental Design Inventory Observations Plants: PlantData

Plants: PlantData

PlantData

Define Observation Details

TRAITS  SELECTIONS

Name	Description	Input Variables	Name	Description

Observations

Select Environment: 1 - Mbe Filter by status: All

Batch Actions

Selected: 0  Select all pages

<input type="checkbox"/>	ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	CROSS	SEED_SOURCE	PLOT_NO	REP_NO	BLOCK_NO	PLANT_NO
<input type="checkbox"/>	Test entry	1161448	IR 75518-84-1-1-B	6	IR 60080-46 A/IR 53236-275-1	St Louis 2019 harvest	1	1	1	1
<input type="checkbox"/>	Test entry	1161448	IR 75518-84-1-1-B	6	IR 60080-46 A/IR 53236-275-1	St Louis 2019 harvest	1	1	1	2


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 PLTGHG – 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;

Add Traits


Plant height (Agronomic)

**PLANT HEIGHT (Agronomic)**

JPHT\_100DAG  + Add


Method: IRGC WILD RICE \_Juvenile Plant 100 DAG Scale: cm

---

JPHT\_75DAG  + Add

Method: IRGC WILD RICE \_Juvenile Plant 75 DAG Scale: cm

---

PlntHt\_Av\_cm 

Method: Plant height average Scale: cm

Calculation: Input Variables:

fn:avg(PLTHGT) PLTHGT

This variable has a formula – avg(PLTHGT) which we can use 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.

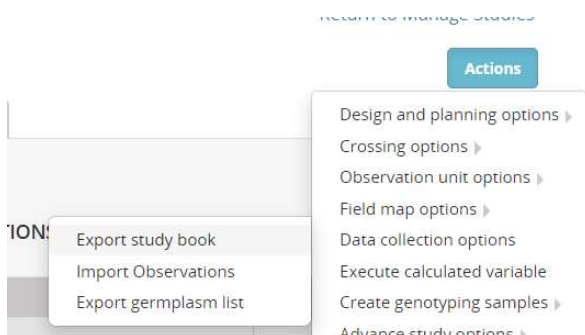
Specify Environment Details

10 Showing 1 to 3 of 3 entries Manage Locations 

Environment	PLOTSIZE	LOCATION_NAME	SEEDING_DATE
 1	5.2	Mbe - (MBE)	20200710
 2	5.2	IITA - INTERNATIONAL INST. OF TROP. AGRICULTURE;IBADAN	20200703
 3	5.2	AFRICA RICE CENTER - (AFC)	20200914

< 1 >

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**.

**EXPORT FORMAT**

Choose an export format: \*

**DATA COLLECTION ORDER**

Choose a data collection order \*  ?

**STUDY ENVIRONMENT**

Choose the study environment you would like to export: \*

10

<input checked="" type="checkbox"/>	TRIAL_INSTANCE	LOCATION_NAME
<input checked="" type="checkbox"/>	1	Mbe - (MBE)
<input checked="" type="checkbox"/>	2	IITA - INTERNATIONAL INST. OF TROP. AGRICULTURE;IBADAN - 0
<input checked="" type="checkbox"/>	3	AFRICA RICE CENTER - (AFC)

Showing 1 to 3 of 3 entries

< 1 >

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 sheets, a Description sheet which describes what is on the Observation sheet, and the Observation sheet which will contain the data.

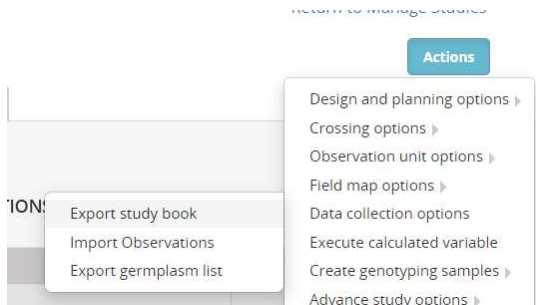
Enter some plausible random data into the columns for FlwDate\_50Flw\_Date, GrYld\_wgh\_gplot, and GRMOIST. (Leave the other traits since these can be calculated by BMS).

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	
1	OBS_UNI	ENTRY_T	GID	DESIGNA	ENTRY_N	CROSS	SEED_SO	PLOT_NO	REP_NO	BLOCK_N	FlwDate_50	Flw_Date	FLW50	GrYld_wgh_gplot	GRMOIST	GYTHA
2	EZSWPL1	T	1161448	IR 75518-	6	IR 60080-	St Louis 2l	1	1	1	20201001		1235		13	
3	EZSWP1	T	70732	CNA 4196	9	CNA 4196	St Louis 2l	2	1	1	20201006		2079		11	
4	EZSWP	as T	790394	YUNLU NC	15	IDSA 6 (IF	St Louis 2l	3	1	1	20201003		1309		12	
5	EZSWP	zC T	1161458	IR 75502-	3	B 6144 F-I	St Louis 2l	4	1	1	20201006		1520		13	
6	EZSWP	1u C	204538	IRRI 132	16	UPL RI 5/I	St Louis 2l	5	1	2	20201005		1997		12	
7	EZSWP	erI T	1161327	IR 76561-	8	CT 13382-	St Louis 2l	6	1	2	20201009		1906		10	
8	EZSWP	ya T	569031	FARO 41	11	IRAT 13/P	St Louis 2l	7	1	2	20201007		1622		15	
9	EZSWP	4E T	904702	IDSA 113	10	IDSA 113	St Louis 2l	8	1	2	20201005		1763		15	
10	EZSWP	1s T	1161444	IR 75516-	4	IR 53236-	St Louis 2l	9	1	3	20201006		1557		14	
11	EZSWP	fln T	406626	UPL RI 5	12	SIGADIS (	St Louis 2l	10	1	3	20201006		1569		13	
12	EZSWP	H T	1161406	IR 72768-	2	IR 60080-	St Louis 2l	11	1	3	20201004		1535		13	
13	EZSWP	M T	1161408	IR 72768-	1	IR 60080-	St Louis 2l	12	1	3	20201006		1506		13	
14	EZSWP	4X T	905029	WAB 534-	14	WAB 181-	St Louis 2l	13	1	4	20201007		2294		12	
15	EZSWP	E T	1161445	IR 75516-	5	IR 53236-	St Louis 2l	14	1	4	20201003		1301		14	
16	EZSWP	7F T	418229	WAB 326-	13	ITA 235 (T	St Louis 2l	15	1	4	20201008		1687		14	
17	EZSWP	M T	1161440	IR 75531-	7	IR 70360-	St Louis 2l	16	1	4	20201003		1939		14	
18	EZSWP	1d T	904702	IDSA 113	10	IDSA 113	St Louis 2l	17	2	1	20201002		1742		14	
19	EZSWP	vp T	1161440	IR 75531-	7	IR 70360-	St Louis 2l	18	2	1	20201002		1995		10	
20	EZSWP	H T	1161408	IR 72768-	1	IR 60080-	St Louis 2l	19	2	1	20201009		2298		11	
21	EZSWP	W T	790394	YUNLU NC	15	IDSA 6 (IF	St Louis 2l	20	2	1	20201005		1747		13	
22	EZSWP	nc T	1161445	IR 75516-	5	IR 53236-	St Louis 2l	21	2	2	20201002		1863		15	
23	EZSWP	Pe6 C	204538	IRRI 132	16	UPL RI 5/I	St Louis 2l	22	2	2	20201007		1595		12	
24	EZSWP	Hy T	1161444	IR 75516-	4	IR 53236-	St Louis 2l	23	2	2	20201001		1949		11	

Save the fieldbook.

Select Actions>Data collection options>Import Observations





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

### Import observations ✕

*\* indicates a mandatory field*

**EXPORT FORMAT**

Please specify the format you are importing:\*

**SELECT FILE**

Please choose the file you would like to import:\*  ✕

Click **Import**

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

Experimental Design **Inventory** Observations

ACCEPTED PENDING

Accept Discard

Show Categorical Description

PLOT_NO	REP_NO	BLOCK_NO	FlwDate_50Flw_Date	GrYld_wgh_gplot	GRMOIST
1	1	1	20201001	1235	13
2	1	1	20201006	2079	11
3	1	1	20201003	1309	12

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:

### Export study book ✕

*\* indicates a mandatory field*

**DATASET**

Please choose the dataset you would like to export: \*

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

Choose an export format: \*

### DATA COLLECTION ORDER

Choose a data collection order \*  ?

### STUDY ENVIRONMENT

Choose the study environment you would like to export: \*

Search:

<input type="checkbox"/>	TRIAL_INSTANCE	LOCATION_NAME
<input checked="" type="checkbox"/>	1	Mbe - (MBE)
<input type="checkbox"/>	2	IITA - INTERNATIONAL INST. OF TROP. AGRICULTURE;IBADAN - ()
<input type="checkbox"/>	3	AFRICA RICE CENTER - (AFC)

Showing 1 to 3 of 3 entries

< 1 >



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	DESIGNA	ENTRY_N	CROSS	SEED_SO	PLOT_NO	REP_NO	BLOCK_N	PLANT_N	PLTHGT
2	EZSWPi3	T	1161448	IR 75518-8	6	IR 60080-4	St Louis 2t	1	1	1	1	76	
3	EZSWP0	T	1161448	IR 75518-8	6	IR 60080-4	St Louis 2t	1	1	1	2	77	
4	EZSWPx6	T	1161448	IR 75518-8	6	IR 60080-4	St Louis 2t	1	1	1	3	777	
5	EZSWP5	T	1161448	IR 75518-8	6	IR 60080-4	St Louis 2t	1	1	1	4	63	
6	EZSWPu	T	1161448	IR 75518-8	6	IR 60080-4	St Louis 2t	1	1	1	5	70	
7	EZSWP8	T	70732	CNA 4196	9	CNA 4196	St Louis 2t	2	1	1	1	67	
8	EZSWPI	T	70732	CNA 4196	9	CNA 4196	St Louis 2t	2	1	1	2	67	
9	EZSWPD	T	70732	CNA 4196	9	CNA 4196	St Louis 2t	2	1	1	3	66	
10	EZSWP1	T	70732	CNA 4196	9	CNA 4196	St Louis 2t	2	1	1	4	64	
11	EZSWPf	T	70732	CNA 4196	9	CNA 4196	St Louis 2t	2	1	1	5	65	
12	EZSWP8	T	790394	YUNLU NC	15	IDSA 6 (IF	St Louis 2t	3	1	1	1	60	
13	EZSWPW	T	790394	YUNLU NC	15	IDSA 6 (IF	St Louis 2t	3	1	1	2	68	
14	EZSWPI	T	790394	YUNLU NC	15	IDSA 6 (IF	St Louis 2t	3	1	1	3	72	
15	EZSWPh	T	790394	YUNLU NC	15	IDSA 6 (IF	St Louis 2t	3	1	1	4	64	
16	EZSWPJ	T	790394	YUNLU NC	15	IDSA 6 (IF	St Louis 2t	3	1	1	5	69	
17	EZSWPg	T	1161458	IR 75502-2	3	B 6144 F-I	St Louis 2t	4	1	1	1	63	
18	EZSWPd	T	1161458	IR 75502-2	3	B 6144 F-I	St Louis 2t	4	1	1	2	69	
19	EZSWPu	T	1161458	IR 75502-2	3	B 6144 F-I	St Louis 2t	4	1	1	3	73	
20	EZSWPQ	T	1161458	IR 75502-2	3	B 6144 F-I	St Louis 2t	4	1	1	4	61	

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

### Import observations ✕

*\* indicates a mandatory field*

**DATASET**

Please choose the dataset you would like to import: \*

Plants: PlantData
▼

Cancel
Continue

Browse to the file just saved - CGM20PVTa-1\_MBE\_PLANT\_PlantData.xls and click **Import**. The data is entered into a staging area waiting for review and approval. We see already one out of bounds value since limits have been set between 40 and 80 cm for PLTHGT.

► Define Observation Details

Observations

ACCEPTED PENDING

Accept Discard

Select Environment: All environments Filter by status: All Show Categorical Description

► Batch Actions

Selected: 0  Select all pages

NTRY_TYPE	GID	DESIGNATION	ENTRY_NO	CROSS	SEED_SOURCE	PLOT_NO	REP_NO	BLOCK_NO	PLANT_NO	PLTHGT
est entry	1161448	IR 75518-84-1-1-B	6	IR 60080-46 A/IR 53236-275-1	St Louis 2019 harvest	1	1	1	1	76
est entry	1161448	IR 75518-84-1-1-B	6	IR 60080-46 A/IR 53236-275-1	St Louis 2019 harvest	1	1	1	2	77
est entry	1161448	IR 75518-84-1-1-B	6	IR 60080-46 A/IR 53236-275-1	St Louis 2019 harvest	1	1	1	3	777
est entry	1161448	IR 75518-84-1-1-B	6	IR 60080-46 A/IR 53236-275-1	St Louis 2019 harvest	1	1	1	4	63
est entry	1161448	IR 75518-84-1-1-B	6	IR 60080-46 A/IR 53236-275-1	St Louis 2019 harvest	1	1	1	5	70

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 imported data.

### Calculate derived variables

Once the data has been accepted you will see it in the full observations 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 calculate the flowering days, select Actions>Execute calculate variable. Continue with Observations, choose the flowering date variable 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 FLW50 has been calculated.

Repeat the calculation operation for the derived variable – GYTHA.

PLOT_NO	REP_NO	BLOCK_NO	FlwDate_50Flw_Date	FLW50	GrYld_wgh_gplot	GRMOIST	GYTHA
1	1	1	20201001	83	1235	13	2.3614
2	1	1	20201006	88	2079	11	4.0666
3	1	1	20201003	85	1309	12	2.5317
4	1	1	20201006	88	1520	13	2.9064
5	1	2	20201005	87	1997	12	3.8623

Now we also have a calculated variable for Plant height:

**PlntHt\_Av\_cm**    Plant height -BY- Plant height measure - IN- cm    **PLTHGT**

Remove

**Observations** ACCEPTED    PENDING

Select Environment: 1 - Mbe    Filter by status: All Show Categorical Description

**Batch Actions**

Selected: 0     Select all pages

	SEED_SOURCE	PLOT_NO	REP_NO	BLOCK_NO	FlwDate_50Flw_Date	FLW50	GrYld_wgh_gplot	GRMOIST	GYTHA	PlntHt_Av_cm
R 53236-	St Louis 2019 harvest	1	1	1	20201001	83	1235	13	2.3614	
	St Louis 2019 harvest	2	1	1	20201006	88	2079	11	4.0666	
DABAIGU-	St Louis 2019 harvest	3	1	1	20201003	85	1309	12	2.5317	
-0-0/R	St Louis 2019	4	1	1	20201006	88	1520	13	2.9064	

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.

## Execute Calculations ✕

\* indicates a mandatory field

Choose the calculation you would like to execute:

Variable:\*

Select the environments where the calculation will be executed:\*

Search:

<input type="checkbox"/>	TRIAL_INSTANCE	LOCATION_NAME
<input checked="" type="checkbox"/>	1	Mbe - (MBE)
<input type="checkbox"/>	2	IITA - INTERNATIONAL INST. OF TROP. AGRICULTURE;IBADAN - ()
<input type="checkbox"/>	3	AFRICA RICE CENTER - (AFC)

Showing 1 to 3 of 3 entries

< 1 >

Click **Execute**.

The plant height averages have been filled in:

	SEED_SOURCE	PLOT_NO	REP_NO	BLOCK_NO	FlwDate_50Flw_Date	FLW50	GrYld_wgh_gplot	GRMOIST	GYTHA	PlntHt_Av_cm
R 53236-	St Louis 2019 harvest	1	1	1	20201001	83	1235	13	2.3614	71.5
	St Louis 2019 harvest	2	1	1	20201006	88	2079	11	4.0666	65.8
DABAIGU-	St Louis 2019 harvest	3	1	1	20201003	85	1309	12	2.5317	66.6
-0-0/IR : RC 9)	St Louis 2019 harvest	4	1	1	20201006	88	1520	13	2.9064	69.2
79-24-1	St Louis 2019 harvest	5	1	2	20201005	87	1997	12	3.8623	71.6
4/IR	St Louis 2019 harvest	6	1	2	20201009	91	1906	10	3.7701	71.6

Notice that the first plot value is 71.5 which is the average of the four no-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 calculate 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.

### 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 trial
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), or the data for different sites may come in 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	<b>ENTRY</b>	<b>DESIGNATION</b>	<b>GID</b>	<b>CROSS</b>	<b>SOURCE</b>
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	<b>LIST NAME</b>	CGM20AVT	
2	<b>LIST DESCRIPTION</b>	2020 AVT for Project CGM	
3	<b>LIST DATE</b>	20200101	
4	<b>LIST TYPE</b>	LST	
5			
6	<b>CONDITION</b>	<b>DESCRIPTION</b>	<b>PROPERTY</b>
7	LIST OWNER	Name of the Principal Investigator	PERSON
8	ID OF LIST OWNER	ID of the Principal Investigator	PERSON
9			
10	<b>FACTOR</b>	<b>DESCRIPTION</b>	<b>PROPERTY</b>
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 germplasm	CROSS NAME
15	SOURCE	The seed source of the germplasm	SEED SOURCE
16	ENTRY CODE	Germplasm entry code	GERMPLASM ENTRY
17	DRVNM	Derivative Name	GERMPLASM ID



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

### ADD GERmplasm DETAILS

You can specify following details to apply to the imported germplasm. These details are optional.

**Germplasm breeding method:**  ?  
 Show only favorite methods [Manage Methods](#)

**Germplasm location:**   
 All locations  Breeding locations [Manage Locations](#)  
 Show only favorite locations

**Seed Storage Location:**   
 All locations  Storage locations [Manage Locations](#)  
 Show only favorite locations

**Germplasm date:**

**Germplasm name type:**

### SELECT GID ASSIGNMENT OPTIONS

**GID Assignment Options:**   
 Automatically accept single matches whenever found

[Back](#) [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):

### Select Matching Germplasm or Add New Entry

Match(es) were found for entry **31 of 32**, with the name **IR 64**. Click on an existing entry below to choose it as the match for this germplasm. You may also choose to ignore the match and add a new entry.

DESIGNATION	GID	IMMEDIATE SOURCE	AVAILABLE	LOCATION	BREEDIN
IR 64-CROSS	110	-	-	Int Rice Research Institute	Single
IR 64	50533	IR 18348-36-3	5.0 kg	International Rice Testing Program, IRRI	Single
IR 64	432785	IR 64	-	Viet Nam	Cultiv
IR 64	432786	IR 64	-	India	Cultiv
IR 64	433635	IR 64	-	Bhutan	Cultiv
IR 18348-36-3-3	510553	IR 64	-	National Small Grain Collection USDA,ARS	Collec
IR 64	522504	IR 64	-	United States	Cultiv



Save the list:

### Save List As ✕

Select a folder to create a new list or select an existing list to edit and overwrite its entries.

#### List Location

#### List Details

\* indicates a mandatory field

**List Name:** \* CGM20AVT

**List Owner:** IBP Trainer

**Description:** Entries for 2020 AVT for project CGM

**List Type:** \* GERMPLASM LISTS

**List Date:** \* 2020-09-08

**Notes:**

Cancel Save

### 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, then it must have a column called PLOT\_NO with a sequence number of 1 to number of plots at each location, then 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 Chesks tab enter the germplasm list we imported and set the last to entries, IR 64 and IR 72 to be check entries.

Test entry	807455	IR 68098-B-78-2-1-12-B	28
Test entry	807462	IR 70182-18-PMI 7-2-B	29
Test entry		IR 70173-29-SRN 2-1-B	30
Test entry		IR 64	31
Test entry		IR 72	32

**EDIT CHECK**

Check entry

Clear List

Save the new trial in your 2020 Trials folder (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.

### Specify Environment Details

10 Showing 1 to 4 of 4 entries

	Environment	PLOTSIZE	LOCATION_NAME
	1	5.2	Raipur RRS - (RPUR)
	2	5.2	Titabar RRS - (TBR)
	3	5.2	Pusa RRS - (PSA)
	4	5.2	Cuttack RRS - (CTK)

< 1 >

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.

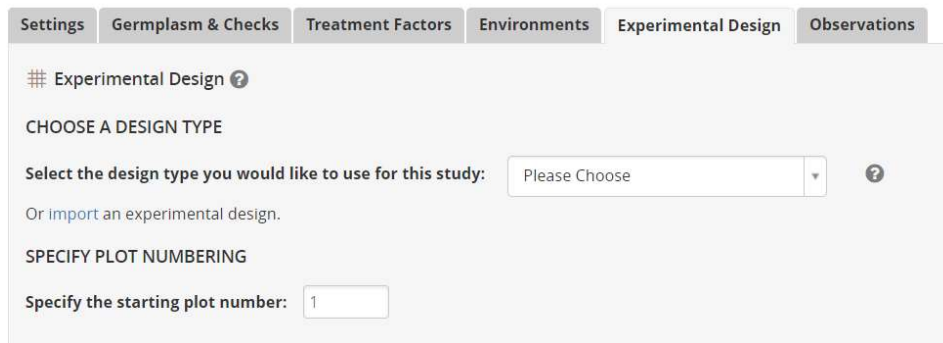
TRAITS ? Add

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



The screenshot shows the 'Experimental Design' tab selected in a navigation bar. Below the tab, there is a section titled '# Experimental Design' with a help icon. Underneath, it says 'CHOOSE A DESIGN TYPE' and 'Select the design type you would like to use for this study:'. A dropdown menu is set to 'Please Choose' with a help icon to its right. Below this, it says 'Or import an experimental design.' and 'SPECIFY PLOT NUMBERING'. A text input field is labeled 'Specify the starting plot number:' and contains the number '1'.

Browse to the layout file and open it:

## Import Experimental Design

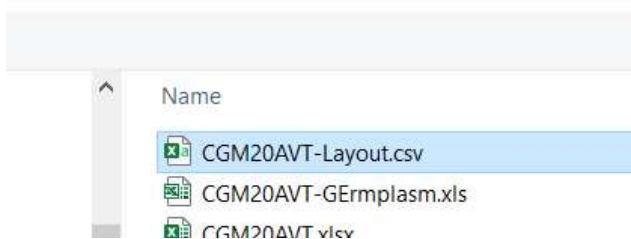
### SELECT DESIGN FILE TO IMPORT

The design file must contain columns of numeric data (**study instance**), **entry number**, and **plot number**. You will be able to map them on the next screen.

**Please specify the format you are importing:\***

Browse

BMS > Tutorials > IRIS > Sample Files



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 remain in the Unmapped Variable box.

### MAP COLUMN HEADERS TO VARIABLES

Drag unmapped headers on the left into one of the three groups on the right. You will be prompted to match the header to an existing variable or create new variables if needed.

#### ► Advanced Options

**Un-Mapped**  
GYGP

**Environmental Factors** ▼  
**TRIAL\_INSTANCE → TRIAL\_INSTANCE** (Required)  
Property: Trial instance      Scale: Number

**Design Factors** ▼  
**PLOT\_NO → PLOT\_NO** (Required)  
Property: Field plot      Scale: Number  
**REP\_NO → REP\_NO**  
Property: Replication factor      Scale: Number  
**BLOCK\_NO → BLOCK\_NO**  
Property: Blocking factor      Scale: Number

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

**Traits** ▼ 6

<b>PANH → PANH</b> Property: Panicles      Scale: Number      Method: Counting	<a href="#">Re-map</a>
<b>FLW → FLW80</b> Property: Time to heading      Scale: Number      Method: 80% Flowering	<a href="#">Re-map</a>
<b>PLNTH_AV_CM → PLNTH_AV_CM</b> Property: Plant height      Scale: cm      Method: Plant height average	<a href="#">Re-map</a>
<b>GYGP →</b> Property:      Scale:      Method:	<a href="#">Apply Mapping</a>
<b>GRMOIST → GRMOIST</b>	<a href="#">Re-map</a>

This will open the Ontology search box. Look for grain yield traits and select GrYld\_wgh\_gplot.

Grain yield (Agronomic)

### GRAIN YIELD (Agronomic)

<b>GRNYLD</b>		➤ Select
Method: Paddy Rice	Scale: Kg/ha	
<b>GrYld_Comp_kgha</b>		➤ Select
Method: Yield measurement	Scale: Kg per ha	
<b>GrYld_wgh_gplot</b>		➤ Select
Method: AYLD_CONT method	Scale: G per plot	
<b>GY_CM_gm2</b>		➤ Select
Method: Calculation - Grain yield from components of yield	Scale: Grams per square meter	
<b>GY_CM_kgha</b>		➤ Select

Close

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

You will get a review panel to check the import:

#### REVIEW DESIGN DETAILS

Type of design: Externally Generated Design

100 ▾ Showing 1 to 100 of 256 entries

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 versatile as a statistical package, such as the full version of Genstat, which is required for research analysis.

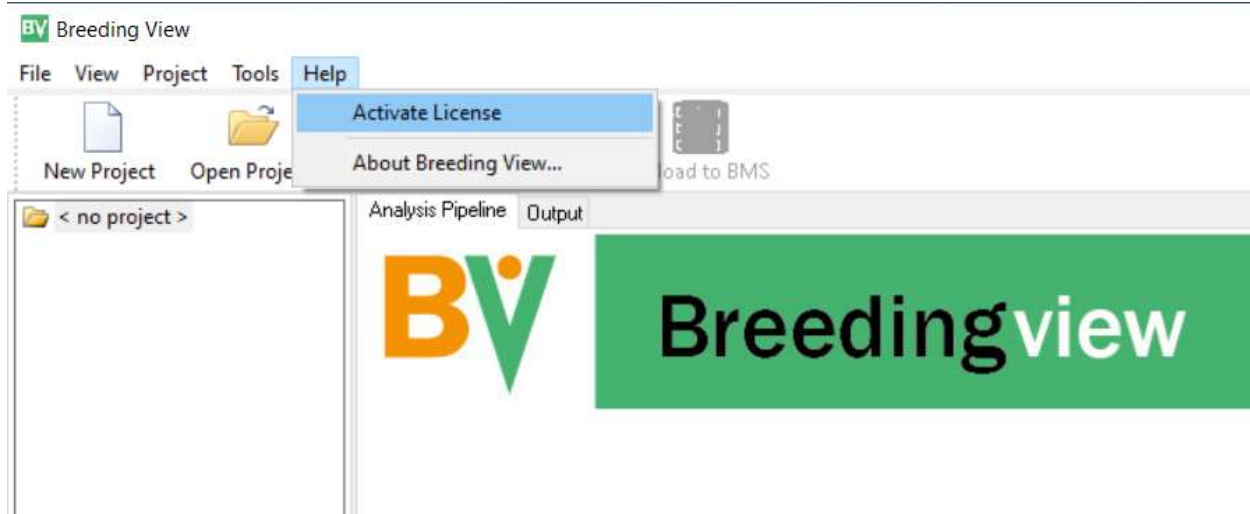
### Objectives

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 ssply a license key by clicking Help>Activate license:



Once the license is activated 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 **Statistical Analysis** menu select **Single-Site Analysis**:

The screenshot shows the BMS interface with a sidebar on the left and a main content area on the right. The sidebar has a menu with the following items: BREEDING ACTIVITIES (Manage Germplasm, Manage Studies, Manage Samples), INFORMATION MANAGEMENT, STATISTICAL ANALYSIS (Single-Site Analysis, Multi-Site Analysis), and INVENTORY MANAGER. The 'Single-Site Analysis' option is highlighted. The main content area has a blue header with a back arrow, the 'B' logo, and 'TUTORIAL IBP'. Below the header is the title 'SINGLE-SITE ANALYSIS' with a help icon. Underneath is a green plant icon and the text 'Select Data for Analysis'. Below that is the instruction: 'Browse for a study to work with or Upload Breeding View output files to BMS.' Further down is a red plant icon and the title 'DATA SELECTED FOR ANALYSIS'. Below this title are labels for 'Study Name:', 'Dataset:', 'Project Type:', 'Description:', and 'Objective:'.

**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:

## SINGLE-SITE ANALYSIS

### Select Data for Analysis

[Browse](#) for a study to work with or [Upload](#) Breeding View output files to BMS.

#### DATA SELECTED FOR ANALYSIS

**Study Name:** CGM20AVT

**Dataset:** CGM20AVT-PLOTDATA

**Project Type:** Field Trial

**Description:** 2020 AVT for project CGM

**Objective:** 2020 AVT for project CGM

#### GERmplasm DESCRIPTORS

NAME	DESCRIPTION
TRIAL_INSTANCE	Trial instance - enumerated (number)
ENTRY_TYPE	Entry type (test/check)- assigned (type)
GID	Germplasm identifier - assigned (DBID)
DESIGNATION	Germplasm identifier - assigned (DBCv)
ENTRY_NO	Germplasm entry - enumerated (number)
OBS_UNIT_ID	Field observation unit id - assigned (text)
CROSS	The pedigree string of the germplasm
SEED_SOURCE	Seed source - Selected (Code)
REP_NO	Replication - assigned (number)
PLOT_NO	Field plot - enumerated (number)
BLOCK_NO	Block - assigned (number)

And the traits it contains:

## TRAITS

The traits in the dataset you have selected are shown below. Select the traits you wish to submit for analysis.

✓	NAME	DESCRIPTION	SCALE
<input checked="" type="checkbox"/>	GrYld_wgh_gpl	Grain yield -BY- AYLD_CONT method -IN- G per plot	G per plot
<input checked="" type="checkbox"/>	GRMOIST	Moisture content of grain. Expressed in percentage.	Percent
<input checked="" type="checkbox"/>	GYTHA	Grain yield in T per Ha corrected for moisture	t/ha
<input checked="" type="checkbox"/>	PlntHt_Av_cm	Plant height -BY- Plant height measure -IN- cm	cm
<input checked="" type="checkbox"/>	PANH	Panicles per hill - count (Number)	Number
<input checked="" type="checkbox"/>	FLW80	Flowering - 80% Flowering (Number)	Number
<input checked="" type="checkbox"/>	BLAST	BLAST	SES Score Blast

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 variables 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.

## CHOOSE SITES/ENVIRONMENT

You can choose one or more sites/environments from the selected dataset to submit for analysis.

Which factor defines the environment? \*

Select the environment you would like to se

SELECT

Please Choose

- Please Choose
- TRIAL\_INSTANCE
- PLOTSIZE
- LOCATION\_NAME
- SEEDING\_DATE
- EXPT\_DESIGN
- EXPT\_DESIGN\_SOURCE

And we will select all the locations for analysis:

Select the environment you would like to send for analysis: \*

SELECT	TRIAL_INS	LOCATION_NAME
<input checked="" type="checkbox"/>	1	Raipur RRS
<input checked="" type="checkbox"/>	2	Titabar RRS
<input checked="" type="checkbox"/>	3	Pusa RRS
<input checked="" type="checkbox"/>	4	Cuttack RRS

Select All

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

# SPECIFY DESIGN DETAILS

If your data includes row and column information, specify them below to include spatial analysis in your results.

Specify the design type: \*

- Incomplete block design
- Randomized block design
- Row-column design
- P-rep design
- Augmented 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 variables are created by the process of making a 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 defines the entries in the trial. You always have ENTRY\_NO available, but usually the DESIGNATION is preferred:

## # SPECIFY DESIGN DETAILS

If your data includes row and column coordinates, you can specify them below to include spatial analysis in your results.

Specify the design type: \*

Specify replicates factor: \*

Specify incomplete block factor: \*

Specify row factor:

Specify column factor:

## GENOTYPES SPECIFY GENOTYPES

Genotypes: \*

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

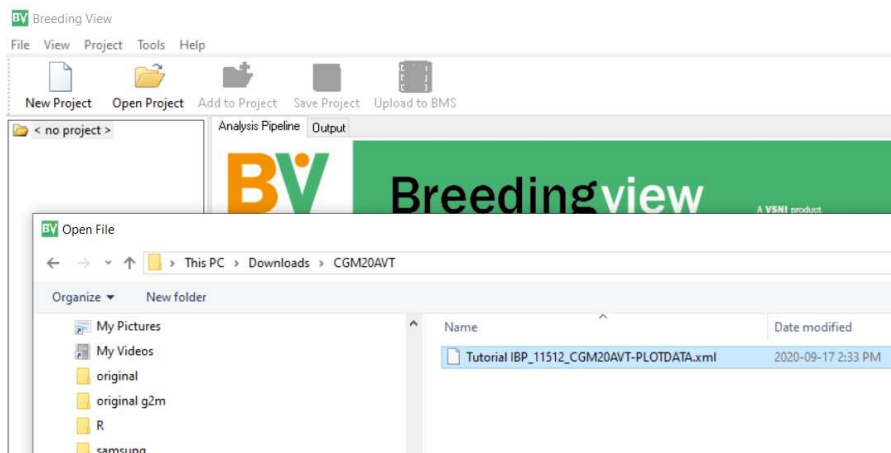


This will download a zip file with the names of the study.zip – CGM20AVT.zip for me.

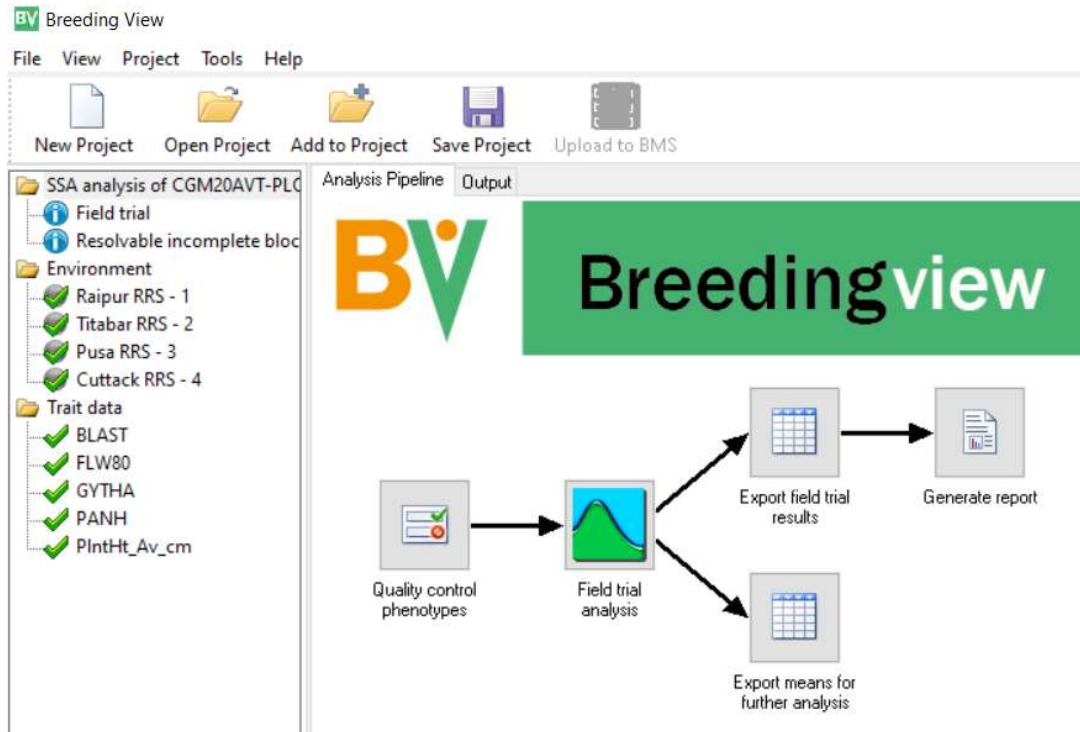
You need to extract the files from this zip file into a directory where the analysis will be performed. There are two files in the zip, one csv file which contains the data to be analysed and one xml file which contains the instructions for the analysis.

## Running Breeding View for Single Site Analysis

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



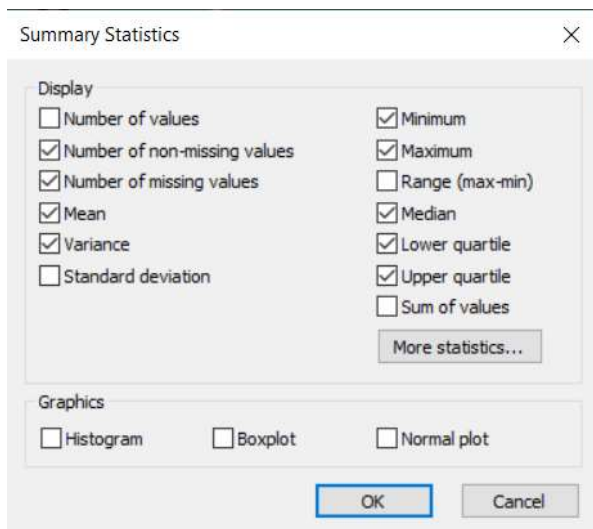
The Single Site Analysis Pipeline will be activated:



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 configured by right-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:

Report Options

Display

Predicted means (BLUEs)

Standard error of estimates

Standard error of differences (s.e.d.)

Approximate LSDs

LSD significance level (%):

Predicted means (BLUPs)

Standard error of estimates

Sort means

Sort order:  Ascending  Descending

Number of genotypes to display:

Sort using trait:

Approximate coefficient of variation

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.

Report Options

Display

Predicted means (BLUEs)

Standard error of estimates

Standard error of differences (s.e.d.)

Approximate LSDs

LSD significance level (%):

Predicted means (BLUPs)

Standard error of estimates

Sort means

Sort order:  Ascending  Descending

Number of genotypes to display:

Sort using trait:

Approximate coefficient of variation



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

Analysis Pipeline | Output | Quality Assurance | Graphs | Report

### Summary report from sequential field trial analysis

**Project: SSA analysis of CGM20AVT-PLOTDATA (run at 2020-09-17\_14:13)**

Date: 2020-09-17T16:43:33

Combined file of predicted means: [Results\\_trait\\_means.xlsx](#)

#### Individual trial reports

Raipur RRS - 1: [Raipur RRS - 1/2020-09-17T16:43:33/FieldTrial\\_report.htm](#)

Titabar RRS - 2: [Titabar RRS - 2/2020-09-17T16:43:33/FieldTrial\\_report.htm](#)

Pusa RRS - 3: [Pusa RRS - 3/2020-09-17T16:43:33/FieldTrial\\_report.htm](#)

Cuttack RRS - 4: [Cuttack RRS - 4/2020-09-17T16:43:33/FieldTrial\\_report.htm](#)

#### Heritability values

To understand how to interpret the Breeding View output you can consult the Manual 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.

Name	Date modified
Combined	2020-09-17 4:43 PM
Cuttack RRS - 4	2020-09-17 4:44 PM
Pusa RRS - 3	2020-09-17 4:44 PM
Raipur RRS	2020-09-17 2:47 PM
Raipur RRS - 1	2020-09-17 4:43 PM
Titabar RRS - 2	2020-09-17 4:44 PM
upload	2020-09-17 4:46 PM
Datastore.qsv	2020-09-17 4:43 PM
Tutorial IBP_11512_CGM20AVT-PLOTDATA.csv	2020-09-17 2:33 PM
Tutorial IBP_11512_CGM20AVT-PLOTDATA.xml	2020-09-17 2:33 PM

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



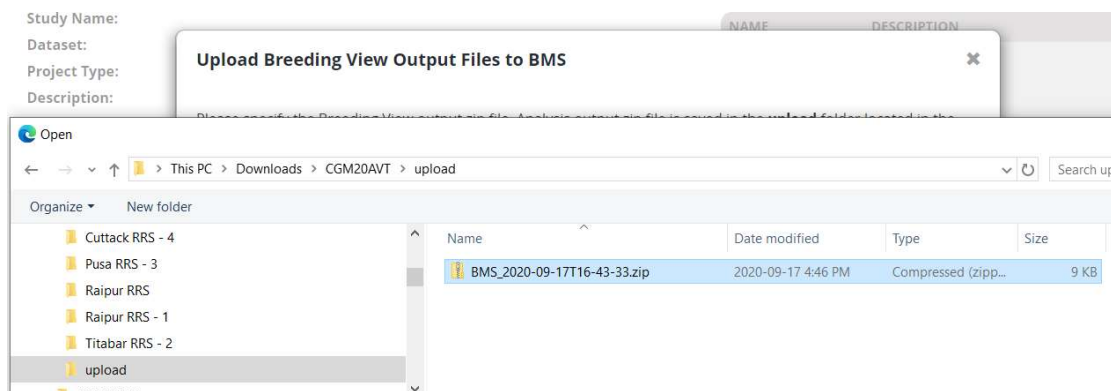
# SINGLE-SITE ANALYSIS ?

## Select Data for Analysis

[Browse](#) for a study to work with or [Upload](#) Breeding View output files to BMS.

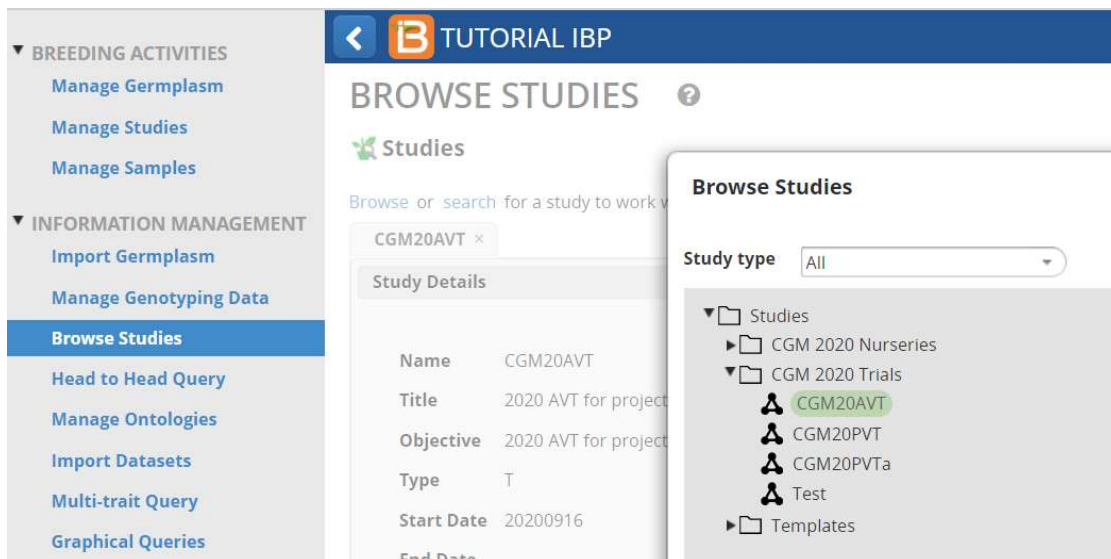
Select the study for which the analysis has been completed – CGM20AVT for me.

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:

Study Details							
Factors							
Variates							
Datasets							
Dataset of CGM20AVT-MEANS							
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

Export to Fieldbook Excel File    Open in Table Viewer

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

### Specify a multi-site analysis for a trial in BMS

From the **Statistical Analysis** 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 analysis 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.

## MULTI-SITE ANALYSIS

### Select Data for Analysis

[Browse](#) for a study to work with.

CGM20AVT ×

**DEFINE ENVIRONMENTS AND GROUPS**

Which factor defines the environment?

Which factor defines the genotype?

Specify a grouping factor if you wish to split your environments into groups.

Specify a factor to define environment groups:

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 (DCV)
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

<input checked="" type="checkbox"/>	NAME	DESCRIPTION
<input type="checkbox"/>	BLAST	BLAST
<input type="checkbox"/>	FLW80	Flowering - 80% Flowering (Number)
<input checked="" type="checkbox"/>	GYTHA	Grain yield in T per Ha corrected for moisture
<input type="checkbox"/>	PANH	Panicles per hill - count (Number)
<input type="checkbox"/>	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 or for which the heritability is too low, and similarly at the bottom you can eliminate traits. We 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 analysis 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
<input checked="" type="checkbox"/>	1	Raipur RRS	32 (0.452443873146702)
<input type="checkbox"/>	2	Titabar RRS	32 (3.85412131875817e-07)
<input checked="" type="checkbox"/>	3	Pusa RRS	32 (0.365209863186716)
<input checked="" type="checkbox"/>	4	Cuttack RRS	32 (0.593190077323482)

Select all environments

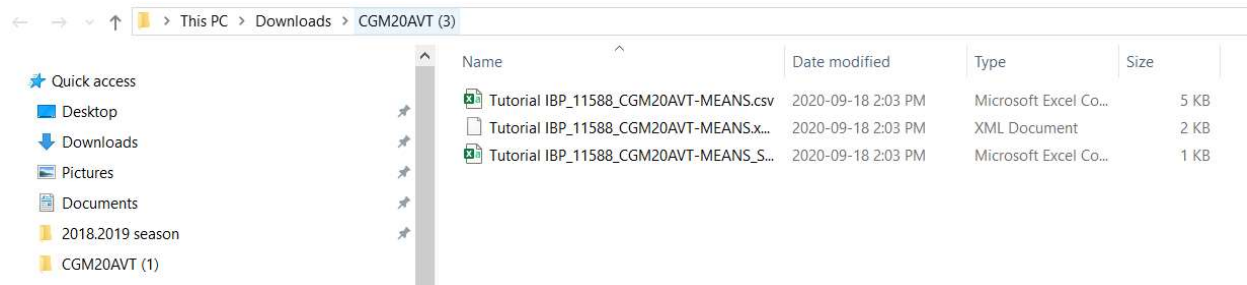
Select the trait(s) you would like to send for analysis:

GYTHA
<input checked="" type="checkbox"/>

Select all traits

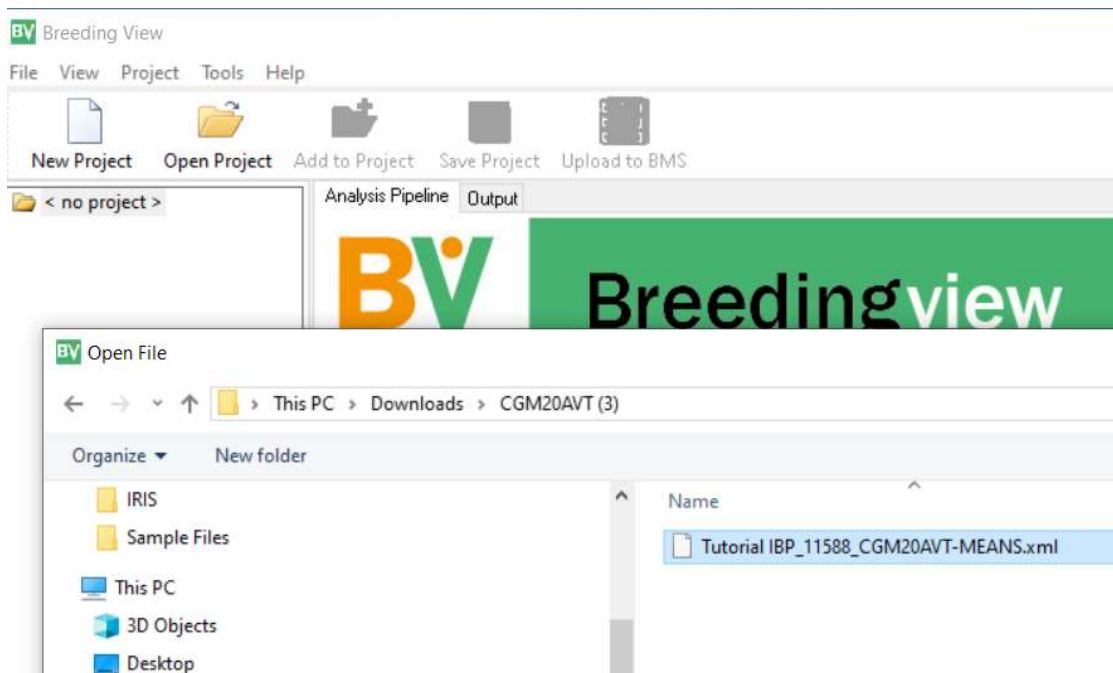
Click Download Input Files at the bottom of the form.

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.

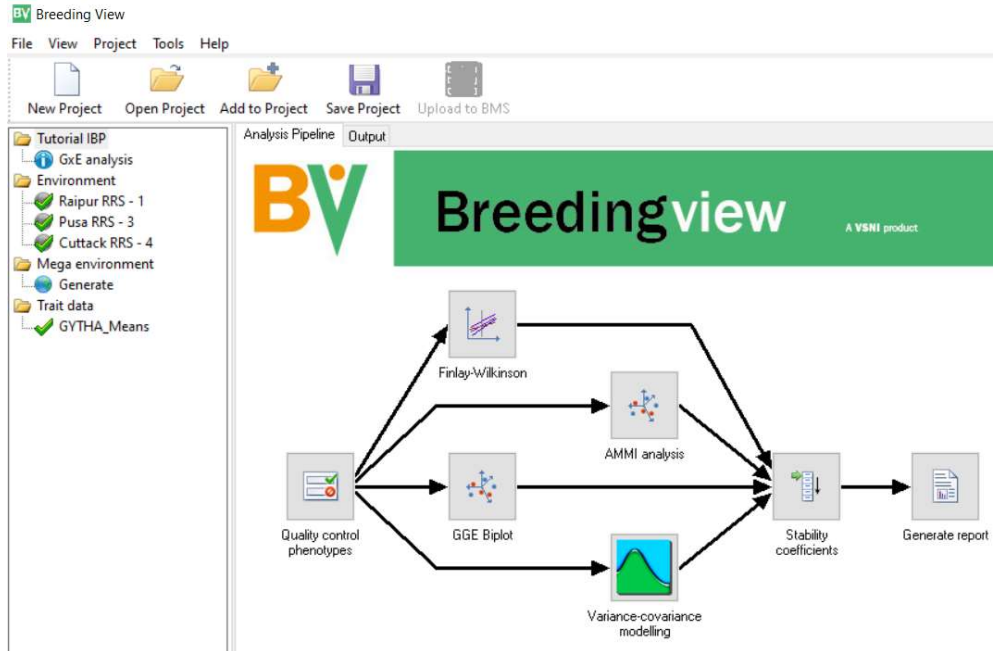


### Run a multi-site analysis with Breeding View

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:

**Report from GxE analysis**

**Project: Tutorial IBP**

Date: 2020-09-18T14-09-41

File containing means: [GxE\\_Means.xlsx](#)

File containing AMMI estimates: [GxE\\_AMMI.xlsx](#)

**Summary statistics**

**Trait: GYTHA\_Means**

	No. of observations	No. of missing values	Mean	Median	Min	Max	Lower quartile
Pusa RRS	32.00	0	3.876	3.886	3.778	3.969	3.834
Raipur RRS	32.00	0	3.747	3.745	3.664	3.853	3.704
Cuttack RRS	32.00	0	3.738	3.742	3.652	3.820	3.691

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>