

BMS Training – Exercises for Durum Wheat

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Getting Started Durum Wheat

1. Germplasm Search

1. Log on to your account on BMS
2. Select Durum Tutorial Program from the Workbench.
3. Germplasm Search
 - a. Click on View Germplasm tab in Manage Germplasm
 - b. Enter Assasa in the search box and click search
 - c. Click on Assesa in the results page
 - d. Click on Names in the Germplasm Details Page
 - e. Click on pedigree.
 - f. Now enter Huitle in the search box – search
 - g. Click on the name in the results page
 - h. Then click on Names in The Germplasm details page and then pedigree, then view pedigree.
 - i. Now try it for DW11903.

2. List management

4. View Lists
 - a. Click on the View Lists tab in Manage Germplasm
 - b. Click Browse
 - c. Select list 2019CrossesF1
 - d. Click on one of the cross names and then view the pedigree.
 - e. Click Browse again
 - f. Select list 2019CB Parents
5. Make a new list
 - a. Highlight five lines by checking in the select box
 - b. Right-click on the green space in the CROSS column and select “Add selected entries to a new list”
 - c. Click on the 2019CrossesF1 tab (or open the list from Browse if it is not there)
 - d. Select 5 entries well spaced down the list and add then to new list
 - e. In the new list box (under Build a New List click actions>list editing options>save list.
 - f. Make a new folder under Program Lists called Tutorial<your username>
 - g. Save the file there with the name TutorialParents<your username>

Design a crossing nursery

1. Create nursery

- Start a new study
- Specify Study Name and Description. I.e. : “Crossing Nursery <your username>”
- Specify Study Type to **Nursery**

The screenshot shows the 'MANAGE STUDIES' interface with the 'Create Study' form. The form includes fields for 'Study name', 'Description', 'Study type', and 'Objective'. The 'Study name' field contains 'Crossing Nursery', 'Description' contains 'Crossing nursery 2019', and 'Study type' is set to 'Nursery'. There are also fields for 'Save in', 'Created by', 'Creation date', and 'Completion date'. The 'Created by' field is filled with 'Mariano Crimi' and 'Creation date' is '2019-09-25'. A 'Save' button and an 'unsaved data' indicator are visible. Below the form, there are tabs for 'Settings', 'Germplasm & Checks', and 'Environments'. The 'STUDY SETTINGS' section is currently active, showing an 'Add' button and a message: 'Click Add to begin selecting items to record in this section.'

2. Germplasm and Checks

- Browse for your parents list **TutorialParents<your username>**
- Define which entries you want to consider as checks (if any)

The screenshot shows the 'Germplasm and Checks' interface. It features a table with columns for 'ENTRY_TYPE', 'GID', 'DESIGNATION', and 'ENTRY_NO'. The table contains 10 rows of test entries. An 'EDIT CHECK' dialog box is open over the 7th row, showing a dropdown menu with 'Test entry' selected and a green checkmark icon. The table also has a 'Clear List' button at the bottom left and an 'Actions' button at the bottom right.

ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO
Test entry	901000488	DW173186	1
Test entry	901000070	DW173204	2
Test entry	901000583	DW181309	3
Test entry	901000585	DW183311	4
Test entry	901000587	DW183313	5
Test entry	901000614	DW191004	6
Test entry	901000734	DW191124	7
Test entry	901000752	DW191142	8
Test entry	901000795	DW191185	9
Test entry	901000706	DW191096	10

3. Environments

- Search for the location name where you want to place your environment. If you don't find your desired location, you can broaden the scope of your search by disabling the favorites filter and searching by **All location types**

- d. Click on **Save**
- e. Select the folder where you want to save your study

After Save you will see that new tabs **Treatment Factors**, **Experimental Design** and **Observations** will be enabled for the study.

4. Experimental Design

- a. You will see all the available designs available in the BMS. Given that for the crossing nursery one would not typically need randomization, we will choose “**Entry list order**” which will place the entries in the plots according with the order of the entry list.

- b. **(Optional)** If check entries have been defined for this study, you can specify the spacing parameter so those . In this case use the following parameters to avoid increasing the number of plots generated for the upcoming steps:

- c. Click on Generate design

5. Observations tab

- d. You will see here that your Plots (Observation units) have been generated and your entries have been assigned to them according to your design parameters. We're now going to map those plots with physical coordinates in the field.

Create a fieldmap

1. Map Details

- a. Go to **Actions>Fieldmap Options>Make fieldmap**
- b. Our Nursery will be selected by default, so we click on **Next**
- c. Our environment will be selected by default, so we click on **Ok**
- d. You will see the following form specifying the # of environments, the # of entries and most importantly the number of **Plots Needed** (plot quantity might differ based on the check spacing defined)

2. Field Details

- a. We will now have to define the Field and Block details:
- b. Enter Field Location, for which we will select the same location that we specified for the environment in step 6
- c. We will create a new field **Field<your username>** and new **Block (BL1)** for our experiment using the **Add fields** and **Add Blocks** links

- d. Given that I will need capacity to allocate **10 plots**, I'll create a block with **2 rows and 5 ranges**. In any case the # Plots needed needs to be \leq than the total number of plots available in the block. Click **Next**

3. Assign Entries to the plots in the field

- a. Select Layout Order (Serpentine or Row/column) and click Next
- b. We'll see the final layout in the field

SUMMARY OF STUDY, FIELD AND PLANTING DETAILS

Selected Studies:

Order	Study	Environment	# of Entries	# of Reps	Plots Needed
1	Crossing Nursery	1	10	1	10

Total Number of Plots : 10

FIELD AND BLOCK DETAILS

Field Location: Kulumsa - (KU)

Field Name: FieldMC

Block Name: BL1

ROW, RANGE AND PLOT DETAILS

Block Capacity: 2 Rows, 5 Ranges

Rows per Plot: 1

Columns: 2

PLANTING DETAILS

Starting Coordinates: Column 1, Range 1

Plot Layout Order: Row/Column

Row Capacity of Planting Machine: 1

FIELD MAP

Arrows indicate direction of travel of the planting machine.

Actions

Rows	1	2
	↑	↓
	Column 1	Column 2
Range 5	Crossing Nursery-9 Entry 1 Rep 1	Crossing Nursery-10 Entry 10 Rep 1
Range 4	Crossing Nursery-7 Entry 8 Rep 1	Crossing Nursery-8 Entry 9 Rep 1
Range 3	Crossing Nursery-5 Entry 6 Rep 1	Crossing Nursery-6 Entry 7 Rep 1
Range 2	Crossing Nursery-3 Entry 4 Rep 1	Crossing Nursery-4 Entry 5 Rep 1
Range 1	Crossing Nursery-1 Entry 2	Crossing Nursery-2 Entry 3

Back
Finish

- c. Once we're satisfied with the layout we click on **Finish**
- d. If you go to the Observations tab you will notice that two new labels were added to your plots FIELDMAP_COLUMN, FIELDMAP_RANGE. These variables store the field coordinates of each plot.

Observations

Define Observation Details

TRAITS ⓘ

Name	Description	Input Variables

SELECTIONS ⓘ

Name	Description

Observations ACCEPTED PENDING

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

Batch Actions ⌵

ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	PLOT_NO	FIELDMAP_COLUMN	FIELDMAP_RANGE
Test entry	901000070	DW173204	2	1	1	1
Test entry	901000583	DW181309	3	2	2	1
Test entry	901000585	DW183311	4	3	1	2
Test entry	901000587	DW183313	5	4	2	2
Test entry	901000614	DW191004	6	5	1	3
Test entry	901000734	DW191124	7	6	2	3
Test entry	901000752	DW191142	8	7	1	4
Test entry	901000795	DW191185	9	8	2	4
Check entry	901000488	DW173186	1	9	1	5
Test entry	901000706	DW191096	10	10	2	5

Showing 1 to 10 of 10 entries Records per page: 50

Make crosses using a Crossing Template

1. Fill in a Crossing Template

- a. Go to **Actions** then **Crossing Options>Export Crossing Template**
- b. Open the crossing template
- c. In this excel file you will be able to reflect the crosses that you want to perform for in the crossing nursery. You would be able to specify with plot you're using as **female** and the plot that you're using as **male**.
- d. First thing to notice is that there is a **Study List** tab in the template that has all the plots of your study with the corresponding GID's and Designation. This will be useful to work through the crosses definition

FEMALE STUDY	FEMALE PLOT	ENTRY TYPE	GID	MGID	DESIGNATION	CROSS	FIELDMAP COLUMN	FIELDMAP RANGE	OBS UNIT ID
Crossing Nursery	1	Test Entry	901000070	901000070	DW173204	-	1	1	XFTDPBvCy0WZL
Crossing Nursery	2	Test Entry	901000583	901000583	DW181309	-	2	1	XFTDPX6hsNCzo
Crossing Nursery	3	Test Entry	901000585	901000585	DW183311	-	1	2	XFTDPVM7pI7mQ
Crossing Nursery	4	Test Entry	901000587	901000587	DW183313	-	2	2	XFTDPVWbjNxfi7
Crossing Nursery	5	Test Entry	901000614	901000614	DW191004	-	1	3	XFTDPPOkYumFw
Crossing Nursery	6	Test Entry	901000734	901000734	DW191124	-	2	3	XFTDPRycDUP4c
Crossing Nursery	7	Test Entry	901000752	901000752	DW191142	-	1	4	XFTDPcQ5INSBZ
Crossing Nursery	8	Test Entry	901000795	901000795	DW191185	-	2	4	XFTDPcQHSemth
Crossing Nursery	9	Check Entry	901000488	901000488	DW173186	-	1	5	XFTDPjCH6g1LJ
Crossing Nursery	10	Test Entry	901000706	901000706	DW191096	-	2	5	XFTDPZcjAt10

- e. In this example, the crossing plan will be to cross the first 5 plots (1 to 5) with all the combinations of the remaining 5 plots (plots 6 to 10)

FEMALE PLOT	MALE STUDY	MALE PLOT
1		6
2		6
3		6
4		6
5		6
1		7
2		7
3		7
4		7
5		7
1		8
2		8
3		8
4		8
5		8
1		9
2		9
3		9
4		9
5		9
1		10
2		10
3		10
4		10
5		10

- f. Save your file

2. Import your crossing template

- Go to **Actions>Crossing Options>Import Crosses**
- Select your file and click **Continue**
- In Specify Breeding Method, select Use Parental Status so that the system infers the breeding methods by traversing the pedigree tree

- For Naming, select “Use automatic naming generation” and select Harvest Location and Estimated Harvest date

- Click on Finish
- Save your CrossList, **F1 Germplasm <your username>** when done

ENTRY_NO	DESIGNATION	CROSS	FEMALE PARENT	FGID	MALE PARENT	MGID	GID	SEED SOURCE	GROUP ID	DUPLICATE
1	DW2019091001	DW173204/DW191124	DW173204	90100070	DW191124	901000734	901000852	Crossing Nursery-Kulumsa.201909-1/Crossing Nursery-Kulumsa.201909-6	-	-
2	DW2019091002	DW181309/DW191124	DW181309	901000583	DW191124	901000734	901000853	Crossing Nursery-Kulumsa.201909-2/Crossing Nursery-Kulumsa.201909-6	-	-
3	DW2019091003	DW183311/DW191124	DW183311	901000585	DW191124	901000734	901000854	Crossing Nursery-Kulumsa.201909-3/Crossing Nursery-Kulumsa.201909-6	-	-
4	DW2019091004	DW183313/DW191124	DW183313	901000587	DW191124	901000734	901000855	Crossing Nursery-Kulumsa.201909-4/Crossing Nursery-Kulumsa.201909-6	-	-
5	DW2019091005	DW191004/DW191124	DW191004	901000614	DW191124	901000734	901000856	Crossing Nursery-Kulumsa.201909-5/Crossing Nursery-Kulumsa.201909-6	-	-
6	DW2019091006	DW173204/DW191142	DW173204	901000070	DW191142	901000752	901000857	Crossing Nursery-Kulumsa.201909-1/Crossing Nursery-Kulumsa.201909-7	-	-
7	DW2019091007	DW181309/DW191142	DW181309	901000583	DW191142	901000752	901000858	Crossing Nursery-Kulumsa.201909-2/Crossing Nursery-Kulumsa.201909-7	-	-
8	DW2019091008	DW183311/DW191142	DW183311	901000585	DW191142	901000752	901000859	Crossing Nursery-Kulumsa.201909-3/Crossing Nursery-Kulumsa.201909-7	-	-
9	DW2019091009	DW183313/DW191142	DW183313	901000587	DW191142	901000752	901000860	Crossing Nursery-Kulumsa.201909-4/Crossing Nursery-Kulumsa.201909-7	-	-
10	DW2019091010	DW191004/DW191142	DW191004	901000614	DW191142	901000752	901000861	Crossing Nursery-Kulumsa.201909-5/Crossing Nursery-Kulumsa.201909-7	-	-
11	DW2019091011	DW173204/DW191185	DW173204	901000070	DW191185	901000795	901000862	Crossing Nursery-Kulumsa.201909-1/Crossing Nursery-Kulumsa.201909-8	-	-
12	DW2019091012	DW181309/DW191185	DW181309	901000583	DW191185	901000795	901000863	Crossing Nursery-Kulumsa.201909-2/Crossing Nursery-Kulumsa.201909-8	-	-
13	DW2019091013	DW183311/DW191185	DW183311	901000585	DW191185	901000795	901000864	Crossing Nursery-Kulumsa.201909-3/Crossing Nursery-Kulumsa.201909-8	-	-
14	DW2019091014	DW183313/DW191185	DW183313	901000587	DW191185	901000795	901000865	Crossing Nursery-Kulumsa.201909-4/Crossing Nursery-Kulumsa.201909-8	-	-

3. Look at some crossing results

- a. If we look into the details of the newly generated germplasm. We'll see that breeding methods were inferred and we can look at a few interesting cases. **These will not be the same as your crosses because you chose different prents but there should be some similar cases.**

- If we look at the first entry (GID 901000852, Desogation **DW2019091001**) we can see that a **Three way cross** was inferred ($A \times (B \times C)$)

Germplasm Details: DW2019091001 (GID: 901000852)

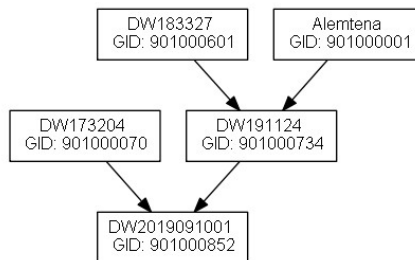
▼ BASIC DETAILS
Preferred Name: DW2019091001 Creation Date: 20191000 GID: 901000852
Creation Method: Three-way cross Location: Kulumsa Reference:
 Grouped Line Group Id (MGID): 0

▼ ATTRIBUTES

▼ PEDIGREE TREE
 Include derivative and maintenance lines Apply View Pedigree Graph

▶ DW2019091001(901000852) - 3 generations

You can verify this by looking at the pedigree graph:



- If we look at the 5th entry (GID: 901000856) DW2019091005 we can see that a **Double cross** was inferred ($A \times B) \times (C \times D)$)

Germplasm Details: DW2019091005 (GID: 901000856)

▼ BASIC DETAILS
Preferred Name: DW2019091005 Creation Date: 20191000 GID: 901000856
Creation Method: Double cross Location: Kulumsa Reference:
 Grouped Line Group Id (MGID): 0

▶ ATTRIBUTES

▶ PEDIGREE TREE

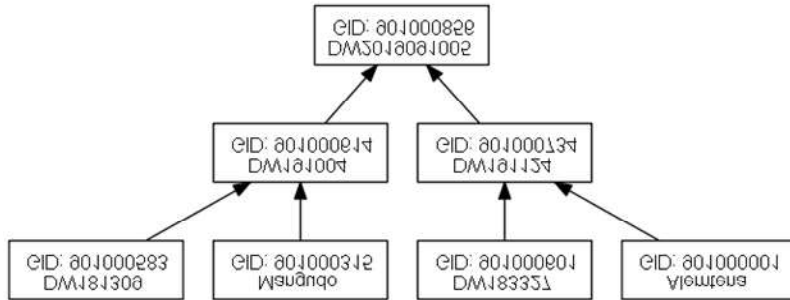
▶ NAMES

▶ INVENTORY INFORMATION

▶ LISTS

▶ SAMPLES

You can verify this by looking at the pedigree graph:



- If we look at the 8th entry DW2019091008 (GID: 901000859) we can see that a **Backcross** was inferred (A x B) x A

Germplasm Details: DW2019091008 (GID: 901000859)

▼ BASIC DETAILS

Preferred Name: DW2019091008	Creation Date: 20191000	GID: 901000859
Creation Method: Backcross	Location: Kulumsa	Reference:
<input type="checkbox"/> Grouped Line	Group Id (MGID): 0	

▶ ATTRIBUTES

▶ PEDIGREE TREE

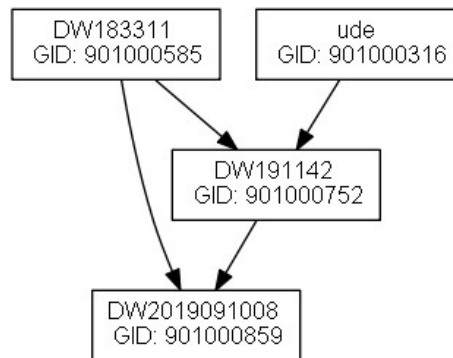
▶ NAMES

▼ INVENTORY INFORMATION

There is no Inventory information available for this germplasm.

▶ LISTS

You can verify this by looking at the pedigree graph:



Make an F1 Nursery to advance the crosses

1. Create a nursery

- From the Study Manager click Start a new study
- Specify study name and description. I.e. : “**F1 Nursery <your username>**”
- Speify study type to Nursery

MANAGE STUDIES ⓘ

Create Study [Return to Manage Studies](#)

BASIC DETAILS
** indicates a mandatory field*

Study name: * ⓘ

Description: *

Study type: * ▼

Objective:

Save in: * [Change Folder](#)

Created by: *

Creation date: * ⓘ

Completion date: ⓘ

Use a previously created study as a template

- Go to **Germplasm and Checks**
- Browse list that you created in the previous exercise list **TutorialParents<your username>**
- Go to **Environments**
- Search for the location name where you want to place your environment. If you don't find your desired location, you can broaden the scope of your search by disabling the favorites filter and searching by All location types
- Click on **Save**
- Select the folder where (Tutorial<your username> you want to save your study

2. Specify Layout and Traits

- After Save you will see that new tabs **Treatment Factors, Experimental Design and Observations** will be enabled for the study.
- Go to **Experimental Design** tab
- You will see all the avialable designs available in the BMS. Given that for the crossing nursery one would not typically need randomization, we will choose “**Entry list order**” which will place the entries in the plots according with the order of the entry list.

MANAGE STUDIES ?

F1 Nursery MC

Save

► BASIC DETAILS

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:

[Generate Design](#)

[Delete Design](#)

SUMMARY OF DESIGN DETAILS

Number of environments: 1

Treatment factor: ENTRY_NO

Plot factor: PLOT_NO

- d. Click on Generate design
- e. Go to **Observations** tab
- f. You will see here that your plots have been generated and your entries have been assigned to them according to your parameters.

MANAGE STUDIES ?

F1 Nursery MC

Save

[Return to Manage Studies](#)

► BASIC DETAILS

[Actions](#)

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

Observations

Define Observation Details

TRAITS ? [Add](#) SELECTIONS ? [Add](#)

Name	Description	Input Variables
------	-------------	-----------------

Name	Description
------	-------------

Observations ACCEPTED PENDING

Select Environment: Filter by status:

[Show Categorical Description](#)

► Batch Actions

ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	PLOT_NO
Test entry	901000852	DW2019091001	1	1
Test entry	901000853	DW2019091002	2	2
Test entry	901000854	DW2019091003	3	3
Test entry	901000855	DW2019091004	4	4
Test entry	901000856	DW2019091005	5	5
Test entry	901000857	DW2019091006	6	6
Test entry	901000858	DW2019091007	7	7
Test entry	901000859	DW2019091008	8	8
Test entry	901000860	DW2019091009	9	9

3. Advance your germplasm

- Select Advance study from the Advance study options in the Actions menu.
- Your instance and location will be selected by default. Click on Continue
- Choose the Random bulk breeding method to produce F2 generation by selecting the F1 population and bulking all seed from each plot. Select Finish.

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
KULUMSA

- Review the pending F2 lines and select Finish.

Advance study ✕

REVIEW ADVANCED LINES

▼ Advance List Entries

Total Entries: 25 Selected: 0

<input checked="" type="checkbox"/>	ENTRY_NO	DESIGNATION	CROSS	GID	SEED_SOURCE	TRIAL_INSTANCE	REP_NO
<input type="checkbox"/>	1	DW2019091001-RB		Pending	F1 Nursery MC:KULUMSA:201909:1:	1	
<input type="checkbox"/>	2	DW2019091002-RB		Pending	F1 Nursery MC:KULUMSA:201909:2:	1	
<input type="checkbox"/>	3	DW2019091003-RB		Pending	F1 Nursery MC:KULUMSA:201909:3:	1	
<input type="checkbox"/>	4	DW2019091004-RB		Pending	F1 Nursery MC:KULUMSA:201909:4:	1	
<input type="checkbox"/>	5	DW2019091005-RB		Pending	F1 Nursery MC:KULUMSA:201909:5:	1	
<input type="checkbox"/>	6	DW2019091006-RB		Pending	F1 Nursery MC:KULUMSA:201909:6:	1	
<input type="checkbox"/>	7	DW2019091007-RB		Pending	F1 Nursery MC:KULUMSA:201909:7:	1	
<input type="checkbox"/>	8	DW2019091008-RB		Pending	F1 Nursery MC:KULUMSA:201909:8:	1	
<input type="checkbox"/>	9	DW2019091009-RB		Pending	F1 Nursery MC:KULUMSA:201909:9:	1	
<input type="checkbox"/>	10	DW2019091010-RB		Pending	F1 Nursery MC:KULUMSA:201909:10:	1	
<input type="checkbox"/>	11	DW2019091011-RB		Pending	F1 Nursery MC:KULUMSA:201909:11:	1	
<input type="checkbox"/>	12	DW2019091012-RB		Pending	F1 Nursery MC:KULUMSA:201909:12:	1	
<input type="checkbox"/>	13	DW2019091013-RB		Pending	F1 Nursery MC:KULUMSA:201909:13:	1	
<input type="checkbox"/>	14	DW2019091014-RB		Pending	F1 Nursery MC:KULUMSA:201909:14:	1	
<input type="checkbox"/>	15	DW2019091015-RB		Pending	F1 Nursery MC:KULUMSA:201909:15:	1	
<input type="checkbox"/>	16	DW2019091016-RB		Pending	F1 Nursery MC:KULUMSA:201909:16:	1	

Select All

- Save list as F2 Germplasm<your username>

F2 Nursery – Measurements and selections

1. Create nursery

- a. From the Study Manager click Start a new study
- b. Specify study name and description. I.e. : “F2 Nursery <your username>”
- c. Speify study type to Nursery
- d. Go to **Germplasm and Checks**
- e. Browse for the list that you created in the previous excercise list - **F2 Germplasm<your username>**
- f. Go to **Environments**
- g. Search for the location name where you want to place your environment. If you don’t find your desired location, you can broaden the scope of your search by disabling the favorites filter and searching by All location types.
- h. Click on **Save**
- i. Select the folder where you want to save your study – Tutorial<your username>

2. Specify Layout

- a. After Save you will see that new tabs **Treatment Factors, Experimental Design and Observations** will be enabled for the study.
- b. Go to **Experimental Design** tab
- c. We will choose “**Entry list order**” which will place the entries in the plots according with the order of the entry list.

MANAGE STUDIES ?

F1 Nursery MC Save

► BASIC DETAILS

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: Entry list order ?

Or import an experimental design.

SPECIFY PLOT NUMBERING

Specify the starting plot number: 1

Generate Design

Delete Design

SUMMARY OF DESIGN DETAILS

Number of environments: 1

Treatment factor: ENTRY_NO

Plot factor: PLOT_NO

- d. Click on Generate design

3. Specify Layout

- Go to **Observations** tab
- You will see here that your plots have been generated and your entries have been assigned to them according to your parameters.
- Add your **Traits** for measurement and your **Selection** variables
- In this case I've added PHT (Plant height measured in centimeters) and PGY (Grain yield measured in grams per plot) as my Trait variables
- I've also added NPSEL (Number of plants selected) as my Selection variable

MANAGE STUDIES

F2 Nursery MC

Save

Return to Manage Studies

Actions

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

Observations

Define Observation Details

TRAITS Add

Name	Description	Input Variables
PHT	PH_M_cm	
PGY	Grain yield-BY-GY Measurement-IN-g/plot	

Remove

SELECTIONS Add

Name	Description
NPSEL	Number of plants selected - counted (number)

Remove

Observations

ACCEPTED PENDING

Show Categorical Description

Select Environment: 1 - KULUMSA Filter by status: All

Batch Actions

ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	PLOT_NO	PHT	NPSEL	PGY
Test entry	901000877	DW2019091001-RB	1	1			
Test entry	901000878	DW2019091002-RB	2	2			
Test entry	901000879	DW2019091003-RB	3	3			
Test entry	901000880	DW2019091004-RB	4	4			

4. Data collection

- You're now ready to start collecting some data!
- Go to **Actions, Data collection>Export study book**
- You should get **Observations** selected by default, click on **Continue**

Export study book

* indicates a mandatory field

DATASET

Please choose the dataset you would like to export: *

Observations

Cancel Continue

Add SELECTIONS

- f. Select **Excel** as the export format and **Plot order** as the data collection order (this should be selected by default) and click on Export

Export Study Book ✕

** indicates a mandatory field*

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: *

Search:

<input checked="" type="checkbox"/>	TRIAL_INSTANCE	LOCATION_NAME
<input checked="" type="checkbox"/>	1	KULUMSA - ()

Showing 1 to 1 of 1 entries

< 1 >

- g. Open the **Excel file** and go to the **Obersvations** tab
- h. Fill in the values for your Trait Values (PHT and PGY in my case)

	A	B	C	D	E	F	G	H	I
1	OBS_UNIT	ENTRY_T	GID	DESIGNA	ENTRY_N	PLOT_NO	PHT	PGY	NPSEL
2	XFTDPMW	T	901000877	DW20190	1	1	85	2420	
3	XFTDPic1j	T	901000878	DW20190	2	2	76	2201	
4	XFTDPAOi	T	901000879	DW20190	3	3	75	2063	
5	XFTDPON	T	901000880	DW20190	4	4	89	1152	
6	XFTDPS9	T	901000881	DW20190	5	5	89	1517	
7	XFTDPO3v	T	901000882	DW20190	6	6	80	1762	
8	XFTDPDaC	T	901000883	DW20190	7	7	75	1243	
9	XFTDPQbr	T	901000884	DW20190	8	8	84	2258	
10	XFTDP0vE	T	901000885	DW20190	9	9	86	1715	
11	XFTDPSXV	T	901000886	DW20190	10	10	86	2529	
12	XFTDP5n5	T	901000887	DW20190	11	11	76	2887	
13	XFTDPCTc	T	901000888	DW20190	12	12	89	1522	
14	XFTDPPM	T	901000889	DW20190	13	13	76	2002	
15	XFTDPN0E	T	901000890	DW20190	14	14	79	2883	
16	XFTDPMfi	T	901000891	DW20190	15	15	82	1553	
17	XFTDPjqhv	T	901000892	DW20190	16	16	85	2270	
18	XFTDPGA	T	901000893	DW20190	17	17	84	2500	
19	XFTDPTYC	T	901000894	DW20190	18	18	80	2329	
20	XFTDPVrw	T	901000895	DW20190	19	19	90	2552	
21	XFTDPv4Q	T	901000896	DW20190	20	20	83	1845	
22	XFTDPGrL	T	901000897	DW20190	21	21	88	2870	
23	XFTDPZ2F	T	901000898	DW20190	22	22	78	1298	
24	XFTDPcuN	T	901000899	DW20190	23	23	82	1825	
25	XFTDPNPk	T	901000900	DW20190	24	24	82	1299	
26	XFTDPEqI	T	901000901	DW20190	25	25	84	2140	
27									
28									

- i. Save your file changes

5. Data import, review and cleaning

- a. Now we're going to import your measurements into the BMS.
- b. Go to Actions>Data Collection Options>Import Observations
- c. You should get **Observations** selected by default, click on **Continue**
- d. Excel should be selected by default for the file format
- e. Browse your measurements file
- f. Click on **Import**
- g. You'll get a success message saying. "Your data was successfully imported and needs correspondence"
- h. You'll now see that the observation tab has an orange **Observations** indicator
- j. This is indication that you have data pending confirmation for a this dataset (Pending Data)
- k. You can toggle between the **Accepted** and **Pending Data** view with this control

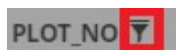


- i. In the Accepted view, you will only see the observations that have been Accepted
 - ii. In the **Pending view**, you will see all the incoming observations that haven't been accepted yet
- l. We will now Accept of the pending data.
- m. You can do this on a cell by cell basis
- i. If you right click on a given cell you will get a pop up with two options: **Accept values as-is** or **Set value to missing**
 - ii. Clicking on **Accept value as is** should move the observation from the **Pending** data into the Accepted

The screenshot shows the 'Observations' interface. At the top, there are 'ACCEPTED' and 'PENDING' toggle buttons, with 'PENDING' selected. Below the toggles are 'Accept' and 'Discard' buttons. The main area contains a table with columns: TRIAL_INSTANCE, ENTRY_TYPE, GID, DESIGNATION, ENTRY_NO, PLOT_NO, PHT, and PGY. A context menu is open over the PHT cell of the first row, showing 'Accept value as-is' and 'Set value to missing' options.

TRIAL_INSTANCE	ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	PLOT_NO	PHT	PGY
1	Test entry	901000877	DW2019091001-RB	1	1	85	
1	Test entry	901000878	DW2019091002-RB	2	2	76	
1	Test entry	901000879	DW2019091003-RB	3	3	75	2063
1	Test entry	901000880	DW2019091004-RB	4	4	89	1152
1	Test entry	901000881	DW2019091005-RB	5	5	89	1517
1	Test entry	901000882	DW2019091006-RB	6	6	80	1762

- iii. You can also filter Accept a subset of the pending data
- iv. For example, go to the **PLOT_NO** column and click on the filter icon



- v. Filter by an existing PLOT_NO (i.e 5) and Click on **Apply**



- vi. You should now get the observations for the PLOT_NO you selected. Now by right clicking on the observations (same as in step i)

- n. Finally we'll accept all of the remaining **Pending data**

- i. In the Pending View, click on **Accept**



- ii. You'll see that the pending observation have moved to the **Accepted view**

ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	PLOT_NO	PHT	NPSEL	PGY
Test entry	901000877	DW2019091001-RB	1	1	85		2420
Test entry	901000878	DW2019091002-RB	2	2	76		2201
Test entry	901000879	DW2019091003-RB	3	3	75		2063
Test entry	901000880	DW2019091004-RB	4	4	89		1152
Test entry	901000881	DW2019091005-RB	5	5	89		1517
Test entry	901000882	DW2019091006-RB	6	6	80		1762
Test entry	901000883	DW2019091007-RB	7	7	75		1243
Test entry	901000884	DW2019091008-RB	8	8	84		2258
Test entry	901000885	DW2019091009-RB	9	9	86		1715
Test entry	901000886	DW2019091010-RB	10	10	86		2529

6. Make selections

- We will use **NPSEL** selection variable to indicate the number of plants that we would like to advance to the F3 generation from each plot
- By clicking on the cells you can input the numbers manually. Changes will be saved automatically

NPSEL ▼	PGY ▼
2	2420
2	2201
	2063

- Once you've indicated the number of plants that you want to advance for each plot (let's say 2 plants for 5 plots), select **Advance study** from the Advance study options in the Actions menu.
- Your instance and location will be selected by default. Click on **Continue**
- Choose the **Single plant selection** to produce your F3 seed
- Uncheck "Same number of lines is selected for 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

Lines Selected per Plot:

1

LOCATION DETAILS

LOCATION_NAME

KULUMSA

Back

Finish

- g. Choose **NPSEL** as the variable that defines the variate that 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

KJLUMSA

- h. Click on **Finish**
- i. Review the pending F3 lines and select **Finish**.

Advance study ✕

REVIEW ADVANCED LINES

▼ Advance List Entries

Total Entries: 4 Selected: 0

<input checked="" type="checkbox"/>	ENTRY_NO	DESIGNATION	CROSS	GID	SEED_SOURCE	TRIAL_INSTANCE	REP_NO
<input type="checkbox"/>	1	DW2019091001-RB-3		Pending	F2 Nursery MC:KJLUMSA:201909:1:	1	
<input type="checkbox"/>	2	DW2019091001-RB-4		Pending	F2 Nursery MC:KJLUMSA:201909:1:	1	
<input type="checkbox"/>	3	DW2019091002-RB-3		Pending	F2 Nursery MC:KJLUMSA:201909:2:	1	
<input type="checkbox"/>	4	DW2019091002-RB-4		Pending	F2 Nursery MC:KJLUMSA:201909:2:	1	

Select All

- j. Save list as **F3 Germplasm <your username>**

Import Germplasm

1. Complete a Germplasm Import Template

- Under Information Management select Germplasm Import (Only available for Crop Admins)
- Download a template by clicking on the message
- Open the template in excel make the Observation Sheet the active sheet
- Open the file 51IDYN_008.xls which comes from CIMMYT make the FieldBook sheet active
- Copy the selection histories for the entries in rep 1 from cells E12 to E61 to clipboard
- Paste them into the Designation column (column B) of the Observation Sheet of the Germplasm Import Template.
- Enter the name of the Local check in the blank cell B2 (I chose Assesa)
- Copy the corresponding cross names from Cells D12 to D61. Paste them under CROSS in cell D2.
- Copy the Origins from F12 to F61 and paste them under SOURCE in E2.
- Copy the Entry number from J2 to J61 under ENTRY_CODE in cell F2
- Fill column A of the Observation sheet of the Germplasm Import Template with sequential ENTRY-Nos, from 1 to 50 in this case.
- On the Description sheet enter the name of the list 51IDYT<your username> in cell B2 and a description and date below.
- You can copy the name and ID of the list owner from the users section of the CODES sheet into the VALUE cells of List Owner and ID of List Owner (Cells G7 and G8).

The Description sheet will look something like this:

	A	B	C	D	E	F	G
1	LIST NAME	51IDYTCGM		Enter a list name here, or add it when saving in the BMS			
2	LIST DESCRIPTION	51st International Durum Yield Trial		Enter a list description here, or add it when saving in the BMS			
3	LIST DATE	20190923		Accepted formats: YYYYMMDD or blank			
4	LIST TYPE	LST					
5							
6	CONDITION	DESCRIPTION	PROPERTY	SCALE	METHOD	DATA TYPE	VALUE
7	LIST OWNER	Name of the Principal Investigator	PERSON	DBC	ASSIGNED	C	Christopher McLaren
8	ID OF LIST OWNER	ID of the Principal Investigator	PERSON	DBID	ASSIGNED	N	2

We want to provide an introduction number as another name for the new germplasm. On the Codes sheet you will see all the NAME_TYPES available. The NAME_TYPE we want to use if GENOTYPE:

59	FACTOR	NAME_TYPES	ALIAS1	First Alias
60	FACTOR	NAME_TYPES	FACCN	FOREIGN ACCESSION NUMBER
61	FACTOR	NAME_TYPES	ACCNAME	GENBANK ACCESSION NAME
62	FACTOR	NAME_TYPES	GENOTYPE	GENOTYPE NAME
63	FACTOR	NAME_TYPES	ACCNO	GERMPLASM BANK ACCESSION NUMBER
64	FACTOR	NAME_TYPES	ITEST	INTERNATIONAL TESTING NUMBER
65	FACTOR	NAME_TYPES	INTRID	IWIS2 INTRID

- n. Copy cte contents of cells 62C and D to 17A and B overwriting the name type DRVNM and its description. Then on the Observation sheet replace the heading DRVNM for column G with GENOTYPE.
- o. Fill the GENOTYPE column with the next series of introduction numbers. This requires you to remember what the last one you used was. In this case we just start with DW203001 for a new year.
- p. You can also add seed stock amounts for the imported seed and this can have different units as described in the section on INVENTORY on the Codes sheet:

88	FACTOR	NAME_TYPES	VARNM	VARIETY NAME
89	INVENTORY	SCALES_FOR_INVENTORY_UNI	SEED_AMOUNT_g	Seed inventory amount deposited or withdrawn (g)
90	INVENTORY	SCALES_FOR_INVENTORY_UNI	SEED_AMOUNT_No	Seed inventory amount deposited or withdrawn (no)
91	INVENTORY	SCALES_FOR_INVENTORY_UNI	SEED_AMOUNT_kg	Seed inventory amount deposited or withdrawn (kg)
92	INVENTORY	SCALES_FOR_INVENTORY_UNI	SEED_AMOUNT_Packets	Seed inventory amount deposited or withdrawn (packets)
93	INVENTORY	SCALES_FOR_INVENTORY_UNI	SEED_AMOUNT_t	Seed inventory amount deposited or withdrawn (t)
94	VARIATE	ATTRIBUTE_TYPES	ACQ_DATE	Acquisition date

- q. We can suppose CIMMYT supplied us with 4 packets of seed for each entry for planting two reps at two locations, so replace the name and description for grams on the description sheet in row 20 with the name and description for packets from row 92 of the Codes sheet: Put SEED_AMOUNT_Packets as the head of column H and fill the column with 4 since we have 4 packets of each line.

15	SOURCE	The seed source of the germplasm	SEED SOURCE	NAME	Seed Source	C
16	ENTRY CODE	Germplasm entry code	GERMPLASM ENTRY	CODE	ASSIGNED	C
17	GENOTYPE	GENOTYPE NAME	GERMPLASM ID	NAME	ASSIGNED	C
18						
19	INVENTORY	DESCRIPTION	PROPERTY	SCALE	METHOD	DATA TYPE
20	SEED_AMOUNT_Packets	Seed inventory amount deposited or withdrawn (packets)	INVENTORY AMOUNT	g	Weighed	N
21	STOCKID	ID of an inventory deposit	Germplasm stock ID	DBCV	ASSIGNED	C

- r. The Observation sheet will look something like this:

	A	B	C	D	E	F	G	H	I	J	K
1	ENTRY	DESIGNATION	GID	CROSS	SOURCE	NTRY COD	GENOTYPE	SEED_AMOUNT_Packets	STOCKID	NOTE	
2	1	Assesa		LOCAL CHECK	\0	701	DW203001	4			
3	2	CM470-1M-3Y-0M		MEXICALI C75	MX117-18\DWTES	702	DW203002	4			
4	3	CM9799-126M-1M-5Y-0M		YAVAROS 79	MX117-18\DWTES	703	DW203003	4			
5	4	CD22344-A-8M-1Y-1M-1Y-2Y-1M-0Y		ALTAR 84	MX117-18\DWTES	704	DW203004	4			
6	5	CD91Y636-1Y-040M-030Y-1M-0Y-0B-1Y-0B-0M		JUPARE C 2001	MX117-18\DWTES	705	DW203005	4			
7	6	CDSS11Y00203S-099Y-019M-3Y-0M-06Y-0B		GUAYACAN IIIA/GU	MX117-18\C51IDY	706	DW203006	4			
8	7	CDSS10B000304T-099Y-051M-33Y-0M-06Y-0B		GUAYACAN IIIA/GU	MX117-18\C51IDY	707	DW203007	4			
9	8	CDSS11Y00431S-099Y-032M-4Y-0M-06Y-0B		MOHAWK/6/LOTUS	MX117-18\C51IDY	708	DW203008	4			
10	9	CDSS11Y00431S-099Y-032M-53Y-0M-06Y-0B		MOHAWK/6/LOTUS	MX117-18\C51IDY	709	DW203009	4			
11	10	CDSS12Y00834T-017Y-033M-40Y-0M		CIT71/DIPPER_1//	MX117-18\C51IDY	710	DW203010	4			
12	11	CDSS11B00212T-080Y-034M-1Y-0M		BHA/3/SORA/2*PL	MX117-18\C51IDY	711	DW203011	4			
13	12	CDSS11B00002S-0133Y-055M-1Y-0M		ALTAR 84/STINT//S	MX117-18\C51IDY	712	DW203012	4			
14	13	CDSS11B00002S-0133Y-055M-2Y-0M		ALTAR 84/STINT//S	MX117-18\C51IDY	713	DW203013	4			
15	14	CDSS12Y00128S-065Y-050M-2Y-0M		CBC 509 CHILE/6/E	MX117-18\C51IDY	714	DW203014	4			
16	15	CDSS12Y00128S-065Y-050M-10Y-0M		CBC 509 CHILE/6/E	MX117-18\C51IDY	715	DW203015	4			
17	16	CDSS11B00071S-082Y-055M-1Y-0M		SILVER_14/MOEWE	MX117-18\C51IDY	716	DW203016	4			
18	17	CDSS11B00072S-097Y-048M-33Y-0M		SILVER_14/MOEWE	MX117-18\C51IDY	717	DW203017	4			
19	18	CDSS11B00104S-0101Y-041M-13Y-0M		1A.1D 5+1-06/3*W	MX117-18\C51IDY	718	DW203018	4			
20	19	CDSS11B00104S-0101Y-041M-23Y-0M		1A.1D 5+1-06/3*W	MX117-18\C51IDY	719	DW203019	4			
21	20	CDSS11B00319T-044Y-028M-15Y-0M		CBC 509 CHILE/6/E	MX117-18\C51IDY	720	DW203020	4			
22	21	CDSS11B00328T-044Y-047M-19Y-0M		GUAYACAN IIIA/GU	MX117-18\C51IDY	721	DW203021	4			

- s. Save the template as 51IDYT<your username>

2. Use Germplasm Import to import the template

- a. Go to Information Management>Import Germplasm>Browse and select the template file just made. Click Continue.
- b. Check the Yes box to make the GENOTYPE introduction name the preferred name of the lines.
- c. Add the following germplasm details:

ADD GERmplasm DETAILS

You can specify following details to apply to the imported germplasm. Seed Storage Location is required when inventory information is present in the imported spreadsheet.

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

Germplasm location: IMPROVEMENT OF MAIZE AND WHEAT - (CIMMYT) ?
 All locations Breeding locations [Manage Locations](#)
 Show only favorite locations

Seed Storage Location: Default Seed Store - (DSS) ?
 All locations Storage locations [Manage Locations](#)
 Show only favorite locations

Germplasm date: 2019-09-29 ?

Germplasm name type: SELECTION HISTORY

- d. And specify “Select existing germplasm whenever found”. Click Finish
- e. You will see some requests to select from multiple matching germplasm such as:

Select Matching Germplasm or Add New Entry ✕

Match(es) were found for entry **2 of 50** , with the name **CM470-1M-3Y-0M** . 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
MEXICALI C75	1137	CM470-1M-3Y	-	CIMMYT - TOLUCA
327-04	5780462	MEXICALI C75	-	INT CENTER FOR THE IMPROVEMENT OF MAIZE AND
BW163226	900004443	327-04	-	Kulumsa

- 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


- f. Select the most appropriate match, select Use this match for other instances and click continue.
- g. You will be asked for a prefix for StockIDs for the inventory, enter <your username>.

- h. Save the list in the Tutorial<your username> when done.

Seed Increase – Durum Wheat

1. Create a seed increase nursery for the imported seed.
 - a. From Manage Studies click Start a New Study
 - b. Give the Study name 51IDYTSI<your username> and fill in some details.
 - c. Don't check 'Use previous study as template.'

MANAGE STUDIES 

 **Create Study**

BASIC DETAILS

** indicates a mandatory field*

Study name: *

Description: *

Study type: *

Objective:

Use a previously created study as a template

- d. On settings tab click Add and add the following variables:
 - i. Product_Concept
 - ii. Responsible-Person
 - iii. Trial_Year
 - iv. Trial_Type
 - v. Target_Region

Settings **Germplasm & Checks** Environments

STUDY SETTINGS ? Add

Product_concept: BWP - Activities for external collaborations no... ▼

Responsible_Person: Christopher McLaren ▼

TRIAL_YEAR: 2019 ▼

Trial_Type: Z- Introduction Trial ▼

Agro_Ecology: E - Early/medium ▼

Select All Remove

- e. On the Germplasm Tab select 51IDYT<your username>
- f. On the environment tab check 'Show only favorite locations' and select DebreZeit.
- g. Click Add opposite Environment Details and add the variables SEEDING_DATE and PlotArea.

Specify Environment Details

10 ▼ Showing 1 to 1 of 1 entries Ma

Environment	PlotAreaHvst_m2	LOCATION_NAME	SEEDING_DATE
1	10	Kulumsa - (KU) ▼ <input checked="" type="radio"/> Breeding locations <input type="radio"/> All locations types <input checked="" type="checkbox"/> Show only favorite locations	2019-09-21

- h. Click Save at the top of the form and save the study in folder Tutorial<your username>
- i. On Experimental Design tab select Entry List Order and click Generate Design.
- j. On the Observation Sheet click Add opposite SELECTIONS and add the variable NPSEL
- k. On the Observation tab click Add opposite Traits and add the following traits:

Observations

▼ Define Observation Details

TRAITS ? Add SELECTIONS ? Add

Name	Description	Input Variables
<input type="checkbox"/> DTH	Heading time-BY-Hd DS55 days Computation-IN-day	
<input type="checkbox"/> DTM	Maturity time-BY-Mat DS87 DT Computation-IN-day	
<input type="checkbox"/> PHT	PH_M_cm	
<input type="checkbox"/> MST	Grain moisture content-BY-GMoi Estimation-IN-%	
<input type="checkbox"/> PGY	Grain yield-BY-GY Measurement-IN-g/plot	
<input type="checkbox"/> GY_Calc_tha	Grain yield-BY-GY Computation (t/ha)-IN-t/ha	GY_M_gPlot , GMoi_E_pct , PlotAreaHvst_m2

Remove

Name	Description
<input type="checkbox"/> NPSEL	Number of plants selected - counted (number)

Remove

ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	PLOT_NO	DTH	DTM	PHT	MST	NPSEL	PGY	GY_Calc_tha
Test entry	901000815	Assesa	1	1							
Test entry	5780462	CM470-1M-3Y-0M	2	2							
Test entry	5780466	CM9799-126M-1M-5Y-0M	3	3							
Test entry	30374	CD22344-A-8M-1Y-1M-1Y-2Y-1M-0Y	4	4							
Test entry	3828077	CD91Y636-1Y-040M-030Y-1M-0Y-0B-1Y-0B-0MEX	5	5							
Test entry	7383430	CD5S11Y00203S-099Y-019M-3Y-0M-06Y-0B	6	6							
Test entry	7383636	CD5S10B00304T-099Y-051M-33Y-0M-06Y-0B	7	7							

2. Collect some data

- ON the ACTIONS menu at the top right of the form select Data collection options>Export study book. Click Continue for the Observation sheet and the click Export to get an excel fieldbook downloaded - 51IDYTSICGM-1_DZ_PLOT_51IDYTSICGM-PLOTDATA.xls
- Add some data to the observation sheet. You can copy it from file 51IDYTSI_data.csv. Make sure the data goes to the correct columns so the fieldbook should look like this:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	
1	OBS	UNIT	ENTRY_T	GID	DESIGNA	ENTRY_N	PLOT_NO	DTH	DTM	PHT	MST	PGY	GY_Calc_tha	NOTES	NPSEL
2	XFTDPRU	T		901000815	Assesa	1	1	70	119	95	15	1357		Good Aspect	29
3	XFTDPFK	T		5780462	CM470-1M	2	2	74	121	90	14	1082			25
4	XFTDPZO	T		5780466	CM9799-1	3	3		122	85	13	1316		Poor Aspect	0
5	XFTDP9g	T		30374	CD22344-	4	4	68	118	95	15	1231		Diseased	0
6	XFTDP1rE	T		3828077	CD91Y636	5	5	70	116	80	15	610			36
7	XFTDPUA	T		7383430	CDSS11Y	6	6		125	100	13	1496		Good Aspect	37
8	XFTDPqJ	T		7383636	CDSS10B	7	7	70	119	90	14	1728			31
9	XFTDPmF	T		7384124	CDSS11Y	8	8	70	117	85	13	884			21
10	XFTDPzK	T		7384135	CDSS11Y	9	9	68	116	90	14	526			22
11	XFTDPvG	T		7407142	CDSS12Y	10	10	73	118	90	13	848		Poor Aspect	0
12	XFTDPVY	T		7407209	CDSS11B	11	11	73	119	95	14	786		Good Aspect	46
13	XFTDPJc	T		7407575	CDSS11B	12	12	73	116	85	14	554			27
14	XFTDPE9	T		7407576	CDSS11B	13	13	71	119	95	15	968			50
15	XFTDPDw	T		7407944	CDSS12Y	14	14	71	117	90	14	1186		Diseased	0
16	XFTDPTW	T		7407946	CDSS12Y	15	15	75	118	95	14	1585			44
17	XFTDPqu	T		7408961	CDSS11B	16	16	75	121	95	14	1014		Poor Aspect	0
18	XFTDPqY	T		7408984	CDSS11B	17	17	72	117	80	14	981			43
19	XFTDPEr	T		7409179	CDSS11B	18	18	70	118	85	13	1051			38
20	XFTDPTOr	T		7409181	CDSS11B	19	19		120	80	14	1124		Diseased	0

- From ACTIONS>Data collection options>Import observations choose Observations and click Continue
- Browse for the fieldbook file you just saved and click Import.
- The data will be loaded and saved as PENDING. Missing values and outliers will be colour coded and actions can be taken to correct then singly or in batches.

Observations

▶ Define Observation Details

Observations

ACCEPTED PENDING

Accept Discard

Select Environment: All environments Filter by status: All

[Show Categorical Description](#)

▶ Batch Actions

TRIAL_INSTANCE	ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	PLOT_NO	DTH	DTM	PHT	MST	NPSEL	PGY	NOTES
1	Test entry	901000815	Assesa	1	1	70	119	95	15	29	1357	Good Aspect
1	Test entry	5780462	CM470-1M-3Y-0M	2	2	74	121	90	14	25	1082	
1	Test entry	5780466	CM9799-126M-1M-5Y-0M	3	3		122	85	13	0	1316	Poor Aspect
1	Test entry	30374	CD22344-A-8M-1Y-1M-1Y-2Y-1M-0Y	4	4	68	118	95	15	0	1231	Diseased

- When the data are acceptable click Accept to approve the data.
- On the Environments tab enter the harvest plot size 10m2 and the seeding date 20190505. Click Save.

3. Calculate the derived variable

- Open the observation sheet. GY_Calc_tha is shown in green because it can be calculated from the existing variables:

Observations ACCEPTED PENDING

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

► Batch Actions

ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	PLOT_NO	DTH	DTM	PHT	MST	NPSEL	PGY	GY_Calc_tha	NOTES
Test entry	901000815	Assesa	1	1	70	119	95	15	29	1357		Good Aspect
Test entry	5780462	CM470-1M-3Y-0M	2	2	74	121	90	14	25	1082		
Test entry	5780466	CM9799-126M-1M-5Y-0M	3	3		122	85	13	0	1316		Poor Aspect
Test entry	30374	CD22344-A-8M-1Y-1M-1Y-2Y-1M-0Y	4	4	68	118	95	15	0	1231		Diseased
Test entry	3828077	CD91Y636-1Y-040M-030Y-1M-0Y-0B-1Y-0B-0MEX	5	5	70	116	80	15	36	610		
Test entry	7383430	CDSS11Y00203S-099Y-019M-3Y-0M-06Y-0B	6	6		125	100	13	37	1496		Good Aspect

- b. From ACTIONS>Execute calculated variable. Choose Observations and continue then choose GY_Calc_tha and click Execute.
- c. The calculates values will be filled in and saved.

Observations ACCEPTED PENDING

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

► Batch Actions

ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	PLOT_NO	DTH	DTM	PHT	MST	NPSEL	PGY	GY_Calc_tha	NOTES
Test entry	901000815	Assesa	1	1	70	119	95	15	29	1357	1.357	Good Aspect
Test entry	5780462	CM470-1M-3Y-0M	2	2	74	121	90	14	25	1082	1.0947	
Test entry	5780466	CM9799-126M-1M-5Y-0M	3	3		122	85	13	0	1316	1.347	Poor Aspect
Test entry	30374	CD22344-A-8M-1Y-1M-1Y-2Y-1M-0Y	4	4	68	118	95	15	0	1231	1.231	Diseased
Test entry	3828077	CD91Y636-1Y-040M-030Y-1M-0Y-0B-1Y-0B-0MEX	5	5	70	116	80	15	36	610	0.61	
Test entry	7383430	CDSS11Y00203S-099Y-019M-3Y-0M-06Y-0B	6	6		125	100	13	37	1496	1.5312	Good Aspect

4. Advance the Study

- a. From ACTION>Advance study options>Advance Study
- b. Select the site (selected by default) and click Continue

Advance study

* indicates a mandatory field

METHODS

Breeding Method is the same for each advance

Seed increase - NSI ?

Derivative and Maintenance methods

All methods

Show only favorite methods [Manage Methods](#)

BULKS

All plots are selected

Choose a variate that defines which plots were selected

NPSEL

LOCATION DETAILS

LOCATION_NAME

Kulumsa

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

- Choose the method Seed increase – NSI.
- Deselect the option “All plots are selected” so that the variable NPSEL will be selected with positive values indicating how many plants were harvested and bulked to give the increased seed. (You can also just use 0 and 1 values in NPSEL to indicate which plots are not harvested and which plots are bulked).
- Click Finish to see a list of pending advanced lines. The name of each new line is derived by appending :19 – the trial_year to the preferred name of the source line.

Advance study

REVIEW ADVANCED LINES

▼ Advance List Entries

Total Entries: 36 Selected: 0

[Actions](#)

<input checked="" type="checkbox"/>	ENTRY_NO	DESIGNATION	CROSS	GID	SEED_SOURCE	TRIAL_INSTANCE	REP_NO
<input type="checkbox"/>	1	Assesa:19		Pending	51IDYTSICGM:Debrezeit:19:1:	1	
<input type="checkbox"/>	2	327-04:19		Pending	51IDYTSICGM:Debrezeit:19:2:	1	
<input type="checkbox"/>	3	DW203050:19		Pending	51IDYTSICGM:Debrezeit:19:5:	1	
<input type="checkbox"/>	4	DW203051:19		Pending	51IDYTSICGM:Debrezeit:19:6:	1	
<input type="checkbox"/>	5	DW203052:19		Pending	51IDYTSICGM:Debrezeit:19:7:	1	
<input type="checkbox"/>	6	DW203053:19		Pending	51IDYTSICGM:Debrezeit:19:8:	1	
<input type="checkbox"/>	7	DW203054:19		Pending	51IDYTSICGM:Debrezeit:19:9:	1	
<input type="checkbox"/>	8	DW203056:19		Pending	51IDYTSICGM:Debrezeit:19:11:	1	
<input type="checkbox"/>	9	DW203057:19		Pending	51IDYTSICGM:Debrezeit:19:12:	1	

- Click Finish and save the list of advanced lines as 51IDYTSI<your username> in the Tutorial<your username> folder.

5. Add Inventory

- In the study 51IDYTI<your username>, on the Advance List tab, click Advance List Actions>Generate Stock List

- Enter your username in the Stock ID prefix box
- Click Continue to obtain an Stock List tab with generated StockIDs
- Click Stock List Actions>Export inventory file
- Open the exported file. It has columns for seed storage LOCATION, LOCATION_ABBR and SEED_AMOUNT_G. Add seed amounts.
- If the seed storage location(s) has/have an abbreviation you only need to supply the abbreviation(s). Ours is DSS for Default seed store but they can be customized for any type of store.
- Add the seed amount in g, or change the heading to one of:

SEED_AMOUNT_g	Seed inventory amount deposited or withdrawn (g)
SEED_AMOUNT_No	Seed inventory amount deposited or withdrawn (no)
SEED_AMOUNT_kg	Seed inventory amount deposited or withdrawn (kg)
SEED_AMOUNT_Packets	Seed inventory amount deposited or withdrawn (packets)
SEED_AMOUNT_t	Seed inventory amount deposited or withdrawn (t)

	A	B	C	D	E	F	G	H	I	J
1	ENTRY_NO	DESIGNATION	CROSS	GID	SEED_SOURCE	LOCATION	LOCATION ABBR	SEED_AMOUNT_G	STOCKID	COMMENT
2	1	Assesa:19	-	901000816	51IDYTSICGM:Debrezeit:19:1:		DSS	187.0	CGM1-1	
3	2	327-04:19	-	901000817	51IDYTSICGM:Debrezeit:19:2:		DSS	193.0	CGM1-2	
4	3	DW203050:19	-	901000818	51IDYTSICGM:Debrezeit:19:5:		DSS	198.0	CGM1-3	
5	4	DW203051:19	-	901000819	51IDYTSICGM:Debrezeit:19:6:		DSS	199.0	CGM1-4	
6	5	DW203052:19	-	901000820	51IDYTSICGM:Debrezeit:19:7:		DSS	149.0	CGM1-5	
7	6	DW203053:19	-	901000821	51IDYTSICGM:Debrezeit:19:8:		DSS	109.0	CGM1-6	
8	7	DW203054:19	-	901000822	51IDYTSICGM:Debrezeit:19:9:		DSS	199.0	CGM1-7	
9	8	DW203056:19	-	901000823	51IDYTSICGM:Debrezeit:19:11:		DSS	116.0	CGM1-8	
10	9	DW203057:19	-	901000824	51IDYTSICGM:Debrezeit:19:12:		DSS	118.0	CGM1-9	
11	10	DW203058:19	-	901000825	51IDYTSICGM:Debrezeit:19:13:		DSS	165.0	CGM1-10	
12	11	DW203060:19	-	901000826	51IDYTSICGM:Debrezeit:19:15:		DSS	110.0	CGM1-11	
13	12	DW203062:19	-	901000827	51IDYTSICGM:Debrezeit:19:17:		DSS	102.0	CGM1-12	
14	13	DW203063:19	-	901000828	51IDYTSICGM:Debrezeit:19:18:		DSS	147.0	CGM1-13	
15	14	DW203065:19	-	901000829	51IDYTSICGM:Debrezeit:19:20:		DSS	176.0	CGM1-14	

- Click Stock List Actions>Import inventory on the Stock List tab to import the inventory:

Stock List: **51DYTCGMSI** Notes: [View List Details](#)

Total Entries: 36 Selected: 0 [Stock List Actions](#)

100 Showing 1 to 36 of 36 entries

<input type="checkbox"/>	ENTRY_NO	DESIGNATION	CROSS	GID	SEED_SOURCE	GROUP ID	LOCATION	AMOUNT	UNITS	STOCKID	COMMENT
<input type="checkbox"/>	1	Assesa:19	-	901000816	51IDYTSICGM:Debrezeit:19:1:	-	Default Seed Store	187.0	SEED_AMOUNT_g	CGM1-1	
<input type="checkbox"/>	2	327-04:19	-	901000817	51IDYTSICGM:Debrezeit:19:2:	-	Default Seed Store	193.0	SEED_AMOUNT_g	CGM1-2	
<input type="checkbox"/>	3	DW203050:19	-	901000818	51IDYTSICGM:Debrezeit:19:5:	3828077	Default Seed Store	198.0	SEED_AMOUNT_g	CGM1-3	
<input type="checkbox"/>	4	DW203051:19	-	901000819	51IDYTSICGM:Debrezeit:19:6:	7383430	Default Seed Store	199.0	SEED_AMOUNT_g	CGM1-4	
<input type="checkbox"/>	5	DW203052:19	-	901000820	51IDYTSICGM:Debrezeit:19:7:	7383636	Default Seed Store	149.0	SEED_AMOUNT_g	CGM1-5	
<input type="checkbox"/>	6	DW203053:19	-	901000821	51IDYTSICGM:Debrezeit:19:8:	7384124	Default Seed Store	109.0	SEED_AMOUNT_g	CGM1-6	
<input type="checkbox"/>	7	DW203054:19	-	901000822	51IDYTSICGM:Debrezeit:19:9:	7384135	Default Seed Store	199.0	SEED_AMOUNT_g	CGM1-7	
<input type="checkbox"/>	8	DW203056:19	-	901000823	51IDYTSICGM:Debrezeit:19:11:	7407209	Default Seed Store	116.0	SEED_AMOUNT_g	CGM1-8	

6. Make reservations for a trial.

- a. Go to Manage Germplasm and on the View Lists tab browse to the list for the advanced germplasm – 51IDYTSI<your username> and select the list.
- b. The list now shows available seed inventory. In order to reserve or withdraw it you must view the list in inventory view. From ACTIONS select Inventory view. This view shows you the seed available, the reservations and the withdraws from each seed lot of each entry.
- c. To make reservations select the seedlots you want to reserve from, in our case check all rows, then check ACTIONS>Seed inventory options>Reserve inventory.
- d. In the popup specify the amount to be reserved in g and write a note to the packer:

Seed Preparation




Specify the amount of seed you would like to prepare for each selected lot. (36 selected)

Amount to Reserve Specify amount in SEED_AMOUNT_g
 Prepare all available seed

Notes

Pack 25g of seed in each of four planting packets for a trial with two locations and 2 reps per location

Commit seed withdrawal on saving 

Cancel

Finish

- e. Click Finish and then save the reservations by selecting ACTIONS>Inventory management options>Save changes.

Create a Multi-location trial

1. Set up the study settings

- Select Manage Studies and click Start a New Study
- Enter basic details for a study called PVT1<your username>
- Check the 'Use a previously created study as a template'

MANAGE STUDIES ?

Create Study Save unsaved data

BASIC DETAILS

** indicates a mandatory field*

Study name: *

Description: *

Study type: *

Objective:

Use a previously created study as a template Choose Clear Tabs

- Click Choose and select your seed increase nursery – 51IDYTSI<your username> as a template. You will see that the Study settings were imported from the template. Select new settings as appropriate:

Settings **Germplasm & Checks** **Environments**

STUDY SETTINGS ? Add

TRIAL_YEAR:

Product_concept:

Agro_Ecology:

Responsible_Person:

Trial_Type:

Select All Remove

- On the Germplasm & Checks tab, click add next to Germplasm Descriptors and add variable StockID to the list of germplasm descriptors.
- Click Browse and choose the seed increase list where we have just made the reservations:

2. Specify Germplasm and Environments

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 (DBCv)
<input type="checkbox"/>	ENTRY_NO	Germplasm entry - enumerated (number)
<input type="checkbox"/>	OBS_UNIT_ID	Field observation unit id - assigned (text)
<input type="checkbox"/>	StockID	ID of an inventory deposit

[Remove](#)

Study List
Browse a list to work with.
Total Entries: **36** [View Header](#)

ENTRY_TYPE	GID	DESIGNATION
Test entry	901000816	Assesa:19
Test entry	901000817	327-04:19
Test entry	901000818	DW203050:19
Test entry	901000819	DW203051:19
Test entry	901000820	DW203052:19
Test entry	901000821	DW203053:19

- d. On the Environments tab, enter 2 in the number of environments box and click ok.
- e. In the second location name box, check Show only favorite locations, and select appropriate locations for each environment. Leave the plot size and planting date blank for now since you may not know them.

Specify Environment Details

10 Showing 1 to 2 of 2 entries Manage Locations

Environment	PlotAreaHvst_m2	LOCATION_NAME	SEEDING_DATE
<input type="checkbox"/> 1	<input type="text"/>	Asasa - (AA) <input checked="" type="radio"/> Breeding locations <input type="radio"/> All locations types <input checked="" type="checkbox"/> Show only favorite locations	yyyy-mm-dd <input type="text"/>
<input type="checkbox"/> 2	<input type="text"/>	Alem Tena - (AT) <input type="radio"/> Breeding locations <input checked="" type="radio"/> All locations types <input checked="" type="checkbox"/> Show only favorite locations	yyyy-mm-dd <input type="text"/>

- f. Click save and select the folder Tutorial<your username> to save the study.

3. Generate the trial design

- g. On the Experimental Design tab choose Resolvable Incomplete Block Design, enter 2 replications and block size of 6, then click Generate Design.

- h. On the observations tab you will see that the traits from the template study have been automatically added. Remove trait GY_Calc_tha by checking the box next to the trait and clicking remove.
- i. Click Add opposite Traits and add the leaf runs traits LrS and LrR.
- j. The observations sheet now looks something like this:

ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	StockID	REP_NO	PLOT_NO	BLOCK_NO	DTH	DTM	PHT	MST	PGY	NOTES	LrS	LrR
Test entry	901000825	DW203060-19	11	CGM1-11	1	1	1								
Test entry	901000824	DW203057-19	9	CGM1-9	1	2	1								
Test entry	901000823	DW203056-19	8	CGM1-8	1	3	1								
Test entry	901000839	DW203080-19	24	CGM1-24	1	4	1								
Test entry	901000838	DW203078-19	23	CGM1-23	1	5	1								
Test entry	901000840	DW203081-19	25	CGM1-25	1	6	1								
Test entry	901000848	DW203090-19	33	CGM1-33	1	7	2								

- k. Select ACTIONS>Data collection options>Export study book. Select Observations and click Continue and then click Export to export a zip file with one Excel fieldbook for each environment. These can be transferred to Fieldscorer for data collection.

4. Prepare information file for packing/planting labels

- To obtain fields for packing/planting labels select ACTIONS>Design and planting options>Create planting labels
- Select Observations and click Continue. Choose CSV Data for Output format.
- Select the following fields for the label.

Study Details	Dataset Details	Selected Fields
Responsible_Person	REP_NO	StockID
TRIAL_YEAR	ENTRY_TYPE	ENTRY_NO
Product_concept	GID	DESIGNATION
Agro_Ecology	Parentage	Study Name
Trial_Type		TRIAL_INSTANCE
NREP		LOCATION_NAME
BSIZE		Plot No.
PlotAreaHvst_m2		

- Check Yes for Barcode, and Yes for automatically generated barcodes. Save the settings with code PPL (Packing and planting labels)

Barcode options

Do you need barcodes on your labels? Yes No

Do you want to use automatically generated unique barcodes? Yes No

Specify the name of the label file

Filename: *

Save label settings

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

Preset name

- Click Export Label to get a CSV file with the label fields for each plot.
- Sort the file by ENTRY_NO, TRIAL_INSTANCE and PLOT_NUMBER. Then the labels will be ready for packing the six packets of each entry in turn.

	A	B	C	D	E	F	G	H
1	StockID	ENTRY_NC	DESIGNATION	Study Name	TRIAL_INSTANCE	LOCATION_NAME	Plot No.	Barcode
2	CGM1-1	1	Assesa:19	PVT1CGM		1 Asasa	13	XFTDP5S3JDpeD
3	CGM1-1	1	Assesa:19	PVT1CGM		1 Asasa	56	XFTDPHHub8gIm
4	CGM1-1	1	Assesa:19	PVT1CGM	2	Alem Tena	14	XFTDPU5Obvbgf
5	CGM1-1	1	Assesa:19	PVT1CGM	2	Alem Tena	52	XFTDPyKvH0ZdG
6	CGM1-2	2	327-04:19	PVT1CGM		1 Asasa	23	XFTDPdTgPwBRk
7	CGM1-2	2	327-04:19	PVT1CGM		1 Asasa	62	XFTDPo6zgmOes
8	CGM1-2	2	327-04:19	PVT1CGM	2	Alem Tena	15	XFTDPIklaHBgG
9	CGM1-2	2	327-04:19	PVT1CGM	2	Alem Tena	56	XFTDPOv18666p
10	CGM1-3	3	DW203050:19	PVT1CGM		1 Asasa	35	XFTDPk0TpEJ88
11	CGM1-3	3	DW203050:19	PVT1CGM		1 Asasa	61	XFTDP8X06IXWo
12	CGM1-3	3	DW203050:19	PVT1CGM	2	Alem Tena	23	XFTDPjAVXW7pt
13	CGM1-3	3	DW203050:19	PVT1CGM	2	Alem Tena	40	XFTDPZn7ELKfk
14	CGM1-4	4	DW203051:19	PVT1CGM		1 Asasa	36	XFTDPobpHjx8p
15	CGM1-4	4	DW203051:19	PVT1CGM		1 Asasa	45	XFTDPzflkp4cX
16	CGM1-4	4	DW203051:19	PVT1CGM	2	Alem Tena	8	XFTDPSJA4IUYB
17	CGM1-4	4	DW203051:19	PVT1CGM	2	Alem Tena	68	XFTDPGd2tpjfl

Make a trial fieldbook with an externally generated design

1. Prepare the layout file

- a. Open the CIMMYT nursery fieldbook 51IDYN_008.xls to the Fieldbook sheet.
- b. Copy Plot, Rep, Subblock, Entry from cells G11 to J111 to a new excel file.
- c. Rename the sheet Layout.
- d. Insert a column before Plot with heading TRIAL_INSTANCE and fill the column with 1s.

	A	B	C	D	E	F
1	TRIAL_INSTANCE	Plot	Rep	SubBlock	Entry	
2	1	701	1	1	701	
3	1	702	1	1	702	
4	1	703	1	1	703	
5	1	704	1	1	704	
6	1	705	1	1	705	
7	1	706	1	1	706	
8	1	707	1	1	707	
9	1	708	1	1	708	
10	1	709	1	1	709	
11	1	710	1	1	710	
12	1	711	1	2	711	
13	1	712	1	2	712	

- e. If the trial is to be conducted at multiple sites, add the Plot Plot, Rep, Subblock, Entry values (without headings) for the other sites to the bottom of the list and fill the TRIAL_INSTANCE column with sequential numbers 2,3, 4 for each location. In our case just 2.
- f. Rename Plot to PLOT_CODE, Rep to REP_NO, SubBlock to BLOCK_NO and Entry to ENTRY_CODE.
- g. Add a column before PLOT_CODE and call it PLOT_NO. Fill the column with numbers 1-100 for each location.
- h. Add a column before ENTRY_CODE and call it ENTRY_NO. ENTRY_NO needs to be filled with the number 1 to 50 matching the # column in the list 51IDYT<your username> which you imported earlier. These numbers are in fact the values of ENTRY_CODE – 700 but you need to be sure to get this right and each case may be different. If you use the formula ENTRY_CODE – 700 to compute the ENTRY_NOs you must paste the values (not keep the formula) in the ENTRY_NO column.
- i. If you want row and column layout add columns headed FLD_ROW and FLD_COL and fill them with row and column coordinates. Here we assume a 10x10 layout.
- j. Save the file as 51IDYLayout.xls. The top of the layout file now looks like this:

	A	B	C	D	E	F	G	H	I
1	TRIAL_INSTANCE	PLOT_NO	PLOT_CODE	REP_NO	BLOCK_NO	ENTRY_NO	ENTRY_CODE	FLD_ROW	FLD_COL
2	1	1	701	1	1	1	701	1	1
3	1	2	702	1	1	2	702	1	2
4	1	3	703	1	1	3	703	1	3
5	1	4	704	1	1	4	704	1	4
6	1	5	705	1	1	5	705	1	5
7	1	6	706	1	1	6	706	1	6
8	1	7	707	1	1	7	707	1	7
9	1	8	708	1	1	8	708	1	8
10	1	9	709	1	1	9	709	1	9
11	1	10	710	1	1	10	710	1	10
12	1	11	711	1	2	11	711	2	1
13	1	12	712	1	2	12	712	2	2

2. Set up the study settings

- Select Manage Studies and click Start a New Study
- Enter basic details for a study called PVT1<your username>
- Check the 'Use a previously created study as a template'

MANAGE STUDIES ?



Create Study

Save

BASIC DETAILS

* indicates a mandatory field

Study name: *	<input type="text" value="51IDYTINCGM"/>
Description: *	<input type="text" value="51st International Durum Yield Trial"/>
Study type: *	<input type="text" value="Trial"/>
Objective:	<input type="text" value="Evaluate 51st International Durum Yield Trial"/>

Use a previously created study as a template

Choose

Clear Tabs

- Click Choose and select your seed increase nursery – 51IDYTSI<your username> as a template. You will see that the Study settings were imported from the template. Select new settings as appropriate:

Settings | **Germplasm & Checks** | Environments

STUDY SETTINGS ? Add

<input type="checkbox"/> TRIAL_YEAR:	<input type="text" value="2020"/>
<input type="checkbox"/> Product_concept:	<input type="text" value="DWP - Activities for external collaborations no..."/>
<input type="checkbox"/> Agro_Ecology:	<input type="text" value="E - Early/medium"/>
<input type="checkbox"/> Responsible_Person:	<input type="text" value="Christopher McLaren"/>
<input type="checkbox"/> Trial_Type:	<input type="text" value="Z - Introduction Trial"/>

Select All Remove

3. Specify Germplasm and Environments

- g. On the Germplasm & Checks tab, click add next to Germplasm Descriptors and add variable StockID to the list of germplasm descriptors.
- h. Click Browse and choose the list we imported 40ESWYT<your username>. You will see that the StockID column is blank because we did not load any stock on the Germplasm Import Template.

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"/>	StockID	ID of an inventory deposit

Remove

Study List
Browse a list to work with.
Total Entries: 50 [View Header](#)

ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	StockID
Test entry	901000815	Assesa	1	
Test entry	5780462	CM470-1M-3Y-0M	2	
Test entry	5780466	CM9799-126M-1M-5Y-0M	3	
Test entry	30374	CD22344-A-8M-1Y-1M-1Y-2Y-1M-0Y	4	
Test entry	3828077	CD91Y636-1Y-040M-030Y-1M-0Y-0B-1Y-0B-0MEX	5	
Test entry	7383430	CD551Y002035-099Y-019M-3Y-0M-06Y-0B	6	
Test entry	7383636	CD5510800304T-099Y-051M-33Y-0M-06Y-0B	7	
Test entry	7384124	CD551Y00431S-099Y-032M-4Y-0M-06Y-0B	8	
Test entry	7384135	CD551Y00431S-099Y-032M-53Y-0M-06Y-0B	9	
Test entry	7407142	CD5512Y00834T-017Y-033M-40Y-0M	10	
Test entry	7407209	CD551B00212T-080Y-034M-1Y-0M	11	
Test entry	7407575	CD551B00002S-0133Y-055M-1Y-0M	12	
Test entry	7407576	CD551B00002S-0133Y-055M-2Y-0M	13	

- i. On the Environments tab, enter 2 in the number of environments block and click ok.
- j. In each location name box, check Show only favorite locations, and select appropriate locations for each environment. Leave the plot size and planting date blank for now since you may not know them.

Settings **Germplasm & Checks** Environments

Define Environments

ENVIRONMENT DETAILS Add ENVIRONMENTAL CONDITIONS ?

<input type="checkbox"/>	Name	Description
<input type="checkbox"/>	PlotAreaHvst_m2	Plot area harvested
<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

Showing 1 to 2 of 2 entries

Environment	PlotAreaHvst_m2	LOCATION_NAME	SEEDING_DATE
1	<input type="text"/>	Asasa - (AA) <input checked="" type="radio"/> Breeding locations <input type="radio"/> All locations types <input checked="" type="checkbox"/> Show only favorite locations	<input type="text" value="yyyy-mm-dd"/>
2	<input type="text"/>	Alem Tena - (AT) <input type="radio"/> Breeding locations <input checked="" type="radio"/> All locations types <input checked="" type="checkbox"/> Show only favorite locations	<input type="text" value="yyyy-mm-dd"/>

- k. Click save and select the folder Tutorial<your username> to save the study.

4. Import the trial design

- f. On the Experimental Design tab click 'import' in the line Or import an experimental design. Change the setting to XLS file and click Browse. Choost the layout file you just made – 40ESWYT-Layout.xlsx.
- g. All the variables should map to the sam-named ones from the BMS ontology. IF not you may have miss-typed a column heading or you may want a different one in which case you can map your choice to the matching variable in the BMS ontology. (Do not vary the names of the columns TRIAL_INSTANCE, PLOT_NO and ENTRY_NO these are structural variables for the Study).

The screenshot shows a configuration interface for an experimental design. It is divided into two main sections: 'Environmental Factors' and 'Design Factors'. Each section contains a list of variables with their properties, scales, and methods, along with a 'Re-map' button.

Environmental Factors 1			
TRIAL_INSTANCE → TRIAL_INSTANCE (Required)	Scale: Number	Method: Enumerated	Re-map
Property: Trial instance			

Design Factors 6			
PLOT_NO → PLOT_NO (Required)	Scale: Number	Method: Enumerated	Re-map
Property: Field plot			
PLOT_CODE → PLOT_CODE	Scale: Code of PLOT_CODE	Method: Assigned	Re-map
Property: Field plot			
REP_NO → REP_NO	Scale: Number	Method: Enumerated	Re-map
Property: Replication factor			
BLOCK_NO → BLOCK_NO	Scale: Number	Method: Enumerated	Re-map
Property: Blocking factor			
FLD_ROW → FLD_ROW	Scale: Number	Method: Assigned	Re-map
Property: Row in layout			
FLD_COL → FLD_COL	Scale: Number	Method: Assigned	Re-map
Property: Column in layout			

[Cancel](#) [Next](#)

- h. Click Next to see a review of design details. IF they are correct click Finish.

5. Review the traits

- a. On the observation sheet the traits from the template study will be shown. The Fiedbook from CIMMYT has the traits: Heading, Height, Lodging, Grain-Yield, 1000-Kernel, Agronomic-Score, Check-Mark. DTH and PHT are in the fieldbook already. Clcik the Add button opposite Traits and type Lodging, add Lodge_E_pct as this seems to be the one that matches the CIMMYT trait. Grain-Yield g/plot is there already as GYLD, type 1000 in the search box and the variable that matches 100-Kernel seems to be GW_M_g100grn so add this to the fieldbook. Your code for Agronomic Score is AgrSc. If this is the same as CIMMYT's variable add this to the fieldbook.
- b. The final variable Check-Mark, I would guess is a selection variable, not a trait. So click the Add button opposite SELECTIONS and add the variable called SelChkMark which is there.
- c. Now you can remove traits that were inherited from the template – like GY-Calc_tha and MC if you want and you can add more variable you would like to measure.

d. So finally the Observation sheet looks like:

The screenshot shows a software interface for managing observations. At the top, there are sections for 'TRAITS' and 'SELECTIONS'. The 'TRAITS' section contains a list of variables with checkboxes and descriptions:

Name	Description	Input Variables
<input type="checkbox"/> DTH	Heading time-BY-Hd D555 days Computation-IN-day	
<input type="checkbox"/> DTM	Maturity time-BY-Mat D587 DT Computation-IN-day	
<input type="checkbox"/> PHT	PH_M_cm	
<input type="checkbox"/> MST	Grain moisture content-BY-GMol Estimation-IN-%	
<input type="checkbox"/> PGY	Grain yield-BY-GY Measurement-IN-g/plot	
<input type="checkbox"/> GY_Calc_tha	Grain yield-BY-GY Computation (t/ha)-IN-t/ha	GY_M_gPlot, GMol_E_pct, PlotAreaHvst_m2
<input type="checkbox"/> NOTES	Field notes - observed (text)	

Below the traits list, there are 'Observations' and 'Batch Actions' sections. The 'Observations' section includes a dropdown for 'Select Environment: 1 - Asasa' and a 'Filter by status: All' dropdown. The 'Batch Actions' section has 'ACCEPTED' and 'PENDING' buttons. At the bottom, a data table is displayed with the following columns: ENTRY_TYPE, GID, DESIGNATION, ENTRY_NO, StockID, FLD_ROW, FLD_COL, PLOT_NO, REP_NO, BLOCK_NO, PLOT_CODE, DTH, DTM, PHT, MST, PGY, GY_Calc_tha, and NOTES. The table contains 7 rows of test entry data.

ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	StockID	FLD_ROW	FLD_COL	PLOT_NO	REP_NO	BLOCK_NO	PLOT_CODE	DTH	DTM	PHT	MST	PGY	GY_Calc_tha	NOTES
Test entry	901000815	Assesa	1		1	1	1	1	1	701							
Test entry	5780462	CM470-1M-3Y-0M	2		1	2	2	1	1	702							
Test entry	5780466	CM9799-126M-1M-5Y-0M	3		1	3	3	1	1	703							
Test entry	30374	CD22344-A-8M-1Y-1M-1Y-2Y-1M-0Y	4		1	4	4	1	1	704							
Test entry	3828077	CD91Y636-1Y-040M-030Y-1M-0Y-0B-1Y-0B-0MEX	5		1	5	5	1	1	705							
Test entry	7383430	CD5511Y002035-099Y-019M-3Y-0M-06Y-0B	6		1	6	6	1	1	706							
Test entry	7383636	CD5510800304T-099Y-051M-33Y-0M-	7		1	7	7	1	1	707							

e. You can now export the fieldbook for data collection.