

BMS Training – Exercises for Bread Wheat

Contents

- Getting Started - Bread Wheat 3
 - 1. Germplasm Search 3
 - 2. List management..... 3
- Design a crossing nursery 4
 - 1. Create nursery..... 4
 - 2. Germplasm and Checks..... 4
 - 3. Environments 4
 - 4. Experimental Design 5
 - 5. Observations tab..... 6
- Create a fieldmap..... 6
 - 1. Map Details 6
 - 2. Field Details..... 6
 - 3. Assign Entries to the plots in the field 7
- Make crosses using a Crossing Template..... 8
 - 1. Fill in a Crossing Template 8
 - 2. Import your crossing template 9
 - 3. Look at some crossing results 10
- Make an F1 Nursery to advance the crosses 12
 - 1. Create a nursery..... 12
 - 2. Specify Layout and Traits 12
 - 3. Advance your germplasm 14
- F2 Nursery – Measurements and selections..... 15
 - 1. Create nursery..... 15
 - 2. Specify Layout 15
 - 3. Specify Layout 16
 - 4. Data collection 16
 - 5. Data import, review and cleaning..... 18
 - 6. Make selections 20
- Import Germplasm..... 22
 - 1. Prepare the Germplasm Import Template 22

| | |
|--|----|
| 2. Use Germplasm Import to import the template..... | 24 |
| Seed Increase Nursery | 25 |
| 1. Create a seed increase nursery for the imported seed. | 25 |
| 2. Collect some data..... | 27 |
| 3. Calculate the derived variable | 28 |
| 4. Advance the Study | 29 |
| 5. Add Inventory | 30 |
| 6. Make reservations for a trial..... | 31 |
| Create a Multi-location trial..... | 32 |
| 1. Set up the study settings..... | 32 |
| 2. Specify Germplasm and Environments | 33 |
| 3. Generate the trial design | 34 |
| 4. Prepare information file for packing/planting labels..... | 35 |
| Make a trial fieldbook with an externally generated design | 36 |
| 1. Prepare the layout file | 36 |
| 2. Set up the study settings..... | 37 |
| 3. Specify Germplasm and Environments | 38 |
| 4. Import the trial design | 39 |
| 5. Review the traits | 39 |

Getting Started - Bread Wheat

1. Germplasm Search

- a. Log on to your account on BMS
- b. Select Wheat Tutorial Program from the Workbench.
- c. Germplasm Search
 - a. Click on View Germplasm tab in Manage Germplasm
 - b. Enter Kingfisher in the search box and click search
 - c. Click on the name in the results page
 - d. Click on Names in the Germplasm Details Page
 - e. Click on pedigree.
 - f. Now enter BW162664 in the search box – search
 - g. Click on the name in the results, then pedigree, then view pedigree.
 - h. Now try it for BW180004.

2. List management

- a. View Lists
 - a. Click on the View Lists tab in Manage Germplasm
 - b. Click Browse
 - c. Select list 2018 F1 Lines
 - d. Click on one of the cross names and then view the pedigree.
 - e. Click Browse again
 - f. Select list 2018 Crossing Block
- b. Make a new list
 - a. Highlight any five lines by checking in the select box for each
 - b. Right-click on the green space in the CROSS column and select “Add selected entries to a new list”
 - c. Click on the 2018 F1 Lines 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**

MANAGE STUDIES My Programs ? mcrimi

Create Study

[Save](#) [unsaved data](#) [Return to Manage Studies](#)

** indicates a mandatory field*

Study name: [📄](#) **Save in:** Mariano Crimi [Change Folder](#)

Description: **Created by:** Mariano Crimi

Study type: **Creation date:** [📅](#)

Objective:

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.

2. Germplasm and Checks

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

▼ 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 [Actions](#)

Browse a list to work with.

Total Entries: 10 [View Header](#)

| 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 |

EDIT CHECK

Test entry

[Clear List](#)

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 | XFTDPjZcjAt10 |

- 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)

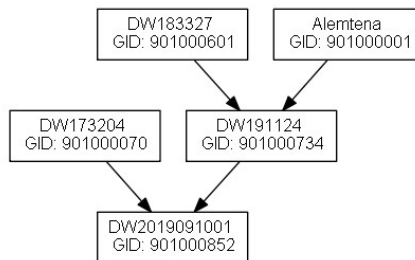
BASIC DETAILS
Preferred Name: DW2019091001 Creation Date: 20191000 GID: 901000852
Creation Method: Three-way cross Location: Kulumsa Reference:
 Grouped Line Group Id (MGID): 0

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

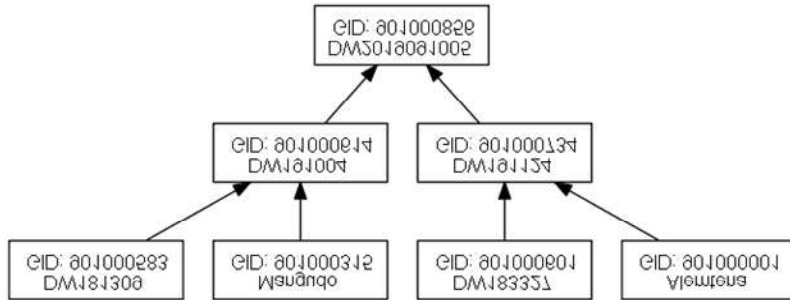
NAMES

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

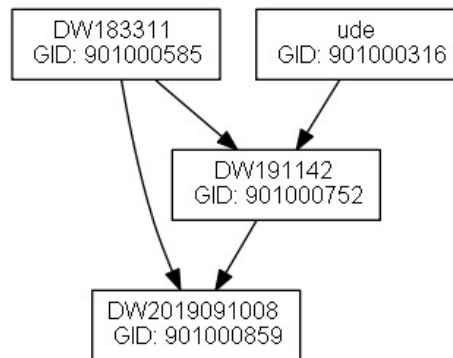
▶ NAMES

▼ 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: * TutorialCGM [Change Folder](#)

Created by: * Mariano Crimi

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 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.

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

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

Back
Finish

- Review the pending F2 lines and select Finish.

Advance study ✕

REVIEW ADVANCED LINES

▼ Advance List Entries Actions

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

Back
Finish

- 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. Specify study type to Nursery
- d. Go to **Germplasm and Checks**
- e. Browse for the list that you created in the previous exercise 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: ?

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

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 (**Better DTH and SrS and SRL etc**)
- I've also added NPSEL (Number of plants selected) as my Selection variable

MANAGE STUDIES

F2 Nursery MC

Return to Manage Studies

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

Observations

Define Observation Details

TRAITS Add SELECTIONS Add

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

Remove

Observations

ACCEPTED PENDING

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

- 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

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

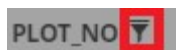


- In the Accepted view, you will only see the observations that have been Accepted
 - In the **Pending view**, you will see all the incoming observations that haven't been accepted yet
- We will now Accept of the pending data.
- You can do this on a cell by cell basis
 - If you right click on a given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

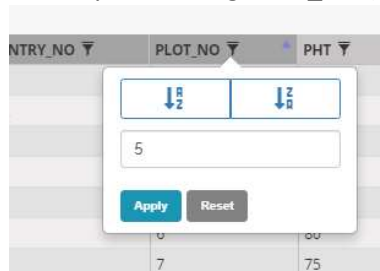
The screenshot shows the 'Observations' interface. At the top, there are 'ACCEPTED' and 'PENDING' toggle buttons, with 'PENDING' selected. Below this are 'Accept' and 'Discard' buttons. The main area contains a table with columns: TRIAL_INSTANCE, ENTRY_TYPE, GID, DESIGNATION, ENTRY_NO, PLOT_NO, PHT,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

| 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 |

- You can also filter Accept a subset of the pending data
- 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. Prepare the Germplasm Import Template

- a. Under Information Management select Germplasm Import (Only available for Admins)
- b. Download a template by clicking on the message
- c. Open the template in excel make the Observation Sheet the active sheet
- d. Open the file 40ESWYT_024.xls which comes from CIMMYT make the FieldBook sheet active
- e. Copy the selection histories for the entries in rep 1 from cells E12 to E61 to clipboard (including the blank cell for the local check)
- f. Paste them into the Designation column (column B) of the Observation Sheet of the Germplasm Import Template.
- g. Enter the name of the Local check in the blank cell B2 (I chose Kingfisher)
- h. Copy the corresponding cross names from Cells D12 to D61. Paste them under CROSS in cell D2.
- i. Copy the Origins from F12 to F61 and paste them under SOURCE in E2.
- j. Copy the Entry number from J2 to J61 under ENTRY_CODE in cell F2
- k. Fill column A of the Observation sheet of the Germplasm Import Template with sequential ENTRY-Nos, from 1 to 50 in this case.
- l. On the Description sheet enter the name of the list 40ESWYT<Your username> in cell B2 and a description and date below.
- m. 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 | 40ESWYTCGM | | Enter a list name here, or add it when saving in the BMS | | | |
| 2 | LIST DESCRIPTION | Germplasm for 40th ESWYT | | Enter a list description here, or add it when saving in the BMS | | | |
| 3 | LIST DATE | 20190924 | | 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 |

- n. 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 |

- o. Copy the 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.
- p. 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 BW202001 for a new year.
- q. 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 |

- r. We can suppose CIMMYT supplied us with 8 packets of seed for each entry for planting two reps at four 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 8 since we have 8 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 |

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

| ENTRY | DESIGNATION | GID | CROSS | SOURCE | NTRY COD | GENOTYPE | SEED_AMOUNT_Packets | STOCKID | NOTE |
|-------|--|---------------------|-------------|---------|----------|----------|---------------------|---------|------|
| 1 | Kingfisher | | LOCAL CHECK | W0 | 101 | BW202001 | 8 | | |
| 2 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-099Y- | MUCUY | | MX18-19 | WTEST0 | 102 | BW202002 | 8 | |
| 3 | CMSS10Y00374S-099Y-099M-1WGY-0B | KACHU/SAUAL/4/A | | MX18-19 | WTEST0 | 103 | BW202003 | 8 | |
| 4 | CMSS11Y00507S-099Y-099M-099NJ-099NJ-191 | NELOKI//SOKOLL/E | | MX18-19 | WTEST0 | 104 | BW202004 | 8 | |
| 5 | CMSS12Y00070S-099Y-099M-099NJ-099NJ-211 | BORL14//BECARD/I | | MX18-19 | W40ES2 | 105 | BW202005 | 8 | |
| 6 | CMSS12Y00241S-099Y-099M-099NJ-099NJ-1Y | KACHU//WBLL1*2/ | | MX18-19 | W40ES2 | 106 | BW202006 | 8 | |
| 7 | CMSS12Y00711T-099TOPM-099Y-099M-099NJ | FRANCOLIN #1//WB | | MX18-19 | W40ES2 | 107 | BW202007 | 8 | |
| 8 | CMSS12Y00831T-099TOPM-099Y-099M-099NJ | SAUAL/3//ACHTAR* | | MX18-19 | W40ES2 | 108 | BW202008 | 8 | |
| 9 | CMSS12Y00966T-099TOPM-099Y-099M-099NJ | MUCUY/3//PBW343* | | MX18-19 | W40ES2 | 109 | BW202009 | 8 | |
| 10 | CMSS12B00016S-099M-099NJ-099NJ-9Y-0WG | FRET2*2//SHAMA//I | | MX18-19 | W40ES2 | 110 | BW202010 | 8 | |
| 11 | CMSS12B00159S-099M-099NJ-099NJ-8Y-0WG | ITP40//AKURI//FRK | | MX18-19 | W40ES2 | 111 | BW202011 | 8 | |
| 12 | CMSS12B00171S-099M-099NJ-099NJ-17Y-0WG | FRINCLN*2//TECUE #1 | | MX18-19 | W40ES2 | 112 | BW202012 | 8 | |
| 13 | CMSS12B00561S-099M-099NJ-099NJ-3Y-0WG | SITL/3//KACHU//W | | MX18-19 | W40ES2 | 113 | BW202013 | 8 | |
| 14 | CMSS12B00644T-099TOPY-099M-099NJ-099NJ | COPIO*2//MUCUY | | MX18-19 | W40ES2 | 114 | BW202014 | 8 | |
| 15 | CMSS12B00713T-099TOPY-099M-099NJ-099NJ | WBLL1*2//BRAMBLI | | MX18-19 | W40ES2 | 115 | BW202015 | 8 | |
| 16 | CMSS12B00767T-099TOPY-099M-099NJ-099NJ | NADI#1*2//3//MUTU | | MX18-19 | W40ES2 | 116 | BW202016 | 8 | |
| 17 | CMSS12B00767T-099TOPY-099M-099NJ-099NJ | NADI#1*2//3//MUTU | | MX18-19 | W40ES2 | 117 | BW202017 | 8 | |
| 18 | CMSS12B00871T-099TOPY-099M-099NJ-099NJ | MUCUY//STLN//MUN | | MX18-19 | W40ES2 | 118 | BW202018 | 8 | |

- t. Save the template as 40ESWYT<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. Add germplasm details:

ADD GERMLASM 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 ?

- c. And specify “Select existing germplasm whenever found”. Click Finish
- d. 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 **CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY** . 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 |
|---|-----------|---|
| CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY | 6341870 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M |
| BW182002 | 900000053 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY |
| BW182176 | 900000230 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY |
| BW172004 | 900001694 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY |
| BW172304 | 800001194 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY |


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

- e. Select the most appropriate match, select Use this match for oterh instancves and click continue.
- f. Save the list in the Tutorial<Your username> when done.

Seed Increase Nursery

1. Create a seed increase nursery for the imported seed.
 - a. From Manage Studies click Start a New Study
 - b. Give the Study name 40ESWYTSI<Your username> and fill in some details.
 - c. Don't check 'Use previous study as template.'

MANAGE STUDIES ?

 **40ESWYTSICGM** Save

▼ BASIC DETAILS

** indicates a mandatory field*

| | |
|-----------------------|--|
| Study name: * | 40ESWYTSICGM |
| Description: * | <input type="text" value="Seed increase nursery for 40ESWYT"/> |
| Study type: * | Nursery |
| Objective: | <input type="text" value="Seed increase nursery for 40ESWYT"/> |

- 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

| | |
|---|---|
| <input type="checkbox"/> Product_concept: | <input type="text" value="BWP - Activities for external collaborations no..."/> |
| <input type="checkbox"/> Responsible_Person: | <input type="text" value="Christopher McLaren"/> |
| <input type="checkbox"/> TRIAL_YEAR: | <input type="text" value="2019"/> |
| <input type="checkbox"/> Trial_Type: | <input type="text" value="Z- Introduction Trial"/> |
| <input type="checkbox"/> Agro_Ecology: | <input type="text" value="E - Early/medium"/> |

Select All Remove

- e. On the Germplasm Tab select 40ESWYT<Your username>
- f. On the environment tab check 'Show only favorite locations' and select Kulumsa.
- g. Click Add opposite Environment Details and add the variables SEEDING _DATE and PlotAreaHvst_m2.

Specify Environment Details

10 Showing 1 to 1 of 1 entries

| 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

| <input type="checkbox"/> 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"/> MC | Grain moisture content-BY-GMoi Estimation-IN-% | |
| <input type="checkbox"/> GYLD | 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 |
| <input type="checkbox"/> NOTES | Field notes - observed (text) | |

Remove

SELECTIONS ? Add

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

Remove

| ENTRY_TYPE | GID | DESIGNATION | ENTRY_NO | PLOT_NO | DTH | DTM | PHT | MC | GYLD | GY_Calc_tha | NOTES | NPSEL |
|------------|---------|---|----------|---------|-----|-----|-----|----|------|-------------|-------|-------|
| Test entry | 1848 | Kingfisher | 1 | 1 | | | | | | | | |
| Test entry | 6341870 | CMS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY | 2 | 2 | | | | | | | | |
| Test entry | 6933502 | CMS10Y00374S-099Y-099M-1WGY-0B | 3 | 3 | | | | | | | | |
| Test entry | 7400769 | CMSA11Y00507S-099Y-099M-099NJ-099NJ-19WGY-0B | 4 | 4 | | | | | | | | |
| Test entry | 8048669 | CMS12Y00070S-099Y-099M-099NJ-099NJ-21Y-0WGY | 5 | 5 | | | | | | | | |
| Test entry | 8049004 | CMS12Y00241S-099Y-099M-099NJ-099NJ-1Y-0WGY | 6 | 6 | | | | | | | | |
| Test entry | 8049754 | CMS12Y00711T-099TOPM-099Y-099M-099NJ-099NJ-22Y-0WGY | 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 - 40ESWYTSICGM-1_KU_PLOT_40ESWYTSICGM-PLOTDATA.xls
- Add some data to the fieldbook. You can copy it from file 40ESWYTSI_data.csv. Make sure the data goes to the correct columns so the fieldbook should look like this:

| G | H | I | J | K | L | M | N |
|-----|-----|-----|----|------|------------|-------------|-------|
| DTH | DTM | PHT | MC | GYLD | GY_Calo_th | NOTES | NPSEL |
| 70 | 119 | 95 | 15 | 1357 | | Good Aspect | 29 |
| 74 | 121 | 90 | 14 | 1082 | | | 25 |
| | 122 | 85 | 13 | 1316 | | Poor Aspect | 0 |
| 68 | 118 | 95 | 15 | 1231 | | Diseased | 0 |
| 70 | 116 | 80 | 15 | 610 | | | 36 |
| | 125 | 100 | 13 | 1496 | | Good Aspect | 37 |
| 70 | 119 | 90 | 14 | 1728 | | | 31 |
| 70 | 117 | 85 | 13 | 884 | | | 21 |
| 68 | 116 | 90 | 14 | 526 | | | 22 |
| 73 | 118 | 90 | 13 | 848 | | Poor Aspect | 0 |
| 73 | 119 | 95 | 14 | 786 | | Good Aspect | 46 |
| 73 | 116 | 85 | 14 | 554 | | | 27 |
| 71 | 119 | 95 | 15 | 968 | | | 50 |
| 71 | 117 | 90 | 14 | 1186 | | Diseased | 0 |
| 75 | 118 | 95 | 14 | 1585 | | | 44 |
| 75 | 121 | 95 | 14 | 1014 | | Poor Aspect | 0 |
| 72 | 117 | 80 | 14 | 981 | | | 43 |
| 70 | 118 | 85 | 13 | 1051 | | | 38 |
| | 120 | 80 | 14 | 1124 | | Diseased | 0 |
| 74 | 119 | 85 | 15 | 848 | | | 36 |
| 72 | 119 | 95 | 14 | 1508 | | | 37 |
| 73 | 124 | 95 | 14 | 1373 | | Poor Aspect | 0 |
| 70 | 119 | 90 | 14 | 1311 | | Good Aspect | 49 |
| 71 | 121 | 95 | 13 | 1252 | | | 45 |
| 71 | 118 | 95 | 15 | 1206 | | | 28 |
| | 122 | 100 | 13 | 1330 | | | 34 |
| 71 | 120 | 95 | 14 | 1000 | | Poor Aspect | 0 |
| 72 | 119 | 100 | 13 | 906 | | | 29 |
| 71 | 118 | 90 | 14 | 940 | | | 26 |
| 71 | 116 | 85 | 13 | 784 | | | 28 |
| 73 | 118 | 85 | 13 | 966 | | Poor Aspect | 0 |
| 67 | 119 | 95 | 15 | 1151 | | Diseased | 0 |
| | 119 | 100 | 15 | 612 | | | 32 |
| | 116 | 90 | 14 | 374 | | Poor Aspect | 0 |
| | 125 | 100 | 13 | 1412 | | | 24 |
| 71 | 117 | 85 | 15 | 631 | | | 36 |
| 74 | 120 | 100 | 15 | 1118 | | Good Aspect | 21 |
| | 122 | 95 | 15 | 1294 | | | 31 |
| 71 | 118 | 95 | 13 | 1216 | | | 38 |
| 72 | 121 | 95 | 13 | 1255 | | Diseased | 0 |
| 70 | 118 | 85 | 13 | 1169 | | | 49 |
| 71 | 119 | 85 | 14 | 1001 | | | 31 |
| 71 | 120 | 90 | 15 | 863 | | | 41 |
| | 118 | 95 | 14 | 875 | | | 45 |
| 70 | 116 | 90 | 13 | 1040 | | | 29 |
| 75 | 120 | 110 | 13 | 1886 | | Poor Aspect | 0 |
| 70 | 116 | 100 | 15 | 607 | | | 42 |
| 70 | 119 | 100 | 13 | 1132 | | Diseased | 0 |
| 70 | 118 | 90 | 13 | 751 | | | 43 |
| 70 | 116 | 90 | 15 | 897 | | Good Aspect | 28 |

- Save the fieldbook.

- d. From ACTIONS>Data collection options>Import observations choose Observations and click Continue
- e. Browse for the fieldbook file you just saved and click Import.
- f. 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.
- g. When the data are acceptable click Accept to approve the data.

Observations ACCEPTED PENDING

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

► Batch Actions ☰

| ENTRY_TYPE | GID | DESIGNATION | ENTRY_NO | PLOT_NO | DTH | DTM | PHT | MC | GYLD | GY_Calc_tha | NOTES | NPSEL |
|------------|---------|---|----------|---------|-----|-----|-----|----|------|-------------|-------------|-------|
| Test entry | 1848 | Kingfisher | 1 | 1 | 70 | 119 | 95 | 15 | 1357 | | Good Aspect | 29 |
| Test entry | 6341870 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY | 2 | 2 | 74 | 121 | 90 | 14 | 1082 | | | 25 |
| Test entry | 6933502 | CMSS10Y00374S-099Y-099M-1WGY-0B | 3 | 3 | | 122 | 85 | 13 | 1316 | | Poor Aspect | 0 |
| Test entry | 7400769 | CMSA11Y00507S-099Y-099M-099NJ-099NJ-19WGY-0B | 4 | 4 | 68 | 118 | 95 | 15 | 1231 | | Diseased | 0 |
| Test entry | 8048669 | CMSS12Y00070S-099Y-099M-099NJ-099NJ-21Y-0WGY | 5 | 5 | 70 | 116 | 80 | 15 | 610 | | | 36 |
| Test entry | 8049004 | CMSS12Y00241S-099Y-099M-099NJ-099NJ-1Y-0WGY | 6 | 6 | | 125 | 100 | 13 | 1496 | | Good Aspect | 37 |

- h. On the Environments tab enter the harvest plot size 10m2 and the seeding date 20190505. Click Save.

3. Calculate the derived variable

- a. Open the observation sheet. GY_Calc_tha is shown in green because it can be calculated from the existing variables.
- 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 - Kulumsa Filter by status: All Show Categorical Description

► Batch Actions ☰

| ENTRY_TYPE | GID | DESIGNATION | ENTRY_NO | PLOT_NO | DTH | DTM | PHT | MC | GYLD | GY_Calc_tha | NOTES | NPSEL |
|------------|---------|---|----------|---------|-----|-----|-----|----|------|-------------|-------------|-------|
| Test entry | 1848 | Kingfisher | 1 | 1 | 70 | 119 | 95 | 15 | 1357 | 1.357 | Good Aspect | 29 |
| Test entry | 6341870 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY | 2 | 2 | 74 | 121 | 90 | 14 | 1082 | 1.0947 | | 25 |
| Test entry | 6933502 | CMSS10Y00374S-099Y-099M-1WGY-0B | 3 | 3 | | 122 | 85 | 13 | 1316 | 1.347 | Poor Aspect | 0 |
| Test entry | 7400769 | CMSA11Y00507S-099Y-099M-099NJ-099NJ-19WGY-0B | 4 | 4 | 68 | 118 | 95 | 15 | 1231 | 1.231 | Diseased | 0 |
| Test entry | 8048669 | CMSS12Y00070S-099Y-099M-099NJ-099NJ-21Y-0WGY | 5 | 5 | 70 | 116 | 80 | 15 | 610 | 0.61 | | 36 |
| Test entry | 8049004 | CMSS12Y00241S-099Y-099M-099NJ-099NJ-1Y-0WGY | 6 | 6 | | 125 | 100 | 13 | 1496 | 1.5312 | Good Aspect | 37 |
| Test entry | 8048754 | CMSS12Y00711T-099TOPM-099Y-099M-099Y-40M-0WGY | 7 | 7 | 70 | 119 | 90 | 14 | 1338 | 1.7482 | | 31 |

4. Advance the Study

- From ACTION>Advance study options>Advance Study
- 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

- 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 name of the source line.

Advance study ✕

REVIEW ADVANCED LINES

▼ Advance List Entries

Total Entries: 36 Selected: 0

| ✓ | ENTRY_NO | DESIGNATION | CROSS | GID | SEED_SOURCE |
|--------------------------|----------|---|-------|---------|----------------|
| <input type="checkbox"/> | 1 | KINGFISHER:19 | | Pending | 40ESWYTSICGM:f |
| <input type="checkbox"/> | 2 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY:19 | | Pending | 40ESWYTSICGM:f |
| <input type="checkbox"/> | 3 | CMSS12Y00070S-099Y-099M-099NJ-099NJ-21Y-0WGY:19 | | Pending | 40ESWYTSICGM:f |
| <input type="checkbox"/> | 4 | CMSS12Y00241S-099Y-099M-099NJ-099NJ-1Y-0WGY:19 | | Pending | 40ESWYTSICGM:f |
| <input type="checkbox"/> | 5 | CMSS12Y00711T-099TOPM-099Y-099M-099NJ-099NJ-22Y-0WGY:19 | | Pending | 40ESWYTSICGM:f |
| <input type="checkbox"/> | 6 | CMSS12Y00831T-099TOPM-099Y-099M-099NJ-099NJ-29Y-0WGY:19 | | Pending | 40ESWYTSICGM:f |
| <input type="checkbox"/> | 7 | CMSS12Y00966T-099TOPM-099Y-099M-099NJ-099NJ-19Y-0WGY:19 | | Pending | 40ESWYTSICGM:f |
| <input type="checkbox"/> | 8 | CMSS12B00159S-099M-099NJ-099NJ-8Y-0WGY:19 | | Pending | 40ESWYTSICGM:f |

- Click Finish and save the list of advanced lines as 40ESWYTSI<Your username> in the Tutorial<Your username> folder.

5. Add Inventory

- g. In the study 40ESWYTSI<Your username>, on the Advance List tab, click Advance List Actions>Generate Stock List.
- h. Enter Your username in the Stock ID prefix box.
- i. Click Continue to obtain an Stock list tab with generated StockIDs
- j. Click Stock List Actions>Export inventory file
- k. Open the exported file. It has columns for seed storage LOCATION, LOCATION_ABBR and SEED_AMOUNT_G. Add seed amounts.
- l. 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.
- m. The following inventory units are available (more can be added):

| | |
|---------------------|--|
| 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) |
- n. Change the SEED_AMOUNT_G to SEED_AMMOUNT_KG and add some values:

| A | B | C | D | E | F | G | H | I | J |
|----------|---|-------|-----------|-----------------------------|----------|---------------|----------------|---------|---------|
| ENTRY_NO | DESIGNATION | CROSS | GID | SEED_SOURCE | LOCATION | LOCATION_ABBR | SEED_AMOUNT_KG | STOCKID | COMMENT |
| 1 | KINGFISHER:19 | - | 900006238 | 40ESWYTSICGM:Kulumsa:19:1: | | DSS | 1.0 | CGM1-1 | |
| 2 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY:19 | - | 900006239 | 40ESWYTSICGM:Kulumsa:19:2: | | DSS | 1.0 | CGM1-2 | |
| 3 | CMSS12Y00070S-099Y-099M-099NJ-099NJ-21Y-0WGY:19 | - | 900006240 | 40ESWYTSICGM:Kulumsa:19:5: | | DSS | 0.8 | CGM1-3 | |
| 4 | CMSS12Y00241S-099Y-099M-099NJ-099NJ-1Y-0WGY:19 | - | 900006241 | 40ESWYTSICGM:Kulumsa:19:6: | | DSS | 1.1 | CGM1-4 | |
| 5 | CMSS12Y00711T-099TOPM-099Y-099M-099NJ-099NJ-22Y-0WGY:19 | - | 900006242 | 40ESWYTSICGM:Kulumsa:19:7: | | DSS | 0.9 | CGM1-5 | |
| 6 | CMSS12Y00831T-099TOPM-099Y-099M-099NJ-099NJ-29Y-0WGY:19 | - | 900006243 | 40ESWYTSICGM:Kulumsa:19:8: | | DSS | 0.9 | CGM1-6 | |
| 7 | CMSS12Y00966T-099TOPM-099Y-099M-099NJ-099NJ-19Y-0WGY:19 | - | 900006244 | 40ESWYTSICGM:Kulumsa:19:9: | | DSS | 1.4 | CGM1-7 | |
| 8 | CMSS12B00159S-099M-099NJ-099NJ-8Y-0WGY:19 | - | 900006245 | 40ESWYTSICGM:Kulumsa:19:11: | | DSS | 0.6 | CGM1-8 | |
| 9 | CMSS12B00171S-099M-099NJ-099NJ-17Y-0WGY:19 | - | 900006246 | 40ESWYTSICGM:Kulumsa:19:12: | | DSS | 0.7 | CGM1-9 | |
| 10 | CMSS12B00561S-099M-099NJ-099NJ-3Y-0WGY:19 | - | 900006247 | 40ESWYTSICGM:Kulumsa:19:13: | | DSS | 0.8 | CGM1-10 | |
| 11 | CMSS12B00713T-099TOPY-099M-099NJ-099NJ-11Y-0WGY:19 | - | 900006248 | 40ESWYTSICGM:Kulumsa:19:15: | | DSS | 0.6 | CGM1-11 | |
| 12 | CMSS12B00767T-099TOPY-099M-099NJ-099NJ-35Y-0WGY:19 | - | 900006249 | 40ESWYTSICGM:Kulumsa:19:17: | | DSS | 0.8 | CGM1-12 | |
| 13 | CMSS12B00871T-099TOPY-099M-099NJ-099NJ-46Y-0WGY:19 | - | 900006250 | 40ESWYTSICGM:Kulumsa:19:18: | | DSS | 1.1 | CGM1-13 | |
| 14 | CMSS12Y00043S-099Y-099M-099Y-2M-0WGY:19 | - | 900006251 | 40ESWYTSICGM:Kulumsa:19:20: | | DSS | 0.9 | CGM1-14 | |

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

Stock List: **40ESWYTSI** Notes: [View List Details](#)

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

100 Showing 1 to 36 of 36 entries

| ENTRY_NO | DESIGNATION | CROSS | GID | SEED_SOURCE | GROUP ID | LOCATION | AMOUNT | UNITS | STOCKID | COMMENT |
|--------------------------|---|-------|-----------|----------------------------|----------|--------------------|--------|----------------|---------|---------|
| <input type="checkbox"/> | 1 KINGFISHER:19 | - | 900006238 | 40ESWYTSICGM:Kulumsa:19:1: | 1848 | Default Seed Store | 1.01 | SEED_AMOUNT_kg | CGM1-1 | |
| <input type="checkbox"/> | 2 CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY:19 | - | 900006239 | 40ESWYTSICGM:Kulumsa:19:2: | - | Default Seed Store | 0.988 | SEED_AMOUNT_kg | CGM1-2 | |
| <input type="checkbox"/> | 3 CMSS12Y00070S-099Y-099M-099NJ-099NJ-21Y-0WGY:19 | - | 900006240 | 40ESWYTSICGM:Kulumsa:19:5: | - | Default Seed Store | 0.781 | SEED_AMOUNT_kg | CGM1-3 | |
| <input type="checkbox"/> | 4 CMSS12Y00241S-099Y-099M-099NJ-099NJ-1Y-0WGY:19 | - | 900006241 | 40ESWYTSICGM:Kulumsa:19:6: | - | Default Seed Store | 1.09 | SEED_AMOUNT_kg | CGM1-4 | |
| <input type="checkbox"/> | 5 CMSS12Y00711T-099TOPM-099Y-099M-099NJ-099NJ-22Y-0WGY:19 | - | 900006242 | 40ESWYTSICGM:Kulumsa:19:7: | - | Default Seed Store | 0.909 | SEED_AMOUNT_kg | CGM1-5 | |

6. Make reservations for a trial.

- p. Go to Manage Germplasm and on the View Lists tab browse to the list for the advanced germplasm – 40ESWYTSI<Your username> and select the list.
- q. 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.
- r. 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.
- s. 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_kg
 Prepare all available seed

Notes

Commit seed withdrawal on saving ?

Cancel **Finish**

- t. 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

BASIC DETAILS

** indicates a mandatory field*

| | |
|----------------|--|
| Study name: * | <input type="text" value="PVT1CGM"/> |
| Description: * | <input type="text" value="CGMs PVT1 trial for selected imported lines"/> |
| Study type: * | <input type="text" value="Trial"/> |
| Objective: | <input type="text" value="Preliminary trial to evaluate selected imported lines"/> |

Use a previously created study as a template

Choose

Clear Tabs

- Click Choose and select your seed increase nursery – 40ESWYTSI<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="BW1 - Medium to late pan-bread varieties for ..."/> |
| <input type="checkbox"/> Agro_Ecology: | <input type="text" value="L - Medium/late"/> |
| <input type="checkbox"/> Responsible_Person: | <input type="text" value="Christopher McLaren"/> |
| <input type="checkbox"/> Trial_Type: | <input type="text" value="P - Preliminary Variety"/> |

Select All [Remove](#)

2. Specify Germplasm and Environments

- 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:

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 | ENTRY_NO | StockID |
|------------|-----------|-----------------------------------|----------|---------|
| Test entry | 900006238 | KINGFISHER:19 | 1 | CGM1-1 |
| Test entry | 900006239 | CMSS07Y01083T-099TOPM-099Y-099M | 2 | CGM1-2 |
| Test entry | 900006240 | CMSS12Y00070S-099Y-099M-099NJ-099 | 3 | CGM1-3 |
| Test entry | 900006241 | CMSS12Y00241S-099Y-099M-099NJ-099 | 4 | CGM1-4 |
| Test entry | 900006242 | CMSS12Y00711T-099TOPM-099Y-099M | 5 | CGM1-5 |
| Test entry | 900006243 | CMSS12Y00831T-099TOPM-099Y-099M | 6 | CGM1-6 |

- On the Environments tab, enter 4 in the number of environments block and click ok.
- 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.

Specify Environment Details

10 Showing 1 to 4 of 4 entries Manage Locations

| Environment | PlotAreaHvst_m2 | LOCATION_NAME | SEEDING_DATE |
|-------------|----------------------|---|--------------|
| 1 | <input type="text"/> | Kulumsa - (KU) <input checked="" type="radio"/> Breeding locations <input type="radio"/> All locations types <input checked="" type="checkbox"/> Show only favorite locations | yyyy-mm-dd |
| 2 | <input type="text"/> | Asasa - (AA) <input type="radio"/> Breeding locations <input checked="" type="radio"/> All locations types <input checked="" type="checkbox"/> Show only favorite locations | yyyy-mm-dd |
| 3 | <input type="text"/> | Dhera - (DR) <input type="radio"/> Breeding locations <input checked="" type="radio"/> All locations types <input checked="" type="checkbox"/> Show only favorite locations | yyyy-mm-dd |
| 4 | <input type="text"/> | Melkasa - (MK) <input type="radio"/> Breeding locations <input checked="" type="radio"/> All locations types <input checked="" type="checkbox"/> Show only favorite locations | yyyy-mm-dd |

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

3. Generate the trial design

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

- 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.
- Click Add opposite Traits and add the leaf runs traits LrS and LrR.
- The observations sheet now looks something like this:

| ENTRY_TYPE | GID | DESIGNATION | ENTRY_NO | StockID | REP_NO | PLOT_NO | BLOCK_NO | DTH | DTM | PHT | MC | GYLD | NOTES | LrS | LrR |
|------------|-----------|--|----------|---------|--------|---------|----------|-----|-----|-----|----|------|-------|-----|-----|
| Test entry | 900006238 | KINGFISHER-19 | 1 | CGM1-1 | 1 | 1 | 1 | | | | | | | | |
| Test entry | 900006247 | CMSS12B00561S-099M-099N-099N-3Y-0WGY-19 | 10 | CGM1-10 | 1 | 2 | 1 | | | | | | | | |
| Test entry | 900006268 | CMSS13B005865-099M-09Y-29M-0WGY-19 | 31 | CGM1-31 | 1 | 3 | 1 | | | | | | | | |
| Test entry | 900006250 | CMSS12B00871T-099TOPY-099M-099N-099N-46Y-0WGY-19 | 13 | CGM1-13 | 1 | 4 | 1 | | | | | | | | |
| Test entry | 900006246 | CMSS12B00171S-099M-099N-099N-17Y-0WGY-19 | 9 | CGM1-9 | 1 | 5 | 1 | | | | | | | | |
| Test entry | 900006271 | CMSS13B01730T-099TOPY-099M-099N-17M-0WGY-19 | 26 | CGM1-26 | 1 | 6 | 1 | | | | | | | | |

- 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:* Labels-for-PVT1CGM-4-20190927

Save label settings

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

Preset name PPL

- 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_NO | DESIGNATION | Study Name | TRIAL_INSTANCE | LOCATION_NAME | Plot No. | Barcode |
| 2 | CGM1-1 | 1 | KINGFISHER:19 | PVT1CGM | 1 | Kulumsa | 1 | X124PAOnwiHIA |
| 3 | CGM1-1 | 1 | KINGFISHER:19 | PVT1CGM | 1 | Kulumsa | 55 | X124PPFkGOHS0 |
| 4 | CGM1-1 | 1 | KINGFISHER:19 | PVT1CGM | 2 | Asasa | 22 | X124Pmimfreeg |
| 5 | CGM1-1 | 1 | KINGFISHER:19 | PVT1CGM | 2 | Asasa | 55 | X124Pi0vHD2Dx |
| 6 | CGM1-1 | 1 | KINGFISHER:19 | PVT1CGM | 3 | Dhera | 23 | X124PEWZTFTbj |
| 7 | CGM1-1 | 1 | KINGFISHER:19 | PVT1CGM | 3 | Dhera | 37 | X124Pmlgwfnh7 |
| 8 | CGM1-1 | 1 | KINGFISHER:19 | PVT1CGM | 4 | Melkasa | 27 | X124PLrX6HLqJ |
| 9 | CGM1-1 | 1 | KINGFISHER:19 | PVT1CGM | 4 | Melkasa | 56 | X124P1kGcbyi |
| 10 | CGM1-2 | 2 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY:19 | PVT1CGM | 1 | Kulumsa | 21 | X124PK9BYbNc |
| 11 | CGM1-2 | 2 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY:19 | PVT1CGM | 1 | Kulumsa | 70 | X124Pt0wgjNPQ |
| 12 | CGM1-2 | 2 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY:19 | PVT1CGM | 2 | Asasa | 26 | X124Pqil8EHbt |
| 13 | CGM1-2 | 2 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY:19 | PVT1CGM | 2 | Asasa | 47 | X124Po1qFZvfG |
| 14 | CGM1-2 | 2 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY:19 | PVT1CGM | 3 | Dhera | 26 | X124PzldaQrol |
| 15 | CGM1-2 | 2 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY:19 | PVT1CGM | 3 | Dhera | 49 | X124Pd3wwCLjo |
| 16 | CGM1-2 | 2 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY:19 | PVT1CGM | 4 | Melkasa | 30 | X124PIGSBzuzK |
| 17 | CGM1-2 | 2 | CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY:19 | PVT1CGM | 4 | Melkasa | 71 | X124P1kGcbyi |

Make a trial fieldbook with an externally generated design

1. Prepare the layout file

- Open the CIMMYT nursery fieldbook 40ESWYT_024.xls to the Fieldbook sheet.
- Copy Plot, Rep, Subblock, Entry from cells G11 to J111 to a new excel file.
- Rename the sheet Layout.
- 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 | 101 | 1 | 1 | 101 | |
| 3 | 1 | 102 | 1 | 1 | 102 | |
| 4 | 1 | 103 | 1 | 1 | 103 | |
| 5 | 1 | 104 | 1 | 1 | 104 | |
| 6 | 1 | 105 | 1 | 1 | 105 | |
| 7 | 1 | 106 | 1 | 1 | 106 | |
| 8 | 1 | 107 | 1 | 1 | 107 | |
| 9 | 1 | 108 | 1 | 1 | 108 | |
| 10 | 1 | 109 | 1 | 1 | 109 | |
| 11 | 1 | 110 | 1 | 1 | 110 | |
| 12 | 1 | 111 | 1 | 2 | 111 | |

- If the trial is to be conducted at multiple sites, add the 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.
- Rename Plot to PLOT_CODE, Rep to REP_NO, SubBlock to BLOCK_NO and Entry to ENTRY_CODE.
- Add a column before PLOT_CODE and call it PLOT_NO. Fill the column with numbers 1-100 for each location.
- 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 40ESWYT<Your username> which you imported earlier. These numbers are in fact the values of ENTRY_CODE – 100 but you need to be sure to get this right and each case may be different. If you use the formula ENTRY_CODE – 100 to compute the ENTRY_NOs you must paste the values (not keep the formula) in the ENTRY_NO column.
- 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.
- Save the file as 40ESWYTLAYOUT.xls. The top of the layout file now looks like this:

| | A | B | C | D | E | F | G | H | I |
|----|-----------|---------|-----------|--------|----------|----------|------------|---------|---------|
| 1 | TRIAL_INS | PLOT_NO | PLOT_CODE | REP_NO | BLOCK_NO | ENTRY_NO | ENTRY_CODE | FLD_ROW | FLD_COL |
| 2 | 1 | 1 | 101 | 1 | 1 | 1 | 101 | 1 | 1 |
| 3 | 1 | 2 | 102 | 1 | 1 | 2 | 102 | 1 | 2 |
| 4 | 1 | 3 | 103 | 1 | 1 | 3 | 103 | 1 | 3 |
| 5 | 1 | 4 | 104 | 1 | 1 | 4 | 104 | 1 | 4 |
| 6 | 1 | 5 | 105 | 1 | 1 | 5 | 105 | 1 | 5 |
| 7 | 1 | 6 | 106 | 1 | 1 | 6 | 106 | 1 | 6 |
| 8 | 1 | 7 | 107 | 1 | 1 | 7 | 107 | 1 | 7 |
| 9 | 1 | 8 | 108 | 1 | 1 | 8 | 108 | 1 | 8 |
| 10 | 1 | 9 | 109 | 1 | 1 | 9 | 109 | 1 | 9 |
| 11 | 1 | 10 | 110 | 1 | 1 | 10 | 110 | 1 | 10 |
| 12 | 1 | 11 | 111 | 1 | 2 | 11 | 111 | 2 | 1 |
| 13 | 1 | 12 | 112 | 1 | 2 | 12 | 112 | 2 | 2 |

2. Set up the study settings

- a. Select Manage Studies and click Start a New Study
- b. Enter basic details for a study called PVT1<Your username>
- c. 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="40ESWYTINCGM"/> |
| Description: * | <input type="text" value="40th ESWYT International Nursery CGM"/> |
| Study type: * | <input type="text" value="Trial"/> |
| Objective: | <input type="text" value="40th ESWYT International Nursery CGM"/> |

Use a previously created study as a template

Choose

Clear Tabs

- d. Click Choose and select your seed increase nursery – 40ESWYTSI<Your username> as a template. You will see that the Study settings were imported from the template. Select new settings as appropriate:

Use a previously created study as a template Choose Clear Tabs

Settings **Germplasm & Checks** Environments

STUDY SETTINGS ? Add

| | |
|--|---|
| <input type="checkbox"/> TRIAL_YEAR: | <input type="text" value="2019"/> |
| <input type="checkbox"/> Product_concept: | <input type="text" value="BWP - 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

- k. On the Germplasm & Checks tab, click add next to Germplasm Descriptors and add variable StockID to the list of germplasm descriptors.
- l. 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 |
|----------------------------------|---|
| 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) |
| <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 | 1848 | Kingfisher | 1 | |
| Test entry | 6341870 | CMSS07Y01083T-099TOPM-099Y-099M | 2 | |
| Test entry | 6933502 | CMSS10Y00374S-099Y-099M-1WGY-0B | 3 | |
| Test entry | 7400769 | CMSA11Y00507S-099Y-099M-099NJ-09S | 4 | |
| Test entry | 8048669 | CMSS12Y00070S-099Y-099M-099NJ-09S | 5 | |
| Test entry | 8049004 | CMSS12Y00241S-099Y-099M-099NJ-09S | 6 | |
| Test entry | 8049754 | CMSS12Y00711T-099TOPM-099Y-099M | 7 | |
| Test entry | 8050267 | CMSS12Y00831T-099TOPM-099Y-099M | 8 | |

- m. On the Environments tab, enter 4 in the number of environments block and click ok.
- n. 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.

Specify Environment Details

10 Showing 1 to 4 of 4 entries Manage L

| Environment | PlotAreaHvst_m2 | LOCATION_NAME | SEEDING_DATE |
|-------------|-----------------|---|--------------|
| 1 | | Kulumsa - (KU) <input type="radio"/> Breeding locations <input type="radio"/> All locations types <input checked="" type="checkbox"/> Show only favorite locations | yyyy-mm-dd |
| 2 | | Asasa - (AA) <input type="radio"/> Breeding locations <input checked="" type="radio"/> All locations types <input checked="" type="checkbox"/> Show only favorite locations | yyyy-mm-dd |
| 3 | | Dhera - (DR) <input type="radio"/> Breeding locations <input checked="" type="radio"/> All locations types <input checked="" type="checkbox"/> Show only favorite locations | yyyy-mm-dd |
| 4 | | Melkasa - (MK) <input type="radio"/> Breeding locations <input checked="" type="radio"/> All locations types <input checked="" type="checkbox"/> Show only favorite locations | yyyy-mm-dd |

- o. Click save and select the folder Tutorial<Your username> to save the study.

4. Import the trial design

- p. 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.
- q. 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 displays a mapping interface for an experimental design. On the left, there is a red header 'Un-Mapped' above an empty box. On the right, there are two sections: 'Environmental Factors' and 'Design Factors'. Each section lists variables and their corresponding BMS ontology properties and scales.

| Section | Variable | Property | Scale |
|-----------------------|--|--------------------|-------------------|
| Environmental Factors | TRIAL_INSTANCE → TRIAL_INSTANCE (Required) | Trial instance | Number |
| Design Factors | PLOT_NO → PLOT_NO (Required) | Field plot | Number |
| | PLOT_CODE → PLOT_CODE | Field plot | Code of PLOT_CODE |
| | REP_NO → REP_NO | Replication factor | Number |
| | BLOCK_NO → BLOCK_NO | Blocking factor | Number |
| | FLD_ROW → FLD_ROW | Row in layout | Number |
| | FLD_COL → FLD_COL | Column in layout | Number |

At the bottom right of the Design Factors section, there are 'Cancel' and 'Next' buttons.

- r. 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 Fledbook 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 displays the 'TRAITS' and 'SELECTIONS' sections of the observation sheet. The 'TRAITS' section lists various variables such as DTH, DTM, PHT, GYLD, NOTES, Lodg_E_pct, GW_M_g1000grn, and AgrSc. The 'SELECTIONS' section includes a 'SelChkMark' option. Below these sections, there are filters for 'Observations' (Environment: 1 - Kulumusa, Filter by status: All) and a 'Batch Actions' button. The main data table has columns for ENTRY_TYPE, GID, DESIGNATION, ENTRY_NO, StockID, REP_NO, PLOT_NO, BLOCK_NO, PLOT_CODE, FLD_ROW, FLD_COL, DTH, DTM, PHT, GYLD, NOTES, Lodg_E_pct, GW_M_g1000grn, AgrSc, and Sel.

| ENTRY_TYPE | GID | DESIGNATION | ENTRY_NO | StockID | REP_NO | PLOT_NO | BLOCK_NO | PLOT_CODE | FLD_ROW | FLD_COL | DTH | DTM | PHT | GYLD | NOTES | Lodg_E_pct | GW_M_g1000grn | AgrSc | Sel |
|------------|---------|---|----------|---------|--------|---------|----------|-----------|---------|---------|-----|-----|-----|------|-------|------------|---------------|-------|-----|
| Test entry | 1848 | Kingfisher | 1 | | 1 | 1 | 1 | 101 | 1 | 1 | | | | | | | | | |
| Test entry | 6341870 | CMSS07Y01083T-099T0PM-099Y-099M-099Y-40M-DWGY | 2 | | 1 | 2 | 1 | 102 | 1 | 2 | | | | | | | | | |
| Test entry | 6933502 | CMSS10Y00374S-099Y-099M-1WGY-0B | 3 | | 1 | 3 | 1 | 103 | 1 | 3 | | | | | | | | | |
| Test entry | 7400769 | CMMS11Y00507S-099Y-099M-099NJ-099NJ-19WGY-0B | 4 | | 1 | 4 | 1 | 104 | 1 | 4 | | | | | | | | | |

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