

Tutorial on managing hybrid crossing and Line by Tester analysis

This tutorial assumes that the user has a good knowledge of the basic functions and operation of BMS and shows how these functions can be used to facilitate a hybrid breeding program. The user is expected to obtain their own input lists and follow the steps with their own germplasm.

Contents

Introduction	1
Fixing and coding some inbred lines.....	2
Make some hybrid test crosses	4
Make a Line x Tester Trial	8
Analyse the Line x Tester Trial	10
Make a second generation of test crosses using the Cross Design Tool	12
Advance the selected lines and the testers	12
Make a new Crossing nursery	14
Annex 1. Review of coding functionality as specified for CIMMYT GMP.....	18

Introduction

In a typical hybrid breeding program line development follows a traditional pedigree or DH program and when lines are considered reasonable candidates to be tested as hybrids, they are marked as ‘fixed’ and may be given a code name. In fact, in a pedigree breeding program for lines they may not be genetically fixed at this stage but subsequent inbred generations will be grouped with the first ‘fixed’ line. These lines are crossed to testers, or to other candidate lines so that the lines and their combining ability can be evaluated through the performance of those candidate hybrids. As the ‘fixed’ lines are further selected based on the results of the hybrid tests and on other evaluations, the selected descendants are grouped with their earliest fixed ancestor. When crosses are made with hybrid crossing methods between ‘fixed’ (grouped) lines BMS checks to see if a previous hybrid cross was made between members of the same parental groups and if so, the new cross is grouped with the previous ones. So, all crosses between lines having the same male and female parental groups from a group of hybrids. These groups of hybrids can also be given a code name.

BMS has several methods assigned for producing candidate or more advanced hybrids, and the method IDs of these hybrid crossing methods is customized in the file
C:\BMS4\infrastructure\tomcat\webapps\Fieldbook\WEB-INF\classes\crossing.properties. These are set by default to the following methods.

Hybrid methods			
ID	Code	Name	Description
321	VHY	Hybrid formation	Forming a hybrid cultivar
416	TNL	Narrow based tester, line	Test (Top) cross between a known plant and a narrow based (1 or few plants) population. For practical reasons the tester population or line is used as the male which can be stored pollen.
417	TNP	Narrow based tester, pop	Test (Top) cross between a known population and a narrow based tester population. For practical reasons the tester population or line is used as the male which can be stored pollen.
418	TBL	Broad based tester, line	Test (Top) cross between a known plant and a broad based (many plants) tester. For practical reasons the tester population is used as the male which can be stored pollen.
419	TBP	Broad based tester, pop	Test (Top) between a known population and a broad based tester. For practical reasons the tester population is used as the male which can be stored pollen.
426	TCR	Test cross	Crosses made for generating hybrids for early generation testing. The females can be lines in any generation of inbreeding or DH lines, and the male is usually a fixed inbred line, or a F1 single cross between two fixed inbred lines.

More methods could be added and then added to the configuration file.

Fixing and coding some inbred lines

For this tutorial, pick any list with five inbred lines and mark them as fixed.

View Lists View Germplasm

List Details [Show List Builder](#)
Browse or search for a list to work with. [Close All Tab](#)

AVT500 x

List entries
Total Entries: 5 Selected: 5

✓	#	DESIGNATION	CROSS	LOTS
<input checked="" type="checkbox"/>	1	CL02101-RR1	Pob21C5HC57-1	
<input checked="" type="checkbox"/>	2	CL02102-RR1	Pob21C5HC78-3	
<input checked="" type="checkbox"/>	3	CL02103-RR1	Pob21C5HC84-2-1-B-3-B	- - E0003
<input checked="" type="checkbox"/>	4	CL02104-RR1	Pob21C5HC109-3-1-5-4-B-1-#-BB-1-B	- - E0004
<input checked="" type="checkbox"/>	5	CL02105-RR1	Pob21C5HC133-1-B-##-B	- - E0005

Assign codes
Mark lines as fixed

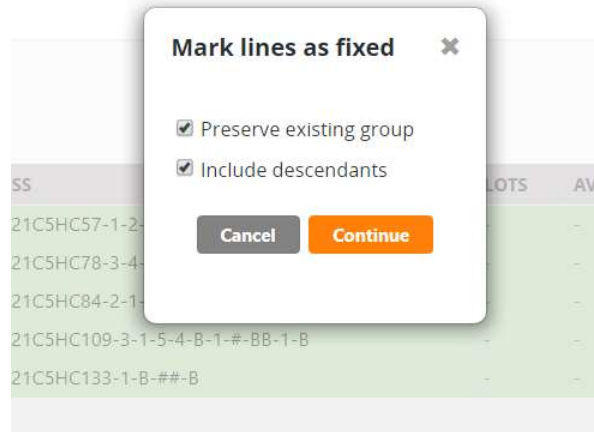
Inventory view
List editing options
Export list
Coding and Fixing Options
Remove selected germplasm

Check the options “Preserve existing group” and “Include descendants”.

Preserve existing Group means that if the line you are fixing is already fixed don't start a new group but leave the line in the group it currently has. If this is unchecked the line would start a new group. This

could be desirable if you decided that the original line had not been ready to be fixed and you had to do some purification and start the grouping again.

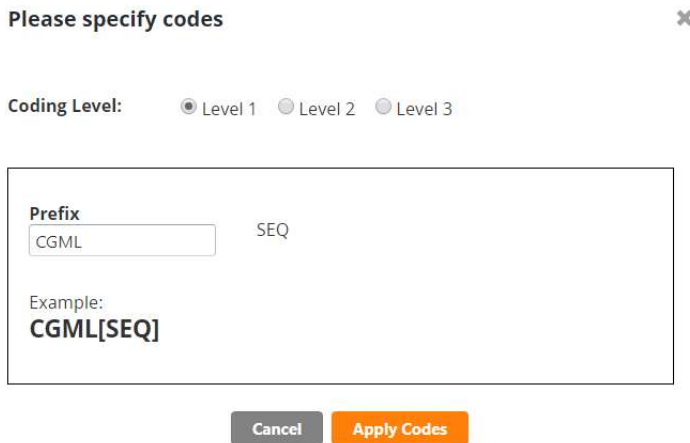
Include Descendants is simply an option in case the line you are grouping has already been advanced (not usual) in which case you have the choice to bring those advances into the group as well. Normally you would want to, so again the default seems the less usual case.



Next assign codes by going to the Assign code item in the Coding and Fixing options sub menu.

Codes are names assigned to lines at a certain level of development. These become the preferred name for the lines and are inherited as the preferred names of descendants in the same group. There are three levels of codes which can be assigned at different stages of development and each level supersedes the other as the preferred name for the group as it is assigned to any member of the group.

Enter a prefix which reflects the project producing the germplasm (CGM) and the type of germplasm (L for line). A sequence number reflecting the next code with the specified prefix will be added to produce the code name.



You can see the codes applied by filling the ENTRY CODE column with preferred name (right-click on the ENTRY CODE header).

List Details

Browse or search for a list to work with.

[Show List Build](#)

AVT500 x

List entries

Total Entries: 5 Selected: 0

✓	#	DESIGNATION	CROSS	L	ENTRY_CODE	CGID	GROUP ID	STOCKID	SEE
<input type="checkbox"/>	1	CL02101-RR1	Pob21C5HC57-1-2-B-##	-	CGML1				
<input type="checkbox"/>	4	CL02104-RR1	Pob21C5HC109-3-1-5-4-B-1-#-BB-1-	-	CGML2				
<input type="checkbox"/>	5	CL02105-RR1	Pob21C5HC133-1-B-##-B	-	CGML3				
<input type="checkbox"/>	2	CL02102-RR1	Pob21C5HC78-3-4-B-#-B	-	CGML4				
<input type="checkbox"/>	3	CL02103-RR1	Pob21C5HC84-2-1-B-3-B	-	CGML5				

- Make Column Empty
- Fill With Preferred ID
- Fill With Germplasm Date
- Fill With Preferred Name
- Fill With Attribute
- Fill With Breeding Method Information
- Fill with Cross-Female Information
- Fill with Cross-Male Information
- Fill with Sequence Number

For this tutorial, you also need a set of tester lines which should also be 'Fixed' (grouped). For example, the CML lines.

Make some hybrid test crosses

Create a list for the crossing block with five testers (CML lines in this example) and our five inbreds. Notice that the inbreds appear with their codes in the new list since these are now the preferred names of these lines.

List Details

Browse or search for a list to work with.

[Hide List Builder](#) [Build a New List](#)

Close All Tabs Build or revise your list by dragging in entries from the left.

CML Lines 2 x AVT500 x

List entries

Total Entries: 5 Selected: 5

✓	#	DESIGNATION	CROSS
<input checked="" type="checkbox"/>	1	CL02101-RR1	Pob21C5HC57-1-2-B-##
<input checked="" type="checkbox"/>	2	CL02102-RR1	Pob21C5HC78-3-4-B-#-B
<input checked="" type="checkbox"/>	3	CL02103-RR1	Pob21C5HC84-2-1-B-3-B
<input checked="" type="checkbox"/>	4	CL02104-RR1	Pob21C5HC109-3-1-5-4-B-1-#-BB-1-B
<input checked="" type="checkbox"/>	5	CL02105-RR1	Pob21C5HC133-1-B-##-B

List entries

Total Entries: 10 Selected: 0

✓	#	DESIGNATION	CROSS	LOTS
<input type="checkbox"/>	1	CML320	P501c0F112-2-5-1-1-B*4	1
<input type="checkbox"/>	2	CML360	SA4C2HC(21X26)-1-2-2-2-B	1
<input type="checkbox"/>	3	CML370	MBR-ET(W)F2-14-3-1-3-B-B-B	1
<input type="checkbox"/>	4	CML432	KTX3752F2-7-1-1-1-B-B-B	1
<input type="checkbox"/>	5	CML444	P43C9-1-1-1-1-1-BBBB	1
<input type="checkbox"/>	6	CGML1	Pob21C5HC57-1-2-B-##	
<input type="checkbox"/>	7	CGML4	Pob21C5HC78-3-4-B-#-B	
<input type="checkbox"/>	8	CGML5	Pob21C5HC84-2-1-B-3-B	
<input type="checkbox"/>	9	CGML2	Pob21C5HC109-3-1-5-4-B-1-	
<input type="checkbox"/>	10	CGML3	Pob21C5HC133-1-B-##-B	

We are going to use a matrix crossing layout to facilitate the crossing as follows:

Male Testers	Female Line 1	Female Line 2	Female Line 3	Female Line 4	Female Line 5
Plot 1 Entry 1	Plot 2 Entry 6	Plot 3 Entry 7	Plot 4 Entry 8	Plot 5 Entry 9	Plot 6 Entry 10
Plot 7 Entry 2	Plot 8 Entry 6	Plot 9 Entry 7	Plot 10 Entry 8	Plot 11 Entry 9	Plot 12 Entry 10
Plot 13 Entry 3	Plot 14 Entry 6	Plot 15 Entry 7	Plot 16 Entry 8	Plot 17 Entry 9	Plot 18 Entry 10
Plot 19 Entry 4	Plot 20 Entry 6	Plot 21 Entry 7	Plot 22 Entry 8	Plot 23 Entry 9	Plot 24 Entry 10
Plot 25 Entry 5	Plot 26 Entry 6	Plot 27 Entry 7	Plot 28 Entry 8	Plot 29 Entry 9	Plot 30 Entry 10

Translate this table into a csv file as follows. This layout file can be used whenever the same layout is required (CGMTCLayout.csv). Any layout design can be accommodated in this way.

	A	B	C
1	TRIAL_INSTANCE	ENTRY_NO	PLOT_NO
2	1	1	1
3	1	6	2
4	1	7	3
5	1	8	4
6	1	9	5
7	1	10	6
8	1	2	7
9	1	6	8
10	1	7	9
11	1	8	10
12	1	9	11
13	1	10	12
14	1	3	13
15	1	6	14
16	1	7	15
17	1	8	16
18	1	9	17
19	1	10	18
20	1	4	19
21	1	6	20
22	1	7	21
23	1	8	22
24	1	9	23
25	1	10	24
26	1	5	25
27	1	6	26
28	1	7	27
29	1	8	28
30	1	9	29
31	1	10	30

You should do seed preparation. Start by reserving seed by switching to inventory view and using the menu item Inventory management options > Reserve inventory. Save the reservations, Print labels, Export the seed preparation list, pack the seed into sufficient packets dictated by the layout and then Import the seed preparation list to update the inventory.

MANAGE GERmplasm ?

View Lists
View Germplasm

List Details

Browse or search for a list to work with.

[Show List Builder](#)

CGM17TCB List ×

Inventory

Total Lots: 5 Selected: 0

✓	#	DESIGNATION	LOCATIO	Reserve inventory	Save changes	Cancel Reservations	Close lots
<input type="checkbox"/>	1	CML320	Default S				
<input type="checkbox"/>	2	CML360	Default S				
<input type="checkbox"/>	3	CML370	Default S				
<input type="checkbox"/>	4	CML432	Default Seed Store	53.1999999999998g	0.0g	0.0g	From Lis
<input type="checkbox"/>	5	CML444	Default Seed Store	54.3999999999998g	0.0g	0.0g	From Lis

ACTIONS

- Return to List entries view
- List editing options
- Inventory management options
- Export Seed preparation list
- Import Seed preparation list
- Print Labels

Create a crossing block nursery with the Nursery Manager. Add the Management Details (Project_prefix, Target_Region, LOCATION_ABBR, Crop_season_code) that you want to be part of your cross codes. Add the list you created. Import the design from file CGMTCLayout.csv you made above and save the

Nursery. (You must do the whole process without saving to avoid a bug in importing the design in v6 – fixed in V6.2).

MANAGE NURSERIES ?

Create Nursery Save Return to Manage Nurseries

BASIC DETAILS
* indicates a mandatory field

Nursery name: *

Description: *

Objective:

Save in: *

Created by: * Christopher McLaren

Creation date: *

Completion date:

Use a previously created nursery as a template

Actions
Import Crosses
Import Design

Nursery Settings | **Germplasm & Checks** | **Measurements**

MANAGEMENT DETAILS ? Add

PL_NAME:

Project_Prefix:

Target_Region:

LOCATION_ABBR:

Crop_season_Code:

NURSERY CONDITIONS ? Add
Click Add to begin selecting items to record in this section.

TRAITS ? Add

Trait	Description

Now export the crossing template. Fill in the description sheet:

	A	B	C
1	LIST NAME	CGM17TC List	
2	LIST DESCRIPTION	2017 Test crosses for project CGM	
3	LIST DATE	20170728	

And add the crossing plan to the observation sheet:

	A	B	C	D	E	F
1	FEMALE PLOT	MALE NURSERY	MALE PLOT	BREEDING METHOD	CROSSING DATE	NOTES
2	2		1	TCR	20170728	
3	3		1	TCR	20170728	
4	4		1	TCR	20170728	
5	5		1	TCR	20170728	
6	6		1	TCR	20170728	
7	8		7	TCR	20170728	
8	9		7	TCR	20170728	
9	10		7	TCR	20170728	
10	11		7	TCR	20170728	
11	12		7	TCR	20170728	
12	14		13	TCR	20170728	
13	15		13	TCR	20170728	
14	16		13	TCR	20170728	
15	17		13	TCR	20170728	
16	18		13	TCR	20170728	
17	20		19	TCR	20170728	
18	21		19	TCR	20170728	
19	22		19	TCR	20170728	
20	23		19	TCR	20170728	
21	24		19	TCR	20170728	
22	26		25	TCR	20170728	
23	27		25	TCR	20170728	
24	28		25	TCR	20170728	
25	29		25	TCR	20170728	
26	30		25	TCR	20170728	

This crossing plan can be copied into the crossing template of future test cross nurseries which use the same layout. Fill in the date that the crosses are made and any notes before Importing the crosses. Use the method TCR (Test cross) specified in the template, but check 'Apply grouping to new crosses only' as in the screenshot below. This means that if the cross has been made before with a hybrid crossing method between lines in the same parental inbred groups and therefore grouped then that group will be preserved and the new cross added to it. Only new crosses which have not been made before will start new groups.

Specify Breeding Method ✕

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

- Use the breeding methods specified in the import file
 - Use parental status
 - Select a method to use for all crosses :

?

 - All methods
 - Generative methods
- Show only favorite methods [Manage Methods](#)
- Apply grouping to new crosses only

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

You can see the crosses which have been imported and that they are grouped. The cross names have been constructed following the [CIMCRS] rules as Projectr_Prefix + Target_Region + Crop_season_Code + LOCATION_ABBR+[SEQUENCE] and this is customizable.

Nursery: CGM17TCB [Save](#)
[Return to Manage Nurseries](#)

▶ BASIC DETAILS [Actions](#)

Nursery Settings | **Germplasm & Checks** | **Experimental Design** | **Measurements** | **Imported Crosses: [CGM17TC List] ✕**

Cross List: *CGM17TC List* Notes:

Total Entries: 25 Selected: 0 [View List Details](#)

[Cross List Actions](#)

100 Showing 1 to 25 of 25 entries

ENTRY_NO	DESIGNATION	CROSS	FEMALE PARENT	FGID	MALE PARENT	MGID	GID	SEED_SOURCE	GROUP ID	DUPLICATE
1	PBR317MH1	CGML1/CML320	CGML1	13543	CML320	16	13667	CGM17TCB:2/CG	13667	
2	PBR317MH2	CGML4/CML320	CGML4	13544	CML320	16	13668	CGM17TCB:3/CG	13668	
3	PBR317MH3	CGML5/CML320	CGML5	13545	CML320	16	13669	CGM17TCB:4/CG	13669	
4	PBR317MH4	CGML2/CML320	CGML2	13546	CML320	16	13670	CGM17TCB:5/CG	13670	
5	PBR317MH5	CGML3/CML320	CGML3	13547	CML320	16	13671	CGM17TCB:6/CG	13671	
6	PBR317MH6	CGML1/CML360	CGML1	13543	CML360	1480	13672	CGM17TCB:8/CG	13672	
7	PBR317MH7	CGML4/CML360	CGML4	13544	CML360	1480	13673	CGM17TCB:9/CG	13673	

You should continue to add inventory by one of the available methods for the new test hybrids.

Make a Line x Tester Trial

First you must add the line and tester names to the list containing the test cross germplasm from our nursery. To do this in the GERMPPLASM MANAGER, right-click on the ENTRY CODE column header and fill it with Cross-Female Preferred Name. In the same way fill the SEED SOURCE column with the Cross-Male Preferred Name.

MANAGE GERMLASM ?

[View Lists](#) [View Germplasm](#)

List Details

Browse or search for a list to work with.

CGM17TC List ×

List entries

Total Entries: 25 Selected: 0

✓	#	DESIGNATION	CROSS	LOTS	AVAILABLE	ENTRY_CODE	GID	GROUP ID	STOCKID	SEED_SOURCE
<input type="checkbox"/>	1	PBR317MH1	CGML1/CML320	-	-	1				CB:2/CGI
<input type="checkbox"/>	2	PBR317MH2	CGML4/CML320	-	-	2				CB:3/CGI
<input type="checkbox"/>	3	PBR317MH3	CGML5/CML320	-	-	3				CB:4/CGI
<input type="checkbox"/>	4	PBR317MH4	CGML2/CML320	-	-	4				CB:5/CGI
<input type="checkbox"/>	5	PBR317MH5	CGML3/CML320	-	-	5				CB:6/CGI
<input type="checkbox"/>	6	PBR317MH6	CGML1/CML360	-	-	6				CB:8/CGI
<input type="checkbox"/>	7	PBR317MH7	CGML4/CML360	-	-	7				CB:9/CGI
<input type="checkbox"/>	8	PBR317MH8	CGML5/CML360	-	-	8				CB:10/CC
<input type="checkbox"/>	9	PBR317MH9	CGML2/CML360	-	-	9				CB:11/CC
<input type="checkbox"/>	10	PBR317MH10	CGML3/CML360	-	-	10	13676	13676		CGM17TCB:12/CC
<input type="checkbox"/>	11	PBR317MH11	CGML1/CML370	-	-	11	13677	13677		CGM17TCB:14/CC
<input type="checkbox"/>	12	PBR317MH12	CGML4/CML370	-	-	12	13678	13678		CGM17TCB:15/CC
<input type="checkbox"/>	13	PBR317MH13	CGML5/CML370	-	-	13	13679	13679		CGM17TCB:16/CC
<input type="checkbox"/>	14	PBR317MH14	CGML2/CML370	-	-	14	13680	13680		CGM17TCB:17/CC

- Make Column Empty
- Fill With Preferred ID
- Fill With Germplasm Date
- Fill With Preferred Name
- Fill With Attribute
- Fill With Breeding Method Information
- Fill with Cross-Female Information
- Fill with Cross-Male Information
- Fill with Sequence Number

- Fill with Cross-Female GID
- Fill with Cross-Female Preferred Name

The list now looks like this:

List Details

Browse or search for a list to work with.

[Show List Builder](#)

CGM17TC List ×

List entries

Total Entries: 25 Selected: 0

ACTIONS

✓	#	DESIGNATION	CROSS	ENTRY_CODE	GID	GROUP ID	SEED_SOURCE
<input type="checkbox"/>	1	PBR317MH1	CGML1/CML320	CGML1	13667	13667	CML320
<input type="checkbox"/>	2	PBR317MH2	CGML4/CML320	CGML4	13668	13668	CML320
<input type="checkbox"/>	3	PBR317MH3	CGML5/CML320	CGML5	13669	13669	CML320
<input type="checkbox"/>	4	PBR317MH4	CGML2/CML320	CGML2	13670	13670	CML320
<input type="checkbox"/>	5	PBR317MH5	CGML3/CML320	CGML3	13671	13671	CML320
<input type="checkbox"/>	6	PBR317MH6	CGML1/CML360	CGML1	13672	13672	CML360
<input type="checkbox"/>	7	PBR317MH7	CGML4/CML360	CGML4	13673	13673	CML360

In the TRIAL MANAGER, start a new trial (CGM17LXT) add the same Trial Settings as for the Nursery. On the GERMLASM tab add ENTRY CODE (change its name to LINE) and SEED SOURCE (change its name to TESTER) variables to the germplasm variable list. Add the list of test crosses.

Settings Germplasm Environments Experimental Design Measurements

▼ Define Germplasm Details Add

GERMPLASM DESCRIPTORS

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)
PLOT_ID	Field plot id - assigned (text)
<input type="checkbox"/> LINE	Germplasm ID - Assigned (Code)
<input type="checkbox"/> TESTER	Seed source - Selected (Code)

Select All Remove

Trial List

Browse a list to work with.

Total Entries: 25 View Header

ENTRY_TYPE	GID	DESIGNATION	ENTRY_NO	LINE	TESTER
Test entry	13697	PBR317MH26	1	CGML1	CML320
Test entry	13698	PBR317MH27	2	CGML4	CML320
Test entry	13699	PBR317MH28	3	CGML5	CML320
Test entry	13700	PBR317MH29	4	CGML2	CML320
Test entry	13701	PBR317MH30	5	CGML3	CML320
Test entry	13702	PBR317MH31	6	CGML1	CML360

Add one environment with a LOCATION_NAME and whatever Trial Conditions you usually record (irrigation, rainfall, fertilizer etc.).

Generate an appropriate design and add traits you want to measure. Collect the data.

Analyse the Line x Tester Trial

Prepare the standard SSA analysis for the design you chose. You can analyse this preparation and it will do the usual analysis ignoring the Line x Tester decomposition. To obtain the Line x Tester analysis you must edit the Breeding View project xml file. Simply insert the text in red into the xml file with a text editor. Then run the Breeding View analysis again.

```
<?xml version="1.0" encoding="UTF-8" standalone="yes"?>
<Session>
  <IBWS InputDataSetId="25470" OutputDataSetId="0"
  StudyId="25468" WorkbenchProjectId="2"/>
  <Datafile name="Maize_25470_CGM17LXT1-PLOTDATA.csv"/>
  <BreedingViewProject name="SSA analysis of CGM17LXT1-PLOTDATA
  (run at 2017-07-28_22:21)" version="1.2">
    <Pipelines>
      <Pipeline type="SEA">
        <DataConfiguration>
          <Design type="Resolvable incomplete block
          design">
            <Blocks name="BLOCK_NO"/>
            <PlotNo name="PLOT_NO"/>
            <Replicates name="REP_NO"/>
          </Design>
          <Environments name="LOCATION_NAME">
            <Environment active="true" name="ART
            FARM; HARARE"/>
          </Environments>
          <Genotypes entry="ENTRY_NO"
          name="DESIGNATION" line="LINE" tester="TESTER"/>
          <Traits>
            <Trait active="true" name="GY_Adj_tha"/>
          </Traits>
        </DataConfiguration>
      </Pipeline>
    </Pipelines>
  </BreedingViewProject>
</Session>
```

I generated data with the following parameters:

LINES	LValue	TESTERS	Tvalue	CROSSES	Gvalue
CGML1	1	CML320	1	1	3
CGML2	2	CML360	2	2	0
CGML3	3	CML370	3	3	0
CGML4	4	CML432	4	4	0
CGML5	5	CZL99029	5	5	-3
				6	0
				7	3
				8	0
				9	-3
				10	0
				11	0
				12	0
				13	0
				14	0
				15	0
				16	0
				17	-3
				18	0
				19	3
				20	0
				21	-3
				22	0
				23	0
				24	0
				25	3

The standard analysis report from Breeding View is not very different from the usual SSA analysis, except that it shows the significance of the LINE, TESTER and LINExTESTER effects:

Estimated generalized heritability

Term	Heritability
LINE	0.4012
LINE.TESTER	0.6679

Tests for combinability effects

	Deviance	d.f.	Chi pr.
LINE	8.04	1	0.005
LINE.TESTER	29.35	1	<0.001

Wald/F tests when genotypes modelled as fixed effects

Term	Wald statistic	n.d.f.	F statistic	d.d.f.	F pr.
REP_NO	0.2	2	0.12	48	0.887
TESTER	58.5	4	14.62	48	<0.001
LINE	55.0	4	13.76	48	<0.001
TESTER.LINE	121.0	16	7.56	48	<0.001

However the report on the Output tab is more informative and has estimates of GCA:

LINE BLUPs (GCA effects)

LINE	GCA	s.e.
CGML3	-0.1173	0.8648
CGML4	0.4748	0.8655
CGML1	-0.6611	0.8652
CGML2	-0.5714	0.8651
CGML5	0.8750	0.8648

and SCA:

LINE.TESTER BLUPs (SCA effects)

TESTER	CML370 SCA	s.e.	CML320 SCA	s.e.
LINE				
CGML3	-0.440	1.605	-3.221	1.607
CGML4	0.072	1.609	1.196	1.603
CGML1	-2.982	1.608	1.952	1.608
CGML2	0.426	1.604	-0.810	1.602
CGML5	2.925	1.615	0.884	1.608

TESTER	CML360 SCA	s.e.	CML432 SCA	s.e.
LINE				
CGML3	0.770	1.607	-1.652	1.609
CGML4	2.862	1.605	-3.429	1.604

... table continued.

If you rearrange the SCA table to match the crossing layout you can see that the SCA values used in generating the data were reasonably well recovered (except for cross 13 in the middle).

TESTER		LINE	CGML1	CGML4	CGML5	CGML2	CGML3
CML320	SCA		1.952	1.196	0.884	-0.81	-3.221
	s.e.		1.608	1.603	1.608	1.602	1.607
CML360	SCA		-1.01	2.862	0.507	-3.129	0.77
	s.e.		1.607	1.605	1.604	1.605	1.607
CML370	SCA		-2.982	0.072	2.925	0.426	-0.44
	s.e.		1.608	1.609	1.615	1.604	1.605
CML432	SCA		1.354	-3.429	2.057	1.67	-1.652
	s.e.		1.602	1.604	1.608	1.607	1.609
CZL99029	SCA		-3.626	2.397	-0.665	-1.885	3.779
	s.e.		1.602	1.607	1.604	1.605	1.605

Make a second generation of test crosses using the Cross Design Tool

Advance the selected lines and the testers

Although the GCA values are not significantly different they have been estimated in the same order that they were supplied as parameters, so deciding to keep CGML4 and CGML5 would not have been a bad decision. Although normally you would have separate nurseries to advance lines we can illustrate the process using the crossing block. You might use this nursery to bulk new seed for the tester lines (which seems reasonable). We will also use it to demonstrate the advance of the lines CGML4 and CGML5 (which is less practical). To do this add the variables NPSEL and BM_CODE_VTE to the Selection group on

the Nursery Settings Page. Add 1 to the variable NPSEL for the male plots (CML lines) and for the first plots containing CGML4 and CGML5 which we wish to advance. Put the method code Seed Increase Bulk (NBK) in the variate BM_CODE_VTE next to the selected male plots, and Selected Bulk (DSB) next to the plots for CGML4 and CGML5 using the pull down list.

MANAGE NURSERIES ?

Nursery: CGM17TCB Save

► BASIC DETAILS

Nursery Settings | Germplasm & Checks | Experimental Design | Measurements | Imported Crosses: [CGM17TCx List]

Measurements

100 Showing 1 to 30 of 30 entries

Action	ENTRY_NO	CROSS	PLOT_NO	GID	DESIGNATION	NPSEL	BM_CODE_VTE
	1	P501cOF112-2-5-1-1-B*4	1	16	CML320	1	Seed increase bulk - NBK
	6	Pob21C5HC57-1-2-B-##	2	13543	CGML1		
	7	Pob21C5HC78-3-4-B-#B	3	13544	CGML4	1	Selected bulk - DSB
	8	Pob21C5HC84-2-1-B-3-B	4	13545	CGML5	1	Selected bulk - DSB
	9	Pob21C5HC109-3-1-5-4-B-1-#	5	13546	CGML2		
	10	Pob21C5HC133-1-B-##-B	6	13547	CGML3		
	2	SA4C2HC(21X26)-1-2-2-2-B	7	1480	CML360	1	Seed increase bulk - NBK
	6	Pob21C5HC57-1-2-B-##	8	13543	CGML1		
	7	Pob21C5HC78-3-4-B-#B	9	13544	CGML4		
	8	Pob21C5HC84-2-1-B-3-B	10	13545	CGML5		
	9	Pob21C5HC109-3-1-5-4-B-1-#	11	13546	CGML2		
	10	Pob21C5HC133-1-B-##-B	12	13547	CGML3		
	3	MBR-ET(W)F2-14-3-1-3-B-B-B	13	1490	CML370	1	Seed increase bulk - NBK

Save the data, then use nursery advance from the Actions menu. Uncheck the box for 'Breeding method is the same for each advance' and for 'All plots are selected' and use BM_CODE-VTE to define the breeding method and NPSL to define the plots for advancement.

METHODS

Breeding Method is the same for each advance

Derivative and Maintenance methods

All methods

Show only favorite methods [Manage Methods](#)

Choose a variate that defines the breeding method for each advance:

LINES

Same number of lines is selected for each plot

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

BULKES

All plots are selected

HARVEST DETAILS

Harvest Location: ?

Breeding locations All locations types

Show only favorite locations [Manage Locations](#)

Harvest Date:

Cancel Finish

The resulting bulks will be grouped with the source material. You will see the seed increase list displayed as in the screenshot below. The names have been constructed as source name + Crop_season_Code for the method Seed Increase Bulk and as Source Name+'-SB' for the Selected bulks as customized in the methods table for the seed increase method. Note that the original source name has been used for CGML4, CGML5 and CML5 because these are derivative names and the naming convention specifies these. They also have the group names and to see these you can fill the ENTRSY_CODE column with preferred name in the List Manager.

MANAGE NURSERIES ?

Nursery: **CGM17TCB** Save Return to Manage Nurseries

► BASIC DETAILS Actions

Nursery Settings | Germplasm & Checks | Experimental Design | Measurements

Advance List: **CGM17CD** Notes: View List Details

Advance List

Total Entries: 7 Selected: 0 Advance List Actions

100 Showing 1 to 7 of 7 entries

ENTRY_NO	DESIGNATION	CROSS	GID	SEED_SOURCE	GROUP ID
1	CML320:17M	P501c0F112-2-5-1-1-B*4	13722	CGM17TCB:1	16
2	CL02102-RR1-SB	Pob21C5HC78-3-4-B-#-B	13723	CGM17TCB:3	13544
3	CL02103-RR1-SB	Pob21C5HC84-2-1-B-3-B	13724	CGM17TCB:4	13545
4	CML360:17M	SA4C2HC(21X26)-1-2-2-2-B	13725	CGM17TCB:7	1480
5	CML370:17M	MBR-ET(W)F2-14-3-1-3-B-B-B	13726	CGM17TCB:13	1490
6	CML432:17M	KTX3752F2-7-1-1-1-B-B-B	13727	CGM17TCB:19	1551
7	CZL99029:17M	P43C9-1-1-1-1-BBBB	13728	CGM17TCB:25	13

Again add inventory for the new batches.

Make a new Crossing nursery

CGML4 combined best with CML360 (Cross PBR317MH7) and CGML5 combines best with CML370 (Cross PBR317MH13) so for example we might decide to make these crosses again. Similarly, as an example we might make three-way test hybrids CGML4/CML360// CGML5 (PBR317MH7/CGML5) and CGML5/CML370//CGML4 (PBR317MH13/CGML4). We can assume we will use the new batches of tester lines and the new generation of inbred lines. We will use the Crossing tool to make these crosses and illustrate the grouping of hybrids although normally such crosses would be made in larger nurseries and would use the layout and crossing template features illustrated above.

Make a new nursery and the lines CGML4, CGML5, PBR317MH7, PBR317MH13 from appropriate lists as females. Then add CML360, CML370, CGML5 and CGML4 as male parents.

Total Entries: 7 Selected: 1

✓ #	DESIGNATION	CROSS	ENTRY_CODE	GID	GROUP ID	LOTS	AVAILABLE
<input type="checkbox"/>	1 CML320:17M	P501c0F112-2-5-1-1-B	CML320:17M	13722	16	-	-
<input checked="" type="checkbox"/>	2 CL02102-RR1-SB	Pob21C5HC78-3-4-B-1	CGML4	13723	13544	-	-
<input type="checkbox"/>	3 CL02103-RR1-SB	Pob21C5HC84-2-1-B-1	CGML5	13724	13545	-	-
<input type="checkbox"/>	4 CML360:17M	SA4C2HC(21X26)-1-2-	CML360:17M	13725	1480	-	-
<input type="checkbox"/>	5 CML370:17M	MBR-ET(W)F2-14-3-1-1	CML370:17M	13726	1490	-	-

Select All

Parent Lists

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

Female Parents

List entries

Total Entries: 2 Selected: 2

✓ #	DESIGNATION	CROSS	STO
<input checked="" type="checkbox"/>	1 CL02102-RR1-SB	Pob21C5HC78-3-4-B-#-B	
<input checked="" type="checkbox"/>	2 CL02103-RR1-SB	Pob21C5HC84-2-1-B-3-B	

Male Parents

List entries

Total Entries: 4 Selected: 4

✓ #	DESIGNATION	CROSS	ST
<input checked="" type="checkbox"/>	1 CML360:17M	SA4C2HC(21X26)-1-2-2-2-B	
<input checked="" type="checkbox"/>	2 CML370:17M	MBR-ET(W)F2-14-3-1-3-B-B	
<input checked="" type="checkbox"/>	3 CL02103-RR1-SB	Pob21C5HC84-2-1-B-3-B	
<input checked="" type="checkbox"/>	4 CL02102-RR1-SB	Pob21C5HC78-3-4-B-#-B	

Now browse the CGM17TC List and open it for review. Add PBR317MH7 and PBR317MH13 from this list to the female parent list. So that the parent lists look like this:

Parent Lists

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

Female Parents

List entries

Total Entries: 4 Selected: 4

✓ #	DESIGNATION	CROSS	STO
<input checked="" type="checkbox"/>	1 CL02102-RR1-SB	Pob21C5HC78-3-4-B-#-B	
<input checked="" type="checkbox"/>	2 CL02103-RR1-SB	Pob21C5HC84-2-1-B-3-B	
<input checked="" type="checkbox"/>	3 PBR317MH7	CGML4/CML360	
<input checked="" type="checkbox"/>	4 PBR317MH13	CGML5/CML370	

Male Parents

List entries

Total Entries: 4 Selected: 4

✓ #	DESIGNATION	CROSS	ST
<input checked="" type="checkbox"/>	1 CML360:17M	SA4C2HC(21X26)-1-2-2-2-B	
<input checked="" type="checkbox"/>	2 CML370:17M	MBR-ET(W)F2-14-3-1-3-B-B	
<input checked="" type="checkbox"/>	3 CL02103-RR1-SB	Pob21C5HC84-2-1-B-3-B	
<input checked="" type="checkbox"/>	4 CL02102-RR1-SB	Pob21C5HC78-3-4-B-#-B	

Specify the crossing of matched pairs and generate the crosses:

Crossing Method

Choose how you would like to make your crosses:

Make reciprocal crosses Exclude selfs **Generate Crosses**

Preview Crosses

Total Crosses: 4 Selected: 0

✓ #	FEMALE PARENT	MALE PARENT	FEMALE CROSS	MALE CROSS
<input type="checkbox"/>	1 CGML4	CML360:17M	CL02102	CML360
<input type="checkbox"/>	2 CGML5	CML370:17M	CL02103	CML370
<input type="checkbox"/>	3 PBR317MH7	CGML5	CGML4/CML360	CL02103
<input type="checkbox"/>	4 PBR317MH13	CGML4	CGML5/CML370	CL02102

Specify a hybrid breeding method such as Test Cross and select the option to 'Apply grouping to new crosses only'.

Specify Breeding Method ✕

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

Use parental status
 Select a method to use for all crosses :

?

All methods Generative methods
 Show only favorite methods [Manage Methods](#)

Apply grouping to new crosses only

Continue

Save the germplasm list and add inventory by one of the available methods.

CGM18TC List ✕

List entries

Total Entries: **4** Selected: **0**

ACTIO
i ✎

✓	#	DESIGNATION	CROSS	LOTS	AVAILABLE	ENTRY_CODE	GID	GROUP ID
<input type="checkbox"/>	1	PBR318MH1	CGML4/CML360:17M	1	120.0 g	1	13729	13673
<input type="checkbox"/>	2	PBR318MH2	CGML5/CML370:17M	1	120.0 g	2	13730	13679
<input type="checkbox"/>	3	PBR318MH3	PBR317MH7/CGML5	1	120.0 g	3	13731	13731
<input type="checkbox"/>	4	PBR318MH4	PBR317MH13/CGML4	1	120.0 g	4	13732	13732

Note that the re-made crosses PBR317MH7 and PBR317MH13 have been given their own cross names PBR318MH1 and PBR318MH2 but have been grouped with the original test crosses even though they were made from the next generation of inbred lines, and they have inherited the names of those crosses with name type SELHISFIX.

▼ BASIC DETAILS

Preferred Name: PBR317MH7

Creation Date: 20180300

GID: 13729

Creation Method: Test cross

Location: ART FARM, HARARE

Reference:

Fixed Line

Group Id (MGID): 13673

▶ ATTRIBUTES

▶ PEDIGREE TREE

▼ NAMES

NAME	DATE	LOCATION	TYPE	TYPE DESC	
PBR317MH7	20170731	ART FARM, HARARE	SELHISFIX	Selection history at fixation	
PBR318MH1	20180300	ART FARM, HARARE	CRSNM	CROSS NAME	

If we had not checked the option 'Apply grouping to new crosses only' they would have started new groups and not inherited the original test cross name.

On the other hand, the three-way crosses are first time combinations so they have been assigned as founding members. IF they are made again from subsequent version of the single crosses and subsequent versions of the inbred lines, these new versions will be grouped with the original three-way crosses.

You can also assign codes to test hybrids, as was done in section 1 for inbred lines. These codes will be inherited as the preferred name by all hybrid group members.

Annex 1. Review of coding functionality as specified for CIMMYT GMP

Since the idea of including coding in to BMS tools came from CIMMYT's maize breeding needs, it would be appropriate to discuss and summarize what we understood from CIMMYT's documentation on the subject and compare them with the tutorial.

CIMMYT assigns three different sets of codes to maize germplasm based on the stages of testing.

Code 1 – Every entry that goes in to Stage 1 testing – i.e. preliminary yield trials that are usually made by crossing S2 (or F3) ears to a tester. This is the first time that a breeder is able to test the germplasm generated by crossing two (or more) parents to generate hybrids for testing. If this is done with DH lines, obviously, those lines are fixed while if they are done with S2/S3 lines they are not fixed.

Code 2 – In preliminary yield trials, usually about 10-15% of the best performing entries are retained for stage 2 and stage 3 testing. These entries are assigned a Code 2. Basically, Code 2 superimposes Code 1. The difference between Stage 1 testing and Stage 2 testing is that entries that get to stage 2 testing are tested with more testers and in more environments. The S2/S3 lines that were used for crossing for stage 1 testing are now at S4/S5 stage – (while the hybrid combinations are evaluated in yield trials, in the nurseries, breeders grow the lines, self them to make them more genetically uniform). I believe that entries get a Code 2 assignment when they are ready to be tested outside a specific breeding program – i.e. in regional trials where multiple breeders may have entries contributing to the regional trial.

Code 3 - A code 3 is given to advanced inbreds (such as CMLs) or hybrids or OPVs when they get ready for commercialization in a country.

What is not very clear is that how many of breeders give code 1 and code 2 to hybrids instead of inbreds. Practically, it is obvious that a breeder would have a large number of Code 1s a subset of which will also get Code 2 and a small subset of them (Code 2s) get a Code 3. If a breeder selects a few entries originating from a specific cross (eg. AxB) to enter into Stage 2 trials, these few entries are related since they come from the same original cross and can be considered as 'sister lines' or as a group.