

Implementation new tools and technologies in the AGG-Maize Project

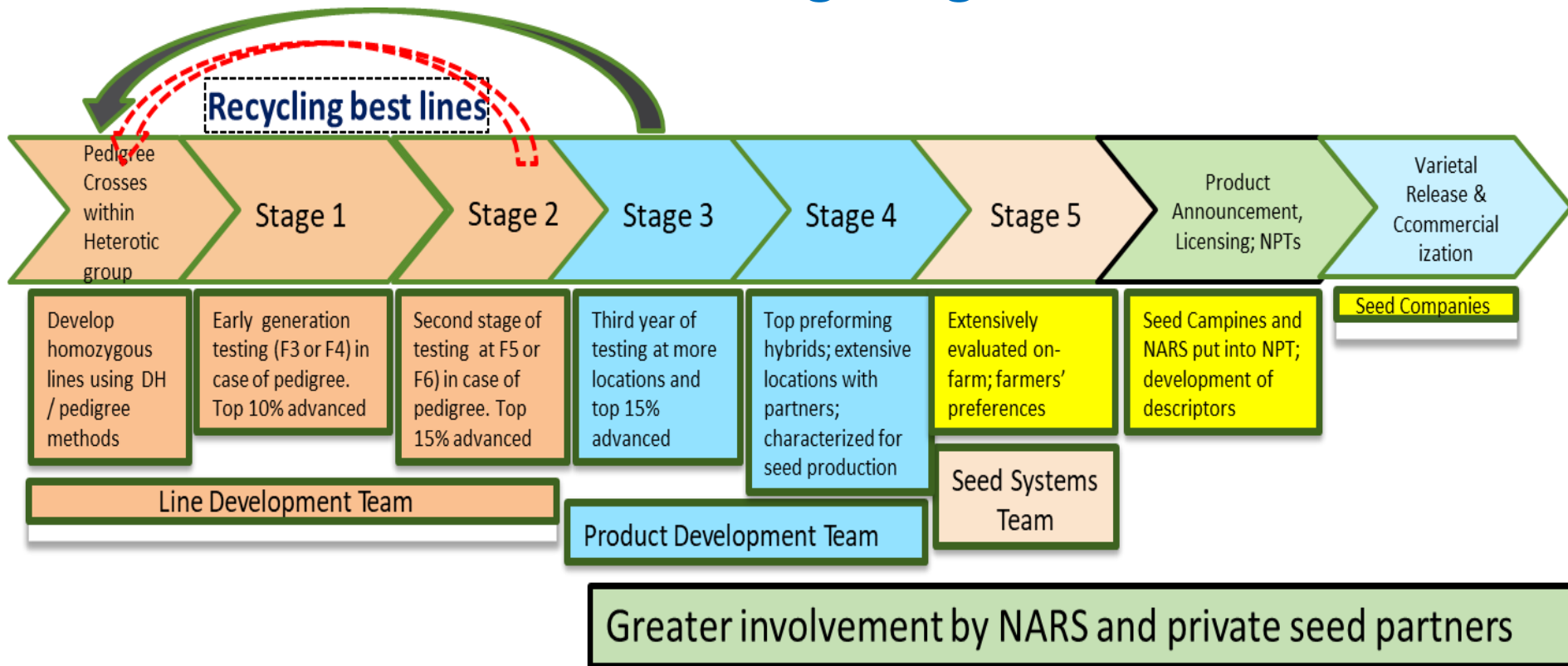
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Regional Maize Breeding Coordinator and AGG Maize Project Leader

**Presentation to the Product Profile Based Breeding for Increased Genetic Gains 6-10
December 2022, Concord Hotel, Nairobi**



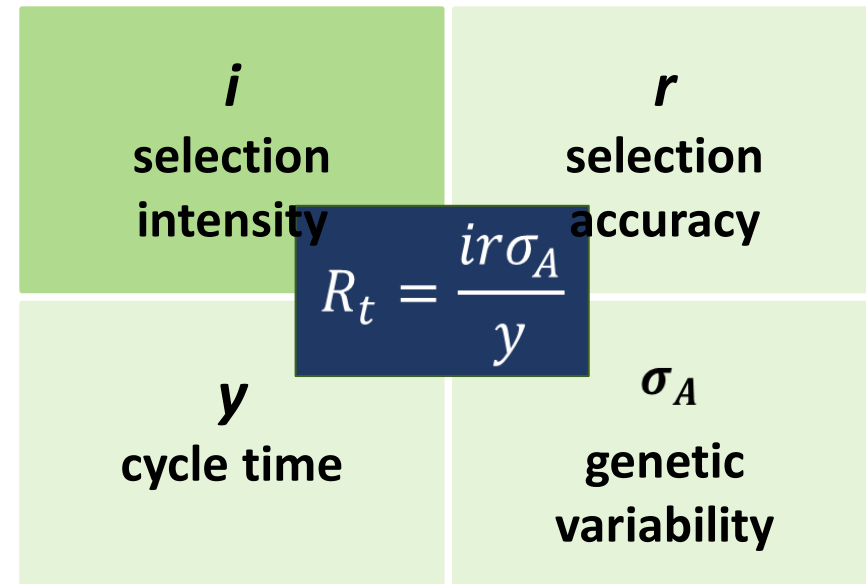
CIMMYT Maize Breeding: Stage-Gate Process



- **Stage 1** – First testcross evaluation; one tester; 2 reps, 3-5 sites
- **Stage 2** – Selected lines (10-15% S.I.) from Stage 1 trials; 3 testers; 2 reps, 8-10 sites
- **Stage 3** – Selected lines from Stage 2 trials (15% S.I.); Cross with 5 testers; 2 reps, 10-15 locations
- **Stage 4 (Regional On-station Trials)** – Best products from Stage 3; 2 rows, 3 reps, 25-35 locations
- **Stage 5 (Regional On-Farm Trials)** – 30-50 on-farm trials per Product Profile; Farmers' preferences
- **Final Product Advancement Meeting** to identify products/pre-commercial hybrids to be announced to the partners through CIMMYT Website

Breeding Schemes Optimization in AGG-Maize

- Recycling lines at an early stage of testing (reduced from 6 yrs. to 4 yrs.)
- Develop suitable selection indices for parental selections (DESIER software)
- Identify optimum number of testing locations and testers for recycling
- Sparse testing and sparse genetic testcrossing (implemented in selected PPs)
- Use of genomic selection (all stage 1 lines being genotyped with medium density markers)
- Estimate predicted genetic gain (done in selected PPs)
- Incorporation of ex-PVP lines into tropical lines improved yield potential
- Refining and strengthening heterotic groups
- Responding to emerging threats



Forward Breeding: Using Msv1 haplotype for selection of MSV resistance at early stage of testcross formation

Sampling leaf tissue in the DH nursery

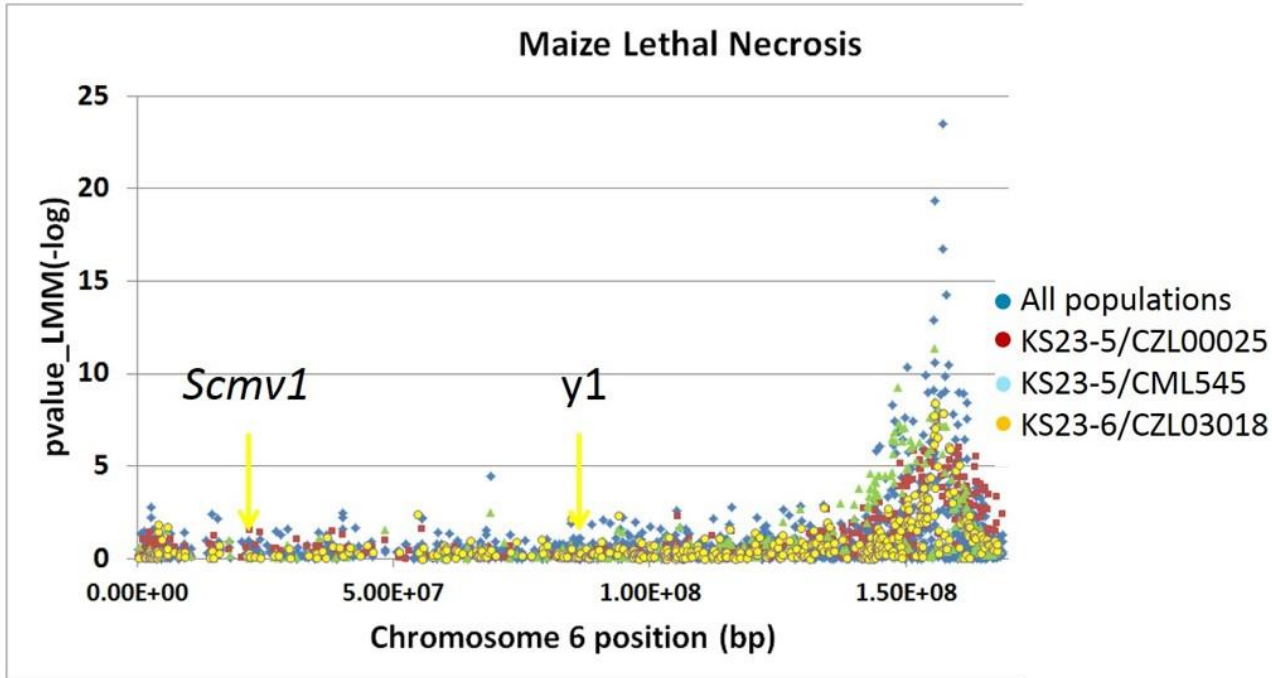


SNP	Trait	Chr	SNP	RR	SS
PZE0186065237	MSV	1	C/T	C:C	T:T
PZE0186365075	MSV	1	C/A	C:C	A:A
PZE-10109395	MSV	1	A/G	A:A	G:G

Population	PZE-101093951	PZE0186065237	PZE0186365075	Comment on msv1 data	Decision
CML312/INTA-F2-192-2-1-1-1-B*7-2-B-10-B-B-B:@	A:A	C:C	C:C	Homozygous for favorable alleles at 3 loci	Select
CML312/INTA-F2-192-2-1-1-1-B*7-2-B-10-B-B-B:@	A:A	C:C	C:C	Homozygous for favorable alleles at 3 loci	Select
CML312/LaPostaSeqC7-F18-3-2-1-1-B-B-B:@	A:A	C:C	C:C	Homozygous for favorable alleles at 3 loci	Select
CML312/LaPostaSeqC7-F18-3-2-1-1-B-B-B:@	A:A	C:C	C:C	Homozygous for favorable alleles at 3 loci	Select
CML312/LaPostaSeqC7-F18-3-2-1-1-B-B-B:@	G:G	T:T	A:A	Homozygous for unfavorable alleles at 3 loci	Reject
CML312/LaPostaSeqC7-F18-3-2-1-1-B-B-B:@	G:G	T:T	A:A	Homozygous for unfavorable alleles at 3 loci	Reject
CML312/LaPostaSeqC7-F18-3-2-1-1-B-B-B:@	G:G	T:T	A:A	Homozygous for unfavorable alleles at 3 loci	Reject
CML312/LaPostaSeqC7-F18-3-2-1-1-B-B-B:@	G:G	T:T	A:A	Homozygous for unfavorable alleles at 3 loci	Reject



Fine-mapping of a major QTL for MLN resistance



- The major QTL on Chr. 6 is being fine-mapped by Corteva team, in collaboration with CIMMYT
- Target for **gene editing** for MLN resistance in collaboration with Corteva

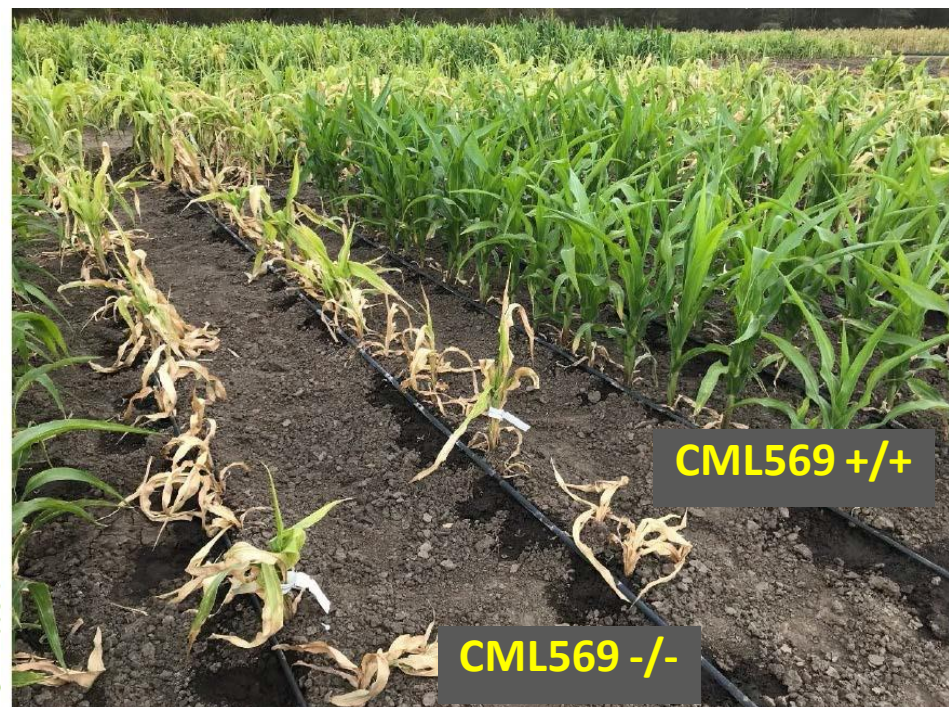
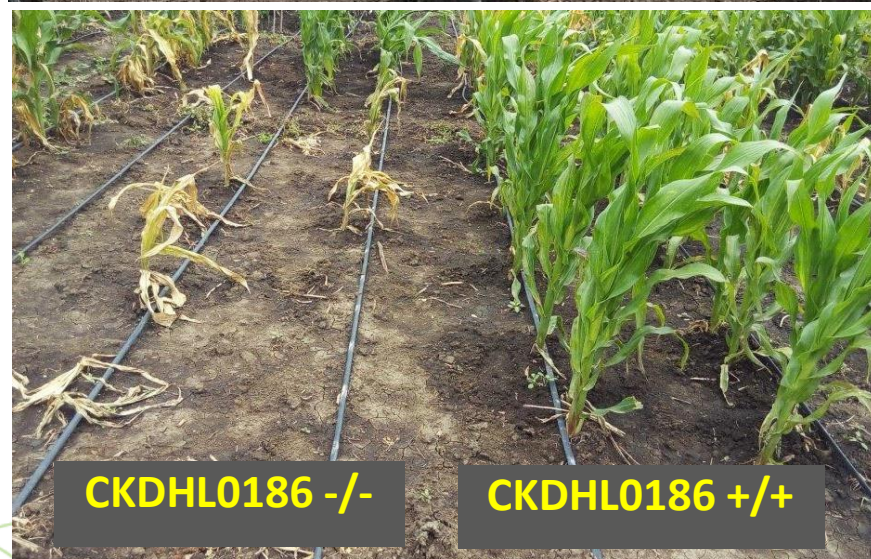


KS23-6: MLN resistant; MSV-susceptible; Yellow kernels

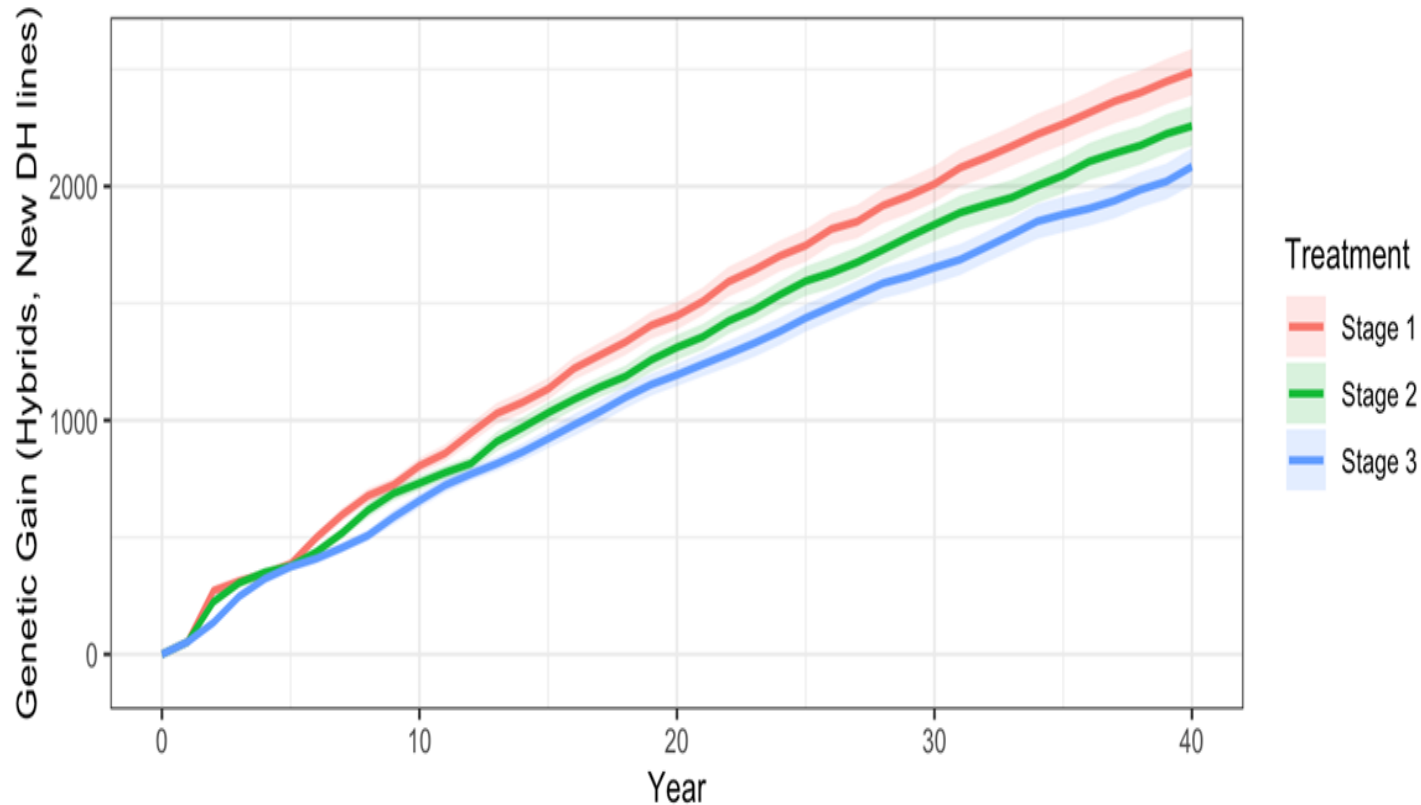


CML395: MLN-susceptible; Drought-tolerant; MSV-resistant; White kernels

MLN Resistance through MABC



Reducing tyhe breeding cylce: Simulation for Recycling Lines at Early Stage of Testing



Simulation results comparing the current recycling at Stage 3 vs recycling after Stage 1 and 2 testing using data from EA-PP1. Recycling after Stage 1 or Stage 2 could deliver increase genetic gain by **17% and 9%** compared to recycling at Stage 3, respectively



Sparse Phenotyping

Background

- Testing of N entries in L locations of a MET.
- Trials can be replicated or unreplicated.
- Trial location shall represent TPE
- Estimate genetic values by (adjusted) means across locations

Idea

- Test each entry only in a subset of locations
- Predict missing information from relatives

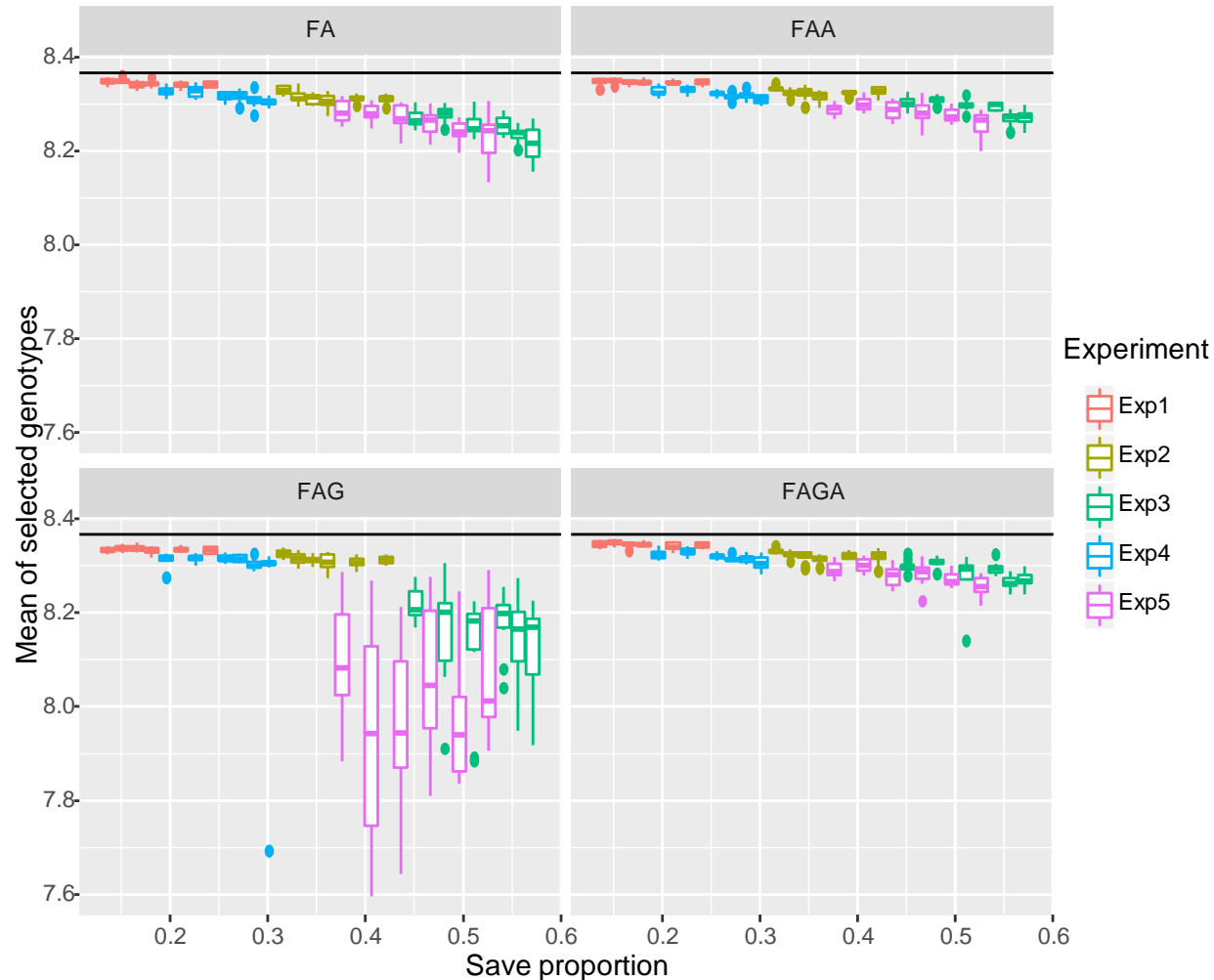
Goals: At same costs

- Test more entries
- Test same entries in more locations
- A combination of both



Sparse phenotyping to sample TPE

- Phenotypic data for 2018 Stage II trials (900 hybrids)
- Evaluated at 5 locations in Kenya
- Genotypic data for lines used in stage II trials
- Different experimental layout for sparse testing
- 4 types of analysis:
- Factorial analysis (FA),
- FA + CoP
- FA+ Marker data
- FA+ Marker + CoP



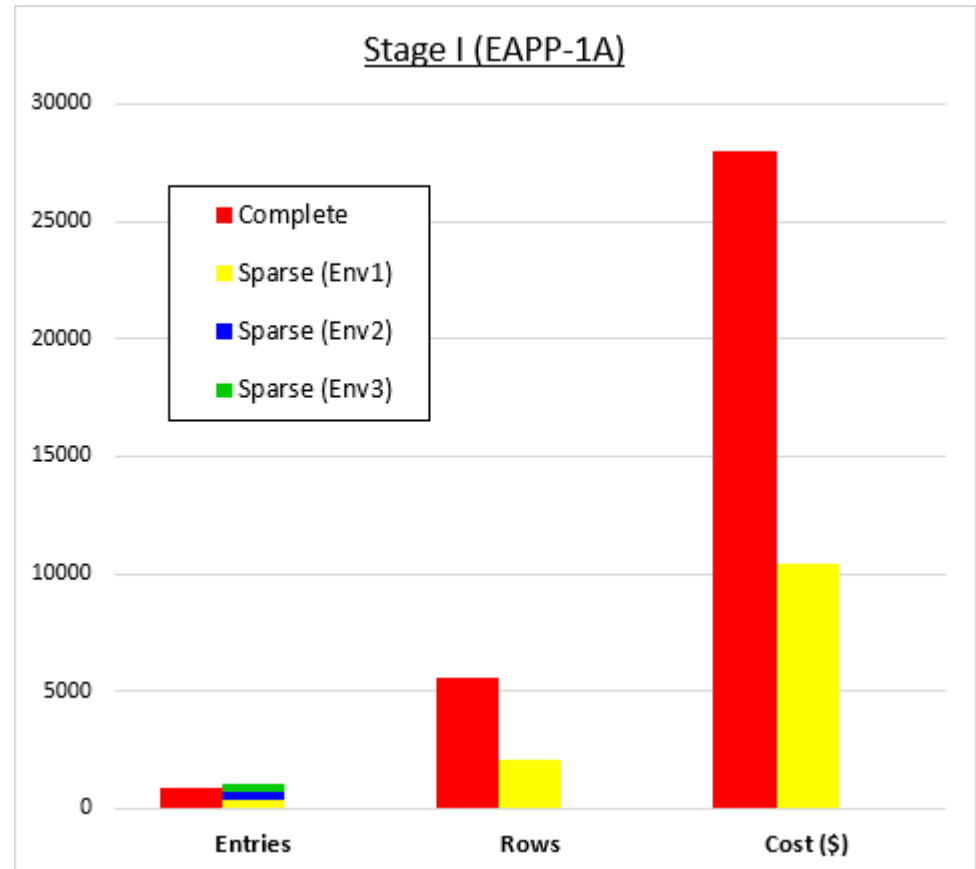
The horizontal black line is the mean of the hybrids selected under complete phenotyping (8.36 t/ha)

Conclusion: By saving 30% the phenotypic cost, 90% of the best hybrids were common between complete phenotyping and sparse phenotyping

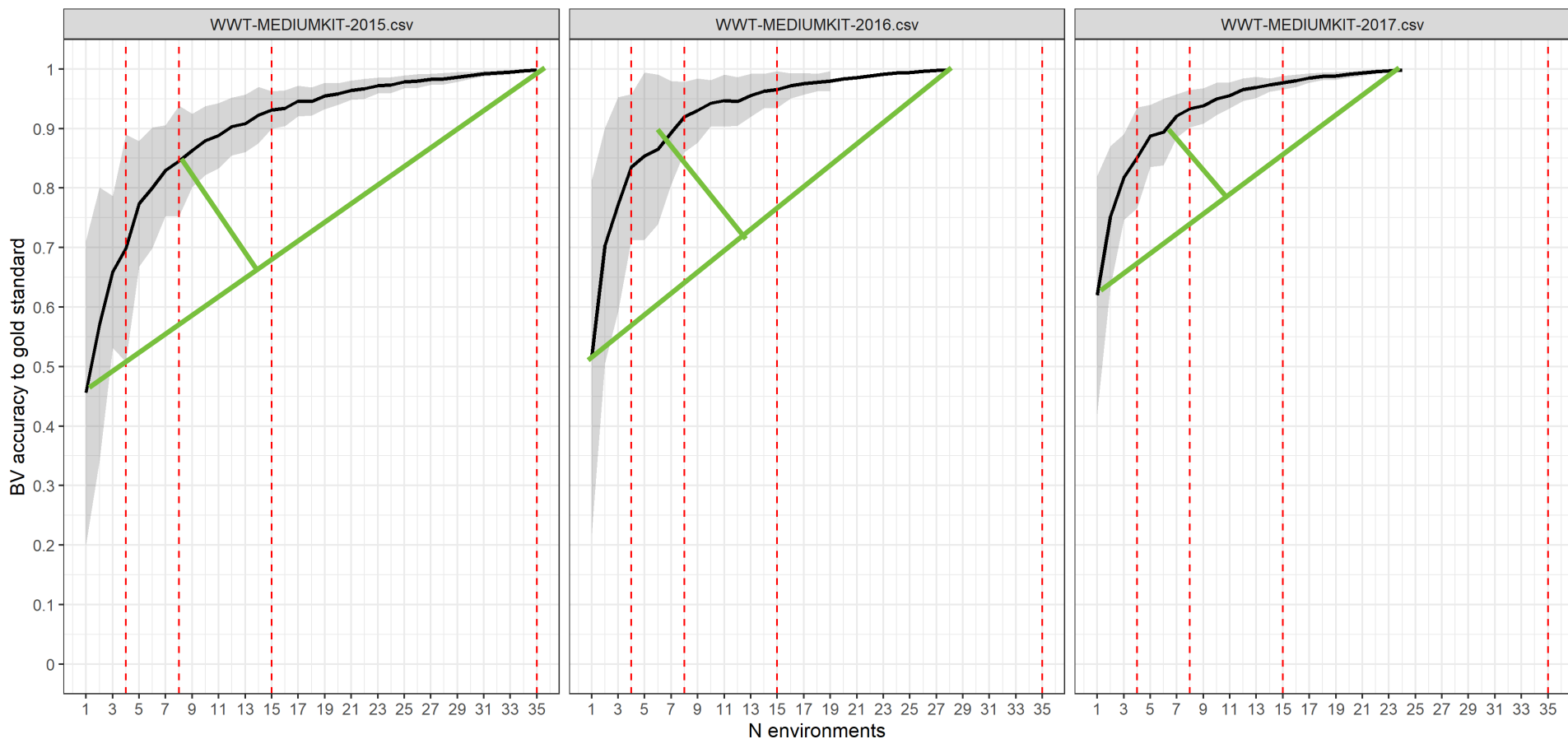
Sparse phenotyping being implemented in ESA

- Total number of stage 1 entries =928
- # Checks =4
- # entries evaluated in all sites=52
- # Entries to be valuated in sparse design (928-52=876)
- # entries evaluated at one of the three site (876/3=292)

	Env1	Env2	Env3	Total
Full set (1)	52	52	52	
Set 2	292	---	---	
Set 3	---	292	---	
Set 4	---	---	292	
# checks	4	4	4	
total # entreis /s	348	348	348	
Entries	348	348	348	932
Reps	2	2	2	2
Locations	1	1	1	3
Rows	696	696	696	2,088
Cost (\$)	3480	3480	3480	10,440



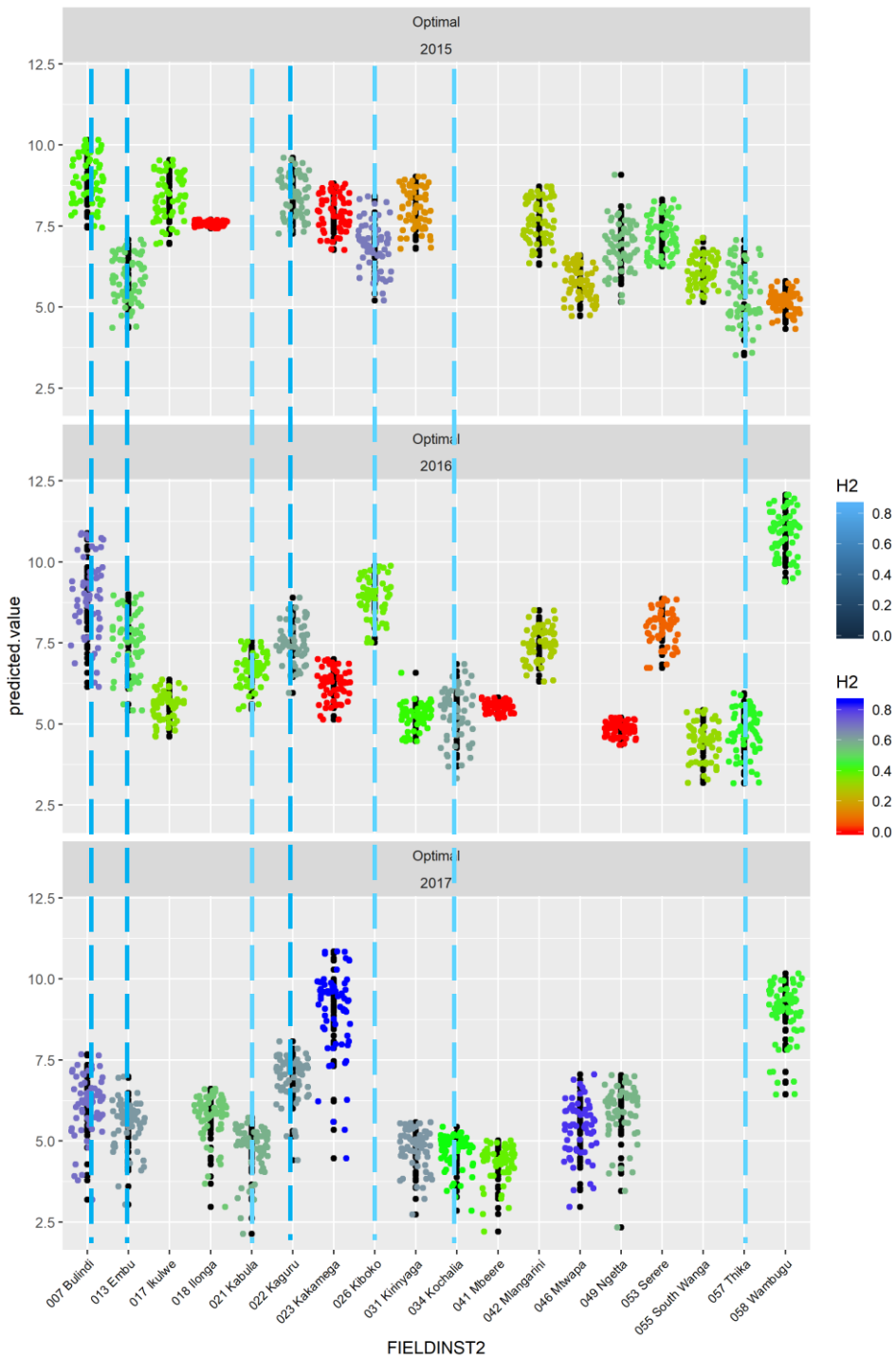
Identification of the optimal number of environment to accurately select across the TPE



Results from cross validation to know the accuracy between real (across the entire TPE) and estimated BV when selecting a given number of environments (we assume the max #of environments represent the real BV).

Optimizing recycling through retrospective analysis to identify locations with high heritability and high genetic variance

Results from single environment heritability across 3 years of data. We assume that environments with highest H2 and genetic variance represent the best locations for applying selection



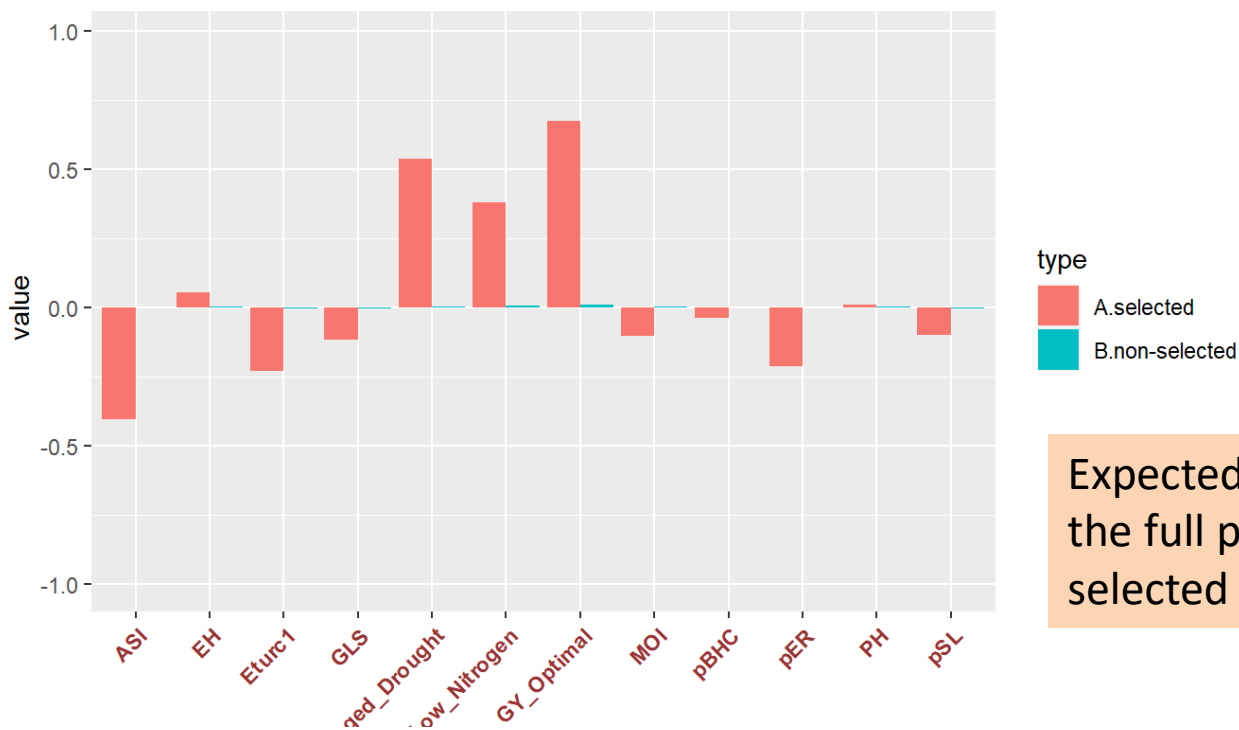
Develop suitable selection indices for parental selections (DESIRE software)

No. of Entries	600
No. of Test Hybrids	588
No. of Checks	12
No. of Lines	198
No. of Testers	3

Traits used for SI	H2
GY_Managed_Drought	0.83
GY_Managed_Low_Nitrogen	0.46
GY_Optimal	0.86
pER	0.90
pSL	0.87
pBHC	0.85
Eturc1	0.81
MOI	0.88
PH	0.95
EH	0.97
GLS	0.73
ASI	0.92

Example of genetic merit

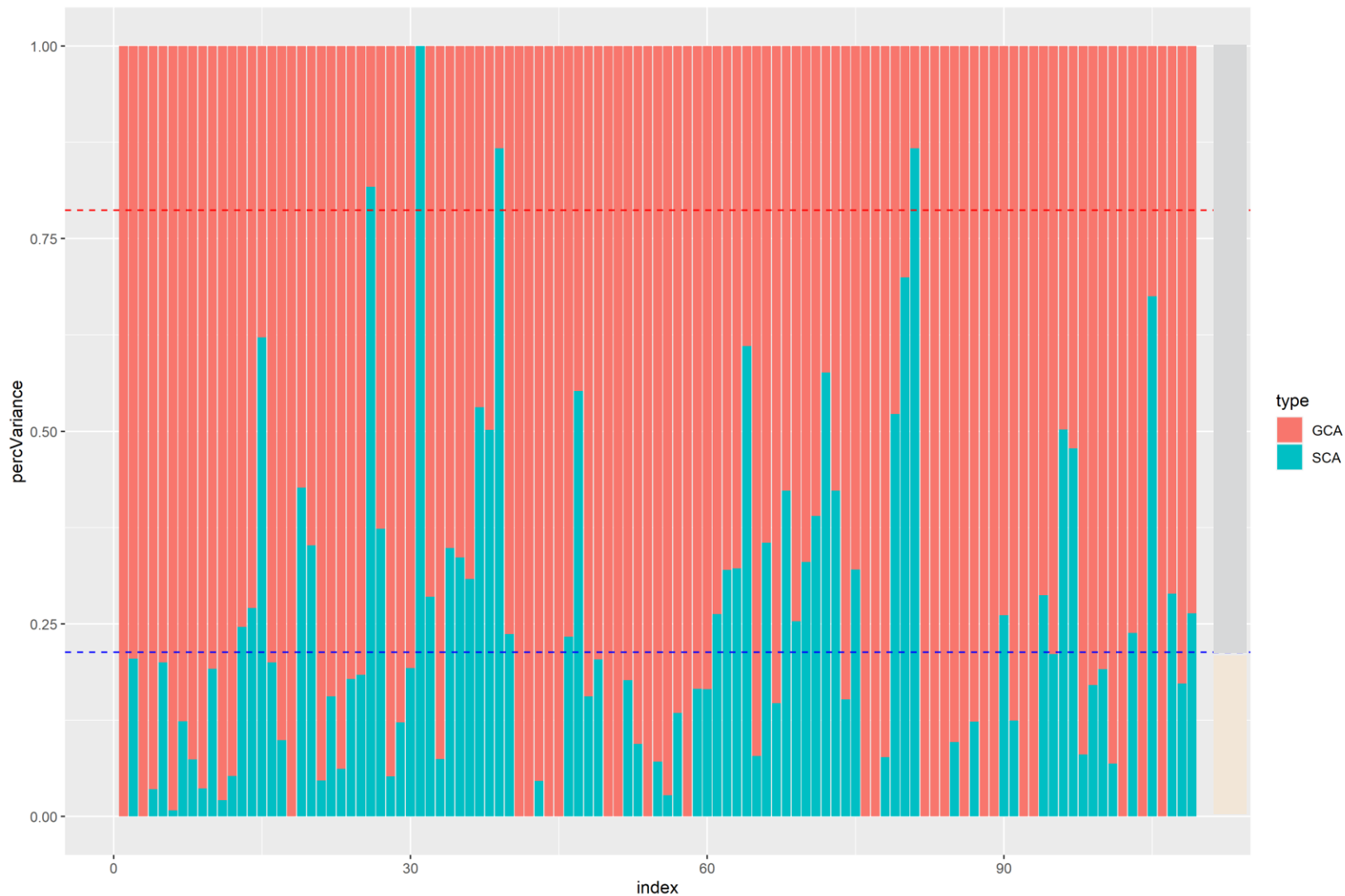
Line	Merit	Rank
CKDHL1715901	1.96	1
CKDHL1715896	1.77	2
CKDHL1715915	1.34	3
CKDHL1715480	-1.33	196
CKDHL1715260	-1.49	197
CKDHL1720872	-1.34	198



Expected changes in mean between the full population of lines versus a selected top 20% the lines using index.

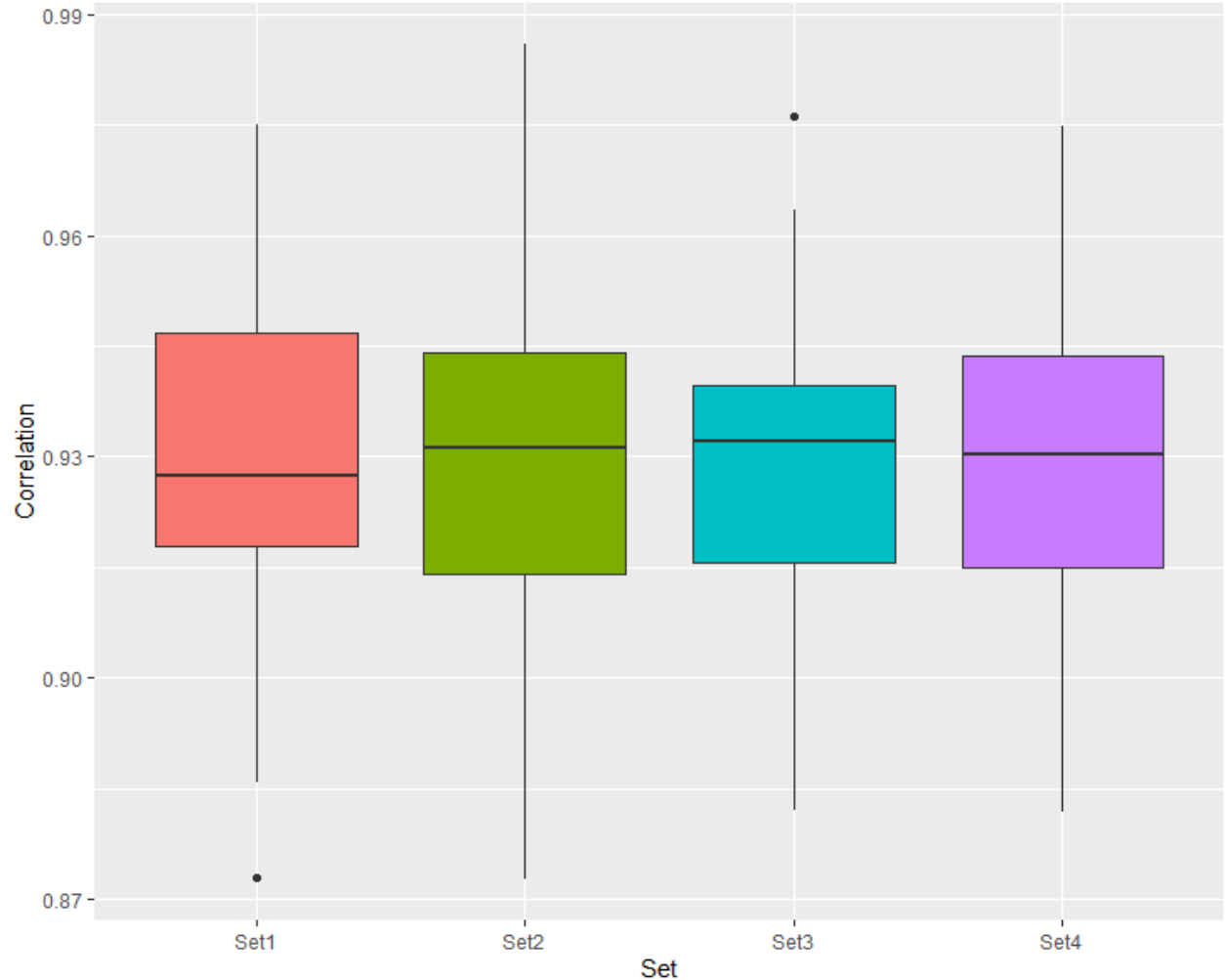


Analyzing mode of inheritance (GCA and SCA)



Sparse genetic testcrossing testcrossing

Option 3			
To phenotype			
Set	Lines	Testers	TC
1	48	1-2-3	144
2	85	1	85
3	85	2	85
4	85	3	85
Total			399
To predict			
Set	Lines	Testers	TC
1	85	2-3	170
2	85	1-3	170
3	85	1-2	170
Total			510



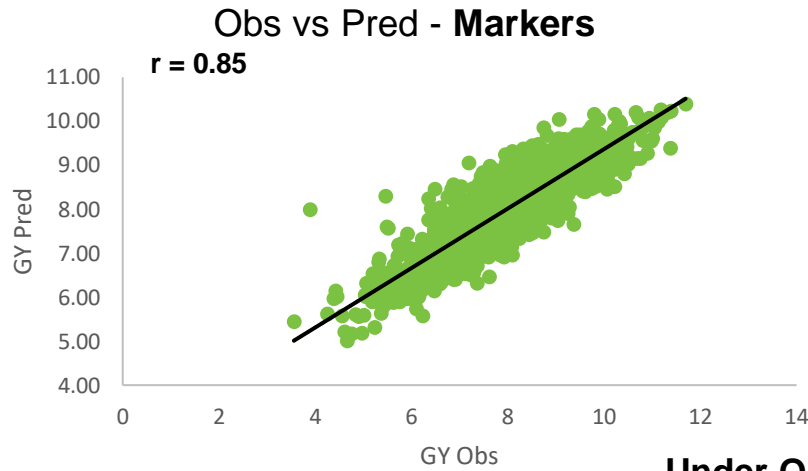
Spearman correlation between observed and predicted line-breeding value (n=50).
 Set 1 line crossed with all testers, set 2-4 lines crossed with one tester, predicted with the other two testers.

Sparse genetic testcrossing being applied on stage 1 in 2022 (EAPP1 and SAPP1) that allow us to estimate BLUP GCA to further reducing the breeding cycle

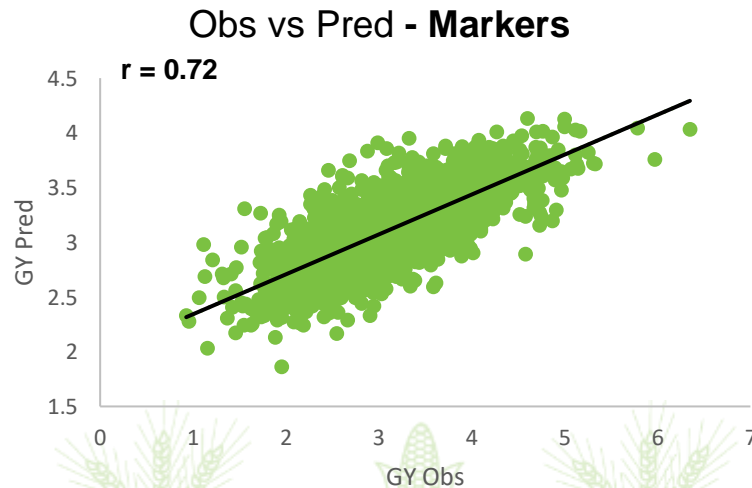
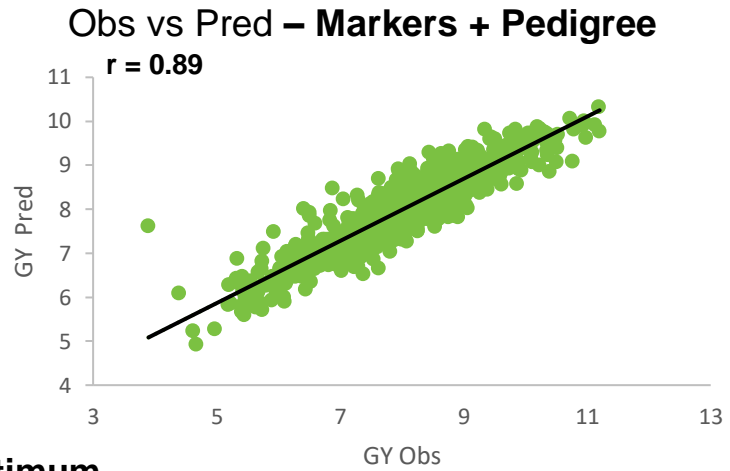
	660 DH lines from heterotic group A divided into three groups and crossed with one of the three testers		
Tester	Group 1 (165 DH lines)	Group 2 (165 DH)	Group 3 (165 DH)
CKDHL0500/CML543	Yes	No	No
CML566/CML607B	No	Yes	No
CML444/CML546	No	No	Yes
	540 DH lines from heterotic group B divided into three groups and crossed with one of the three testers		
	Group 1 (180)	Group 2 (180)	Group 3 (180)
604A/CML539	Yes	No	No
CKDHL120423/CKLTI0344	No	Yes	No
CML568/CML572	No	No	Yes



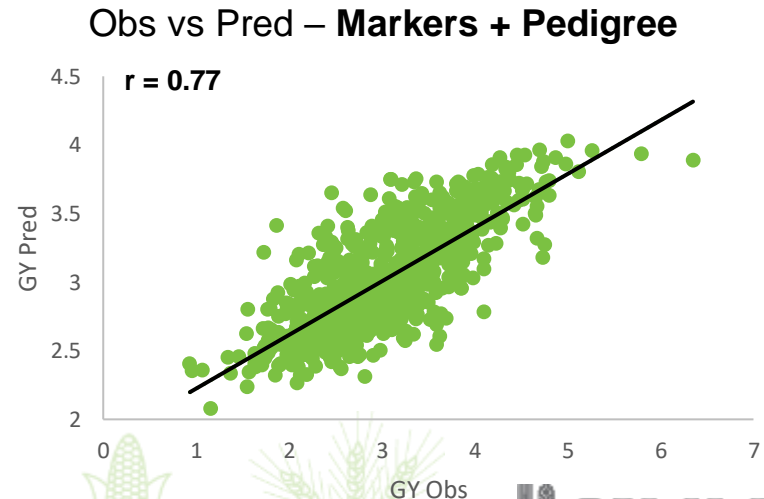
Genomic selection using test half-predict-half strategy –incorporating pedigree



Under Optimum



Under drought stress



Advancement of lines based on GEBV and PS:

Population	CML536/LPS-F64
# DH genotyped	166
# DH lines phenotyped	88
# lines selected based on Phenotype	21
# lines selected based on GEBV	19

Check	GY(t/ha)_Opt	GY(t/ha)_MD	MOI-Opt	PH_Opt
H517	6.5	1.8	16.4	267.4
Pioneer 30G19	6.2	2.9	17.9	254.5
WH505	7.6	3.1	17.9	257.3
Heritability	0.64	0.52	0.3	0.8
Genotype Variance	0.70	0.21	0.3	79.8
GenxLoc Variance	0.13		0.3	16.2
Residual Variance	2.06	0.39	4.0	81.5
Grand Mean	6.81	3.10	18.2	248.8
LSD	1.43	0.93	1.4	11.6
CV	21.07	20.27	10.9	3.6
n Replicates	2	2	2	2
n Locations	3	1	3	3

SN	name	Observed GY_BLUE_optimal	Predicted GY_BLUE_optimal	Observed GY_BLUE_drought	Predicted GY_BLUE_drought
1	CKDHL152921	9.1	7.6	3.1	3.1
2	CKDHL152857	8.8	7.6	4	4
3	CKDHL152610	8.4	7.7	4.7	3.8
4	CKDHL152563	8.4	7.7	4.2	3.6
5	CKDHL152554	8.3	7.7	3.6	3.3
6	CKDHL152653	8.3	7.8	3.3	3.3
7	CKDHL152616	8.2	7.3	4.3	4.1
8	CKDHL152617	8.2	7.2	3.8	3.4
9	CKDHL152821	8.2	7.3	3	3.1
10	CKDHL152733	8.1	7.5	4.2	3.4
11	CKDHL152658	8.1	7.2	3.4	3.2
12	CKDHL152638	8.1	7.5	3.6	3.1
13	CKDHL152976	8	7.5	3.3	3.4
14	CKDHL152591	8	7.6	3.7	3.6
15	CKDHL152906	7.6	7.2	3.6	3.2
16	CKDHL152751	7.5	7.3	3.6	3.8
17	CKDHL152769	7.4	7.2	4.7	3.8
18	CKDHL153005	7.4	7.1	4	3.7
19	CKDHL152929	7.3	7	3.9	3.8
20	CKDHL152866	7.1	7.2	4.3	3.7
21	CKDHL152962	7	7	4.3	3.5
1	CKDHL152820	NA	7.6	NA	3.5
2	CKDHL152994	NA	7.5	NA	3.7
3	CKDHL152529	NA	7.5	NA	3.5
4	CKDHL152590	NA	7.5	NA	3.3
5	CKDHL152811	NA	7.4	NA	3.8
6	CKDHL152682	NA	7.4	NA	3.4
7	CKDHL152579	NA	7.4	NA	3.5
8	CKDHL152927	NA	7.4	NA	3.5
9	CKDHL152759	NA	7.4	NA	3.9
10	CKDHL152890	NA	7.4	NA	3.3
11	CKDHL152689	NA	7.4	NA	3.1
12	CKDHL152632	NA	7.3	NA	3.3
13	CKDHL152773	NA	7.3	NA	3.9
14	CKDHL152862	NA	7	NA	3.9
15	CKDHL152813	NA	7	NA	3.8
16	CKDHL152879	NA	7.2	NA	3.8
17	CKDHL152777	NA	7	NA	3.7
18	CKDHL152849	NA	7.2	NA	3.7
19	CKDHL152778	NA	7.2	NA	3.6

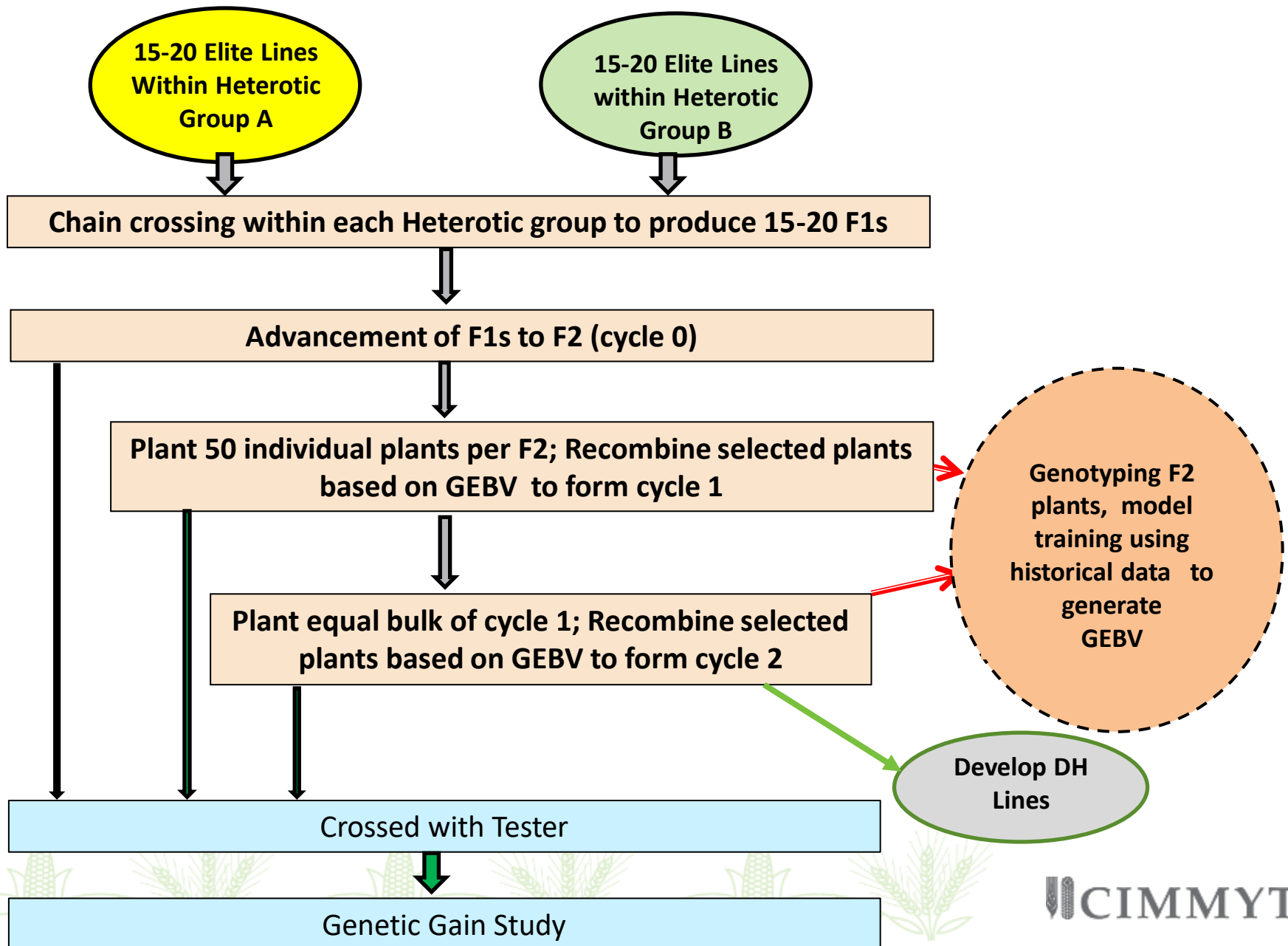


Lines developed through RCGS are being used as the parent of allocated hybrids to partners

Line	Parent in # allocated hybrids
CKLMARS1C3S50268	1
CKLMARS1C3S50080	2
CKLMARS1C3S50113	3
CKLMARS1C3S50140	2
CKLMARS1C3S50137	1



Rapid Cycle of GS Workflow



Mechanization of breeding hubs: Improving efficiency and accuracy

Planter



Seed treater



Combined harvester



Drip Irrigation at Kiboko



**Thank you
for your
interest!**