Molecular Assisted Breeding in Maize

February 21, 2018

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Maize Novel Tools and Germplasm

- **Vision**: To improve input use efficiency and reduce production risk of small holder maize farming systems by **enhancing the rate of genetic gain** for economically important traits through the application of innovative technology and novel germplasm

MAIZE CRP CoA 2.2 Organization

- 2.2.1 – DH cost reduction
- 2.2.2 – Forward Breeding applications (Deployment)
- 2.2.3 – Trait Pipeline (Discovery and Validation)
- 2.2.4 – Genomic Selection

MAIZE CRP CoA 2.2 Organization

- **2.2.3 – Trait Pipeline (Discovery and Validation)**
- Trait teams

Priority 1	Priority 2	Priority 3
TSC	TLB	BLSB
MLN	GLS	PFSR
MSV	Low P	DM
PVA	Low N	QPM
Zinc	Acid Soil	CMS
Striga	Drought	CSC
Aflatoxin	Heat	Waterlogging
(Ms44)	Temperate Introgression	Herbicide susceptibility
FAW		Highland Adaptation

Strategic teams

- QA/QC
- Genomic Selection

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Global Trait Pipeline

Molecular Discovery → Molecular Deployment → Line Development → Product Development → Seed Systems

Discovery
- MLN
- Heat
- Striga

Validation
- MLN
- GLS
- TLB
- Drought
- Low N
- Mycotoxin

Deployment
- MLN
- MSV
- PVA
- **TSC**

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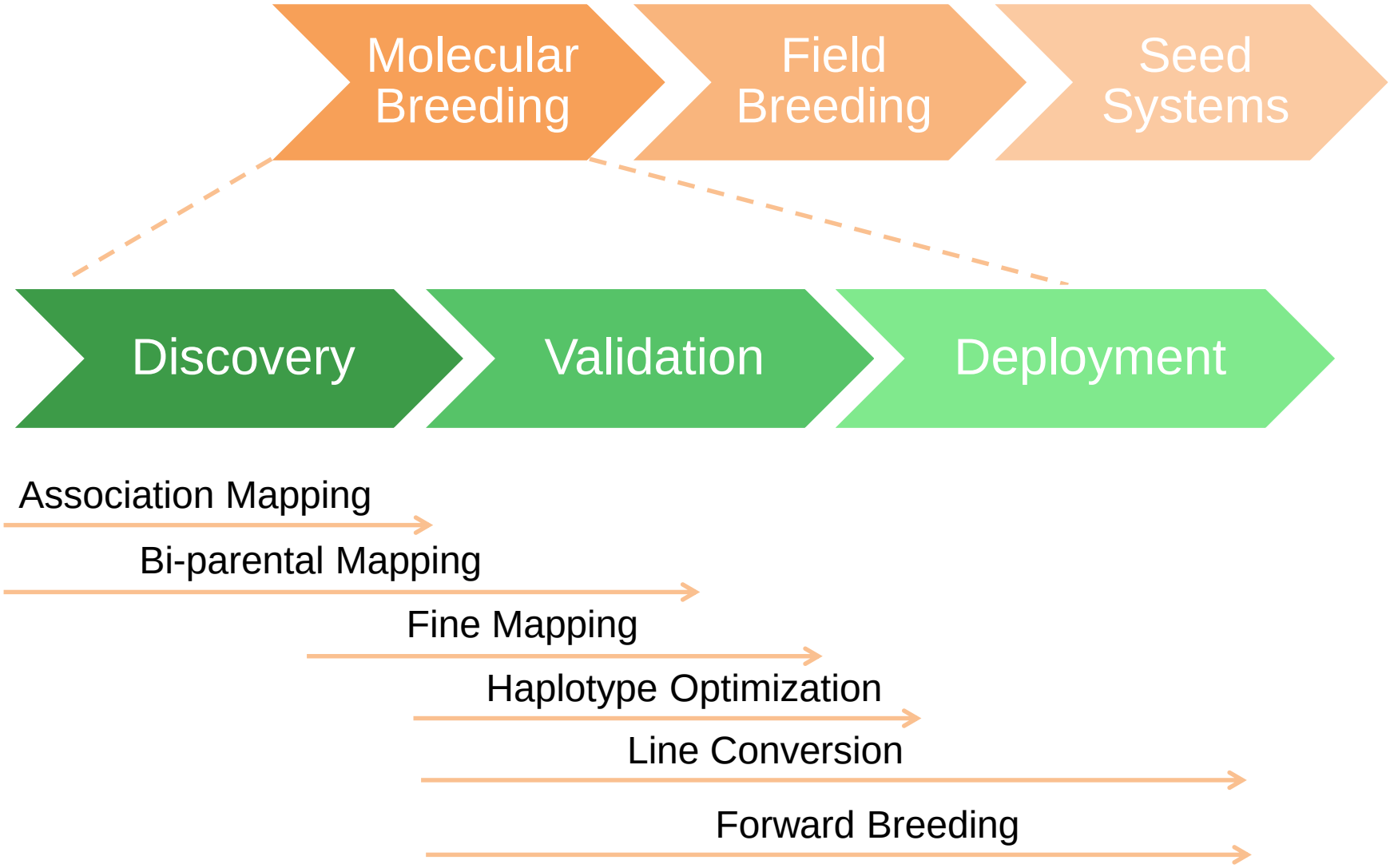
Molecular Breeding
Field Breeding
Seed Systems
Discovery
Validation
Deployment
Association Mapping
Bi-parental Mapping
Fine Mapping
Haplotype Optimization
Line Conversion
Forward Breeding

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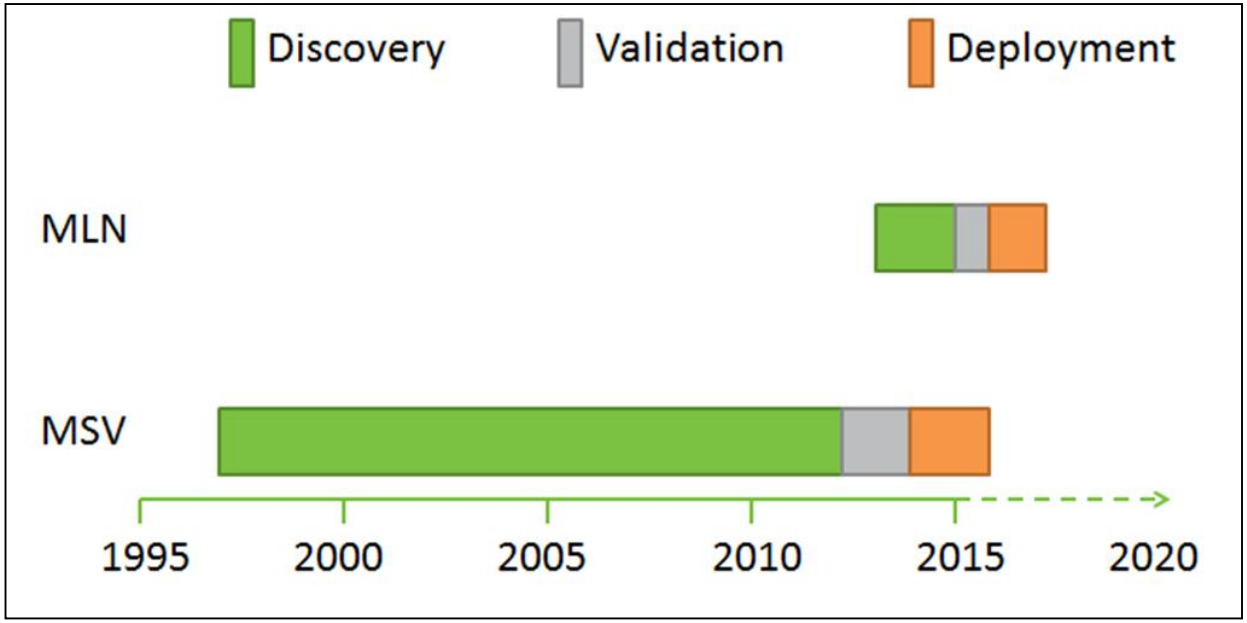
Critical Path Analysis

- Optimization of discovery to deployment pipeline
- Focus on critically time-sensitive steps
- Role specialization to improve efficiency at bottlenecks
- Integration with breeding workflows



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Trait Pipeline

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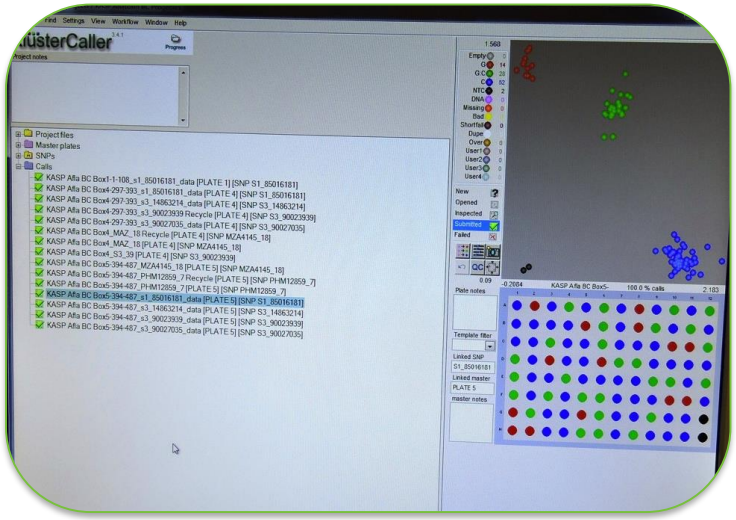
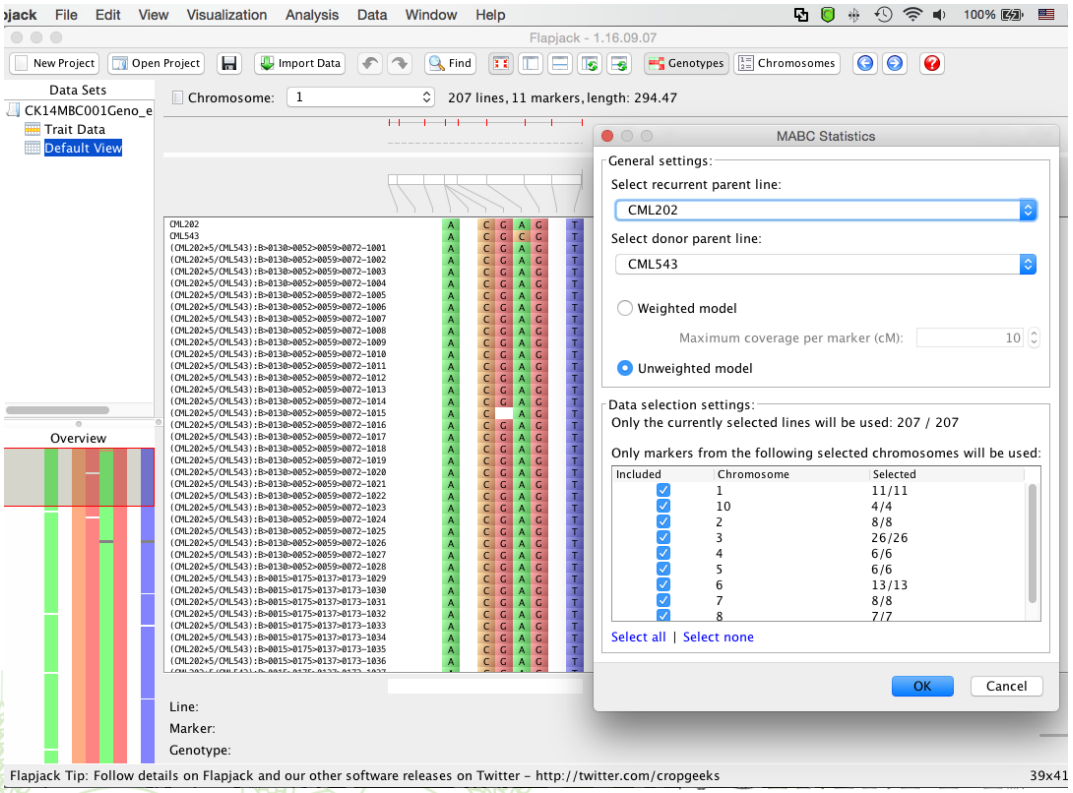
Aflatoxin resistance



- Validated haplotypes from Mississippi State Univ. (M. Warburton) being evaluated for efficacy in Africa
- Marker-assisted backcrossing for introgression of Aflatoxin resistance in Maize
  - 400 BC1 genotyped and about 15% selected for recombination
- MSU x CIMMYT bi-parental populations in field trials 2018



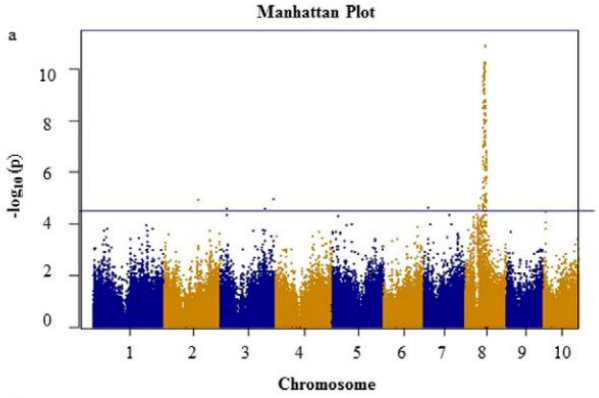
Genome-Wide Analysis of Tar Spot Complex Resistance in Maize Using Genotyping-by-Sequencing SNPs and Whole-Genome Prediction

The Plant Genome [Volume 10, Issue 1, March 2017]

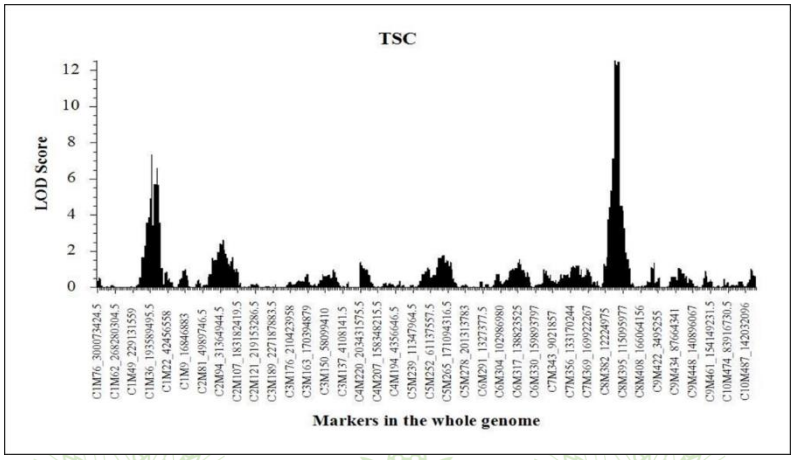
Shiliang Cao, Alexander Loladze, Yibing Yuan, Yongsheng Wu, Ao Zhang, Jiafa Chen, Gordon Huestis, Jingsheng Cao, Vijay Chaikam, Michael Olsen, Boddupalli M. Prasanna, Felix San Vicente*, and Xuecai Zhang*

Tar spot complex

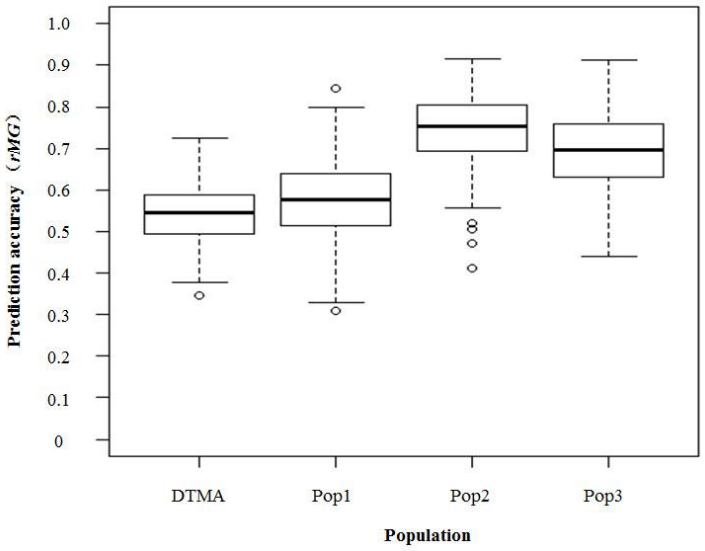
GWAS



Linkage Mapping

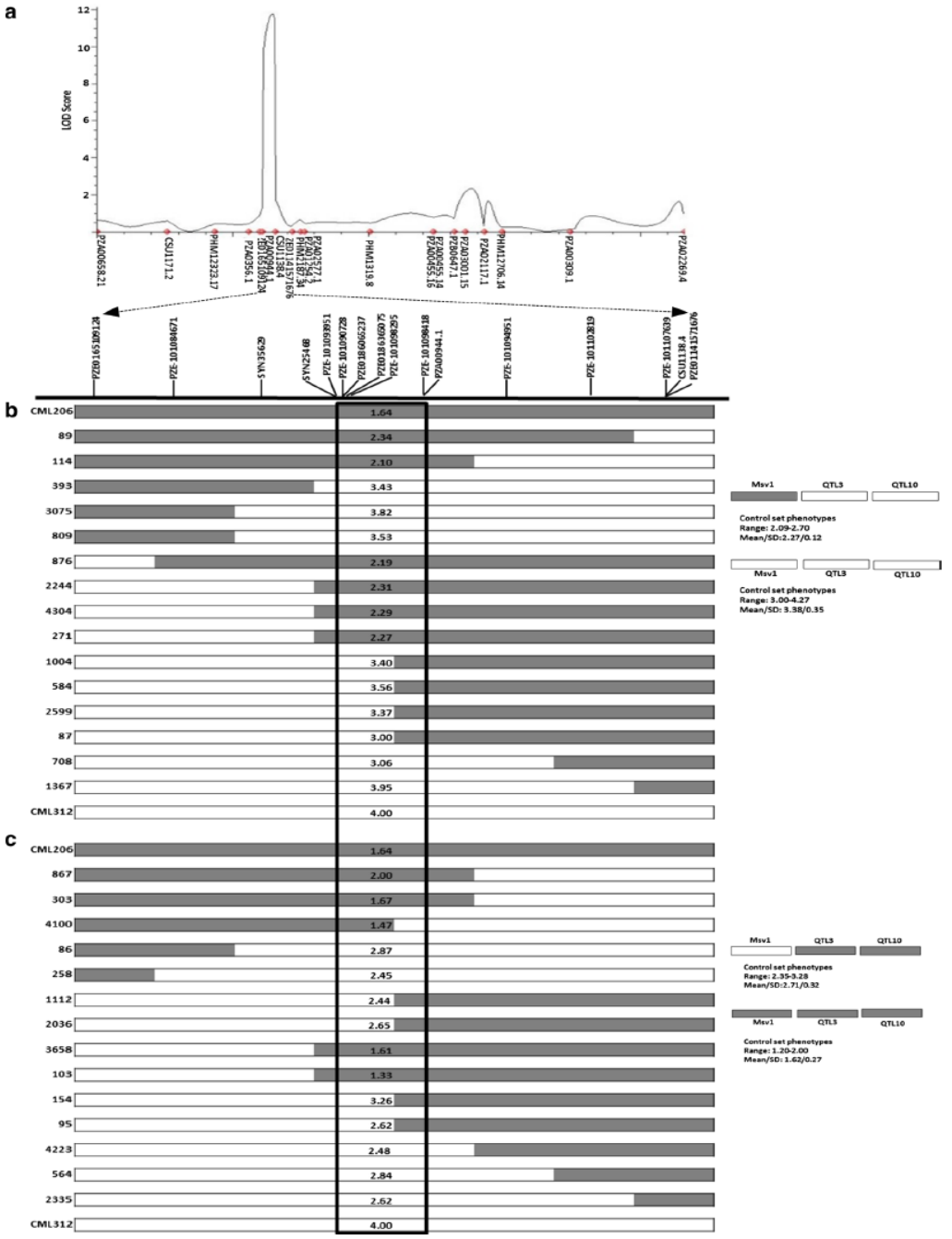


GS



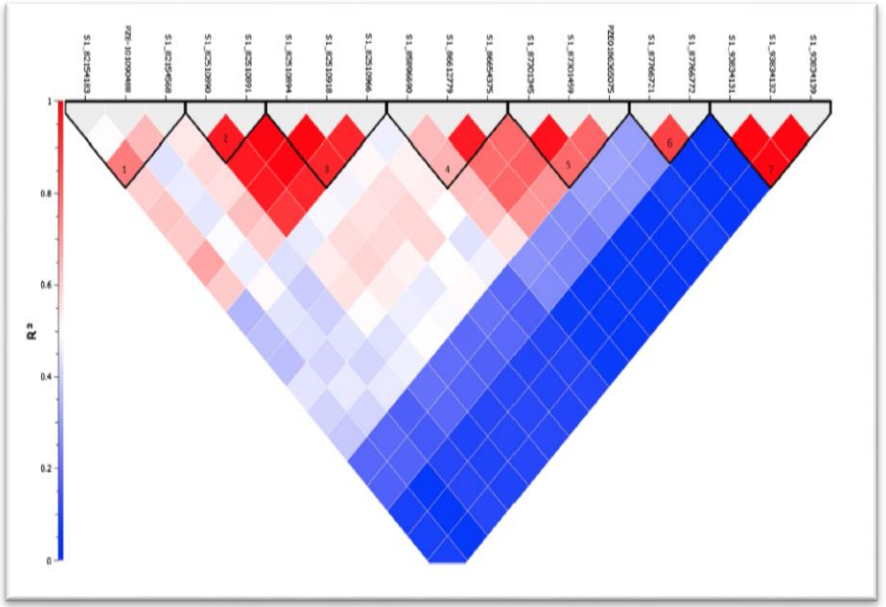
Fine mapping *Msv1* locus for resistance to Maize streak virus in Africa

Followed a QTL isogenic recombinant (QIR) strategy to fine map to a genetic interval of 0.87 cM



Production markers for *Msv1*

- 0.87 cM ~7Mb physical distance
- Validation confirmed 94% accuracy for selection with favorable haplotype
- >50000 lines screened with *Msv1* since 2015



Theor Appl Genet
DOI 10.1007/s00122-015-2551-8

ORIGINAL PAPER

Fine mapping of *Msv1*, a major QTL for resistance to Maize Streak Virus leads to development of production markers for breeding pipelines

Sudha K. Nair[1] · Raman Babu[1] · Cosmos Magorokosho[2] · George Mahuku[3] · Kassa Semagn[3] · Yoseph Beyene[3] · Biswanath Das[3] · Dan Makumbi[3] · P. Lava Kumar[4] · Michael Olsen[3] · Prasanna M. Boddupalli[3]

Maize Lethal Necrosis

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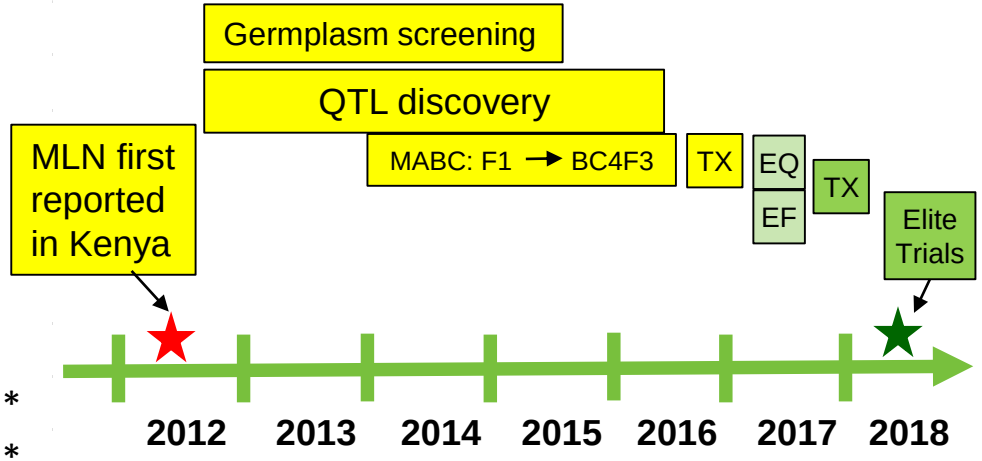
MLN QTL deployment

MLN Conversions			
CML202	CML539	DTPWC9-F67-2-2-1	
CML312	CML540	LPSC7-F103-2-2-2	
CML341	CML544	LPSC7-F180-3-1-1	
CML343	CML545	LPSC7-F64-2-6-2	
CML373	CML546	CKL05015	
CML442	CML547	CLRCY034	**
CML444	CML548	CML574 (CLRCY039)	**
CML445	CML550	CLYN231	**
CML489	CZL052	CLWN270	**
CML507	CZL068	DTPYC9-F46-1-2-1	**

** MLN tolerant lines converted from yellow to white + MSV1



- 3 generation per year nursery
- BC4F3 Testcross evaluation
- BC4F4 Line evaluation

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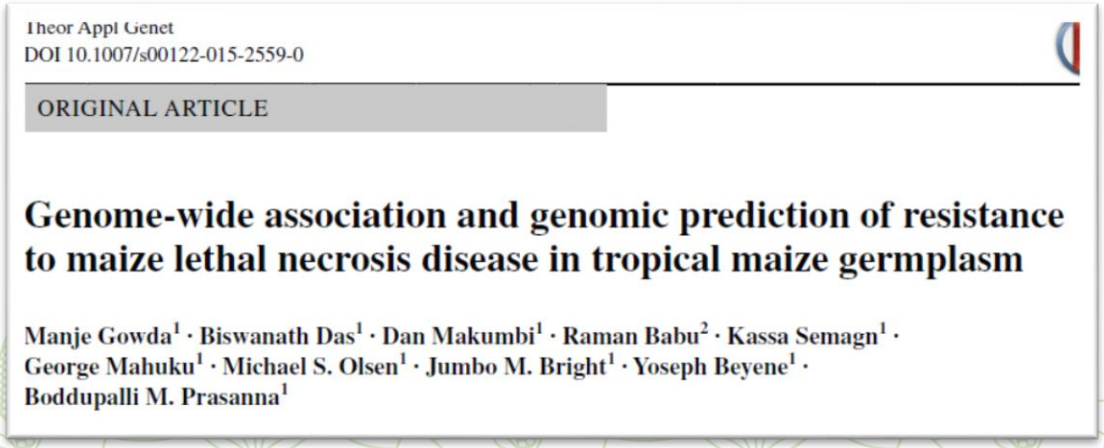
	HG A DONORS				HG B DONORS			
Haplotype	DTPF46	CLWN270	CLYN261	CML509	CLRCY034	CML574	CML494	CML543
MLN_01.002							1	
MLN_02.185			1					
MLN_02.194	1		6			2		1
MLN_03.044	1		8			1		
MLN_03.113			2					
MLN_03.133	3	1	2		1	2		
MLN_03.140								9
MLN_03.171							4	
MLN_03.189	2	1	7		1	2		
MLN_06.020								8
MLN_06.166			5					
MLN_07.142							3	
MLN_07.158								2
MLN_08.074	2					1		
MLN_09.108							4	
MLN_09.146			1					
MSV_01.087				3				3
Y1_06.082				3				2


Theor Appl Genet
DOI 10.1007/s00122-015-2559-0

ORIGINAL ARTICLE

Genome-wide association and genomic prediction of resistance to maize lethal necrosis disease in tropical maize germplasm

Manje Gowda[1] · Biswanath Das[1] · Dan Makumbi[1] · Raman Babu[2] · Kassa Semagn[1] · George Mahuku[1] · Michael S. Olsen[1] · Jumbo M. Bright[1] · Yoseph Beyene[1] · Boddupalli M. Prasanna[1]

MLN QTL Deployment

- 37 MLN MABC projects
- Target: 10% GY increase vs RP in hybrids
- 6 white + MSV1 donor conversion projects

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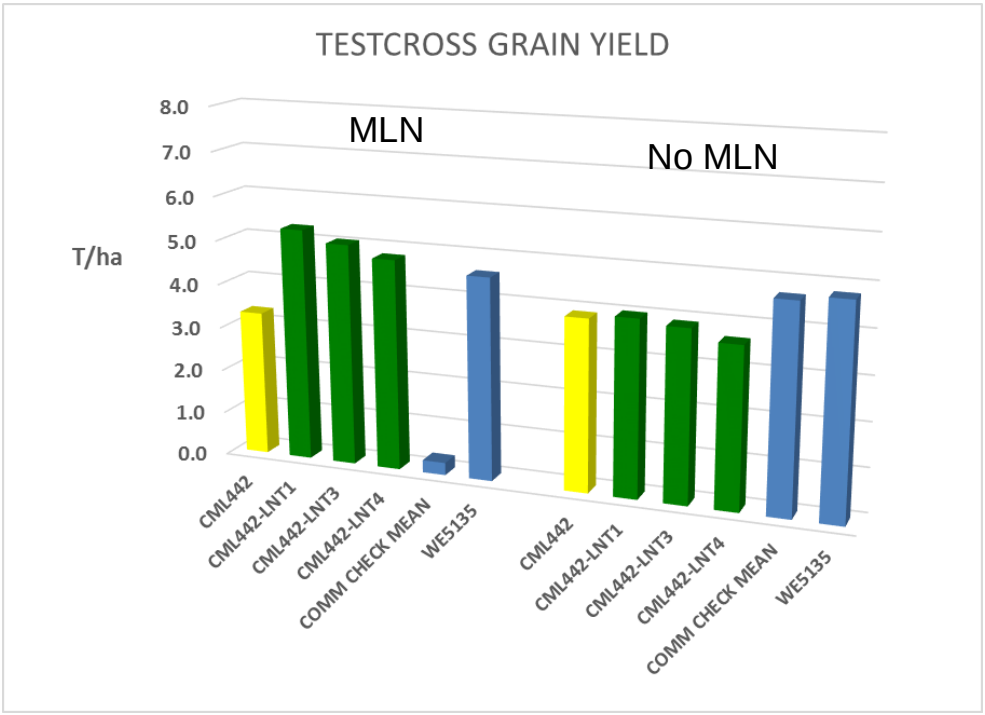
Improved MLN tolerance of elite stress tolerant lines: CML442

CML442*5/CLWN270

CML442



1.8 t/ha testcross yield increase under severe MLN pressure

Yield parity in absence of MLN

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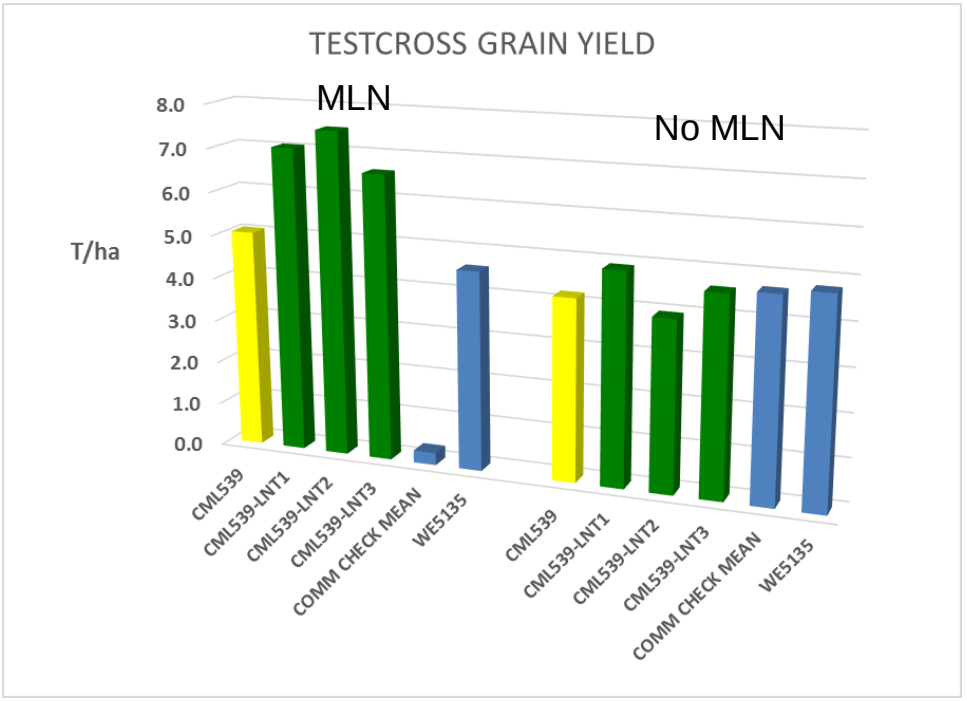
Improved MLN tolerance of elite stress tolerant lines: CML539

CML539*5/DTPYF46 | CML539



2.0 t/ha testcross yield increase under severe MLN pressure

Yield parity in absence of MLN

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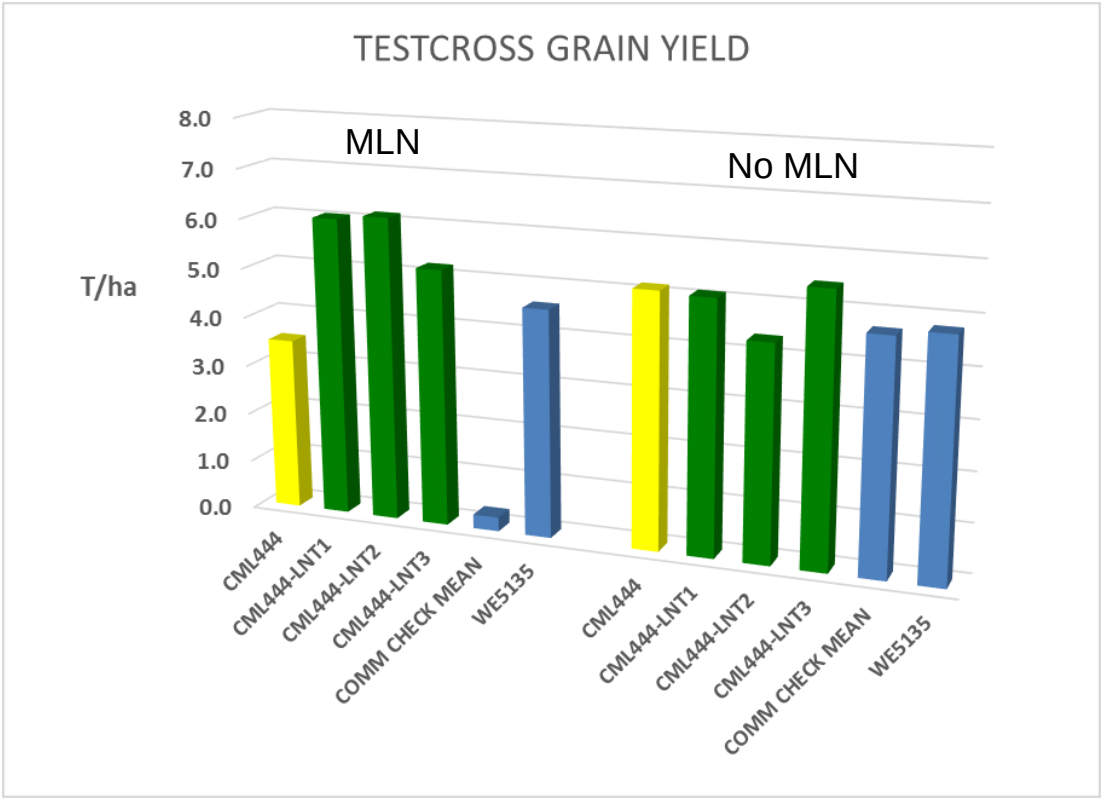
Improved MLN tolerance of elite stress tolerant lines: CML444

CML444*5/CML494

CML444

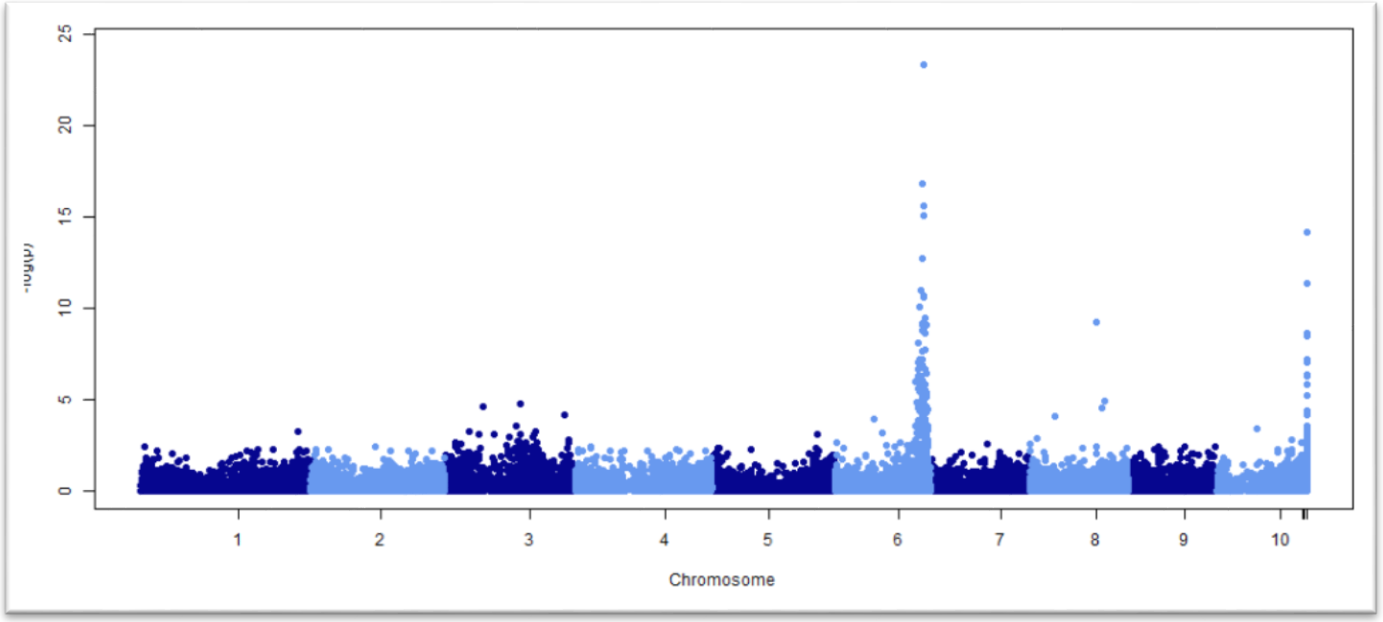
2.3 t/ha testcross yield increase under severe MLN pressure

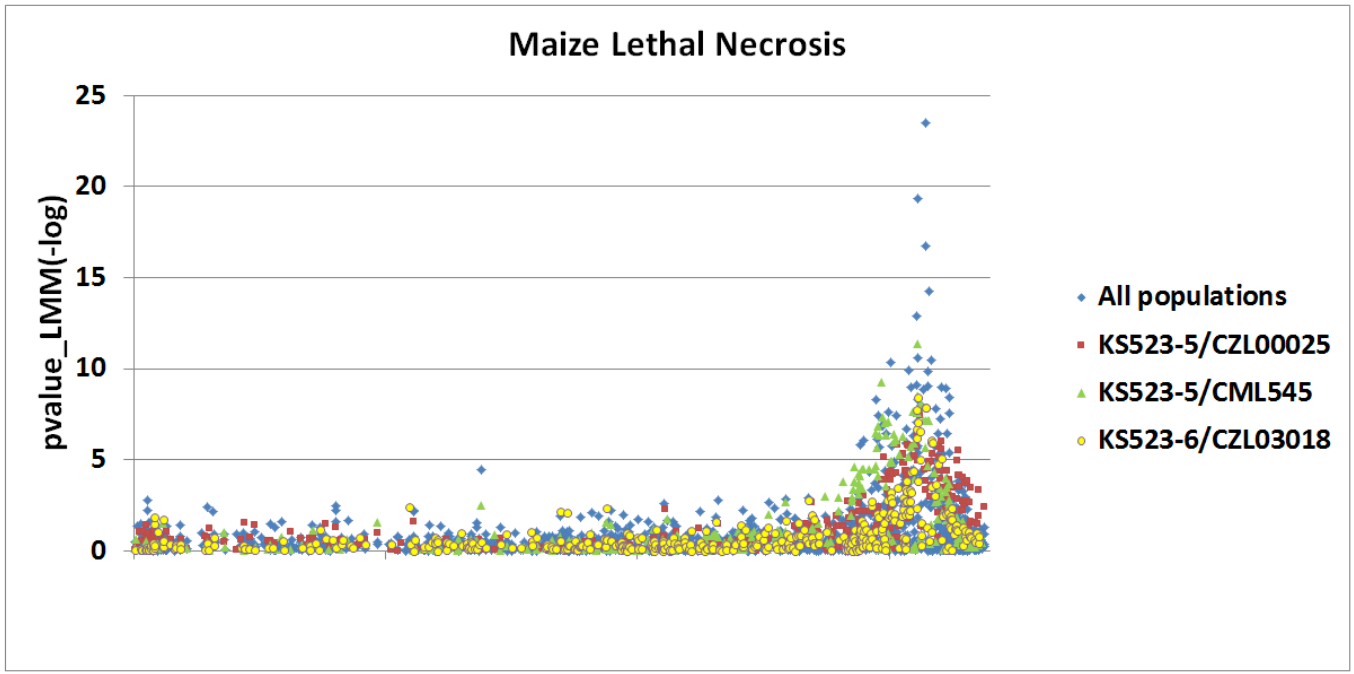
Yield parity in absence of MLN



KS23 MLN QTL

- **Modified QTL seq method**
- **Consistent detection in three populations**





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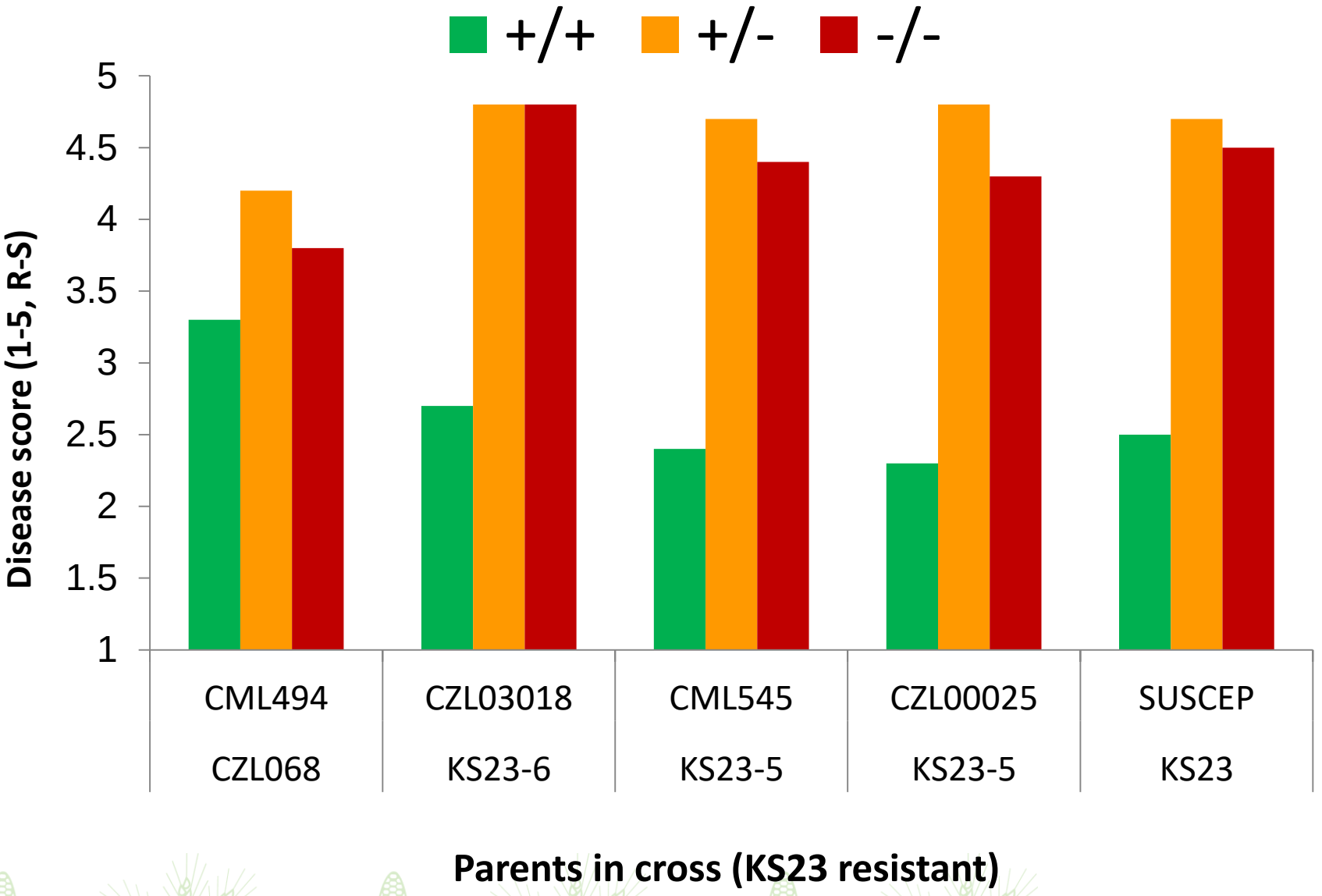
Contribution of MLN_R Locus to Resistance Against MLN



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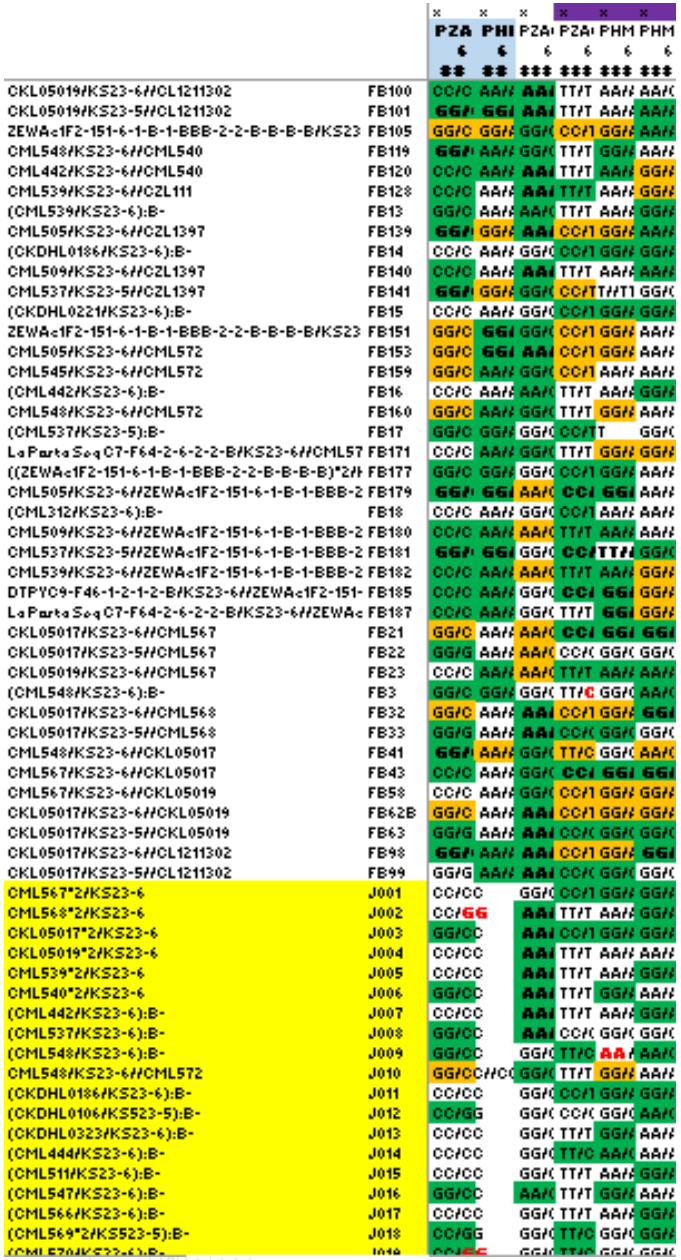
KS23 MLN haplotype deployment

- Six marker haplotype identified for HTPG
- 40 enriched breeding populations to delivered to ESA line development team
- 19 MABC projects at BC2 or BC3 stage
- >10,000 F4 and DH lines being screened currently



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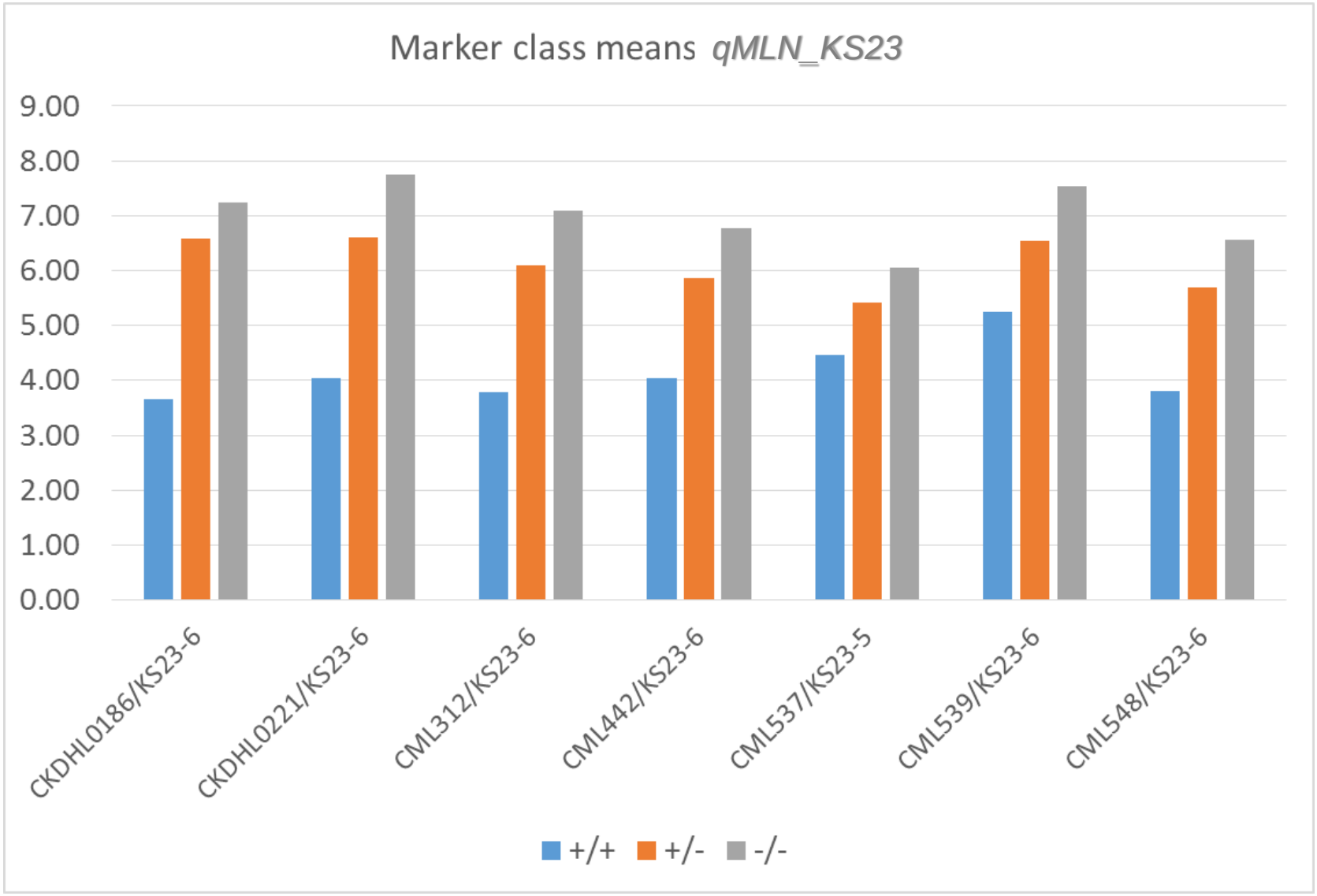
qMLN_KS23 +/-

qMLN_KS23 +/+

qMLN_KS23 +/-


Marker class means qMLN_KS23
9.00
8.00
7.00
6.00
5.00
4.00
3.00
2.00
1.00
0.00
CKDHL0186/KS23-6
CKDHL0221/KS23-6
CML312/KS23-6
CML442/KS23-6
CML537/KS23-5
CML539/KS23-6
CML548/KS23-6
+/+
+/-
-/-

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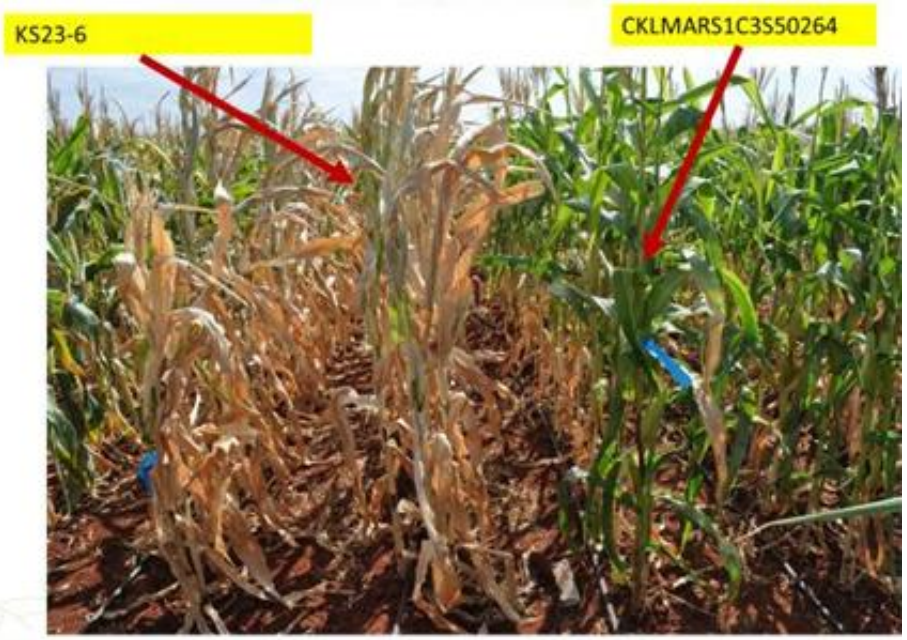
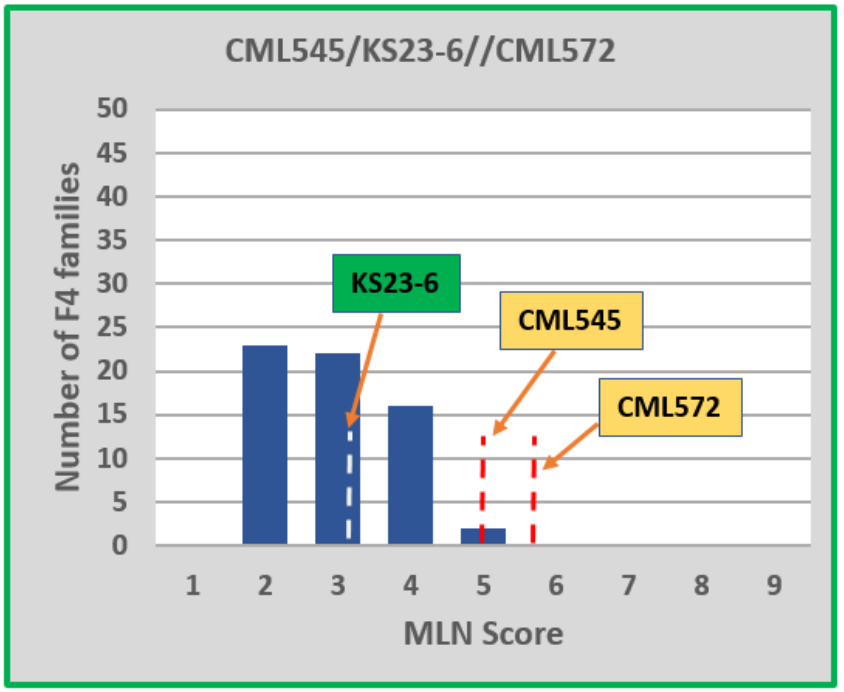
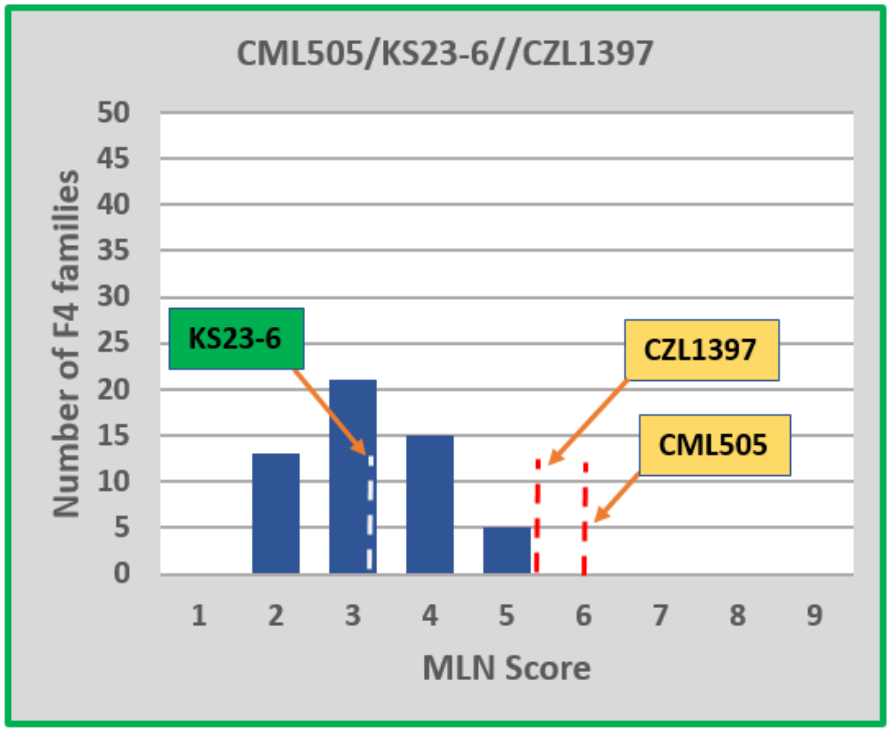
qMLN_06.157 deployment strategy

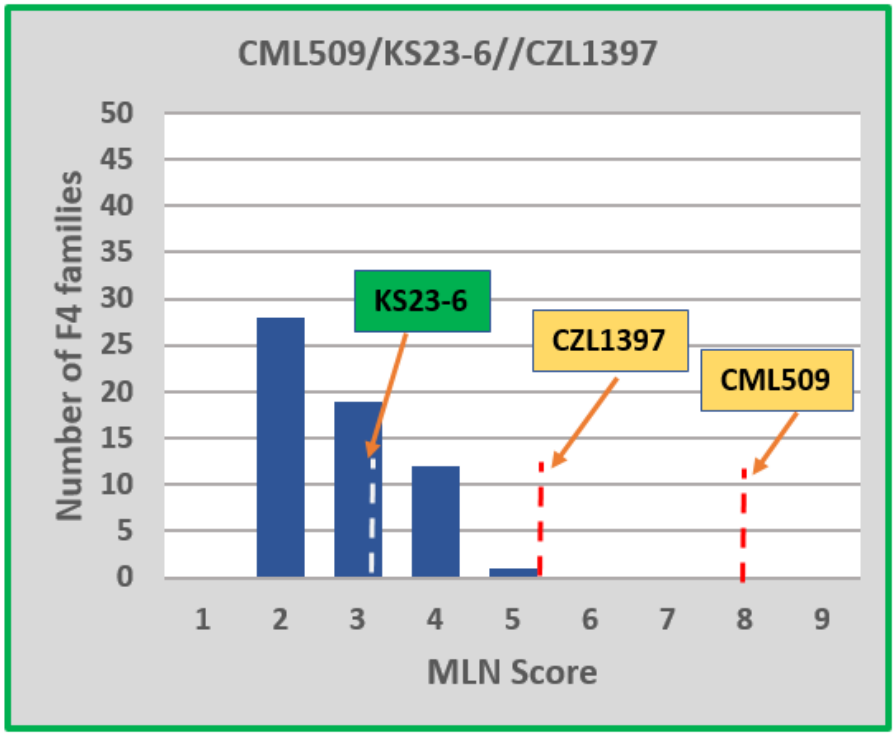
Drought response KS23-6





CIMMYT


CML505/KS23-6//CZL1397
Number of F4 families
50
45
40
35
30
25
20
15
10
5
0
KS23-6
CZL1397
CML505
1
2
3
4
5
6
7
8
9
MLN Score


CML509/KS23-6//CZL1397
Number of F4 families
50
45
40
35
30
25
20
15
10
5
0
KS23-6
CZL1397
CML509
1
2
3
4
5
6
7
8
9
MLN Score

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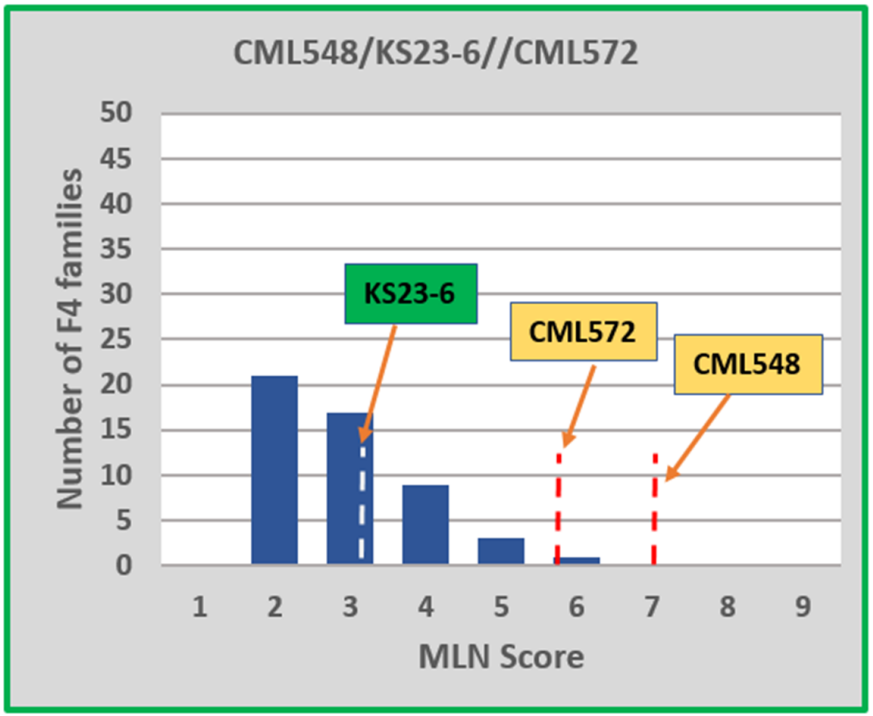
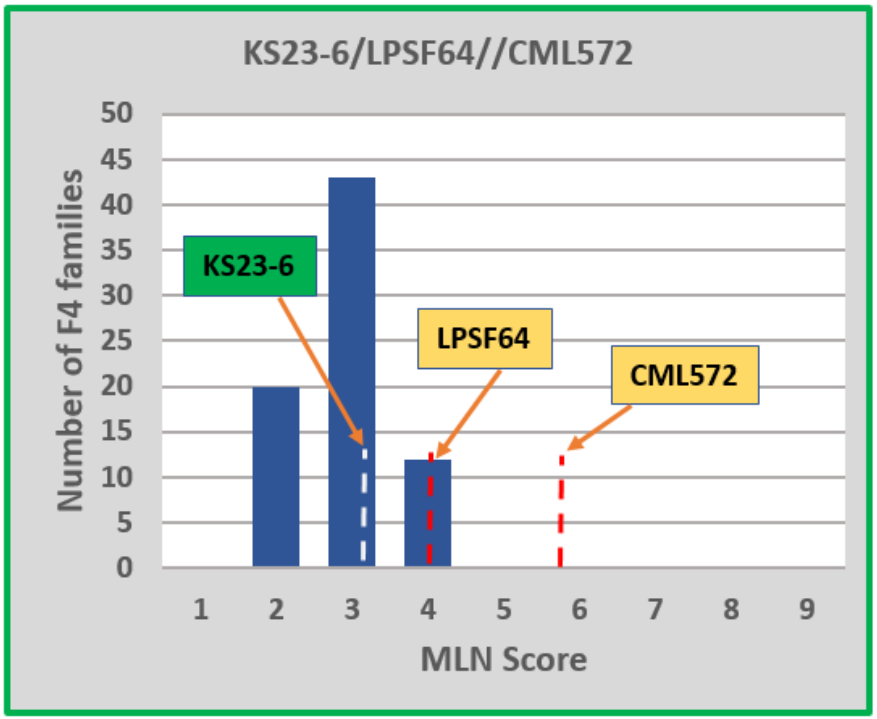

CML548/KS23-6//CML572
Number of F4 families
50
45
40
35
30
25
20
15
10
5
0
KS23-6
CML572
CML548
1
2
3
4
5
6
7
8
9
MLN Score


KS23-6/LPSF64//CML572
Number of F4 families
50
45
40
35
30
25
20
15
10
5
0
KS23-6
LPSF64
CML572
1
2
3
4
5
6
7
8
9
MLN Score

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Forward breeding example: MSV + MLN

Funnel = 400

Output = 6

MSV

MLN

Funnel = 6000

Output = 90

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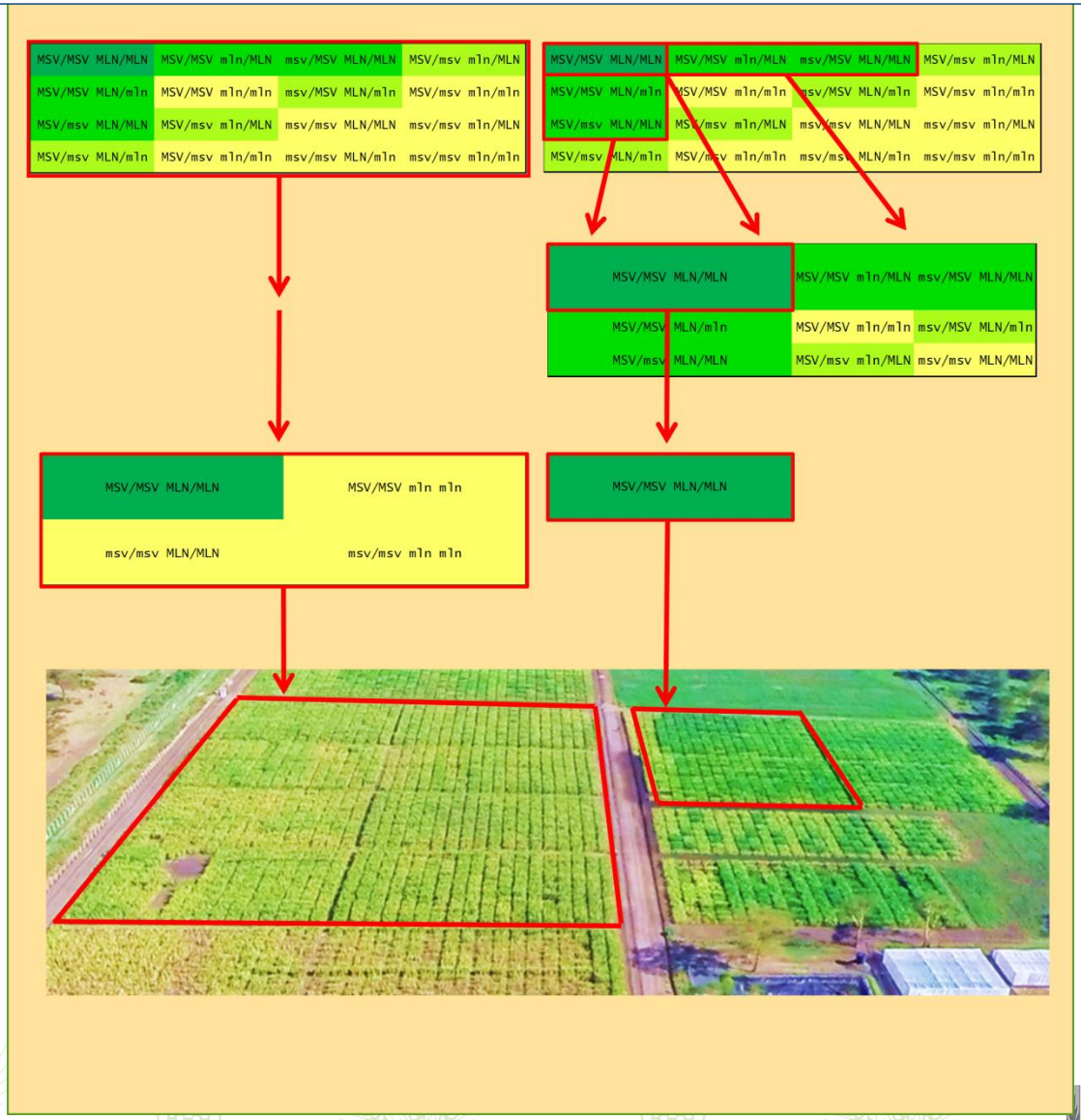
Example: KS23-5/CML442

KS23-5 (msv/msv MLN/MLN) / CML442 (MSV/MSV mln/mln)



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100 MSV/MSV+MLN/MLN F4 ears				
Genotype	Phenotype (MSV + MLN)	Forward Breeding	Conv.	Relative cost
$ 2.50	$ 8.00	$ 2,800	$ 3,200	88%
$ 2.50	$ 10.00	$ 3,000	$ 4,000	75%
$ 2.50	$ 12.00	$ 3,200	$ 4,800	67%
$ 2.00	$ 8.00	$ 2,400	$ 3,200	75%
$ 2.00	$ 10.00	$ 2,600	$ 4,000	65%
$ 2.00	$ 12.00	$ 2,800	$ 4,800	58%
$ 1.50	$ 8.00	$ 2,000	$ 3,200	63%
$ 1.50	$ 10.00	$ 2,200	$ 4,000	55%
$ 1.50	$ 12.00	$ 2,400	$ 4,800	50%
$ 1.00	$ 8.00	$ 1,600	$ 3,200	50%
$ 1.00	$ 10.00	$ 1,800	$ 4,000	45%
$ 1.00	$ 12.00	$ 2,000	$ 4,800	42%

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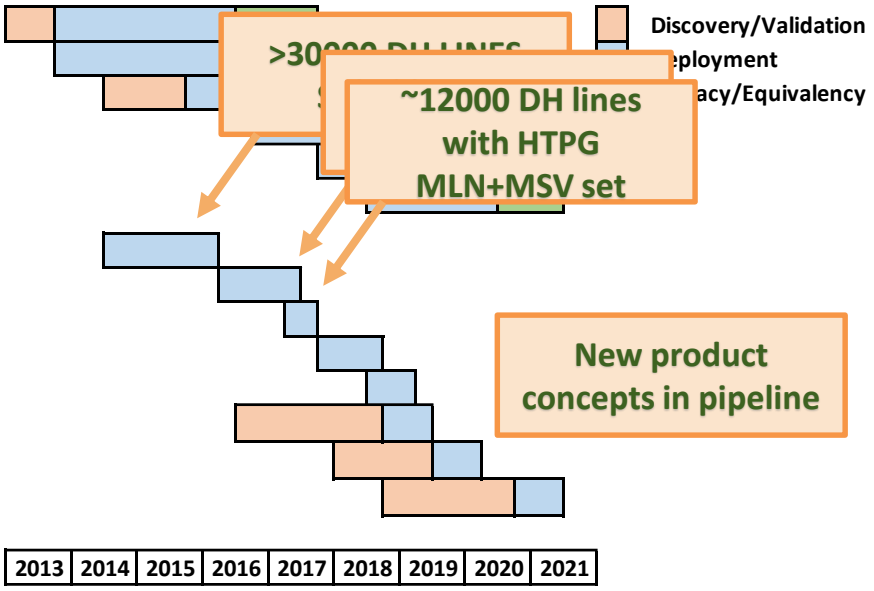
Marker Deployment Strategy: Africa

	Traits Deployed
MABC Cohort 1A	MLN I
MABC Cohort 1B	White, MSV
MABC Cohort 2	MLN II (*qMLN 06.157*)
MABC Cohort 3	MLN II
MABC Cohort 4	MLN II (NARS)
MABC Cohort 5	MSV, MLN II (FAW)
Forward Breeding I	MSV
Forward Breeding II	MSV, MLN II
Forward Breeding III	MSV, MLN II
Forward Breeding IV	MSV, MLN II (NARS)
Forward Breeding V	MSV, MLN II (FAW)
Forward Breeding VI	MLN II, Striga
Forward Breeding VII	MSV, MLN II, Aflatoxin
Forward Breeding VIII	MSV, MLN II, FAW



Genome-wide selection strategies

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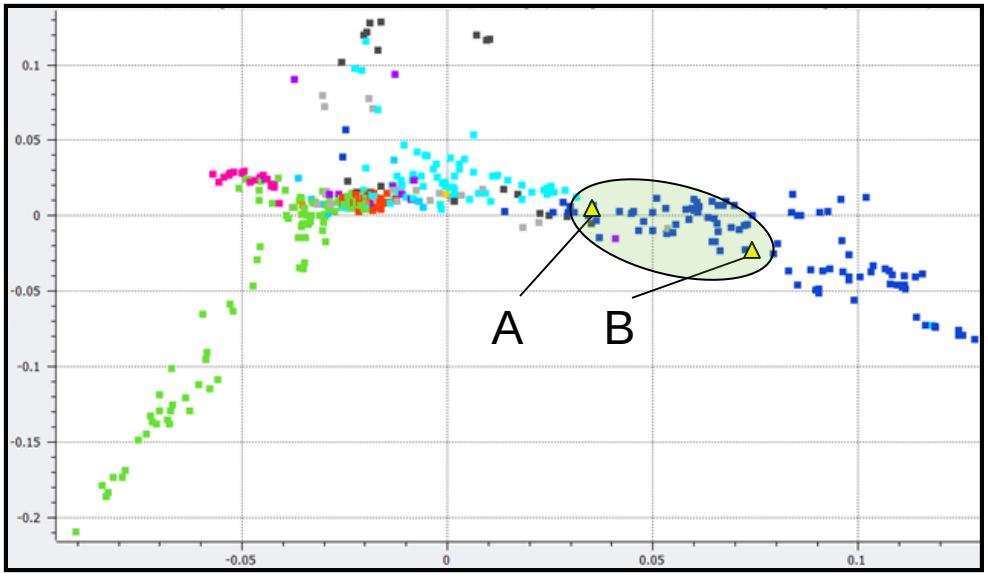
Training set development

- **Windheusen et al. 2013:**
  - ***…emphasizing the need (for) larger training sets with <u>strong genetic relationship</u> to the validation set.***

- **Endelman et al. 2013:**
  - ***…the training population must be expanded beyond the full-sib family under selection, <u>using close relatives of the parents</u> as a source of prediction accuracy.***



- **Jacobsen et al. 2014:**
  - ***GCA model – half-sib populations involving A and B***
  - ***Gain from prediction = 68-76% of phenotypic selection at much lower cost***

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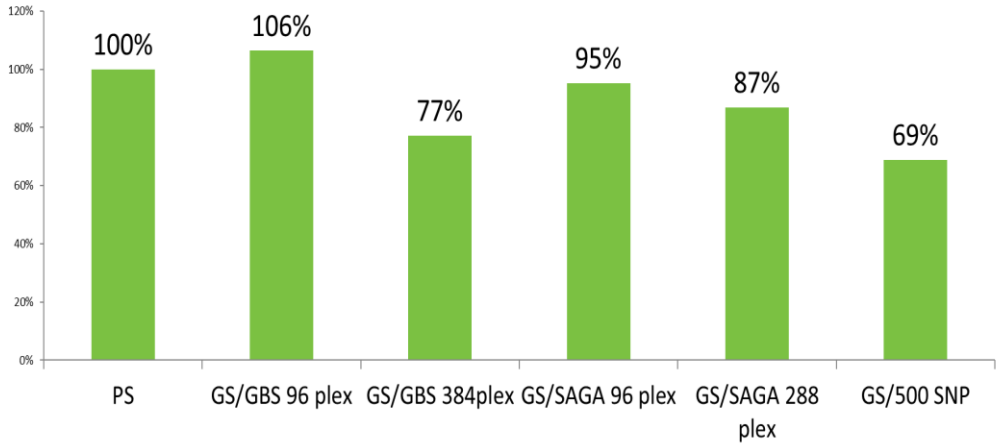
Prediction of untested DH lines

Phase 1

- Phenotype half / predict half
- FS and FS/HS prediction

Operational cost comparison



Breeder selection table

IDs	Pedigree	Yield	Pre_ AF	Rank	Yield	Pre_Cot	Rank	Yield	Predict_TL	Rank	Total Rank
LLTDHW_255	((CLRCW96/CLWN345)-B)-DH42	NA	7.98	7	NA	5.92	57	NA	11.92	106	57
LLTDHW_256	((CLRCW96/CLWN345)-B)-DH43	NA	7.80	20	NA	5.87	62	NA	11.99	98	60
LLTDHW_74	((CLWN216/CLWN241)-B)-DH28	NA	7.52	77	NA	5.51	106	NA	13.20	10	64
LLTDHW_79	((CLWN216/CLWN241)-B)-DH55	NA	7.83	17	NA	5.49	114	NA	12.17	66	66
LLTDHW_254	((CLRCW96/CLWN345)-B)-DH41	NA	7.66	44	NA	5.59	94	NA	12.16	70	69
LLTDHW_90	((CLWN216/CLWN241)-B)-DH97	NA	7.80	21	NA	5.17	173	NA	12.78	24	73
LLTDHW_173	((CLWN216/CLWN345)-B)-DH78	NA	8.35	1	NA	5.05	200	NA	12.90	18	73
LLTDHW_78	((CLWN216/CLWN241)-B)-DH52	NA	7.29	155	NA	5.80	67	NA	13.24	8	77
LLTDHW_264	((CLRCW96/CLWN345)-B)-DH51	NA	7.84	13	NA	5.32	141	NA	12.08	82	79
LLTDHW_84	((CLWN216/CLWN241)-B)-DH84	NA	7.34	135	NA	5.61	91	NA	12.68	28	85
LLTDHW_154	((CLWN216/CLWN345)-B)-DH32	NA	7.83	16	NA	5.12	182	NA	12.17	67	88
LLTDHW_86	((CLWN216/CLWN241)-B)-DH90	NA	7.49	88	NA	5.50	111	NA	12.16	71	90
LLTDHW_263	((CLRCW96/CLWN345)-B)-DH50	NA	8.03	5	NA	6.19	35	NA	11.22	231	90
LLTDHW_537	((CLWN207/CLWN241)-B)-DH46	NA	7.10	220	NA	6.27	23	NA	12.64	34	92
LLTDHW_101	((CLWN216/CLWN241)-B)-DH143	NA	7.39	118	NA	5.28	145	NA	13.00	14	92
LLTDHW_713	((CLWN345/CLWN364)-B)-DH21	NA	7.72	33	NA	5.51	108	NA	11.66	141	94
LLTDHW_82	((CLWN216/CLWN241)-B)-DH81	NA	7.20	186	NA	5.61	92	NA	13.33	5	94
LLTDHW_68	((CLWN216/CLWN241)-B)-DH9	NA	7.34	142	NA	5.33	138	NA	13.46	3	94

Phase 2

- Training set maintenance with established x new pops
- GCA model prediction directly into stage 2 testing

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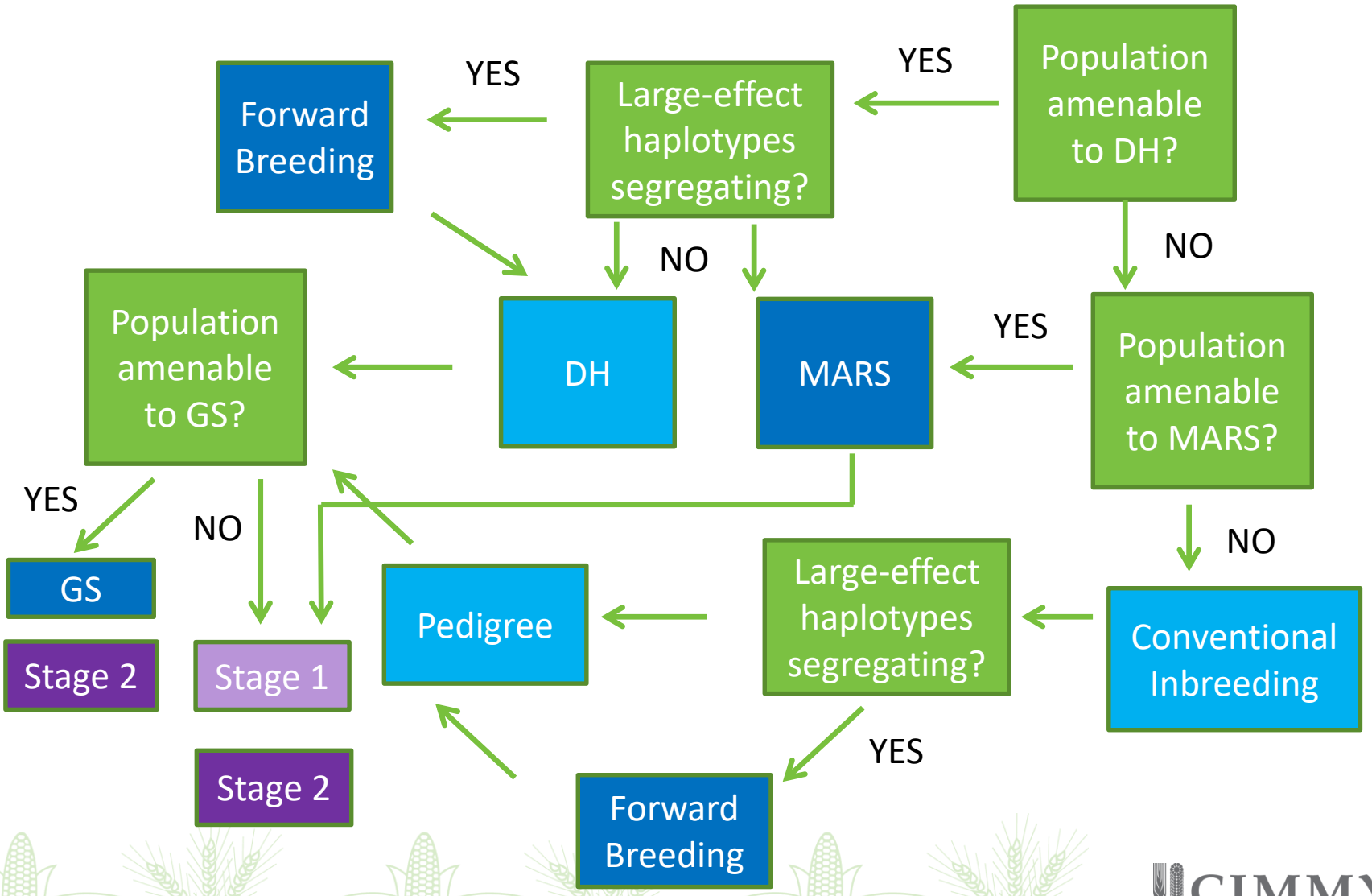
Designing decision trees



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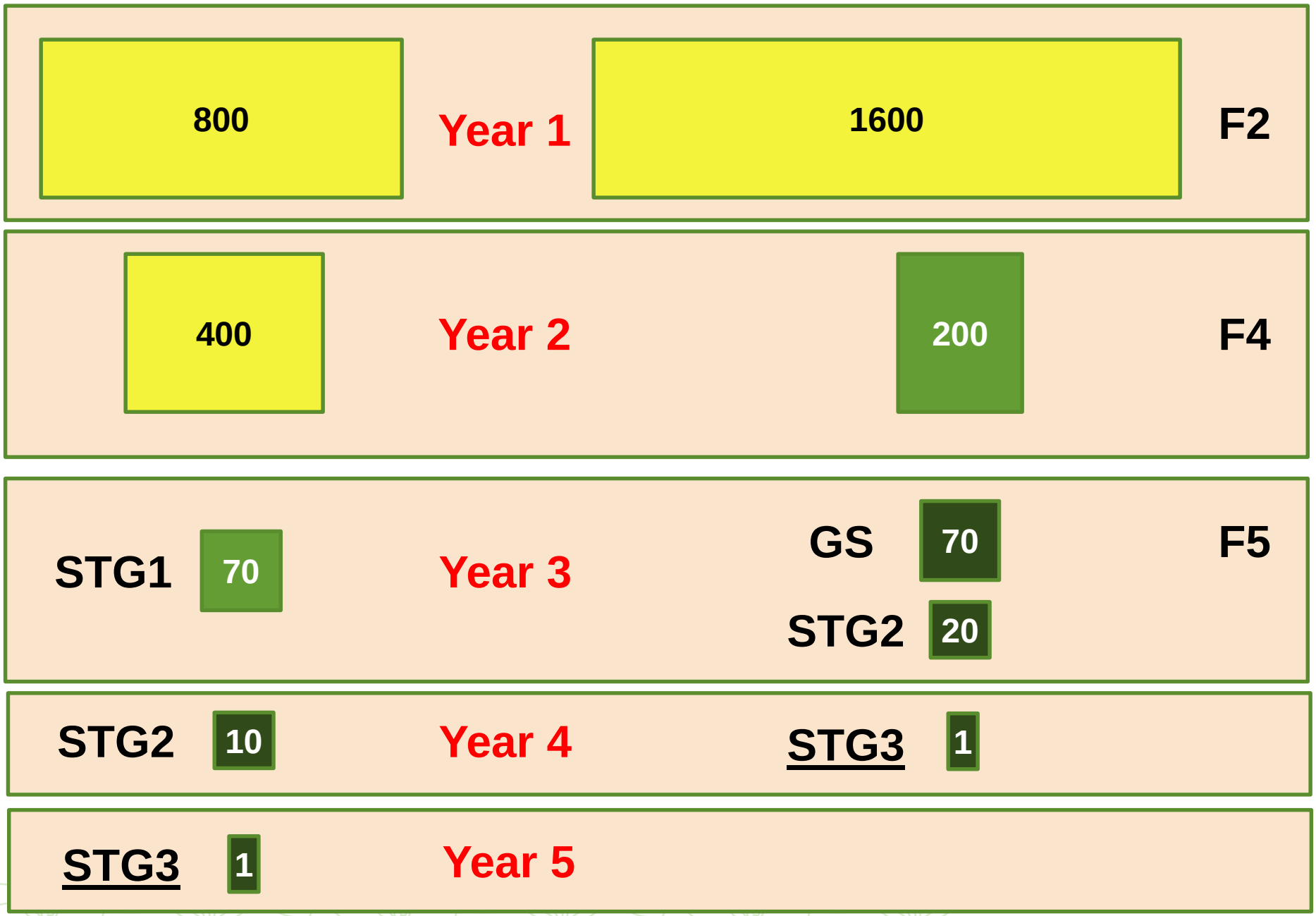
Breeding process comparison – Equivalent cost basis



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