Use of molecular marker technologies to enhance genetic gain in maize

Mike Olsen on behalf of the STMA PO1 team and MAIZE AFS CoA 2.2

Maize training workshop on improving genetic gain

Nairobi, Kenya

June 23, 2017

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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
- 2.2.5 – Gene Editing

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
		Highland Adaptation

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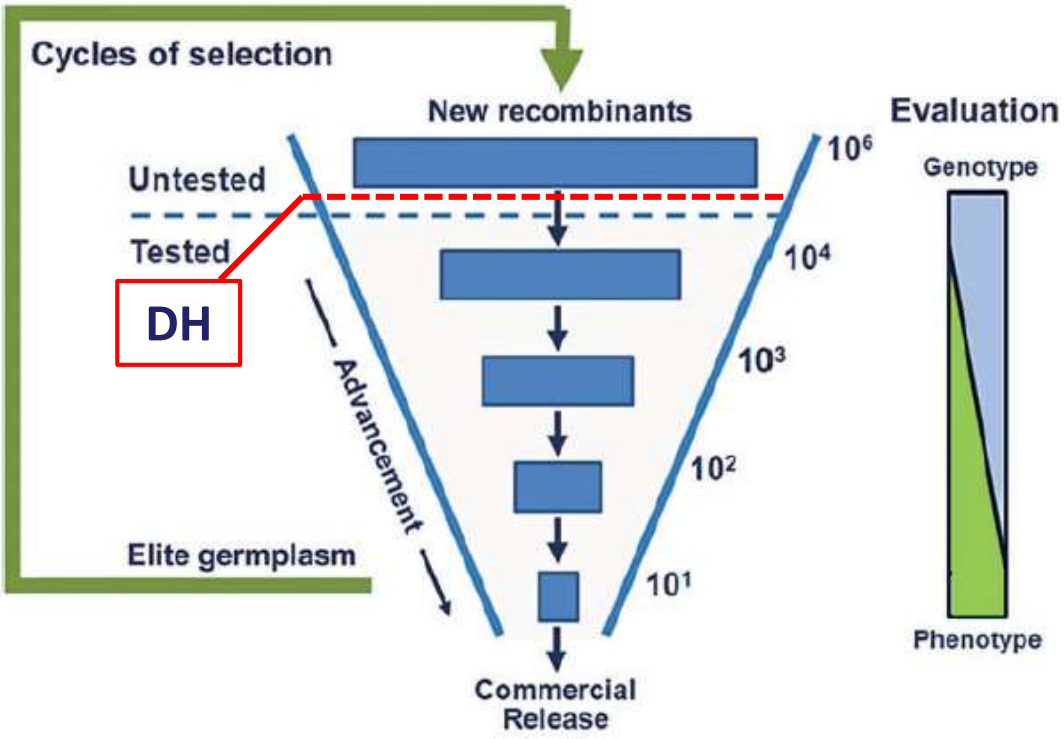
Improved breeding efficiency – increasing genetic gain

Novel Germplasm

- New Haplotypes
- Accelerated donor use



Selection intensity

- Low cost genotyping
- Informatics - GOBII
- Seed chipping

Cycle Time

- Genomic Selection
- Informatics – GOBII
- Mechanization

Heritability

- Phenotyping innovation
- Affordable DH
- Mechanization

Decision Support Tools

- Parent Selection
- Advancement decisions

Adapted from Cooper et al. 2014

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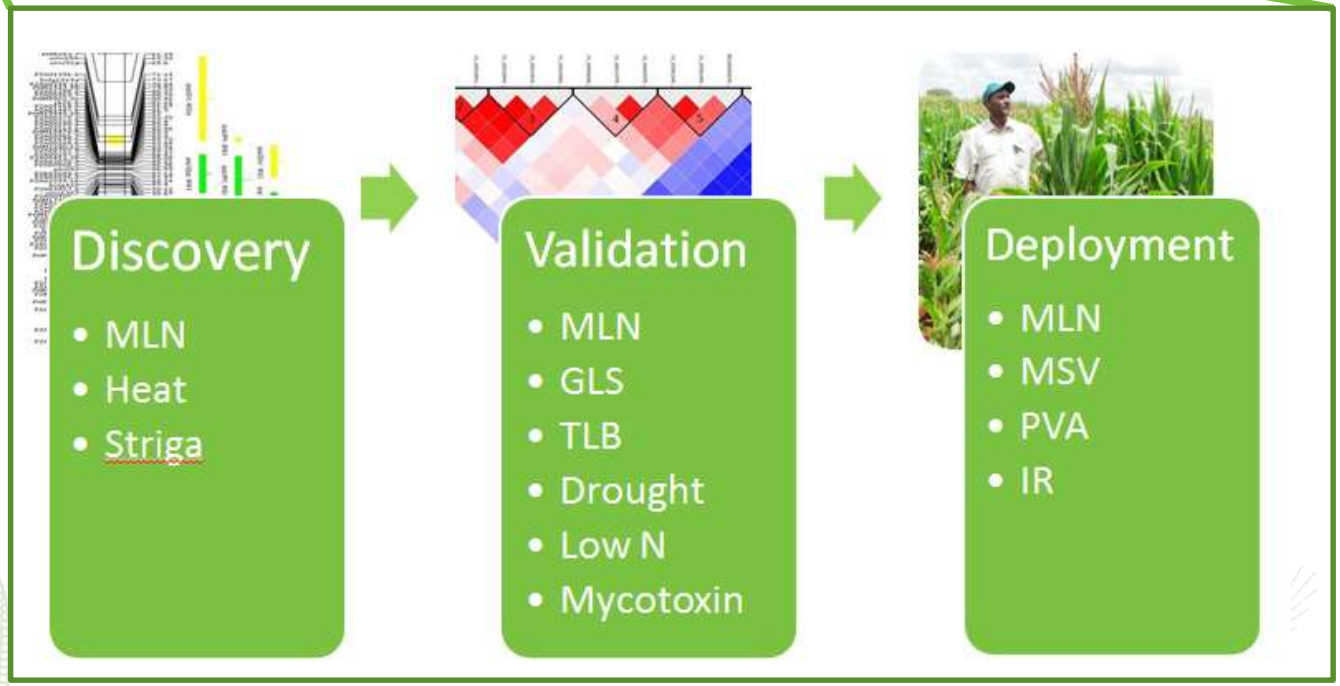
GMP-Africa pipeline

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



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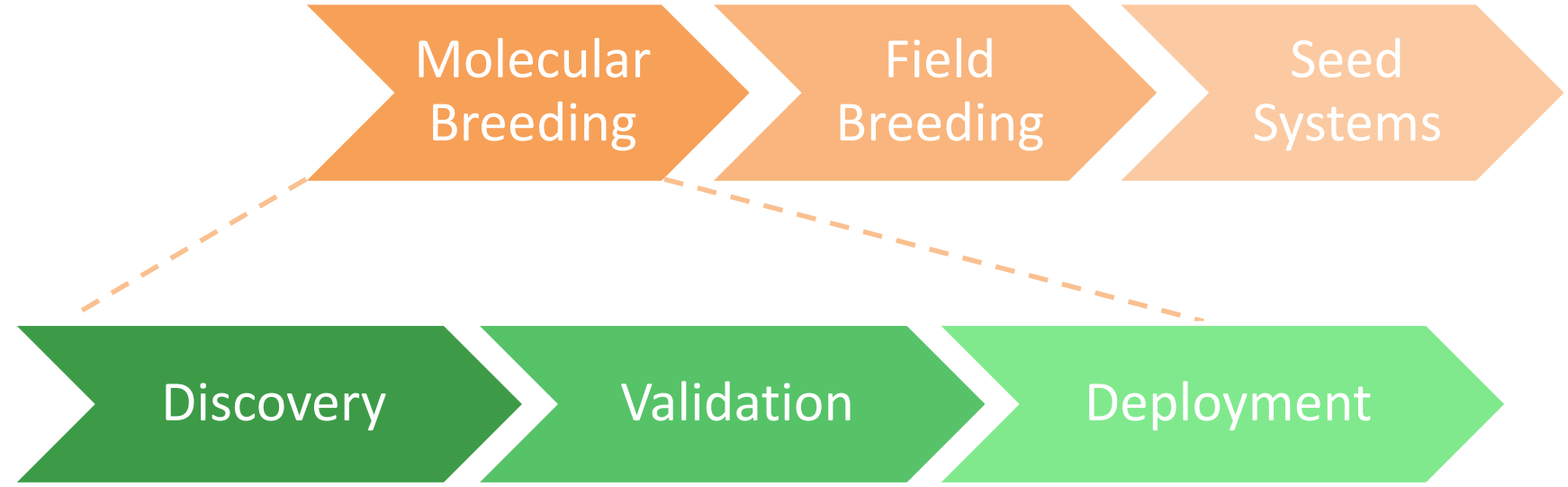

Association Mapping

Bi-parental Mapping

Fine Mapping

Haplotype Optimization

Line Conversion

Forward Breeding

Key Traits

MLN
MSV
Striga

Additional Traits

TLB
GLS
Temperate haplotypes

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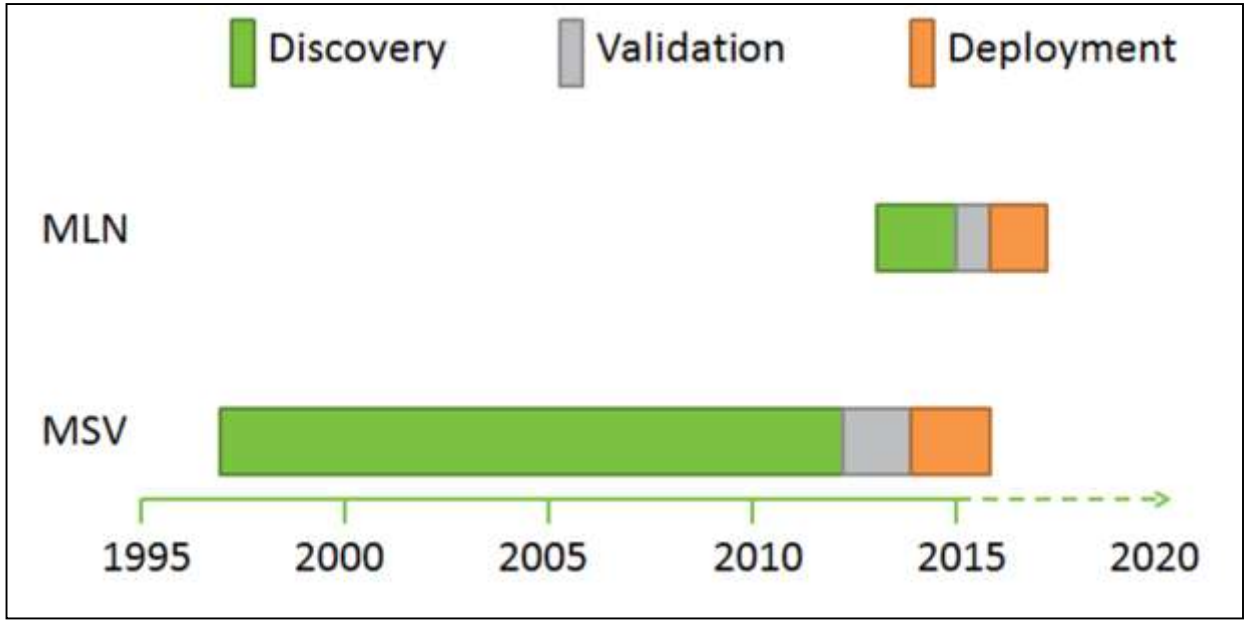
Critical Path Analysis

- Which steps can be done in parallel?
- Cost-benefit of crashing timelines
- Which steps are critically time-sensitive?
- Role specialization to improve efficiency at bottlenecks
- Integration of process workflows



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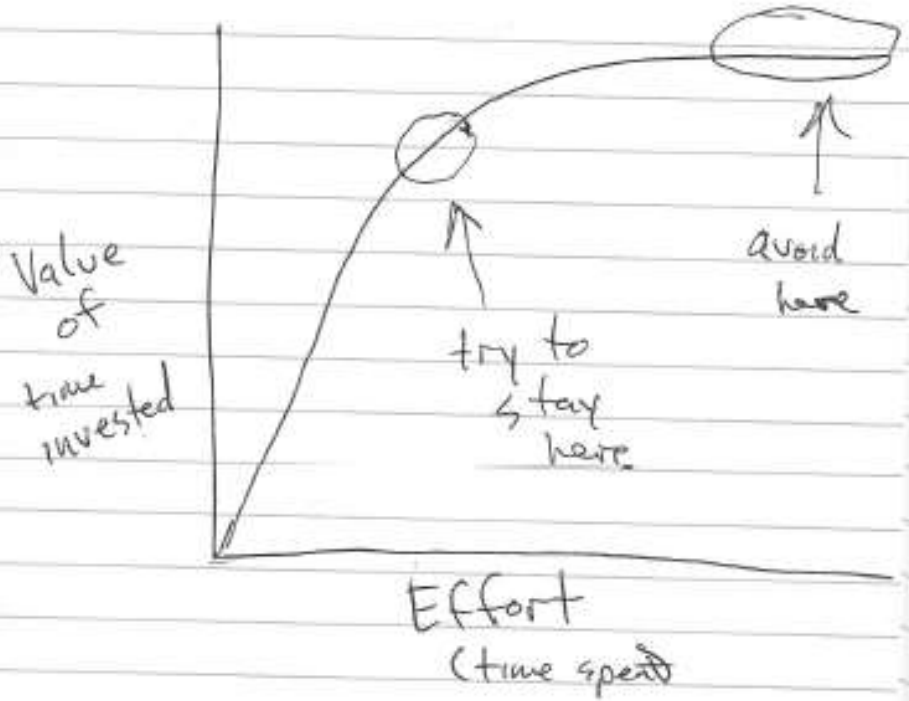

If it takes 2 hours to score 90% on an exam but 6 hours to score 100% take the 90, we have to many other important things we need you for!

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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

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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]

QTL Deployment

- 37 MLN MABC projects
- Target: 10% GY increase vs RP in hybrids
- 6 white + MSV1 donor conversion projects
- Inbred efficacy trial planted
- Hybrid equivalency and efficacy trials in the field

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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

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CML442

CML442*5/CLWN270

CIMMYT

CML488*5/DTPYF46

CML488

CIMMYT

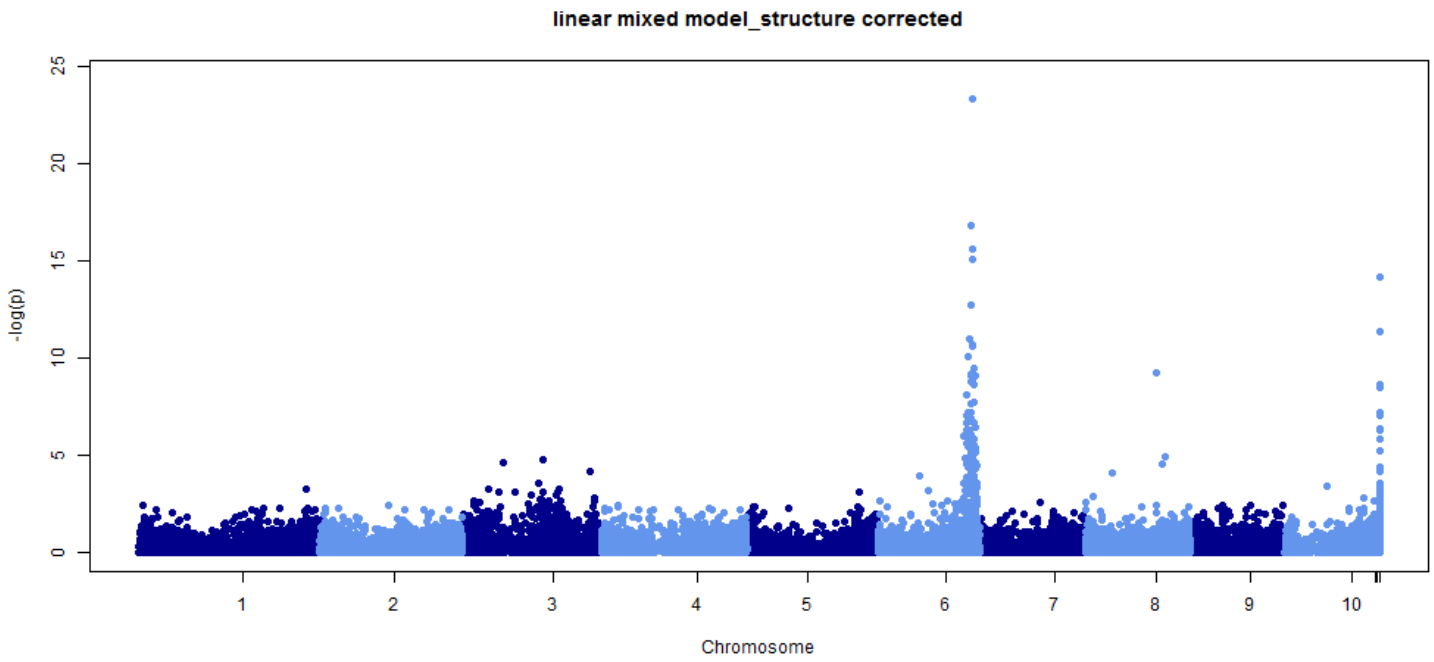
CML539*5/DTPYF46

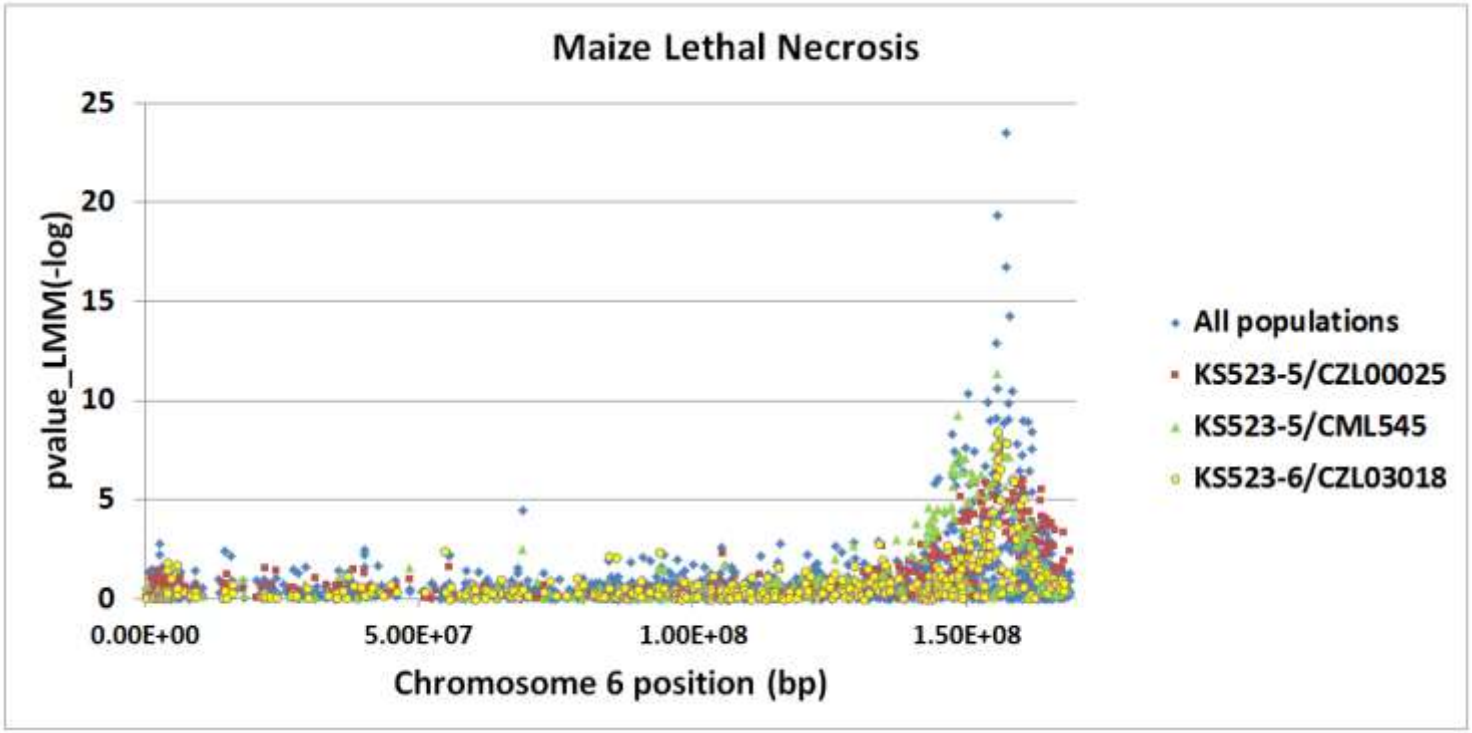
CML539

CIMMYT

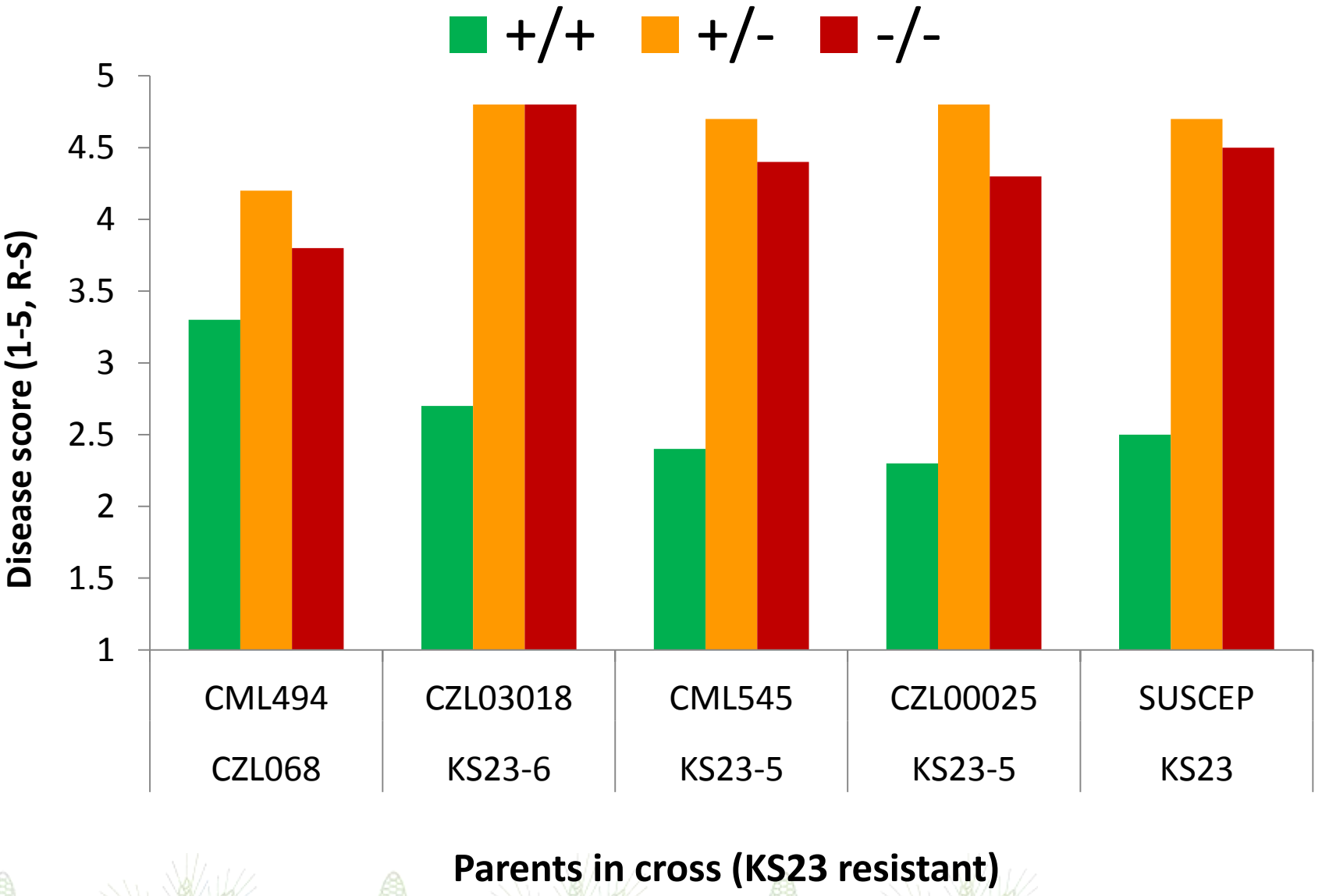
CML444*5/CML494

CML444


linear mixed model_structure corrected
-log(p)
0
5
10
15
20
25
1
2
3
4
5
6
7
8
9
10
Chromosome


Maize Lethal Necrosis
pvalue_LMM(-log)
0
5
10
15
20
25
0.00E+00
5.00E+07
1.00E+08
1.50E+08
Chromosome 6 position (bp)
All populations
KS523-5/CZL00025
KS523-5/CML545
KS523-6/CZL03018

Contribution of MLN_R Locus to Resistance Against MLN



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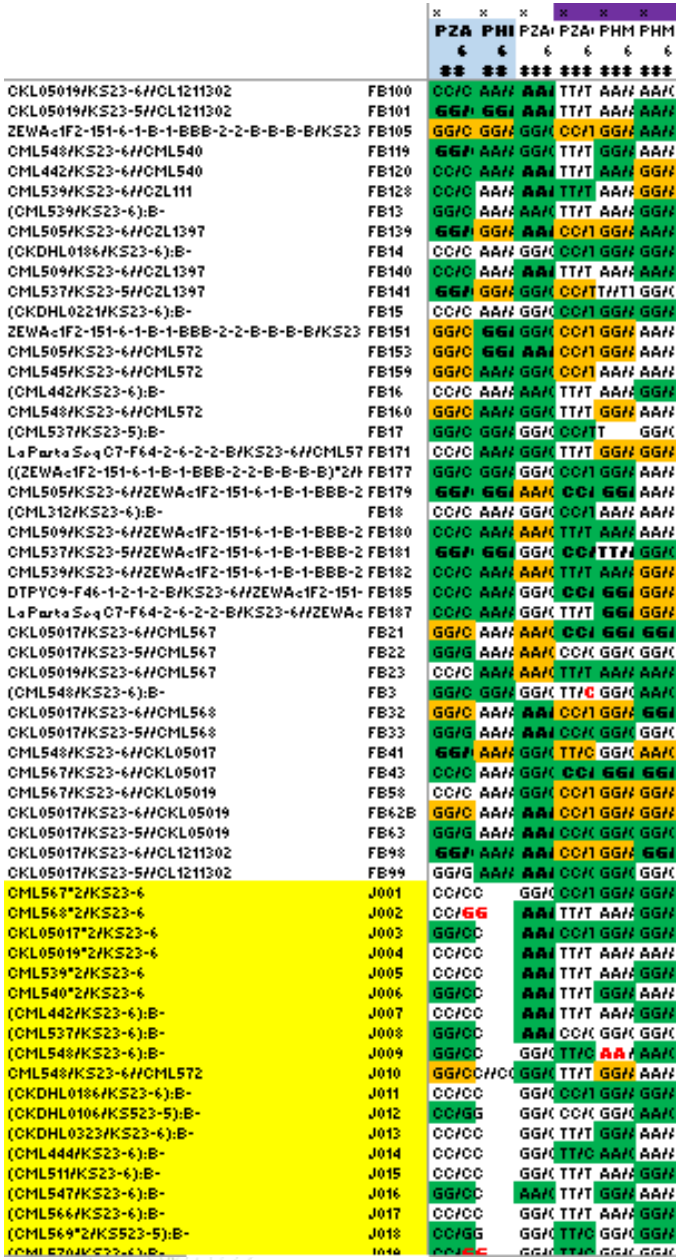
KS23 MLN haplotype deployment

- Six marker haplotype identified for HTPG
- 40 breeding populations to deliver to ESA line development team in June
- 19 MABC projects at BC2 or BC3 stage



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Entries 52&53
CML539 and KS23-6

CIMMYT

Entries 297&298
CML442 and
KS23-6

CIMMYT

Entry 30 (*Left)* and
entry 35 (*Right)*

Class – R/S

CIMMYT

CKDHL 1086

Entry 140 (*Left)* and entry 141 (*Right)*

Class

140 – R/R

141 – R/S

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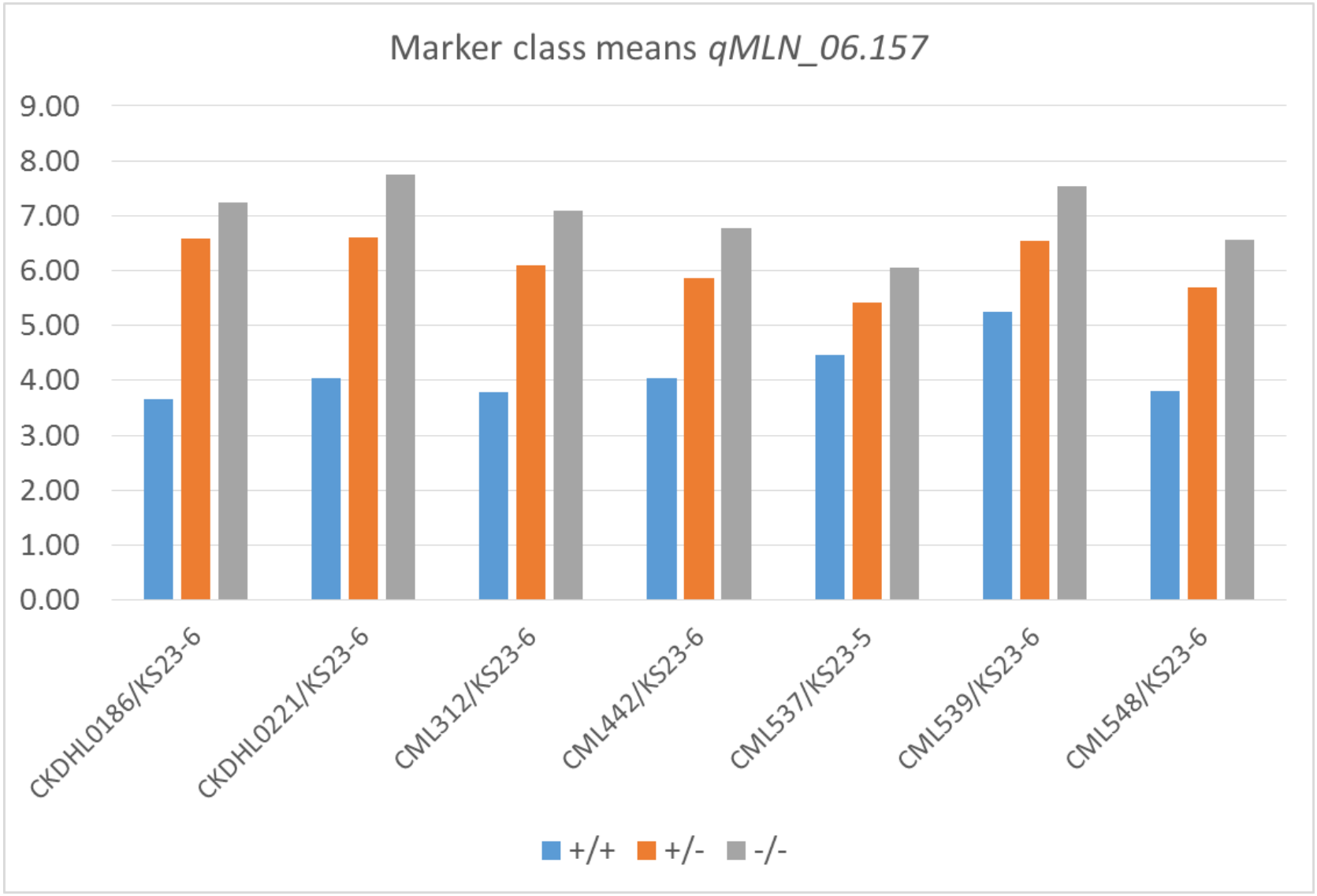
ENTRY	126	126	127	130	130	qMLN	131	132		133	133	AVE MLN	MLN SCORES
KS23-6	C/C	A/A		A/A	G/G	R/R		A/A	G:G	C/C	C/C	4.0	4 4 4 3 3 4 3 | 4 4 4 4 4 4 4 4
CML548/KS23-6	C/C	A/A		A/A	G/G	R/R		A/A	G:G	C/C	C/C	3.0	3 3 3 3 4 4 3 3 4 3 | 4 4 4 3 3 3 4 4 3 3 4
CML548/KS23-6	C/C	A/A		A/A	G/G	R/R		A/A	G:G	C/C	C/C	4.0	4 4 4 4 4 3 3 3 4 | 4 3 3 5 4 4 4 3 3 4 3
CML548/KS23-6	C/C	A/A		A/A	G/G	R/R		A/A	G:G	C/C	C/C	4.0	4 4 3 5 5 3 4 4 4 | 3 4 3 3 3 3 3 4 5
CML548/KS23-6	C/C	A/C		A/A	G/G	R/R		A/A	-	C/C	C/C	4.0	4 4 4 4 4 3 4 4 4 4 4 | 4 4 4 4 4 4 4 4 5 5
CML548/KS23-6	C/C	A/C		A/A	G/G	R/R		A/A	G:G	C/C	C/C	4.0	6 5 5 4 4 4 4 3 4 3 3 4 | 4 4 4 4 4 5 4 4 4 4
CML548/KS23-6	C/C	A/A		A/A	G/G	R/R		A/G	G:A	C/T	C/T	3.8	3 3 3 4 4 4 4 4 3 4 | 3 4 4 4 4 4 4 4 4 4 4
CML548/KS23-6	C/C	A/A		A/A	G/G	R/R		A/G	G:A	C/T	C/T	4.0	4 3 4 3 3 4 3 5 3 | 4 5 4 4 4 4 4 4 6
CML548/KS23-6	C/C	A/A		A/C	G/T	R/S		A/G	G:A	C/T	C/T	6.0	4 3 5 3 5 8 6 4 7 | 6 6 7 4 3 4 9 9 9 8
CML548/KS23-6	C/C	C/C		A/C	G/T	R/S		A/G	G:A	C/T	C/T	5.0	6 4 6 7 4 6 4 6 7 7 6 | 4 5 3 4 4 4 6 7 3
CML548/KS23-6	C/C	C/C		C/C	T/T	S/S		G/G	G:A	C/T	C/T	7.0	6 6 6 5 8 4 9 9 6 | 7 7 8 9 7 8 5 4 9
CML548/KS23-6	C/C	C/C		C/C	T/T	S/S		G/G	A:A	T/T	T/T	7.9	6 9 5 9 8 9 9 8 6 5 9 | 9 7 9 8 8
CML548	C/G	C/C		C/C	T/T	S/S		G/G	A:A	T/T	T/T	7.0	9 5 5 5 5 6 | 9 9 9 7 9 9 5
KS23-6	C/C	A/A	G/G			R/R	A/A	A/A		T/T	T/T	4.0	4 4 5 4 4 4 | 4
CKDHL0221/KS23-6	C/C	A/A	G/G			R/R	A/A	A/A		T/T	T/T	3.0	3 3 3 3 3 4 3 3 4 3 | 3 4 3 4 4 3 3 4 5 4 4 4 4
CKDHL0221/KS23-6	C/C	A/A	G/G			R/S	A/G	A/G		T/T	T/T	6.0	4 4 8 8 4 8 8 8 6 7 | 4 8 4 4 7 4 4 8 7 4 4 4
CKDHL0221/KS23-6	C/C	A/A	A/G			R/S	A/G	A/G		T/T	T/T	7.0	9 9 8 9 9 7 4 9 9 9 | 8 4 8 4 7 5 9 8 4 9
CKDHL0221/KS23-6	C/G	A/C	A/G			R/S	A/G	G/G		T/T	T/T	7.0	9 7 | 7 6 9 4 4 9
CKDHL0221/KS23-6	C/G	A/C	A/G			R/S	A/G	G/G		T/T	T/T	7.0	5 3 9 8 9 4 9 | 8 7 8 9 3 9 5
CKDHL0221/KS23-6	C/G	A/C	A/G			R/S	A/G	A/G		T/T	T/T	7.0	8 5 6 7 5 9 9 5 | 6 7 8 7 8 9 9 4 9 9 9 9
CKDHL0221/KS23-6	G/G	A/C	A/G			S/S	G/G	A/G		T/T	T/T	9.0	9 9 9 9 9 9 9 | 9 5 9 9 9 9 9
CKDHL0221/KS23-6	G/G	C/C	A/A			S/S	G/G	G/G		T/T	T/T	9.0	8 8 7 9 | 9 9 9 9 9 9 9 9
CKDHL0221	G/G	C/C	A/A			S/S	G/G	G/G		T/T	T/T	8.0	9 6 9 9 | 5 4 9 9 9 9


Marker class means qMLN_06.157
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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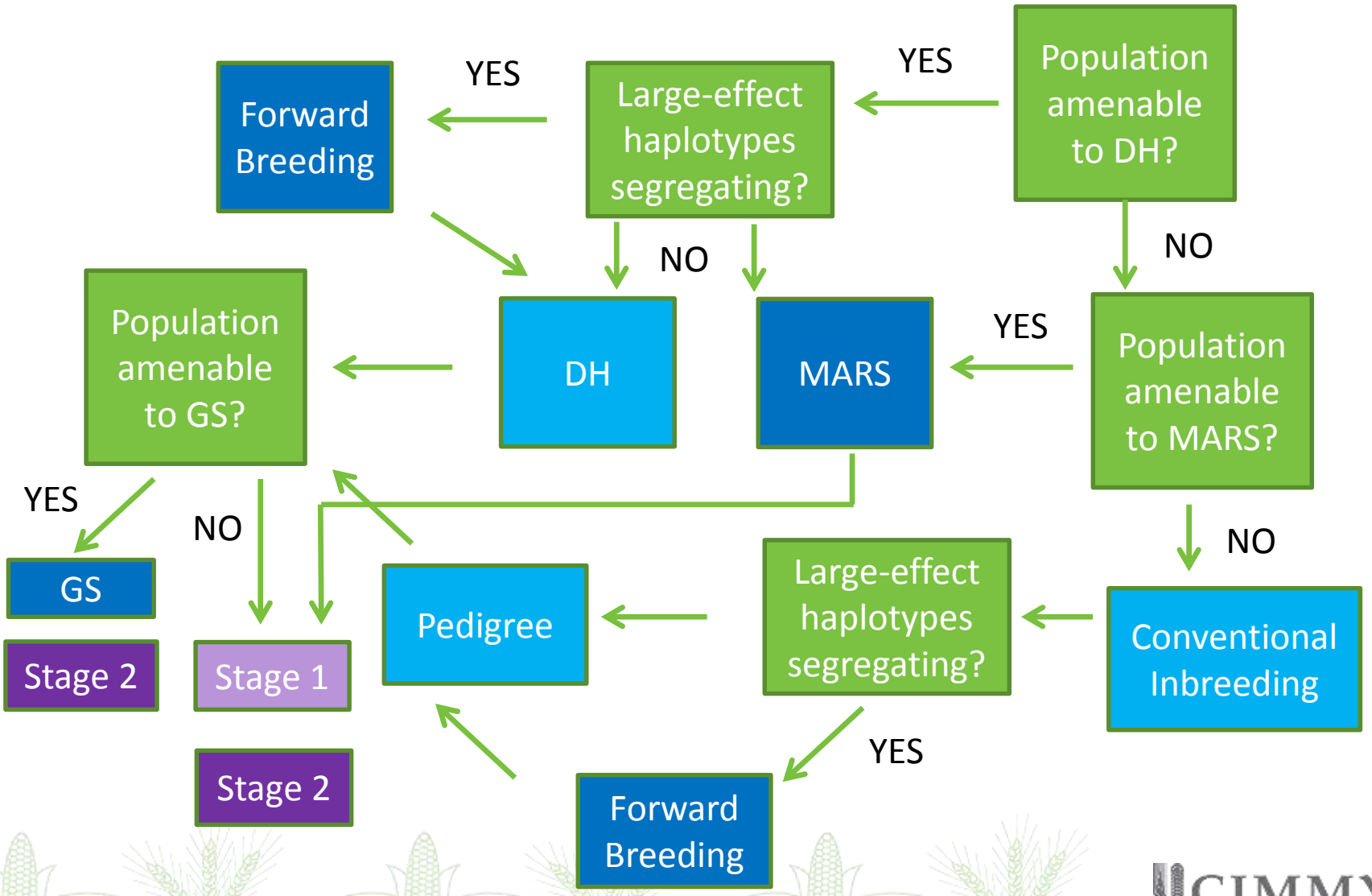
Designing decision trees



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Forward breeding example: MSV + MLN

Funnel = 400

Output = 6

MSV

MLN

Funnel = 6000

Output = 90

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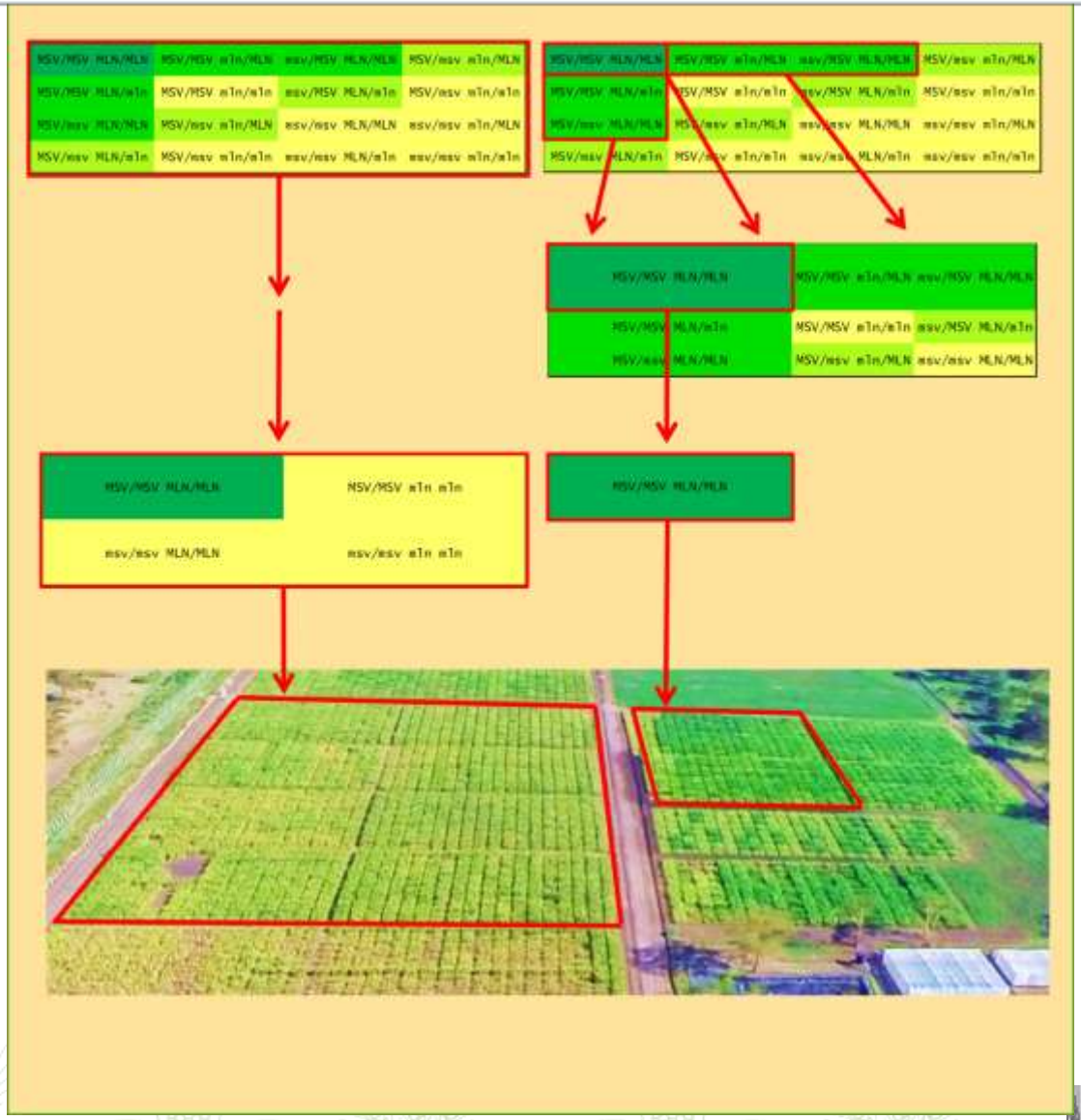
Example: KS23-5/CML442

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



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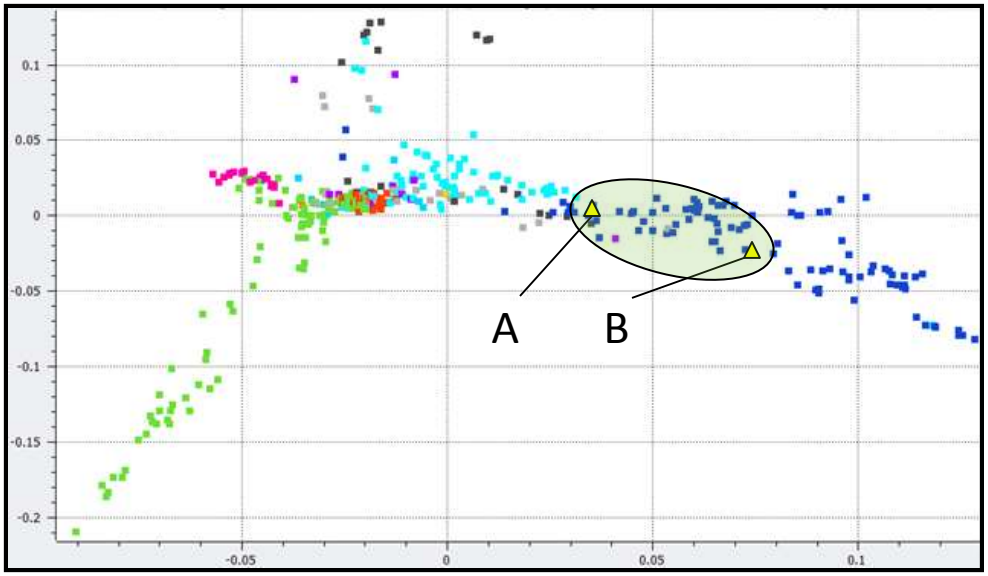
100 MSV/MSV+MLN/MLN F4 ears				
Genotype	Phenotype (MSV + MLN)	Forward Breeding	Conv.	Relative cost
$ 2.50	$ 8.00	$ 2,800	$ 3,200	88%
$ 2.50	$ 10.00	$ 3,000	$ 4,000	75%
$ 2.50	$ 12.00	$ 3,200	$ 4,800	67%
$ 2.00	$ 8.00	$ 2,400	$ 3,200	75%
$ 2.00	$ 10.00	$ 2,600	$ 4,000	65%
$ 2.00	$ 12.00	$ 2,800	$ 4,800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

100 MSV/MSV+MLN/MLN DH lines ($15/DH)				
Genotype	Phenotype (MSV + MLN)	Forward Breeding	Conv.	Relative cost
$ 2.50	$ 8.00	$ 4,300	$ 9,200	47%
$ 2.50	$ 10.00	$ 4,500	$ 10,000	45%
$ 2.50	$ 12.00	$ 4,700	$ 10,800	44%
$ 2.00	$ 8.00	$ 3,900	$ 9,200	42%
$ 2.00	$ 10.00	$ 4,100	$ 10,000	41%
$ 2.00	$ 12.00	$ 4,300	$ 10,800	40%
$ 1.50	$ 8.00	$ 3,500	$ 9,200	38%
$ 1.50	$ 10.00	$ 3,700	$ 10,000	37%
$ 1.50	$ 12.00	$ 3,900	$ 10,800	36%
$ 1.00	$ 8.00	$ 3,100	$ 9,200	34%
$ 1.00	$ 10.00	$ 3,300	$ 10,000	33%
$ 1.00	$ 12.00	$ 3,500	$ 10,800	32%

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***

Breeding process comparison

Next Steps / Challenges

- Migrate to a centralized breeding database
- Implement role specialization / centralization of core functions
- Demonstrate forward breeding value proposition
- Expand impact of GS in wheat
- Develop appropriate GS prediction sets in maize

Special thanks to staff and graduate students

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