Increasing the rate of genetic gain in the CIMMYT maize program using doubled haploids and marker-assisted selection

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CIMMYT Global Maize Program

On behalf of the CIMMYT GMP

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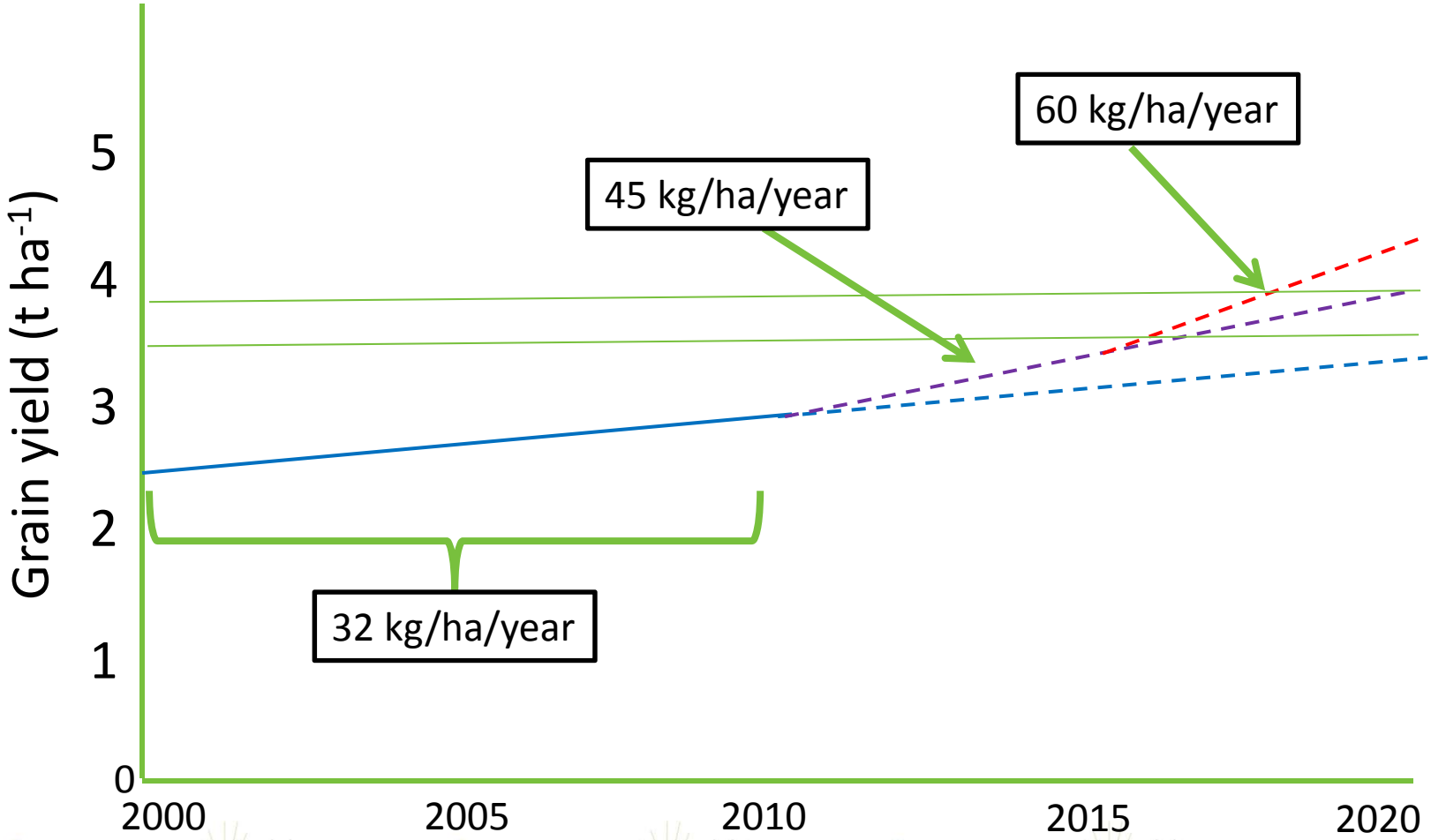
Driving genetic gain



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Driving genetic gain

- Increasing the size of the breeding program - greater selection intensity
- Faster breeding cycles
- More accurate selection (higher heritability)
- Adequate genetic variation
- Decision support tools

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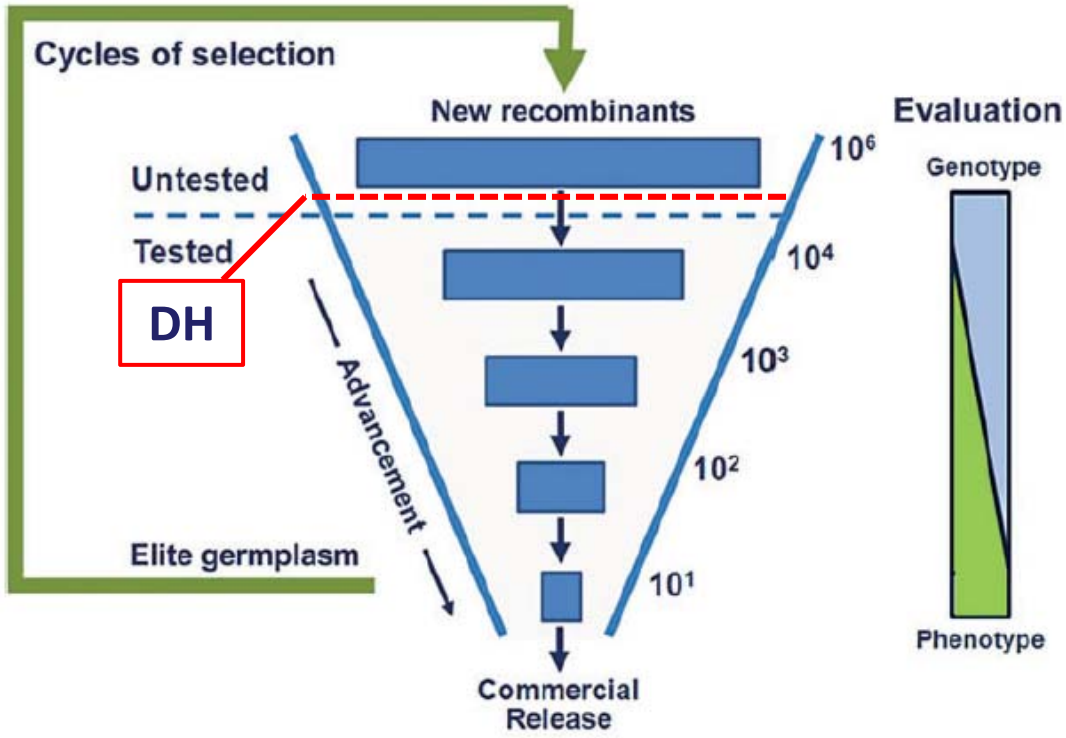
Putting it together – our approach to increasing genetic gain

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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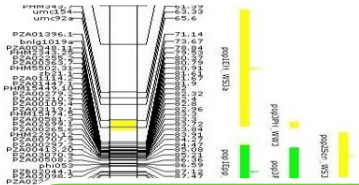
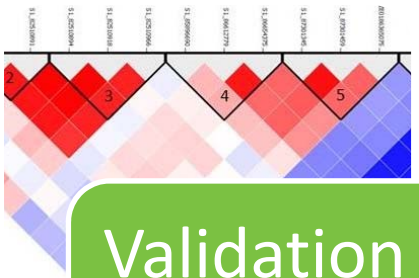
Production markers for high value haplotypes



Discovery

- MLN
- Heat
- Striga



Validation

- MLN
- GLS
- TLB
- Drought
- Low N

Deployment

- MSV
- PVA

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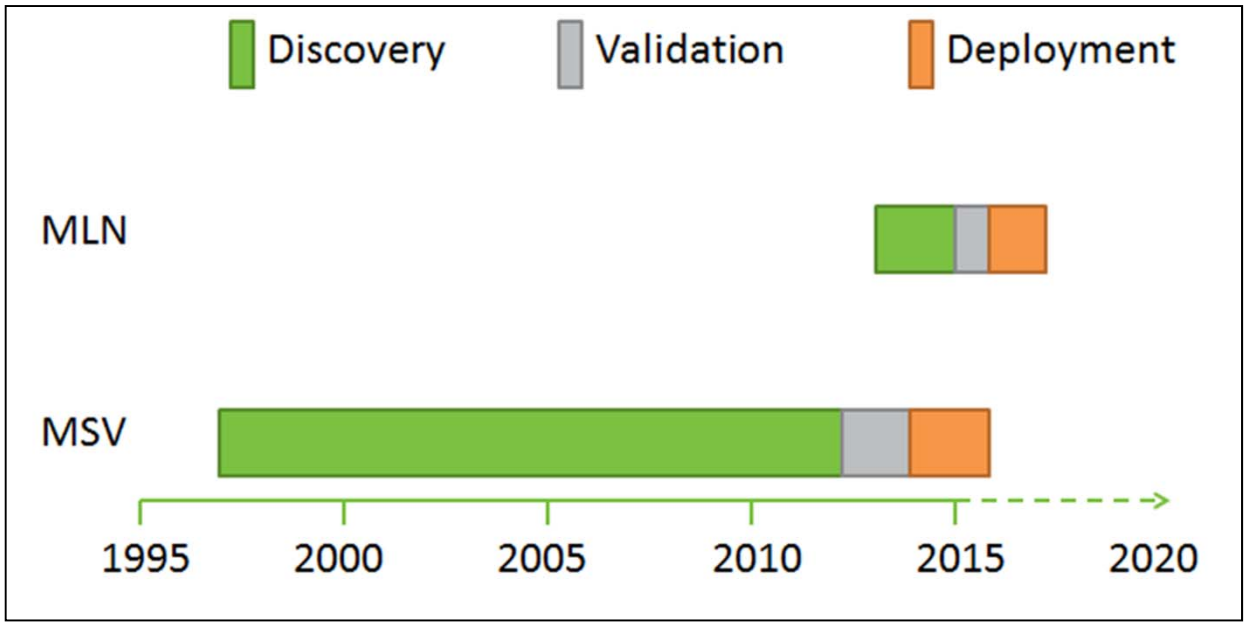
Critical Path Analysis

- 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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Case study

Combining multiple stress tolerance resistance:
Stress Tolerant Maize for Africa (STMA)

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Project deliverables

- Managed drought 45 kg/ha/year
- Low N 45 kg/ha/year
- Optimal 110 kg/ha/year
- Per se female yield 45 kg/ha/year
- MLN 250 kg/ha/year

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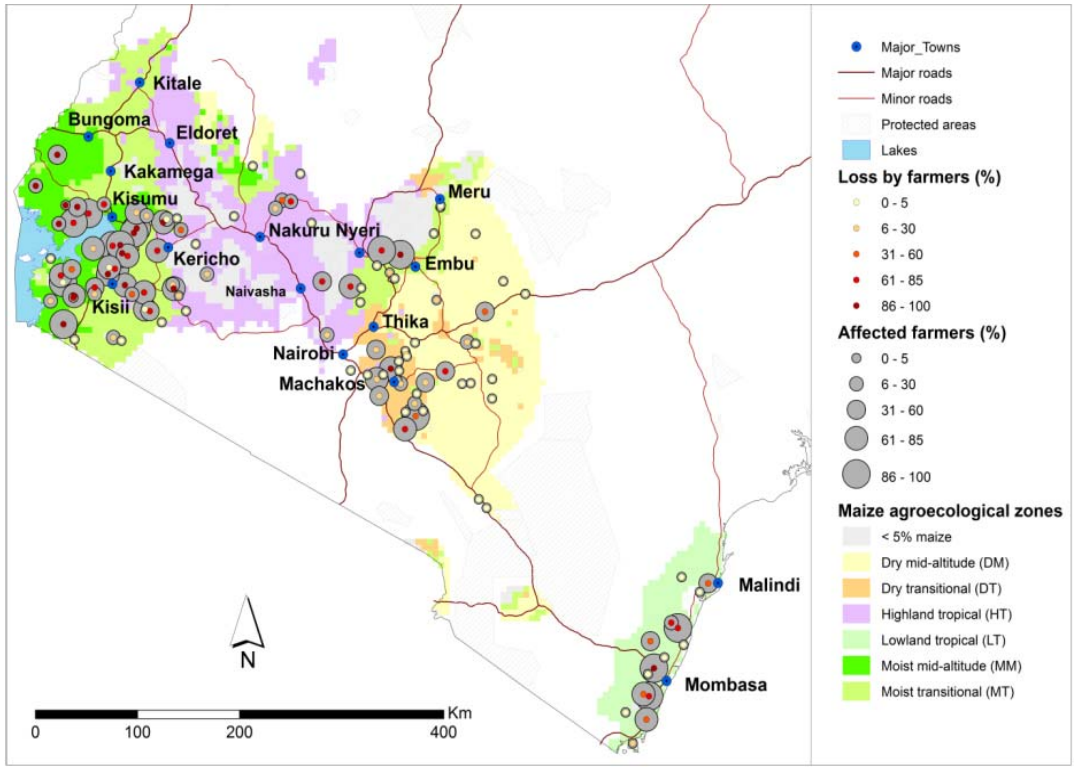
Maize Lethal Necrosis : Impact



- 23% yield loss in Kenya
- 0.3 million metric tons
- US $188 million

De Groote et al. 2015. Geographic distribution and impact of Maize Lethal Necrosis (MLN) disease in Kenya

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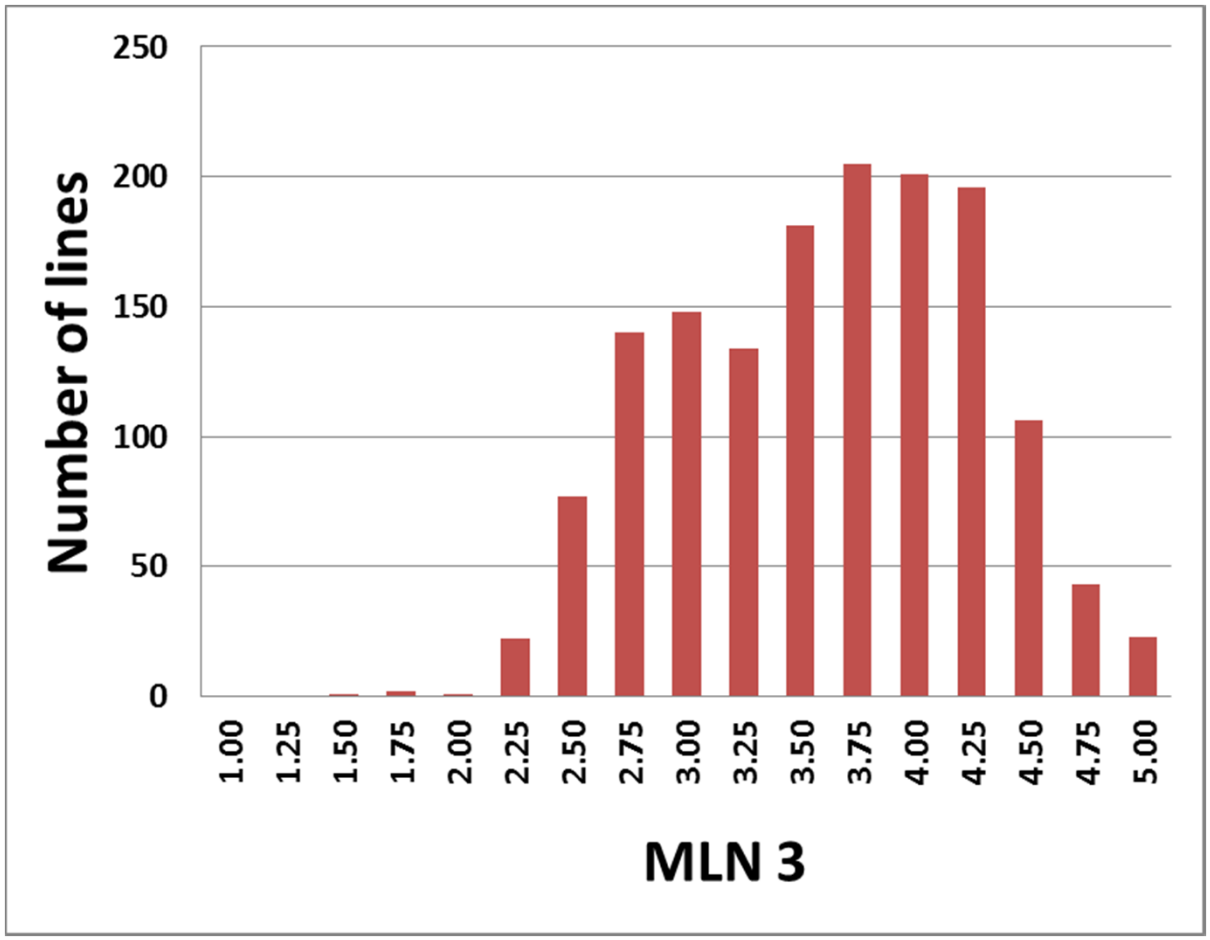

- African germplasm highly susceptible
- 1480 inbred lines evaluated from global germplasm sources

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MLN tolerant line prioritization

Pedigree	Donor	HG	BLUE	SE	N Obs	N Env
KS523-5	YES	A	1.47	0.42	3	2
OhiVI Ril-41			1.59	0.42	3	2
KS23-6	YES	A	1.63	0.31	5	3
(CML494/CML550)PHDH166-B			2.01	0.25	8	4
CKLMLN140287 (CML494*2/LH51)			2.01	0.30	5	3
(CML494/CML550)PHDH185-B			2.03	0.25	8	4
CML574 (CLRCY039)	YES	B	2.16	0.13	26	11
CLYN261	YES	A	2.30	0.19	12	7
CLRCY034	YES	B	2.36	0.13	26	11
CKDHL120918			2.38	0.20	11	6
DTPYC9-F46-1-2-1-2-B	YES	A	2.39	0.13	24	12
CML494	YES	B	2.57	0.12	31	13
CML543 (CKL5003)	YES	B	2.64	0.12	33	15
CML550 (CLWN201)			2.71	0.18	14	7
CML312			3.24	0.12	33	15
CML539			3.40	0.12	40	12
CML444			3.48	0.13	28	13
CML395			3.76	0.10	44	20
CML442			4.49	0.10	47	20

- Combined analysis estimates across trials
- 43 MABC projects ongoing
- BC4F1

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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
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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 Discovery and Validation

- 2 AM Panels
- 5 Bi-Parentals
- 37 MLN MABC projects
- 2 or 3 QTL introgression models
- Target: 10% GY increase vs RP in hybrid combination under natural MLN pressure
- 6 white + MSV1 donor conversion projects

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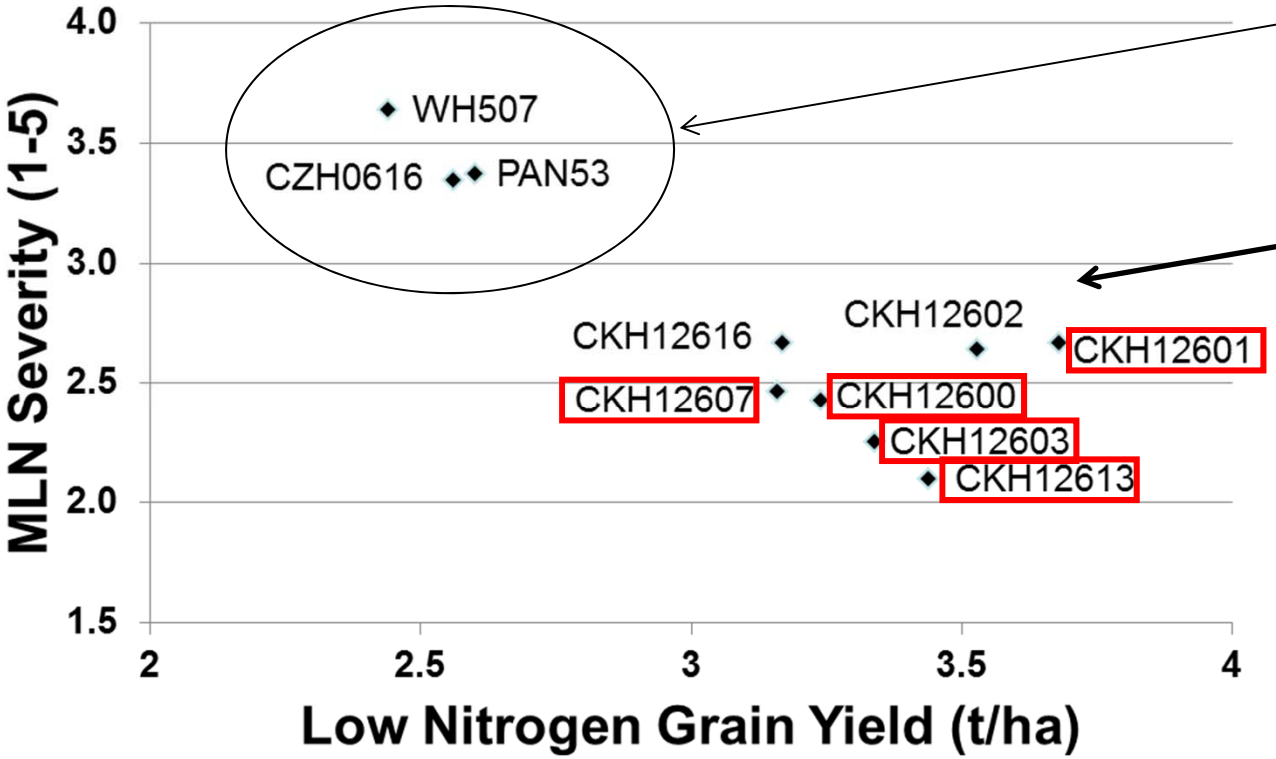
First generation MLN hybrids



Commercial Checks

Hybrids submitted for release on basis of Low N + MLN scores below 3

Hybrids in red boxes have been officially released

Several TWC Hybrids comprised of Elite, Africa adapted lines x Tropical lowland NUE+MLN donors

MLN Tolerant Hybrids versus Susceptible Checks Under natural disease pressure in Babati, Tanzania

CKDHL0221/CML312//(CML494/LH51)-12-2-1-1-2-B-B

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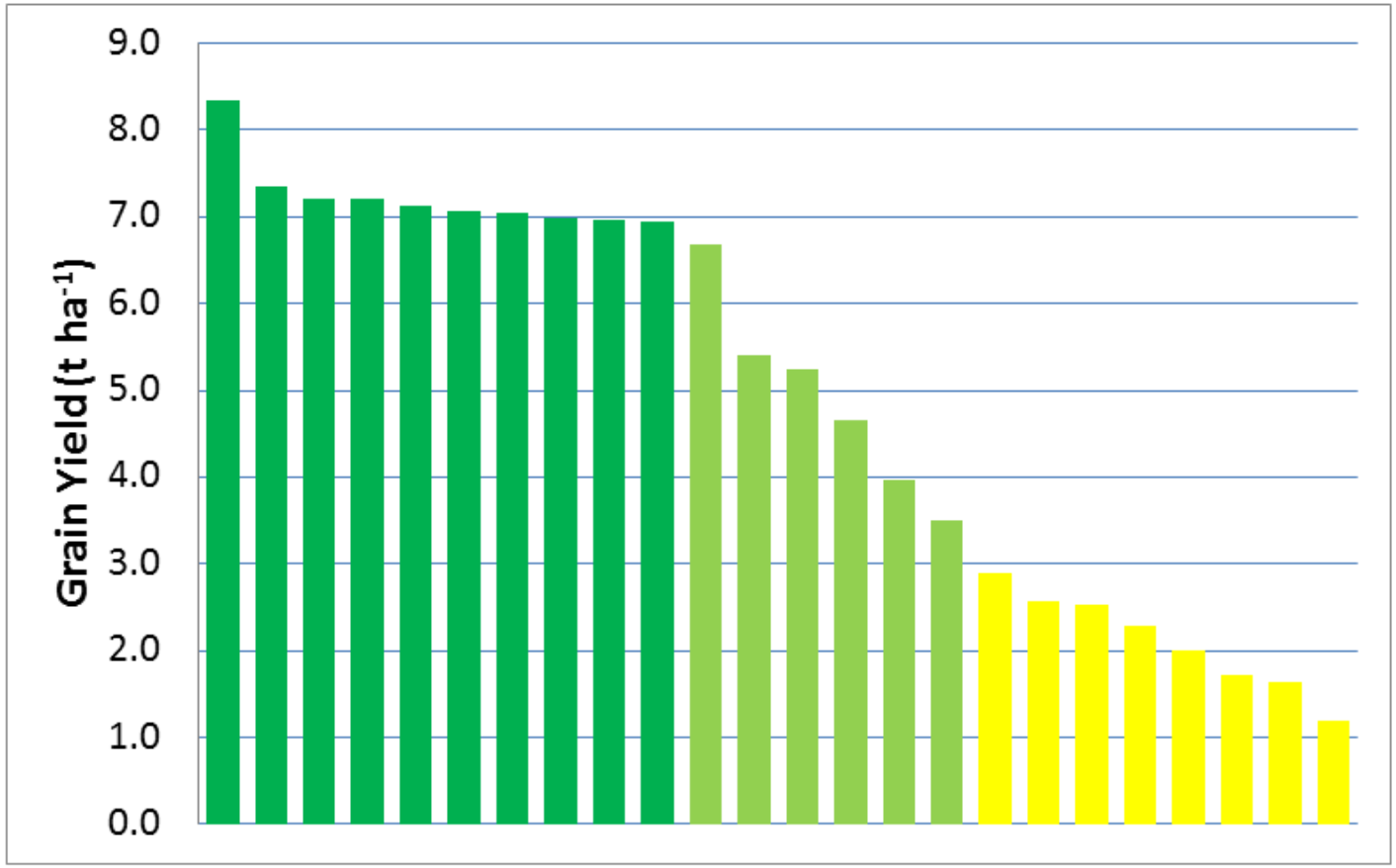
Grain yield : natural MLN pressure - TZ



1 loc; 2 reps

h^2 = 0.59

$LSD_{0.05}$ = 2.9

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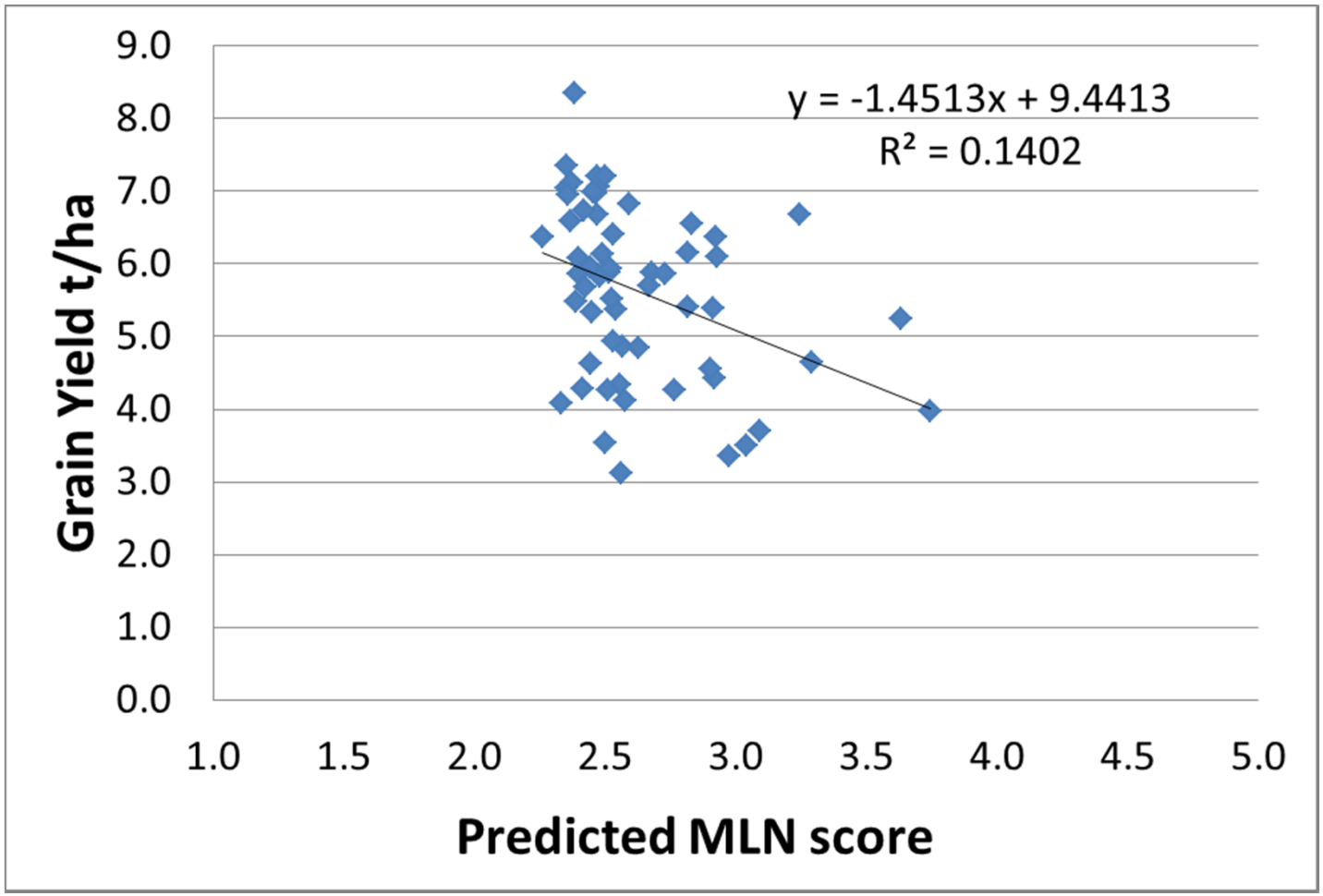
Grain yield : natural MLN pressure - TZ



Coded x Coded
First-Gen MLN NPT
Popular Checks

1 loc; 2 reps

$h^2 = 0.59$

$LSD_{0.05} = 2.9$

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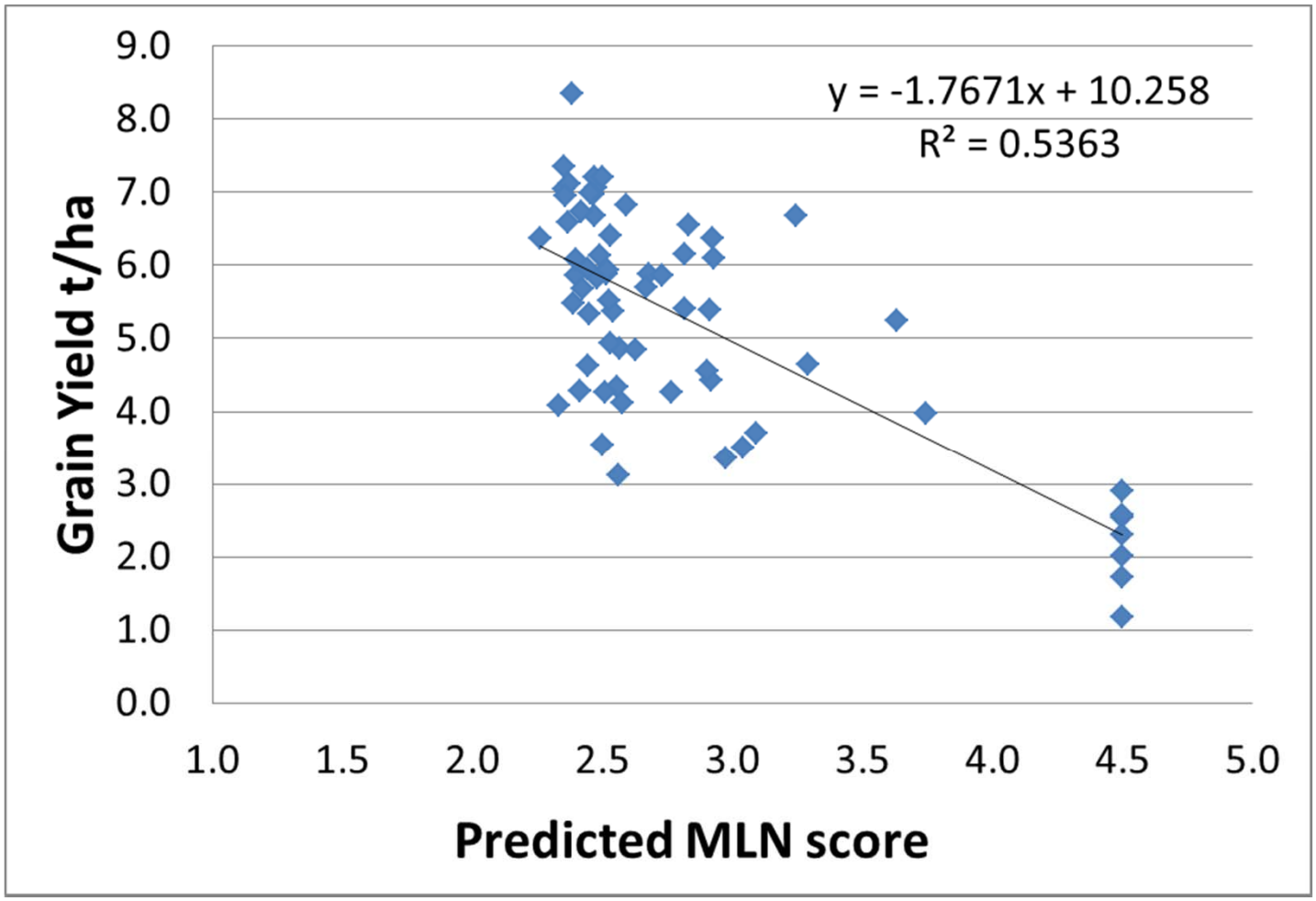
Grain yield : natural MLN pressure - TZ



Coded x Coded
First-Gen MLN NPT
Popular Checks

1 loc; 2 reps

$h^2 = 0.59$

$LSD_{0.05} = 2.9$

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Coded x Coded : Challenges and Opportunities

Category	Number	GY (t ha^{-1})
Coded x Coded	52	5.70
1st Gen MLN Hybrids	6	4.91
Checks	8	2.11

COLOR	Number	GY (t ha^{-1})
Yellow	5	6.97
75% Yellow	15	5.65
50% Yellow	17	5.86
25% Yellow	10	5.19
White	11	4.97
Checks	8	2.11

- White grain preference
- Susceptibility to MSV
- Susceptibility to TLB

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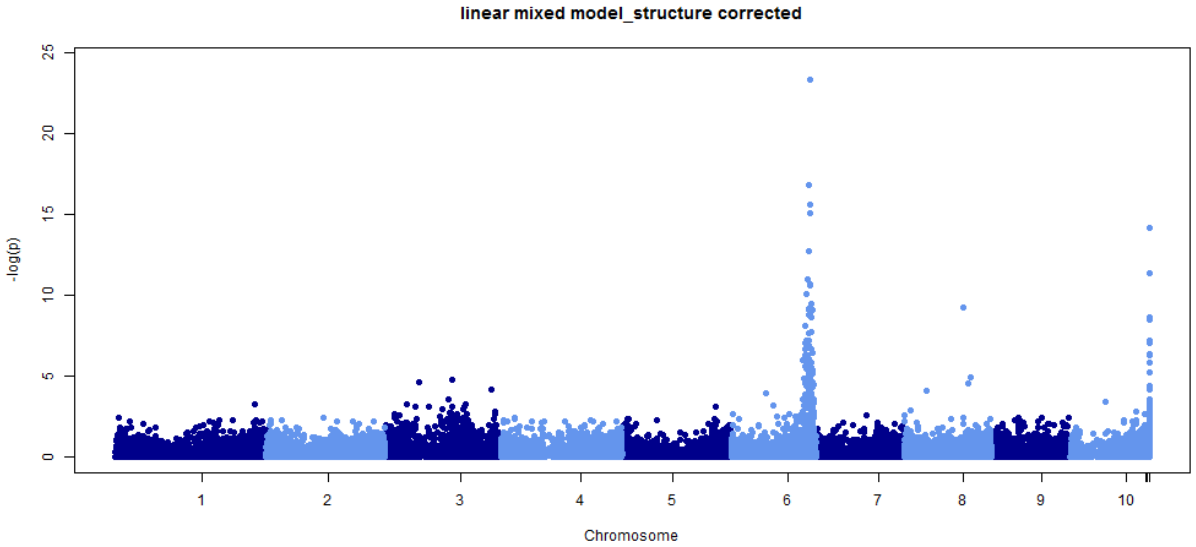
QTL Discovery

- 8 populations evaluated
- 4544 plants tagged and scored
- 5 populations prioritized based on phenotypic distribution

	COLOR	COUNT	MLN1	MLN2	MLN3	MLN4	MLN5
KS523 vs Susc.	W	526	2.4	3.6	3.9	4.2	4.3
	Y	722	2.1	2.9	3.4	3.7	3.9



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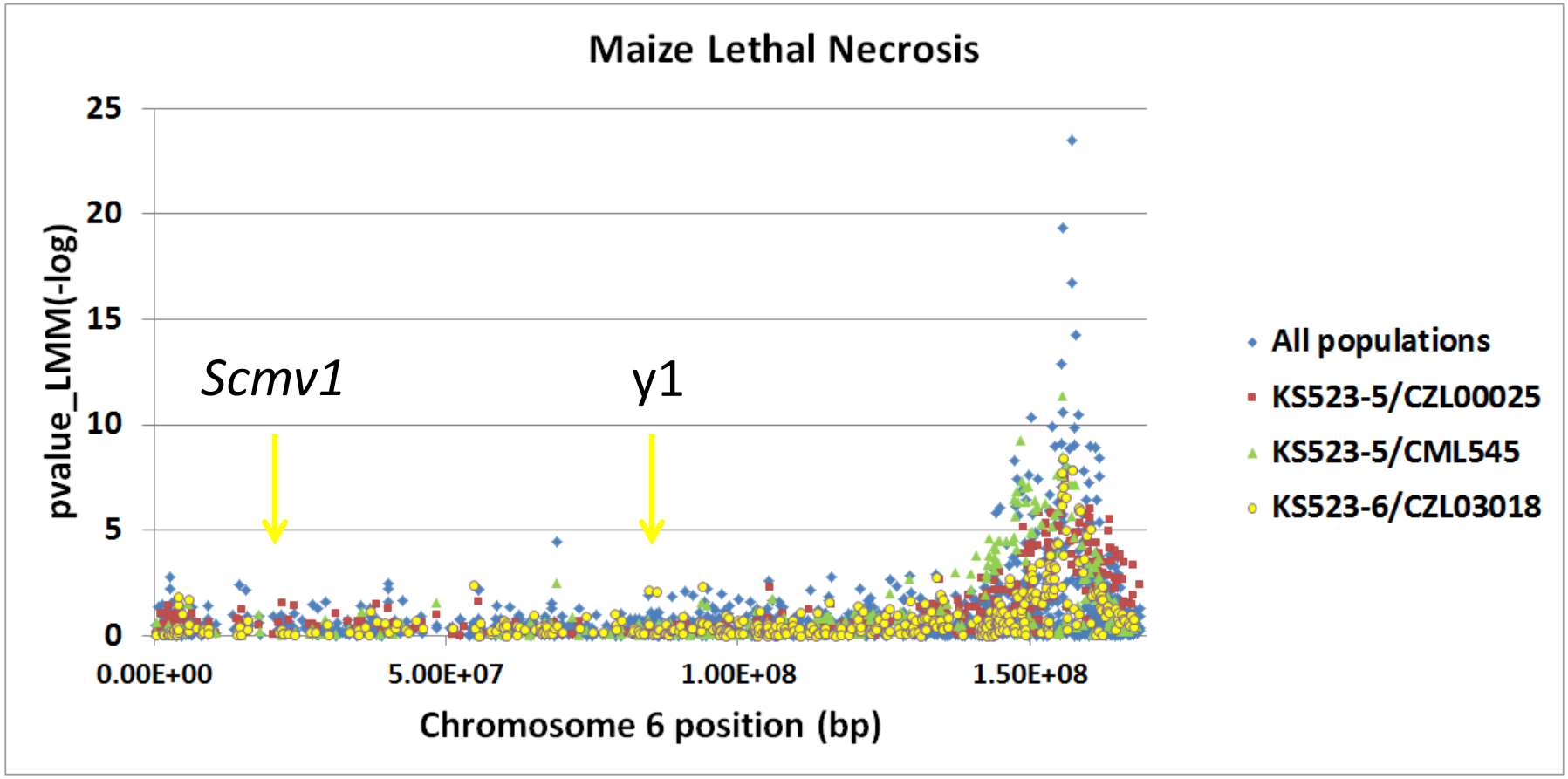
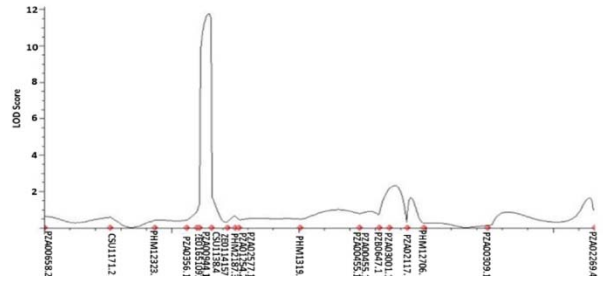

Maize Lethal Necrosis
pvalue_LMM(-log)
25
20
15
10
5
0
Scmv1
y1
0.00E+00
5.00E+07
1.00E+08
1.50E+08
Chromosome 6 position (bp)
All populations
KS523-5/CZL00025
KS523-5/CML545
KS523-6/CZL03018

Marker class means

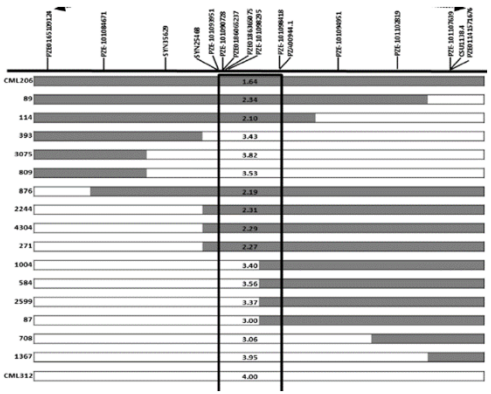
Pedigree	Genotype	COUNT	MLN1	MLN2	MLN3	MLN4	MLN5
CZL068/CML494	+/+	16	2.2	3.3	3.4	3.5	3.3
	+/-	16	2.5	4.0	4.1	4.3	4.2
	-/-	40	2.1	3.7	3.9	3.9	3.8
KS523-6/CZL03018	+/+	42	1.6	2.5	2.3	2.6	2.7
	+/-	22	2.7	4.5	4.8	4.8	4.8
	-/-	44	2.6	4.5	4.8	4.8	4.8
KS523-5/CML545	+/+	55	1.7	2.0	2.1	2.4	2.4
	+/-	23	2.6	4.4	4.9	4.7	4.7
	-/-	48	2.3	3.8	4.3	4.4	4.4
KS523-5/CZL00025	+/+	27	1.9	2.1	2.1	2.3	2.3
	+/-	11	3.0	4.4	4.6	4.8	4.8
	-/-	25	2.6	3.9	4.2	4.3	4.3
KS523 vs Susc.	+/+	124	1.7	2.2	2.2	2.5	2.5
	+/-	56	2.7	4.4	4.8	4.8	4.7
	-/-	117	2.5	4.1	4.4	4.5	4.5

Maize streak virus (MSV)

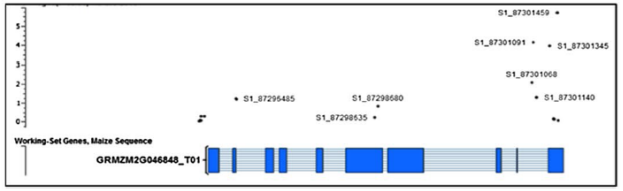


Length: 5.9 cM
Proportion of phenotypic variation: 67.4%

30,000 DH lines screened in 2014-2015



Length: 0.87 cM



3 SNPs
Proportion of phenotypic variation: 45.2%

Nair et al. 2015

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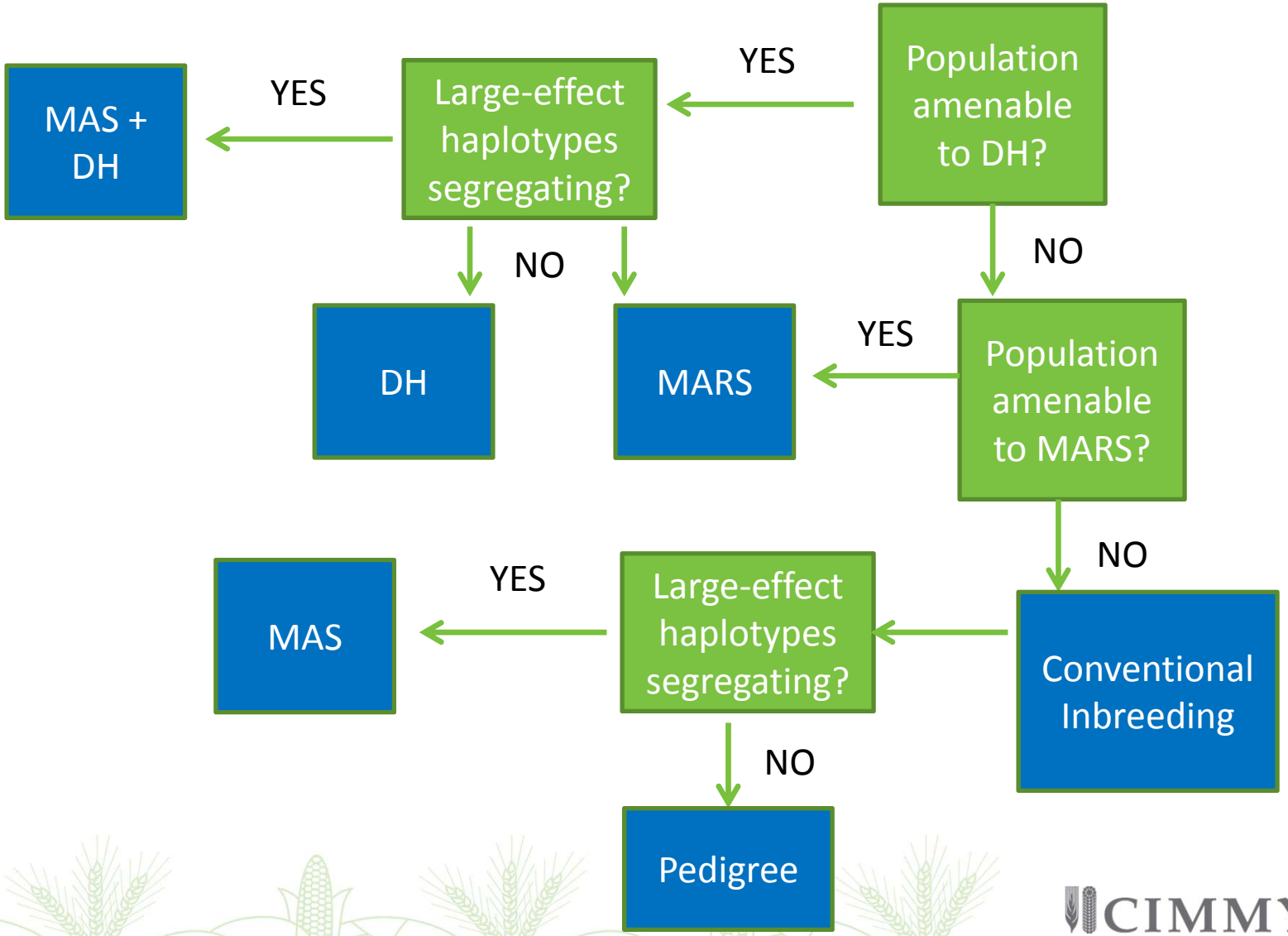
Stakeholder engagement

- Co-development of supported workflows
- Identifying barriers to adoption
- Establishing and budgeting allocations for supported workflows
- Engaging breeders on how to optimally use resources on a population by population basis
- Which tools to use at which stage in which combinations?

Integrating DH and molecular markers

1. Prioritize populations into workflows based on available opportunities
2. Optimize population sizes to match workflows
3. Support few workflow pipelines
4. Develop straightforward access protocols
5. Aggregate populations into workflow pipelines
6. Turn the crank
7. Iteratively optimize workflows

Designing decision trees



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Next Steps

- Implement forward breeding to increase population size at GMP-Africa level by 4x by 2019
- Increase DH utilization in a cost effective way to >50% across GMP-Africa by 2019
- Demonstrate improved genetic gain per unit time per unit invested

Acknowledgements

- Bill and Melinda Gates Foundation
- USAID
- CGIAR Research Program on MAIZE
- Syngenta Foundation for Sustainable Agriculture
- Kenya Agriculture and Livestock Research Organization

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Thank you for your interest!

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Pedigree	GY t/ha	MLN
CML494/CML550//CML543	2.5	3.5
CML550/CML444//CKL13645	2.3	2.2
CML550/CML442//CKL13645	2.3	2.5
CML550/CML494//CKL13647	2.3	3.0
CLRCY039/CLYN261//DTPYC9-F46	2.2	2.0
CLYN261/CML494//CKL13639	2.2	2.5
CML494/CML550//CKL131092	2.1	3.0
CML494/CML550//CKL131016	2.0	2.7
CLYN261/CML494//CKL131089	2.0	3.0
CKH12613 - MLN tolerant	1.9	2.7
CKH12600 - MLN tolerant	1.7	3.2
Commercial Check	0.9	3.2
TegoDrought	0.5	3.7
CKH12616 - MLN tolerant	0.4	3.7
Commercial Check	0.2	4.5
Commercial Check	0.2	3.5
Commercial Check	0.1	5.0
Commercial Check	0.0	4.7
Commercial Check	0.0	5.0
Commercial Check	0.0	4.7

Yield under severe natural MLN pressure

- Preliminary data – 1 location x 2 reps
- CML494 and CML550 being converted with MSV-1
- CLYN261, CLRCY039, DTPYC9-F46 being converted to white and MSV-1
- CML494 and CML550 – key NUE lines
- DTP-F46 Heat+drought tolerant

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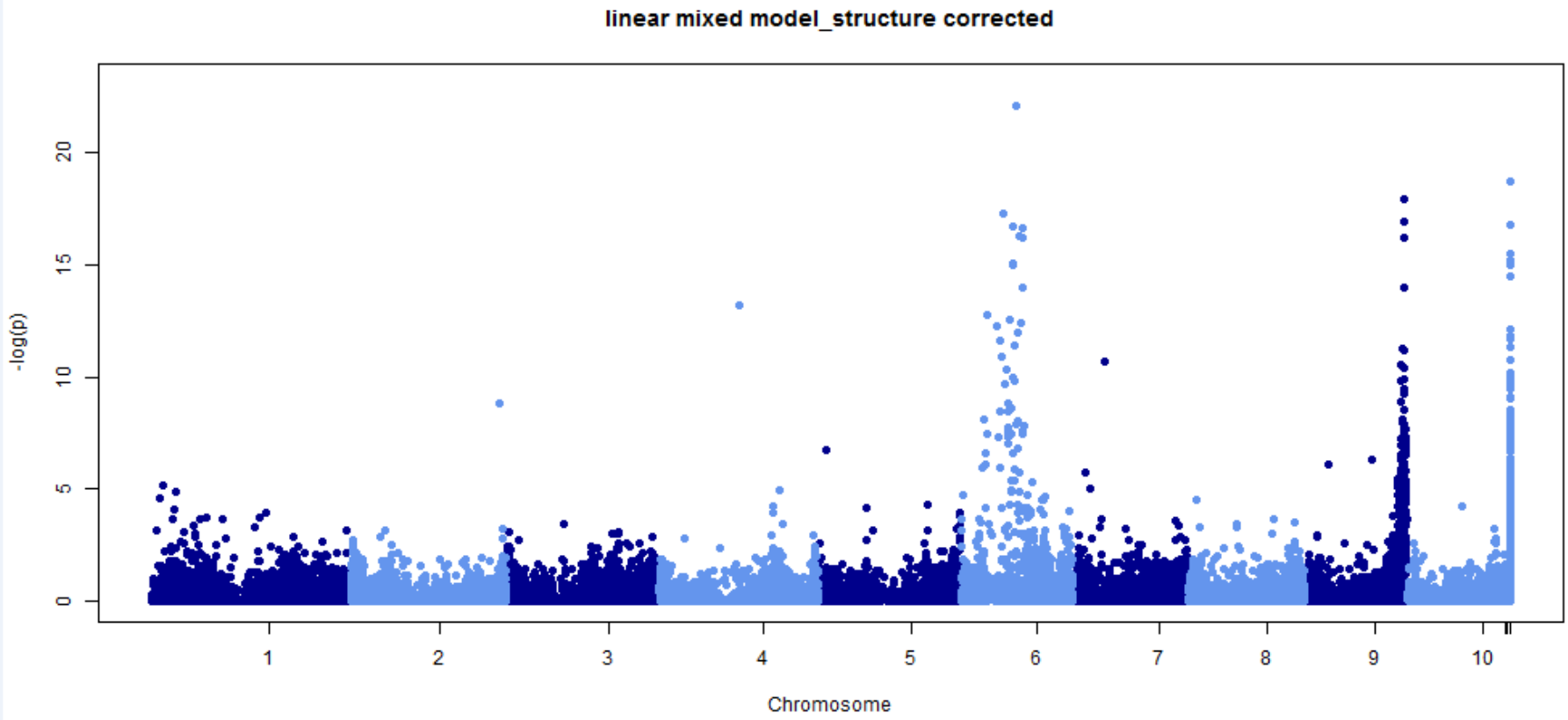
GWAS for grain color