MAIZE strategy: GOBII workshop

Mike Olsen on behalf of
CRP MAIZE AFS CoA2.2
Nairobi, Kenya
February 4, 2017

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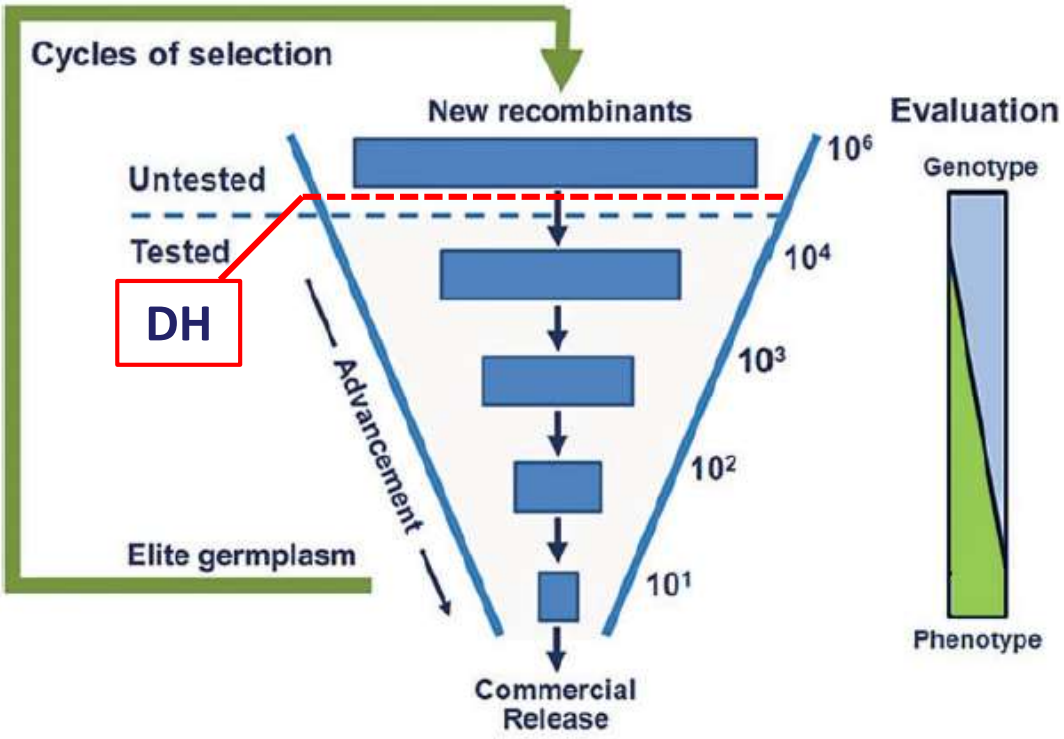
Increasing genetic gain

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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MAIZE AFS 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

Case study- MAIZE

- Brief background of program
  - Latin America
    - Eight maize breeding programs
      - *Applied field breeding programs – 3 GMP; 1 GRP*
      - *Land race improvement breeding – 1 GRP*
      - *Molecular breeding programs – 2 GMP; 1 GRP*
    - Current strategy / Pipeline overview
      - *Deploy large effect haplotype for tar spot complex resistance through forward breeding strategy*
      - *Validate highland adaptation haplotype and develop forward breeding strategy*
      - *Genomic prediction / genomic selection target traits: GLS, TLB, PHT, flowering time, yield under low N, yield under drought*
      - *Discovery pipeline traits: Kernel zinc, yield under low pH*

Case study- MAIZE

- Brief background of program
  - Africa
    - Twelve maize breeding programs
      - *Applied line development programs – 5 CIMMYT; 2 IITA*
      - *Applied product development programs – 2 CIMMYT*
      - *Molecular breeding programs – 2 CIMMYT; 1 IITA*
    - Current strategy / Pipeline overview
      - *Deploy large effect haplotypes for MSV, MLN, and PVA*
        - » Forward breeding all traits
        - » MABC – MLN and PVA
      - *Validate MLN, Striga, Aflatoxin and Drought haplotypes*
      - *Genomic prediction / genomic selection target traits: GLS, TLB, PHT, flowering time, yield under low N, yield under drought, MLN*
      - *Discovery pipeline traits: MLN and Striga*

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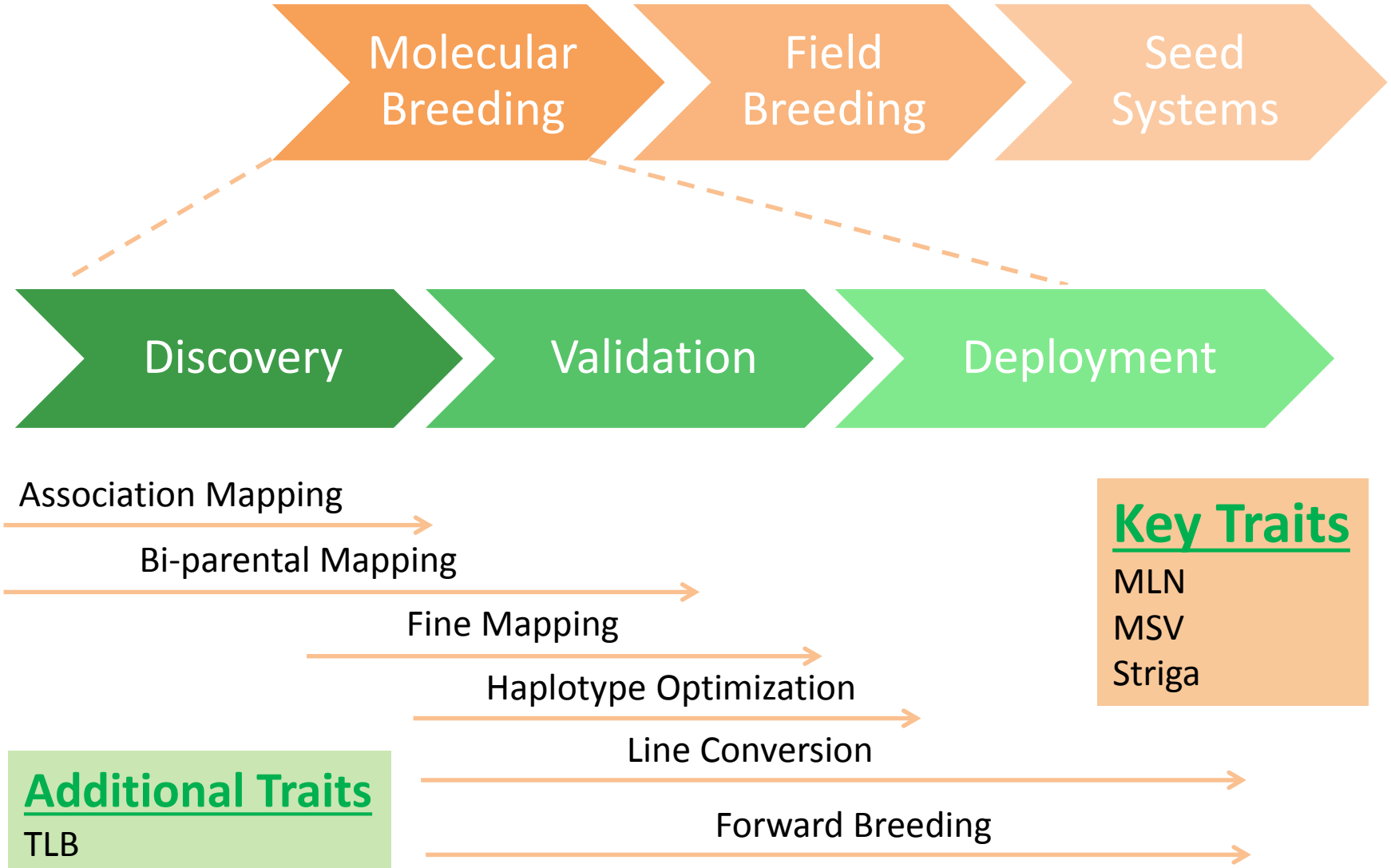
Case study- MAIZE

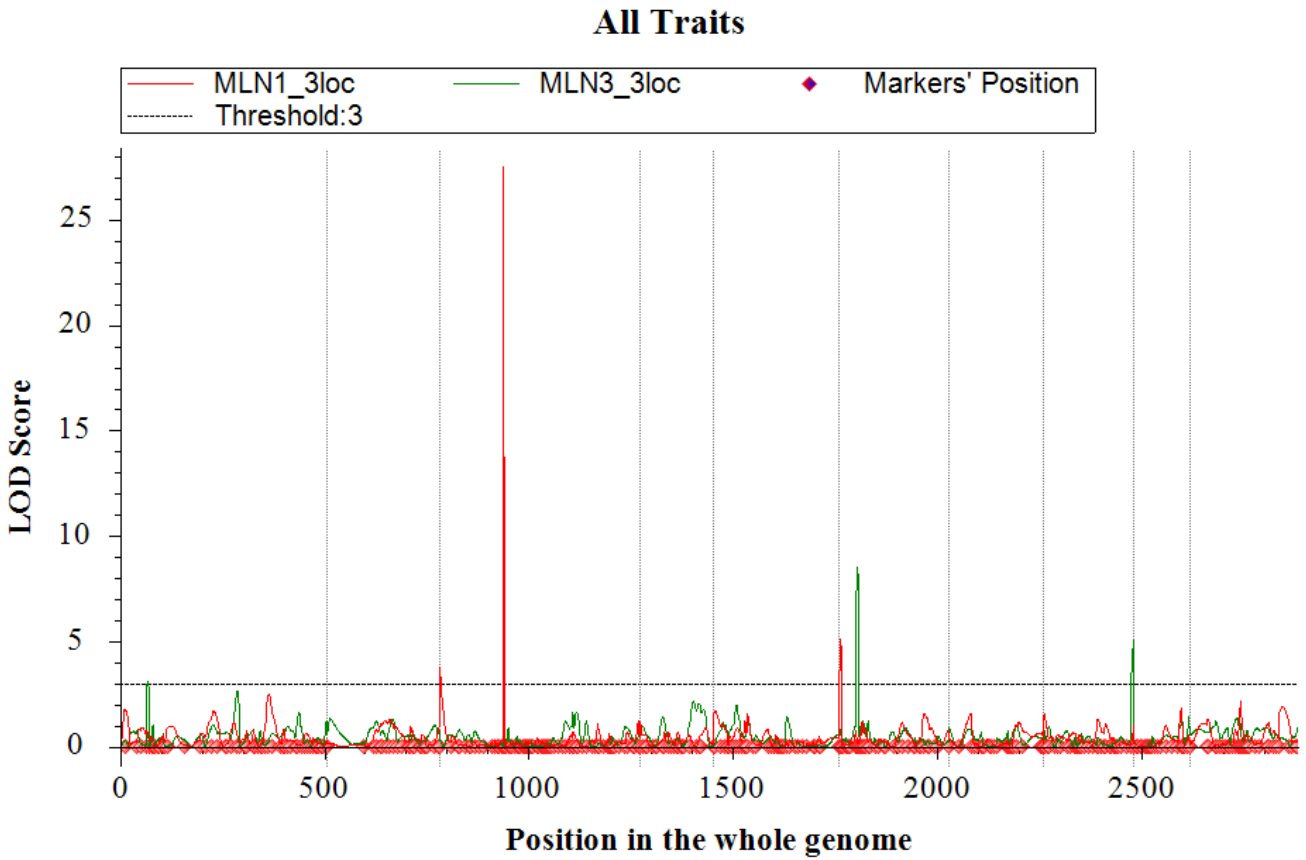
- Brief background of program
  - Asia
    - Six maize breeding programs
      - *Applied line development programs – 4*
      - *Molecular breeding programs – 2*
    - Current strategy / Pipeline overview
      - *MARS / population improvement for drought, waterlogging, heat, GLS and TLB*
      - *Need to assess cost-benefit of forward breeding based on effect size and allele frequency of known haplotypes of importance in Asia*

Case study- MAIZE

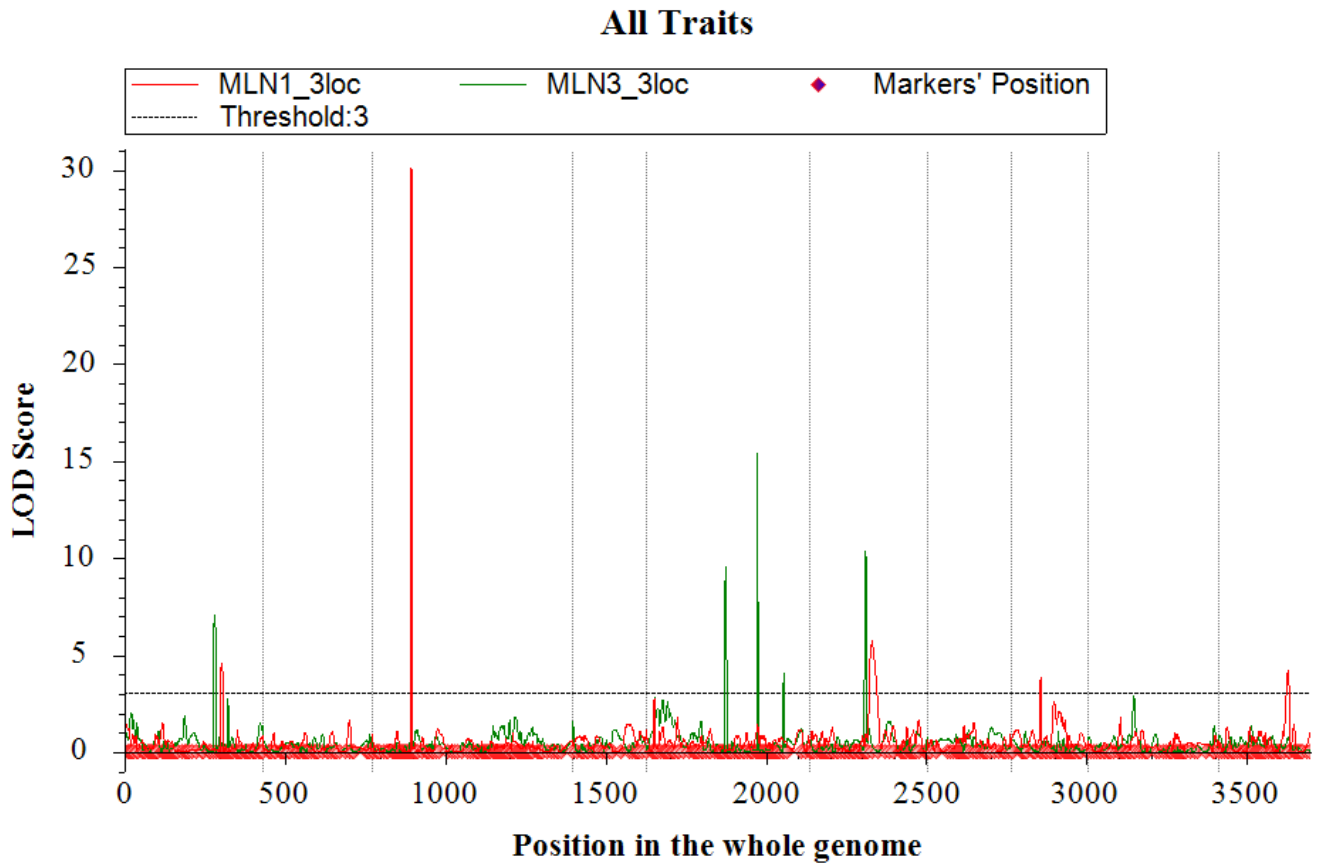
- Products
  - Elite lines developed through WEMA - MARS protocol reaching commercialization
  - Forward bred PVA lines in hybrids in advanced trials
  - Africa DH pipeline screened for MSV1 – materials now in stage 1 yield testing 2016-2017
  - First cohort MABC materials for MLN entering initial efficacy testing – finished versions to hand off in Q3 2017
  - Second cohort MABC materials for MLN at BC2 stage
  - First cohort MLN forward breeding populations to hand off in Q1 2017 (qMLN06.157 + MSV1)


Molecular Breeding
Field Breeding
Seed Systems
Discovery
Validation
Deployment
Association Mapping
Bi-parental Mapping
Fine Mapping
Haplotype Optimization
Line Conversion
Forward Breeding
Key Traits
MLN
MSV
Striga
Additional Traits
TLB
GLS
Temperate haplotypes

MLN QTL mapping – CML543xLPS-C7-F71



MLN QTL mapping – CML543xCML444



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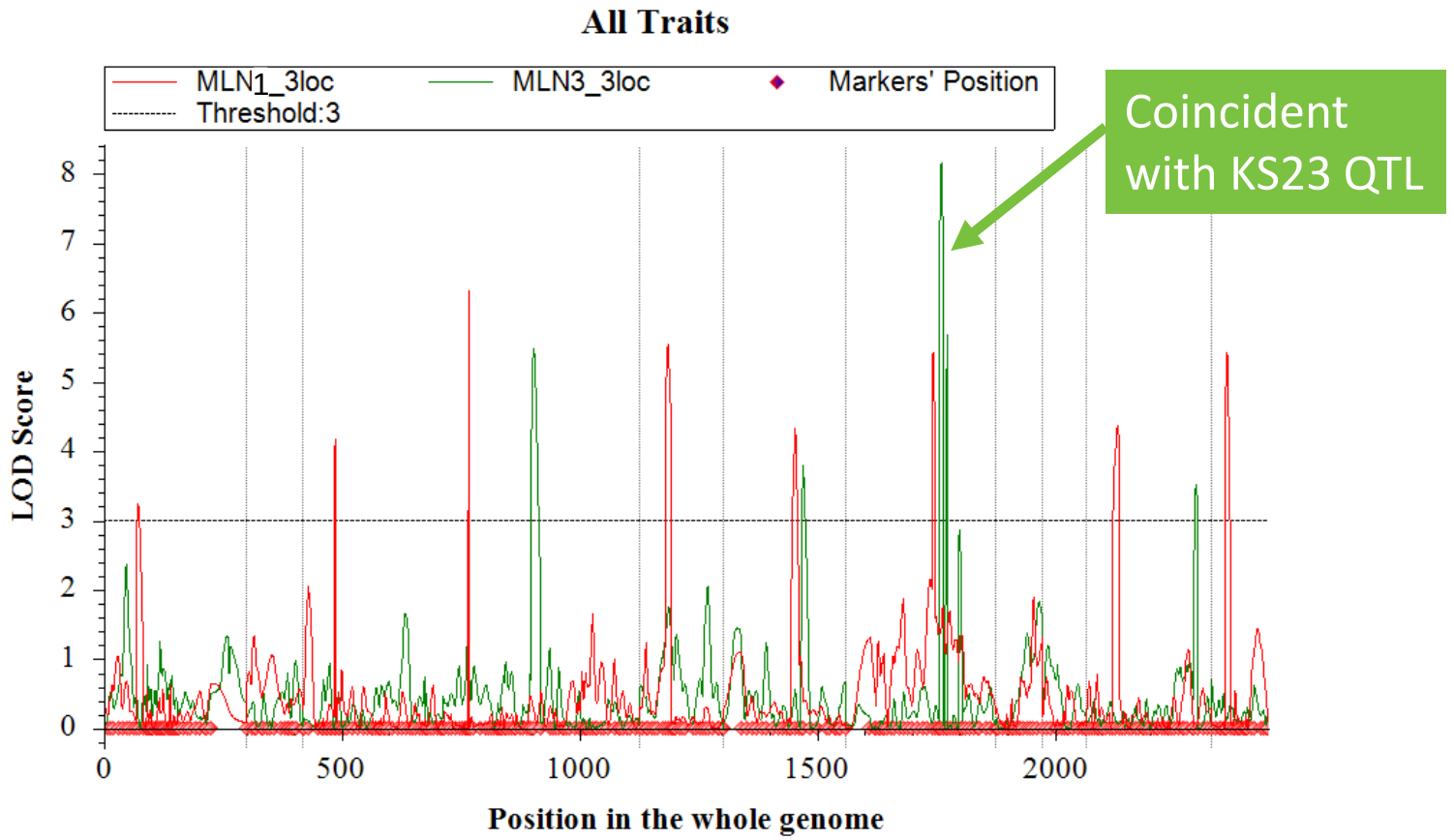
MLN QTL mapping – CML444xCML539



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CML550 x CML504 DH pop

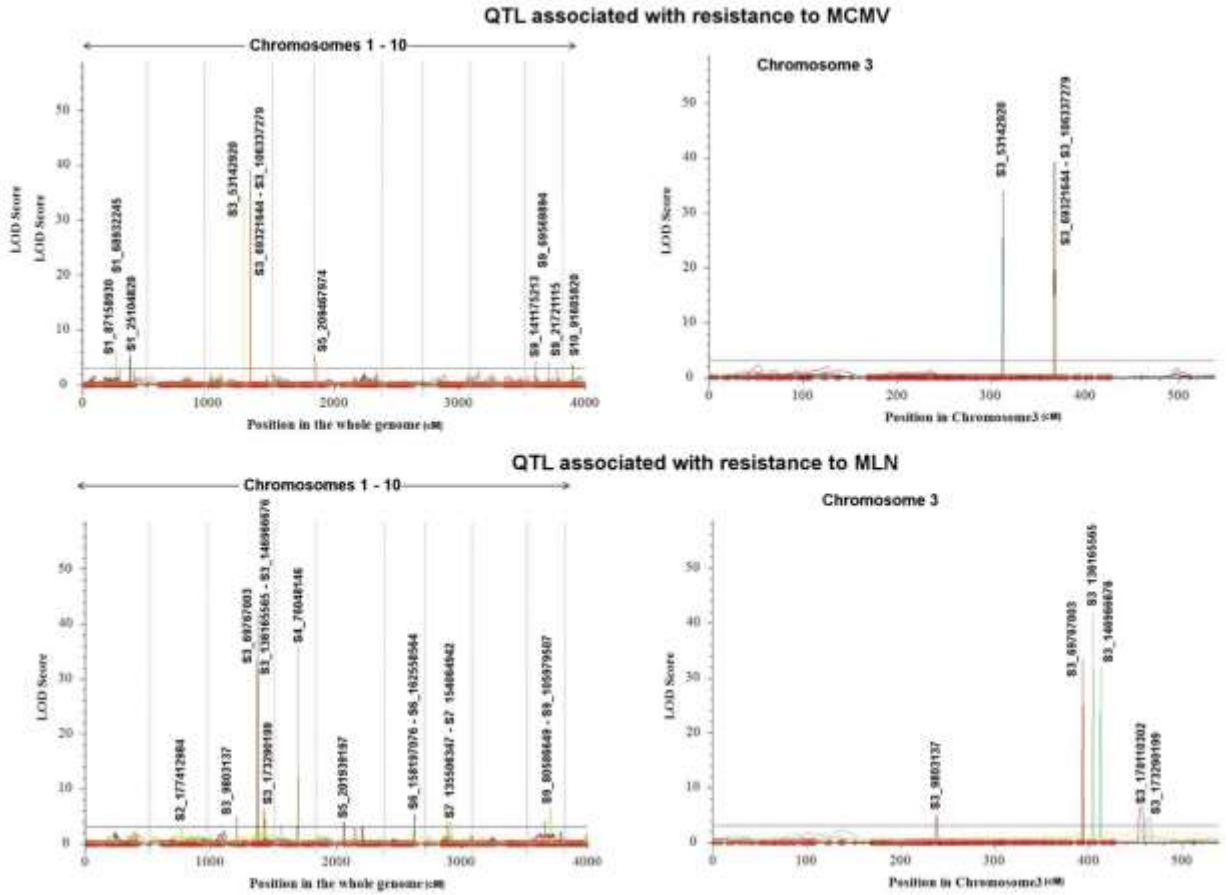

Fig: QTL associated with resistance to MCMV and MLN in same DH population

	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 to be planted in April

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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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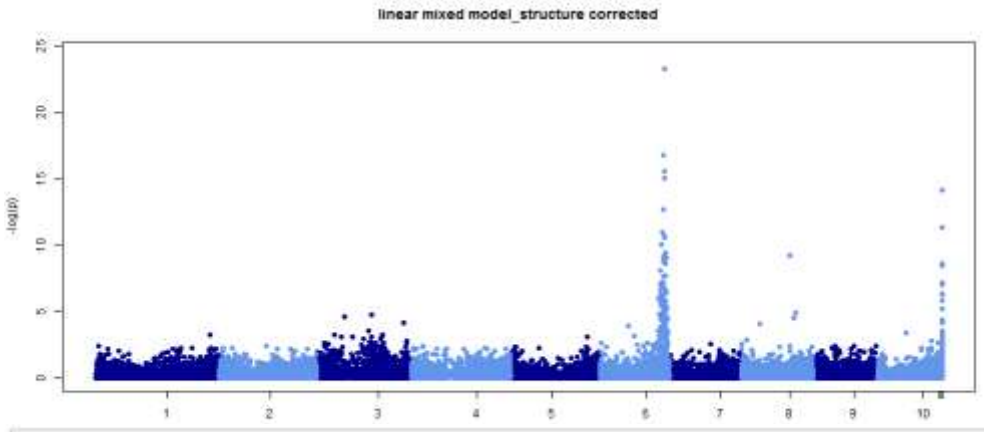
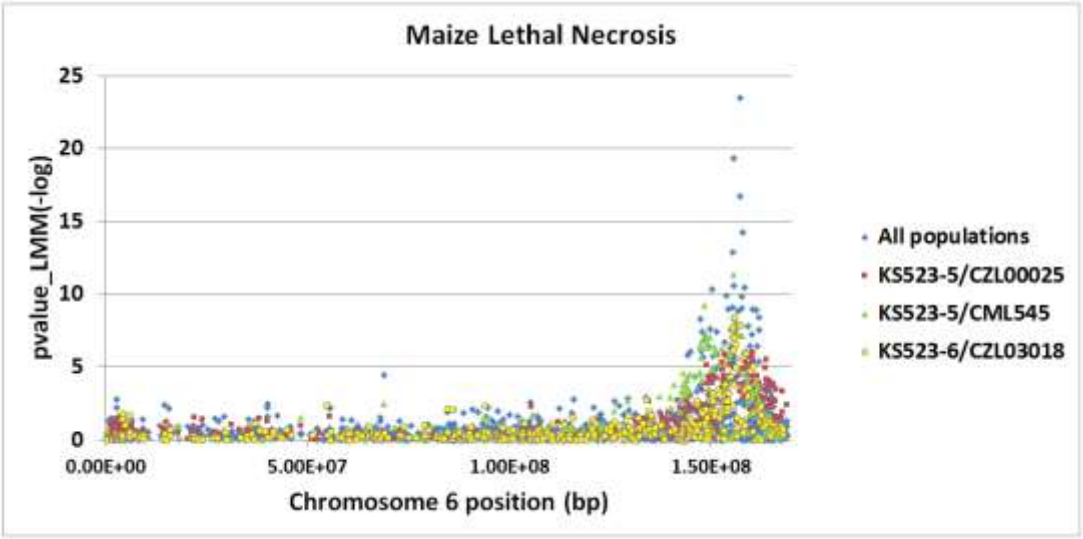
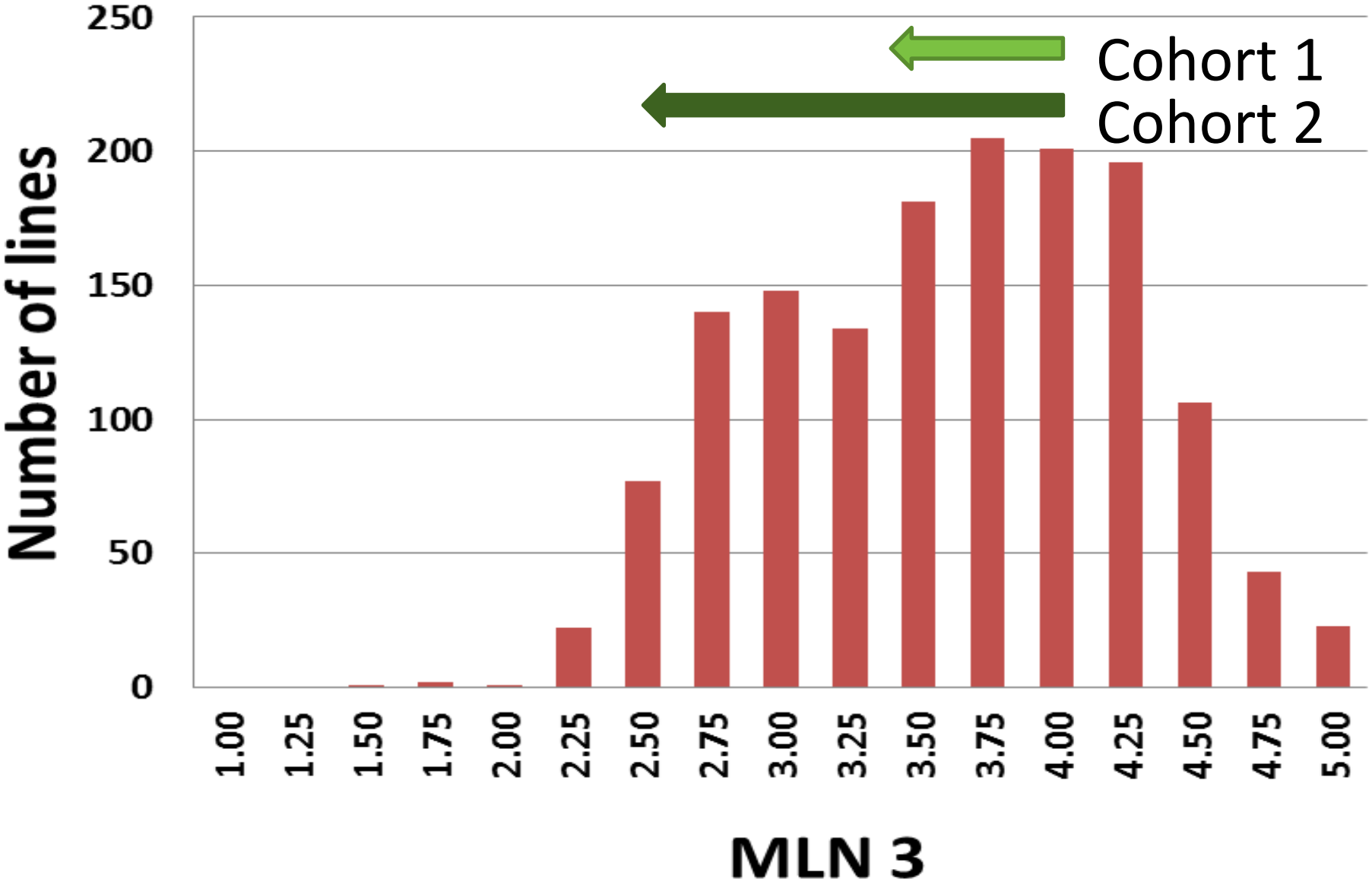
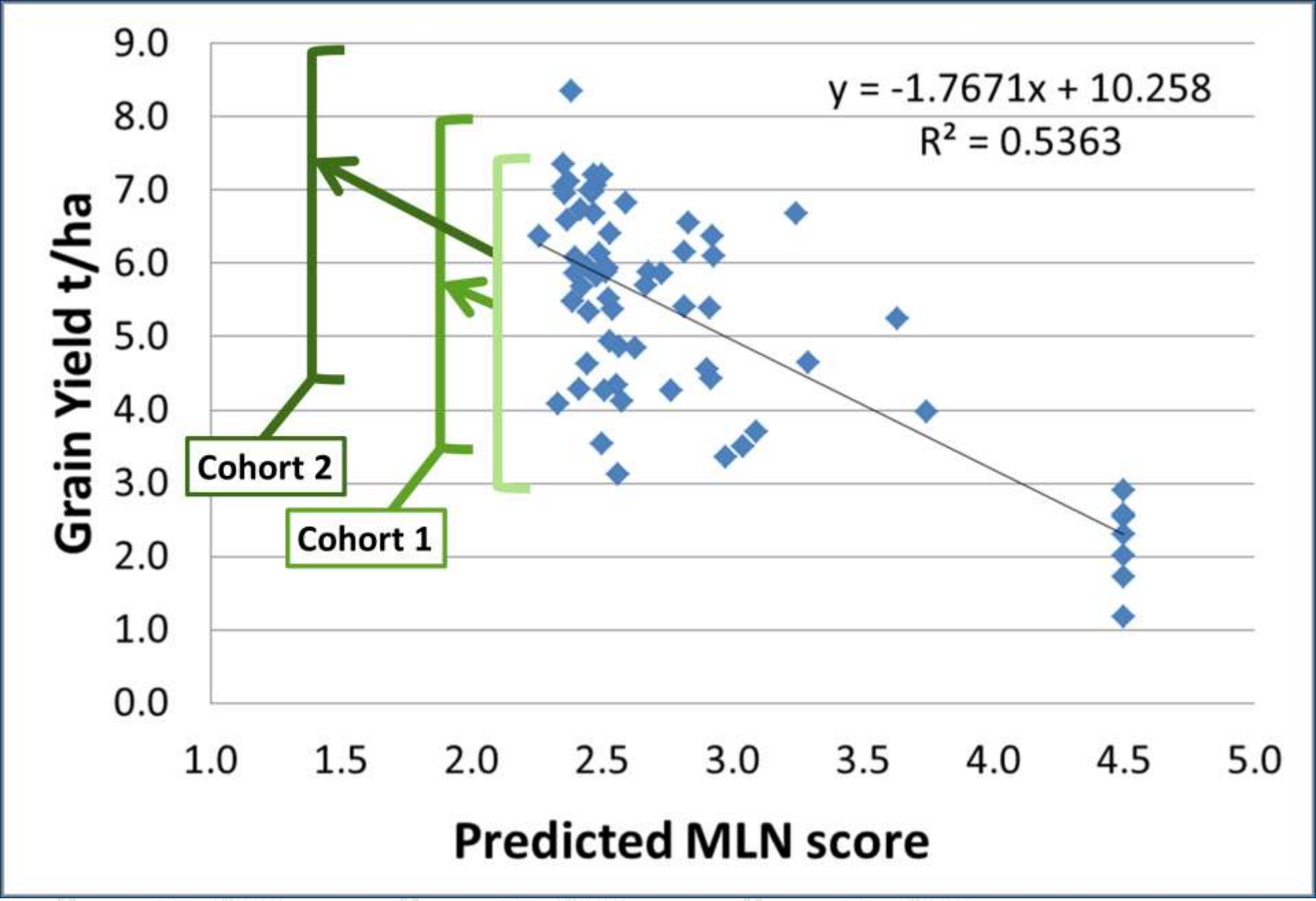
Marker Deployment (MLN)





Pedigree	Genotype	COUNT	MLN1	MLN2	MLN3	MLN4	MLN5
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


Cohort 1
Cohort 2
Number of lines
250
200
150
100
50
0
1.00
1.25
1.50
1.75
2.00
2.25
2.50
2.75
3.00
3.25
3.50
3.75
4.00
4.25
4.50
4.75
5.00
MLN 3


y = -1.7671x + 10.258
R² = 0.5363
Cohort 2
Cohort 1
Grain Yield t/ha
9.0
8.0
7.0
6.0
5.0
4.0
3.0
2.0
1.0
0.0
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
5.0
Predicted MLN score

Forward breeding example: MSV + MLN

Funnel = 400

Output = 6

MSV

MLN

Funnel = 6000

Output = 90

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Widening the funnel

GOBII – forward breeding

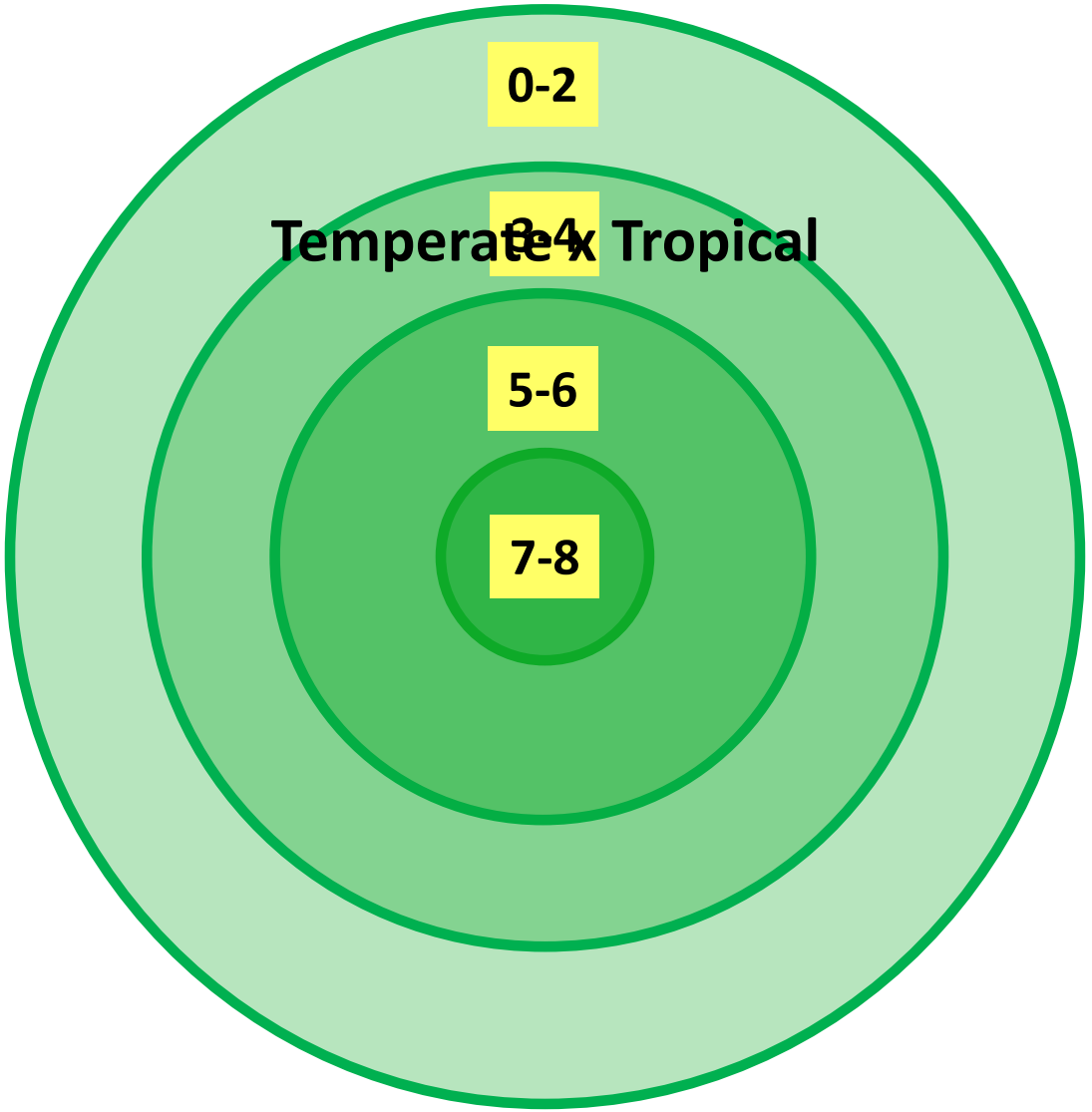
GMP- Africa

Biotic Stresses
- MLN
- MSV
- GLS
- TLB

Abiotic stresses
- Drought
- Low N
- Heat
- Founder haplotypes

Nurtritional quality
- Provitamin A
- Micronutrients

Market Preference
- Cob Color
- Kernel whiteness



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Forward Breeding strategy

Case study- CIMMYT Maize

- Cost, efficiency, logistics for current genotyping platform
  - $2.04 - $3.58 / sample – 6 week data turnaround
  - $2.66 - $4.65 / sample – 3 week data turnaround
  - Price dependent on job size
  - 10 - 92 markers – flexible marker choice
- Logistic challenges
  - Forecasting / price quotation / purchase order / invoice / payment process / import process has led to delays
  - Field sampling workload / accuracy
  - Population QC problems have led to significant complications
    - Need stronger internal processes

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Cost-benefit analysis

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%

Forward Breeding = genotyping 400 individuals in 2 successive cycles (800 total) and phenotyping 100 F4s

Conventional = phenotyping 400 F4 families

Simple assumptions regarding target numbers and QTL effect size

More rigorous analysis previously conducted – needs to be updated with new cost estimates

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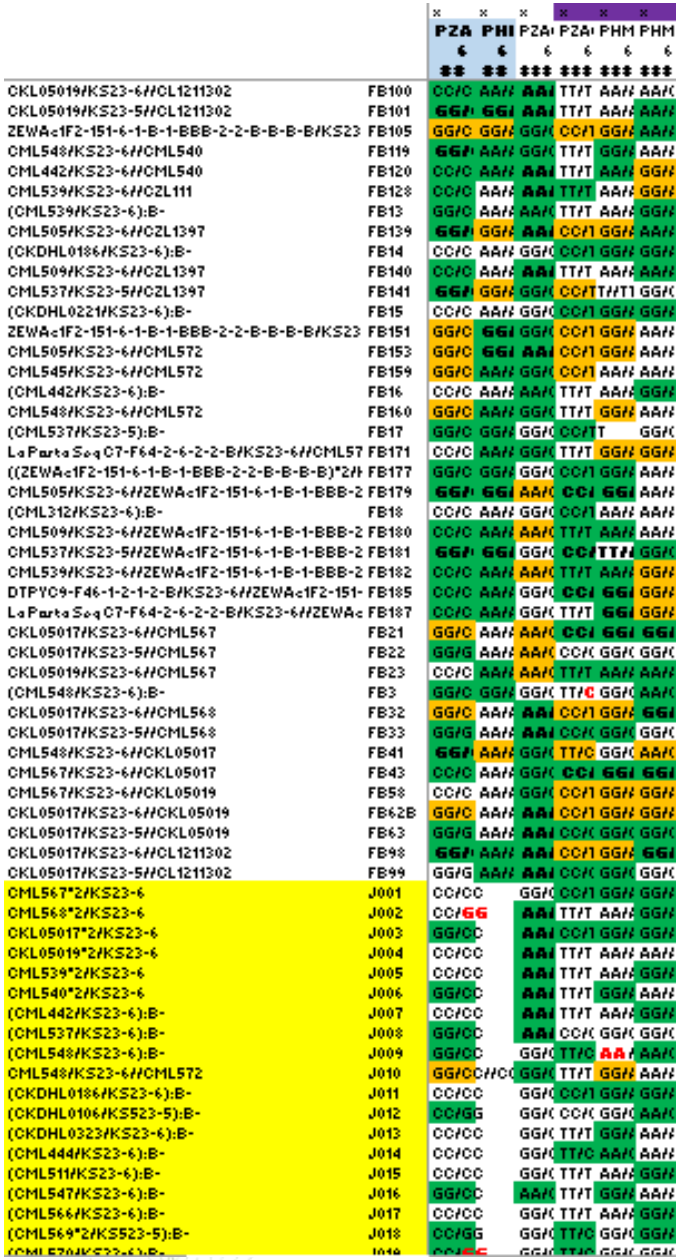
KS23 MLN haplotype deployment

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



Validated haplotypes/SNPs associated with **TLB** and **GLS** resistance in SSA

TLB resistance

Haplotype block/SNP (Physical position)	Av. Effect size (AM)	Effect size (units) (Independent pops)	Comments
S2_208538471	0.48	0.15-0.23	LA and Asia QTL in the region
S2_217335200:S2_217335257	0.53	0.38	
S8_151911732:S8_152767943	0.45	0.25	htn1 isolated from this region (Hurni et al., 2015, PNAS); LA and Asia QTL in the region
S9_151291652:S9_151291657	0.44	0.25-0.46	
S10_137903186:S10_137903272	0.26	0.27	
S6_152167869	0.32	0.24	GWAS and biparental validation for SA
S1_15805542	0.30	0.21	GWAS and biparental validation for SA

GLS resistance

SNP	SF QTL p-value	effect size
S10_5591640	3.92E-04	0.31
S10_105855041	5.83E-04	0.31
S10_128815052	2.94E-02	0.22
S4_202887827	7.85E-06	0.41
S5_176988707	1.18E-05	0.43
S5_191885423	1.49E-03	0.28
S5_198279931	3.44E-05	0.18-0.37
S5_206725263	4.90E-04	0.32
S5_29622434	4.82E-02	0.21
S5_43647429	7.68E-05	0.34
S6_154841719	1.52E-02	0.22
S6_154891169	1.66E-02	0.21
S7_143873505	7.23E-03	0.24
S9_48441376	6.20E-03	0.25
S9_48738880	6.04E-03	0.25

- Summarized a set of 51 SNPs and 58 SNPs from multiple mapping and validation studies for TLB and GLS respectively
- 2017: Allele frequencies and effect sizes will be estimated in breeding lines and populations from SSA breeding programs

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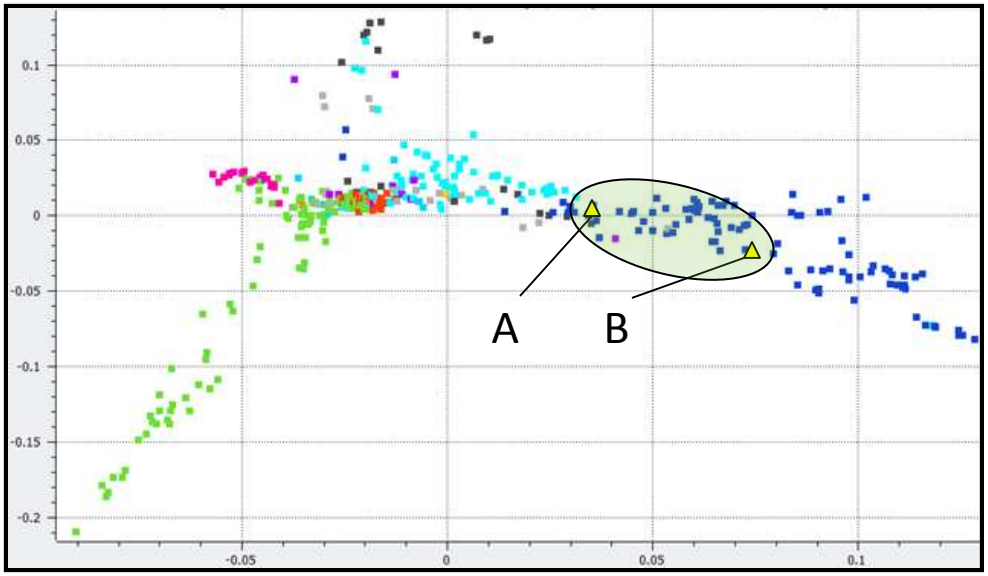
Training set development

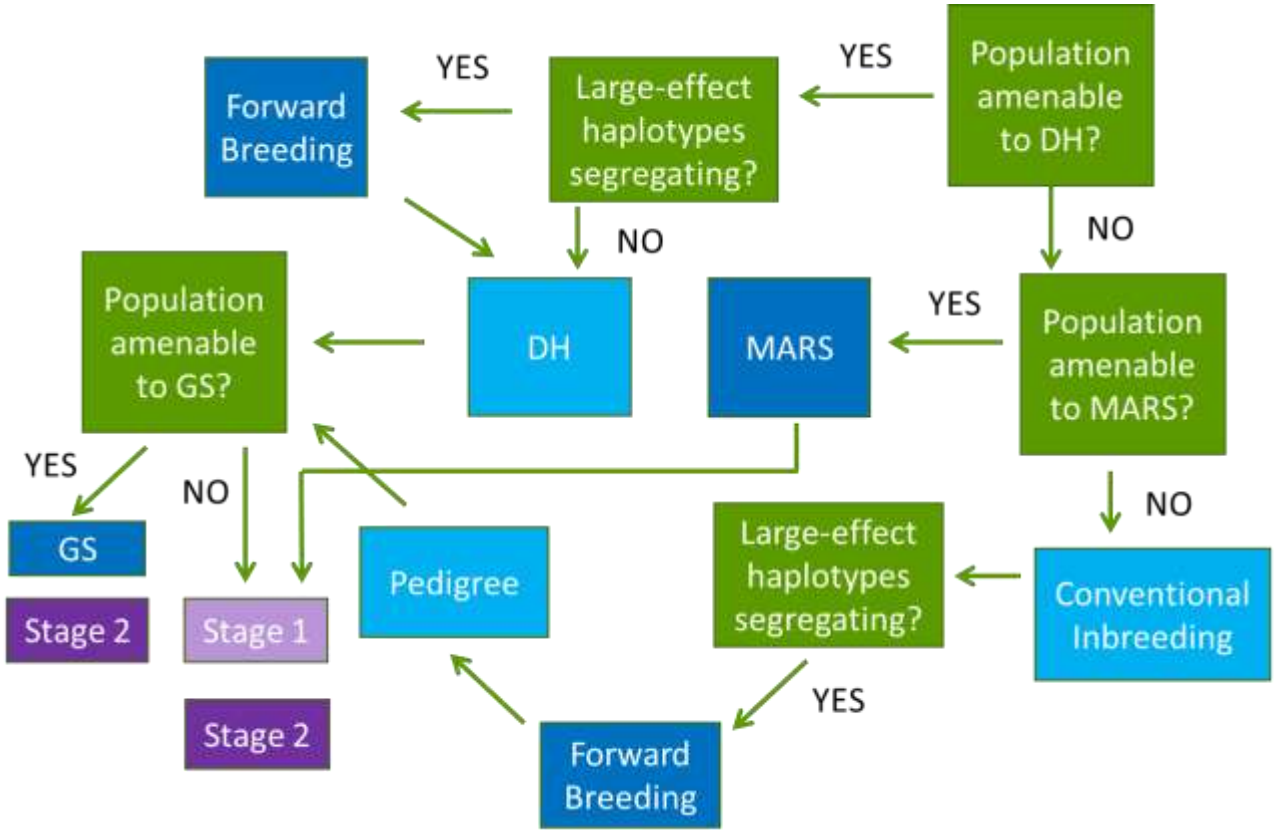
- **Windheusen et al. 2013:**
  - ***…emphasizing the need (for) larger training sets with <u>strong genetic relationship</u> to the validation set.***

- **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***

Deployment breeding: Decision trees and supported workflows



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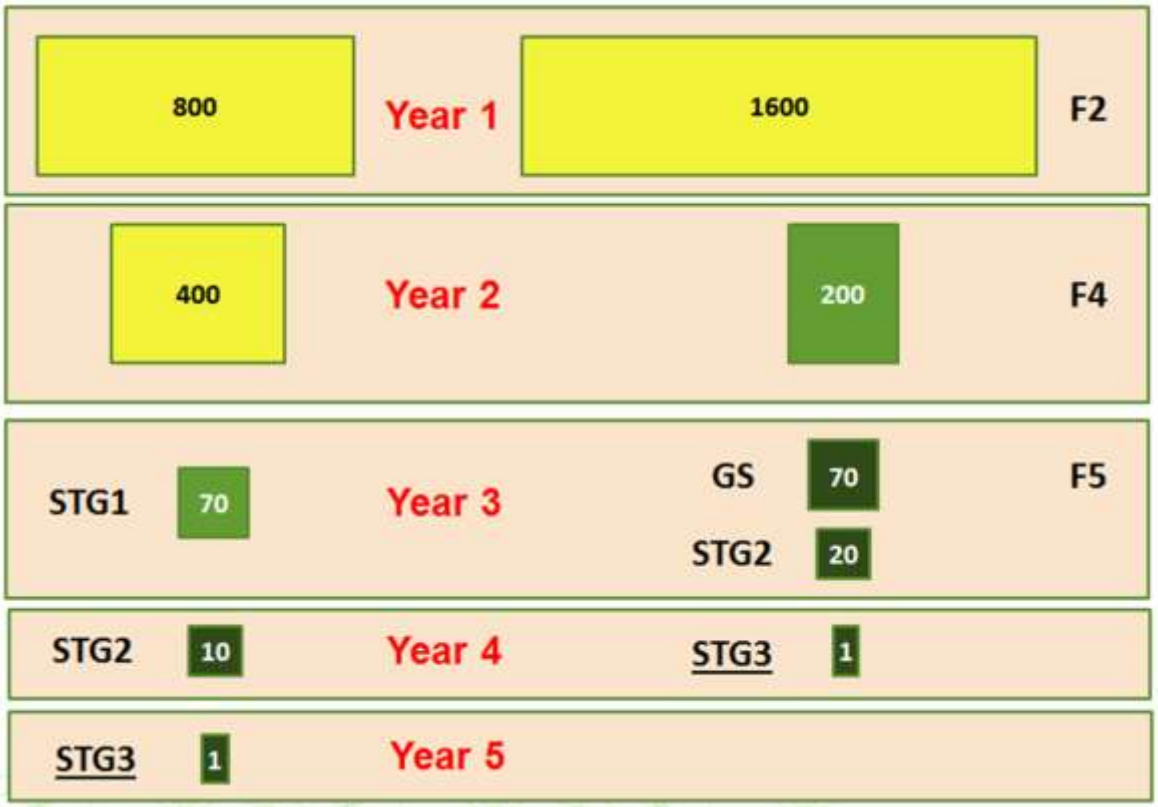
Breeding process comparison = equivalent cost basis (target)



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Thank you

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