Second Part : Boosting breeding efficiency at the EU level

Genomic Selection in Sorghum and Adaptation to Harsh Conditions

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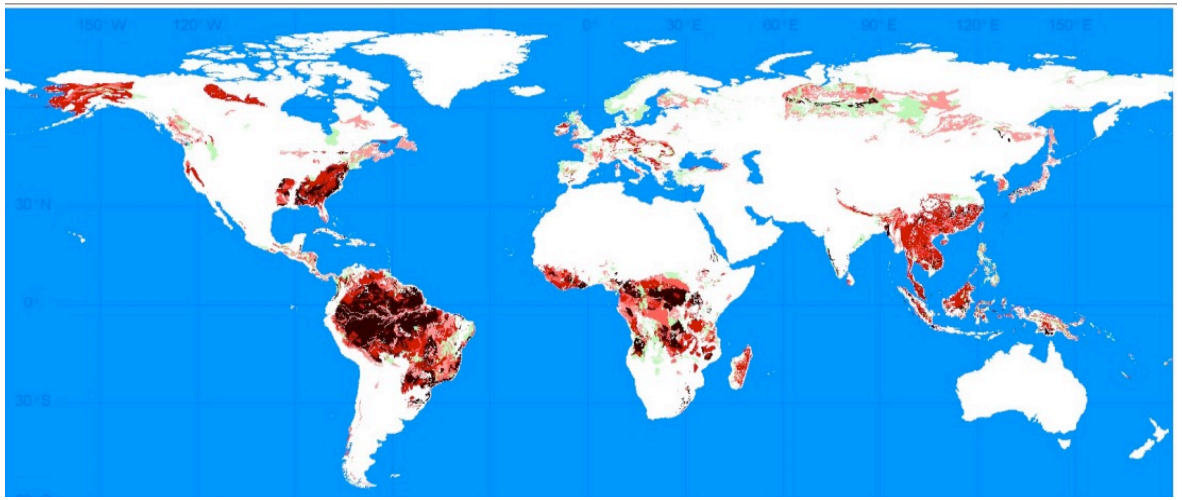
Maize and Sorghum

3rd European Sorghum Congress
Toulouse/France – 12-13 October 2021

Abiotic Stress Tolerance on Tropical Soils

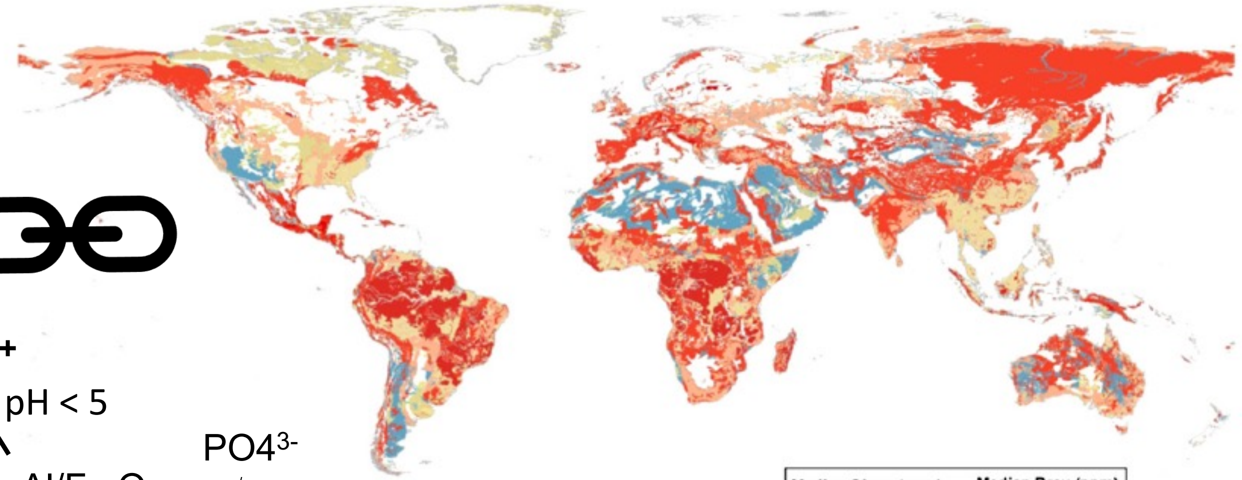
Adaptation to Multipe Stress Factors: Aluminum Toxicity – Phosphorus Deficiency – Drought Stress

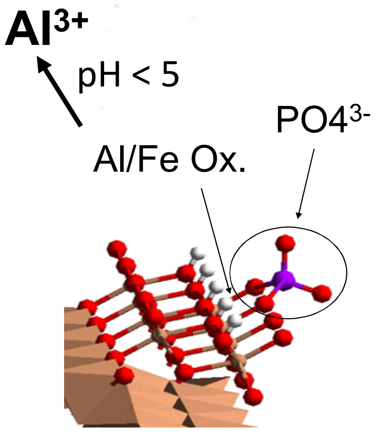
Acid, Al toxic soils



Embrapa Maize and Sorghum
Cartography: E. C. Landau
FAO (1995), ESRI (2000)
Datum: WGS84

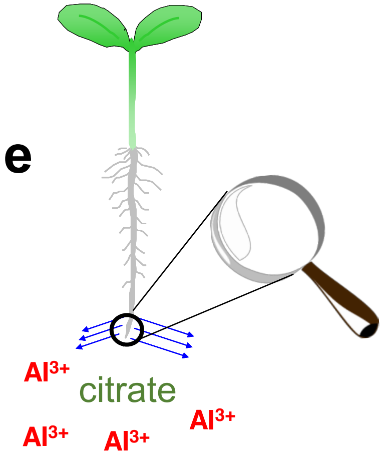
Low P availability

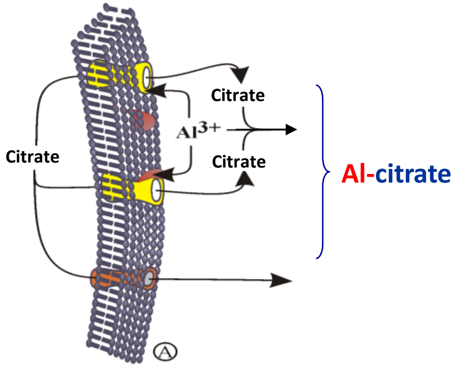




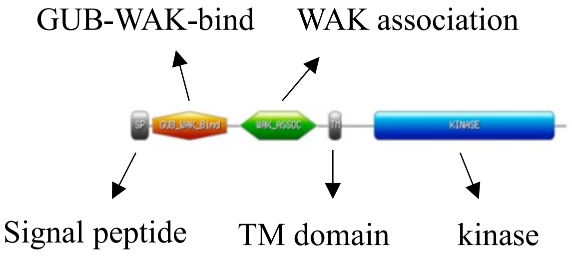
Lynch 2011
Plant Phys 156:141

Major Al tolerance gene
SbMATE
1 ton/ha

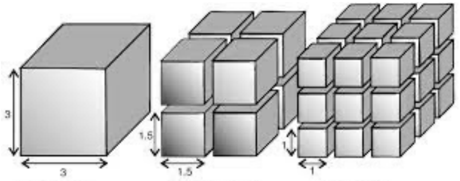




Quantitative inheritance
P efficiency QTL
SbPSTOL1



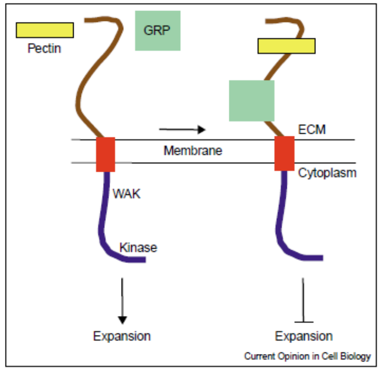
Root Surface Area Enhances Grain Yield Under Low P in the Soil (P diffusion)



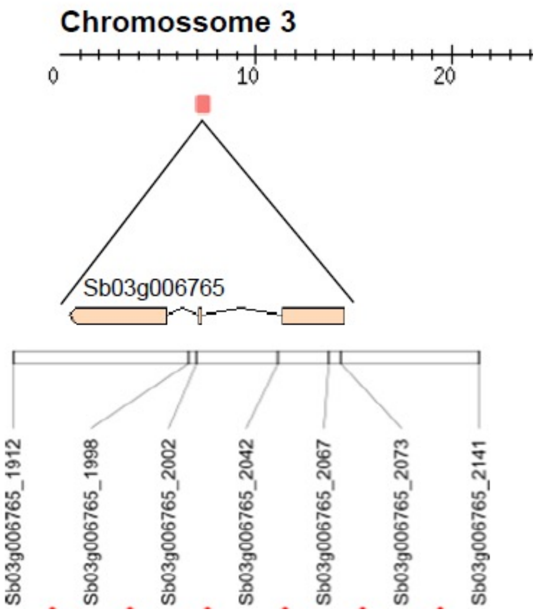
- Botleneck: P diffusion

Bernardino et al. (2019) ***BMC Plant Biology*** **19:87**

- PUE (P use efficiency) = **PAE (acquisition)** x PUTIL (internal utilization)
- PAE highly correlated with grain yield under low-P conditions
- Colocalization of QTLs for root morphology and grain yield

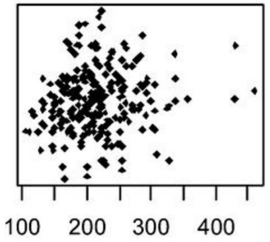


Current Opinion in Cell Biology 2001, 13:529–533

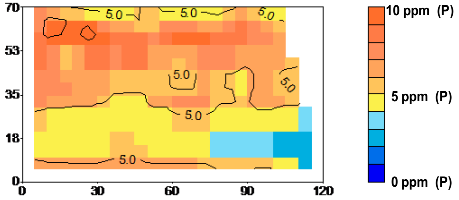


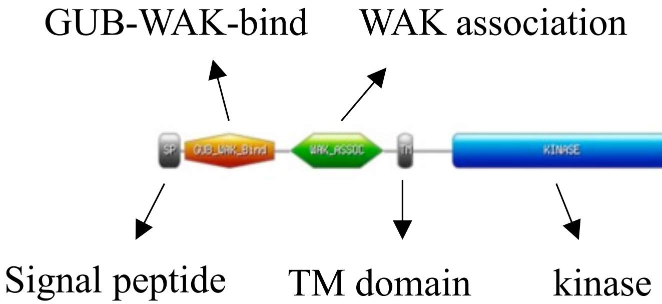
Root surface area

2D imaging



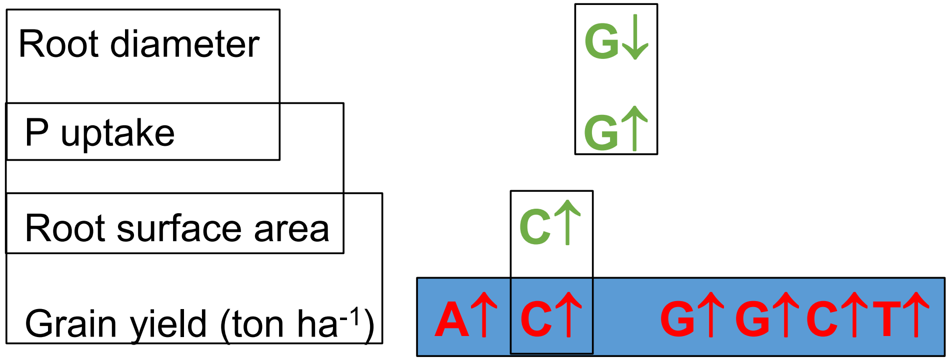
Grain yield (low-P)





- *SbPSTOL1* genes increase grain yield in low-P conditions via changes in root morphology (150 – 200 Kg/ha)
- Deploying multiple genes and regulatory factors into sorghum breeding
- GS with gene-specific markers as fixed effects

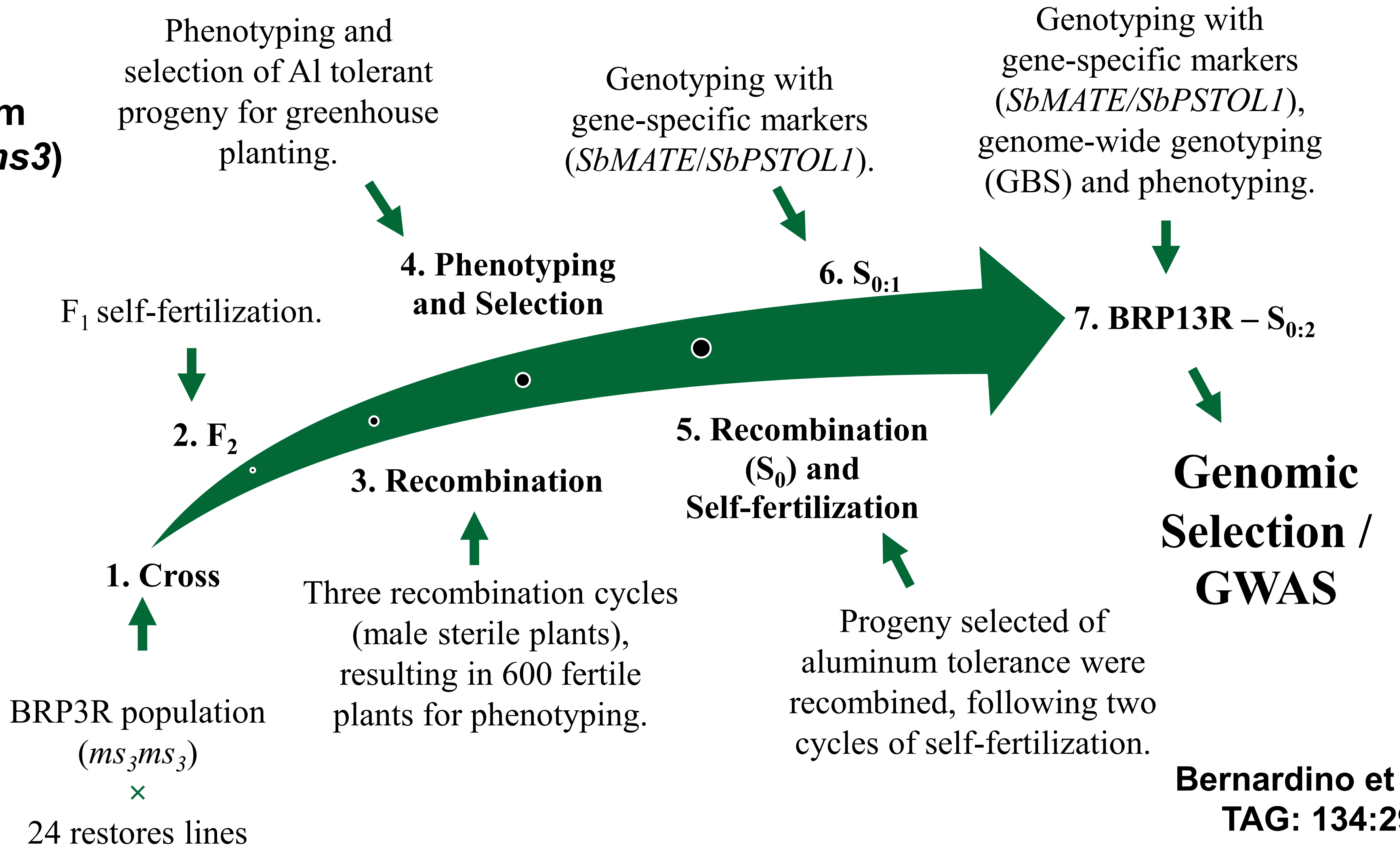
***Hufnagel et al. (2014) Plant Physiology* 166:659-77**



Framework for Candidate Gene Validation and Deployment

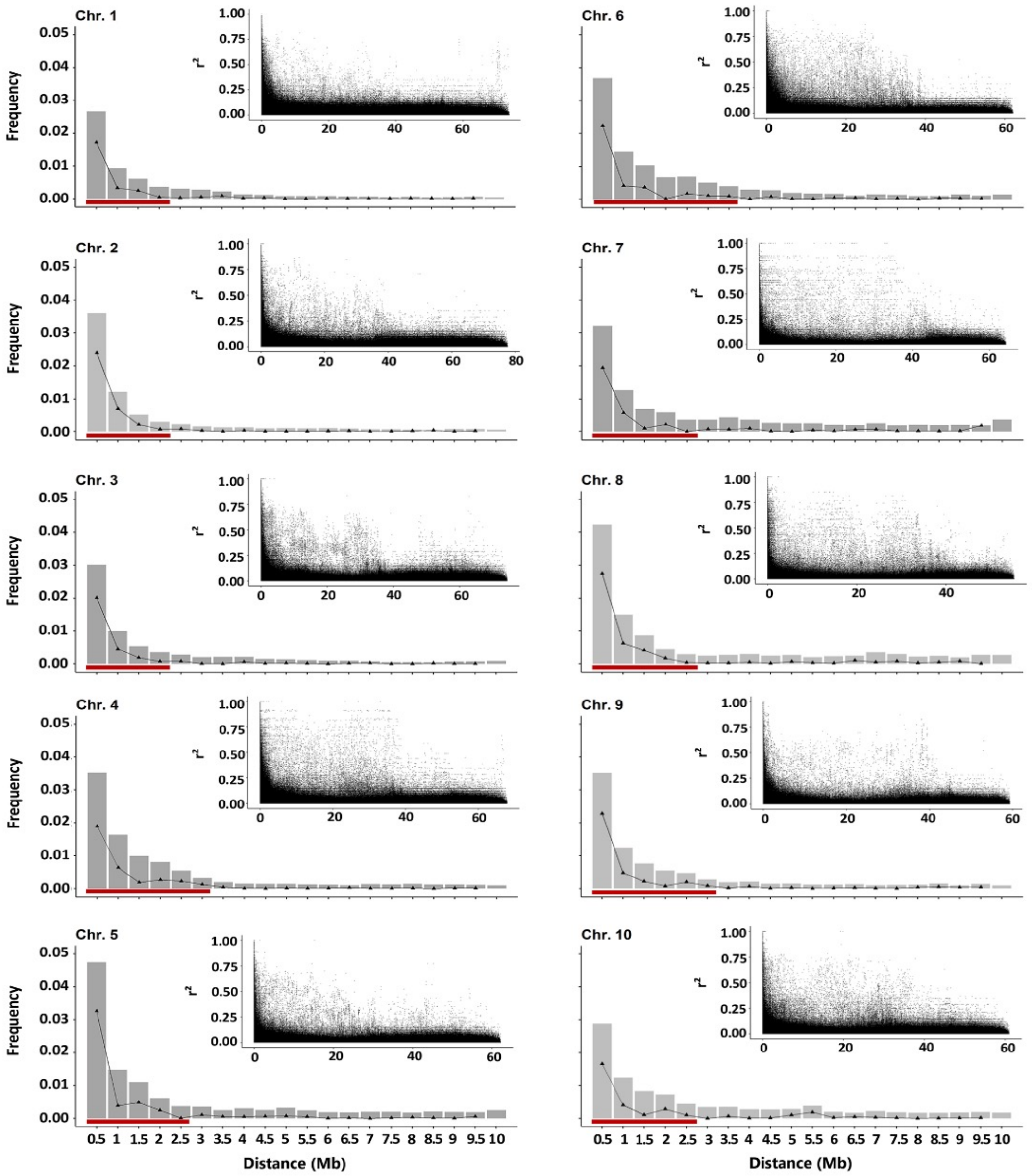
- Complementing populations: extent of LD (resolution), number of segregating alleles and detection power
- RIL population / Sorghum Association Panel / Multi-parent Random Mating Population
- Grain yield, P efficiency traits and root morphology

BRP13R
Multi-parent random mating population (*ms3*)



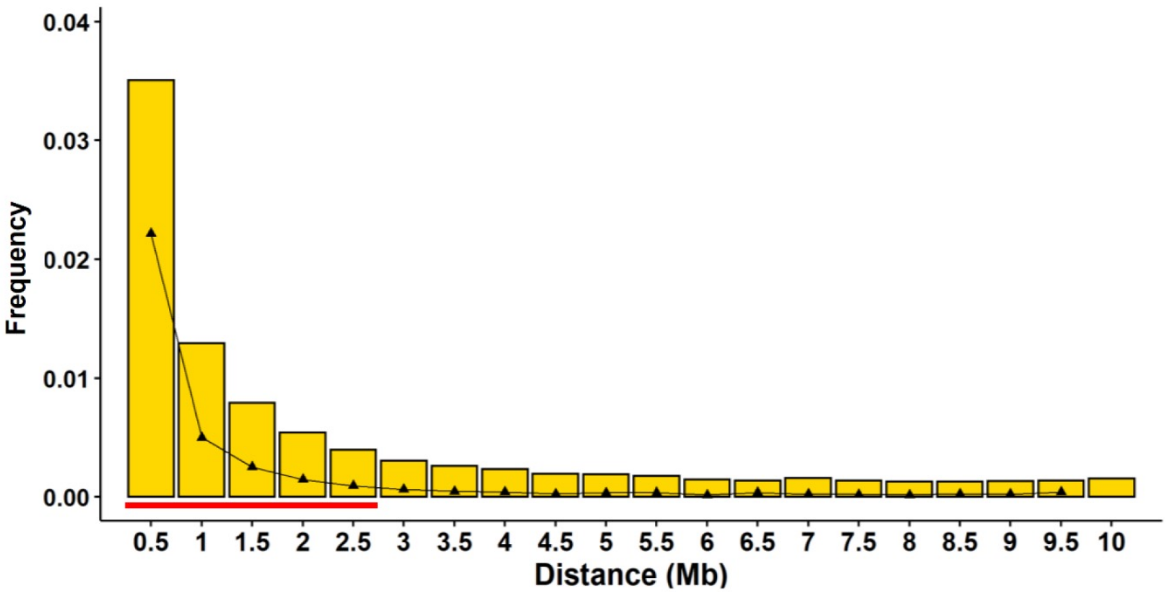
Bernardino et al. (2021)
TAG: 134:295-312

Some Genetic Properties of BRP13R – Linkage Disequilibrium



Frequency of SNP loci under significant LD (r^2) vs physical distance

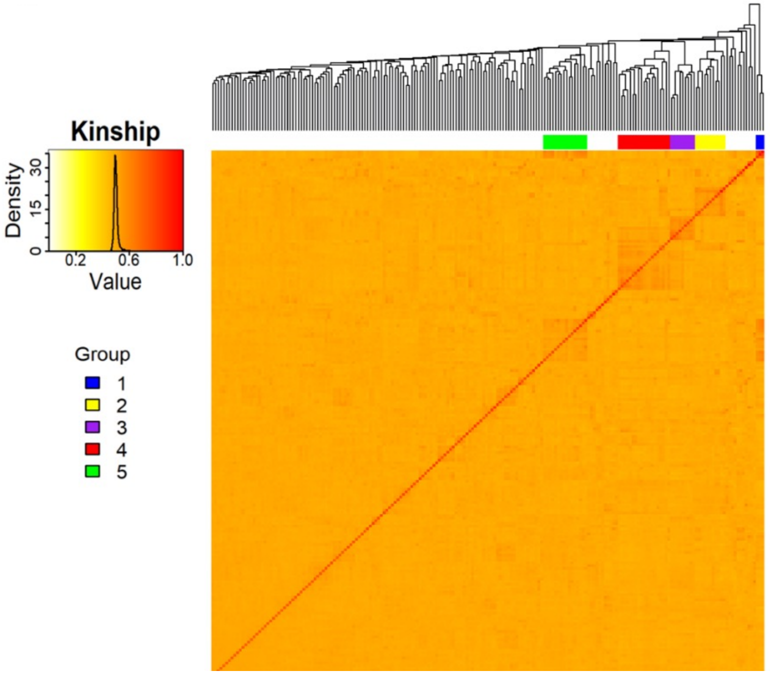
LD extending to 2.5 Mb on average (± 0.5 Mb)

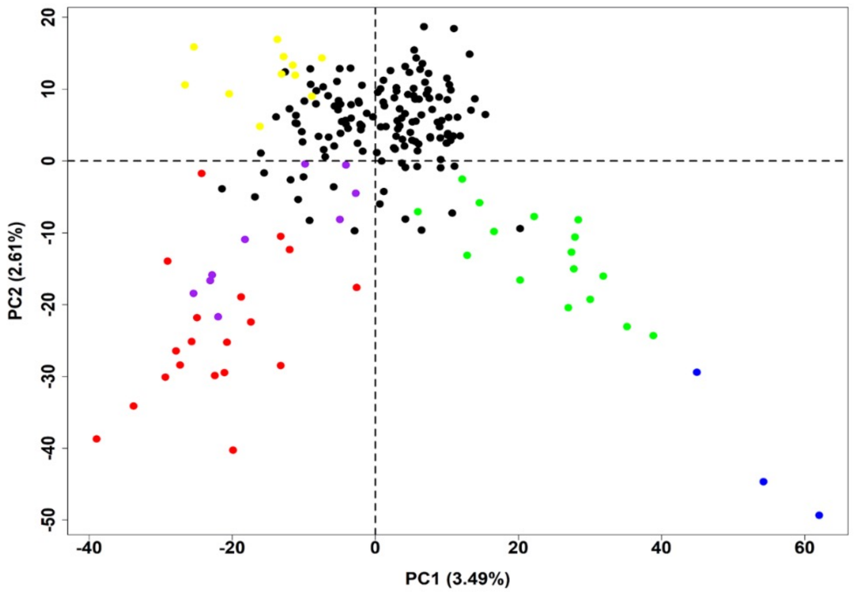


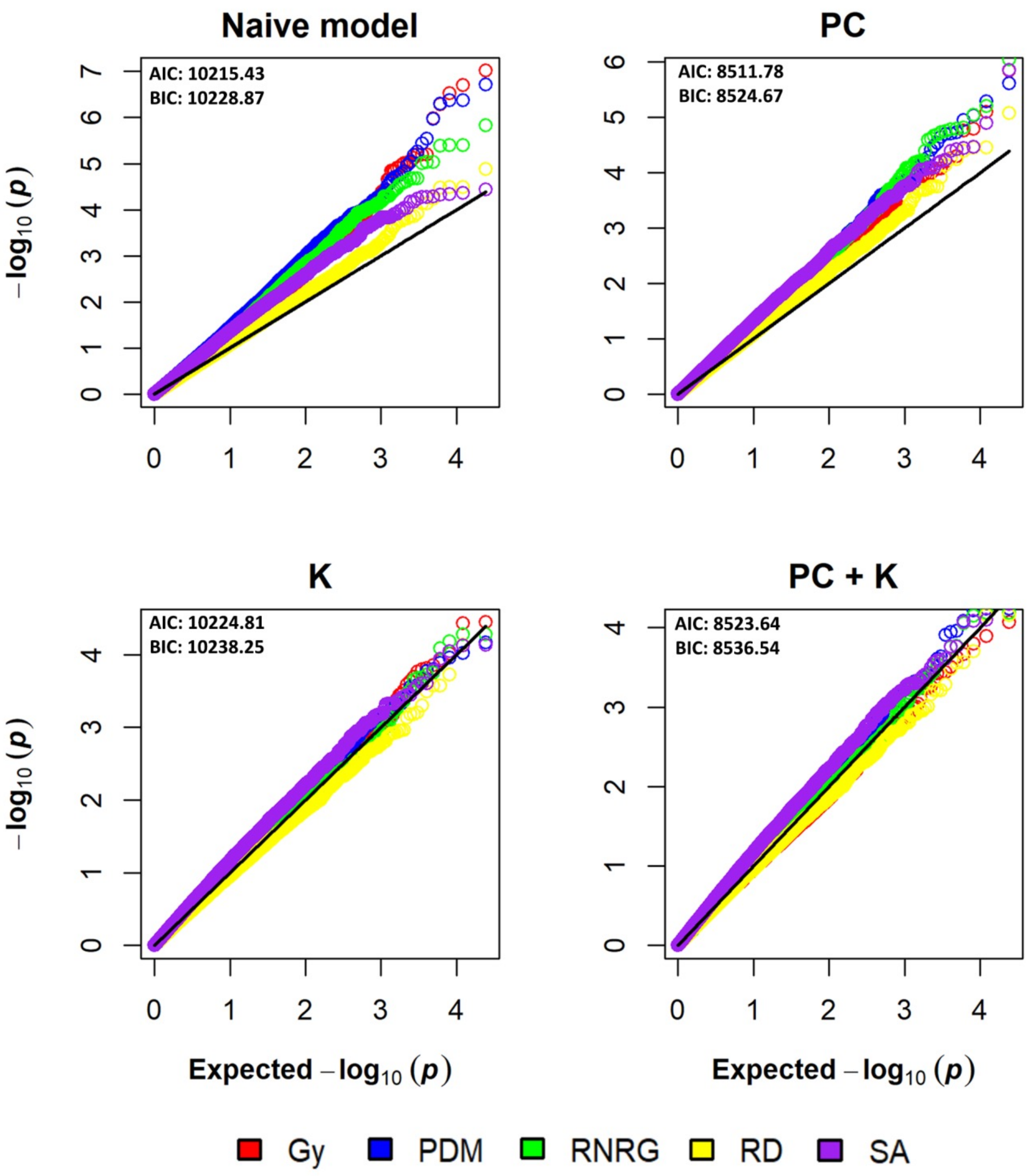
LD RILs > LD BRP13R > Association Panel
(15-20Mb) (2.5 Mb) (10Kb)

Bernardino et al. (2021) TAG: 134:295-312

Some Genetic Properties of BRP13R – Population Structure and Relatedness





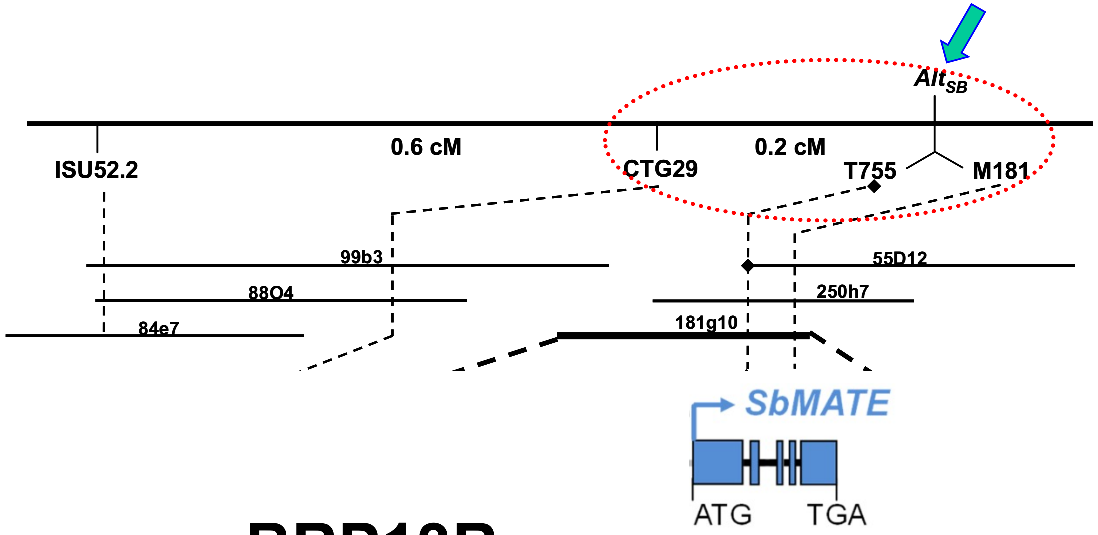


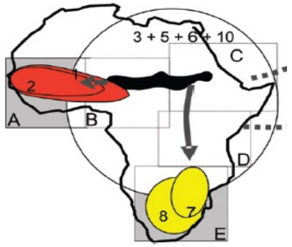
Bernardino et al. (2021) TAG: 134:295-312

Cloning and Validation of Rare, Subpopulation-Specific Variants: *SbMATE*

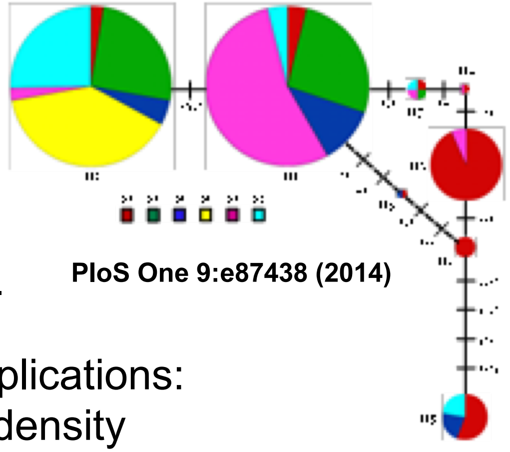
Positional cloning of *SbMATE*

Nature Genetics 39:1156-1161 (2007)





Genetics 179:997-1008 (2008)

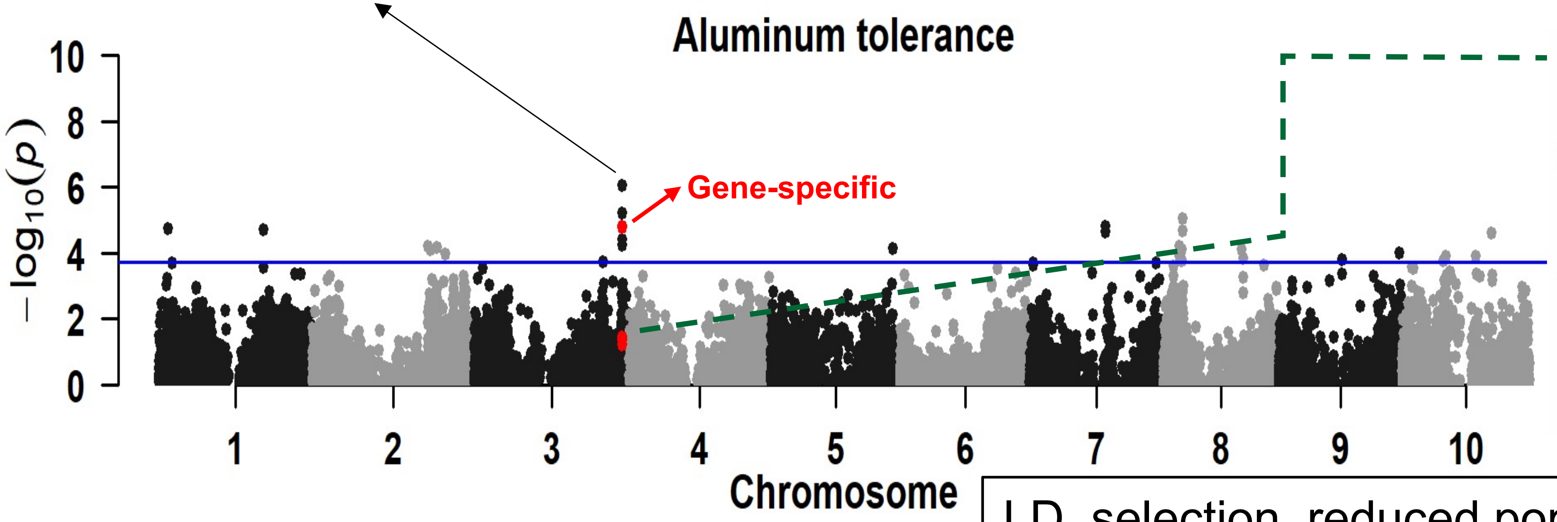


PloS One 9:e87438 (2014)

- Further Complications:
- Low marker density
- Recombination

BRP13R

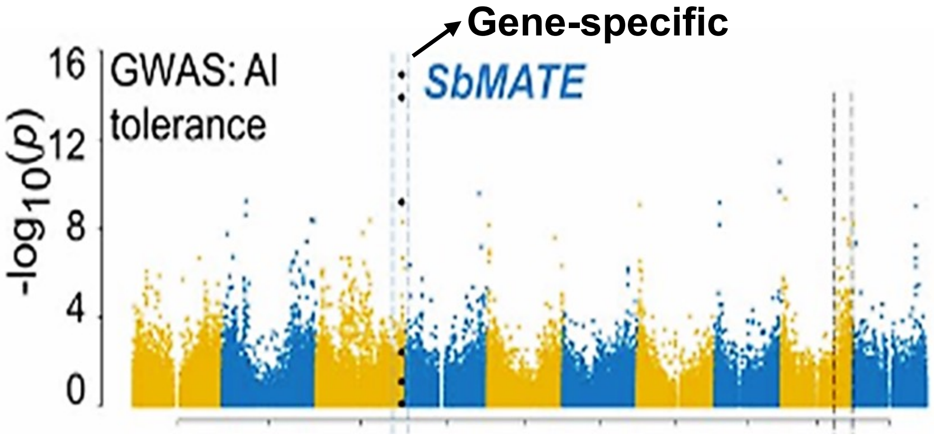
GBS – SNPs 71.1 Mb on chromosome 3: *SbMATE*



200 progeny / 44,000 markers
Bernardino et al. (2021) TAG: 134:295-312

LD, selection, reduced population structure via random mating

CIRAD/EMBRAPA panel



254 lines / 235,000 SNPs
Melo et al. (2019) PNAS 116:313-318

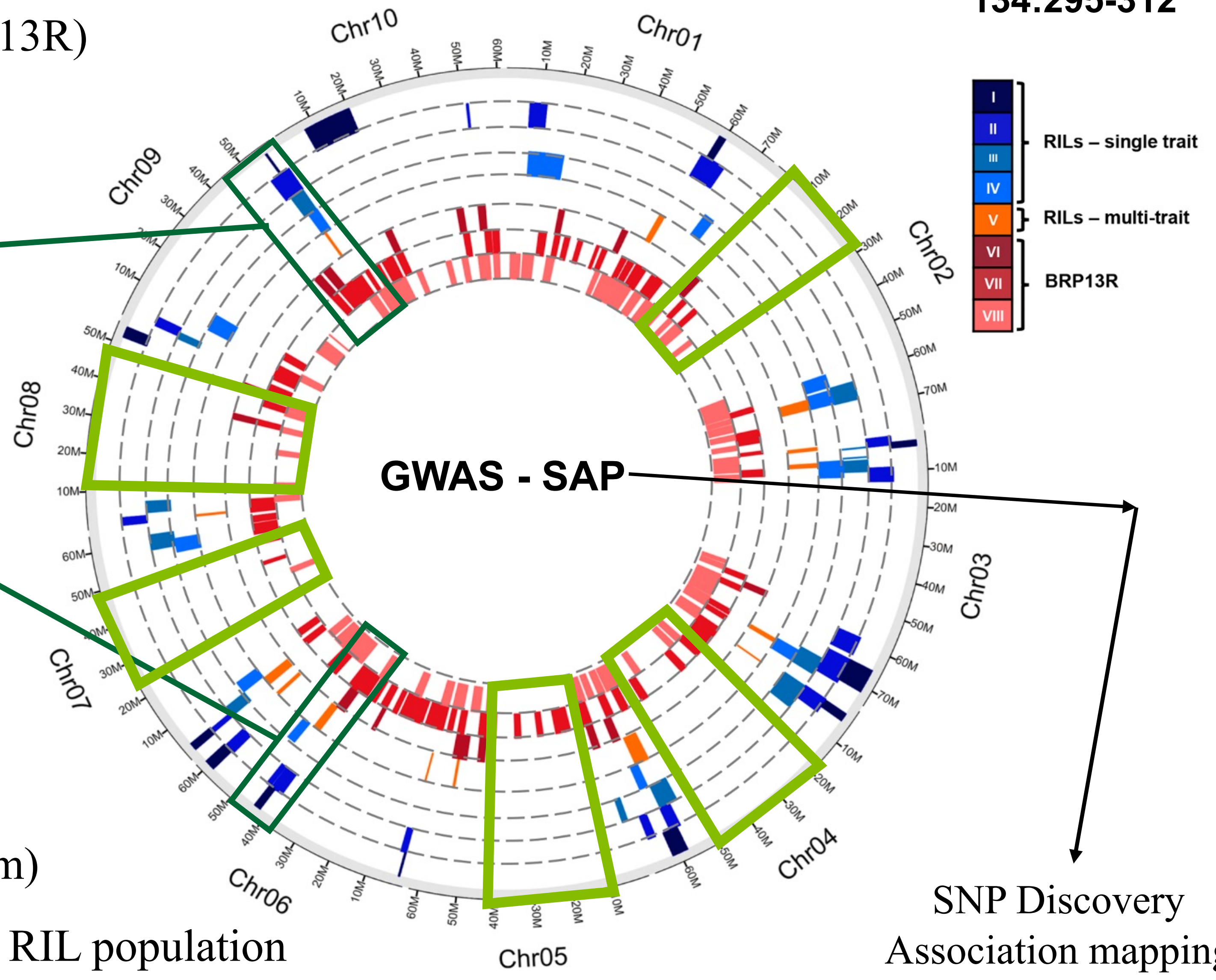
Integrated Pipeline for Gene Cloning and Deployment

Bernardino et al. (2021) TAG: 134:295-312

- Many instances of consensus QTL (RILs vs BRP13R)

55 – 60 Mb (Chr. 9)
Grain yield QTL - RILs
Grain, root and plant dry matter – BRP13R
PHOSPHATE 2 – P efficiency in maize
(Du et al., 2018)

45 – 55 Mb (Chr. 6)
Grain yield QTL - RILs
Grain yield QTL - BRP13R
ALMT - Al tolerance in wheat
ALMT1 - root growth in low-P conditions in Arabidopsis (Mora-Macías et al., 2017)

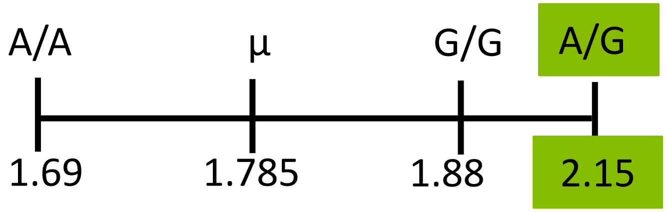


SNP Discovery
Association mapping
Deployment

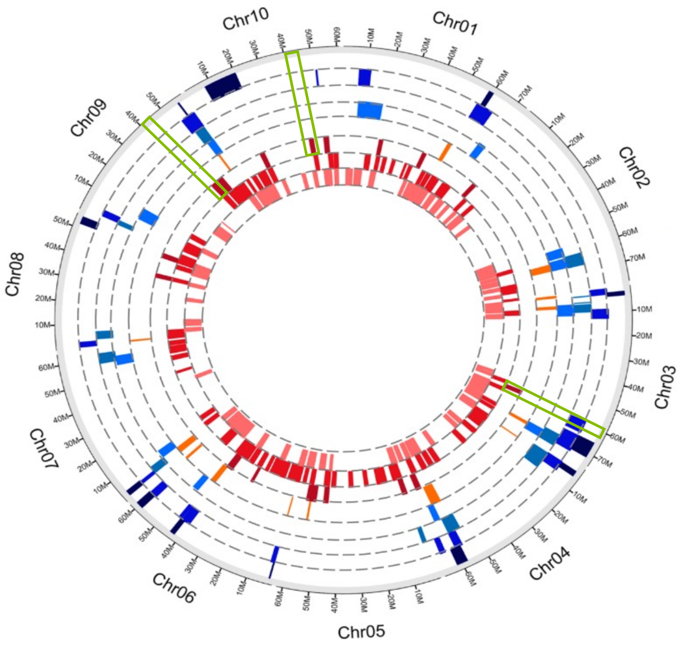
- More QTLs detected in BRP13R (multi-allelism)
- BRP13R complemented QTLs mapping on the RIL population
- Instances of QTLs that are private to BRP13R

Overdominance Contributes to Genetic Gains for Grain Yield

- BRP13R: 20% residual heterozigosity
- Strict overdominance



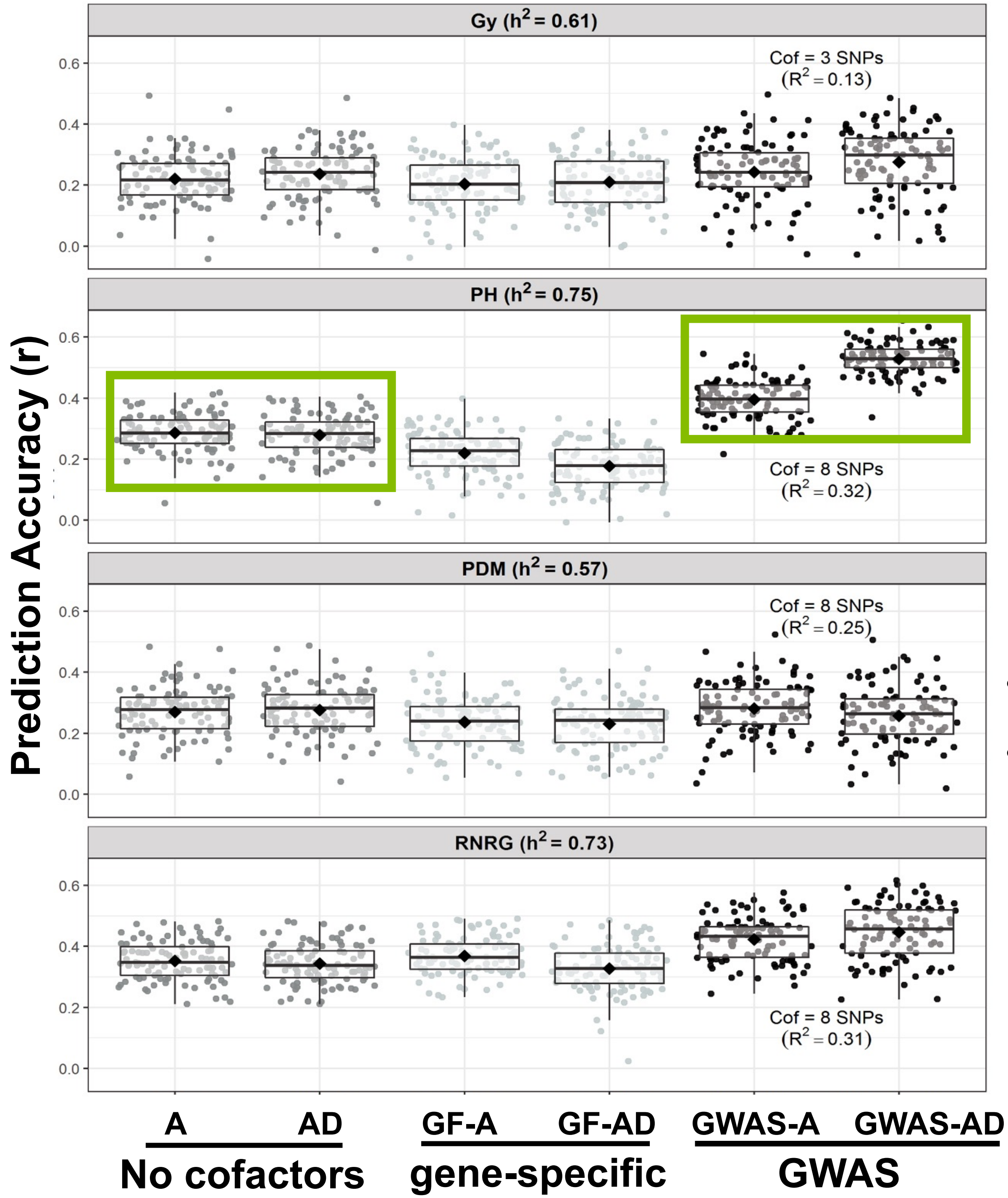
Overdominant QTLs exclusive of BRP13R



Maker	Chr	Genotpypes	Mean	P-value contrasts	Genetic control*
S1_78121019	2	A/A	1.58	A/A - A/G 0.0038	dominance
		A/G	2.10		
		G/G	1.97	A/G - G/G 0.1892	
S1_208828314	3	A/A	1.69	A/A - A/G 0.0245	overdominance
		A/G	2.15		
		G/G	1.88	A/G - G/G 0.0013	
S1_289681597	4	G/G	2.01	G/G - G/T 0.4353	dominance
		G/T	2.10		
		T/T	1.51	G/T - T/T 0.0002	
S1_350323609	5	A/A	1.97	A/A - A/T 0.1187	dominance
		A/T	2.12		
		T/T	1.55	A/T - T/T 0.0043	
S1_582556694	9	C/C	1.86	C/C - G/C 0.0105	overdominance
		G/C	2.12		
		G/G	1.85	G/C - G/G 0.0185	
S1_613208087	10	A/A	1.82	A/A - A/C 0.0309	overdominance
		A/C	2.11		
		C/C	1.85	A/C - C/C 0.0161	
S1_641860550	10	C/C	1.78	C/C - C/T 0.0214	overdominance
		C/T	2.13		
		T/T	1.88	C/T - T/T 0.0077	

Bernardino et al. (2021) TAG: 134:295-312

Genomic selection in BRP13R

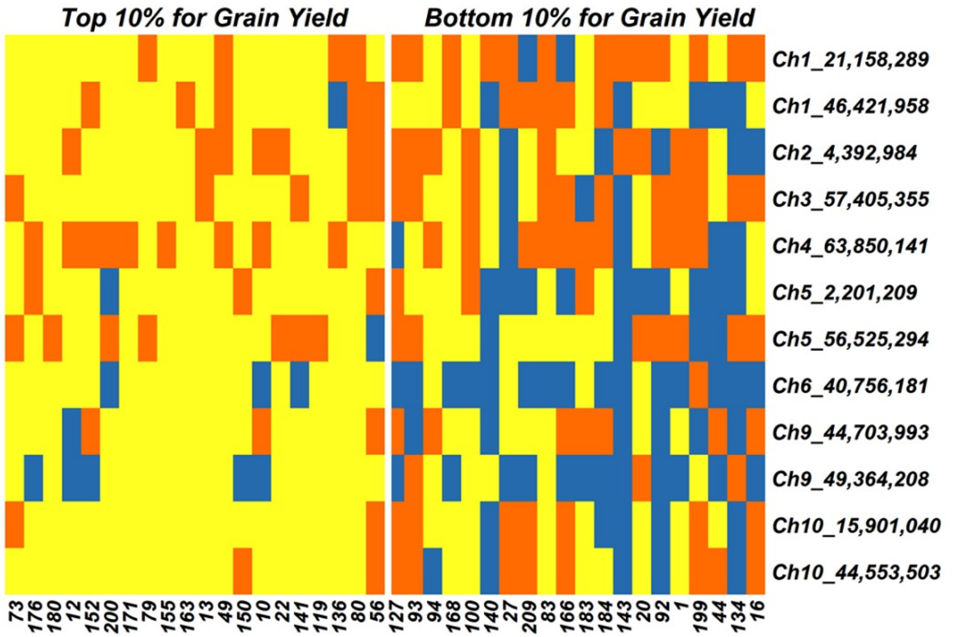


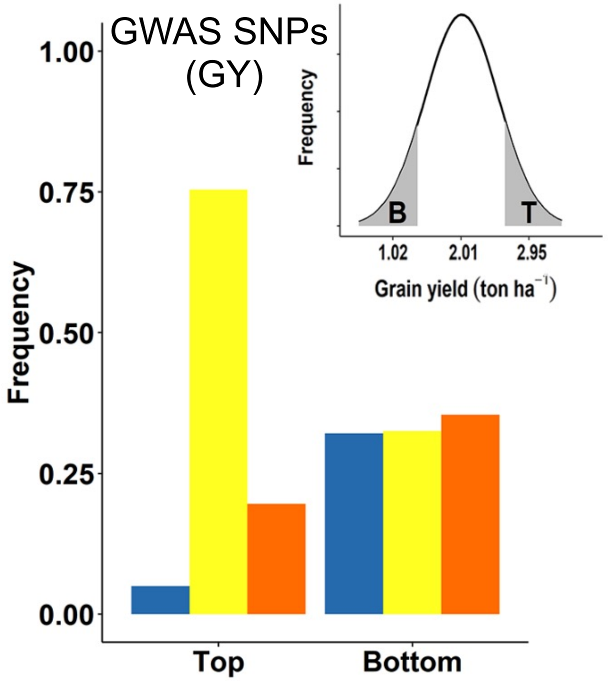
- ➢ Accuracy varied from 0.28 for grain yield to 0.53 for plant height
- ➢ Adding fixed cofactors to the GS models is helpful for grain yield and markedly for plant height (oligogenic and h^2), even in the absence of dominance.
- ➢ Fixed cofactors and GS models: particularly for oligogenic traits and when each major gene explains more than 10% of the genetic variance (Bernardo 2014)
- ➢ Dominance is particularly important in the presence of fixed cofactors (GWAS SNPs):
- • Increased accuracy for grain yield (17%)
- • Produced the highest increase in accuracy – 90%, for plant height
- ➢ No significant improvement caused by gene-specific markers for grain yield

GBLUP Models:

Gene action:	Fixed cofactors:
Aditive (A)	GF – gene-specific markers
Dominance (D)	GWAS – SNPs associated by GWAS

Extreme Mapping in BRP13R - Grain Yield Under Low-P



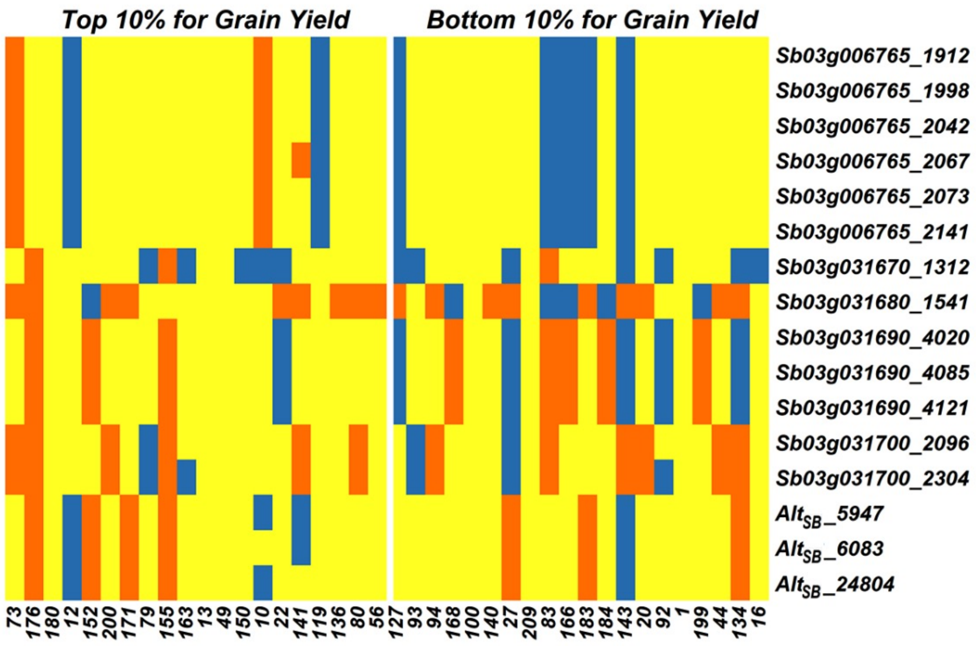


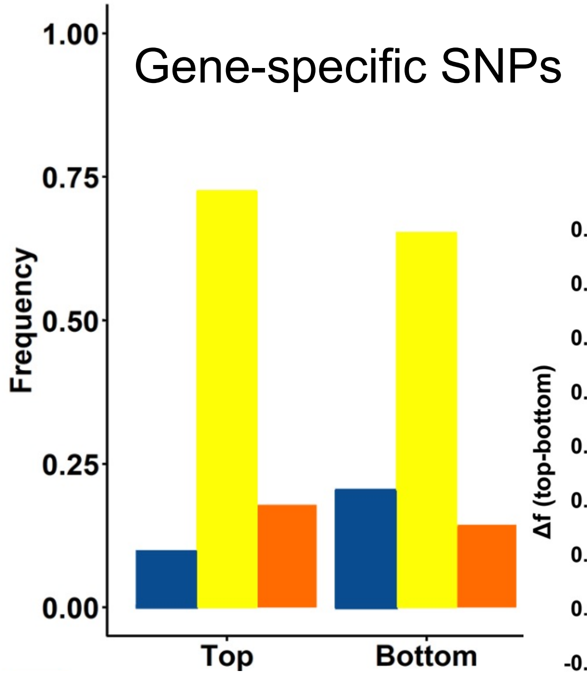
Genotypes

SS (Homozygous for superior allele)

S/I (Heterozygous)

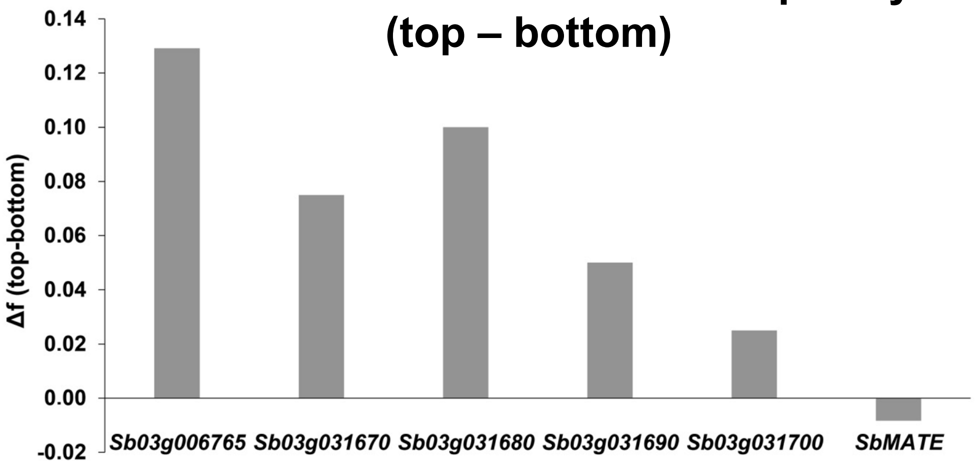
II (Homozygous for inferior allele)





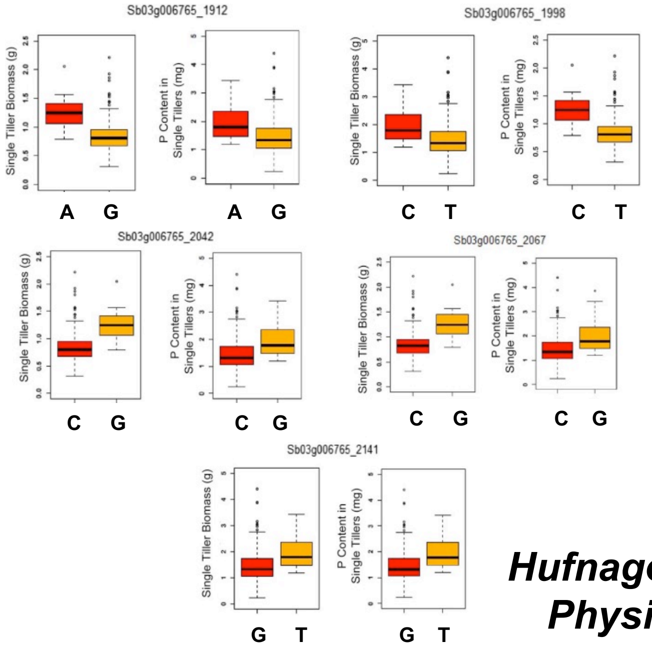
- Overdominance (GY) / aditive SbPSTOL1
- Strongest Δ**f** for *Sb03g006765*

Δf: shifts in favorable allele frequency (top – bottom)

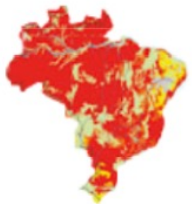


Gene-specific Markers are Associated with Grain Yield in a Low-P Soil

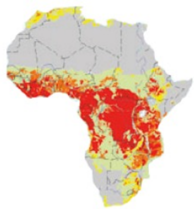
Chr	Gene	Position (bp)	Genotype	Allele Substitution Effect (Kg ha^{-1})
3	Sb03g006765	1912	**A**	173.3
			G	
		1998	**C**	169.1
			T	
		2042	**G**	158.4
			C	
		2067	**G**	181.7
			C	
		2073	**C**	154.5
			T	
		2141	**T**	180.9
			G	
	Sb03g031680	1541	**A**	200.1
			G	



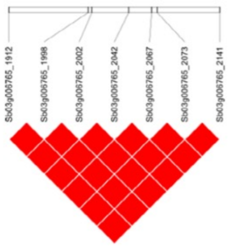
Grain yield effects under low P in Brazil (SAPst)



Biomass and P content under low P in West Africa (WAP)

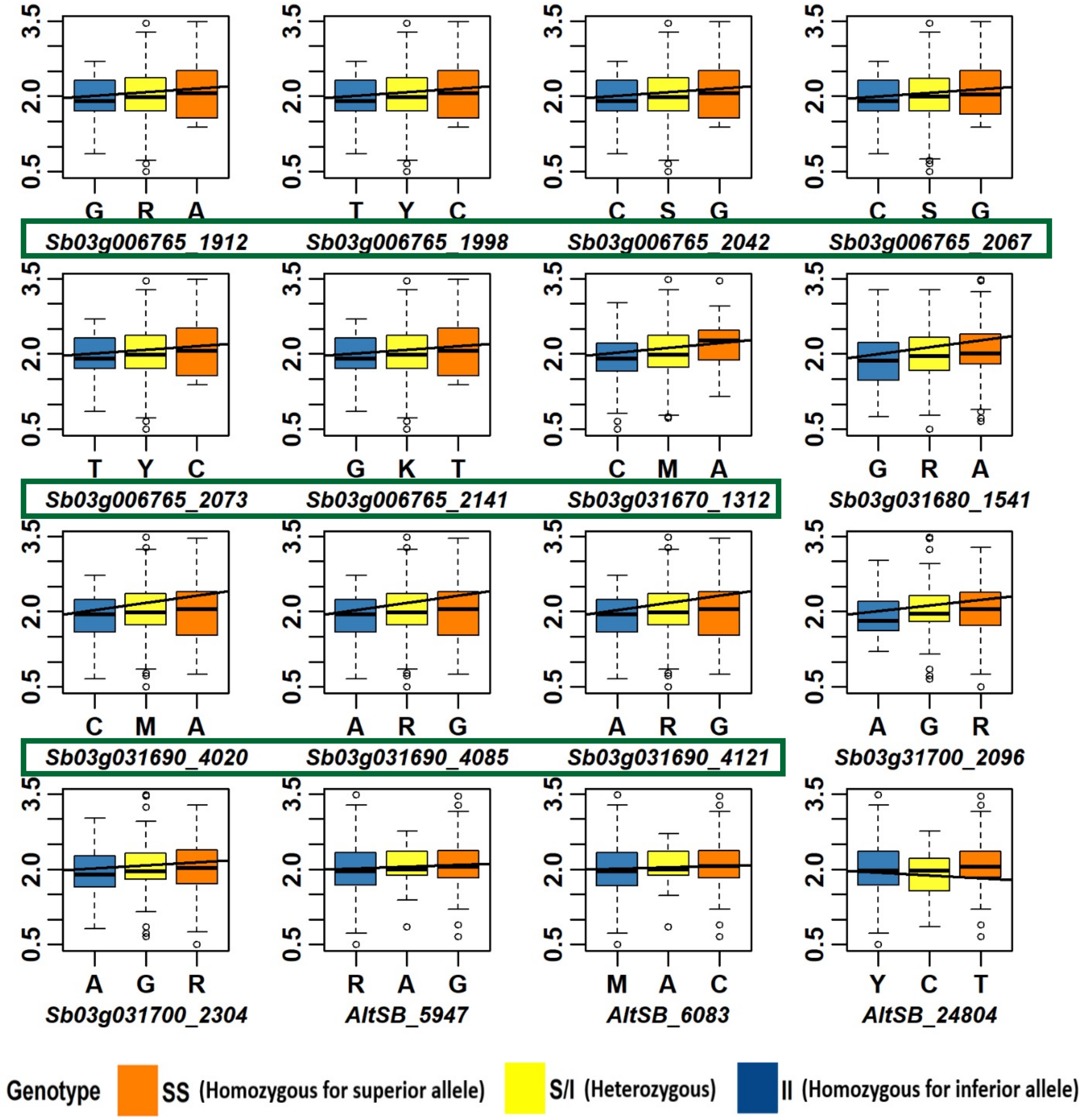


Sb03g006765



Hufnagel et al. (2014) Plant Physiology 166:659-77

Grain yield BRP13R (TAG: 134:295-312)



Summary

- Multi-parent random mating populations can benefit cloning of rare, sub-population-specific alleles, complemeting the genetic properties of other types of populations
- Overdominance is an importante aspect of sorghum adaptation to low-P conditions
- Populations with some degree of heterozygosity are importante both for QTL dectection and candidate gene validation
- Particularly for oligogenic traits, GS models including dominance and SNPs associated with the target traits as fixed cofactors lead to significant increases in prediction accuracy.
- *SbPSTOL1* markers should be used for charactering the base population by allele mining
- The impact of gene-specific markers in GS targeting sorghum adaptation to low-P soils will be assessed with new candidate genes in the cloning pipeline

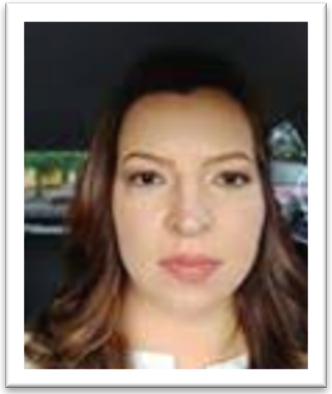
Embrapa

Maize and Sorghum

SEEDS FROM EUROPE

SORGHUM, A KEY TO BUILD OUR FUTURE.

Karine da Costa Bernardino



Maria Marta Pastina

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Generation