



# 1<sup>ST</sup> EUROPEAN SORGHUM CONGRESS

WORKSHOP

*INNOVATIVE RESEARCH TOWARDS GENETIC PROGRESS*

## TACKLING NEW CHALLENGES FOR EUROPEAN SORGHUM THROUGH GENETICS AND NEW BREEDING STRATEGIES

OPTIMIZING GENETIC VALUE PREDICTION USING MOLECULAR  
MARKERS

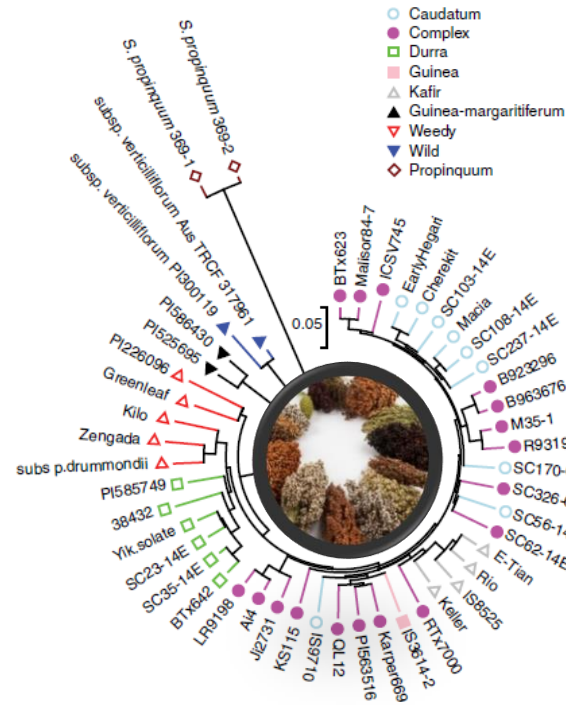
# WHOLE GENOME SEQUENCING : AN ACCELERATOR OF SORGHUM GENETICS AND BREEDING

## Btx623 sequencing



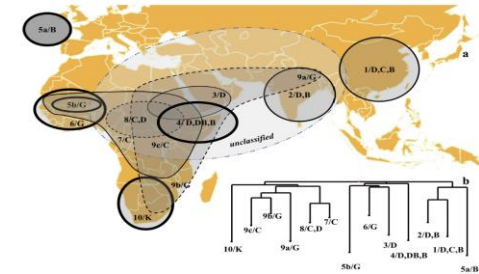
Paterson et al 2009

## Enlarging the diversity coverage



Mace et al 2013

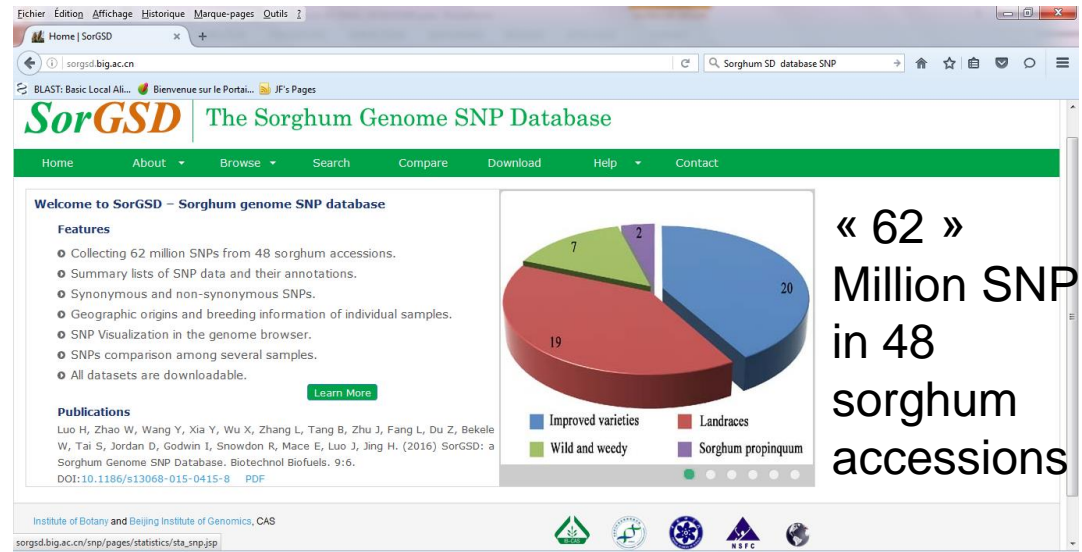
## To 1000's Genomes : « Terra » Project



Mockler et al 2016

Btx623 : ATGCATGCATGC  
 Keller : ATGCCTGC C  
 Tx430 : ATGCATGC C  
 Ji2731 : ATGCCTGCATGC  
 E-Tian : AAGCATGCATGC  
 Rio : AAGCCTGCATGC

SNP (indicated by red arrows pointing to 'A' and 'C' in the Rio sequence)  
 Indels (indicated by a green box around the 'C' in the Keller sequence)



Luo et al 2016

- Polymorphism Database and **Next Generation Sequencing (NGS) methodologies**
  - Characterize the diversity (Jeff's talk)
  - Support breeding efforts (Marker ASSISTED breeding)



# TAKING ADVANTAGE OF GENETIC INFORMATION TO ACCELERATE GENETIC GAINS (PREDICT PHENOTYPES)

- Response to selection:  $R_x = I_x * h_x^2 * Sd_x$  (x = grain yield in low Inputs)

With  $I_x$ : Selection intensity applied on trait<sub>x</sub>

$h_x^2$ : heritability of trait<sub>x</sub>,

$Sd_x$ : Phenotypic standard deviation of trait<sub>x</sub>

- Indirect selection (select trait<sub>x</sub> based on selection on trait<sub>y</sub> (y= grain yield in on-station trial)):

$$CR_x = i_y * h_x * h_y * r_{gxy} * Sd_x$$

With  $r_{gxy}$ : genetic correlation between traits x and y

- Molecular markers allow maximizing  $h_y$ . Assuming a high genetic correlation ( $r_{gxy}$ ) you can expect  $CR_x \gg R_x$

- Challenge : identify the genomic regions (Markers) controlling the traits of interest (high  $r_{gxy}$ ) and combine them in new varieties

# MAJOR GENES AND QTLs (BIPARENTAL) HAVE ALREADY BEEN IDENTIFIED

## Major Genes

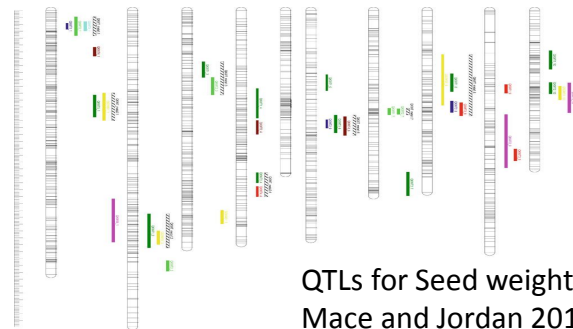


Mace and Jordan 2010

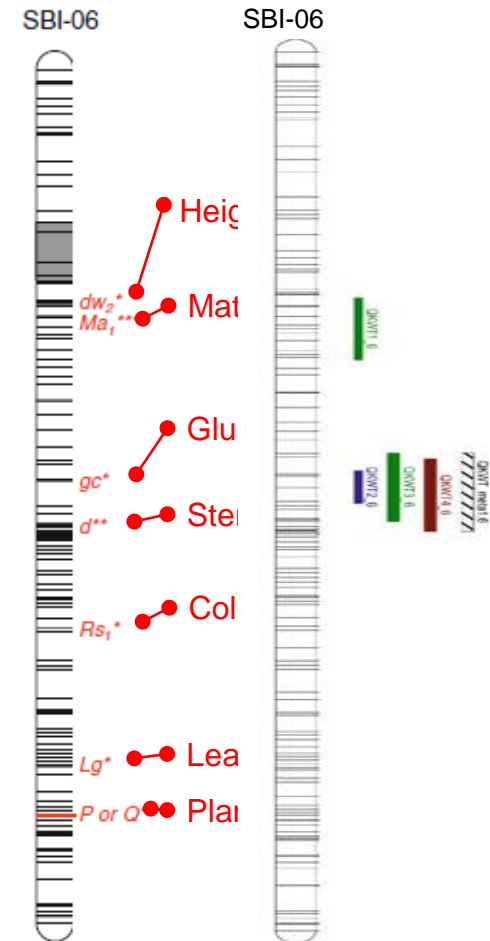
## Some genomic regions affecting quantitative traits

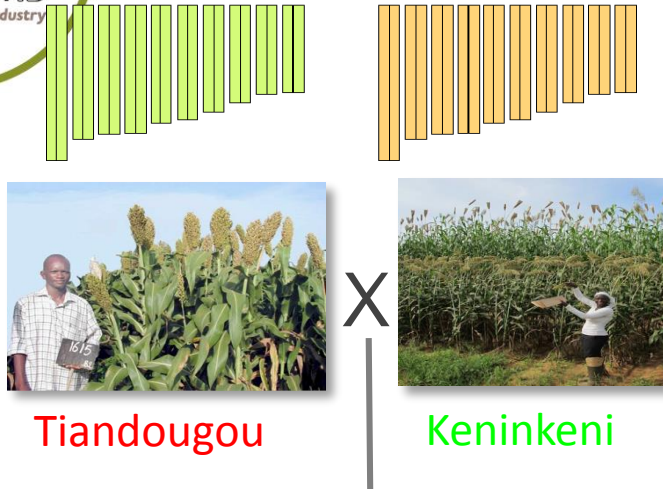
### QTLs in biparental populations

- Grain yield / size...
- Grain quality
- Biomass yield
- Biomass quality
- Biotic and Abiotic stress



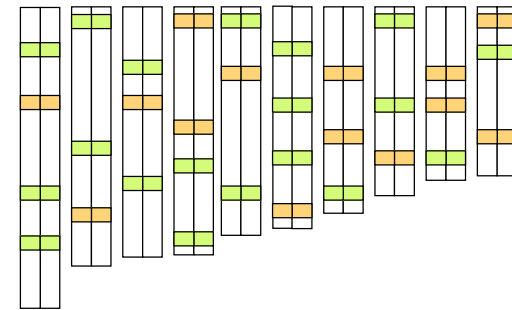
QTLs for Seed weight,  
Mace and Jordan 2011



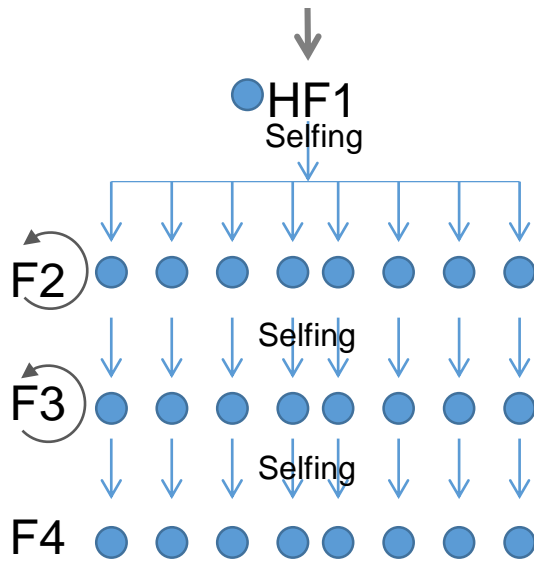


- Multi-trait selection
- Combine favorable alleles from the 2 parents

- What we want : combine « 33 » regions



- Solution : **identify** the genomic regions / favorable alleles and combine them



- Not reachable through genealogic / phenotypic selection : million of progenies would be required...

400 F4

# MET Phenotyping (1/2011)

400 F4

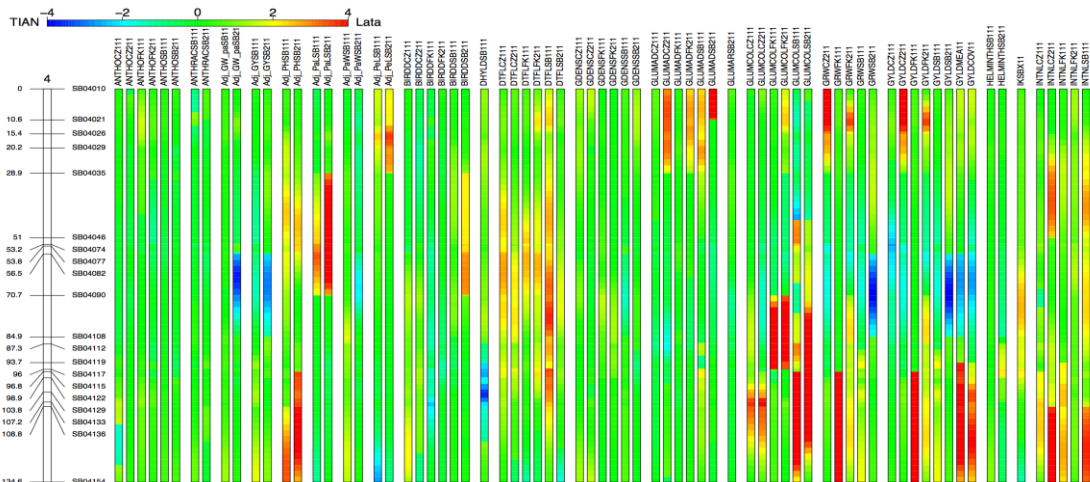
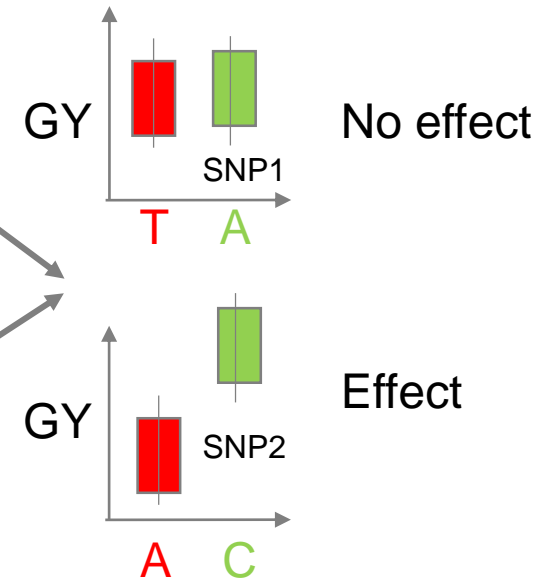


	GY	PH
P1	: 5	130
P2	: 6	170
F4.1	: 2	175
F4.2	: 5	140
F4.3	: 3	120
F4.n	: 8	180

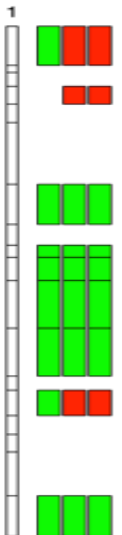
P1 : ATGCATGC  
P2 : AAGCCTGC  
F4.1 : ATGCATGC  
F4.2 : ATGCTGC  
F4.3 : AAGCATGC  
F4.n : AAGCCTGC

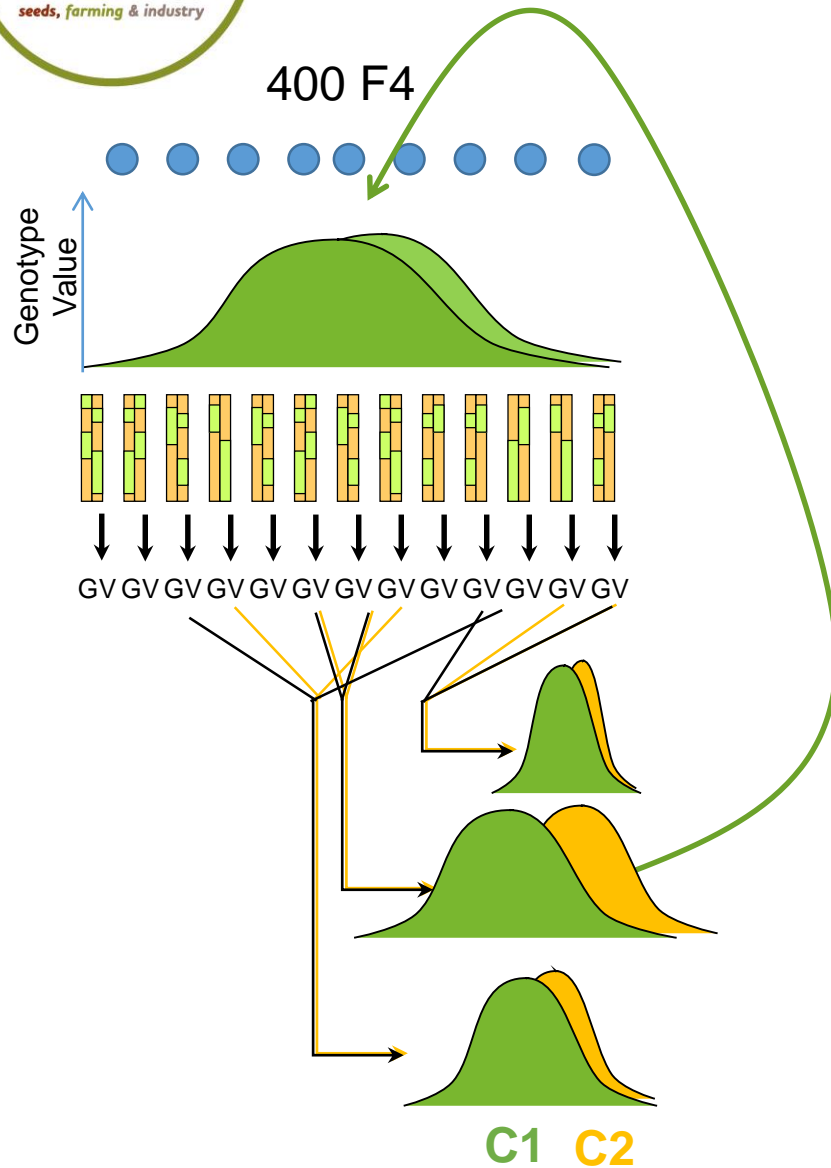
SNP1

SNP2

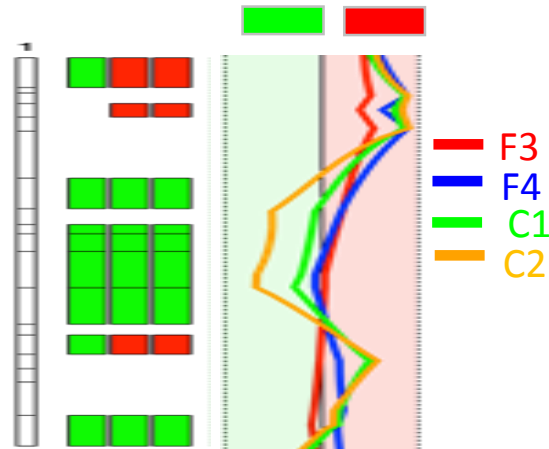


- Molecular target definition

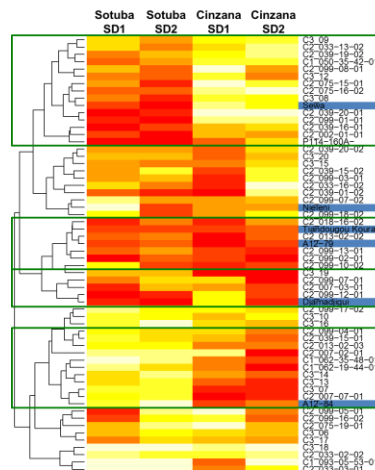




- Evolution towards molecular ideotype (6/2011 – 1/2013)



- Field evaluation (On-Station and on-Farm)



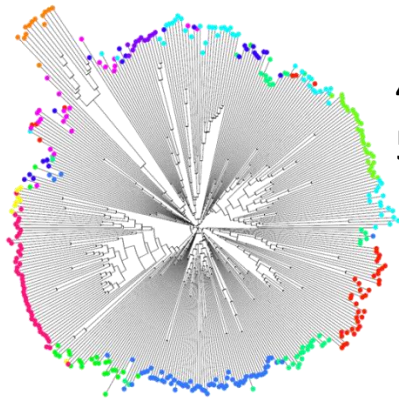
- Comparison with **local varieties**
- Within family MARS works (faster, more accurate)**
- But information is not easily transferred to broad base populations**





Ingrid Vilmus

## Multi-Environments / Panels

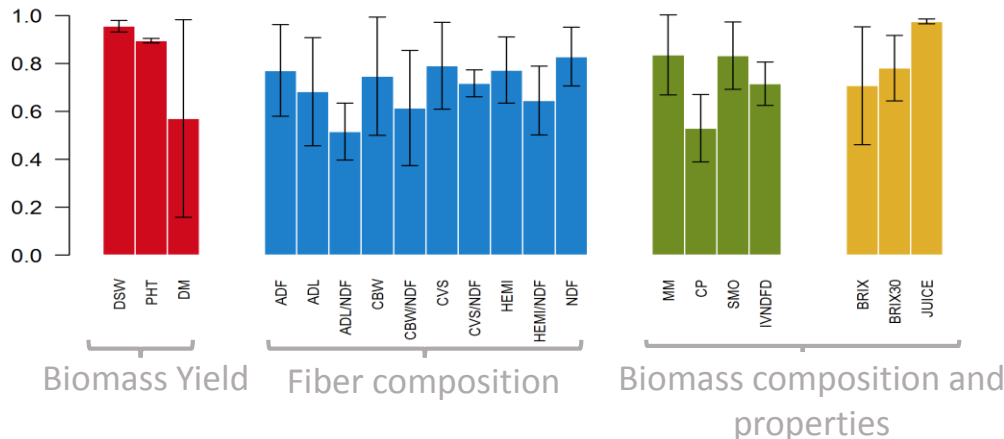


- 413 accessions  
5 trials (100 - 362 genotypes)
- 2 Montpellier
  - 2 Mali
  - 1 Mali Off Season



## GBS : 190ksnp

## Heritabilities

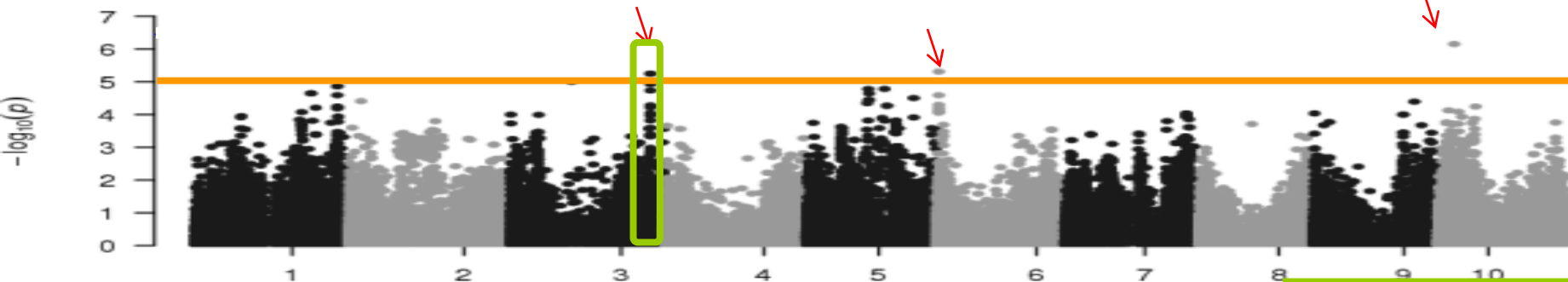


Btx623	:	ATGCATGCATGC
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Tx430	:	ATGCATGC C
Ji2731	:	ATGCCTGCATGC
E-Tian	:	AAGCATGCATGC
Rio	:	AAGCTGCATGC

SNP

Indels

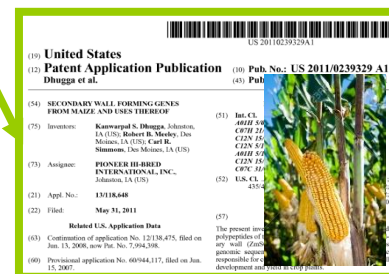
## GWAS for Cell Wall lignin content



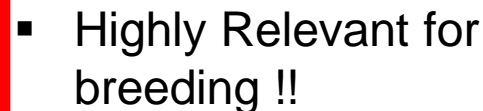
Chrom	Pos(pb)	LOD	Gènes candidats		
			Début	Fin	Fonction
3	67 247 746	5.25	67 242 057	67 244 587	Phenylpropanoids /lignin
6	1 273 618	5.31	1 208 904	1 216 444	TF/TF MYB
10	7 794 293	6.15	7 751 084	7 755 352	TF/TF MADS

LACCASE Is Necessary and Nonredundant with PEROXIDASE for Lignin Polymerization during Vascular Development in Arabidopsis<sup>®</sup>

Qiao Zhao,<sup>1</sup> Jin Nakashima,<sup>2</sup> Feng Chen,<sup>3</sup> Yanbin Yin,<sup>4</sup> Chunxiang Fu,<sup>5</sup> Jian Zeng-Yu Wang,<sup>6</sup> and Richard A. Dixon<sup>1,2</sup>



- Refined genomic regions / genes identification
- GXE + Transfer to breeding programmes (exotic lines...) + Power issues (allelic frequencies)**

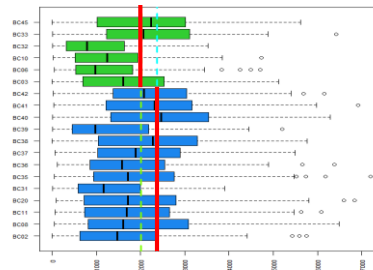
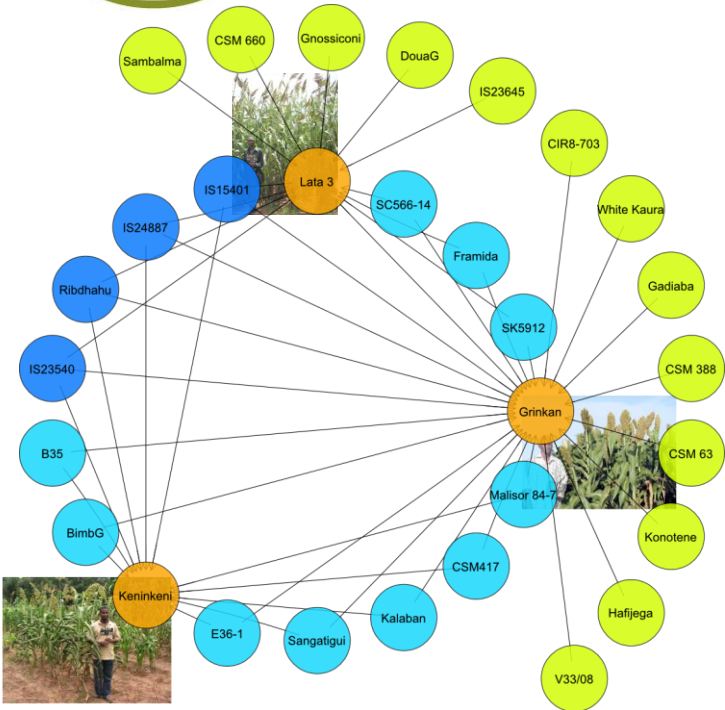


- See also Morris et al 2015 : NAM for Btx623 and Tx430

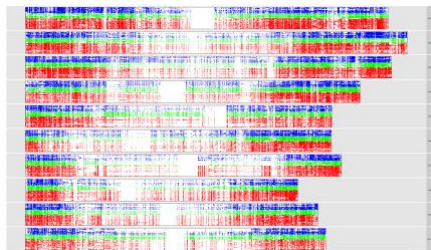




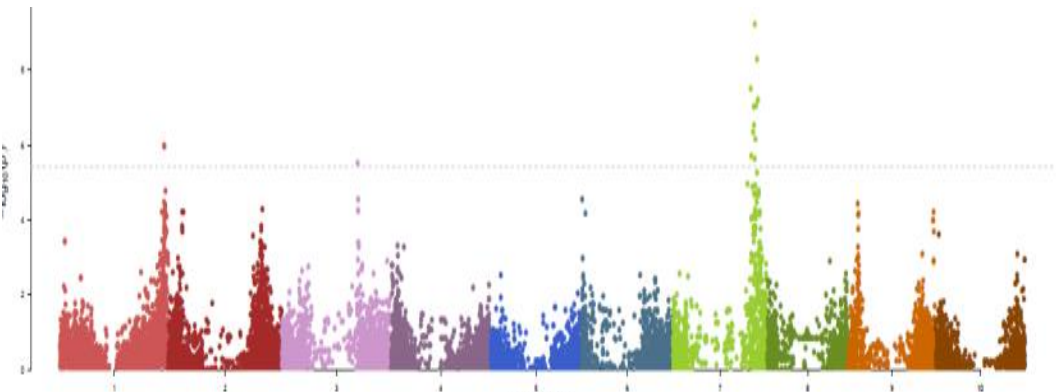
# BC-NAM : GRAIN YIELD AND QUALITY FOR WESTERN AFRICA



Grain yield (kg/ha)



GBS SNP density in 47 populations



BC Nested Association Mapping

47 populations, 4717 BC<sub>1</sub>F<sub>4</sub> families

## Direct variety development through PPB



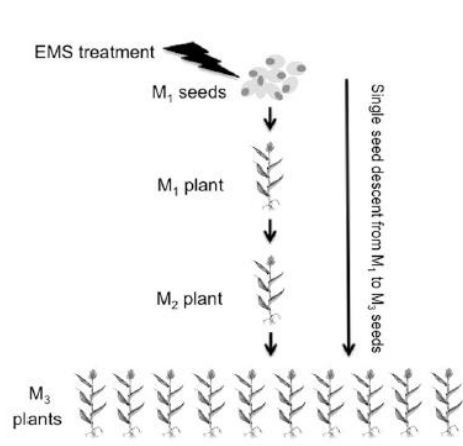
Nom	Pedigree	Diolla	Koutiala	Mande	MOYEN	Rang
Fadda	12A/Lata Hybrid Check	94	242	99	138	1
Lagri	Lata//Grin-8-39-1-1	87	193	92	120	3
Essi	Lata//SC566-6-44-1-1	102	172	89	122	2
Lango	Lata//Ngot-3-6-1-1	89	150	77	104	11
Tieble	CSM335 Local Check	72	148	75	100	14
Djala	Lata//DouaG-1-2-1-1	96	172	71	110	7
Lani	Lata//Gnos-7-13-1-1	81	194	67	107	8
Samboni	Lata//Samb-5-1-1-1	82	196	67	106	9
Dili	Lata//Ribd-3-9-1-1	94	183	57	102	13





# CREATING NEW VARIABILITY THROUGH CHEMICAL MUTATIONS

## EMS Mutant libraries development



Jiao et al 2016 : 6400 M4 mutants



256 mutants lines sequenced.  
A resource for gene validation

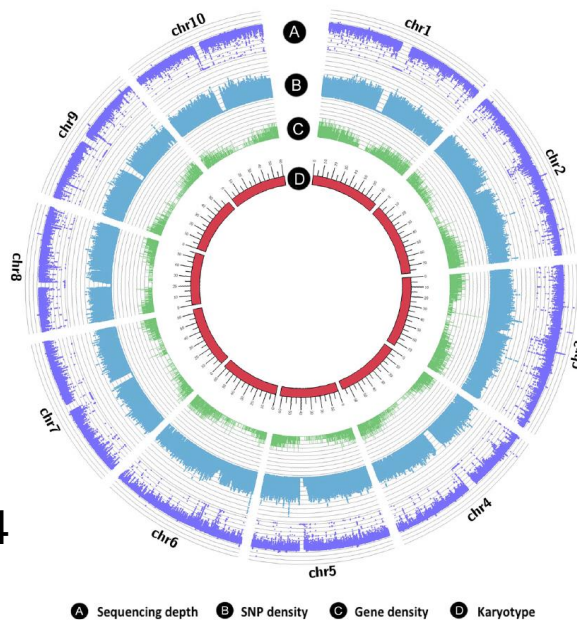


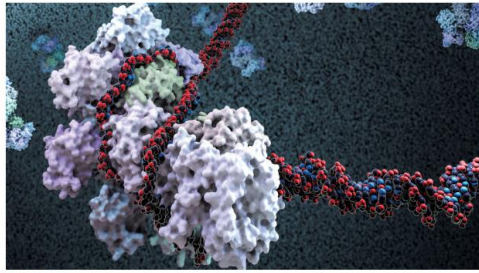
Figure 4. Genome-Wide Distribution of EMS Mutations.

## Identification of mutants relevant for breeding



Sattler et al 2014

SPECIAL COLLECTION  
**The CRISPR Revolution**



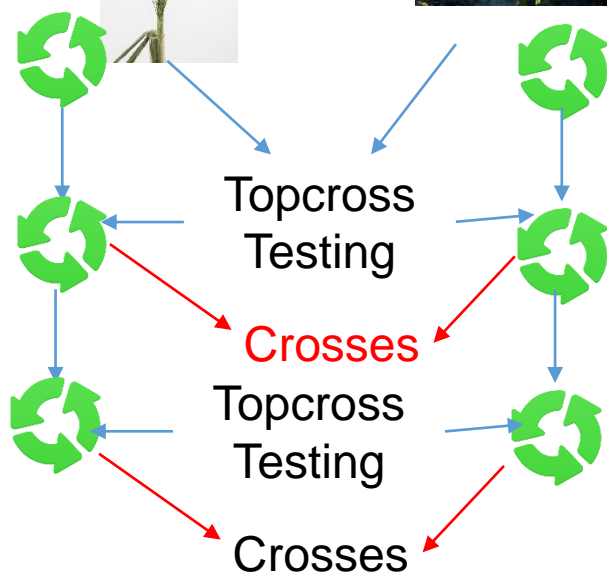
## Demonstration of CRISPR/Cas9/sgrNA-mediated targeted gene modification in Arabidopsis, tobacco, sorghum and rice

Wenzhi Jiang<sup>1</sup>, Huanbin Zhou<sup>2</sup>, Honghao Bi<sup>2</sup>, Michael Fromm<sup>3</sup>, Bing Yang<sup>2</sup> and Donald P. Weeks<sup>1,\*</sup> 2013

- CRISPR Cas9 can be used for :
  - Introduction of large deletions / Rearrangements
  - Introduction of single point mutations
- Interest for Gene function validation ! => acceleration of gene discovery and development of breeding tools
- New Breeding Technology (Creation of targeted variability)

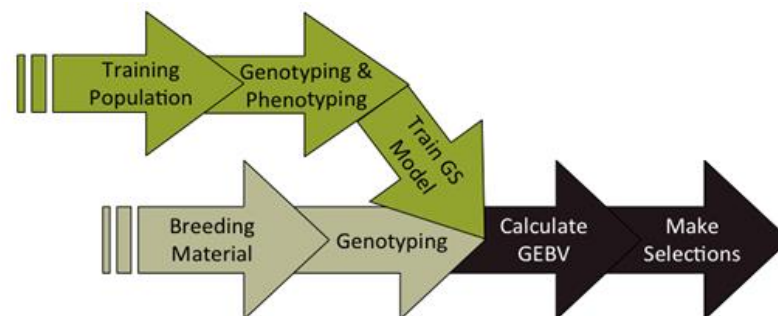
## ● Heterotic groups identified

- Towards dedicated Reciprocal Recurrent Selection schemes



## ● Marker assisted breeding strategies

- Classical QTL / GWAS detection and allele follow up and stacking
- Genomic selection : 1) Calibration of genotypic value based on markers and ii) prediction (no interest in « Genes »)



Heffner et al. 2009 Crop Sci. 49:1–12

## ● Take advantage of the New Breeding Technologies (NBT)

- Functional validation
- Variability development





# SORGHUM GENETICS AND BREEDING IN EU : PERSONAL THOUGHTS

- Sorghum breeding is efficient : an asset to provide producers with genetic materials adapted to their needs and the ones of the end-users (See Jeanson's Talk)
- European sorghum breeding has specificities (target environments). It requires specific research efforts
- Works performed in the US / Africa / India / Australia... are highly valuable and have to be considered
- No need to COORDINATE. But huge benefits to COLLABORATE / AGREGATE results and EXCHANGE EXPERIENCES : **we need a place for that !!**



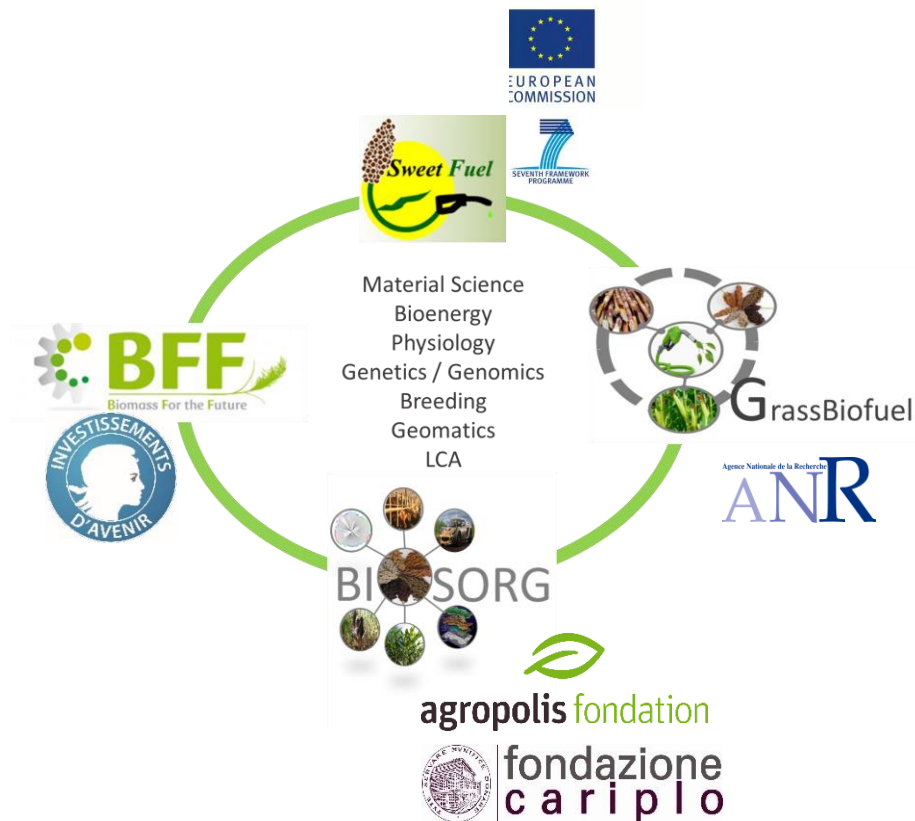
- Gilles Trouche



- Jean-François Rami



## Sorghum Biomass Projects



# QUESTIONS ?

