1ST 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

David Pot, PhD, CIRAD FRANCE

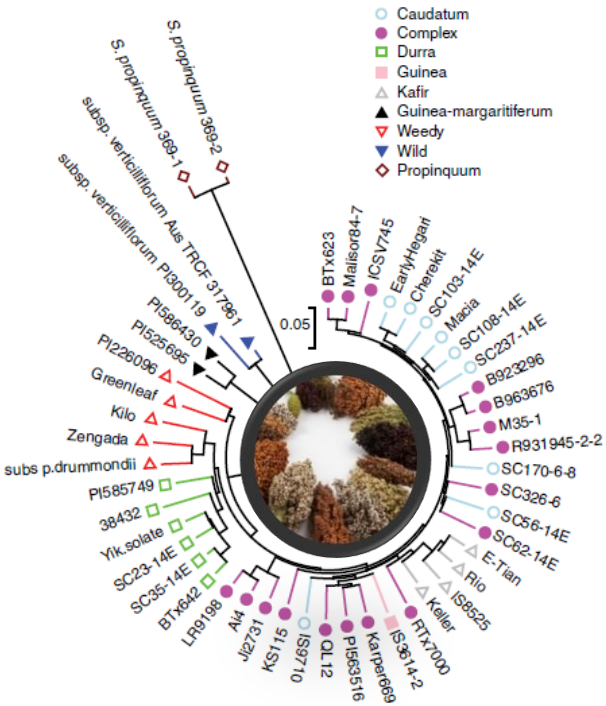
BUCHAREST
3-4 NOVEMBER 2016

WHOLE GENOME SEQUENCING : AN ACCELERATOR OF SORGHUM GENETICS AND BREEDING

Btx623 sequencing

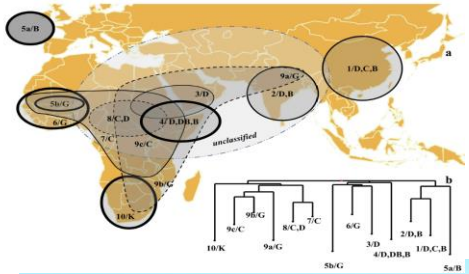
Paterson et al 2009

Enlarging the diversity coverage



Mace et al 2013

To 1000's Genomes : « Terra » Project



Mockler et al 2016

NUCLEOTIDE DIVERSITY INFORMATION

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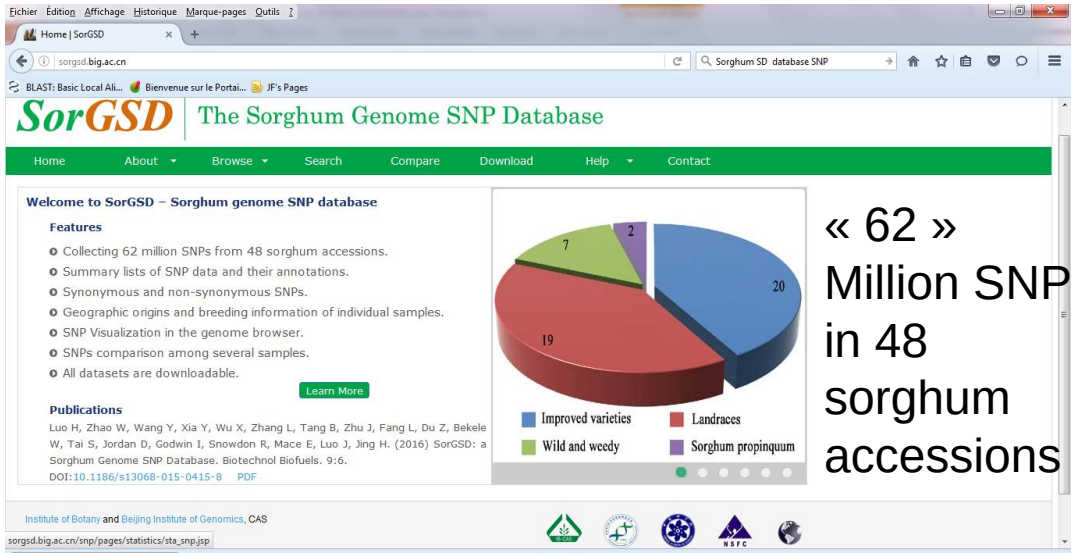
SNP Indels



« 62 » Million SNP in 48 sorghum accessions

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 $trait_x$

  h_x^2: heritability of $trait_x$,

  Sd_x: Phenotypic standard deviation of $trait_x$

- Indirect selection (select $trait_x$ based on selection on $trait_y$ (y= grain yield in on-station trial)):

$$CR_x = i_y * h_x * h_y * r_{g_{xy}} * Sd_x$$

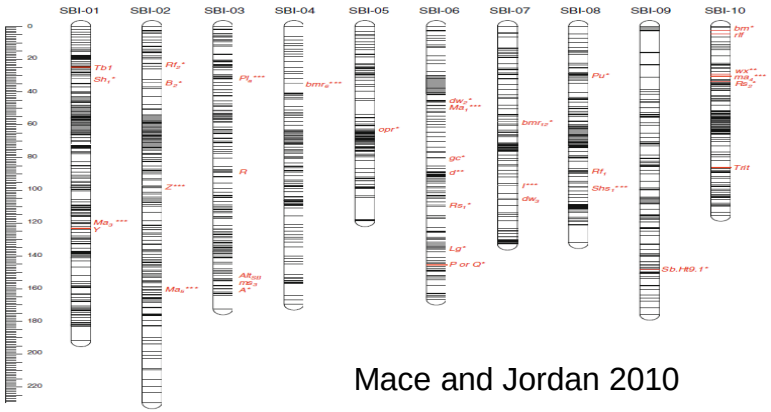
  With $r_{g_{xy}}$: genetic correlation between traits x and y

- Molecular markers allow maximizing h_y. Assuming a high genetic correlation ($r_{g_{xy}}$) you can expect $CR_x >> R_x$

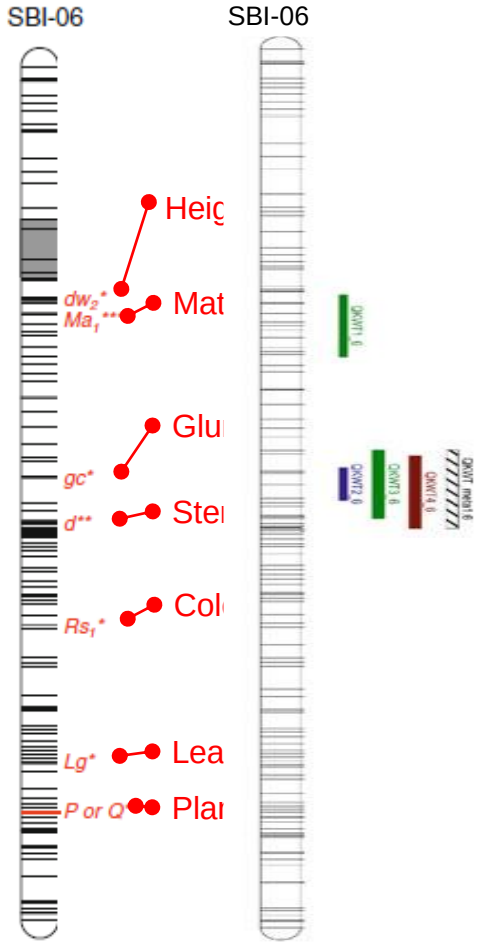
- Challenge : identify the genomic regions (Markers) controlling the traits of interest (high $r_{g_{xy}}$) and combine them in new varieties

MAJOR GENES AND QTLS (BIPARENTAL) HAVE ALREADY BEEN IDENTIFIED

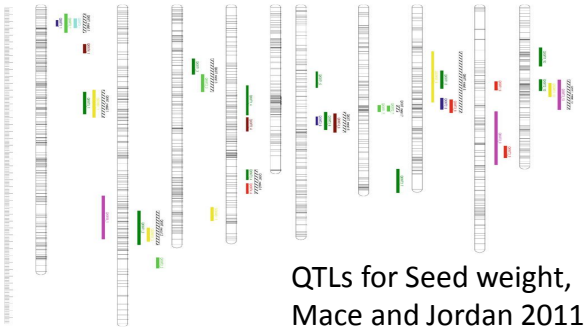
- **Major Genes**



Mace and Jordan 2010



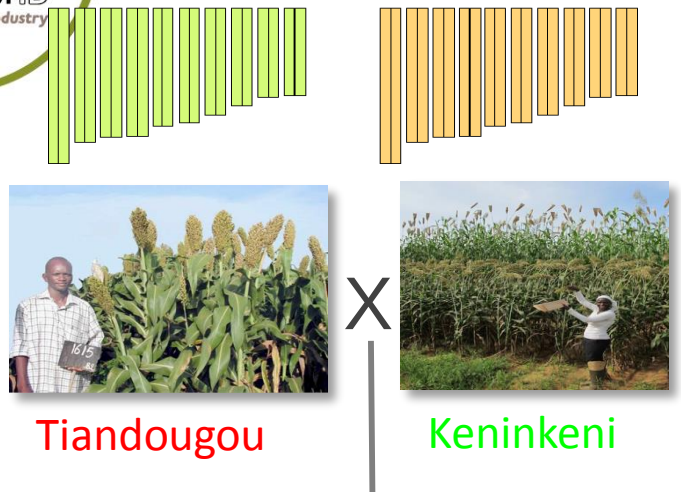
- **Some genomic regions affecting quantitative traits**
  - QTLs in biparental populations
    - Grain yield / size…
    - Grain quality
    - Biomass yield
    - Biomass quality
    - Biotic and Abiotic stress



QTLs for Seed weight,
Mace and Jordan 2011

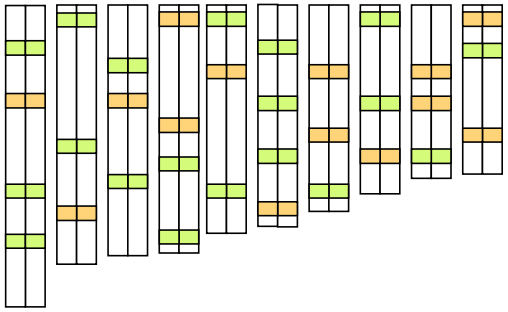
MARKER ASSISTED RECURRENT SELECTION APPLIED TO WITHIN FAMILY BREEDING FOR GRAIN YIELD AND QUALITY IN MALI

Dec 2008

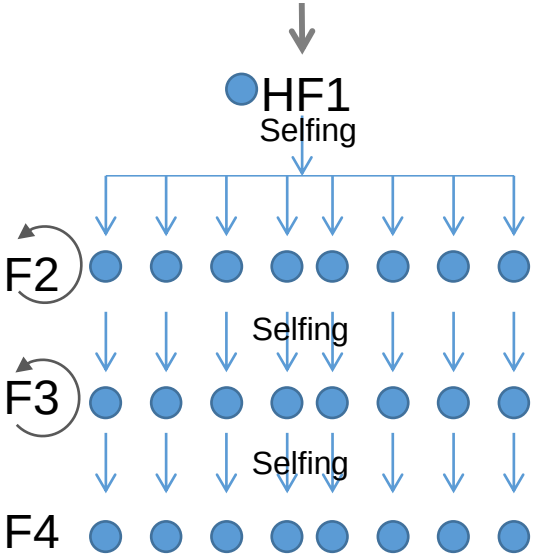


- Multi-trait selection
- Combine favorable alleles from the 2 parents

- What we want : combine « 33 » regions



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



400 F4

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

June 2010

WITHIN FAMILY BREEDING : DEFINING THE MOLECULAR IDEOTYPE

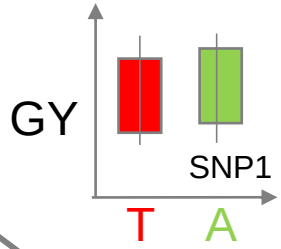
MET Phenotyping (1/2011)

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

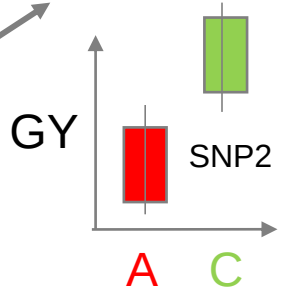
400 F4

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

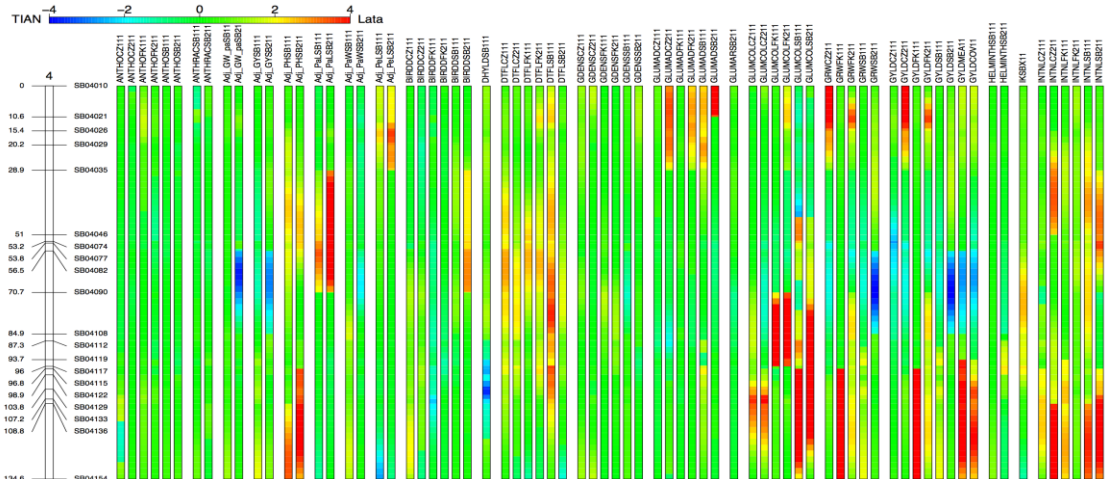
SNP1 SNP2



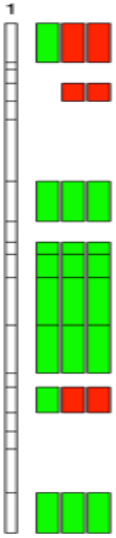
No effect



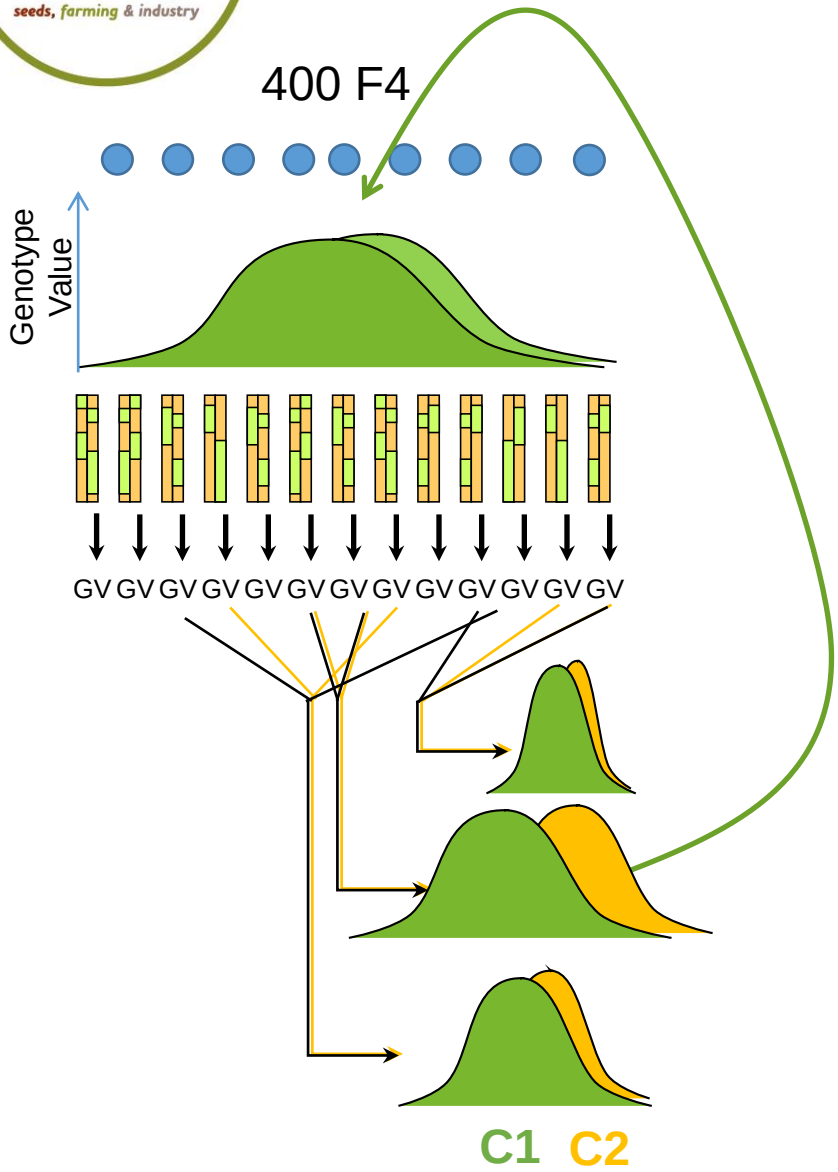
Effect



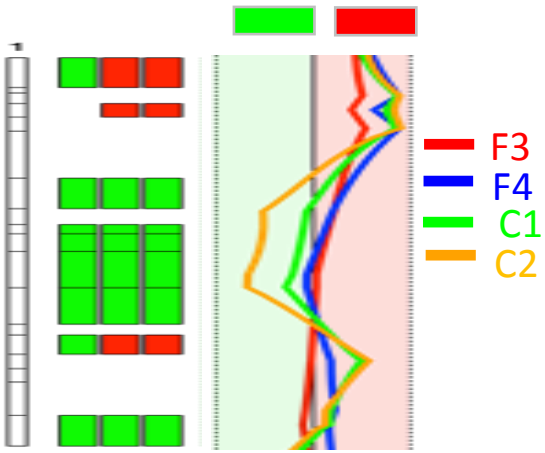
- Molecular target definition



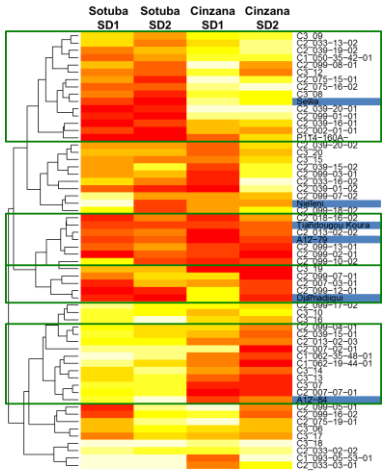
WITHIN FAMILY BREEDING : CONVERGING TOWARDS THE MOLECULAR IDEOTYPE



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

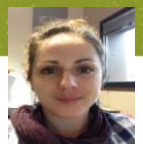


- Field evaluation (On-Station and on-Farm)



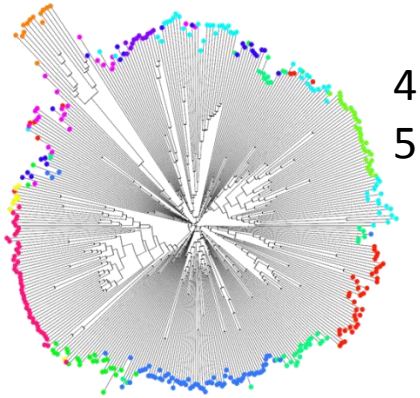
- Comparison with local varieties
- **Within family MARS works (faster, more accurate)**
- **But information is not easily transfered to broad base populations**

GWAS : TRACKING DOWN THE GENES TO MONITOR ALLELES OF INTEREST IN BROAD BASED PANELS



Ingrid Vilmus

Multi-Environments / Panels

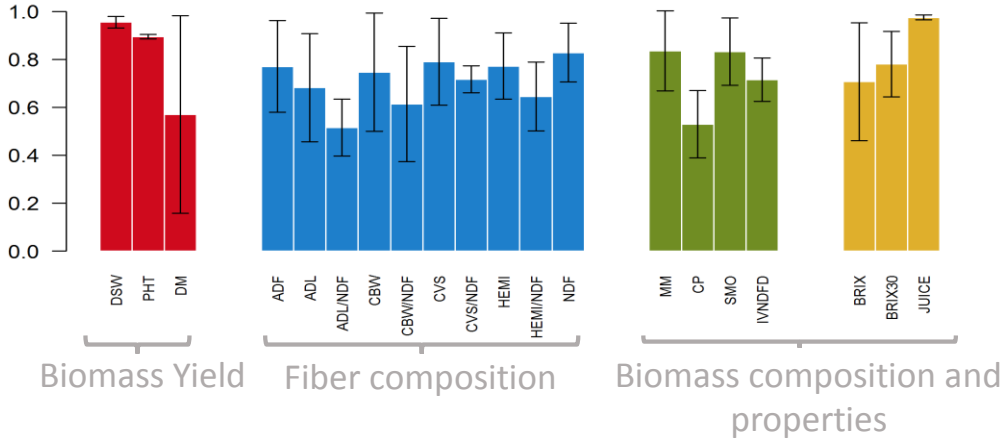


413 accessions

5 trials (100 - 362 genotypes)

- 2 Montpellier
- 2 Mali
- 1 Mali Off Season

Heritabilities



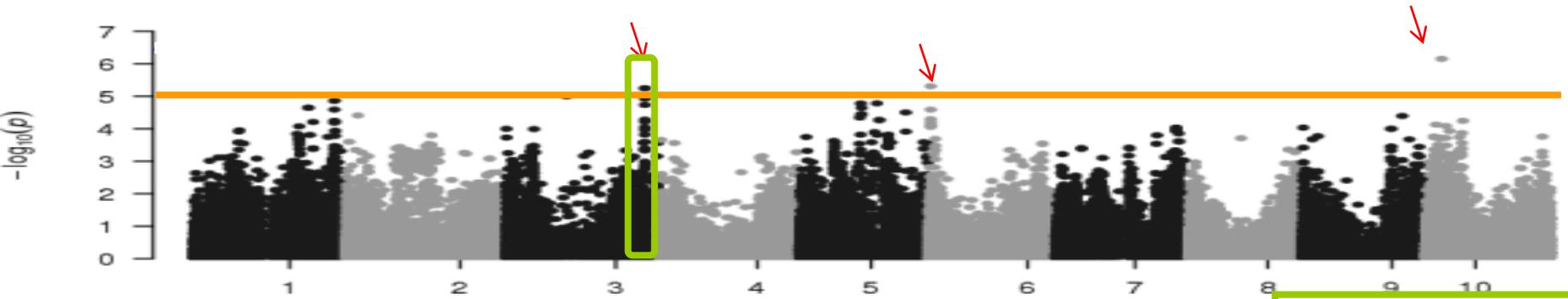
GBS : 190ksnp

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

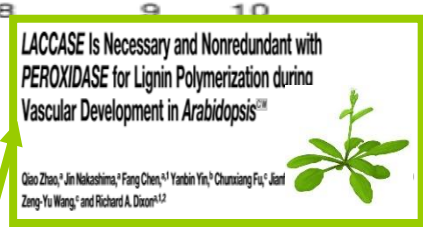
SNP Indels

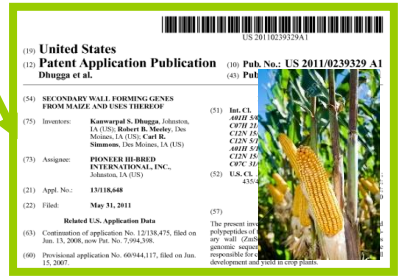
GWAS : GENE IDENTIFICATION, BUT NEEDS FOR MULTI-ENVIRONMENTS ASSESMENTS

GWAS for Cell Wall lignin content



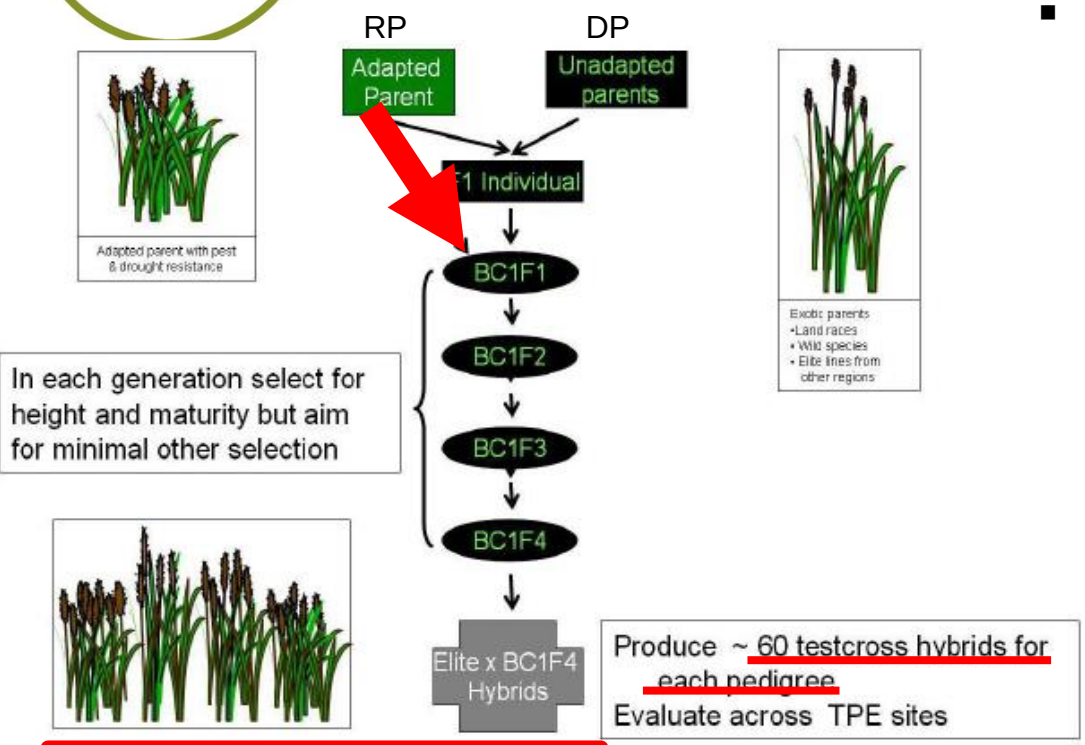
Chrom	Pos(pb)	LOD	Gènes candidats		
			Début	Fin	Fonction
3	67 247 746	5.25	67 242 057	67 244 587	Phenylpropanoids /lignin
6	1 273 618	5.31	1 208 904	1 216 444	TF/TF MYB
10	7 794 293	6.15	7 751 084	7 755 352	TF/TF MADS





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

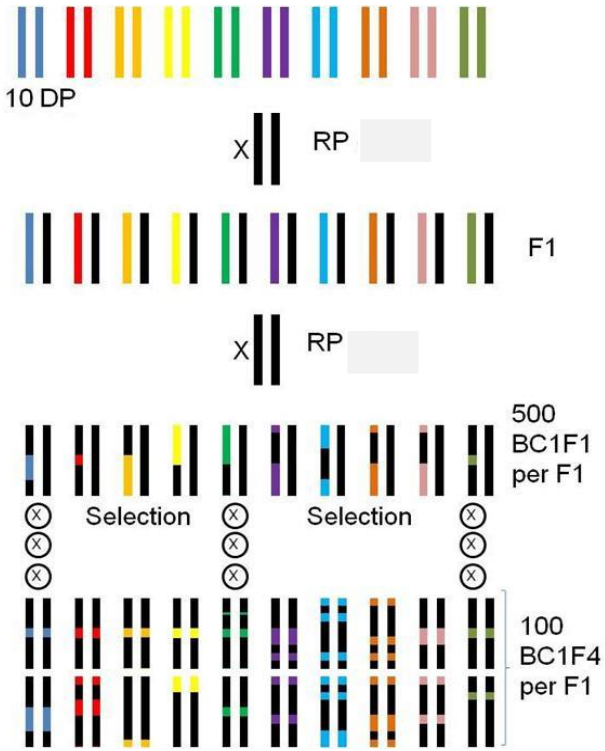
MERGING GENETIC AND BREEDING OBJECTIVES FOR BROAD BASED PANELS : COMBINING BIPARENTAL AND GWAS MAPPING



Jordan et al (2011).

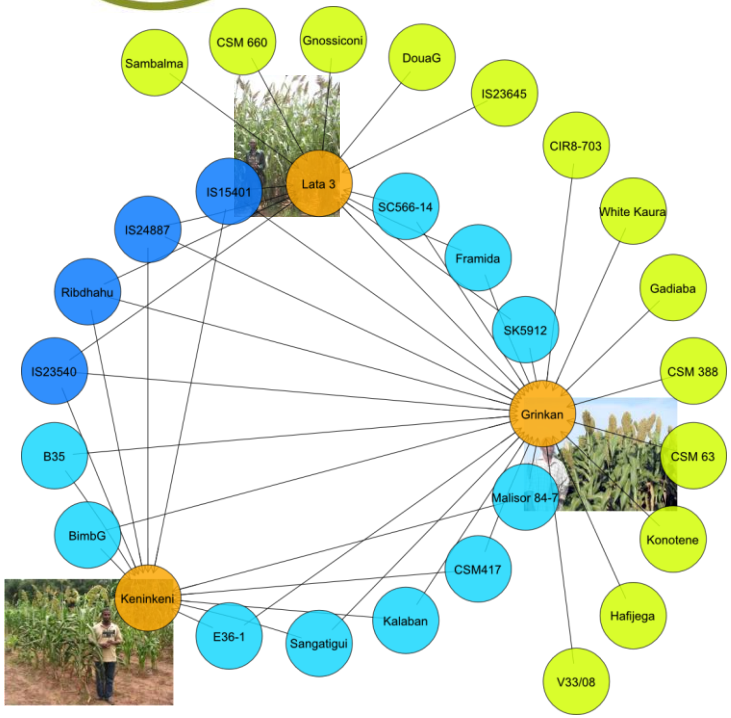
- Highly Relevant for breeding !!

- And high resolution genetic mapping

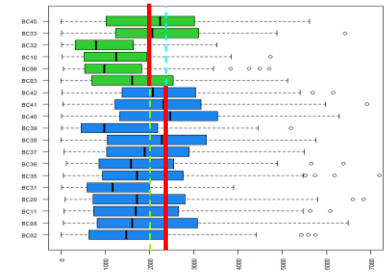


- See also Morris et al 2015 : NAM for Btx623 and Tx430

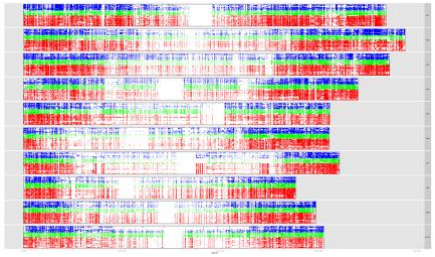
BC-NAM : GRAIN YIELD AND QUALITY FOR WESTERN AFRICA



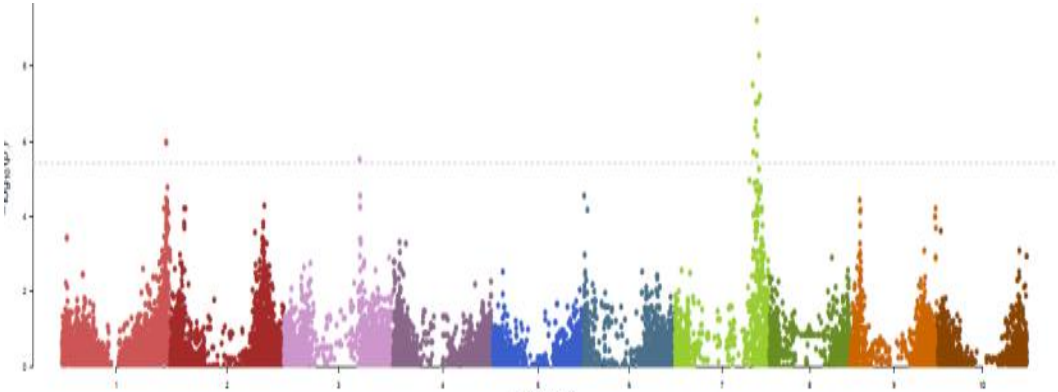
47 populations, 4717 BC_1F_4 families



Grain yield (kg/ha)



GBS SNP density in 47 populations



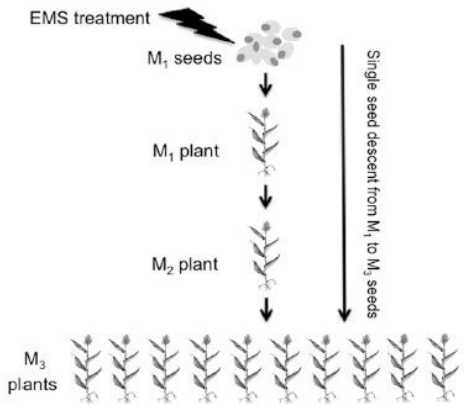
BC Nested Association Mapping

Direct variety development through PPB

Nom	Pedigree	Dioila	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//Ngol-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//Ridb-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

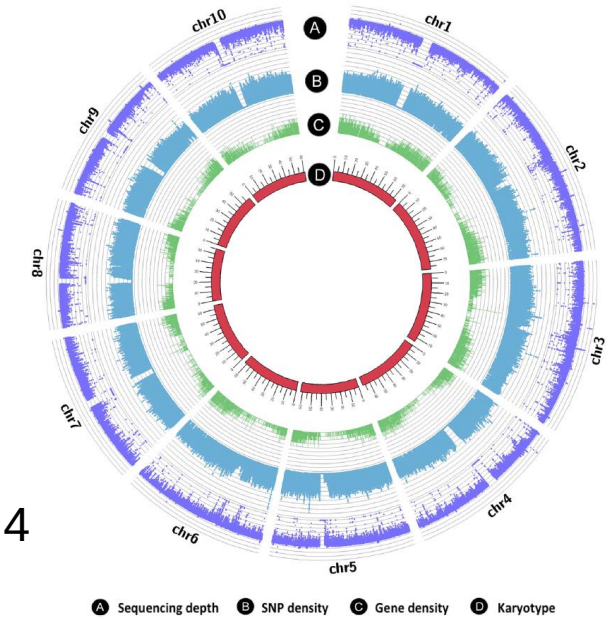


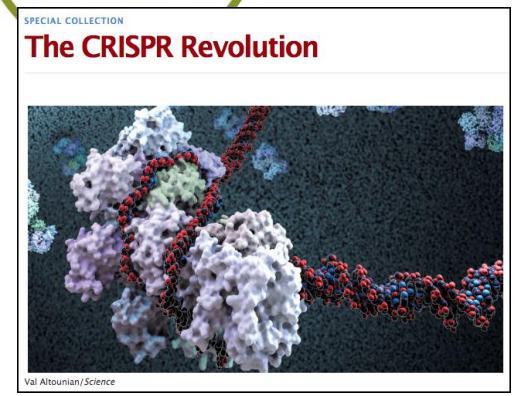
Figure 4. Genome-Wide Distribution of EMS Mutations.

256 mutants lines sequenced.
A ressource for gene validation

- Identification of mutants relevant for breeding

Sattler et al 2014

CREATING NEW VARIABILITY THROUGH GENOME EDITING



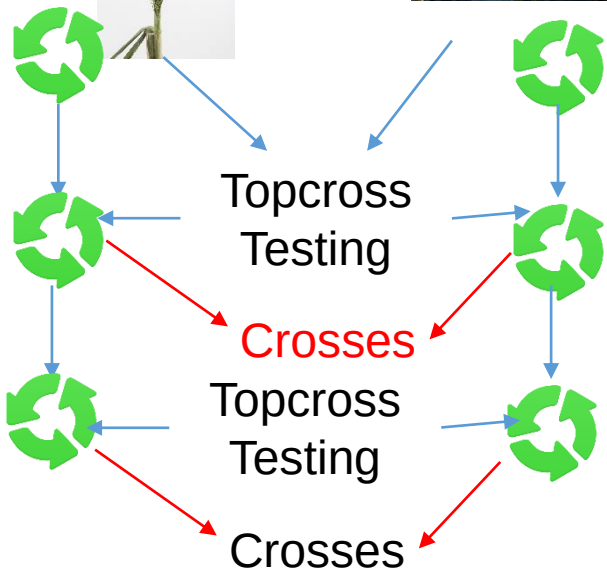
Demonstration of CRISPR/Cas9/sgRNA-mediated targeted gene modification in Arabidopsis, tobacco, sorghum and rice

Wenzhi Jiang[1], Huanbin Zhou[2], Honghao Bi[2], Michael Fromm[3], Bing Yang[2] and Donald P. Weeks[1,*] 2013

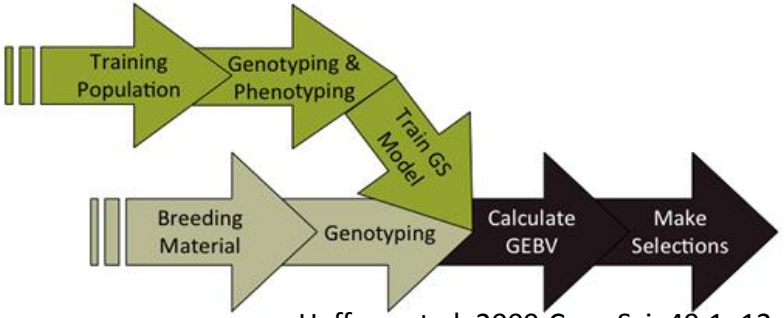
- CRISPR Cas9 can be used for :
  - Introduction of large deletions / Rearrangements
  - Introduction of single point mutations
- Interest for Gene function validation ! => acceleration of gene discovery and development of breeding tools
- New Breeding Technology (Creation of targeted variability)

FUTURE GENOMIC ASSISTED BREEDNG STRATEGIES

- 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 genotyic 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 Tecnhologies (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

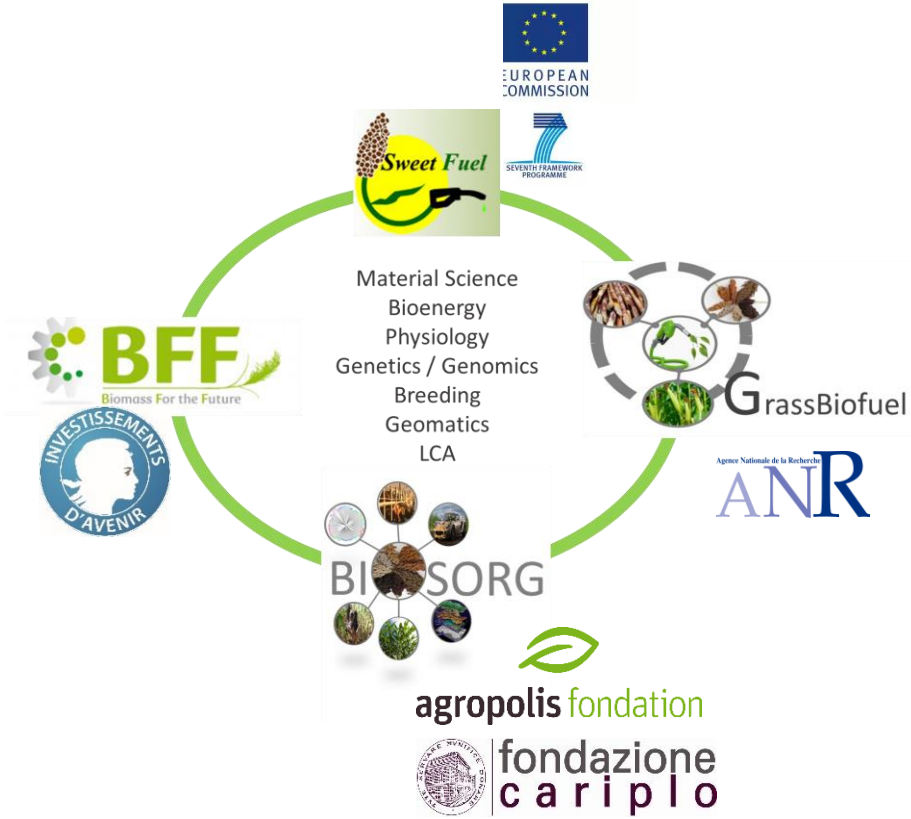
- No need to COORDINATE. But huge benefits to COLLABORATE / AGREGATE results and EXCHANGE EXPERIENCES : **we need a place for that !!**

PEOPLE AND FUNDINGS

- Gilles Trouche

- Jean-François Rami

Sorghum Biomass Projects



QUESTIONS ?