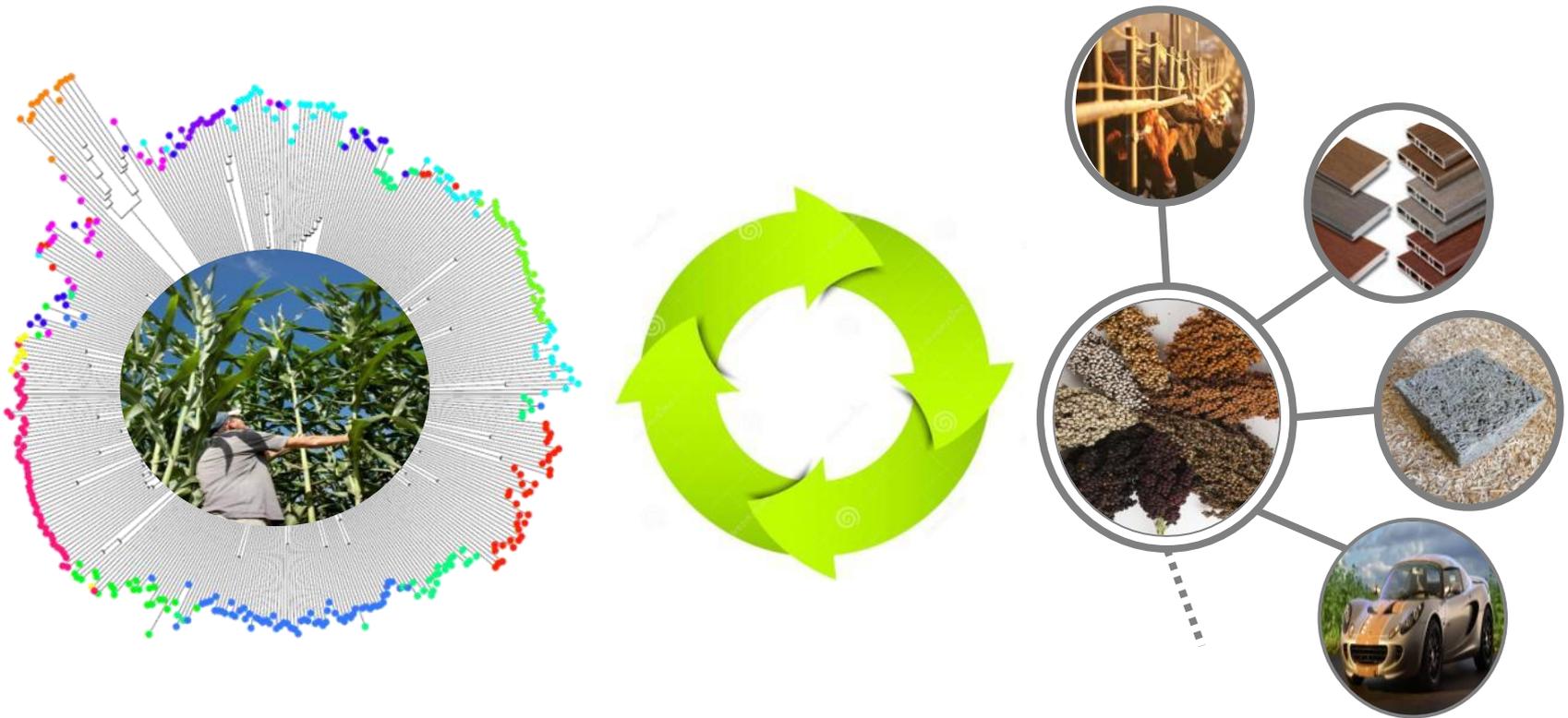


Combining genetic analysis and breeding for multipurpose sorghum

From the development of a “biomass phenotyping tool kit” to the development of dedicated breeding tools and schemes



Sorghum : a key player for a sustainable bioeconomy roadmap



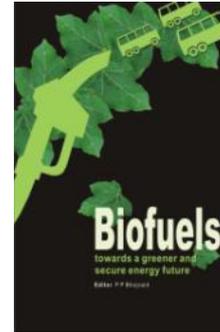
Europe : 250 Kha

France : 50 kha

Mainly for feed



New opportunities



Sorghum features



Biomass yield potential (WUE, NUE...)

Diverse crop management systems

Diversity of biomass composition

Cold tolerance

Weed management



Value chain development based on

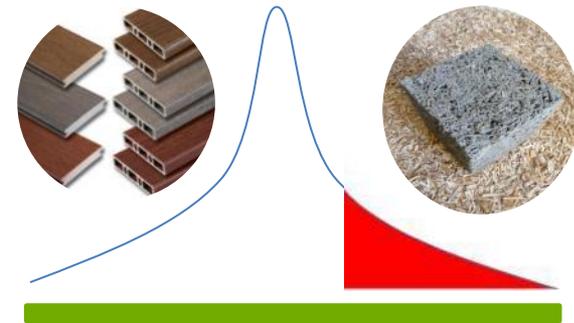
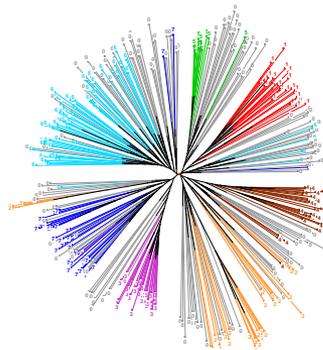
- « offer- demand » convergence
- Availability of relevant varieties



Biomass value chains : Big is « not always » beautiful ! Towards an « industrial ideotype »



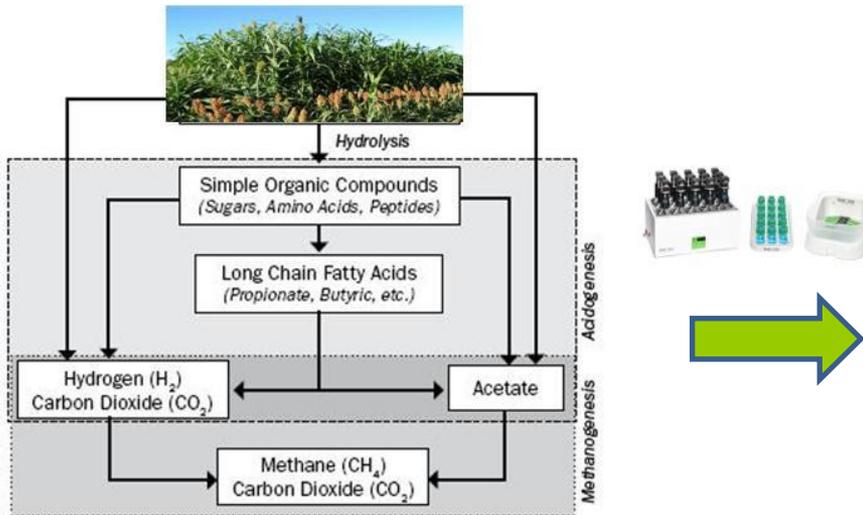
- Biomass Value chain needs Yield !!!
- But : importance of biomass properties
- Biogaz : domestic gaz, cogeneration, transports...
- Biocomposites : automotive industry, decking...
- Biomass key traits impacting end product ?



Genotypes > process > microstructure > performances - durability

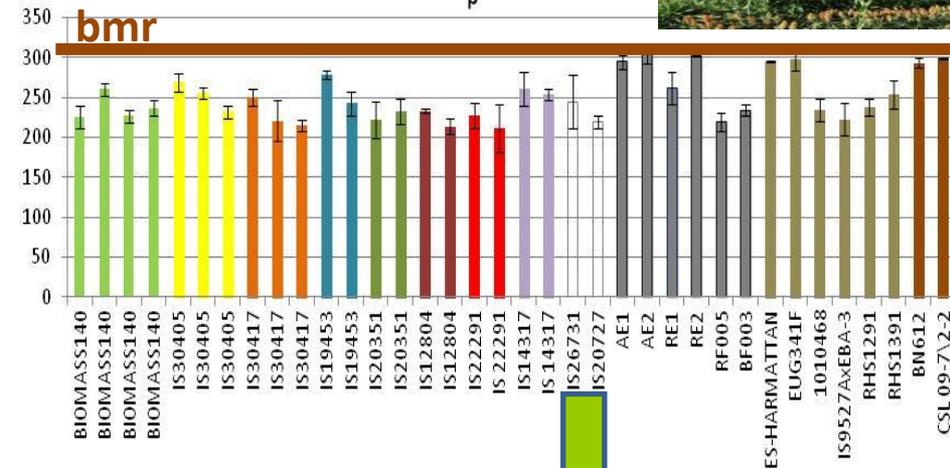


Methane production : Sorghum genetic variability



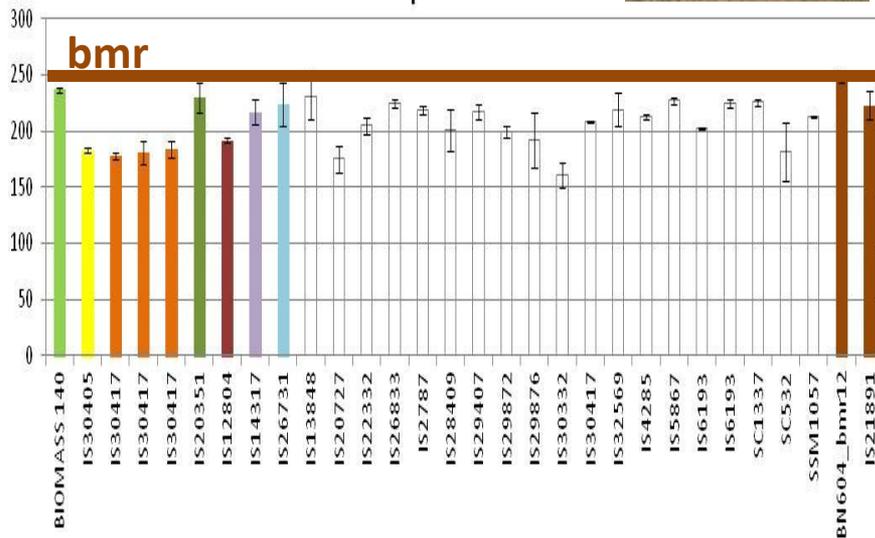
Whole Aboveground Biomass BMP (NmL/gMS)

$Cv_p = 11\%$

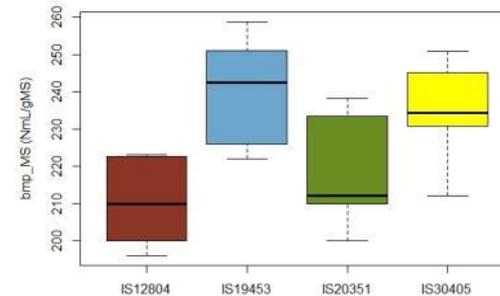


Stem BMP (NmL/gMS)

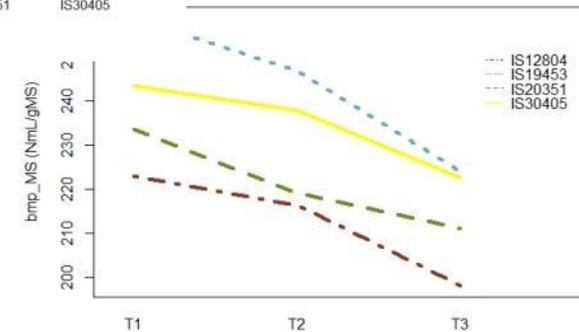
$Cv_p = 10.2\%$



G effect : pvalue=5.10e-4



E Effect : pvalue = 4.10e-4



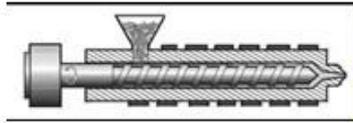
Biocomposites production

Fiber properties

Sorghum stems



+



Polymer matrix (PE, PP ?)

Process optimization

Biocomposites compound

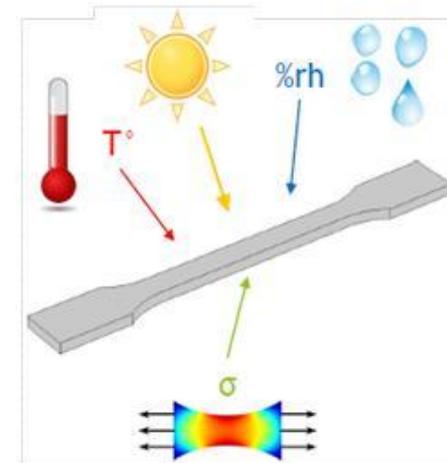


extrusion

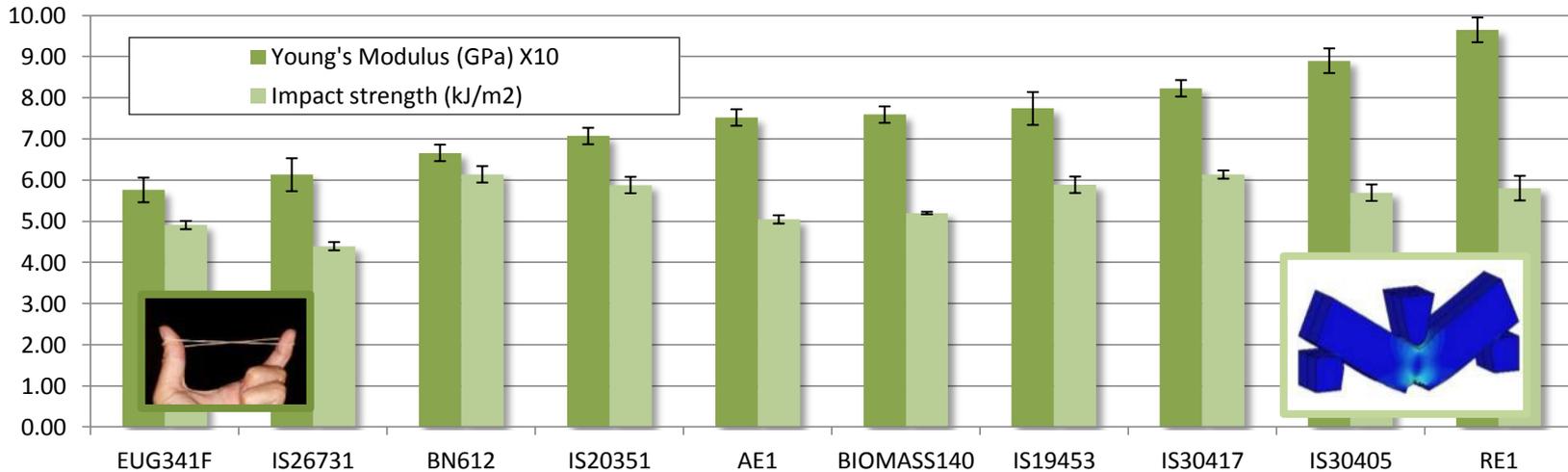
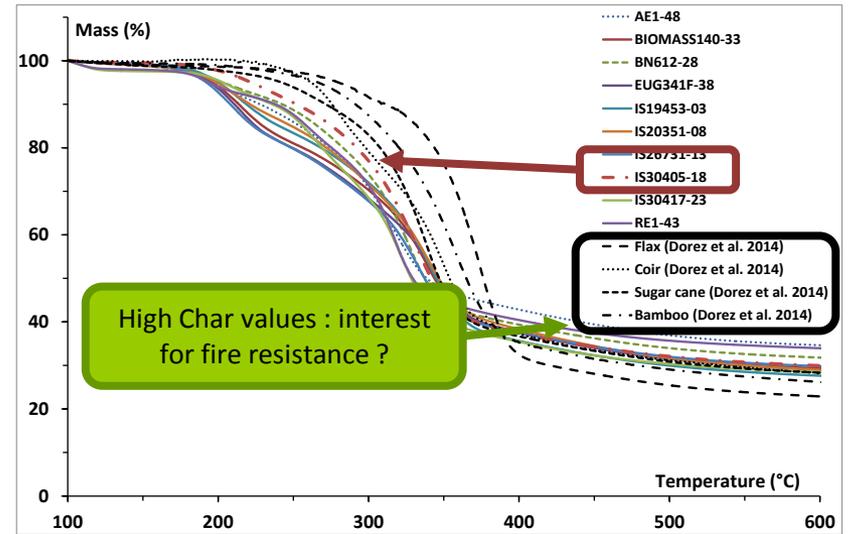
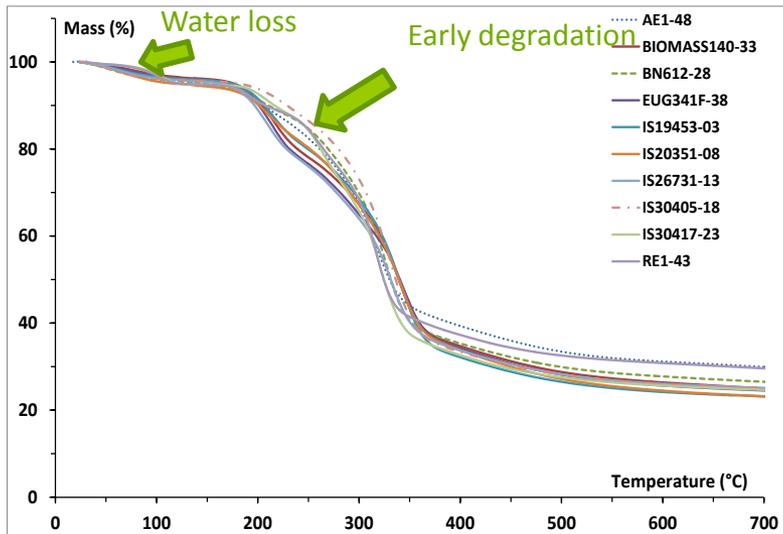


injection

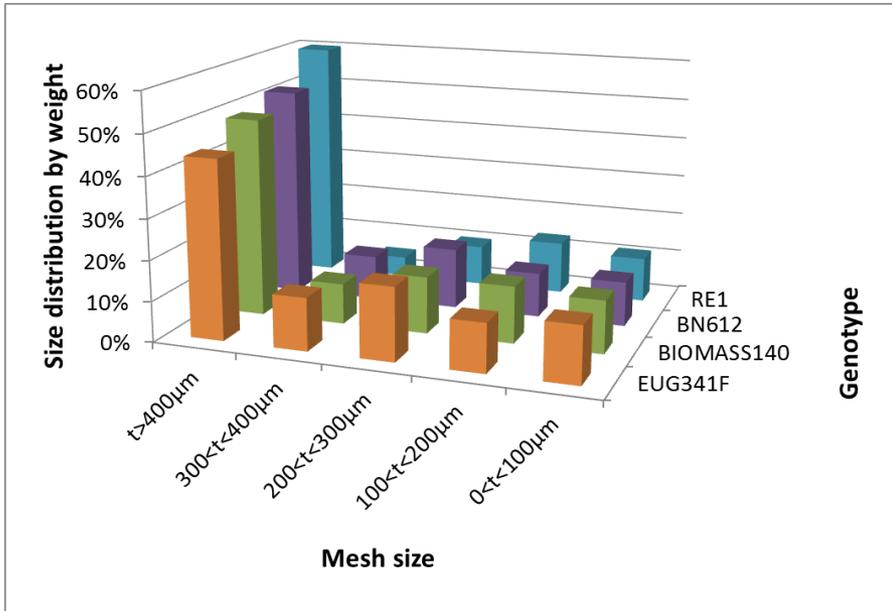
Micro-structure, mechanical properties and durability of biocomposites



Process optimization / end product genetic variability

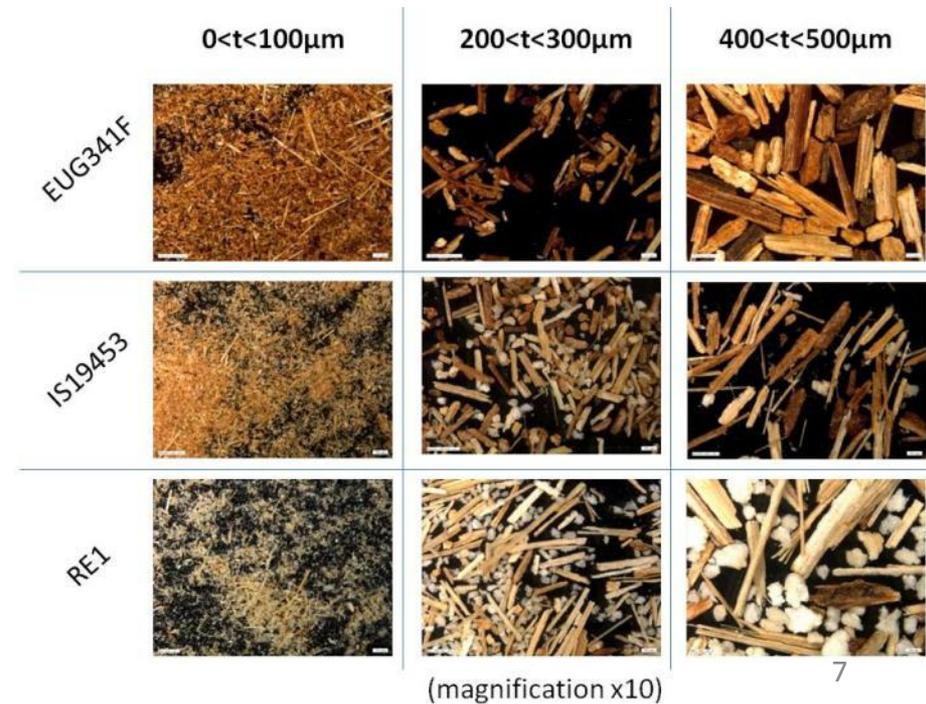


Tracking the biological ideotype : response to milling, Biochemical, histological and physical fibers properties



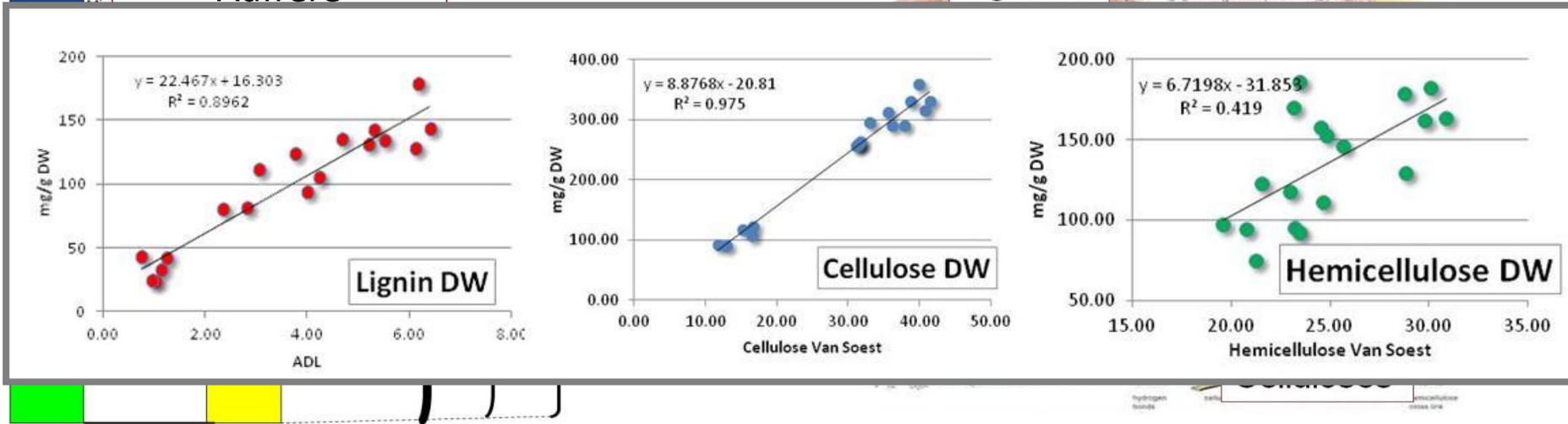
« Genotype » effects on:

- mesh size proportions
- particles morphology



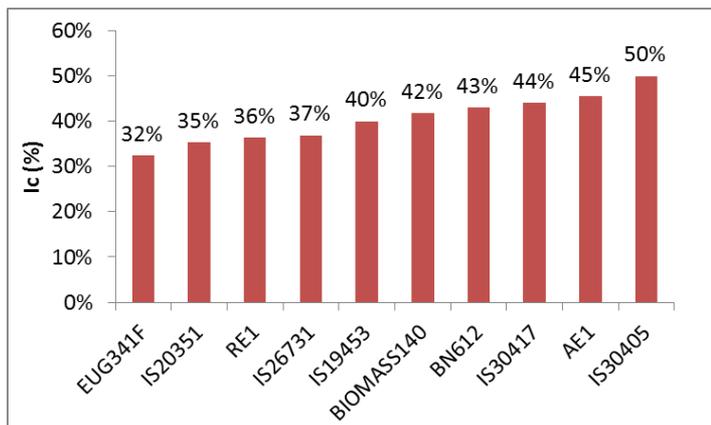
Biomass biochemical composition : increasing the description depth

Van Soest vs « in depth » biochemical analyses

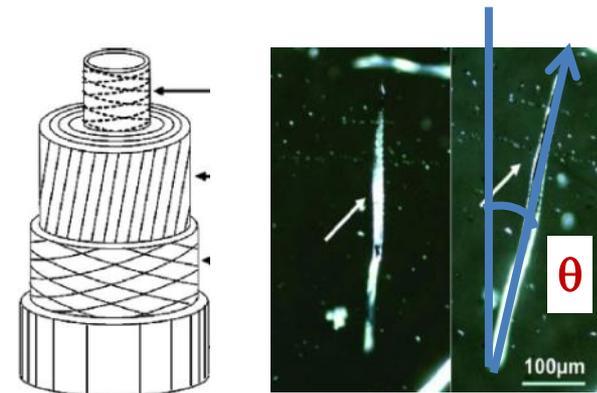


- Genetic variability has already been validated for these traits

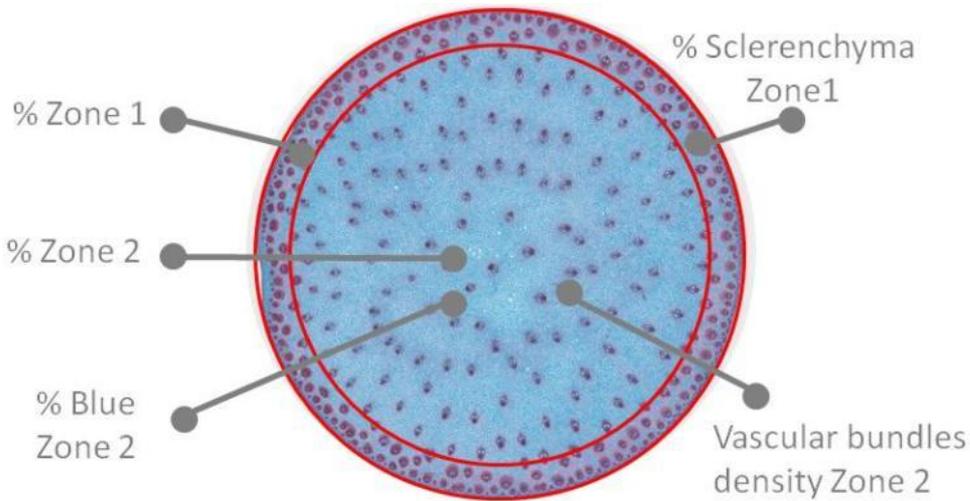
- Cellulose crystallinity : « G » effect



- Microfibrillar angle : on-going



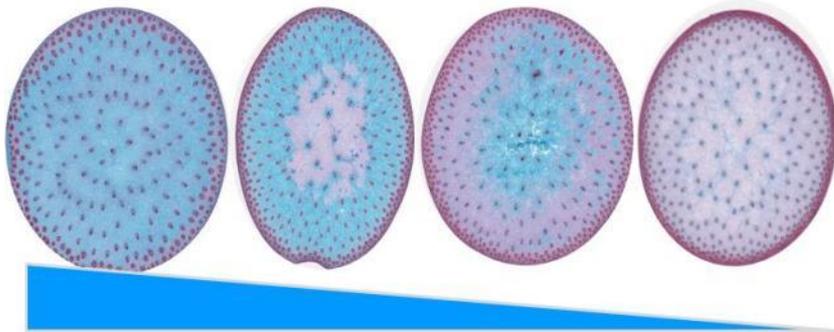
Histology : keys to clarify biochemical composition variability



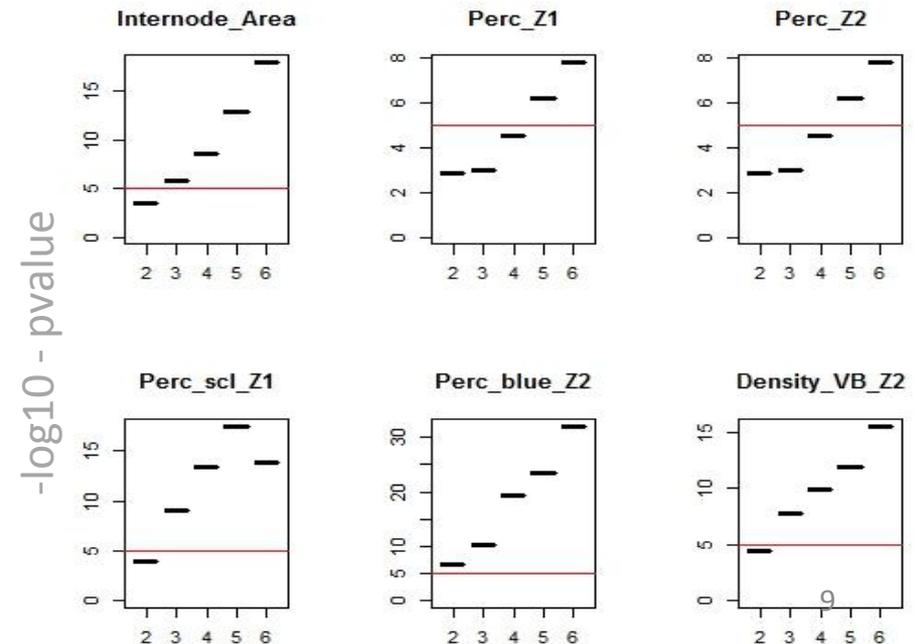
•28 genotypes

trait	G Pvalue	G r ² (%)
Perc_z1	1.66E-08	45
Perc_z2	1.66E-08	45
Perc_sclz1	1.59E-14	57
densitafx2	2.54E-16	59
PercBlueZ2	4.55E-33	78

•G effect on % Blue Zone 2

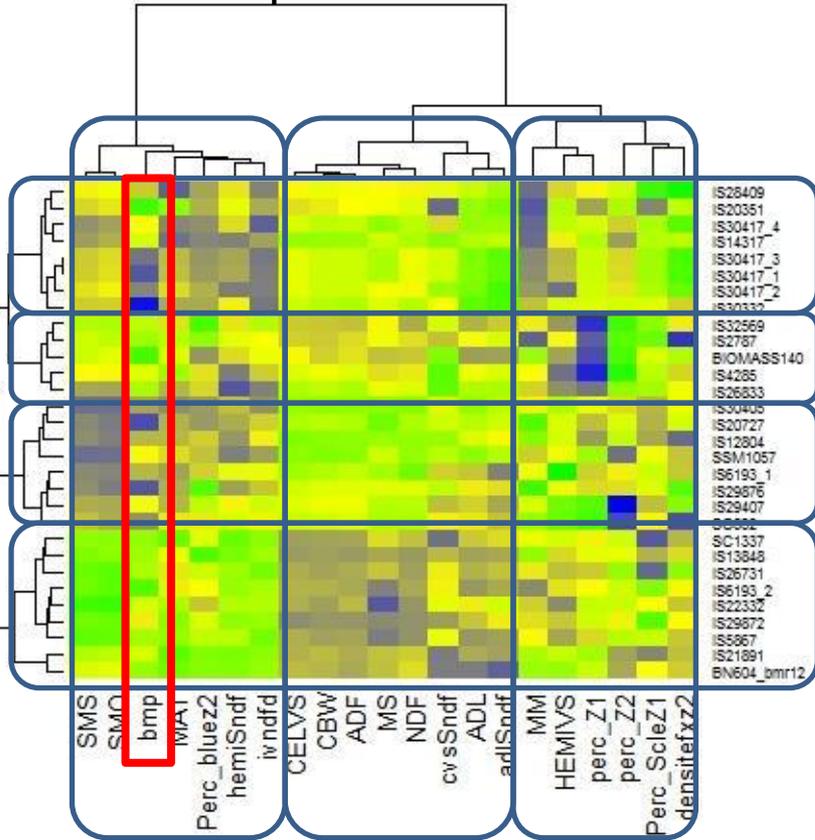


• G effect : plant number

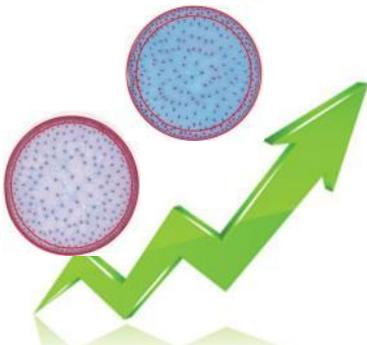


From Industrial ideotype to biological ideotype

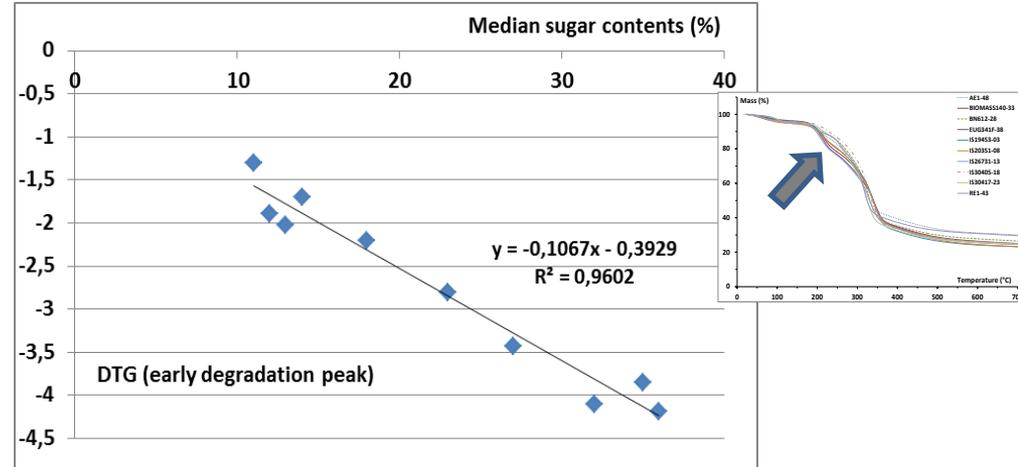
•Methane production



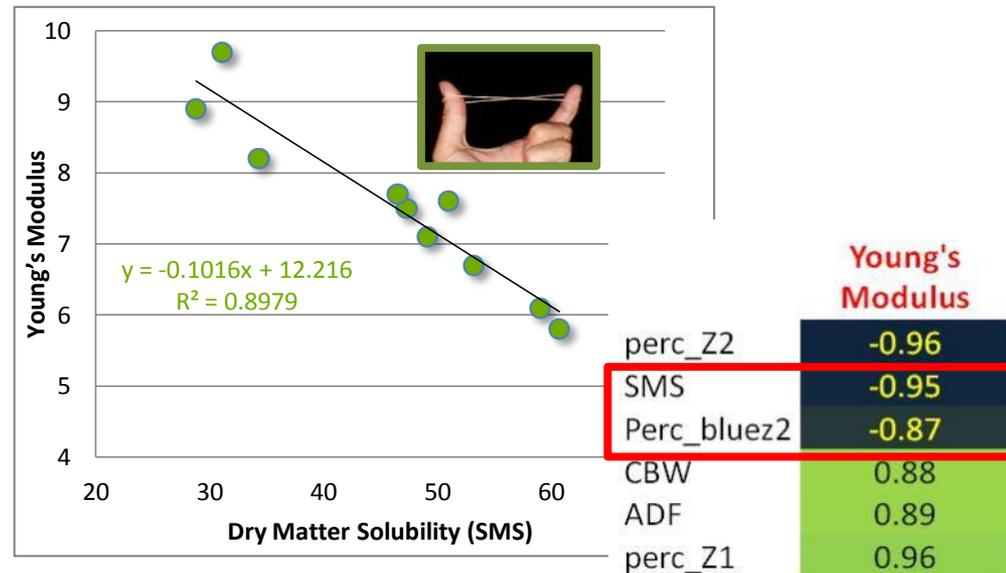
	bmp
adlSndf	-0.62
hemiSndf	0.50
MAT	0.55
Perc_bluez2	0.55
SMS	0.57
IVNDFD	0.62



•Biocomposites

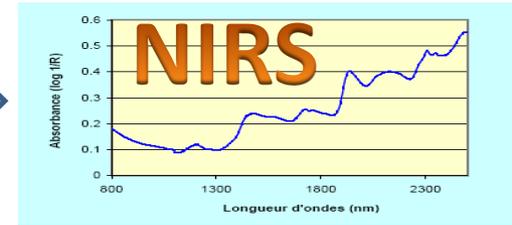
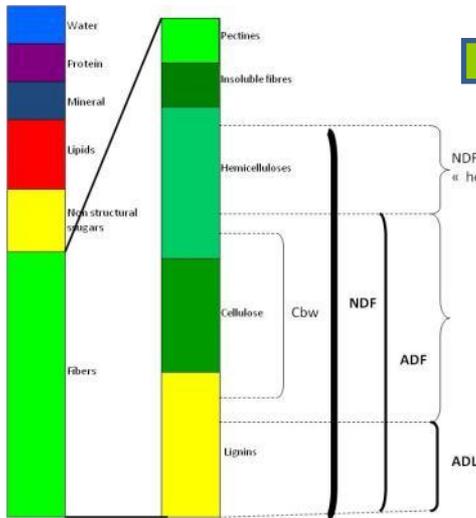


➔ Matrix choice / Pre-treatment / Genotype



	Young's Modulus
perc_Z2	-0.96
SMS	-0.95
Perc_bluez2	-0.87
CBW	0.88
ADF	0.89
perc_Z1	0.96

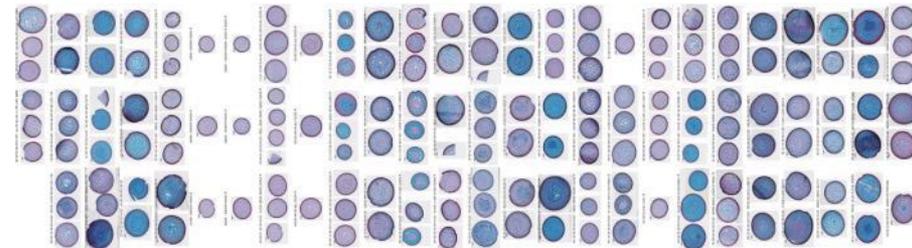
Increasing throughput !



Trait	Analyzed collection				Calibration		Validation	
	N	Mean	SD	CV %	SEC	RSQ	SECV	RPD
MS	523	93.45	1.95	2.09	0.54	0.92	0.61	3.2
MM	517	4.41	2.65	60.14	0.55	0.96	0.68	3.9
MAT	518	3.73	2.21	59.3	0.43	0.96	0.5	4.4
CBW	515	37.74	6.84	18.14	1.02	0.98	1.17	5.9
NDF	455	68.77	10.9	15.85	1.36	0.98	1.57	6.9
ADF	461	41.66	8.58	20.61	1.24	0.98	1.41	6.1
ADL	463	6.46	2.56	39.58	0.56	0.95	0.66	3.9
SMS	467	38.48	12.33	32.04	1.69	0.98	1.91	6.5
SMO	463	36.47	12.16	33.34	1.74	0.98	1.9	6.4

•NIRS calibration on-going for other biochemical (and physical properties)

Time = €

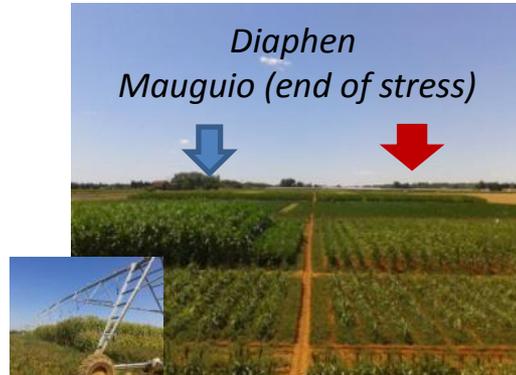
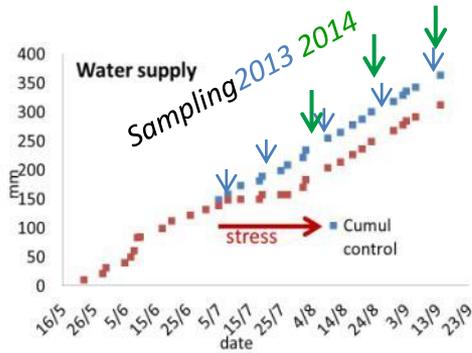


NIRS

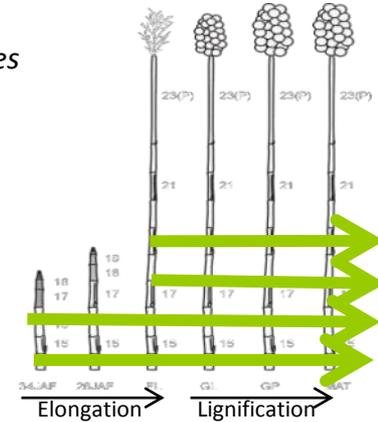
NIRS

Physiological understanding of key traits...

Field Trial : 4 genotypes (2013-2014) , addition of 11 genotypes in 2014
 Water deficit during elongation phase (12 leaves stage, during 1 month)



3-5 harvest stages
 2-4 internodes



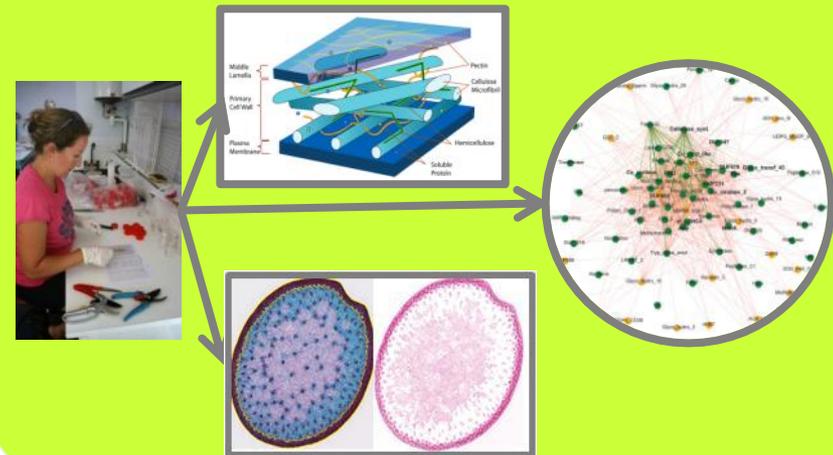
Phenology Architecture



Photosynthesis, C assimilation

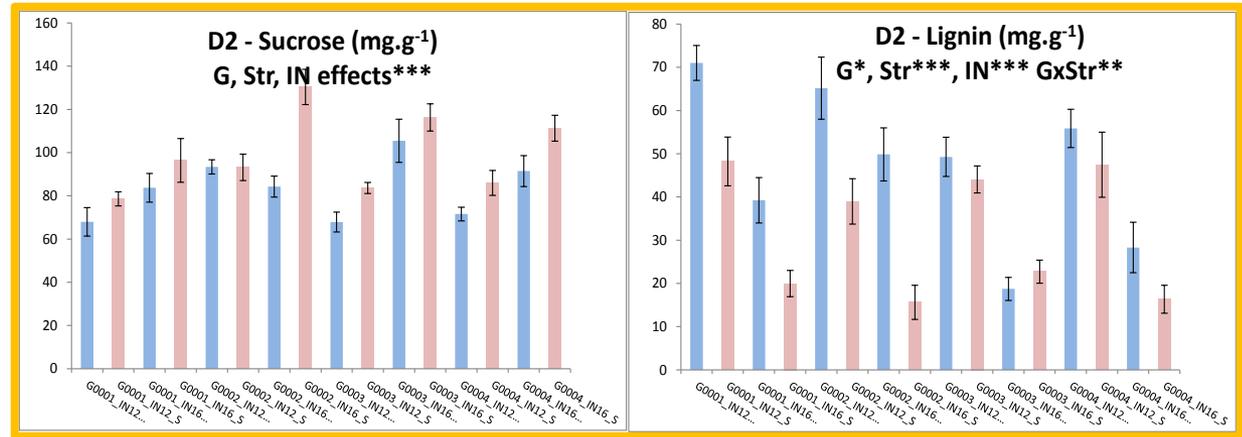
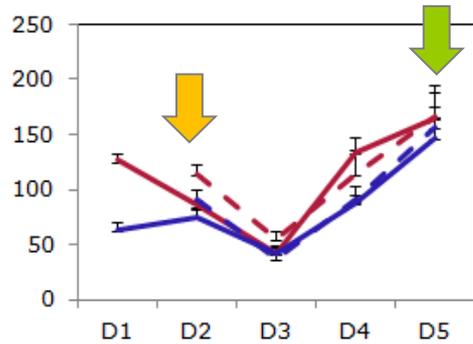


Internode analyses



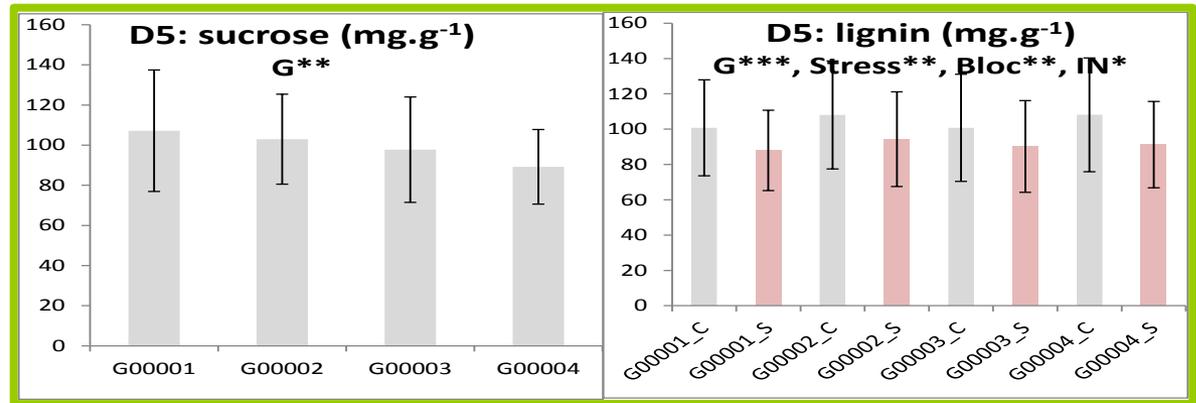
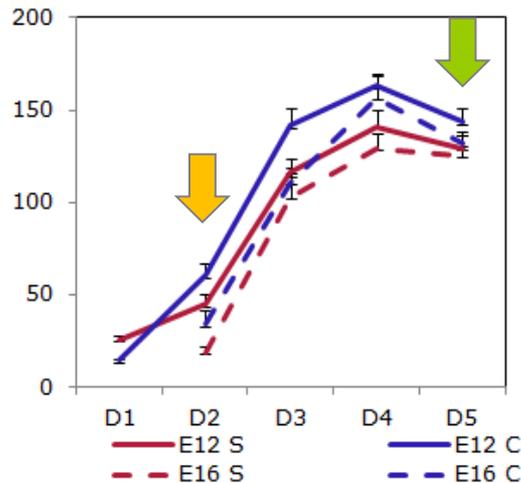
Biochemical composition : Ontogenic, WD , Genotype and interactions effects

[Sucrose] mg/g MS



✓ During WD (D2) : G, WD, Ontogenic and GxWD interactions

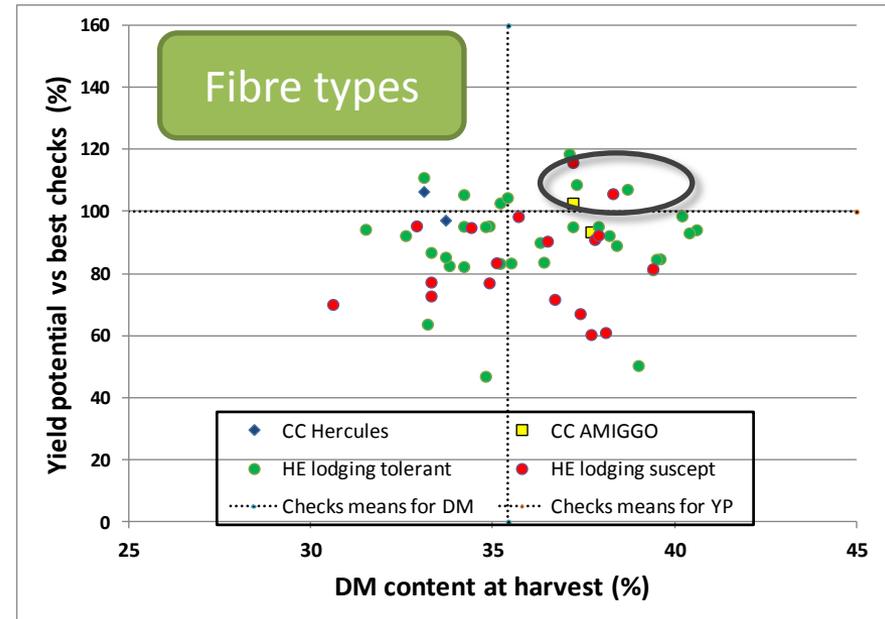
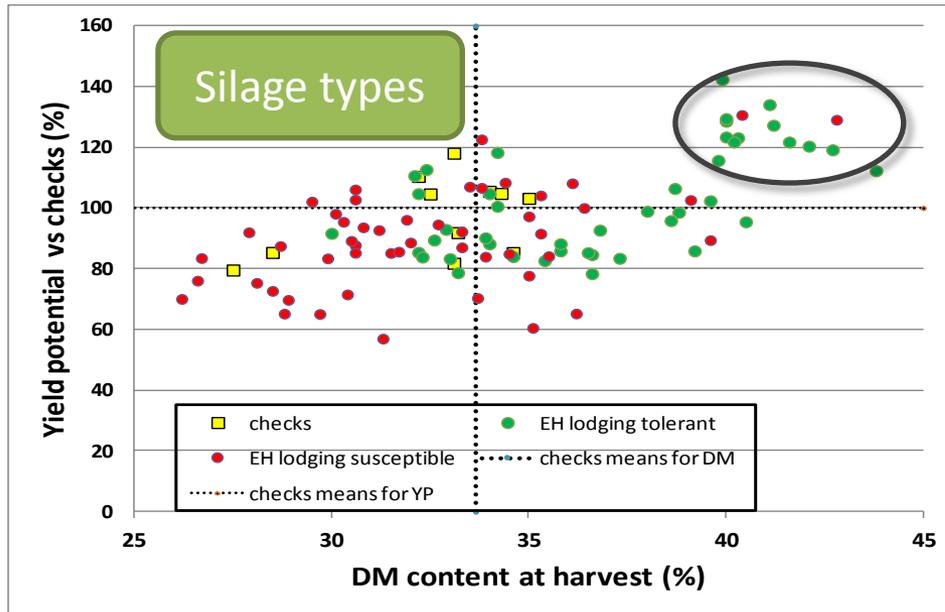
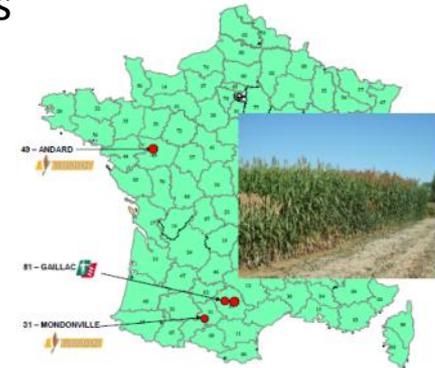
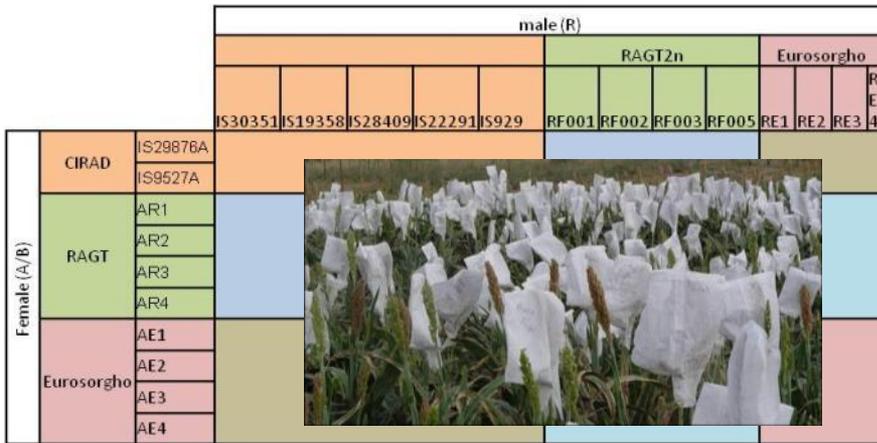
[Lignins] mg/g MS



✓ Dough grain stage (D5 : after recovery period) : G effects, but stress effect only on lignin

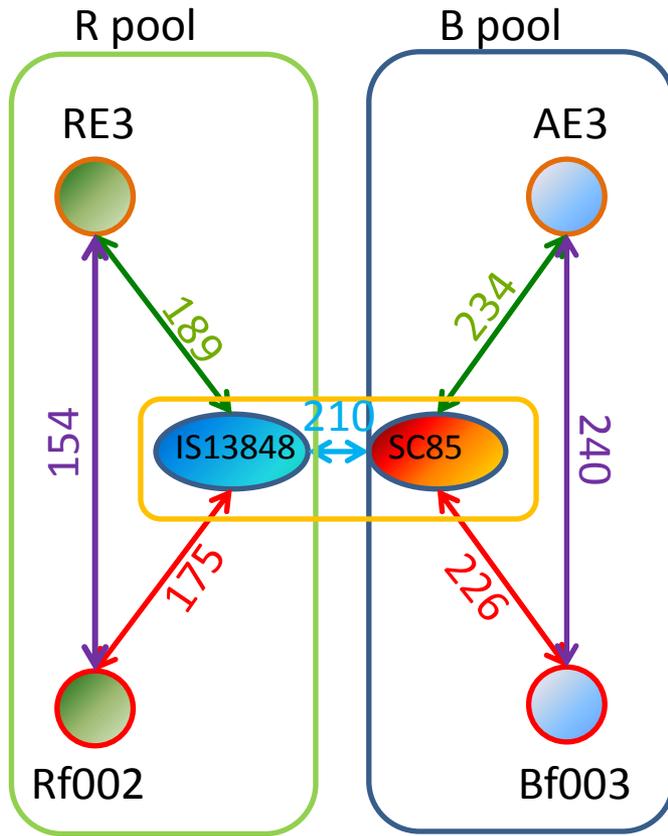
Breeding for biomass . 1- « rapid » 2G hybrid development

2014 : 4 sites, 6 trials, 150 hybrids, 26 parental lines

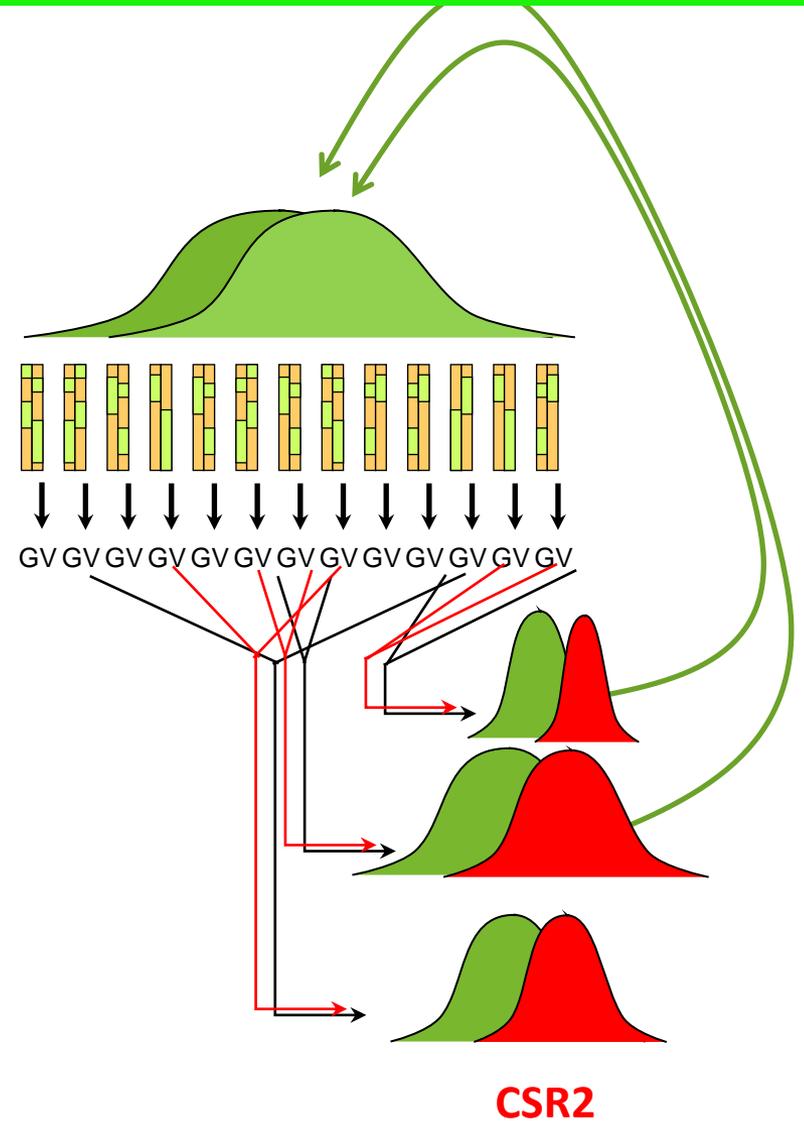
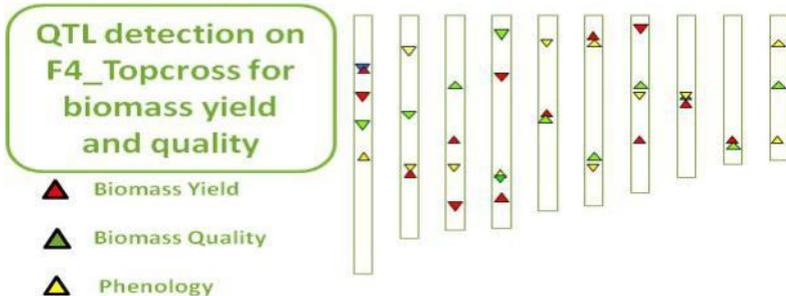


• **Biomass quality also taken into account** : 25 hybrids will be evaluated in 5 sites (5 controls) (1 site : biochemistry + histology + bmp assesment)

Breeding for biomass . 2- Breeding new parental lines for 2G



•Phenotyping in 2016

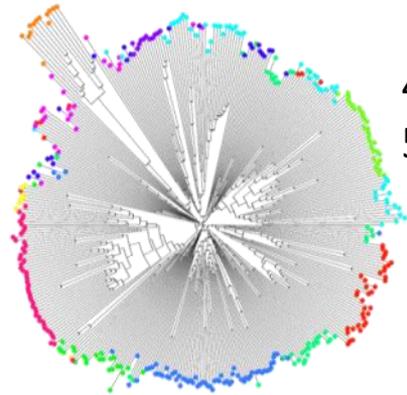


Breeding for biomass . 3- Develop new parental lines for other end-products – World Wide GWAS

Poster I.
Vilmus



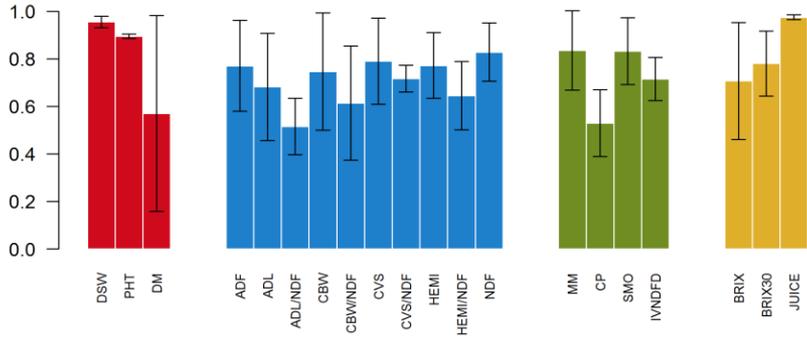
- Identification of biological ideotypes on-going
- Need for broad based populations : GWAS



413 accessions
5 trials (100 - 362 genotypes)

- 2 Montpellier
- 2 Mali
- 1 Mali Off Season

Heritabilities

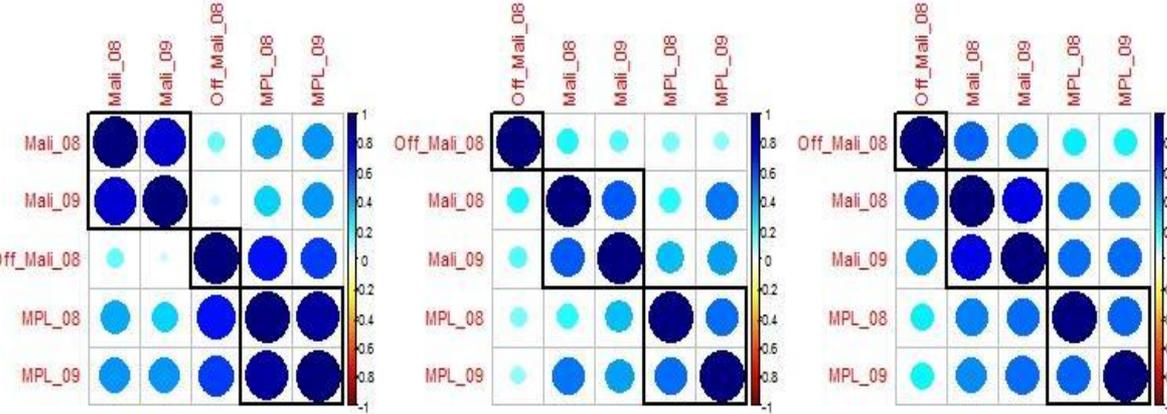


Trials correlations

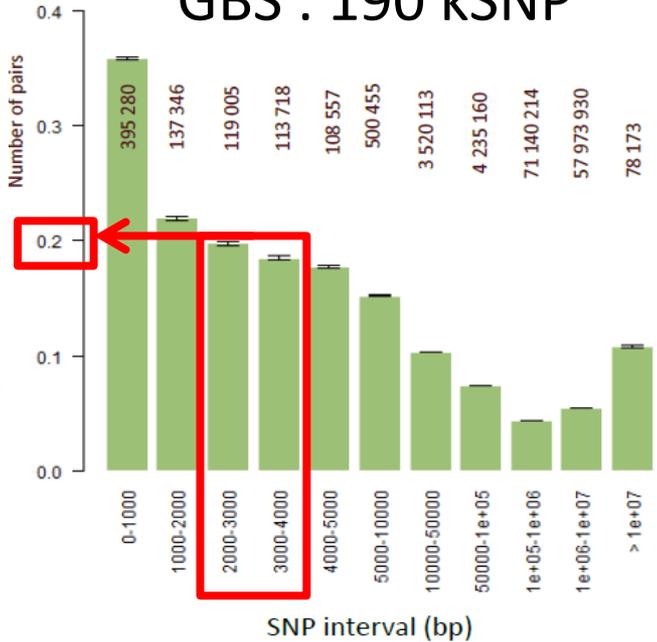
Flowering

adlSndf

IVOMD



GBS : 190 kSNP

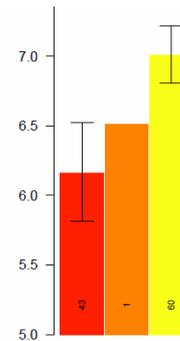
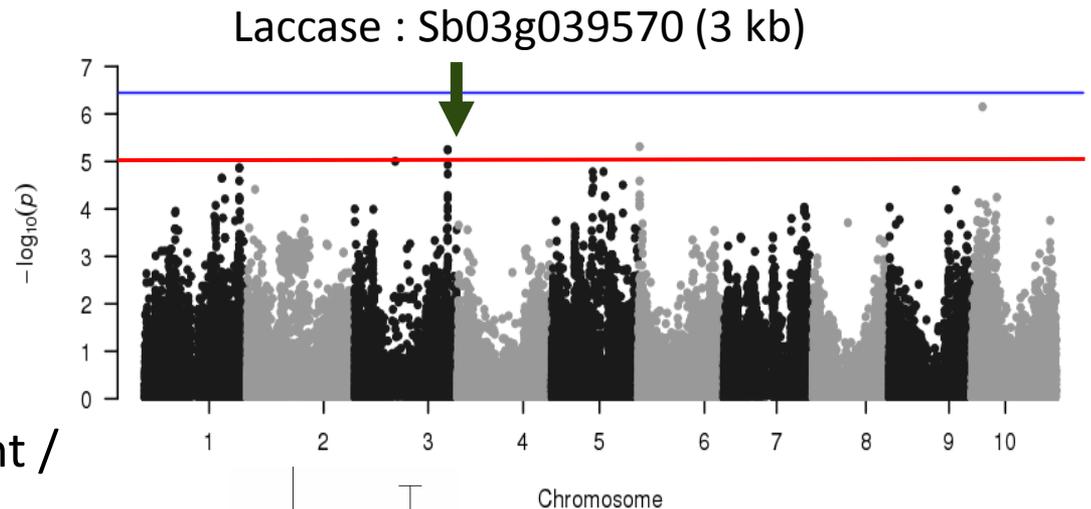


Breeding for biomass . 3- Develop new parental lines for other end-products – World Wide GWAS

•Trial per Trial : $-\log_{10}Pvalue > 5$

Meta-phenotype	Association	CG < 100 kb	SNP < 5kb
Dry matter production	18	8	1
Cell Wall composition	85	43	26
Animal digestibility	50	19	6
Sugar and juice production	18	8	1

•GWAS for *adlSndf*



Zhao et al 2013 : Arabidopsis

Dhugga et al 2011 : Maize US patent

•Most do not colocalize with Height / flowering

•A few replicated associations

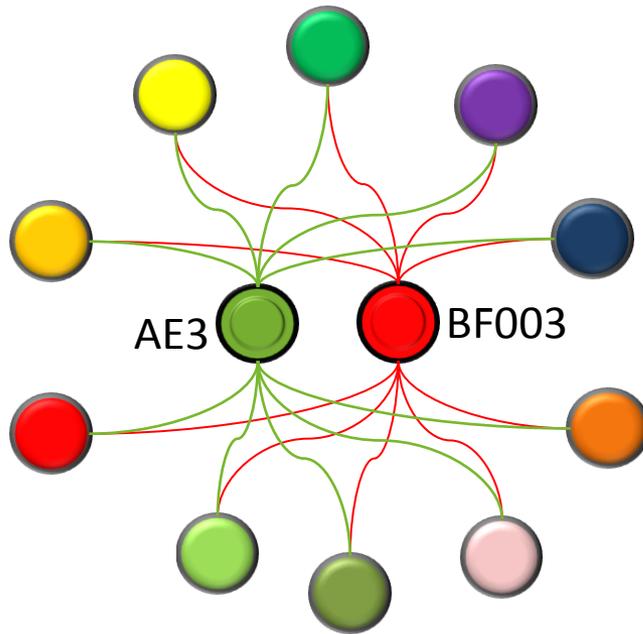
- $-\log_{10}Pvalue > 5$ in 2 trials: *cvsSndf* : (TF)
- 15 associations with > 5 and > 3 in different trials : 9 genes

•Development of new panels on-going : Non Photoperiodic / Photoperiodic (200)

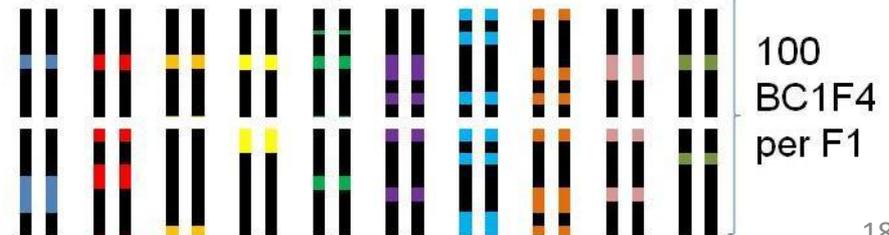
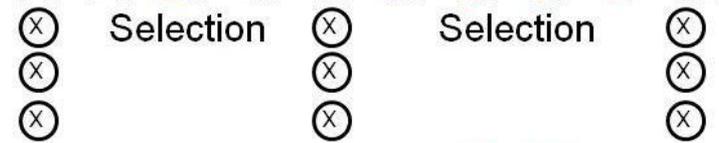
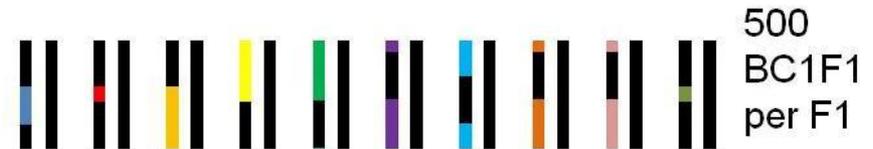
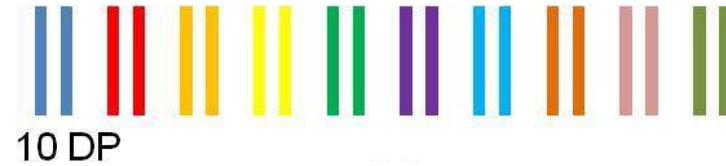
○ Avoid Major genes effects

○ Non Photoperiodic : 2014 : Irrigated (167 topcross), 2015 : WW vs WD (185 topcross)

BCNAM design 1 : a B BCNAM design dedicated to Biomass



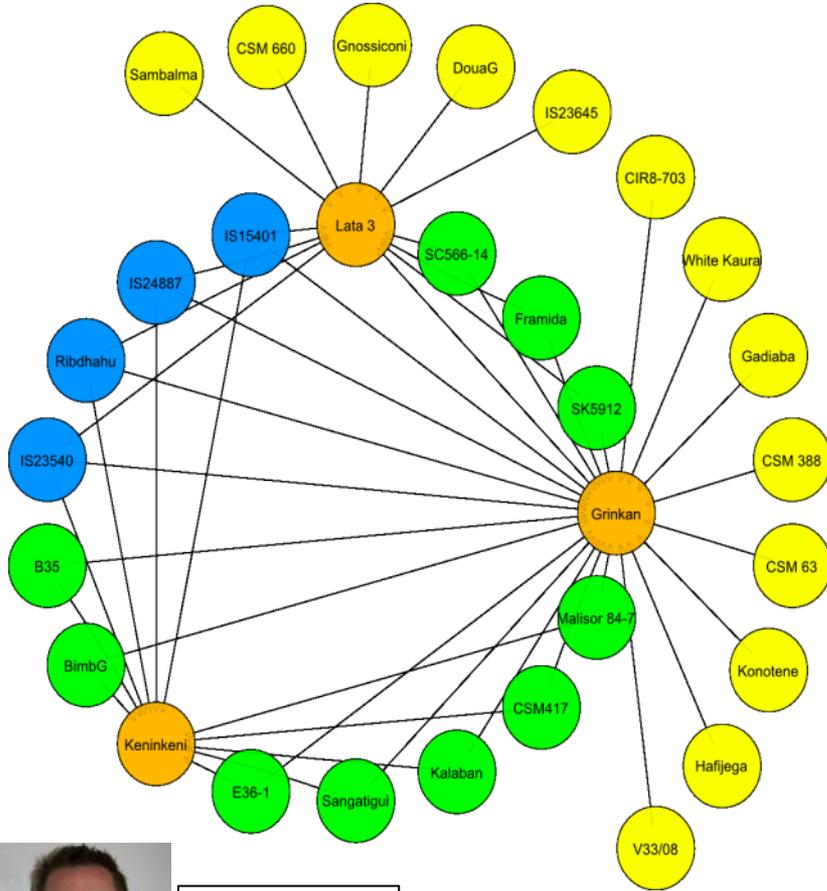
Accession	race	B/R	Trait
BN 612	C	B	Low lignin : Bmr (6 : CAD + 12 : cOMT)
CSL 09-712-2	C	B	Low lignin : Bmr 8 (not yet cloned)
IS 30400	C	B	High lignin, high biomass yield GCA
SSM1057	Gma	B	Diversity optimization
IS30417	BC	B	High lignin
IS29876	C	B	Diversity optimization
IS29407	KC	B	Diversity optimization
SC532	G	B	High Cellulose
SC59	GC	B	High Cell ulose and CWD
SC605	Gma?	B	High Cellulose
IS22332	KC	B	Low lignin
SSM 1284	B	B	Diversity optimization
IS 5972	D	B	Diversity optimization



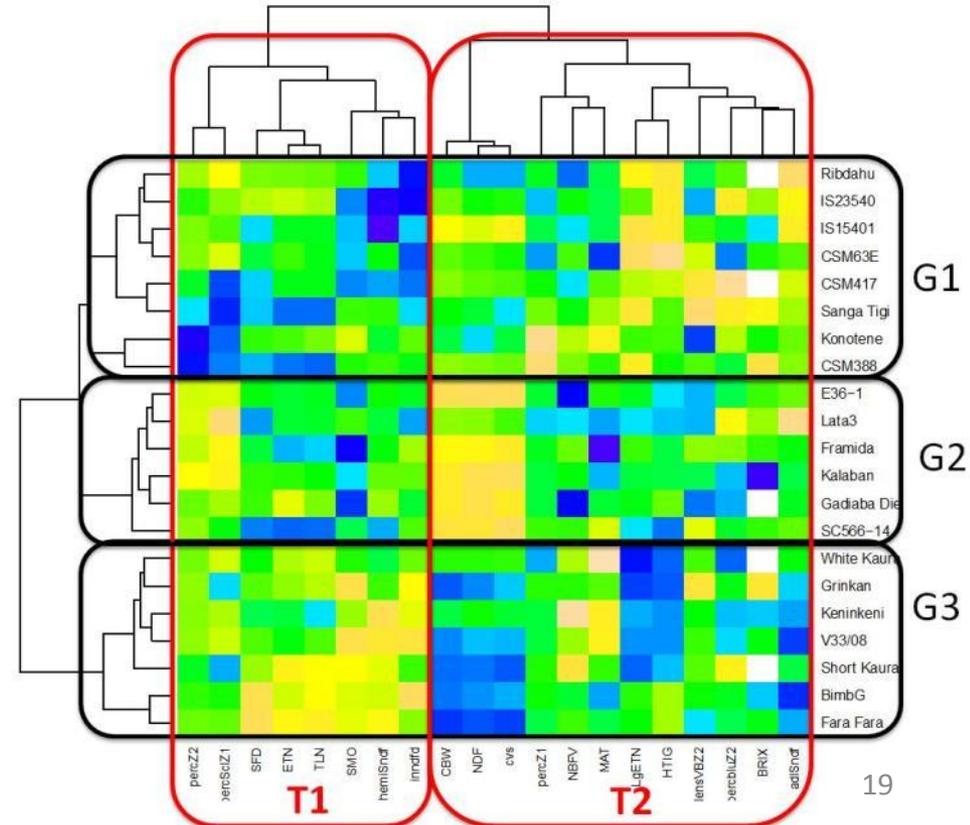
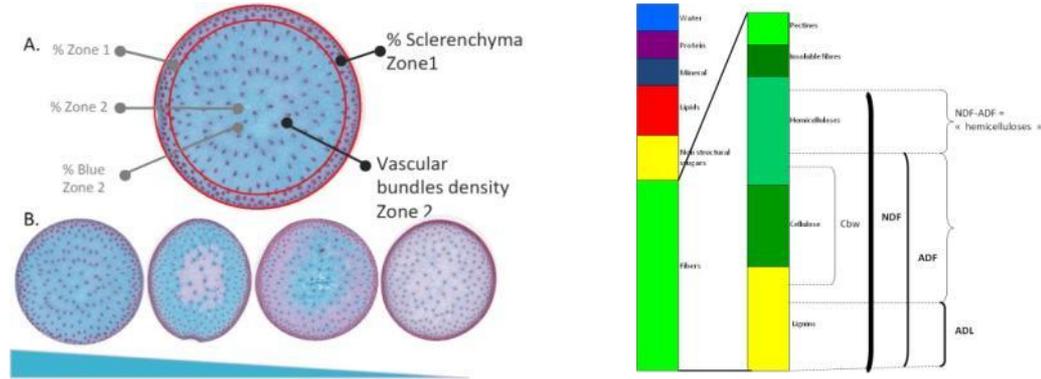
BCNAM design2 : GCP BCNAM design targeted to soudaneo sahelian region but not only !!!



Poster K.
Thera

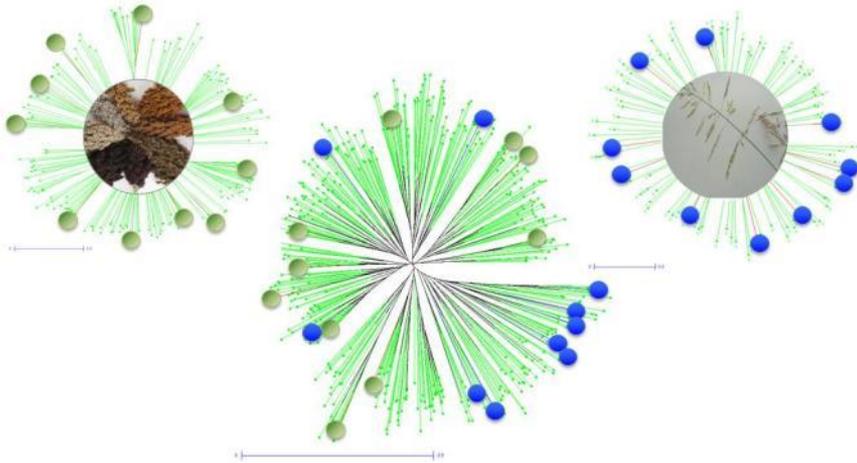


Talk B.
Guitton



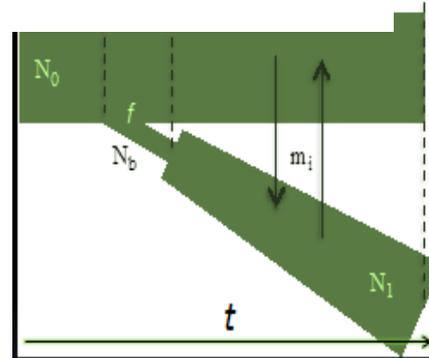
Biomass genetic control : insights from evolutionnary genetics

Domestication



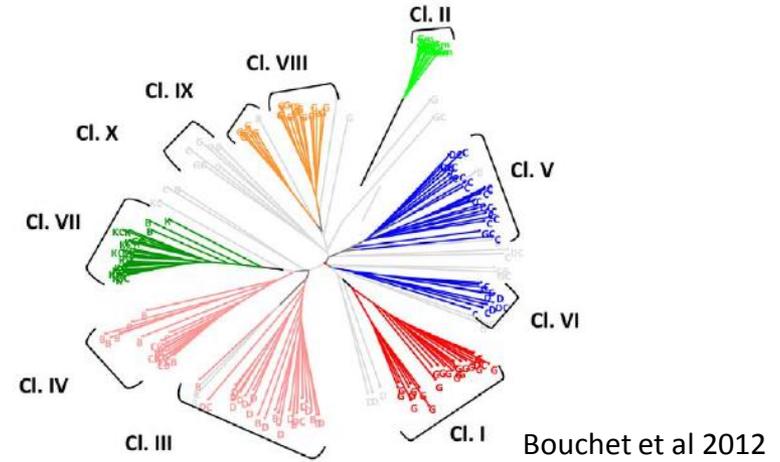
14,784 genes

SNP	Number
Wild	173 042
Specific to Wild	92 304
Cultivated	105 707
Specific to cultivated	25 919
In Wild and Cultivated	79 360



Gene	Theta_CultvsWild	Kst	Tajima's D Cult	Tajima's D Wild
Sb02g025080	no	yes (lower)	no	no
Sb04g015850	no	yes (lower)	no	no
Sb03g031860	no	yes (higher)	no	no
Sb03g034850	yes	no	no	no
Sb10g001970	yes	no	no	no
Sb01g035380	no	no	no	yes
Sb01g040750	no	no	yes	no

Cultivated diversity



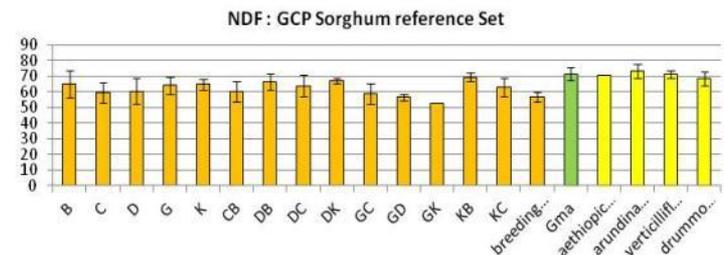
Bouchet et al 2012

Fst « Genome » Scan

1122 DArT markers

33 outliers, 26 (<5kb from gene)

Diversifying selection : 3.3 kb from Beta D xylosidase 4. Guinea margaritifera is the most differentiated :





- + Lisa Perrier (PhD)
- + Ingrid Vilmus (Post Doc)
- + Vaksman Michel
- + Serge Braconnier



Denis Bastianelli
Laurent Bonnal



Yves Barrière



Herman Höfte



Anne Bergeret
Nicolas Le Moigne
Stéphane Corn
Jean-Charles Benezet
Lata Soccalingame (Post Doc)



Patrick Navard
Loan Vo
Lucie Chupin



Laura Rossini (Coord BIOSORG)
Maria Rosaria Stile
Noemi Trabanco (Post Doc)
Martina Balboni



Raffaella Battaglia



Niaba Teme
Korotimi Thera (PhD)
Mamoutou Kouressi



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