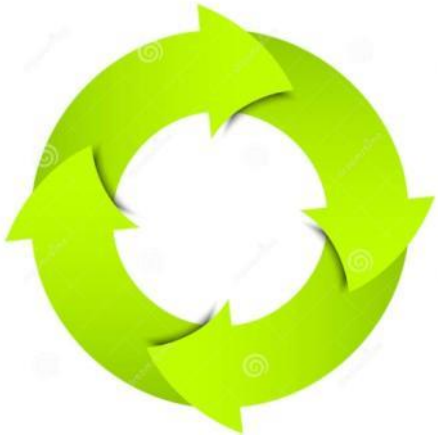
A Sorghum Stem Biomass Quality Genetic Atlas

Integrating GWAS, Multiparental Designs and Transcriptome Analyses



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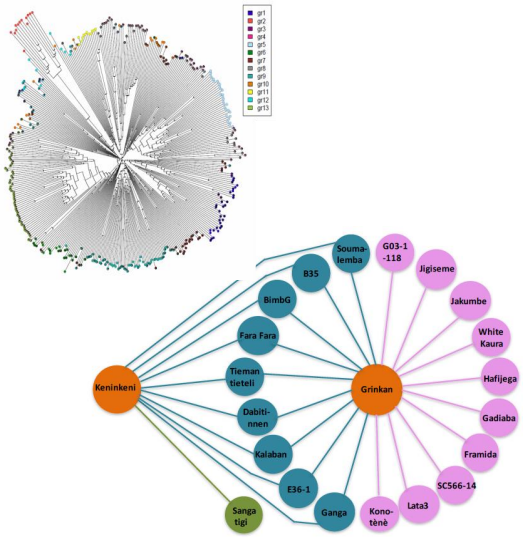
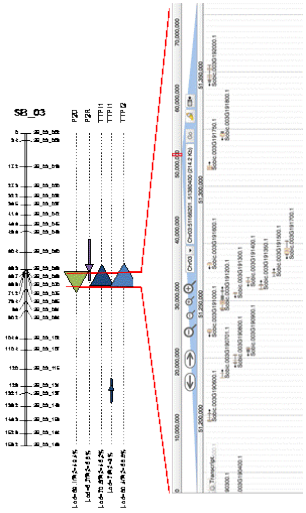
agap cirad

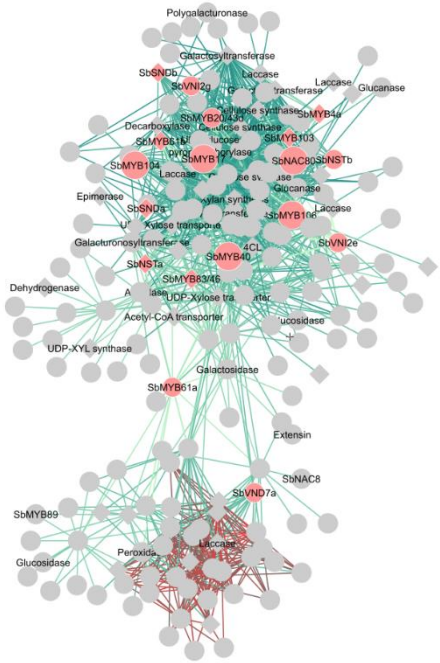
Genetic architecture of stem biomass quality

Genomic regions identification

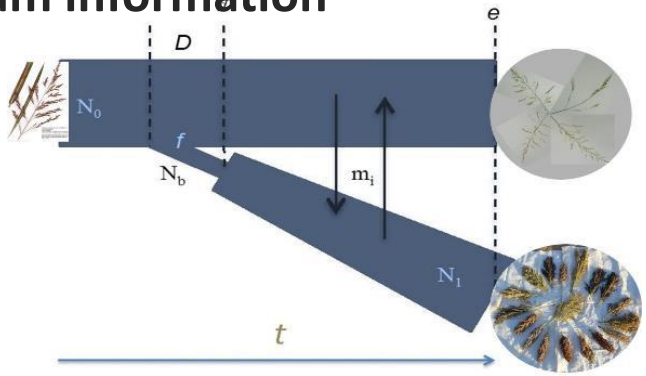




Transcriptome regulation



Combining Maize and sorghum information



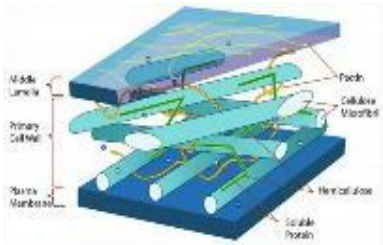
Why we care about stem biomass composition and structure ?

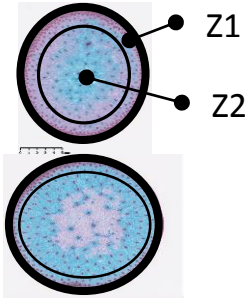
- **The stem :**
  - The support of grain production
    - Lodging
    - Carbon allocations to vegetative vs reproductive organs
  - Large proportion of the whole aboveground biomass
  - Used for feed, energy, plant derived materials

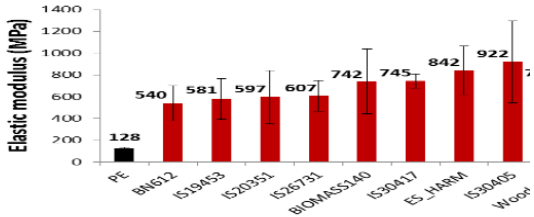
- **A matter of composition**
  - Feed quality
  - Energy yield
  - Fiber re-inforced material properties
  - Communication between grain and stem (T6P…)

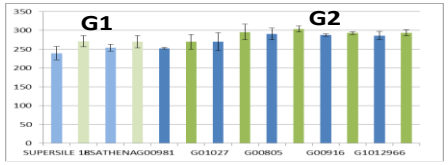
- **Biomass composition is not easily accessible, and the target ideotypes are not always clearly defined**

Biomass value chains :
Yield is still THE key, but others players are acting

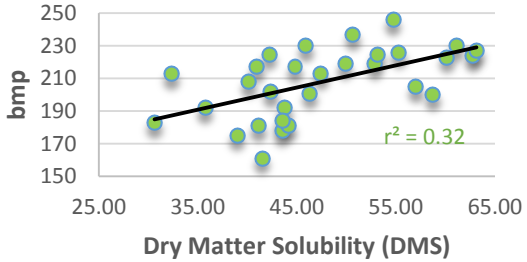


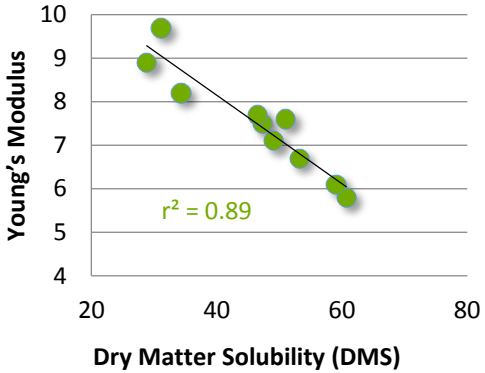






	bmp
Lignin	-0.61
Perc_bluez2	0.55
DMS	0.57



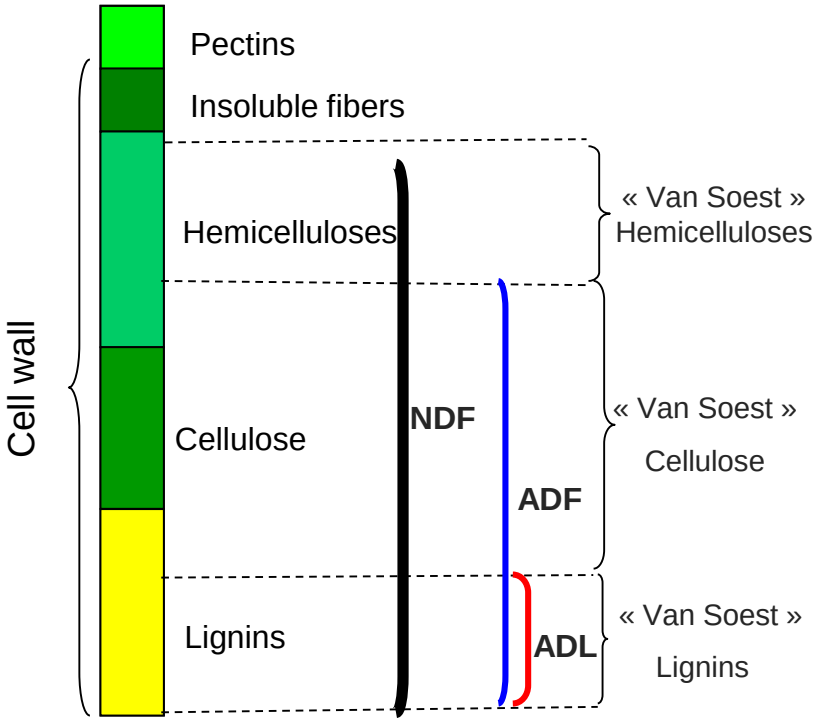


	Young's Modulus
DMS	-0.95
Perc_bluez2	-0.87
Lignin	0.77

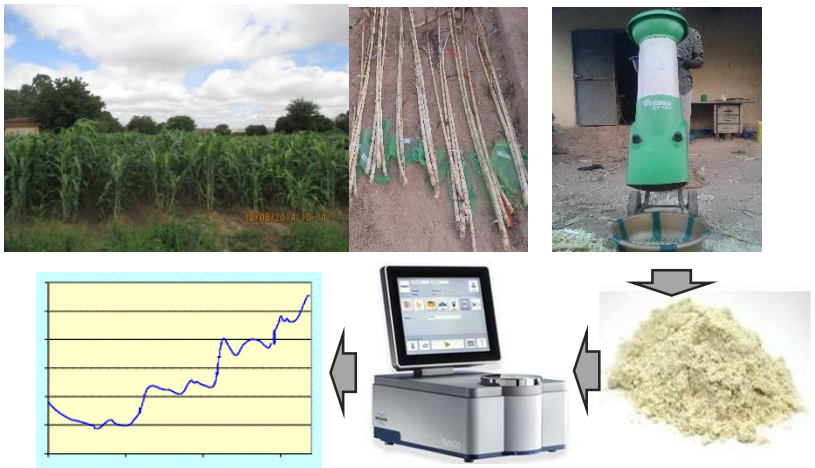
- **Lignin <u>is one of the</u> key traits that contribute to the end products properties**

Characterizing stem biomass quality : increasing the throughput

- **Van Soest Method**



- **Aufrère Method**
  - Dry matter digestibility
  - Cell wall digestibility



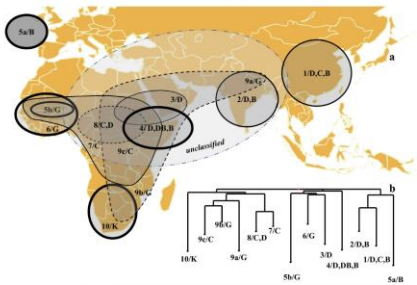
- **Stem : 700 reference data points**

- **Silage / mature stages and developping stem**

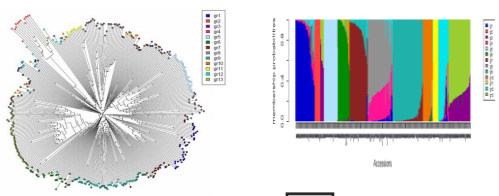
Genetic architecture : Taking advantage of broad based panels

- **World Wide panel**

3367 accessions

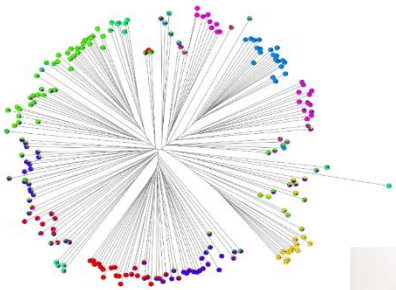


413 accessions



- Line value phenotyping
- 5 trials (100 - 362 genotypes)
  - 2 Montpellier
  - 2 Mali
  - 1 Mali Off Season

- **Non Photoperiodic biomass panel**



- No dwarf gene segregation
- High biomass yielding genotypes
- Diversity coverage

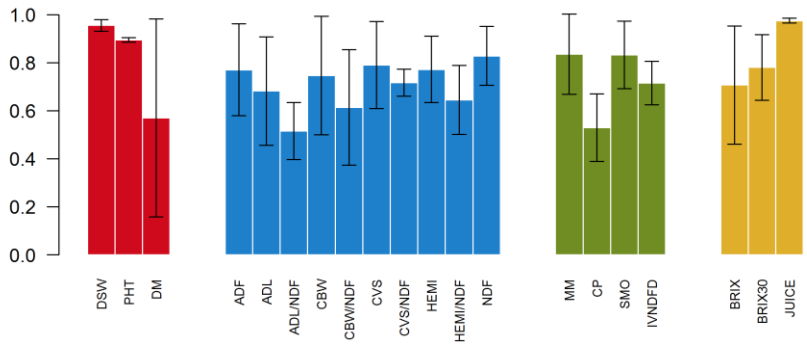
Ingrid Vilmus PostDoc

- Top cross phenotyping
  - 1 tester : high GCA for biomass production

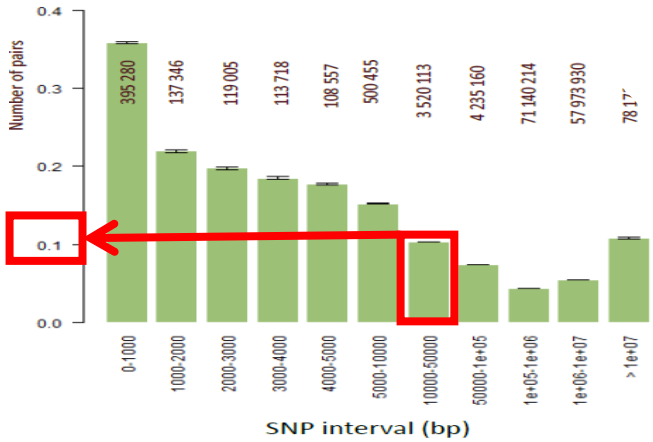
Year	Accessions	Treatment
2014	167	Well Watered
2015	185	Well Watered

GWAS : A set of candidate regions detected

- H^2bs

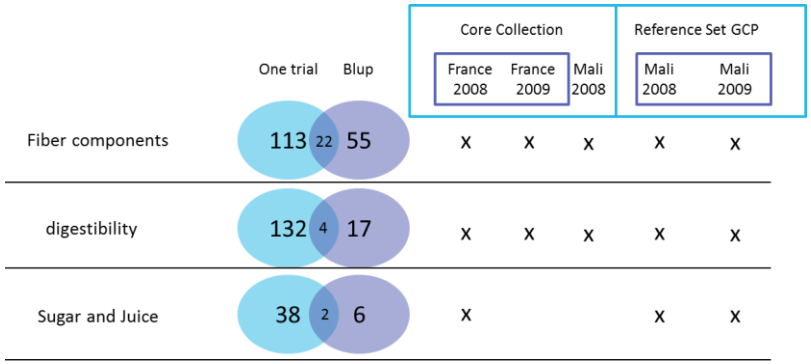


- LD<0.1 : 10 -50 kb



- GWAS : LOP>5 in one trial at least in an other one> 3, and LOP5 for BLUP

- World Wide panel



- 93 genomic regions: 321 genes

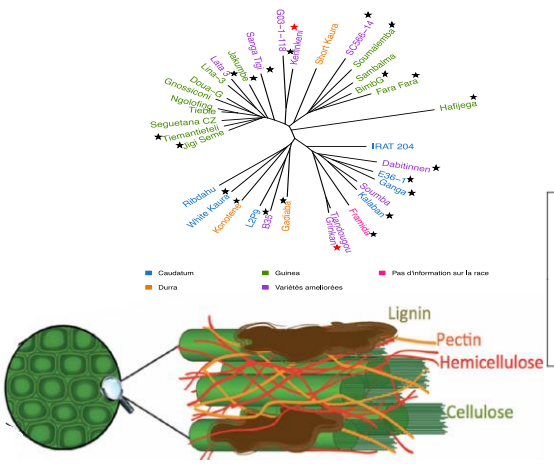
- Non photoperiodic panel

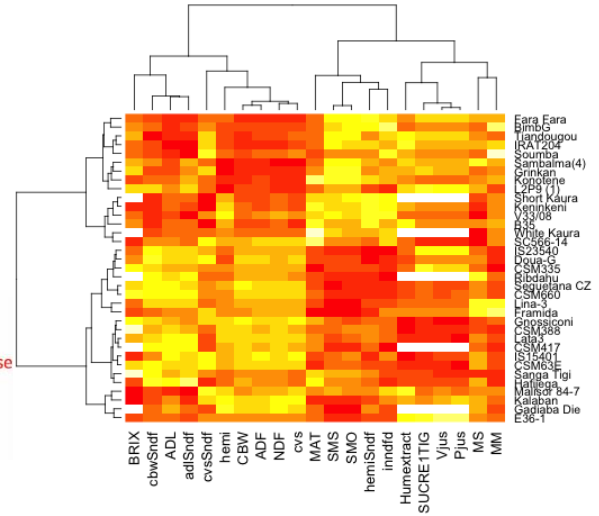
- 55 regions detected: 146 genes

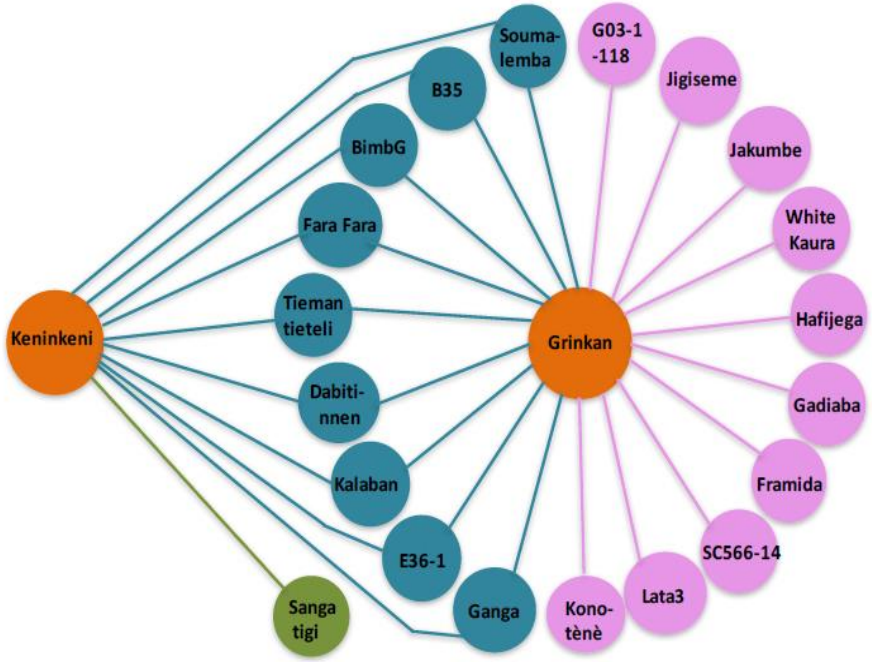
Gene lists comparison coming soon

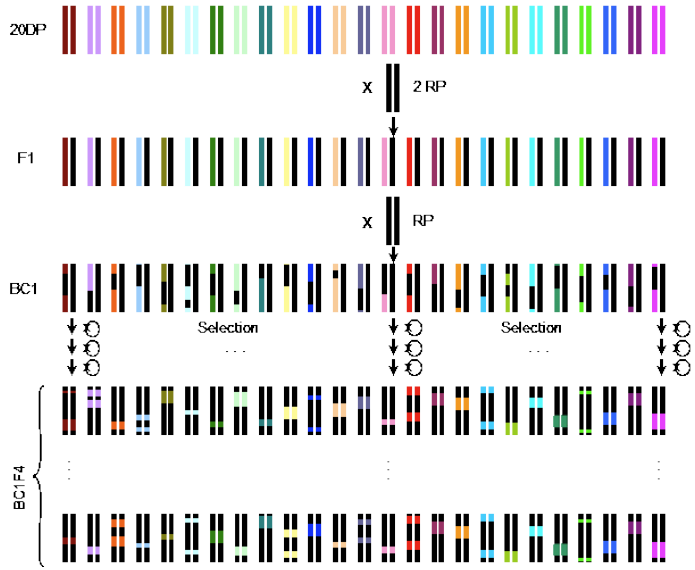
Developping a Back Cross Nested Association mapping population targeting the sudano sahelian region

- **2 recurrent parents (Elites)**
- **20** donors
- **29** populations







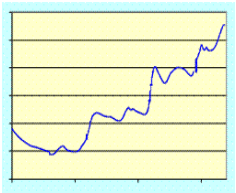


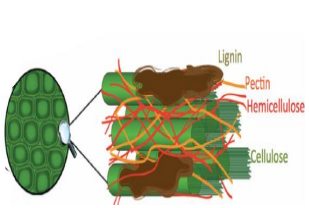
Korotimi Thera PhD

- **1400 BC1F4 obtained (50 /cross)**

Stem quality phenotyping of the BCNAM population

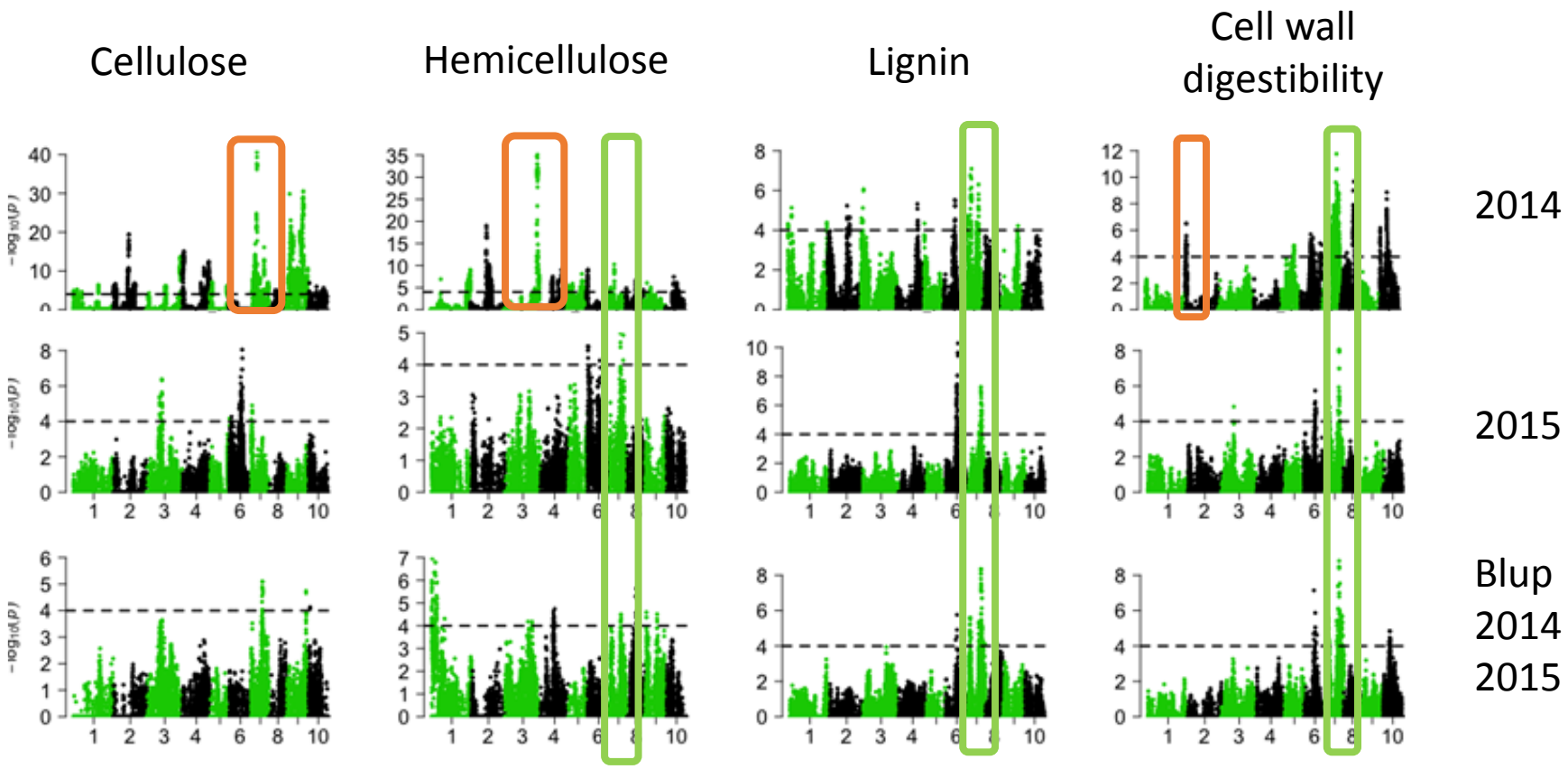
- 2 years
- 1 sowing date
- 5 plants/BC1F4





Genetic architecture in the BCNAM population

- **Genotype-Phenotype association : LOP>5 in one trial and at least 3 in an other one, and LOP5 for BLUP**



- **43 unique regions: 182 genes**

A lack of consistency / A "complementarity" between the different designs

- **632 genes underlying the associations detected**
  - Only 2 genes are common between the 3 panels
    - Sobic.006G145000
    - Sobic.006G144900
  - 13 genes are common between 2 panels
    - Sobic.006G144300
    - Sobic.006G144500
    - Sobic.006G144600
    - Sobic.006G144700
    - Sobic.006G144800
    - Sobic.006G145400
    - Sobic.004G269900
    - Sobic.004G270000
    - Sobic.004G270100
    - Sobic.004G270200
    - Sobic.004G270400
    - Sobic.003G365000
    - Sobic.003G364900

D locus

Casto AL et al., 2018, Fujimoto M et al., 2018, Xia J et al., 2018

Worldwide **Non photoperiodic panel**

hemicellulose

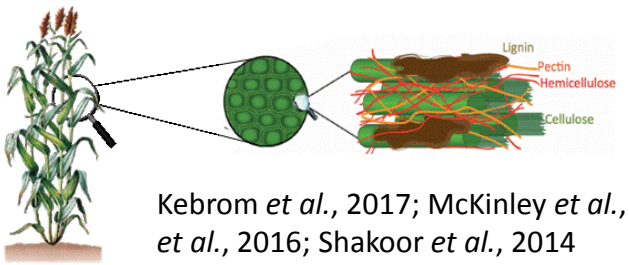
Worldwide **Non photoperiodic panel**

Cell wall composition / Cell wall digestibility

- **617 genes not matching between the different panels : discarding not relevant genes, but not only…**

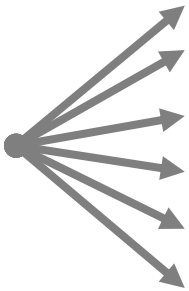
Who are these genes 632 ?

- **A cell wall structural genes library**



Kebrom *et al.*, 2017; McKinley *et al.*, 2016; Rai *et al.*, 2016; Shakoor *et al.*, 2014

655 candidate
Cell wall genes

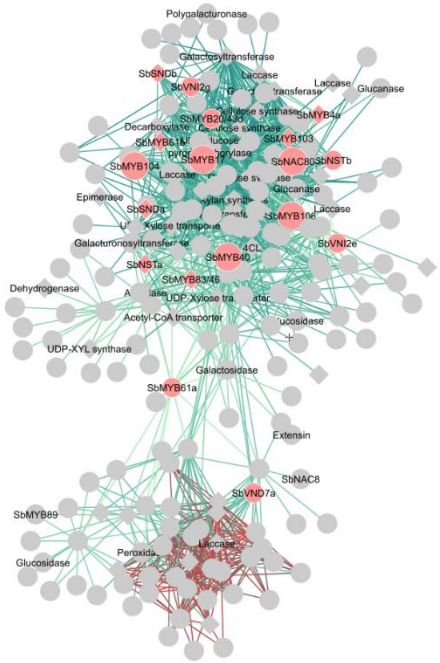


Lignin
Cellulose
Hemicellulose
Pectin
Expansin
…

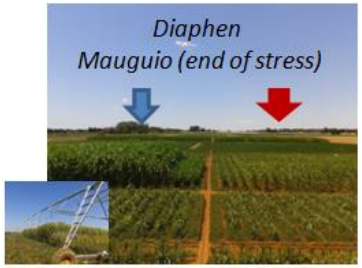
- **632 genes : Only 20 correspond to structural cell wall related genes…**

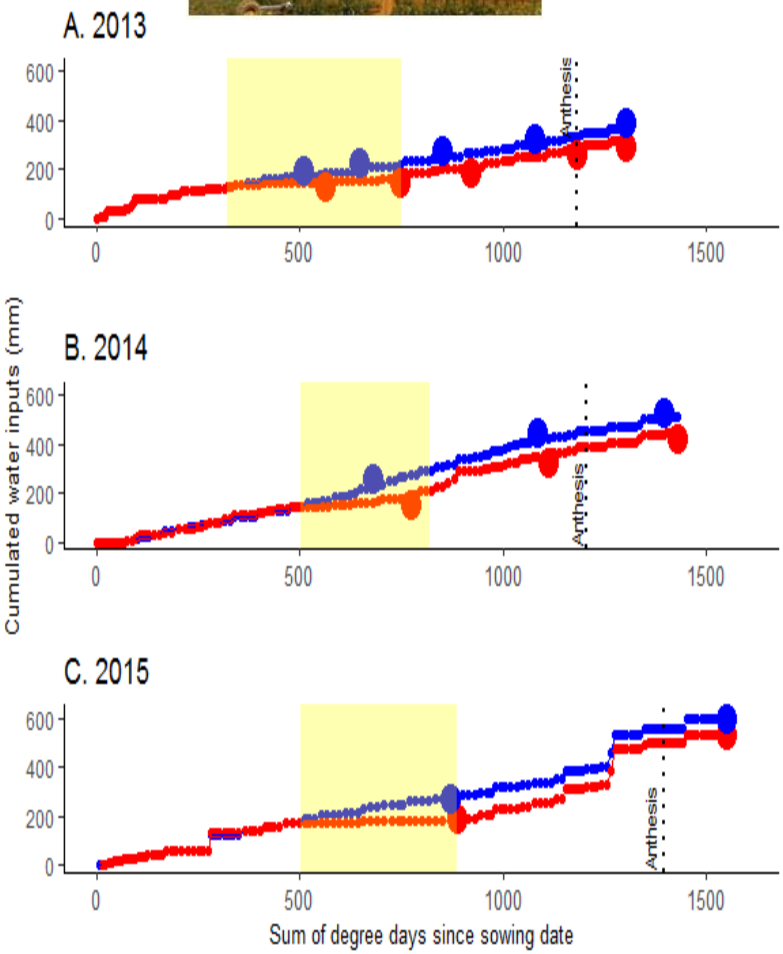
- **A need to reach a better understanding of the key players acting on cell wall establishment**
  - Cell wall gene networks identification

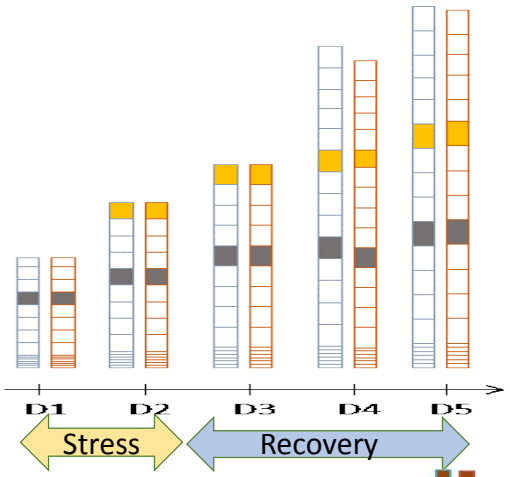
Lauriane
Hennet
PhD



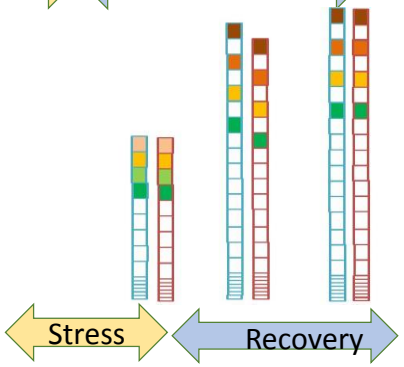
Internode development and cell wall deposition in one biomass hybrid



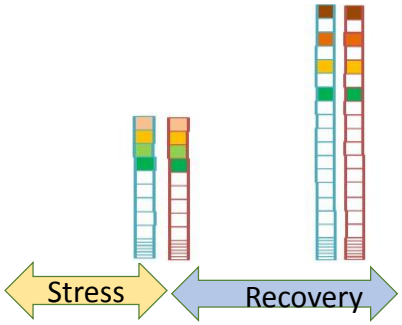




2 Internodes X 5 stages X 2 Water Treatment X 4 rep (80)

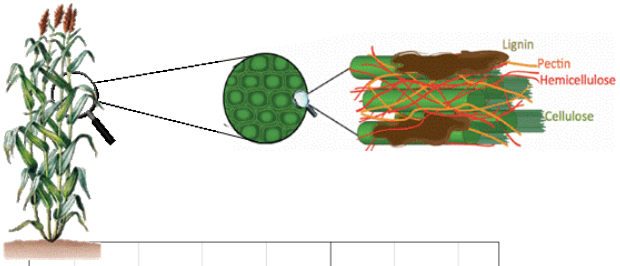


4 Internodes X 3 stages X 2 Water Treatment X 3 rep (72)

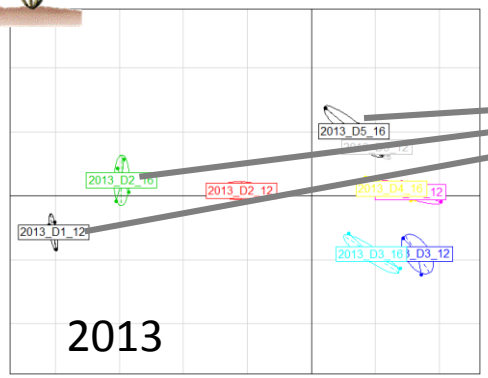


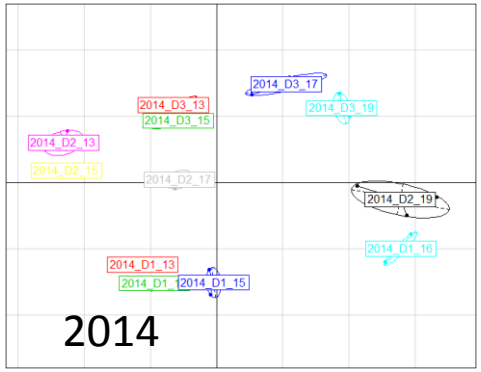
4 Internodes X 2 stages X 2 Water Treatment X 3 rep (48)

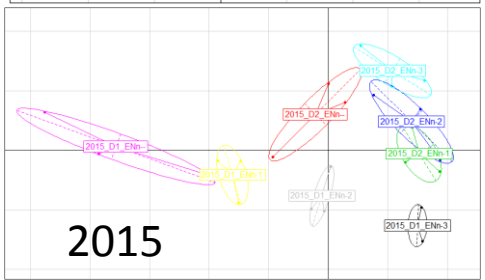
Internode composition evolution

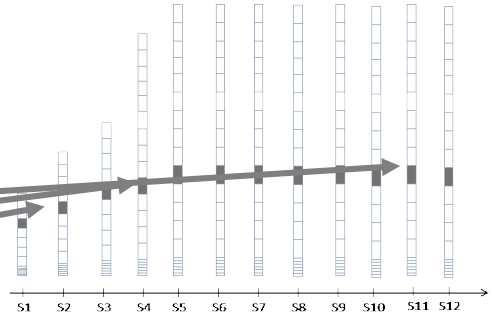


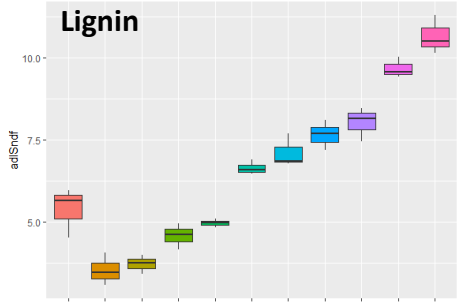
- **2017 : 11 stages analyzed for a single internode**

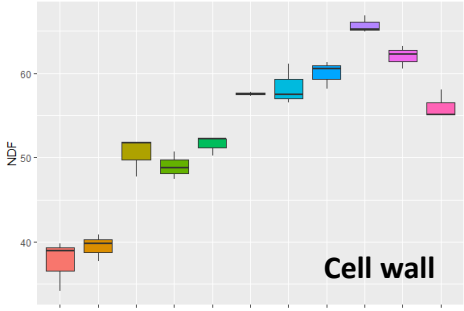


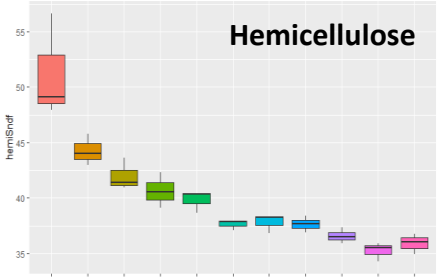


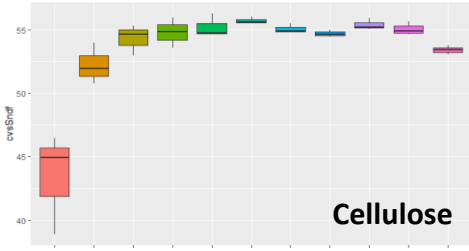


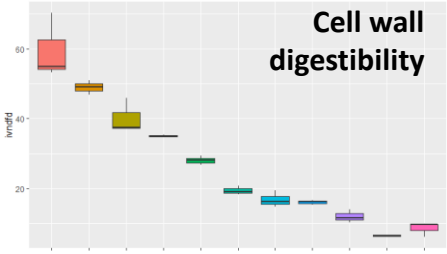










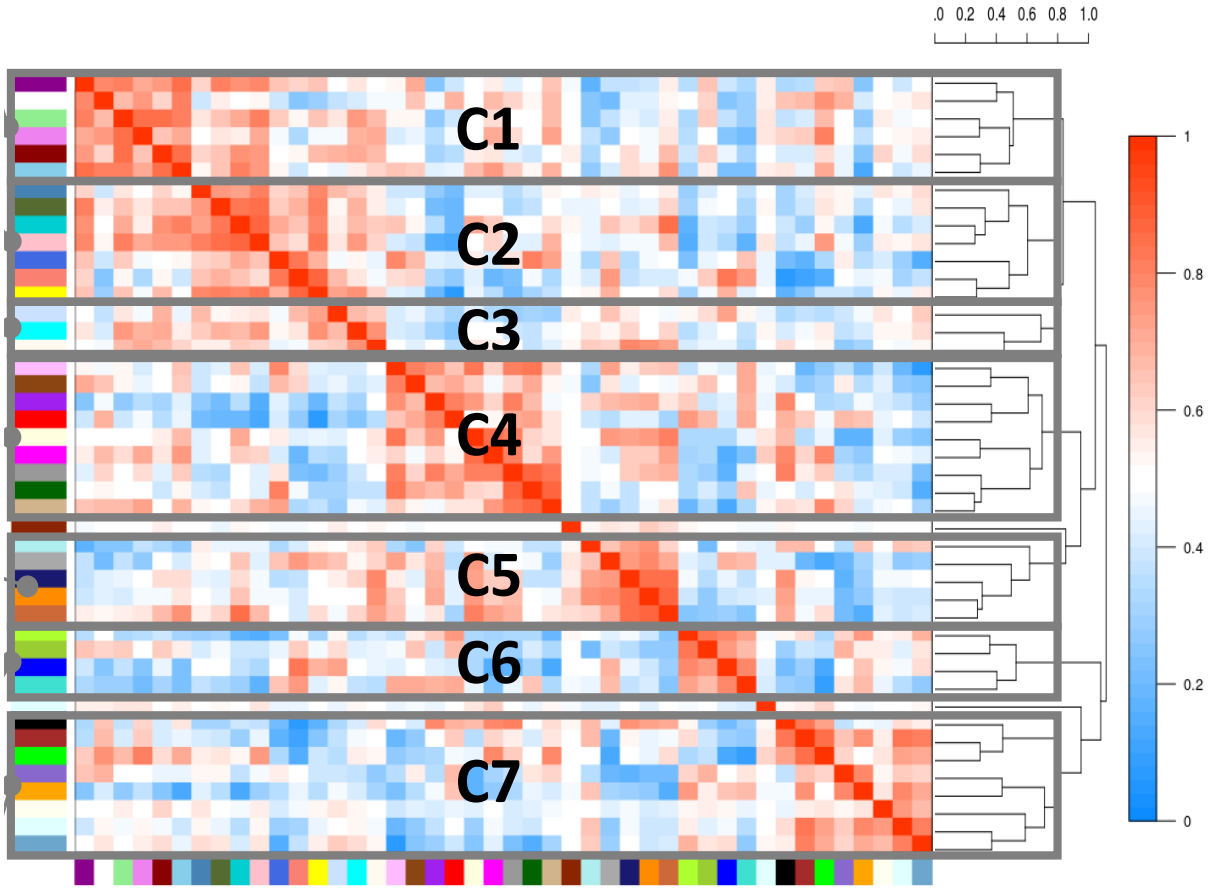


- **« Mapping » of the 2013-2015 samples on the 2017 dynamics => « data validation »**

RNAseq : Gene network identification

- **200 RNA samples produced and sequenced (in duplicate)**
  - 20 294 genes analyzed in the internodes

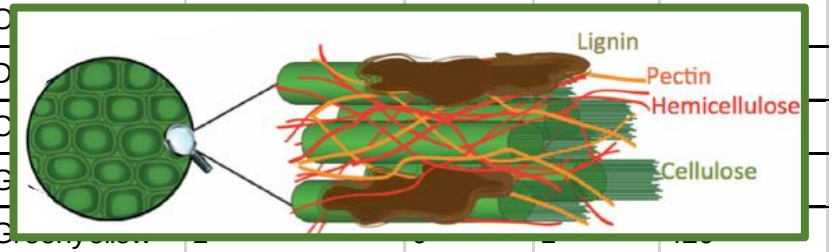
- **Gene networks construction based on all the samples (stages…)**

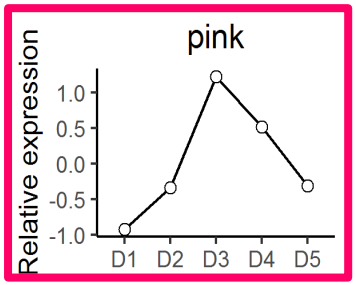


- 30 « signed » modules: 12 422 genes
- 7 clusters of gene networks sharing the same patterns

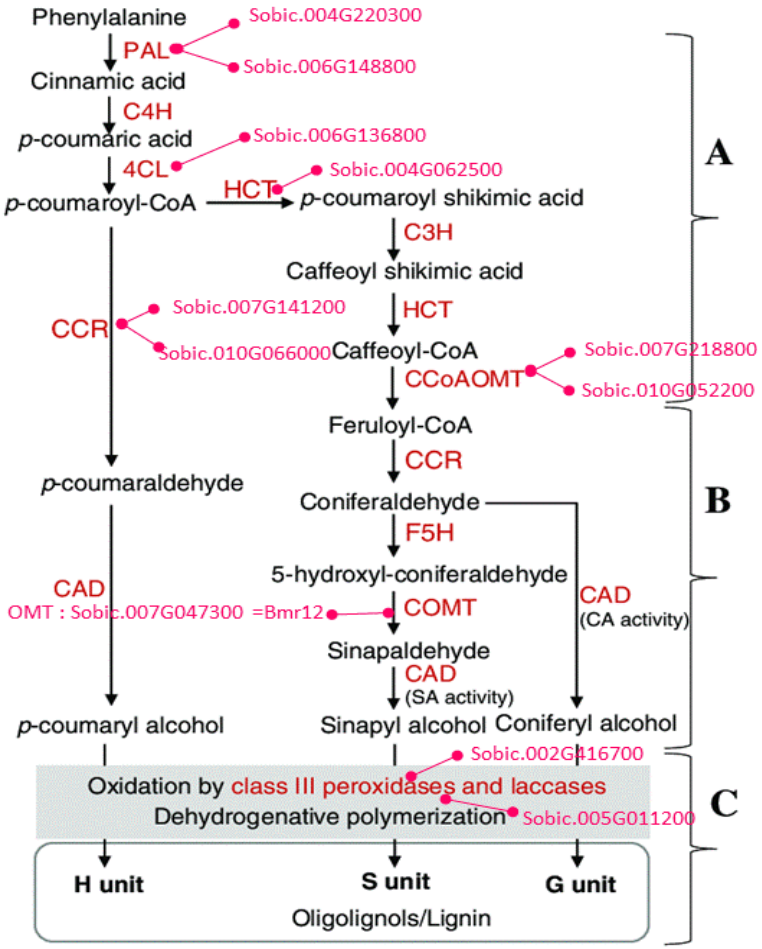
6 modules enriched in cell wall related GO-terms and genes

Module	Cell w all related enzyme list enrichment (p-value)[a]	CW related GO-terms enrichment[b]		Number of genes[c]
		BP	CC	
Yellow	$2.07*10^{-34}$	22	1	1616
Blue	$8.72*10^{-5}$	11	2	2159
Turquoise	0.00173	8	0	2855
Pink	0.0093	7	0	283
Steelblue	$6.01*^{10-5}$	6	1	52
Lightsteelblue	$1.59*10^{-5}$	4	2	9
Darkturquoise	0.16^{ns}	1	0	38
C				
D				
C				
G				
G				
Lightgreen	1^{ns}	0	1	5
SaddleBrow n	1^{ns}	0	1	5
Royalblue	1^{ns}	3	1	63



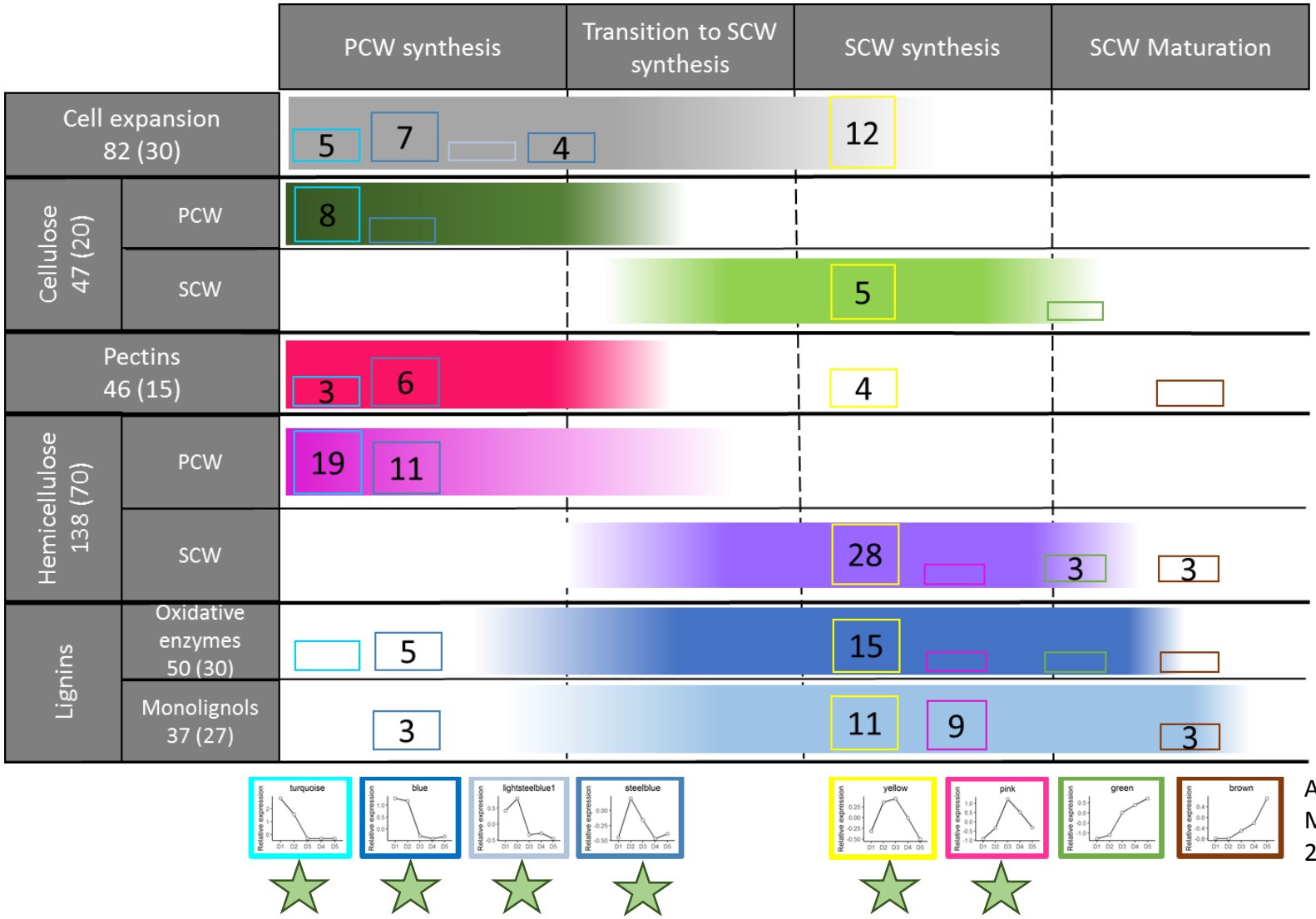


- 283 genes
- 12 structure Cell wall genes



Adapted from Nguyen et al 2016

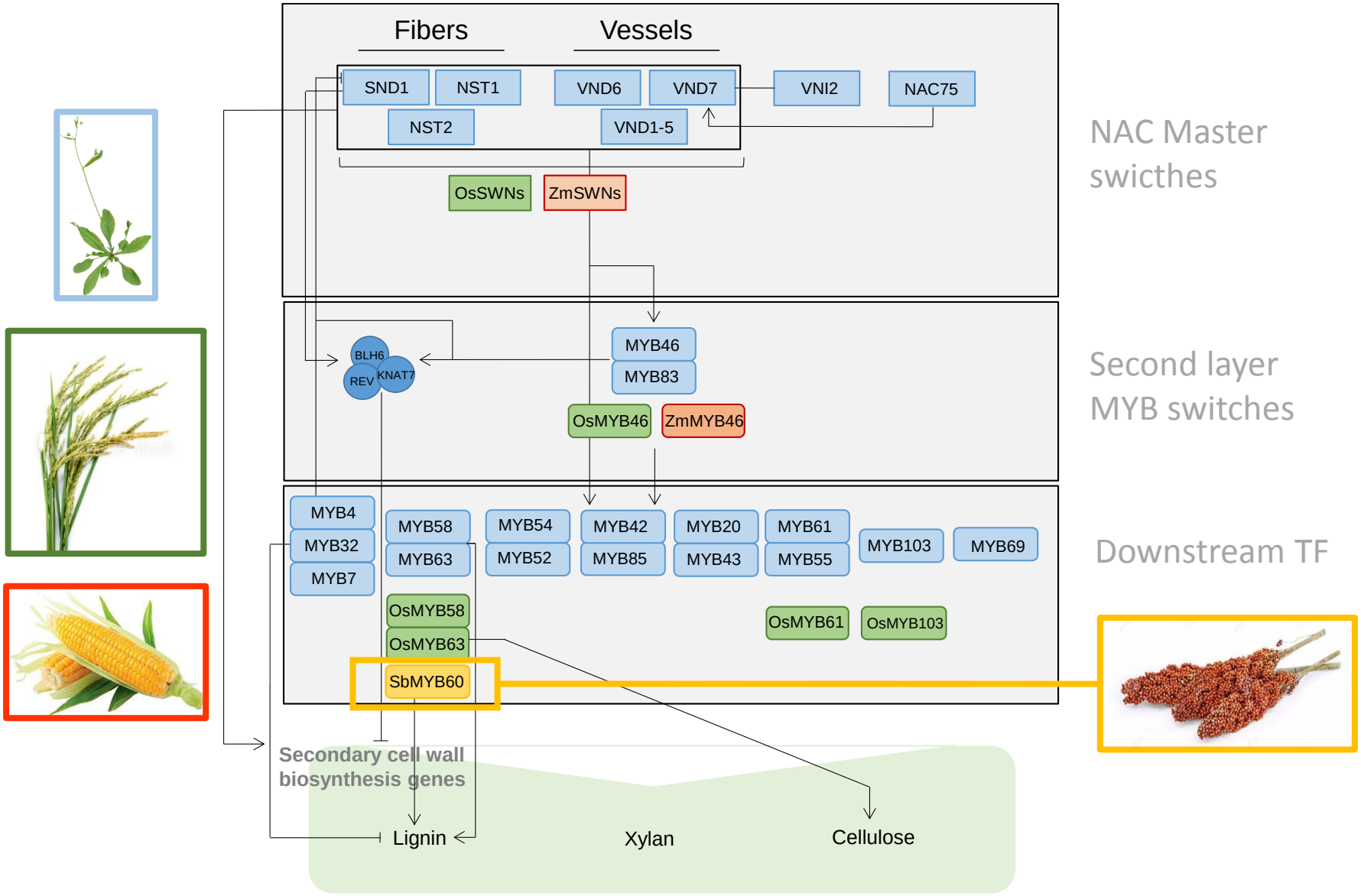
Cell wall related gene Networks : different targets and timings



Adapted from Meents *et al.* 2018

- **What about their regulation?**

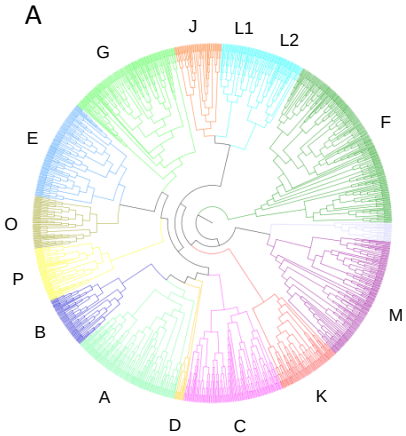
MYB and NAC are key regulators of cell wall building



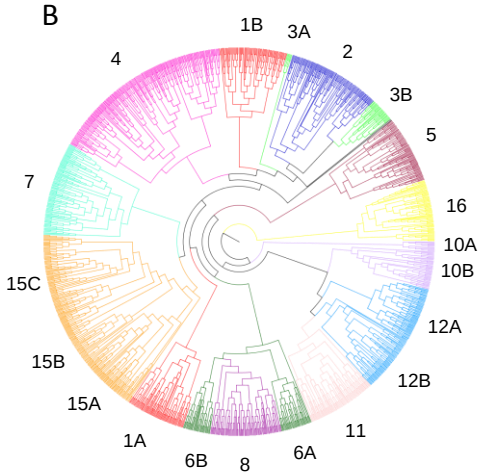
Sorghum NAC and MYB

- **Updating the Phylogenies over 9 species**

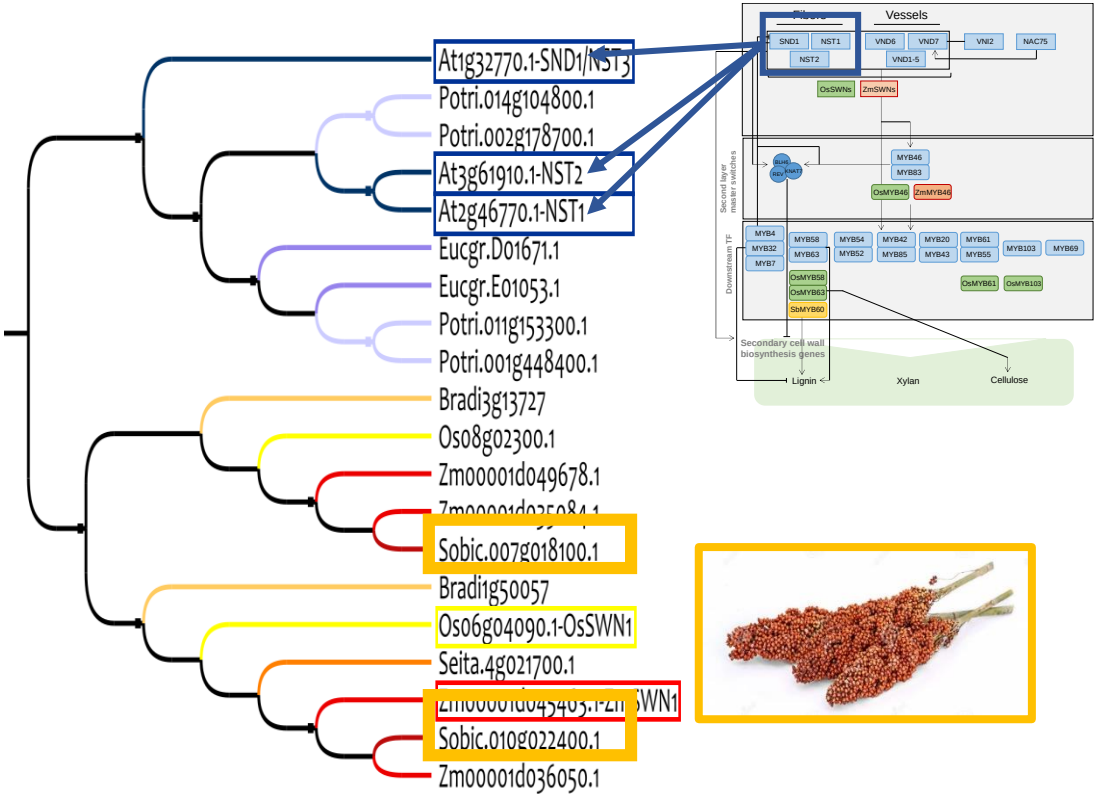
NAC



MYB

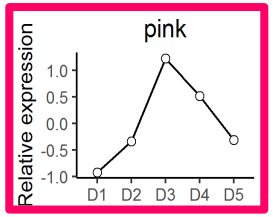


- **Sorghum homologs identification**



Adding « regulation » to the gene netwoks

- **A simplified view of the Pink network**

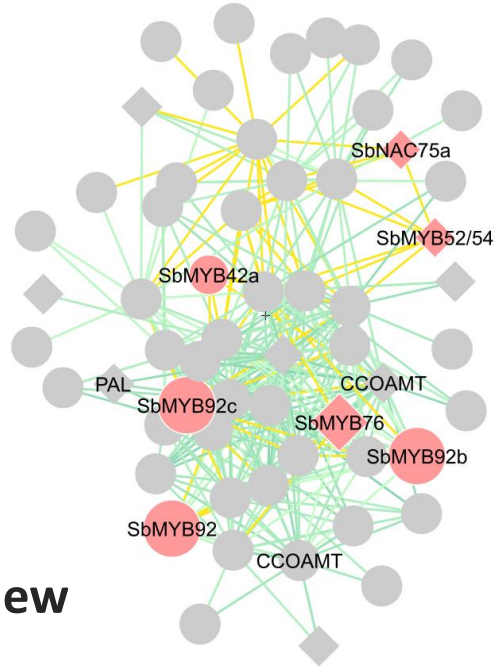


AtNAC75 Sobic.003G035100

Sobic.005g062000
Sobic.008g055800
Sobic.008g055700

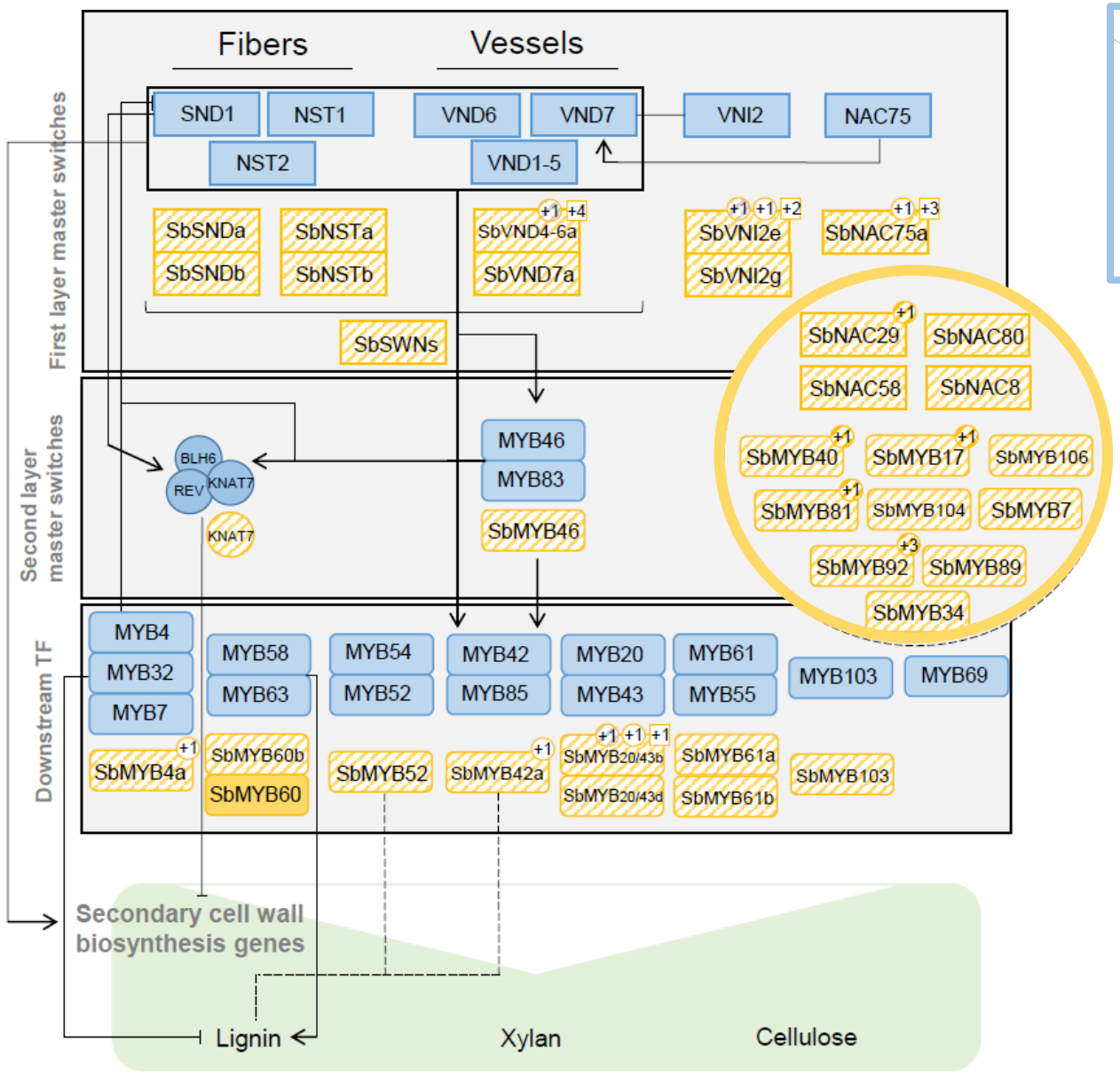
AtMYB52/64 Sobic.001g110900
AtMYB58/63 Sobic.006g199800
AtMYB42 Sobic.002g275500

PAL 4CL HCT CCR CcOAOMT OMT Peroxidase



- **A more realistic view**

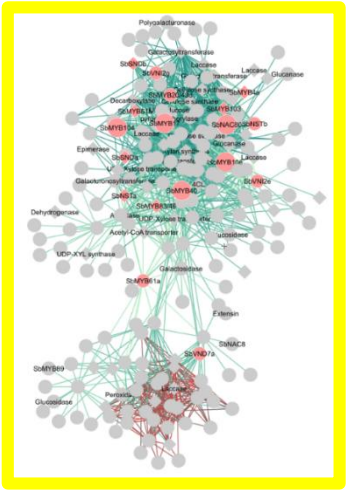
An updated « regulation » network of sorghum Cell wall establishment

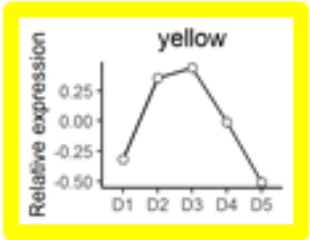
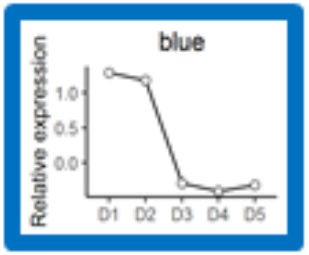
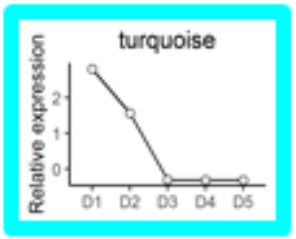


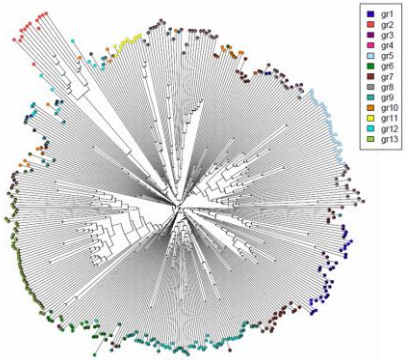
« New » sorghum Cell wall regulation genes

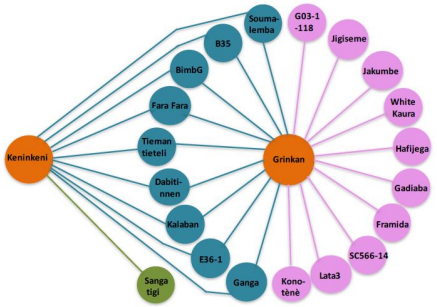
Merging quantitative genetics and transcriptomics : The global picture

- **3 networks significantly enriched in positional candidate genes**



	# Positional candidate genes
	55
	67
	65

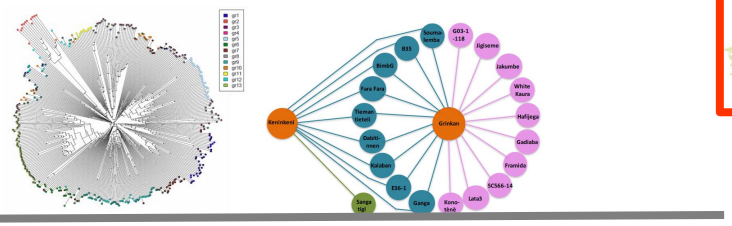


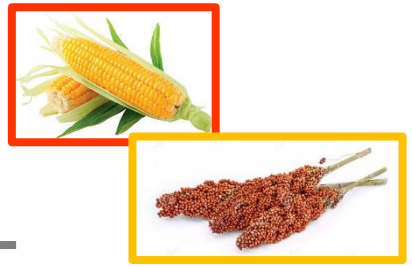


- **632 genes : ≈ 200 « expressional » candidate genes (187 in « enriched » networks)**
- **Sorting out the best candidates !!!**

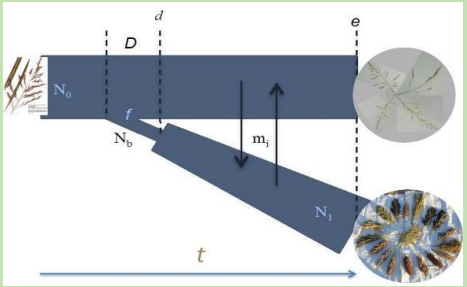
Merging quantitative genetics and transcriptomics : A focus on NAC and MYB

- **3 NAC and MYB associated with cell wall properties**





NAC Master swicthes	SbNST1/2/3	✓ Lignin	✓ Signature of selection
Second layer MYB switches	SbVND4/5/6	✓ Cell wall content	
Downstream TF	SbMYB42	✓ Cell wall digestibility Cell wall content	



- **Molecular signatures of domestication in both maize and sorghum on NST1/2/3**
- **Overall : 55 genes with associations exhibit signature of selection (Mace et al., 2013, Lai et al., 2019 (1843 genes))**

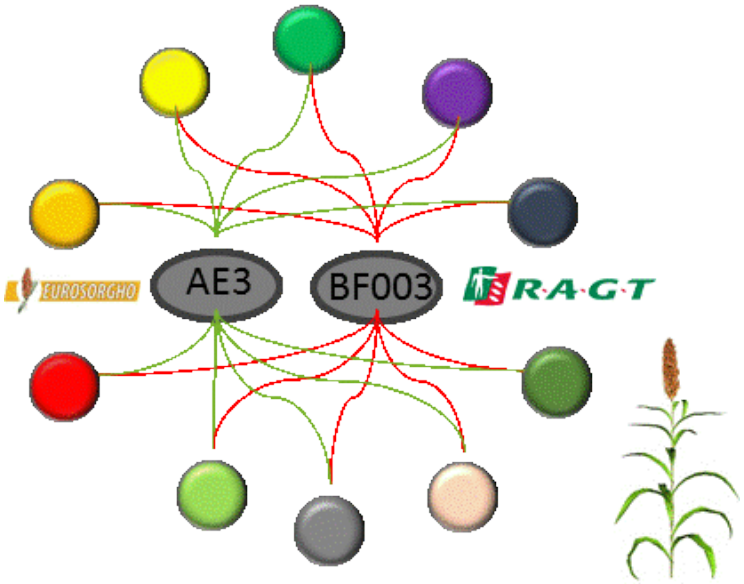
Take home messages

- **632 positional candidates from 3 « independant » designs**
  - Lack of **Consistency / « complementarity** » between the designs
  - 20 structural Cell wall genes only
  - 200 candidate genes belonging to cell wall gene networks
  - 55 genes with signature of selection in sorghum / [sorghum – Maize]

  - **Ability to sort out the « most relevant » candidates**

- **Validation of some of the candidates on-going**
  - Protoplast for Transcription Factor network validation first

- **BCNAM design :**
  - A community resource
  - Relevant to feed the breeding programmes
    - A new design targeting EU
      - B pool



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Lbe

BFF Biomass For the Future

MINES Alès

BCNAM

BIOSORG

iavao Innovation et amélioration variétale en Afrique de l'Ouest

Cemef CENTRE DE MISE EN FORME DES MATERIAUX

Questions ?

Synergies !!!