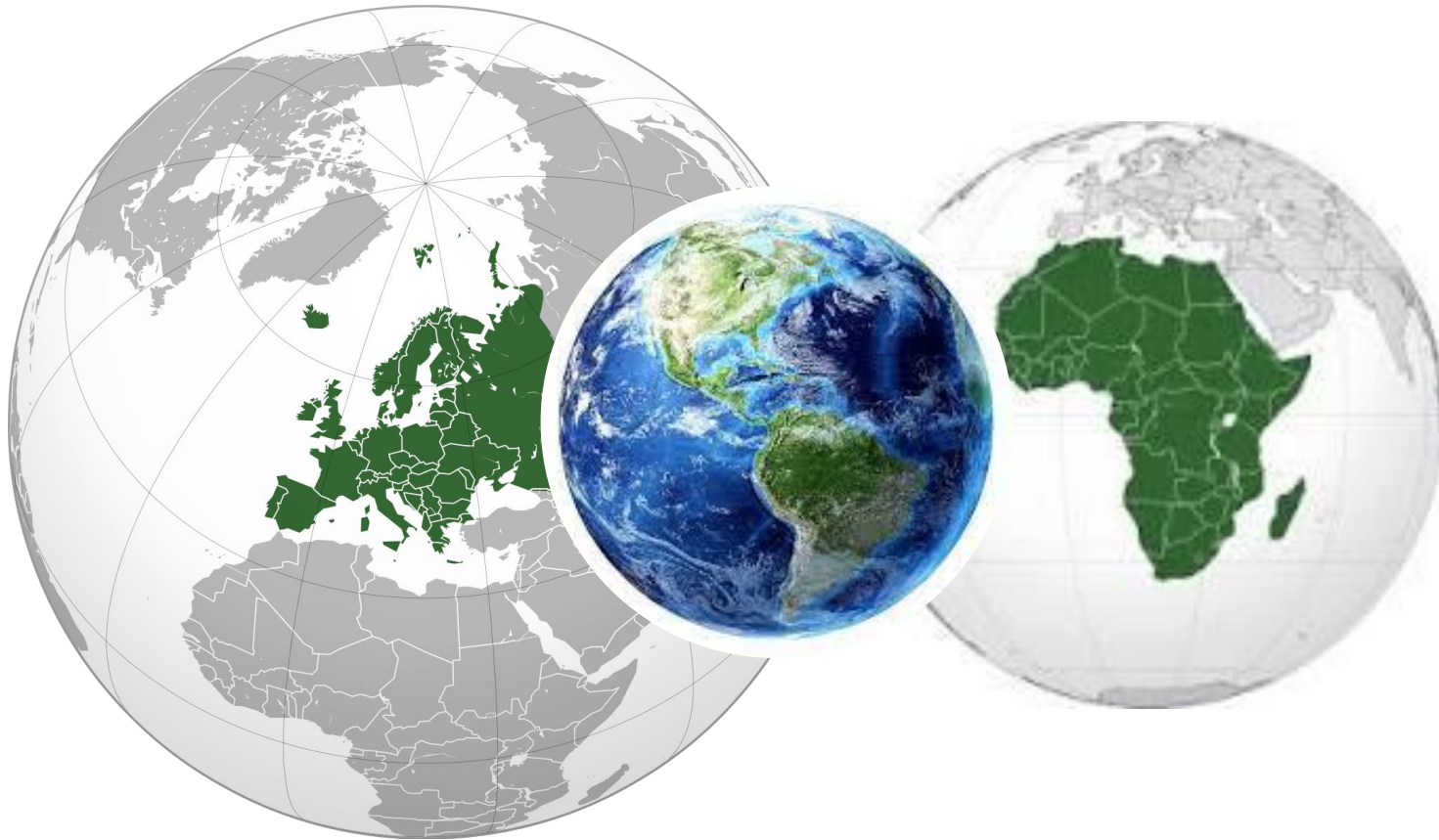


Breaking boundaries in sorghum value chains: the impact of Europe-Africa collaborations and future prospects



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Sorghum in the 21st Century
Global Sorghum Conference

Resiliency and Sustainability in the Face of Climate Change
June 5-9 2023 The Corum Event Center, Montpellier, France

The challenges to support sorghum development in Europe



- Diversifying the “products”
 - New products,
 - Production increase,
 - Confidence between producers and users



- CC in Europe
- Highly heterogeneous
 - Space
 - Time

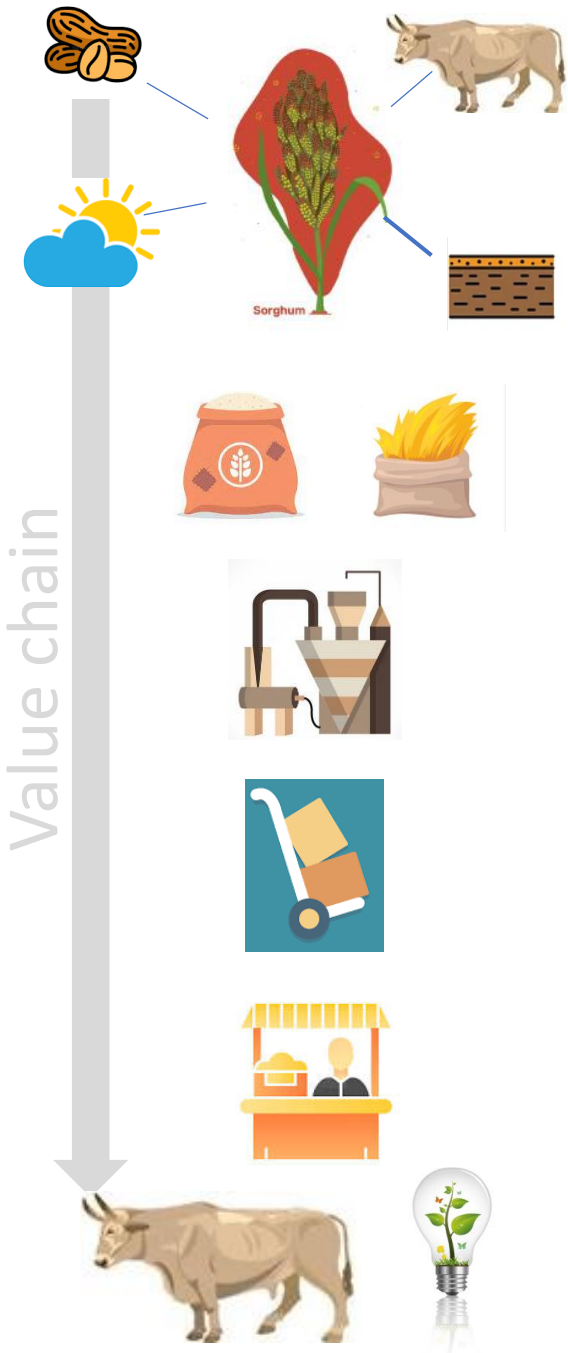


- Mobilizing genetic diversity

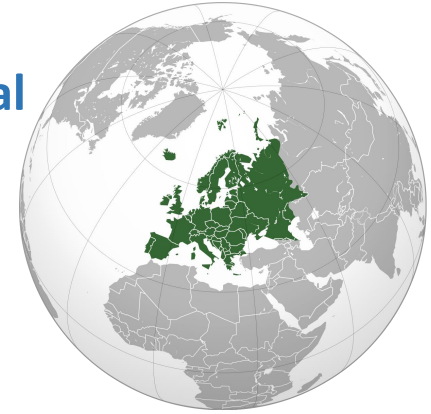


Some specific challenges for Europe BUT most of them are shared with others !!

Supporting value chain development: a multi-level, multiscale approach (not only a matter of politics)

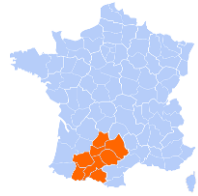
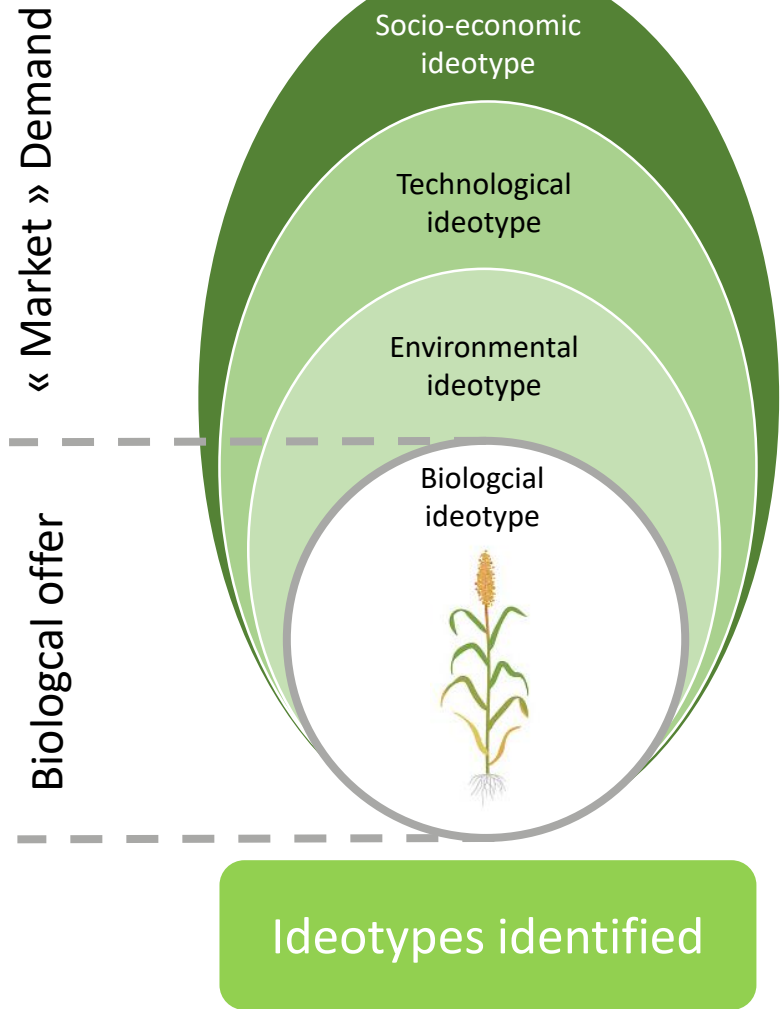


- The needs of producers and users (**Animal nutritionists, material scientists and energy scientists => Process optimization**)
- Understanding the genetic diversity that can be mobilized
- Mining the diversity: Hightroughput phenotyping tools
- A better understanding of the “Plant trait” construction
 - End-product traits = f(Plant traits) + **“Process effect”**
- Pre-breeding population developments and optimization of breeding strategies
- Develop varieties adapted to the “markets”
 - Seed companies and NARS’ mandates

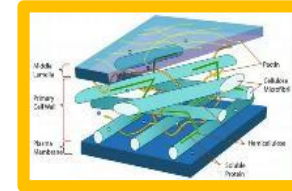
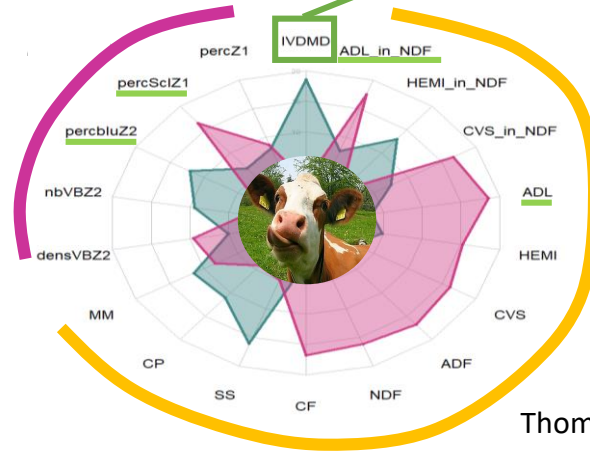
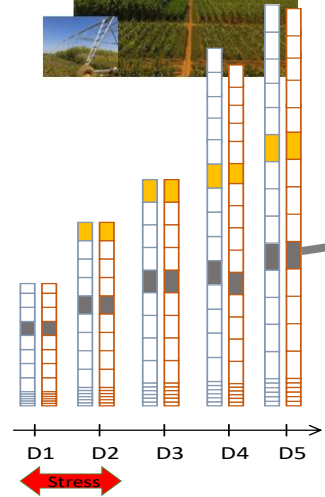
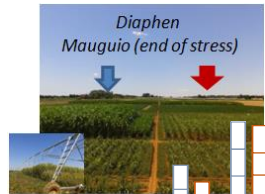
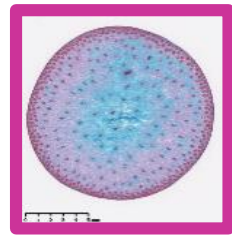


A geneticist oriented point of view with a focus on biomass value chains as an example: “Develop tools to support breeding”

Producers and end-users requirements: Biomass value chain ideotypes

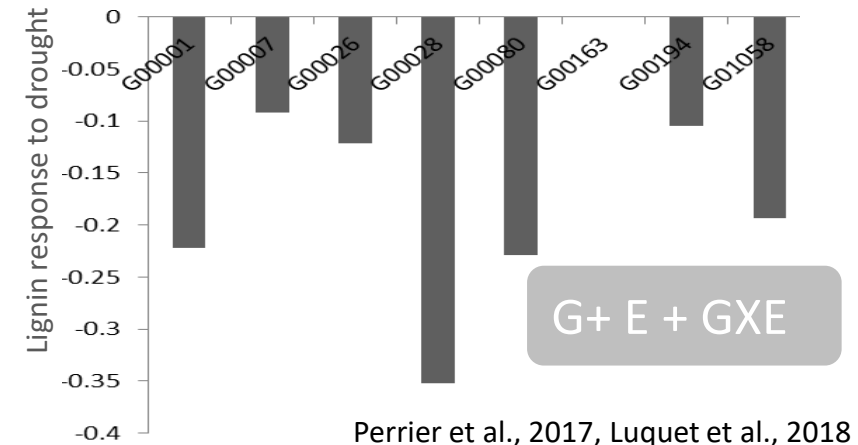
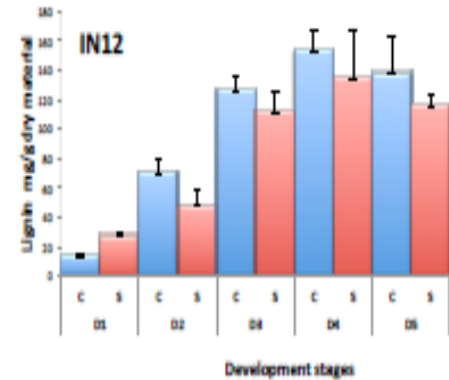


Target area per crop production system / end product
Social acceptance



Lignin content and its locations are key trait (among others)

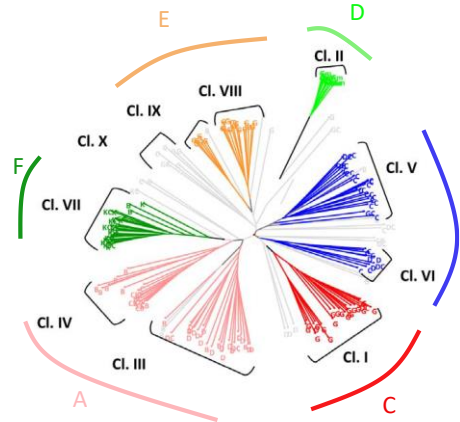
Thomas et al., 2018, 2021



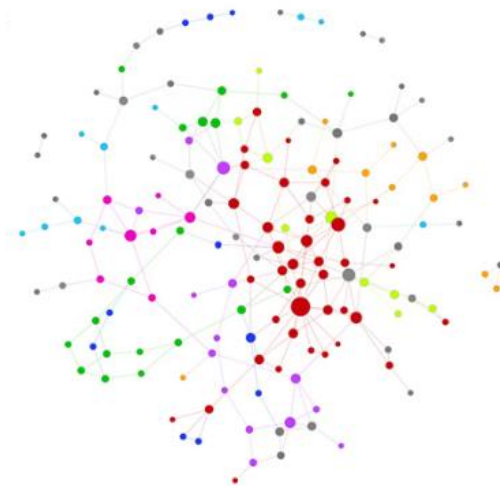
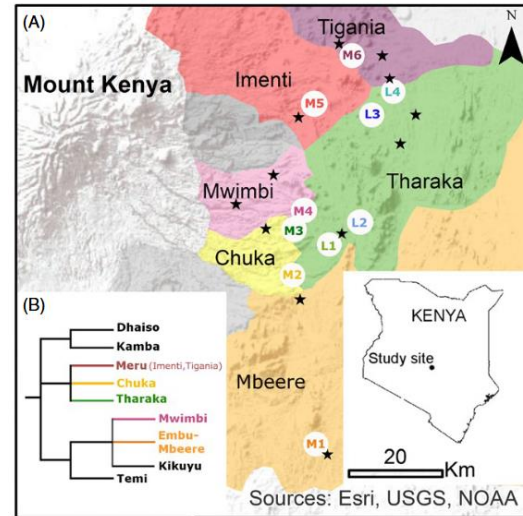
Perrier et al., 2017, Luquet et al., 2018

Identified ideotypes: Before mining the diversity we have to understand it !

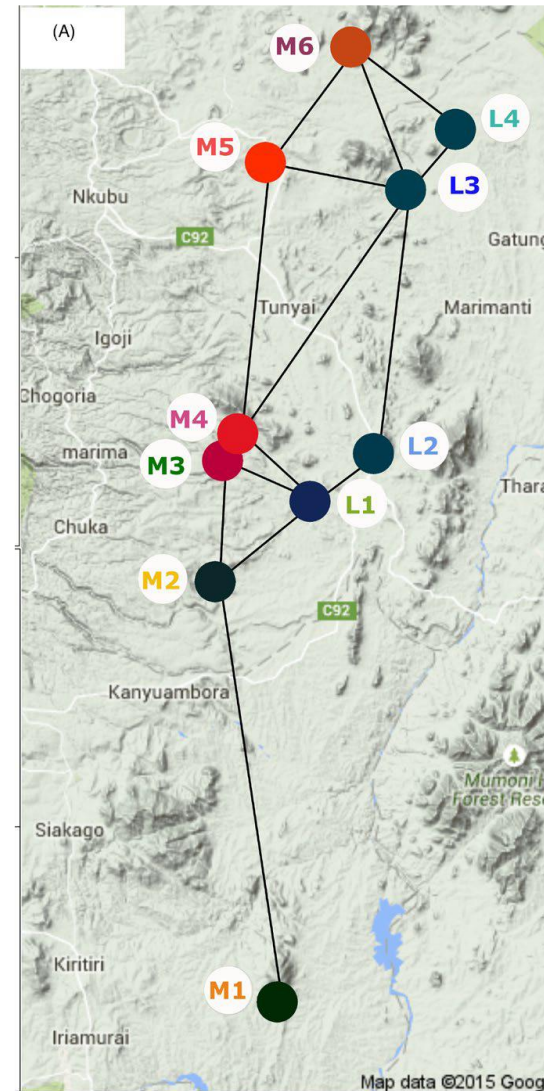
« Population genetics based » strategies



Deu et al., 2006, Bouchet et al 2012

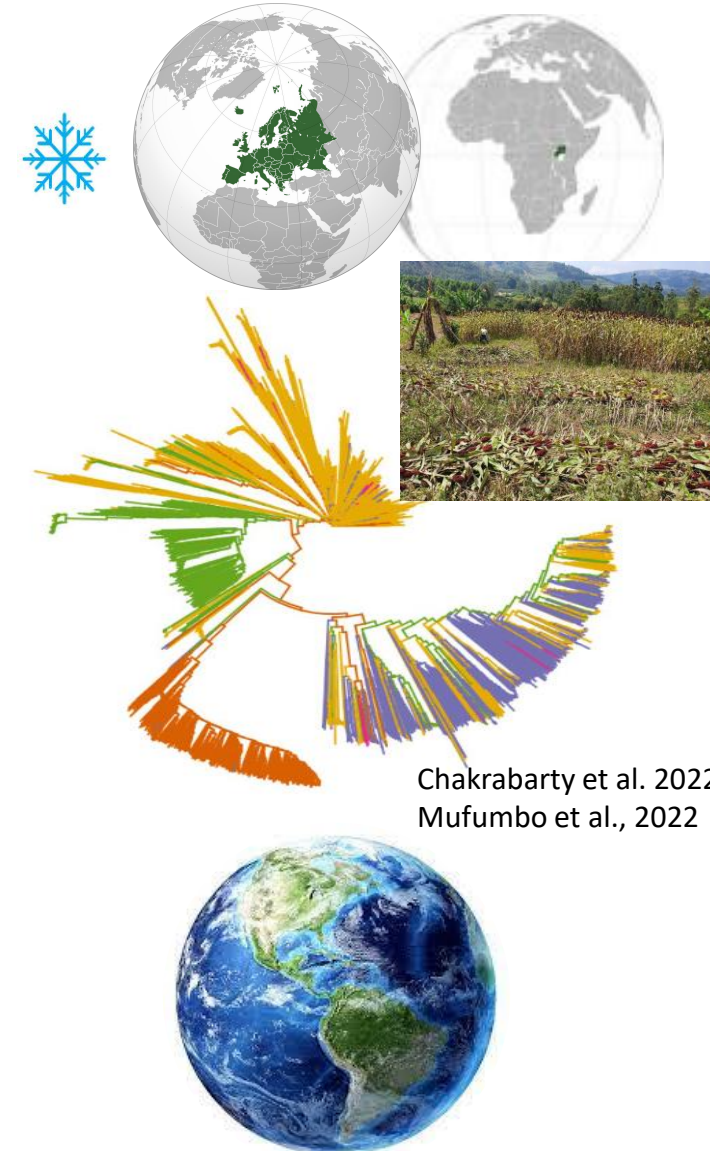


Seed exchange networks



Labeyrie et al., 2016a, b

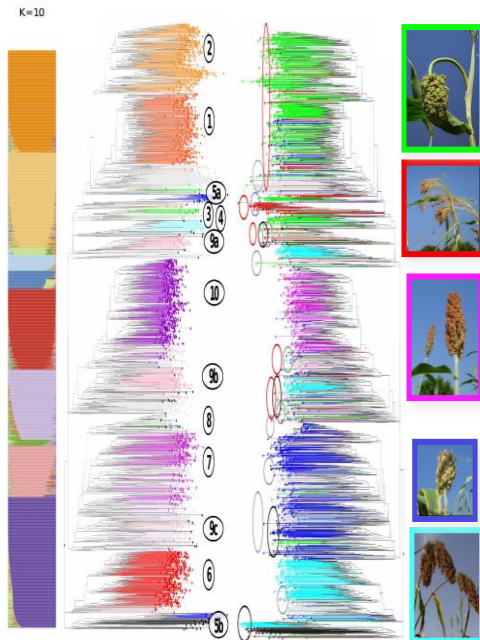
« Trait based » strategies



Chakrabarty et al. 2022
Mufumbo et al., 2022

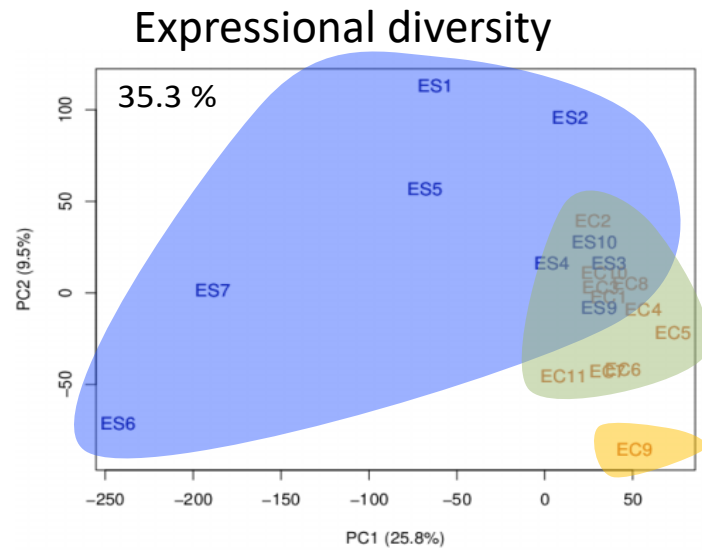
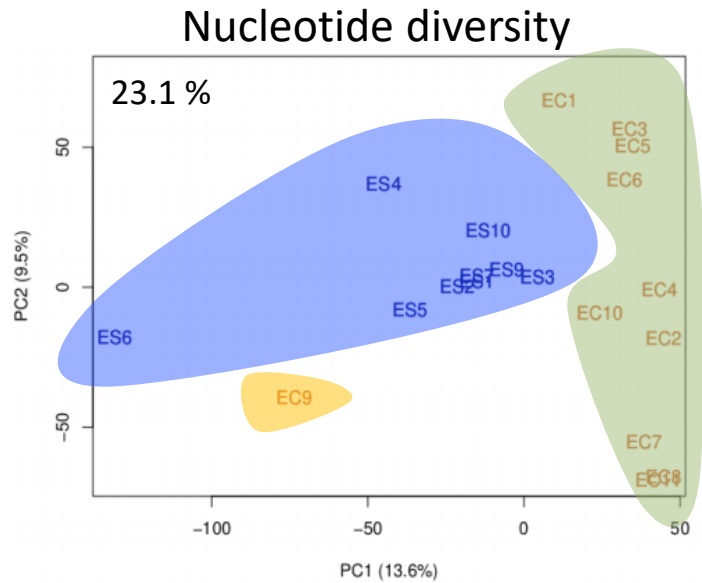
CiRAD Core collection
n = 210

GCP Composite Set, n = 3000

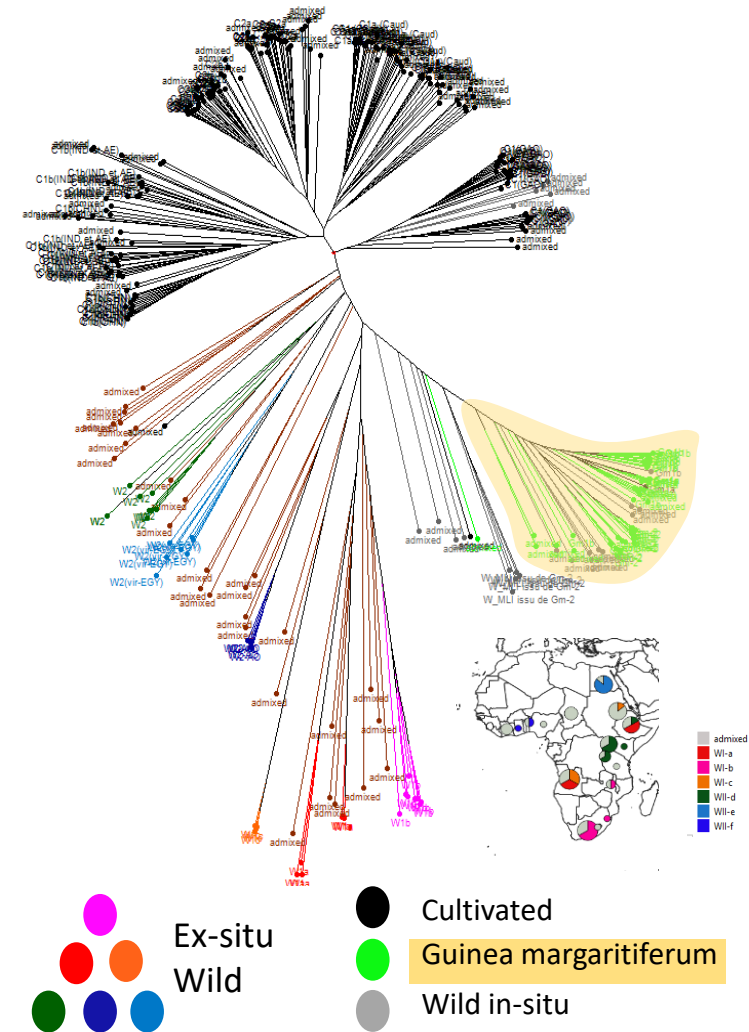


Billot et al., 2013

The “wild pool” a source of relevant diversity that deserves more attention



Burgarella et al., 2021



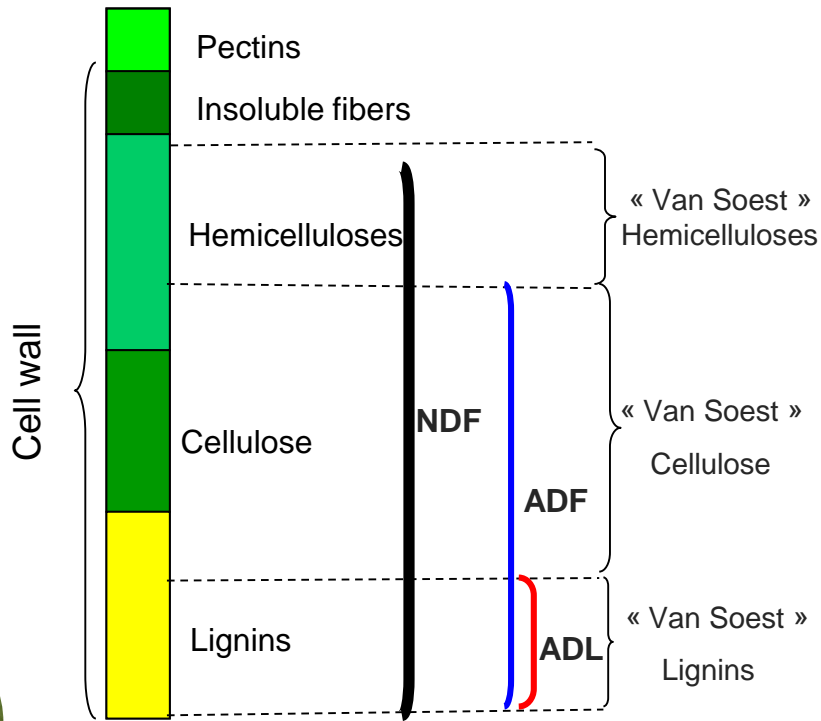
Gilabert et al P36



Mendy et al P53

Characterizing functional diversity: highthroughput phenotyping tools

■ Biomass composition



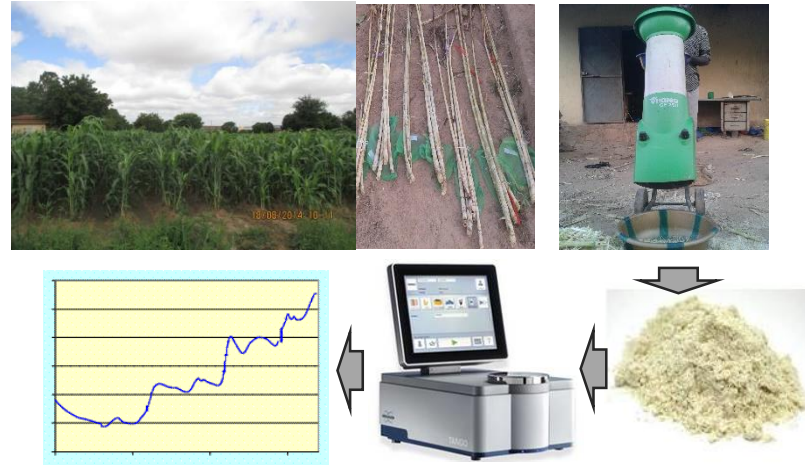
■ Stem : >700 reference data points



■ Biomass properties

- DM / CW digestibility
- Energy

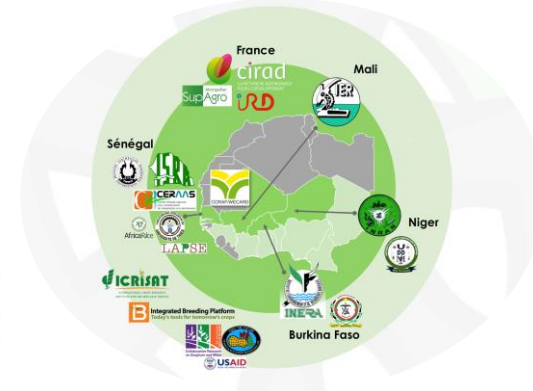
■ NIRS



■ Silage / mature stages and developing stem



Trouche et al., 2014,
Perrier et al., 2017,
Luquet et al., 2018

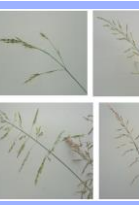


Towards phenomic selection

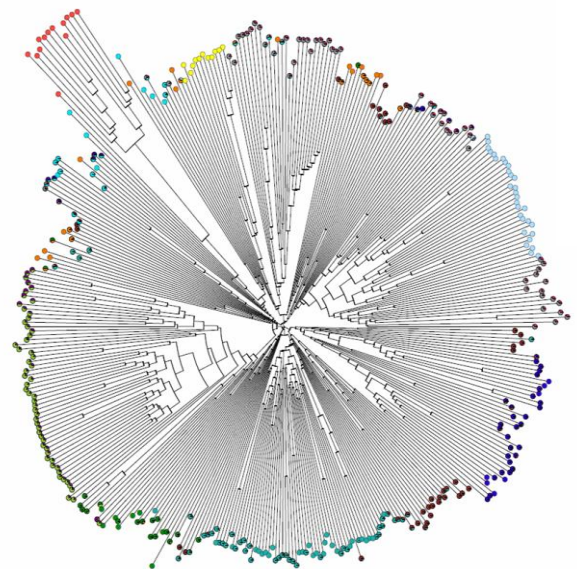
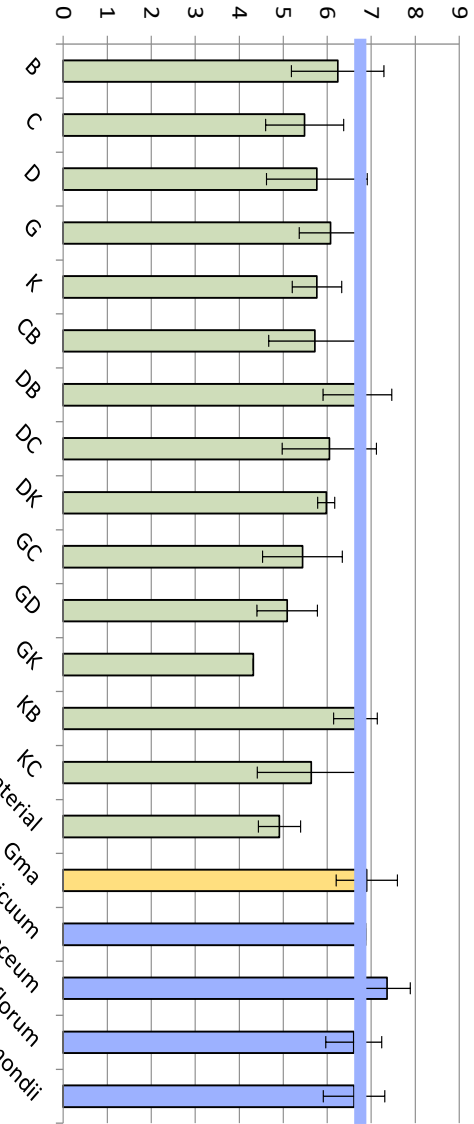


Salas et al 069

Characterizing the wild and cultivated diversity



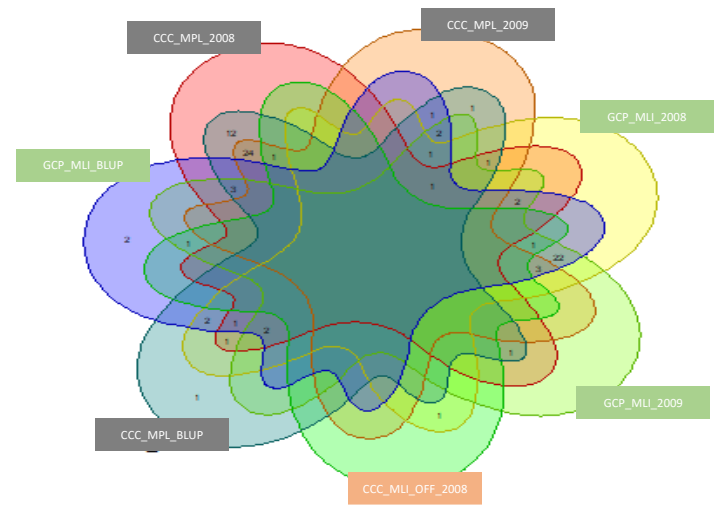
Lignin content



- 413 accessions
- Line value phenotyping
- 5 trials (100 - 362 genotypes)
 - 3 panels (87 genotypes in common)
 - 2 Montpellier (100)
 - 2 Mali (362), rainy season
 - 1 Mali Off Season (210)



87 regions, 321 genes

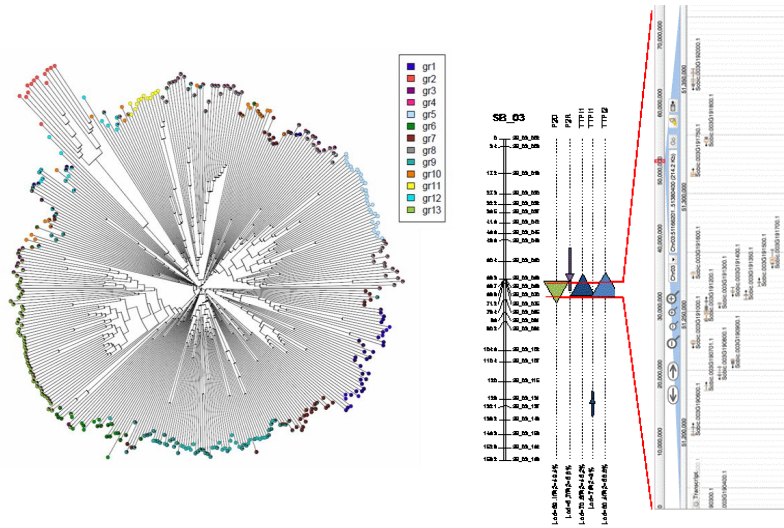


1768 candidates
320 « key » genes

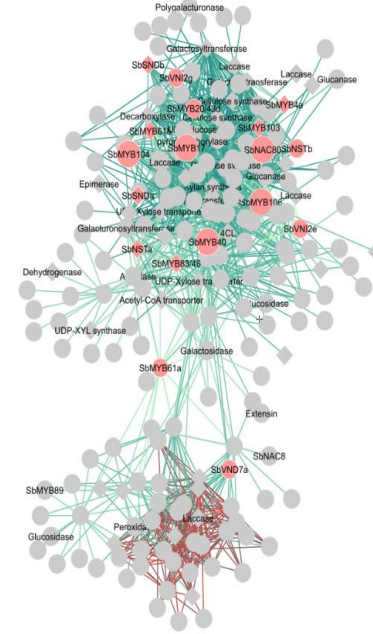
Only 23 genes with previous evidences...

Extracting the most relevant genes: Aggregating « evidences » from the intra and interspecific levels

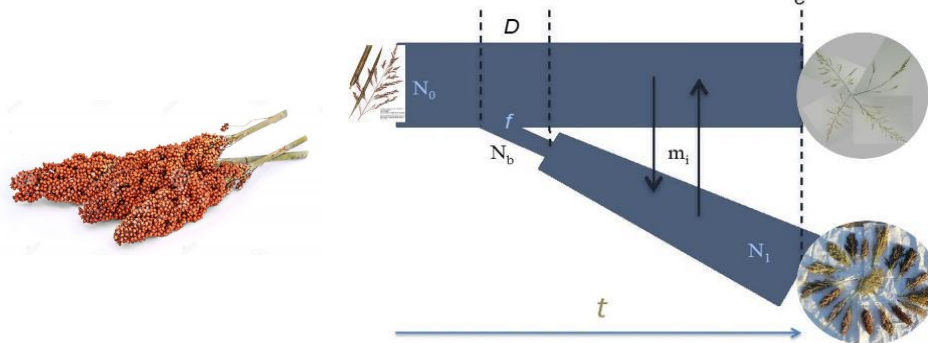
Genomic regions identification



Transcriptome regulation



Evolutionary analyses



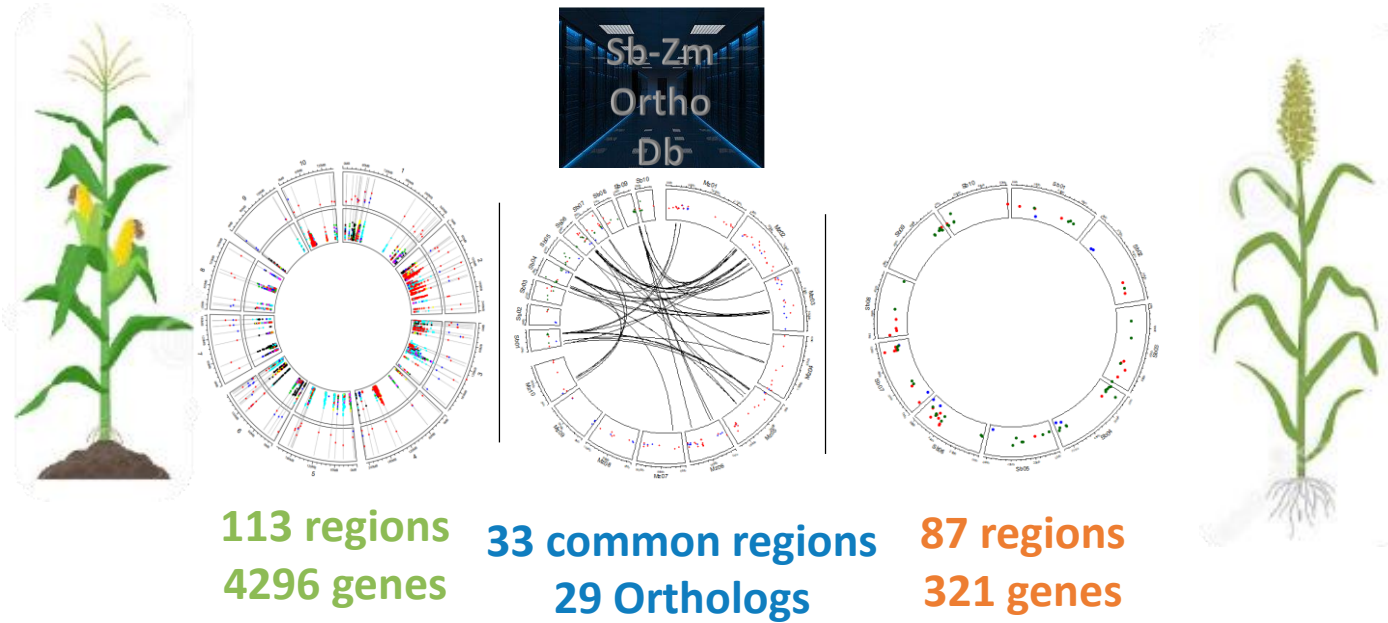
Paterson, Freeling and Schnable groups



Mace et al 2013



Merging GWAS from Sorghum and Maize

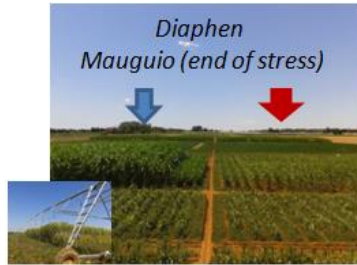


- Higher conservation Zm/Sb than for Root System architecture (Zheng et al., 2020)
- Biomass composition is likely more conserved than root system architecture

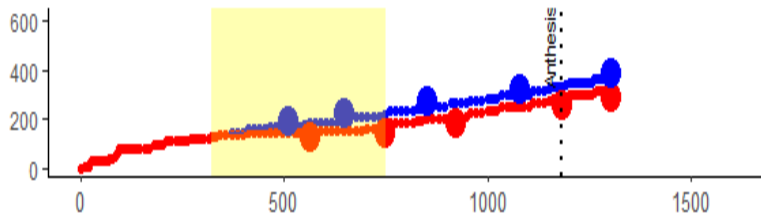
- Additional information regarding cell wall establishment is required

An extremely limited understanding of the genetic determinism of biomass properties

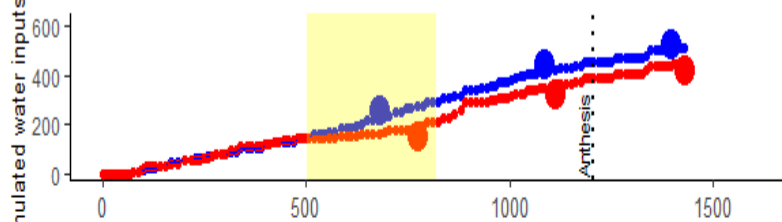
Towards a better understanding of cell wall establishment



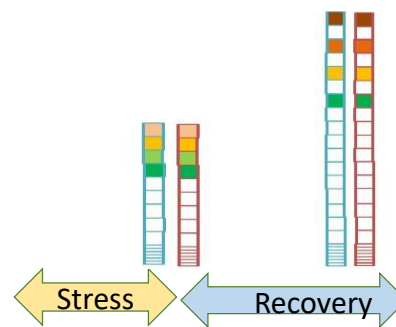
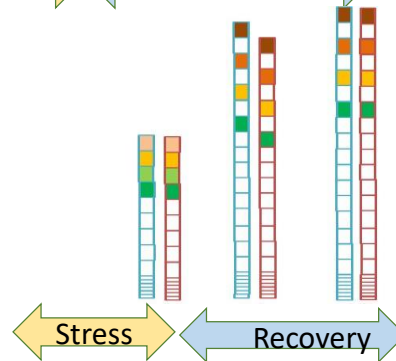
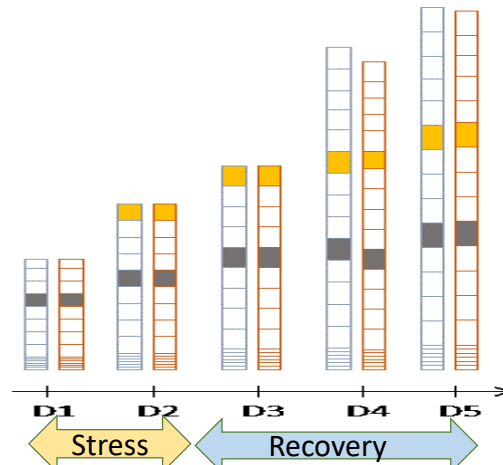
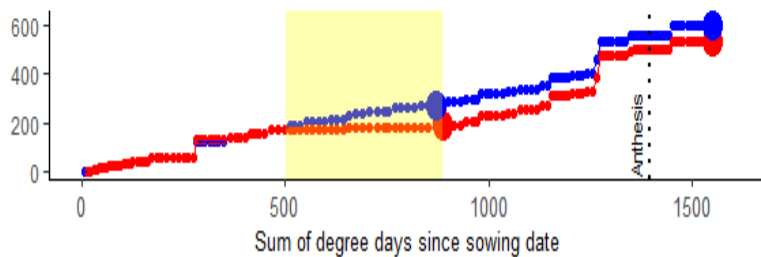
A. 2013



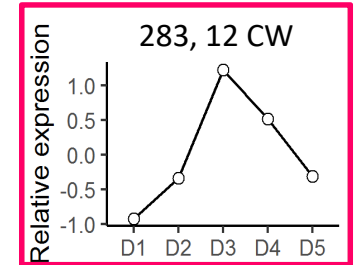
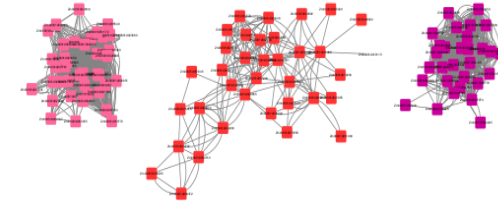
B. 2014



C. 2015



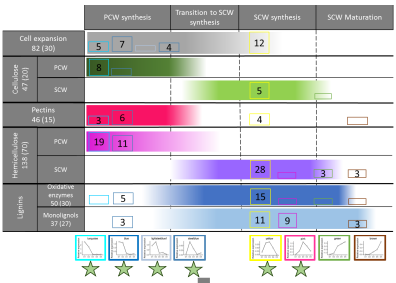
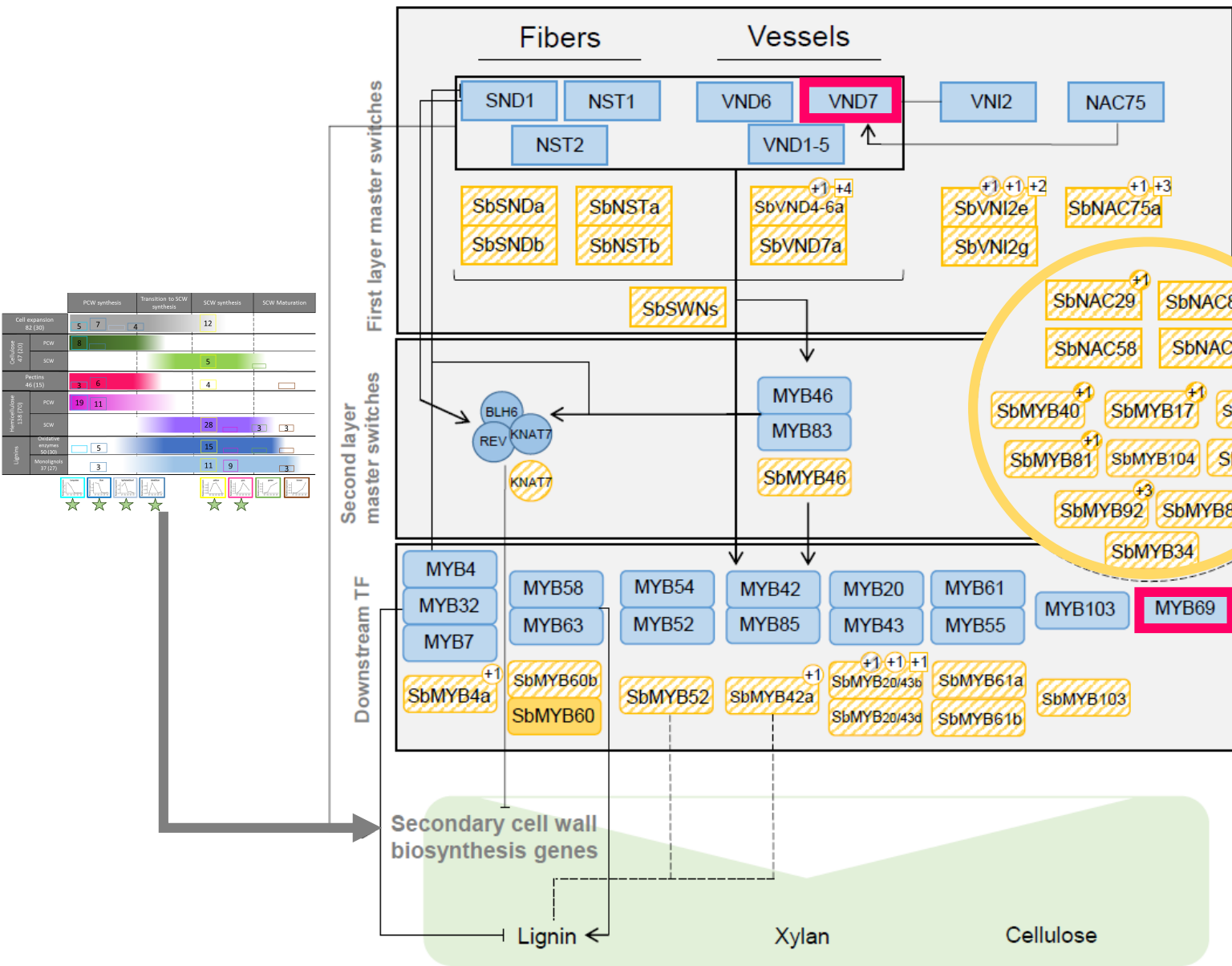
A first focus on Cell wall structural genes



		PCW synthesis	Transition to SCW synthesis	SCW synthesis	SCW Maturation
Cell expansion	82 (30)	5 7 4		12	
Cellulose	47 (20)	8		5	
	PCW				
	SCW				
Pectins	46 (15)	3 6		4	
Hemicellulose	138 (70)	19 11		28	3 3
	PCW				
	SCW				
Lignins	50 (30)	5		15	
	Oxidative enzymes				
	Monolignols	3		11 9	3



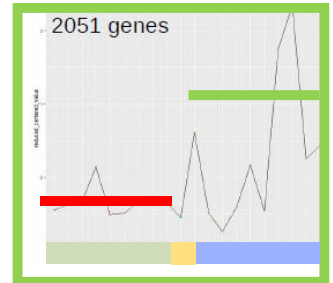
Looking deeper in the regulation of cell wall establishment



At: a relevant model plant

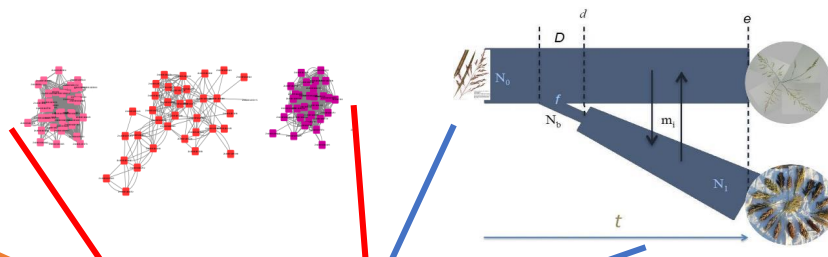
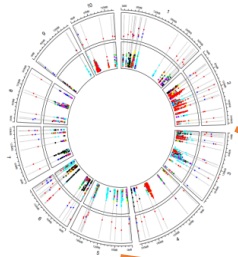
New sorghum transcription factors

VND7 and MYB69 ?
Two key genes in At not detected in sorghum ?

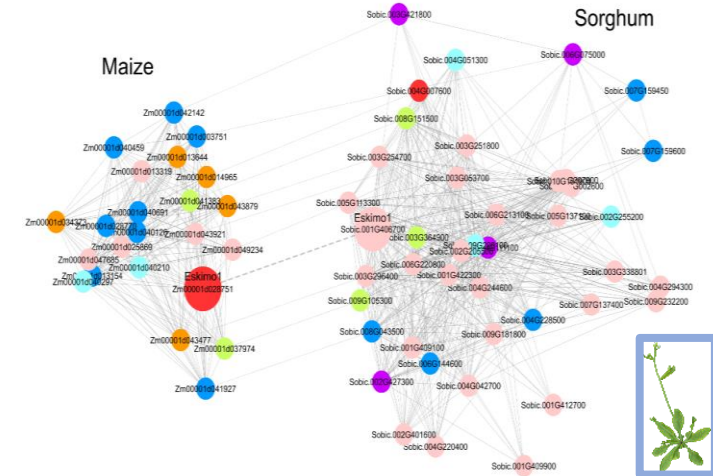


21 SCW Dom + Imp genes

Aggregating evidences at the intra and inter-specific levels and validating the candidates !



Zm and Sb ESKIMO1

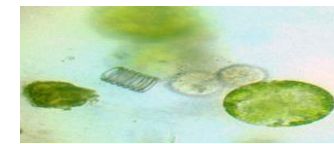


Sb_v3_ID	Zm_v4_ID	Homolog_pair_Zm_Sb	Zm.GWAS	Sb.GWAS	Zm.modulesCW	Sb.modulesCW	Zm_connexion	Sb_connexion	Zm.selected	Sb.selected	Score
Sobic.007G135900	Zm00001d050394	Zm00001d050394_Sobic.007G135900	0	1	1	1	1	1	1	1	7
Sobic.001G406700	Zm00001d028751	Zm00001d028751_Sobic.001G406700	1	0	1	1	1	1	1	1	7
Sobic.001G420700	Zm00001d028620	Zm00001d028620_Sobic.001G420700	1	0	1	1	1	1	1	1	7
Sobic.008G141700	Zm00001d041511	Zm00001d041511_Sobic.008G141700	1	0	1	1	1	1	1	1	7
Sobic.004G227400	Zm00001d041511	Sobic.004G227400	1	0	1	1	1	1	1	0	6
Sobic.006G203400	Zm00001d041511	Sobic.006G203400	0	1	0	1	1	1	1	1	6
Sobic.003G251800	Zm00001d041511	Sobic.003G251800	0	0	1	1	1	1	1	1	6
Sobic.001G026900	Zm00001d041511	Sobic.001G026900	1	0	1	1	1	1	0	1	6
Sobic.001G046800	Zm00001d041511	Sobic.001G046800	0	0	1	1	1	1	1	1	6



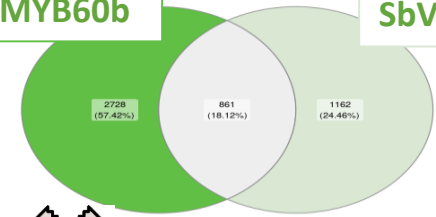
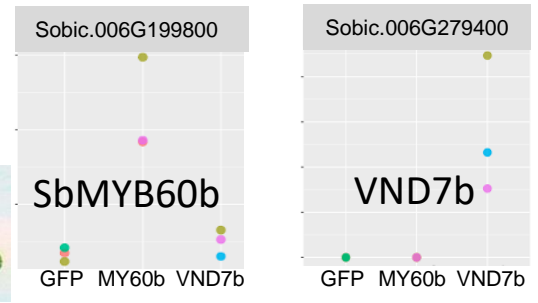
Impacting haplotypes have been identified: we need to deliver them to the breeding programs

Over expression in protoplasts

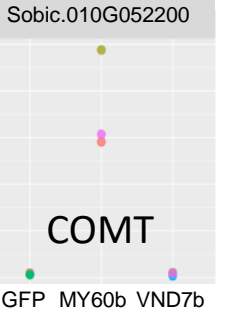


SbMYB60b

SbVND7b



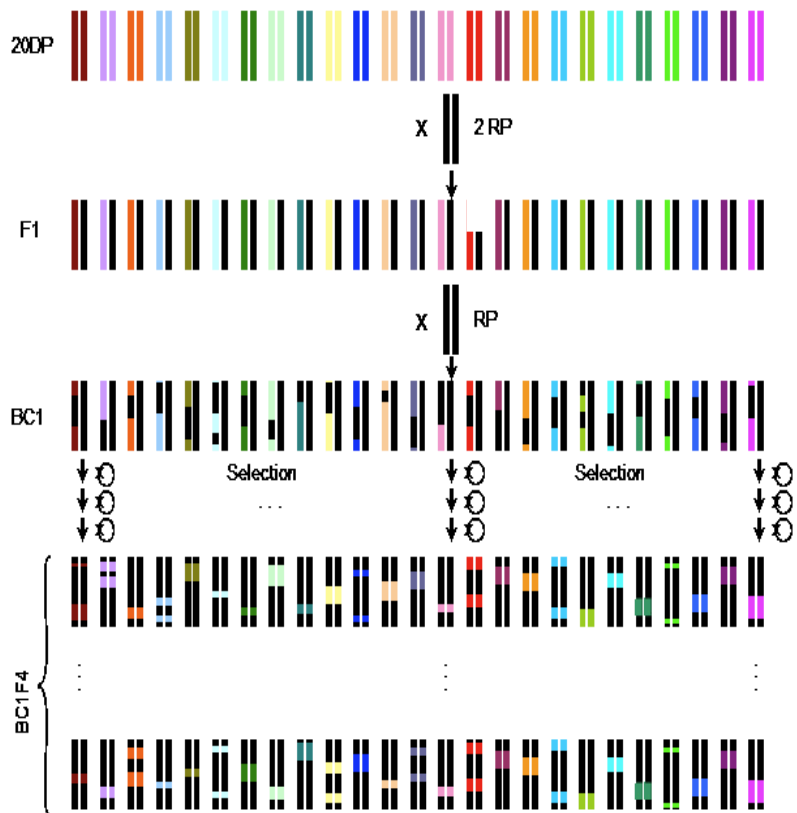
Calatayud, Richaud et al. P19



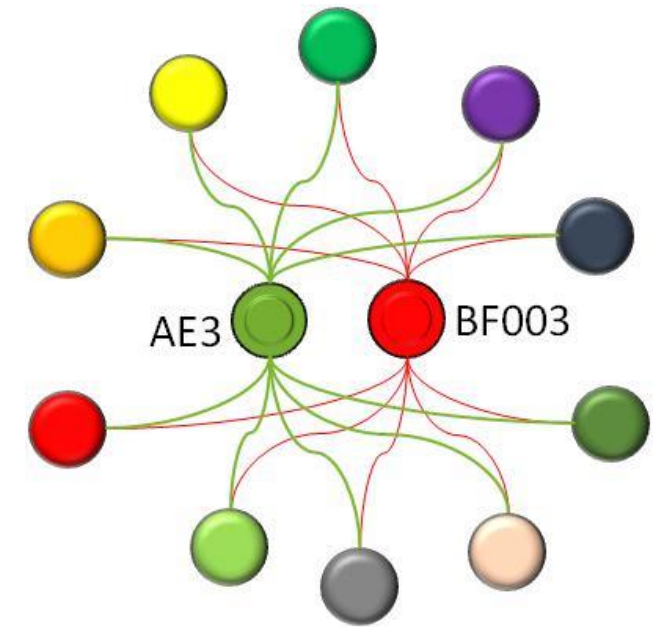
Injecting favorable haplotypes in the elite pools and discovering new ones

- Haplotype's effects need to be evaluated in relevant genetic backgrounds for the breeders
- GWAS power is limited by allelic frequency distribution

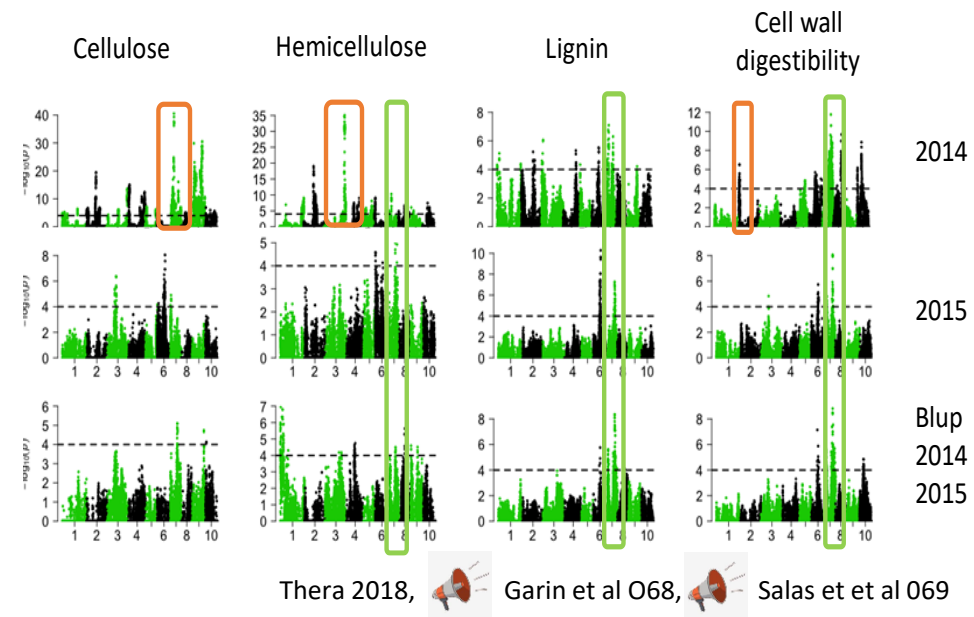
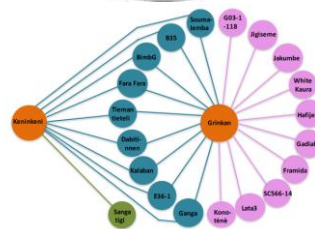
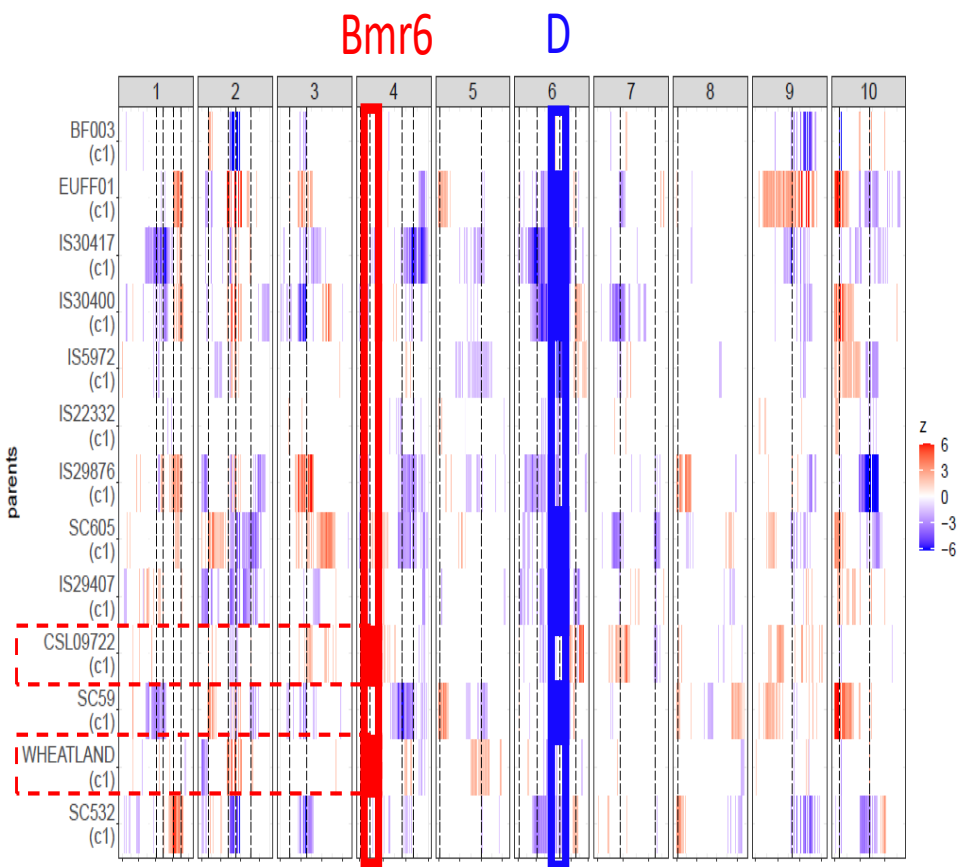
- BCNAM Jordan et al., 2011



- EU Biomass BCNAM: 2RP * 10 DP, 2000 BC1F4 families

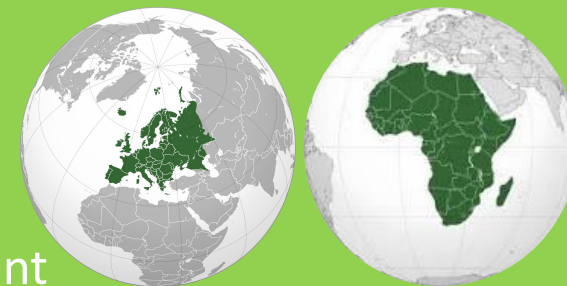


Validation of haplotype effects and discovery of new haplotypes



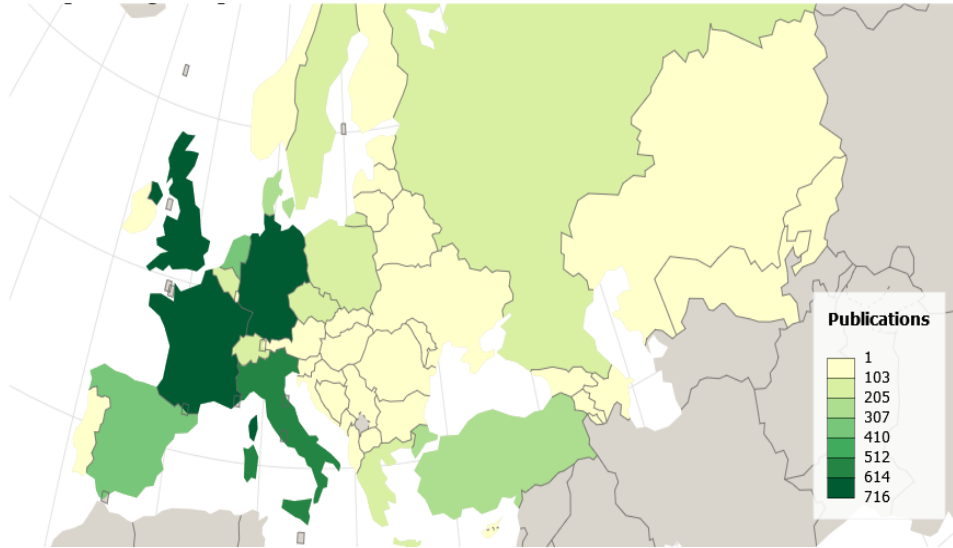
Enriching the elite pool with relevant alleles

- Independent validations of allelic effects in different genetic backgrounds
- Discovery of new haplotypes
- Support for variety development



EU sorghum research: Not only a biomass story !

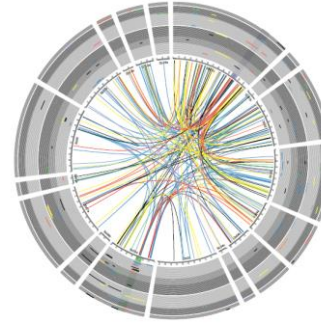
- 2000-2021 : 4724 EU publications



- 22 % of total sorghum publications
- Not too bad as EU production = 2 % of global production



Early stage

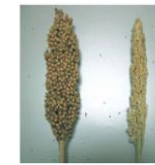


Bekele et al., 2014

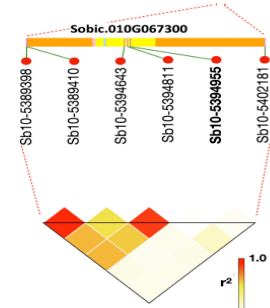
Reproductive stage



Srn39

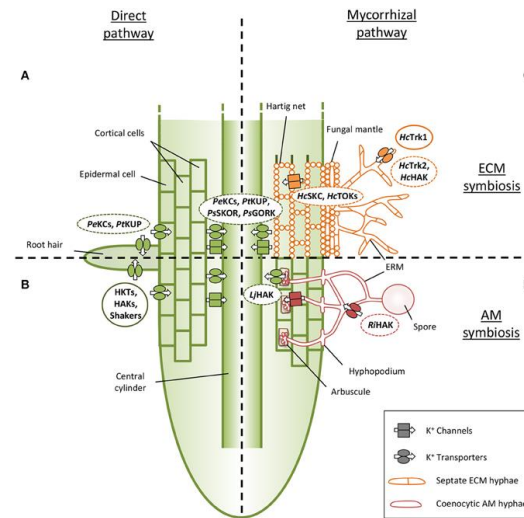


Maulana and Tesso., 2013



Schaffasz et al 2019 a,b
Chakrabarty et al 2021

Sorghum – Arbuscular mycorrhiza



Raphael et al., 2022
Symanczik et al 2018,2020
Koegel et al 2013



Take home messages



A research network to establish
**Not an invitation to join,
An invitation to build together**



Collaborators and Acknowledgements



Thanks a lot for your attention

Questions