

G2MARS a collaborative approach to improve fodder quality of European sorghum germplasm

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- BFF: a 8 years research project funded by the French National Research Agency
- Objective: Address the need of biomass for the new uses: biomaterials, biofuels and the current uses: fodder
 - Sorghum has the ability to maintain a high level of biomass production in stressfull environments
 - Within the BFF project, the G2MARS approach aims to develop highly digestible sorghum germplasm for fodder through a Marker Assisted Recurrent Selection strategy based on an in-depth understanding of the genetic architecture of the traits of interest







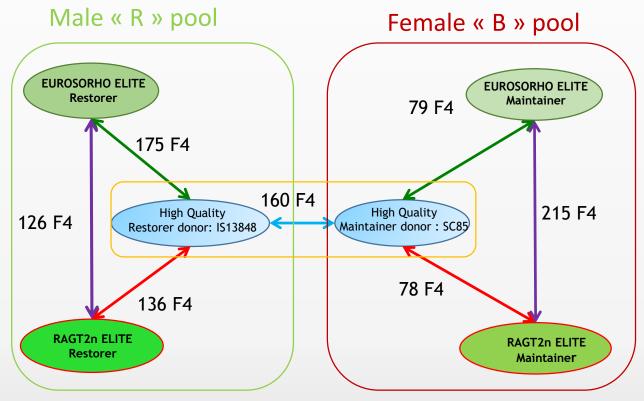


1. Combining elite commercial material with high quality sorghum cultivars



7 F4 populations developped

- 3 restorer populations
- 3 maintainer populations
- 1 connecting population between the 2 high quality donors (high stem digestibility)

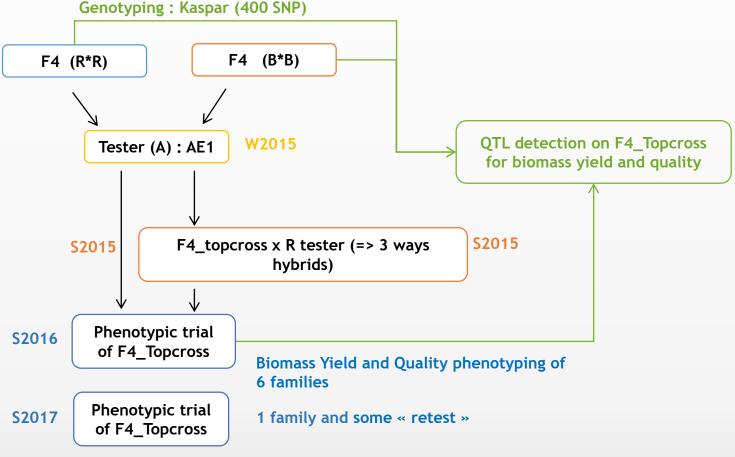




1. Combining elite commercial material with high quality sorghum cultivars



<u>Topcross schemes for the different families</u>:





1. Combining elite commercial material with high quality: BFF sorghum landraces

More than 1000 topcross hybrids developped









- Experimental design:
 - Micro-plot of 18m²
 - 2 locations in south west of France: Gaillac (81) et Mondonville (31)
 - Augmented design with 4 repeated control varieties : Amiggo, Sucro506, ES Athena et Supersile 18
- Scoring of agronomical characters: height, heading date, lodging, biomass yield,...
- Analysis of biomass quality: soluble sugar, starch, cell wall content and composition and digestibility parameters





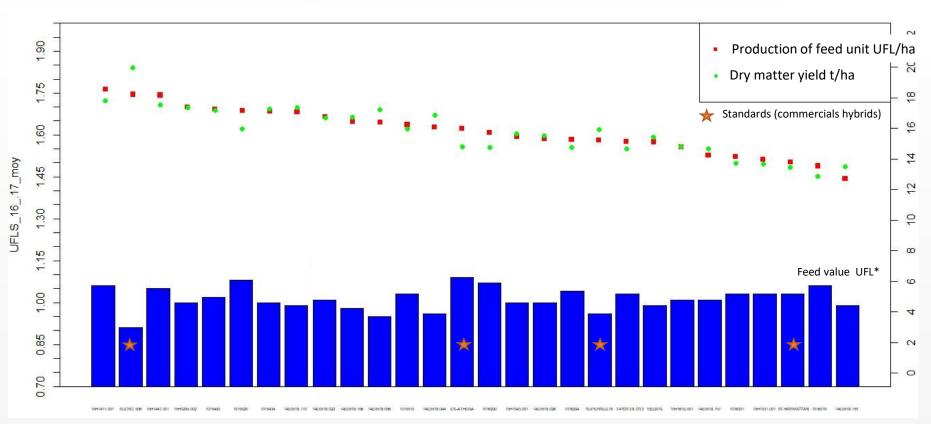




Mondonville trials in september 2017







*UFL: fodder net energy absorbable by a dairy cow 1 UFL = 1700 kcal

Top 30 hybrids: biomass yield and quality data, average 2016-17





- Genotyping with 544 SNPs markers
- Validation of the congruence between the genetic map and the physical map

Pool	Cross	# Informative	
POOI	CIUSS	Markers	
В	RAGT2n B X EUSG B	186	
В	RAGT2n B X SC85	261	
В	SC85 X EUSG B	248	
BxR	SC85 X IS13848	260	
R	EUSG R X IS13848	273	
R	EUSG R X RAGT2n R	231	
R	RAGT2n R X IS13848	274	

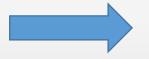


3. Disentangling the genetic architecture of the target traits



- Detection of QTL both for agronomical and quality traits
- QTL detection performed with MCQTL taking advantage of the connected design
- 17 « meta » QTL detected in the R Pool and 6 in the B Pool
- Parental allelic effects ranked

leading date	Soluble sugar Fiber	ADL	Fiber digestibility	Soluble sugar Starch	N content Soluble Sugar	Heading date
The state of the s		Discovery (C) Control discovery in the Control of Contr		The state of the s	Command (C) of the deservation of the command of th	Comment of the American Supple
Chr1	Chr3	Chr4	Chr5	Chr6	Drinners . 415 ber, 81 farten, leight 127	Chr9



Gather all the favorable alleles into the same line



4. Phenotypic and Molecular Ideotypes definitions





Ideotype 1:

- ++ Biomass yield
- + High soluble sugar level
- ++ High fiber digestibility.



Ideotype 2:

- + Biomass yield
- + Starch content (Grain)
- ++ High fiber digestibility.



4. Phenotypic and Molecular Ideotypes definitions



- Translation of the phenotypic ideotypes into molecular ideotypes
- Choice of the best alleles based on QTL detection
- Example for the R pool:
 QTL 11 (chr6) = Soluble Sugar
 CIRAD allele brings higher soluble sugar

Molecular ideotype pool R

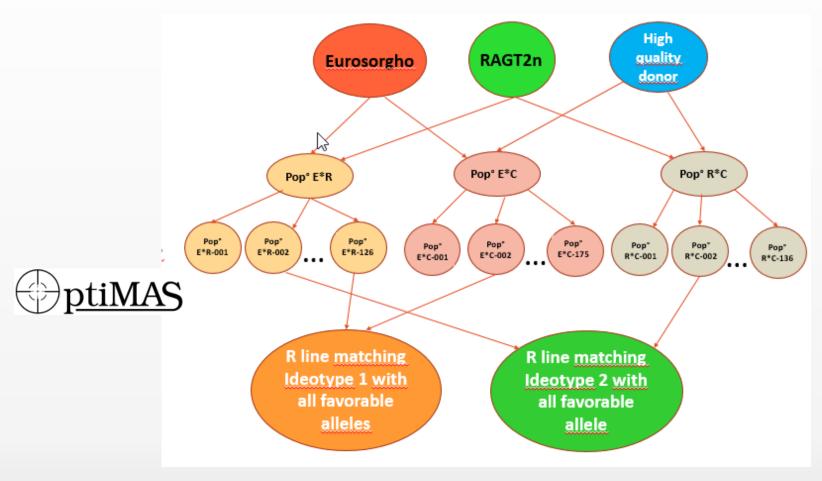
recural racotype poor					
QTL#	Ideotype 1	Ideotype 2			
1	EUG	EUG			
2	EUG	EUG			
3	EUG	CIRAD			
4	EUG	EUG			
5	EUG	EUG			
6	CIRAD	RAGT			
7	RAGT	RAGT			
8	RAGT	RAGT			
9	EUG	EUG			
10	CIRAD	CIRAD			
11	CIRAD	RAGT			
12	RAGT	CIRAD			
13	RAGT	CIRAD			
14	RAGT	CIRAD			
	RAGT/	RAGT/			
15	CIRAD	CIRAD			
16	RAGT	RAGT			
	CIRAD/	CIRAD/			
17	EUG	EUG			



4. towards an optimal recombination strategy



Crossing scheme definition assisted by Optimas software: the R pool example





Conclusion



A private public partnership which brings us a better image of the genetic architecture of biomass quality and yield in an elite germplasm context.

There is still work to do:

- -> need to compare QTL position with litterature and the new results coming from other BFF designs (GWAS, BCNAM)
- -> Assesment of the lines with the aggregated QTL
- -> Make the best use of those hundreds of new lines in our respective breeding program!





Thanks





Thanks





































