

1ST EUROPEAN SORGHUM CONGRESS

WORKSHOP

INNOVATIVE RESEARCH TOWARDS GENETIC PROGRESS

TACKLING NEW CHALLENGES FOR EUROPEAN SORGHUM THROUGH GENETICS AND NEW BREEDING STRATEGIES



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BUCHAREST 3-4 NOVEMBER 2016

WHOLE GENOME SEQUENCING : AN ACCELERATOR OF SORGHUM GENETICS AND BREEDING



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Paterson et al 2009



To 1000's Genomes : Terra Project

Mockler et al 2016







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NUCLEOTIDE DIVERSITY INFORMATION





- Polymorphism Database and Next Generation Sequencing (NGS)
 - Characterize the diversity
 - <u>Support breeding efforts (Marker ASSISTED</u> breeding)

A RESERVOIR OF DIVERSITY : BREEDING POTENTIAL Characterized" genetic resources 10



469 accessions x 265 000 SNP, Morris et al 2014



IX 5b

TAKING ADVANTAGE OF GENETIC INFORMATION TO ACCELERATE GENETIC GAINS

• $R_x = I * h_x^2 * Sd$ (I :Selection intensity, h_x^2 : heritability of trait X, Sd : Phenotypic standard deviation)

- Indirect selection (select trait, based on selection on trait,)
 - $CR_x = i_y * h_x * h_y * r_g (r_g : genetic correlation between traits x and y)$
 - Molecular markers allow maximizing h_v (h²=1)
- Challenge : identify the genomic regions (Markers) controlling the traits of interest and combine them in new varieties



To identify these markers we need PhenotypeSSSS !!! (High-throughput Phenotyping that remains accurate)

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MAJOR GENES AND QTLS (BIPARENTAL) HAVE ALREADY BEEN IDENTIFIED

Major Genes



Some genomic regions affecting quantitative traits

- QTLs in biparental populations
 - Grain yield / size...
 - Grain quality
 - Biomass yield
 - Biomass quality
 - Biotic and Abiotic stress



- New QTLS are detected
- Useful for within family selection, but most of the time useless in broad based breeding programmes

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Ste

Col

Lea

Plai

6

BIPARENTAL VS BROAD BASED POPULATIONS : DIFFERENT MAPPING ACCURACIES REQUIRED



 « Region » identification, relevant for within family breeding « Gene » identification, more relevant in the context of broad based breeding programmes

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GWAS : TRACKING DOWN THE GENES OF INTEREST

Traits analysed through GWAS

- Plant Height, biomass yield
- Flowering
- Agroclimatic traits
- Inflorescence architecture
- Grain weight and yield
- Grain quality
- Tillering

- Anthracnose resistance
- Polyphenol concentrations
- Germinability
- Biomass composition
- Sugar yield
- Aluminium tolerance

Characterizing the variability



GWAS for Biomass « quality »

Screening the variability







Highthrouput phenotyping (NIRS...)



GWAS FOR BIOMASS COMPOSITION



Multi-Environments / Panels



- 413 accessions
- 5 trials (100 362 genotypes)
 - •2 Montpellier
 - •2 Mali
 - •1 Mali Off Season



Ingrid Vilmus







SNP interval (bp)

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properties

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1.0 0.8

0.6 0.4

0.2



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GWAS : EXPECTATIONS AND PERSPECTIVES

- GWAS allows identification of relevant genomic regions
- The detected regions depend on the Site of analysis (High GXE)
- Meta-Analyses are required and GWAS efforts have to be pursued



- GWAS suffers from limitations...
 - Allelic frequencies are not balanced (rare alleles, power issues)
 - Confounding effects with structure
 - Biases due to the genetic context
 - Not always useful directly in breeding programmes (time required to transfer genes identified in poor lines in elites)



Recurrent selection cycles / towards target ideotype (6/2011 – 1/2013)



ΞΔ

 C_2

Field evaluation (On-Station and on-Farm)

Sotuba Sotuba Cinzana Cinzana

SD1

C2_099-07-01 C2_007-03-01 C2_099-12-01

> 013-02-03 007-02-01 062-35-48-01 062-19-44-01

C3 007-07-01 A12-84 C2 099-05-01 C2 099-16-02 C3 06 C3 - 17 C3 - 18 C2 033-02-02 C1 093-05-53-01 C3 - 033-05-53-01

SD2

Multiparental MARS for Biomass quality





COMBINING THE ADVANTAGES OF BIPARENTAL AND ASSOCIATION MAPPING : NESTED ASSOCIATION MAPPING

- Large number of recombination events
- « no » rare alleles

- No population structure effect
- « Same genetic » background





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Jordan et al (2011). Crop Sci 51:1444-1457

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47 populations, 4717 BC_1F_4 families

Direct variety development through PPB



Biomass yield and quality BCNAM Design



- B pool
- 20 BC populations
- 100 BC1F4 / pop
- Topcross phenotyping in 2018





BREEDING SCHEMES AND MARKER USES EVOLUTION AND ADAPTATION

- Heterotic groups identified...
 - Towards dedicated Reciprocal Recurrent Selection schemes



- Marker-use strategies
 - Classical QTL / GWAS detection and allele follow up and stacking
 - Using the « black box » : genomic selection



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TAKIN TRAN

TAKING ADVANTAGE OF COMPARATIVE GENOMICS AND TRANSCRIPTOME ANALYSIS



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CREATING NEW VARIABILITY : EMS MUTANTS !

EMS Mutant libraries : functional tools to identify genes of interest and create variability



AR520

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The CRISPR Revolution

GENOME EDITING THROUGH CRISPR CAS9 : RESEARCH (AND BREEDING) BENEFITS

Vi Atounian/Steiner

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

Wenzhi Jiang¹, Huanbin Zhou², Honghao Bi², Michael Fromm³, Bing Yang² and Donald P. Weeks^{1,*} 2013

CRISPR Cas9 can be used for :

- Iarge 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 AND PERSPECTIVES (I THINK !!!)

- Sorghum breeding is an exciting place able to mobilize relevant genetic and breeding teams
- European sorghum breeding has specificities (target environments)
- Works performed in the US / Africa / India / Australia... are highly valuable and have to be considered
- There is no need to COORDINATE : researchers will search and breeders will breed in their own ways whatever you do !
- But there are huge benefits to COLLABORATE / AGREGATE results and EXCHANGE EXPERIENCES
- Intensifying collaborations in the pre-breeding phase would largely benefits to the EU Sorghum community



PEOPLE, FUNDINGS AND QUESTIONS!

Gilles Trouche



Jean-François Rami





MINES Alès





CENTRE DE MISE EN FORMI DES MATERIAUX