Tailoring Superior Alleles for Abiotic Stress Genes for Deployment into Breeding Programs: A Case Study Based on Association Analysis of $Alt_{SB}$, a Major Aluminum Tolerance Gene in Sorghum (ALTSORGHUM)

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INRAN - Niger -
IGD (Cornell Univ.) - US -
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The breeding Farm mes have access to modern inputs and use intercropping as a strategy to reduce
phenomenon. Soils are usually very sandy and low in nutrients, especially phosphorus. The productivity of sorghum in such systems is very low but most of the farmers are very well adapted. Farmers do not have access to modern inputs and use intercropping as a strategy to reduce risks of crop failure. With the level of poverty in these areas, finding more resilient cultivars with enhanced productivity is the major goal for research in support of farmers.

Despite long term research efforts in Niger, very few cultivars have been effectively adopted by farmers. The potential of many improved varieties is reduced by soil stresses and farmer low capacity to invest in chemical fertilizers. It is very common to find on farm an improved cultivar barely germinating and/or stunted in its growth, when the unimproved landrace does well on the sandy soils. Can upstream genomics be applied to enhance sorghum yield on acid soils (Al/P/N/drought)?

Breeding for sorghum with enhanced tolerance to aluminum (Al) toxicity is likely to improve overall crop performance through better root growth, nutrient acquisition (especially P), and drought tolerance.
Working hypothesis: a thorough scan into the sorghum genetic diversity can be used to identify 'superior' $Alt_{SB}$ haplotypes ('molecular versions' in different lines) to find breeding ideotypes

- Association analysis can be used to define the molecular make-up of these ideotypes,
- Ideotypes can be tagged by an easy-to-use marker system and introgressed into pre-breeding NILs
- The breeding value of these ideotypes can be assessed in acid soil conditions by an adequate strategy
- Field-validated ideotypes can be efficiently deployed into sorghum breeding programs

Association genetics as a means to summarize genetic information and channel it into breeding programs

- Introgression into pre-breeding NILs (Brazil), adapted landraces and improved cultivars (Niger and Mali)
- Allele mining on adapted landraces with focus on the Guinea core collection (Niger and Mali)
ALTSORGHUM Activities

Step 1. Assembly of the Sorghum Association Panel (n=497)
- EMBRAPA Elite (n=47)
- CIRAD Core (n=210)
- CU Landraces (n=200)
- Wilds (n=50)

Step 2. Assessment of multiple levels of relatedness based on genome-wide SSR markers

Step 3. Phenotypic analysis

Step 4.1. SNP discovery and identification of haplotype tag SNPs in a subset of accessions (n=25)

Step 4.2. Genotyping of association panel with htSNPs

Step 5. Unified Mixed-Model: Association tests between Al+++ tolerance and candidate genes

Step 6. Identification of superior haplotypes

Step 7. Pre-breeding – development of NILs
- NILs
- Introgression
- Allele mining (poor-man htSNPs)

Step 8. Breeding connection (INRAN - Niger)

Deployment
Simulated Sorghum Yields in Safrinha Season (Scott Chapman – CSIRO)

- 40 years of weather data for Sete Lagoas
- Al-tolerant (90 cm roots) vs. sensitive (30 cm)
- Similar yields in ‘good rainfall’ years (1991)
- Drought stress in average years
  - 5000 kg/ha tolerant
  - 2500 kg/ha sensitive
- Shows interaction of rainfall amount and distribution on yield
Link with Other Projects

- Concept Note (Assessment of the breeding value of superior haplotypes for \( Alt_{SB} \), a major Al tolerance gene in sorghum: linking upstream genomics to acid soil breeding in Niger and Mali (ALTFIELD) – Bob Schaffert (PI)

- Fred van Eeuwijk and Scott Chapman:
  - multi-trait (exploring genetic correlations between traits) and multi-environment (Africa and Brazil) analysis for performance of selected \( Alt_{SB} \) haplotypes (haplotypexE).
  - multi-trait analysis to assess the impact of Al tolerance on acid soil performance (drought: 1 dryland site vs 2 irrigated sites).
  - Spatial Analysis to account for fertility heterogeneity within field testing sites.
  - ‘phenotypic integration’ of different association panels into one unified set.

Data Format and Release

- Public database for sharing molecular marker information, including summary statistics tables and matrices of population structure and relatedness.
- Aluminum tolerance data for the association panels and related material (tables)
- Detailed physiological and molecular data for selected haplotypes (tables, charts etc)
- Sequence data (FASTA) for selected haplotypes and haplotype tagging-markers
- Field performance data for NILs and converted germplasm.
- Information related to the field testing sites (semi-variograms, etc).

Release: IGD database provisionally (http://cbsuss03.cs.cornell.edu/sorghum/index.html), then PANZEA database, and GCP database