For pragmatic reasons, 2013 Annual Report has been split and published in 10 sections as follows:

1. Overview on the CGIAR Generation Challenge Programme
2. Cassava Research Initiative
3. Legumes Research Initiative
4. Maize Research Initiative
5. Rice Research Initiative
6. Sorghum Research Initiative
7. Wheat Research Initiative
8. Comparative Genomics Research Initiative
9. Integrated Breeding Platform
10. Capacity Building

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Texcoco, Mexico.
Edited by: Robert Koebner and Larry Butler
Cover illustration: Extracts from original artworks by Rhoda Okono entitled *Bountiful African Madonna, Homeward bound and Marketplace at dawn*, recomposed by Eliot Sánchez P
Art direction: Eliot Sánchez P, CIMMYT
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### Acronyms

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<th>Acronym</th>
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<tr>
<td>ARC</td>
<td>Agricultural Research Corporation (Sudan)</td>
</tr>
<tr>
<td>EIAR</td>
<td>Ethiopian Institute of Agricultural Research</td>
</tr>
<tr>
<td>INERA</td>
<td>Institut de l’Environnement et de Recherches Agricoles (Burkina Faso)</td>
</tr>
<tr>
<td>INRAN</td>
<td>Institut National de la Recherche Agronomique du Niger</td>
</tr>
<tr>
<td>KARI</td>
<td>Kenya Agricultural Research Institute</td>
</tr>
<tr>
<td>BCNAM</td>
<td>backcross nested association mapping</td>
</tr>
<tr>
<td>CIRAD</td>
<td>Centre de Coopération Internationale en Recherche Agronomique pour le Développement (France)</td>
</tr>
<tr>
<td>GCP</td>
<td>Generation Challenge Programme</td>
</tr>
<tr>
<td>GY</td>
<td>grain yield</td>
</tr>
<tr>
<td>ICRISAT</td>
<td>International Crops Research Institute for the Semi-arid Tropics (India)</td>
</tr>
<tr>
<td>IER</td>
<td>Institut de l’Économie Rurale (Mali)</td>
</tr>
<tr>
<td>MARS</td>
<td>marker-assisted recurrent selection</td>
</tr>
<tr>
<td>QAFFI</td>
<td>Queensland Alliance for Agriculture and Food Innovation</td>
</tr>
<tr>
<td>SARI</td>
<td>Savannah Agricultural Research Institute (Ghana)</td>
</tr>
<tr>
<td>SG</td>
<td>stay green</td>
</tr>
<tr>
<td>WACCI</td>
<td>West African Centre for Crop Improvement (Ghana)</td>
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Sorghum Research Initiative

Introduction

Sorghum is an important crop in the semi-arid tropics, and particularly in its centre of diversity, the Sudano-Sahelian zone of Africa, where water-intensive crops such as maize cannot thrive. While not as drought tolerant as the millets, sorghum is relatively well adapted to environments which are drought-prone. The production of sorghum in West Africa has doubled over the last 20 years, but mainly as a result of an expansion in the area cropped, rather than by any improvement in per unit area grain yield (GY), which has remained at a relatively low level. In general, local landraces are both well adapted and have been selected over many generations to deliver excellent grain quality. However, they typically respond rather poorly to intensification, a process which is increasingly necessary for the continued viability of cropping in the Sudano-Sahelian zone. As the major abiotic constraint to production in the region is a lack of moisture, the stay green (SG) character has assumed great breeding importance; this trait has proved its worth in both NE Australia and the southern part of the USA. The genetic determination of SG is complex – to date at least 25 SG QTL have been identified, and the link between specific QTL and GY under conditions of terminal drought has yet to be demonstrated for most of them. Nevertheless, the expectation is that the incorporation of combinations of SG QTL should enhance the drought tolerance of sub-Saharan African sorghum. The Sorghum Research Initiative includes four projects: (1) the discovery and development of alleles contributing to drought tolerance, (2) the use of marker assisted recurrent selection (MARS) to breed for increased GY, and (3) the use of the backcross nested association mapping (BCNAM) approach to discover relevant QTL and (4) the exploitation of the SG trait as a means of improving the drought tolerance of African germplasm. (Note that some of the sorghum research supported by the Generation Challenge Programme (GCP) programme is included within the “Comparative Genomics” Research Initiative.)
G3008.05: Sorghum - discovery and development of alleles contributing to drought tolerance

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Achievements

The project’s intention was to enhance terminal drought tolerance in improved sorghum germplasm by evaluating combinations of QTL for the SG trait. Six QTL are known to account for more than half of the variation for SG in the cultivar B35, and it is clear that the presence of just any one of these on its own is insufficient protect GY and grain quality from drought stress. A set of four independent SG introgression lines were intercrossed, and the hybrids selfed to form a range of F₂ populations which were field-sown during the late post-rainy season to ensure that the plants experienced terminal drought stress. A set of 91 lines, each homozygous at two SG QTL, were then evaluated in the field both under irrigation during the dry season and under rain-fed conditions. In both seasons, significant genotypic differences were observed for almost all the agronomic traits followed, and the best ten lines for each trait have been re-evaluated in replicated trials across northern Ghana during the 2013 cropping season. The sorghum genome is the second cereal genome (after rice) to have been fully sequenced, so gaining an understanding of the molecular basis of drought tolerance is a feasible proposition. Total RNA was therefore extracted from thirteen diverse accessions at nine distinct plant growth stages to enable both transcriptome profiling and SNP identification. The number of usable reads per accession ranged from 29 to 57 million. A detailed analysis of these data is in progress. In order to empirically test for any relationship between drought tolerance and the transcription of specific genes or alleles, a RIL population which segregated for SG was evaluated in the field over three years. This data set is currently being assembled for further analysis. Candidate genes identified from the SNP analysis and QTL mapping are to be explored both in the GCP reference sorghum collection (for which data describing the range of variation for GY, transpiration efficiency and water extraction are in hand) and a diversity panel previously identified for SG. Data will be posted to the GCP Central Registry by no later than the end of the project. Much of the data will also be appropriate for, and offered to, other data archives such as the PGML online data dissemination (www.plantgenome.uga.edu), an NSF-funded Comparative Saccharinae Genomics Resource (csgr.agtec.uga.edu), the JGI sorghum genome browser (genome.jgi-psf.org/Sorbi1/Sorbi1.home.html), and Gramene (www.gramene.org). All DNA sequence data will be deposited in Genbank.
**G4008.48: Improving sorghum productivity in semi-arid environments of Mali through integrated MARS**

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**Achievements**

The MARS method has significantly improved breeding efficiency for complex traits in maize, so the focus of this project was to apply it to sorghum improvement. Two separate biparental crosses, targeting two distinct sorghum cropping environments in Mali, were the founders of the two populations developed (#114 and #118). The #114 population is the more advanced. An evaluation made during the 2012 rainy season compared the performance of 79 c1-F$_2$ entries with that of 16 checks, comprising the #114 parents, some improved varieties and three F$_4$ selections of #114 made on the basis of phenotype only. The trials involved two different sowing dates at each of two locations (Sotuba and Cinzana). Three of the c1 families produced the top performers in all four environments, and a further seven produced the best performers in three of the four environments. This was considered positive, as the material had only passed through one cycle of MARS, the GY of the best performers was remarkably stable across environments and the evaluation had been based solely on GY. The characterization of this material for grain quality is ongoing. The second round of MARS was conducted in 2013, at the same two locations, again using two different sowing dates. The test set comprised 64 entries: 36 c2F$_2$ families, 21 c1F$_3$ families and seven checks; and the final cycle, initiated in 2013 in Sotuba only consisted of 345 c2F$_3$ plants (19 C2F$_2$:3 families) and nine c1 families. The process for Population #118 has been initiated, with the first cycle of recurrent selection having started in July 2013; selections were facilitated by OptiMAS software, which was able to exploit a multi-trait selection index. More breeding lines will be evaluated over the coming seasons, as part of and beyond the project, by applying additional MARS cycles to both populations. The expectation is that the programme will deliver productive and stable sorghum germplasm for the IER breeding programme to take forward to on-station and on-farm testing and variety release. The phenotyping data for the two populations have been converted to the IB Field book format. Genotypic, mapping and QTL data will be uploaded into the GDMS module of the IBWS. The local database will be migrated to the GCP Central Registry in the final year of the project.
G7010.05.01: Enhancing sorghum grain yield and quality for the Sudano-Sahelian zone of West Africa using the backcross nested association mapping (BCNAM) approach

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Achievements

This project has featured the use of the BCNAM approach to develop improved germplasm through the introgression of favourable genomic segments, or QTL, into popular and locally adopted germplasm. The research began with the identification and selection of recurrent and donor parents. The characterization of parental lines has been pursued at IER with the evaluation of post flowering drought tolerance of 23 parental lines. Much of the activity has focused on phenotyping the resulting populations, and screening the parental lines for their response to post-flowering drought stress. The phenotyping has been conducted at two contrasting sites, and the parental characterization has involved comparisons between crop performance achieved under limited and full irrigation. Following the choice of parental material (Lata3, Grinkan and Keninkeni, developed out of a participatory breeding programme in Mali as recurrent parents; and a set of 29 donor parents), the final set of 50 BC$_1$F$_3$ populations (each consisting of between 70 and 200 families) was developed for multi-year and multi-site (at both ICRISAT and IER) field evaluation trials in 2012 and 2013.

The phenotypic data collected to date has shown that, for most of the populations, progenies can be identified which express a GY potential superior to that of the relevant recurrent parent. The evaluation of grain quality of these populations is to be conducted as part of the extension project following the purchase and installation of NIRS equipment at IER Sotuba in early 2014. The genotyping strategy was changed in 2013 from KASP-based SNPs at ca. 1,400 loci to genotyping by sequencing to be performed at CIRAD. For this purpose, 50 grains of each of the ca. 6,000 families have been shipped to CIRAD, where DNA is being extracted from a bulk of 20 plants per family. A sub-set of 32 populations (each consisting of at least 100 families) has been advanced to the BC$_1$F$_4$ generation. Phenotyping (GY, grain quality, maturity, plant height and other agronomic traits) has been conducted on 20 BC$_1$F$_4$ populations, using two planting dates per each of the two sites. These are large trials, each involving several thousand plants. Agronomic data are currently held in local files, which can be accessed on request. Grain of the 36 populations is available. Environmental, soil and climatic data for the Sotuba, Cinzana, Farako and Longorola sites have been archived.
G4012.01/G7009.04: Development and evaluation of drought-adapted sorghum germplasm for Africa and Australia (Phase II)

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C Kamau: KARI, Katumani Kenya
A Tirfessa: EIAR, Addis Ababa, Ethiopia
A Mohamed: ARC, Mad Mwedani, Sudan

**Achievements**

Following on from Phase I of the project, in which MAS was used to introduce certain SG QTL into African adapted materials, 68 BC1F2 selections are currently being evaluated at two locations in each of the six participating African countries. The lines being evaluated involve six different SG QTL, with each line harbouring between two and six distinct SG loci. The intention was to expose the material to post-anthesis drought stress, recording both phenology and SG prior to harvest and a set of plant and yield traits post harvest. Most of these trials have already been harvested, and the data is awaiting analysis. A second area of activity was to characterize African germplasm for the presence of known SG QTL. Thus, a 300 line RIL population bred from a cross between an Australian line of known SG content and a Malian line, which had been genotyped during Phase I of the project is currently being evaluated in the field in Mali to enable the identification of which SG QTL are associated with the optimal expression of SG and performance in the local environment. At the same time, six F1 hybrids, combining two Malian lines and three Australian elite lines, where each parental pair presents a contrast in the expression of SG, are being tested under drought conditions at two sites in Mali. An important component of the project was the strengthening of the nascent community of practice for sorghum in Africa. The data will be posted on the GCP Central Registry three months after the end of the project and made available to the subprogram leader at the end of the project if requested.

**Capacity building**

G4008.48 featured a major component of capacity building for the African partners. D Sako has been enrolled in the WACCI PhD programme at the University of Ghana, Legon, D Guindo was based at CIRAD Montpellier for some months, K Thera was hosted by Montpellier SupAgro and CIRAD for two years as an MSc student, M Tékété was hosted by CIRAD for two months and will start a PhD in 2013 in a collaboration involving the University of Bamako and SupAgro. A MARS workshop was organized in Montpellier in May 2013, bringing together partners from Mali, members of the scientific team and students. G7010.05.01 provided training to technicians in how to collect field phenotypic data; K Théra graduated.
with an MSc degree from the University of Montpellier, and is expected to progress to a PhD degree. Two students completed their MSc in Plant Breeding from the University of Ouagadougou, and a further three BSc students have been selected by the University of Ouagadougou to enter the Plant Breeding MSc programme. Training in Australia (G4012.01/G7009.04) has been provided for two Malian and one Ethiopian scientist during February 2012, and a further four scientists (one each from Burkina Faso, Niger, Sudan and Kenya) are to be trained during February 2014. The participants engage with Australian scientists to develop skills in conventional breeding, molecular breeding, crop physiology, pathology, bioinformatics, simulation modelling and leadership/management of science. Visiting Australian scientists will be training personnel in situ in Africa during the first half of 2014. Within project G7010.05.01, an air-conditioned storage facility has been constructed at IER Sotuba to secure the genetic materials developed by the project.

Major accomplishments, challenges & lessons learnt

MAS is a well established breeding method in large commercial programmes enjoying access to a substantial capital and human capacity base. Bringing a version of this technique to a region such as the Sahel was bound to raise numerous technical and manpower challenges. These were manageable where the MAS targets were defined a priori as was the case for the introduction of several SG QTL. However, the MARS project has first to identify the key marker/trait associations, as this is the key process underpinning the success of the method in genetically well understood crops such as maize. Achieving this requires a high standard of phenotyping expertise and infrastructure. Meeting the challenge, the programme was able to demonstrate genetic progress in several breeding populations, whether produced by MARS, BCNAM or backcrossing The robustness of the accumulated QTL still remains to be established, and particularly those which, like many of those underlying drought tolerance do, interact strongly with the environment. This will require continued replication over multiple seasons and locations.

Conclusions & perspectives

The benefits which would flow from an intimate understanding of the genetic and molecular basis of drought tolerance in sorghum are undoubtedly significant. The success of maize breeding in the developed world since the start of the molecular marker age is irrefutable, as is also the gap between current levels of productivity of sorghum in the Sahelian farmers’ fields and the crops’ genetic potential. The Research Initiative has put in place a number of the elements required to embed genotype-based selection into sorghum breeding in the Sahel. These are, prominently, the development of human capacity in the form of trained and motivated personnel, the selection of germplasm well adapted to the local climatic and soil conditions, and the identification of the genetic determinants of the key traits. Genotyping, key to the success to such a strategy, has not proven to be a road-block which it was once thought to be, as the out-sourcing to a service provider of this activity is a model which clearly works (provided that the necessary financial provision is available). Indeed, since the genome sequence of sorghum has already been acquired, it has become feasible to contemplate directly identifying the genes which underlie important QTL effects; if this approach proves to be productive, it would pave the way for producing perfect (within gene) markers for what are still considered as “difficult” traits.
Hosted by CIMMYT
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