Australian Government

Australian Centre for International Agricultural Research

Final report

project	**A targeted approach to sorghum improvement in Ethiopia**
project number	CIM/2013/005
date published	1/06/2019
prepared by	Professor David Jordan
co-authors/ contributors/ collaborators	Professor Graeme Hammer Dr Emma Mace
approved by	Eric Huttner
final report number	FR2019-08
ISBN	978-1-925746-84-6
published by	ACIAR GPO Box 1571 Canberra ACT 2601 Australia

Contents

1 Acknowledgments

The UQ/DAF project team would like to thank Erik Huttner (ACIAR) and Yilma Kebede (BMGF) for their support and advice during the development of the grant and subsequently. The team would also like to acknowledge the tremendous efforts of the sorghum research team at EIAR.

2 Executive summary

This project aimed to address food security issues in Ethiopia by seeking an enduring increase and stability in productivity of sorghum in water-limited production systems through the development of more effective local sorghum crop improvement programs. The project was funded jointly by ACIAR (~$0.7M) and the Bill and Melinda Gates Foundation (~$4.6M). The partners in the project from Australia were The University of Queensland (UQ) and the Queensland Department of Agriculture and Fisheries (DAF) working in collaboration with the Ethiopian Institute of Agricultural Research (EIAR). The project enhanced the capacity of the national sorghum breeding program through improved strategic planning and the implementation of modern methods of plant breeding and agronomic research. In addition the project identified genes associated with drought adaptation mechanisms in sorghum and developing molecular markers and phenotyping approaches to apply this understanding effectively in applied breeding programs. These tools will be used in Australia to improve drought adaption and have also been transferred to the Ethiopia research agencies. The project was successful in substantially improving the capacity crop improvement program and has received praise as model for this type of activity. Subsequently the Bill and Melinda Gates Foundation has invested in a similar program to enhance the capacity of 5 crop improvement programs in Ethiopia with EIAR as the lead and UQ as the partner.

3 Background

This project aimed to address food security issues in Ethiopia by seeking an enduring increase and stability in productivity of sorghum in water-limited production systems through the development of more effective local sorghum crop improvement programs. Sorghum is the world's fifth most important cereal and a staple food crop of millions in the semi-arid tropics. It is crucially important to food security in Africa as it is grown in the drier and resource poor areas, where its capacity to better tolerate drought, high temperature, and low fertility make it a preferred crop to maize. Despite its stress tolerance, drought still causes significant crop losses and food insecurity in major sorghum growing regions, such as those in Ethiopia (1.89 million ha).

The integrated combination of plant breeding and agronomic research has a long track record of generating increased crop productivity and food security. However this type of approach tends to be context dependent and requires crop improvement in the target environment. Unlike other major cereals, sorghum has not had a "green revolution" in the developing world and crop yield in the developed world has increased less rapidly. This is linked with lack of access to inputs and more variable production environments that challenge effective crop improvement. Moreover, in comparison to its importance, sorghum improvement has received limited investment. In sub-Saharan Africa and Asia, the major producing countries are relatively poor, and their sorghum growing regions poorer and less politically influential. In the developed world, sorghum is a low value feed grain and investment has been less than for maize (USA) and wheat (Australia).

While productivity improvements in sorghum have been low in general, there are examples of substantial gains from closely integrated plant breeding and agronomic research. For example, in Australia, where dryland sorghum is grown in areas with 550 to 750mm annual rainfall, seasonally-adjusted yield increases of up to 4% per annum have been reported (Stephens et al., 2012), which is equivalent to the best rates of productivity gain achieved by any cereal improvement program. While direct impacts of improved varieties and of improved management systems contributed to this change, by far the largest impact was made by exploiting favourable interactions between genotypes and management systems to make the most productive use of the water available to crops grown in particular production environments.

Crop improvement for productivity improvement in water limited sorghum is challenged by environment variability and context dependencies. Breeders and agronomists are attempting to identify favourable combinations of varieties and management practices that optimize water use in a complex system where the resources available to search for these combinations are limited. As a result plant breeding solutions (varieties) and agronomic solutions (management systems) are usually developed in isolation even though historically the largest impacts to productivity have been made by exploiting favourable interactions between genotypes and management systems to make the most productive use of the water available to crops grown in particular production environments. In recent years approaches which aim to optimize genotype x environment x management (GxExM) interactions have been made more feasible through the development of crop modelling technologies that permit evaluation of large numbers of potential GxExM combinations in silico and through new marker technologies that allow the rapid development of new varieties with particular combinations of traits. This represents a true paradigm shift but requires a strongly integrated multi-disciplinary systems approach that takes into account variability in production environments and integrates knowledge of crop physiology, genetics and management practices. Such an approach requires a balance of skills and capacities across the relevant areas.

While the integrated combination of plant breeding and agronomic research has a long and credible track record of generating increased crop productivity and food security, this type of approach tends to be context dependant and requires activity in the target environment. In Africa, there is a critical need to strengthen local breeding efforts. New technologies such as genomic selection using whole genome scans, advanced statistical methods, novel selection methods, and crop simulation offer exciting opportunities to accelerate progress. But effective implementation requires integrated multi-disciplinary teams. Poor implementation of these technologies in small scale breeding programs can be worse than no implementation, as resources can be re-directed from conventional breeding activities without sufficient return. This issue is particularly relevant to small African sorghum improvement programs that struggle to sustain the necessary infrastructure and skills. The aim of this project was to implement this type of integrated approach to crop improvement to specific target areas in Ethiopia by raising the capacities of the critical elements of local programs to the necessary level and to supply skills, capacity and expertise to support the building of that local capacity. As well as enhancing capacity, we worked with the local programs on the implementation of this approach through joint applied crop improvement activities targeting specific geographic regions. Finally, we conducted research activities in Australia to understand the physiological and genetic basis of key traits affecting water productivity and provide knowledge and germplasm that can be used to deploy favourable variants in sorghum programs worldwide. We envisaged that through such an approach the program in Ethiopia would have the capacity to assess and make use of the information generated by this more strategic research.

Attempts to apply advanced plant breeding methods in developing country programs tend to be unsuccessful because the necessary infrastructure and skills to deploy the technologies are not available. And attempts to directly deploy elite germplasm developed elsewhere often fail due to lack of local adaptation and consideration of local tastes and cultural practices. One new solution to this problem is to link developing country breeding programs to advanced institutes so that they access capacities they need but cannot easily reproduce, while also building infrastructure and competencies locally. We implemented this approach here by establishing the necessary programmatic and personnel linkages. In the longer term we hope to see the successful changes in methodologies and approaches transmitted to other breeding programs in other crops within the partner organizations and regionally.

4 Objectives

The strategic goal of this project is to improve sorghum productivity and drought adaptation in the 500-750mm rainfall zone in Ethiopia, where moisture stress is a common feature of the environment. The project was originally designed to work in both Ethiopia and Mali however due to the coup and conflict in Mali the scope was restricted to Ethiopia only. Within Ethiopia we specifically targeted the Eastern and Western Hararghe regions. In these regions, sorghum is a staple cereal and drought frequently leads to food shortages but crop improvement programs have had limited impact. As a result a key activity was to build up the plant breeding by improving the technical capacity of national sorghum breeding program in Ethiopia while improving agronomic research through developing the capacity to do local biophysical crop modelling in Ethiopian environments to identify best bet trait combinations of management and genetics to suit the target environments.

The project had three connected objectives that formed an integrated approach to deliver improved breeding practices and improved productivity -

1) enhance the efficiency and capacity of the national sorghum breeding programs

2) improve productivity of sorghum in the target rainfall zones of Ethiopia by a combination of breeding and agronomic research,

3) increase understanding of key drought adaptation mechanisms in sorghum and developing tools to apply this understanding effectively in applied breeding programs.

The approach we used integrates activities from strategic trait discovery, focused on drought, through to the development of efficient and effective breeding pipelines and applied breeding and agronomy.

Activities within these three objectives were interfaced with the existing national crop improvement programs –

(i) Enhancing the efficiency and capacity of the national sorghum breeding programs

Sorghum varieties are adapted to specific sets of challenges. Achieving productivity gains requires appropriately focused long term investment in well-equipped and well-staffed crop improvement programs targeting specific environments. The sorghum breeding programs in Ethiopia lag significantly behind world best practice for conventional plant breeding and have yet to take advantage of recent technological developments such as enhanced statistical methods, crop modelling, molecular marker technologies, and information management systems, all of which provide opportunities for much more rapid progress. A key focus of this component was to enhance the capacity of these programs by providing necessary tools and training linked to the development of appropriate strategic thinking and planning. These new capacities were applied to the problem of crop improvement in the target regions and joint activity between the breeding programs in Australia and Ethiopia developed plant breeding capacity through mentoring and “training by doing”.

(ii) Improving productivity of sorghum in the target rainfall zones Ethiopia by a combination of breeding and agronomic research

In this project component we introduced and applied the newly developed breeding capacities in an applied breeding activity which target the identification of superior genotype and management packages for the target regions. This involved the use of improved statistical design and analysis systems, crop simulation modelling, and molecular breeding capacity within the existing breeding system. As well as delivering breeding products the activity will “bed down” the new approaches and technologies and iron out difficulties in implementation.

(iii) Increasing understanding of key drought adaptation mechanisms in sorghum and developing tools and germplasm sources to apply this understanding effectively in applied breeding programs - A key focus of our approach to sorghum improvement in Australia has been to consider the opportunities presented by understanding the biology and genetic architecture of traits that contribute to water productivity and use crop simulation modelling to scale this understanding to crop production systems with a view to identifying favourable combinations of genes (varieties) and management systems within our production environments. This approach was enabled by the development of cost effective whole genome scanning methods, which have generated the opportunity for breeding programs to change from the paradigm of identifying superior varieties to one of identifying useful genetic regions and combining these regions into varieties that perform well in particular management systems and environments. The trait understanding required for such an approach is equally applicable to the improvement of water productivity in Africa as it is to Australia. The focus of this component was to develop a deeper understanding of the physiology and genetics of traits that determine drought tolerance in sorghum with the view to rapidly using this knowledge in applied crop improvement programs.

In this component, we aimed to identify and map genetic variation in key water productivity traits associated with water capture, transpiration efficiency and harvest index. We made use of natural variation in sorghum varieties adapted to Ethiopia and Australia, as well as the large nested association mapping resources available in Australia. Specific targets of investigation included root angle, variation in the regulation in transpiration patterns, transpiration efficiency, and tillering (for eg see Singh et al (2011) and Mace et al (2012)). Outputs included identification of sources of favourable alleles, knowledge of physiological variation and genetic architecture, and high throughput screening methods. These outputs fed into the enhanced breeding capacity developed in component 1 as well as contributing to global sorghum improvement more widely.

5 Methodology

The vision of success for this project is a step change in the capacity of the Ethiopian national sorghum crop improvement program

Project planning

An initial project planning meeting was conducted with all of the Australian and Ethiopian project staff and a bench marking document was prepared that provided:

1) A summary of the current farming systems in the target region of Ethiopia (climate, soils, farming practices, end uses farm sizes, current a varieties, utilization, markets etc)
2) A summary of the current capacities and resources available to the EIAR crop improvement team (number of staff and their training, equipment for plant breeding and agronomic research, soil and climate data, research stations).
3) A detailed technical description of the sorghum breeding program (number of sites, trial size designs and locations, equipment, breeding methods, statistical methods etc)

Based on an assessment of the benchmarking study a range of interventions were identified (see figure 1 below) and a detailed project work plan was developed jointly with the Ethiopian team including outputs, milestones and detailed activities.

Increased rate of genetic gain in breeding programs

A number of interventions were targets to improve the Ethiopian breeding program

- *Identification of major product types (product concepts) to be targeted by the breeding program.* This activity involved specifying the attributes of the varieties that are required to meet the demands of the customers of the breeding program and provides focus for the breeding program.
- *Redesign of the breeding program to deliver increased genetic gain.* This involved changes to the structure of the breeding program to increase genetic gain per unit time using the “breeder’s equation” as a framework for the changes. Using this framework genetic gain is improved by increasing selection intensity, increasing genetic variance, increasing heritability (selection accuracy) and reducing generation time. In practice these changes required increases in population sizes, the development of a strategic crossing program focused on product concepts, improved use of statistics, greater use of off season nurseries, commencing yield testing at earlier generations, use of molecular markers for population enrichment.
- *Implementation of a range of technologies, systems and breeding program mechanization interventions to support the modifications to the breeding pipelines.* A large range of interventions were employed most of which involved equipment purchases, training and system redesign. The interventions included:
    - Electronic data capture and associated data basing. Use of electronic data capture devices, implementation of barcode based seed inventory, developing seed packet printing capacity, the purchase and set up of a server to allow safe data storage and sharing, data basing of historical performance and pedigree data, standardized pedigree and trait scoring systems.
    - The use of advanced statistics. This involved primarily training and changes to systems.

- The development of the capacity to use outsourced genotyping services. Purchase of freeze drier and geno-grinder inventory and labelling systems.
- The development of the capacity to use NIR to conduct early generation screening for grain quality. This included purchase of an NIR machine for quality screening, training, the development of relevant calibrations for injera quality.

Developing the capacity to use crop modelling to characterize sorghum environments and identify combinations of genotype and management that improve productivity

A number of activities were undertaken to support development and application of sorghum crop modelling

- *Characterisation of phenology of local germplasm.* This activity involved quantifying developmental rate responses to temperature and photoperiod for sorghum germplasm relevant to Ethiopia and developing predictive models for phenology for that germplasm. Nineteen genotypes representing the four major sorghum races (caudatum, caudatum/guinea, kafir, and Ethiopian highland durra) were evaluated in two locations, Melkassa (lowland) and Kulumsa (highland) to quantify developmental responses and develop predictive phenology models. Genotypes were planted on six sowing dates at the two locations over two years to create a range in photoperiod (PP) and temperature relevant to Ethiopian conditions. Observations of phenological stages including days to flag leaf appearance, anthesis, and maturity were recorded to parameterise phenology functions. The optimisation program (DEVEL) was used to fit the model for rate of development as a function of temperature and photoperiod, where rate of development (R) is the daily increment for the phenological phase.
- *Parameterising and validating the APSIM-sorghum crop growth model for Ethiopian germplasm*. Growth analysis experiments were conducted at Melkassa under non-limiting (water and nitrogen) conditions in 2014 and at Miesso for water-limiting dryland conditions in 2016. Canopy development coefficients and crop growth coefficients were derived from the growth analysis experiments. The genotypes used in the growth analysis experiments represented a subset of those used in the phenology experiments (see Table 3.1). Five genotypes (ESH2, Gambella1107, Jigurti, Teshale and Meko) representing landraces, an improved hybrid, and improved varieties were planted in a randomised complete block design with three replications. Aboveground biomass and its partitioning among organs was determined on four occasions by destructively sampling an area of 1 m2 (8.9 plants per m2) in each plot at eight fully expanded leaves, flag leaf full expansion, anthesis and physiological maturity. Data were analysed to quantify partitioning between leaves and stems, crop growth rate, and grain number produced per unit of biomass accumulated. Predictive capacity of the parametised model was tested by comparing simulated and observed biomass and yield accumulation using soil characterisation and weather records at the experimental sites.
- *Environment characterisation for sorghum in Ethiopian dry lowlands.* For 16 sites throughout the dry lowlands sorghum production zone of Ethiopia soil profile information and long-term weather data were collated from all available sources and quality checked. The validated sorghum model was used in simulation studies to characterise production environments for early sowing with a late maturing genotype and late sowing with an early maturing genotype. Environments were

classified based on the trajectory of water limitation predicted throughout the crop life cycle. Some breeding sites were sampled for soil, weather, and crop growth so that environment type for the specific trial could be quantified.

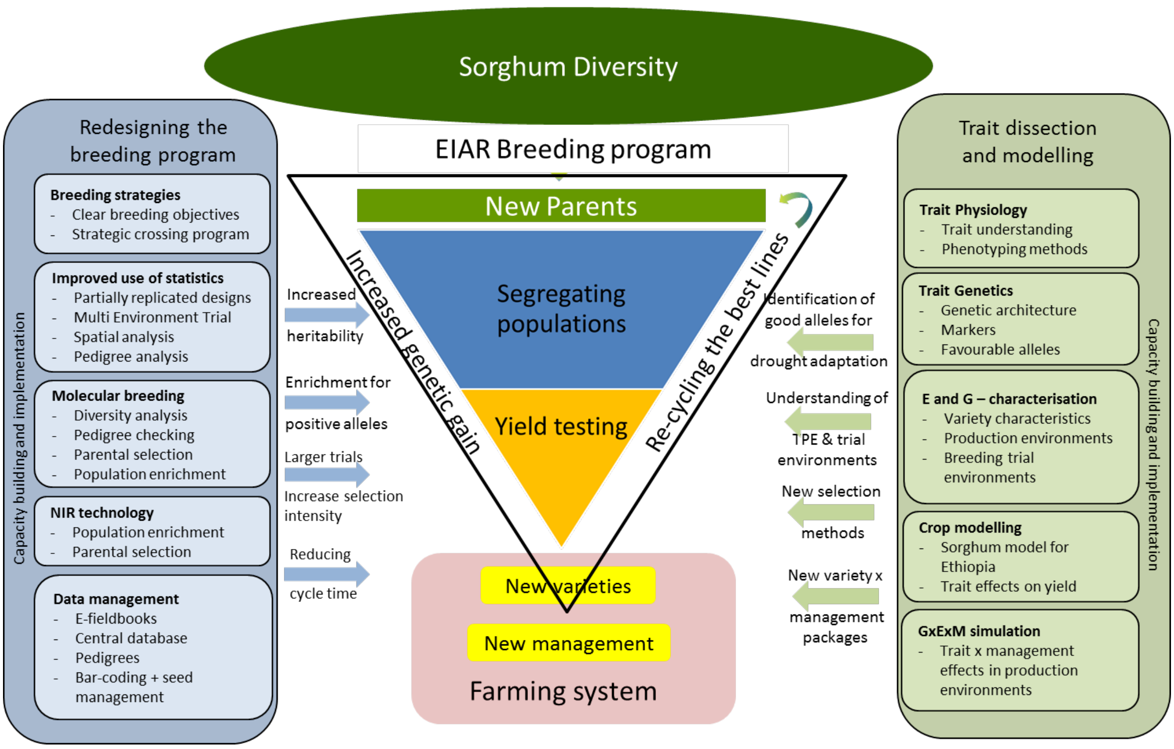
- *Simulating production risks for combinations of genotype and management.* Long-term simulations were conducted using available soil and weather data for both early sowing with a late-maturing type and late sowing with an early maturing type for all regions in the Ethiopian dry lowland sorghum growing areas. Results were analysed to quantify production possibilities and risks for the contrasting scenarios

Increasing understanding of key drought adaptation mechanisms in sorghum and developing tools and germplasm sources to apply this understanding effectively in applied breeding programs

A number of activities were undertaken in relation to the physiological and genetic basis of variation in transpiration efficiency (TE) in sorghum -

- *Exploring variation in TE among Ethiopian germplasm. A set of 25 Ethiopian genotypes that included durra, caudatum, and mixed race lines was grown in 16L lysimeters in an experiment at Melkassa, Ethiopia. In addition, a set of 36 genotypes that included African landraces* and improved lines and hybrids that were all relevant to the Australian program were evaluated in 4L lysimeters in an automated lysimetry platform in three experiments at Gatton, southeast Queensland, Australia. Experiments were harvested around anthesis at Melkassa and at mid-late vegetative stage at Gatton. TE was calculated as the ratio of dry mass at harvest to total water use, with roots only included at Melkassa.

Figure 1 Diagram describing the “iMashilla” project



6 Achievements against activities and outputs/milestones

Objective 1: Enhancing the efficiency and capacity of the national sorghum breeding programs

no.	activity	outputs/ milestones	completion date	comments
1.1	Conduct planning workshop in Ethiopia to develop a detailed strategic and operational plan	Strategic plans for improving sorghum productivity in Ethiopia developed and circulated to key stakeholders. Benchmark document on breeding program produced	Yr 0, m12	A benchmarking document and strategic plan were generated. This was achieved prior to the start of ACIAR involvement. It was key to the smooth implementation of the project and contributed to the subsequent success.
1.2	Collate soil data and historic climatic data for the target regions in Ethiopia and conduct simulation analyses	Environment classifications in target sorghum production zones in Ethiopia completed (report)	Yr 1, m12 (data base) Yr 2, m12 (simulations)	Soil and climate information was collated and simulations conducted once the model validation completed. Environmental characterisation completed for the dry lowlands production regions of Ethiopia.
1.3	Implement electronic data capture and management technologies in breeding program in Ethiopia	Enhanced information management and analysis capability implemented in breeding program in Ethiopia (comparison to benchmark document)	Yr 1, m12 (preliminary) Yr 3, m12 (advanced)	Full implementation of field-scorer data capture was achieved at all EIAR sorghum breeding locations by the end of the project. A server established and used to store and share this and other breeding program data.
1.4	Implement statistical designs and analysis capacity in breeding program in Ethiopia	Enhanced information management and analysis capability implemented in breeding program in Ethiopia (comparison to benchmark document)	Yr 1, m12 (preliminary) Yr 3, m12 (advanced)	These methods were implemented with help from UQ and DAF. The establishment of full autonomous capacity was prevented by the departure of the trained statistician from the program. A subsequent BMGF project which is building on the success of MERCI is building a group of statisticians to provide support all of the breeding programs in EIAR. We feel this approach will be more stable and autonomous.
1.5	Design and develop capacity to conduct high throughput grain and food quality assessment to support breeding program	Enhanced information management and analysis capability implemented in breeding program in Ethiopia (comparison to benchmark document)	Yr 2 m6 (calibrations) Yr 3 m6 (commence implementation)	We implemented high throughput systems for screening for grain quality including NIR and image analysis of injera samples. NIR calibrations were developed for a range of important traits. Image analysis was used to rapidly assess the number and size of bubbles ("eyes") in Injera which is a key quality parameter. Progress has begun into integrating these methods into the selection process within the breeding program to select lines and eliminate lines.
1.6	Conduct training in analysis of information generated by cost-efficient molecular breeding techniques for implementation in breeding program in Ethiopia	Enhanced information management and analysis capability implemented in breeding program in Ethiopia (comparison to benchmark document)	Yr 2, m12	A number of trainings were conducted. Markers for key traits were developed and used in the breeding program to select and eliminate lines.

1.7	Conduct training in crop modelling techniques for implementation in breeding program in Ethiopia	Enhanced information management and analysis capability implemented in breeding program in Ethiopia (comparison to benchmark document)	Yr 1, m6 (preliminary) Yr 2, m12 (advanced)	In this milestone we began the process of integrating the crop modelling with the breeding program by characterizing the types of environments in sampled by breeding program trials with the population of types of environments identified using historical climate and soil data.

PC = partner country, A = Australia

Objective 2: Improving productivity of sorghum in the target rainfall zones of Ethiopia by a combination of breeding and agronomic research

no.	activity	outputs/ milestones	completion date	comments
2.1	Redesign and conduct multi-environment trial (MET) series in target regions to capture efficiencies arising from Objective 1	Improved sorghum germplasm specifically adapted to management system and stress patterns of target regions developed (activity reports and comparison to benchmark document)	Yr 2, m6 (METs) Yr 3, m6 (METs) Yr4, m6 (METs)	A large number of changes have been made to the program to increase the scale of the breeding program. Critically the size of the population at first yield testing has increased from 36 to 430 entries. Breeding cycle time has been reduced by at least 2 years from 8-9 years to 6-7 years.
2.2	Conduct controlled environment and field experiments in Australia and Africa for physiological characterisation of key varieties for paramaterisation of the sorghum model	New combinations of genotype and management system most likely to optimise sorghum productivity in the region identified (activity and technical reports)	Yr 1, m12 (experiments) Yr 2, m12 (experiments) Yr 4 m12 (modelling analysis)	Phenology and crop growth experiments were conducted with key Ethiopian varieties. The model was successfully parameterised for Ethiopian germplasm and validated on field experiments at Melkessa and Miesso. Simulation studies of genotype x management scenarios were conducted.
2.3	Collect soil, crop, and climate data at MET sites for use in crop models. Simulate crop growth and development at MET sites to characterise environment types experienced by each trial	Improved sorghum germplasm specifically adapted to management system and stress patterns of target regions developed	Yr 1, m12 (data base) Yr 2, m12 (simulations) Yr 3, m12 (simulations) Yr 4, m12 (simulations)	Weather stations and soil sampling were established at sample MET sites. Simulation analysis was conducted to classify environment types at sample sites. Systems were put in place for future application for breeding and agronomy studies.
2.4	Conduct simulation studies to explore potential trait and management combinations that could improve yield in target regions in Africa and Conduct field experiments in target regions in Africa to test hypotheses generated in silico	New combinations of genotype and management system most likely to optimise sorghum productivity in the region identified (activity and technical reports)	Yr 2, m12 (design workshop) Yr 3, m12 (simulations) Yr 4, m12 (prelim expts)	Simulations of planting date x maturity were conducted and identified most advantageous combinations Simulations were completed for all regions of dry lowlands. The trade-off of productivity with risk varied with region and rainfall distribution. Specific experiments to test concepts designed were designed but there was insufficient time to conduct them

2.5	Important local landraces and cultivars genotyped to characterise genetic diversity available to Ethiopian sorghum breeders	Improved sorghum germplasm specifically adapted to management system and stress patterns of target regions developed (activity report)	Yr 2, m12	192 important landraces and elite lines from the breeding program were selected for a preliminary diversity analysis, with genotyping out-sourced to Diversity Arrays technology in Australia. Over 50,000 marker data points were generated and used to characterise the genetic diversity within the germplasm set.
2.6	Ethiopian breeding programs generate crosses of local African material identified with superior traits and breeding value and introgress regions known to control key adaptive traits into locally adapted germplasm to produce material for future evaluation	Improved sorghum germplasm specifically adapted to management system and stress patterns of target regions developed (activity reports and comparison to benchmark document)	Yr 2, m12 (crosses) Yr 3, m12 (introgression) Yr 4, m12 (initial evaluation)	Strategic changes made to the crossing program focused on producing specific targets. 1) Local land races enhanced for Striga and drought resistance characteristics using marker assisted backcrossing 2) Improved early maturity varieties with acceptable grain yield and biomass production. Crosses for both targets have been made. Marker assisted introgression has commenced. Segregating materials will be tested for 2) in year 4.
2.7	Interaction with key participants in relevant impact pathway projects: include actors in the local seed system, seed companies, other actors in sorghum seed production, distribution, marketing and extension.	Key participants invited to review and planning meetings to enable 2-way communication and integration. From final meeting: impact pathway (delivery pathway) described in a joint document, listing needs and opportunities for a follow-on project.	Yr 2, m6 (mid-term meeting) Yr 4, m6 (final review meeting)	Project experience has been communicated to the many collaborators of the EIAR program at national sorghum meetings and at meeting for other sorghum projects SMIL, AGRA as well as iMashilla meetings. Communications have been conducted with EIAR senior management and with staff of other EIAR breeding programs. Conduct a final project meeting bring in major stakeholders and collaborators

PC = partner country, A = Australia

Objective 3: Increasing understanding of key drought adaptation mechanisms in sorghum and developing tools and germplasm sources to apply this understanding effectively in applied breeding program

no.	activity	outputs/ milestones	completion date	comments
3.1	Construct phenotyping systems and undertake trait physiology experiments on traits and populations of interest	Medium-high throughput phenotyping systems (lysimeters and rhizotrons) developed for canopy and root traits, TE and biomass partitioning (activity reports and publications)	Yr 1 m12 (trait experiments) Yr 2 m12 (trait experiments) Yr 3 m12 (trait experiments)	New phenotyping platforms were established to screen root architecture and TE in Australia, with ~3000 lines from multiple complementary populations screened for root angle and~1000 lines from the Nested Association Mapping population screened for TE, with substantial phenotypic variation identified for both traits. Both platforms were transferred to Ethiopia for screening Ethiopian germplasm; a TE platform was established at Melkassa and used to screen ~100 entries in 2017 and the root angle screening platform was established at Jimma University and used to screen ~100 entries from the PVT stage of the breeding program, in addition to ~1000 Ethiopian landraces.

3.2	Generate/acquire high density genotypic data on populations and conduct genetic analysis to identify QTL and genes for traits	Genomic regions associated with key traits identified (activity reports and publications)	Yr 3 m12 Yr 4 m12 (trait mapping experiments and genetic analysis)	Whole genome profiles (Diversity Arrays, www.diversityarrays.com) have been generated for 2180 NAM progeny from 35 families, in addition to a set of ~600 breeding lines, and a higher marker density data set for the diversity panel, altogether representing a data set of >250M data-points. Genotypic data were integrated with the phenotypic data generated in 3.1. on root angle and TE and GWAS conducted using the software FarmCPU to identify genomic regions significantly associated with the traits. The QTL analysis conducted for the root angle trait identified 36 genomic regions associated with root angle in the NAM, 43 in the diversity panel and 22 in the breeding populations, with 29 QTL in common between at least 2 populations. An average QTL effect size of approximately 2 degrees and a maximum QTL effect of 3.6 degrees was identified. Publication is underway.
3.3	Incorporate science on traits into APSIM-sorghum to improve its biological functionality and validate improved sorghum model using independent data sets	Improved APSIM-sorghum model validated and released (technical report)	Yr 4, m6	Sorghum model for Ethiopian germplasm and environments developed and preliminary validation conducted. Further experimentation required to enhance validation. Findings on temperature responses for rate of development identified some previously undiscovered results in relation to low base temperature. Simulations identified value of this trait for sorghum production in Australia (via putative cold tolerance for early sowing).

7 Key results and discussion

The integrated combination of plant breeding and agronomic research has a long track record of generating increased crop productivity and food security. However this type of approach tends to be context dependent and requires crop improvement in the target environment. After dropping the planned activity in Mali at the beginning of this project, we focused on the development of more effective local sorghum crop improvement programs in Ethiopia. The aim was to achieve an enduring improvement in capacity of the EIAR program to develop improved combinations of sorghum cultivars and management systems (objectives 1 and 2). A secondary aim of the project was to investigate the basis of two important drought adaptation traits (root architecture and transpiration efficiency) which are potentially valuable in both Ethiopia and Australia.

Objectives 1 and 2

Objectives 1 and 2 of the project are highly related and will be discussed jointly. These objectives focus on building capacity of EIAR to do effective crop improvement and operationalizing those new capacities in the breeding program targeting the dry lowlands. To achieve this we are using a “learning by doing” approach which involved Australian researchers working closely with Ethiopian scientists to improve their capacity, skills, systems and strategies then working with scientists to implement this improved capacity results in their breeding program.

Benchmarking and planning

An initial activity of the project was to benchmark the current situation of the breeding program in Ethiopia and develop a plan for the project. As a first step in achieving objectives 1 and 2 we held a workshop in April 2013 attended by 25 Australian and Ethiopian scientists where we jointly developed the framework for the project by:

- developing a background benchmarking document describing the current status of the sorghum crop improvement program focused on the dry lowlands,
- identifying specific changes to be made,
- developing a detailed work plan of activities. The meeting was very successful and provided both Australian and Ethiopian scientists with a good understanding of mutual capacities. Many of the EIAR scientists were quite young and many commented that they found the project planning exercise very useful as a training activity in itself.

Based on the planning exercise three major work areas were identified

1) Changes to breeding strategies. These included identifying well defined product types, increasing the number of crosses made by the breeding program, increasing generation sizes at all stages of the breeding program to increase selection intensity, and better targeting of trials through understanding of genotype by management interactions.

2) Introduction of new technologies along with associated training and integration into the breeding program. These include: implementation of advanced statistical analysis methods to increase heritability and permit increased selection intensity (spatial analysis, pedigree BLUPs, P-rep trial designs), implementation of breeding program data management systems (E-fieldbooks, databases, barcodes), use of crop modelling to understand target environments and simulate the value of trait and management combinations, and implementation of alternative phenotyping methods (NIR, molecular markers).

3) Crop model based environment characterization and cropping system simulation to identify targets (Genotype*Management*Environment – G*M*E). This activity aimed to characterise the nature of water limitation in production environments in Ethiopia in a manner suitable to enhance genetic gain in breeding, and to quantify the possibilities for yield improvement via G*M*E simulation studies in target environments in Ethiopia.

1) Changes to breeding strategies

Product concepts

One of the key elements of any breeding program is to have a clear well defined breeding strategy. To develop such a strategy requires that the program identifies a set of targets which are called product concepts or product profiles by commercial breeding companies. These product concepts consist of a defined set of traits (eg levels of resistance, quality parameters, maturity and yield) for a defined market (agro-ecology, market size, customer and end-user). These product types provide the framework for designing the breeding programs to deliver the products and help the breeder to prioritize resource allocation to the different product development pipelines (breeding programs). In collaboration with UQ/DAF personnel the EIAR crop improvement team have developed two product concepts around which to build breeding pipelines. In deciding on these targets they have balanced the current preferences of farmers for local landraces particularly due to their interest in biomass with the longer term need for shorter duration varieties which are more suited to increasingly drier seasons. The two product concepts are listed below.

Product concept 1 (PC1): Local landraces with Striga resistance and stay green. Rapid introgression of Striga resistance and stay green traits into popular cultivars. This was a new activity which made use of marker technology to rapidly introduce important traits into popular local varieties.

Product concept 2 (PC2): Early maturing varieties with acceptable yield, quality and biomass production; stable and moderate yielding OPVs for low input systems, combining earliness, good biomass and optimum grain yield with a range of preferred head and kernel traits (eg durra head shape). This was a modification of existing breeding activity but with a new emphasis on developing products that met clients need for biomass and grain quality.

Design of breeding pipelines to deliver product concepts

Breeding pipelines represent the operational design component of a breeding program incorporating breeding methods, breeding generation sizes, selection methods and generation time. Typically they are designed taking into account quantitative genetic principles to maximize genetic gain which are summarised in the “breeder’s equation” and resource limitations which limit factors such as trial size. Optimizing breeding pipelines is a continual process as influenced by changes in costs, priorities and technology. The UQ/DAF team provided training in the design process while working with the EIAR team to develop pipelines for their product concepts. These new pipelines took into account changes in technology that were introduced into the breeding program to enhance efficiency

The new pipeline for PC1 makes use of marker technology to rapidly improve local varieties for resistance to the parasitic weed striga by introgression of the low germination stimulant gene using marker assisted backcrossing. The technological changes introduced here are systems to enable the implementation of markers including systems to collect and freeze-dry leaf tissue samples and track seed and leaf samples. The marker system chosen is LGC KASP assay using markers developed from DArT seq markers by EIAR staff working with Australian scientists,

The PC2 breeding pipeline aims to produce varieties combining earliness with good biomass production and optimum grain yield. PC2 has a longer timeframe and is aimed at producing new varieties with enhanced performance and quality using a forward breeding approach (modified pedigree). The activity is focused on producing improved varieties with earlier maturities that are suitable for later sowing but which have characteristics (particularly increased biomass) that will make them attractive to farmers. Low biomass has been a major contributor to the limited uptake of improved varieties produced by the program. This involved identifying clear achievable breeding strategies and increasing potential genetic gain in the program by increasing selection intensity, heritability and generation time through the use of new technologies. This approach will attempt to change multiple quantitative traits and will involve larger populations and recycling of material. Other changes include reducing cycle time by testing lines at earlier generations. A key change is the introduction of partially replicated designs and pedigree analysis, allowing more genotypes to be included for the same number of plots and for similar heritability. Technologies which increase the scale, efficiency, and effectiveness of the breeding activities (eg see below) were critical to these changes. In terms of population size and selection intensity the aim has been to increase the genotypes evaluated in the first level of yield testing (PVT) to 300-500 entries up from 36 entries prior to intervention (2014 PVT 433, 2015 PVT 300). The number of entries in National variety trials (NVT) has increased from 30-40 prior to the project up to around 100 (2014 NVT 57, NVT 2015 108). In addition yield testing now commences at F5 rather than F8 which reduces the time to the first yield test by 2-3 years and the overall cycle time from 8-9 years from cross to release to 6-7 years from cross to release.

2) Introduction of new technologies

One of the critical elements of this project was the introduction of new technologies to enhance the capacity of the breeding programs to deliver the products they have decided to produce. The EIAR sorghum program was operating at a low level prior to this intervention with low levels of automation, poor data management and antiquated statistical designs and analysis, lack of emphasis on product quality and no use of molecular marker technology.

Improved data management

Modern plant breeding involves management and sharing of multiple interlinked pieces of data as well as physical seed packets. The management of this data requires the use of database systems and the direct capture of data from electronic devices such as scales and NIR machines. These systems can generate large savings in time and labour. EIAR’s use of technology in breeding was at a very low level and this area was a major focus of this project across a range of areas. This activity has achieved or exceeded most of the objectives set and had impacts outside the project with technologies being taken up by other projects and breeding programs. This project activity involved the purchase of equipment such as packet printers and software as well as training and mentoring activities. The sorghum team at EIAR is well on the way to implementing a modern approach to data management.

Data backup, sharing

Prior to this project, breeding program data was held on individual computers and therefore extremely vulnerable to loss as well as being unavailable for sharing with team members. As part of the project a central server computer was set up for the team at Melkassa. This server is being used as the central repository for all of the data produced by the breeding program and is backed up regularly. It protects against data loss and enables sharing of information between team members. The project hosts the breeding program databases and the shared files for digital data capture. The server also provides locations for sharing other breeding program files including barcode labels, presentations and images etc. Sharing has been enabled by the installation of a dedicated wireless router purchased by the project to enable access in the sorghum research lab with UPS systems provided to ensure access when power is out at the station (a frequent occurrence).

Electronic data capture of field notes

EIAR now uses electronic field-books as standard for all of its breeding trials and related experiments and has trained most of its breeding staff and technicians from partner organizations in the use of electronic data capture systems. The phenotypic data points collected in each breeding trial run by the breeding program has increased substantially (eg increase in data points collected from about 1300 per trial (2007-2013) to ~5000 data points per trial in 2014/17). Data from the FieldScorer program is backed up and shared via a central server purchased as part of the project. The use of electronic barcodes to measure plant height and grain yield directly from scales has greatly reduced time taken to collect data and the accuracy of the data collected. A particular advantage of this changes has been the time taken for data entry and the availability of data for analysis in a timely fashion to enable selection decisions to be made. Previously this would take more than a month and often data was not ready for analysis before decisions needed to be made for the next years trials.

Barcode based weighing and seed inventory

Modern plant breeding involves management of many interlinked pieces of data as well as physical seed packets. It is important to be able to have a clear understanding of the location and quantity of seed in thousands of packets of seed and to conduct regular stocktakes. Barcodes are a critical tool in managing these processes. Previously the EIAR team used plastic packets or bottles with hand written labels to manage thousands of packets of seed. As part of this project we provided the team with a packet printer capable of printing barcodes on seed packets, barcode readers and suitable electronic scales which enable a range of improvements in the efficiency of critical operations such as planting, harvest and stocktake. These systems have allowed the teams to handle the larger scale breeding pipelines that were designed. The project has paid for the refitting of the sorghum seed store with efficient shelving and trays for seed packets. The DAF seed management system has been implemented as a temporary measure until the BMS software is installed. Scales and barcode readers and associated data collection software have been purchased and the sorghum program staff trained in their use. This equipment can be used for seed inventory as well as in field digital weighing. In field digital weight capture is now being used in all breeding trials resulting in substantial efficiency gains and error reduction in field trial harvesting and savings in data transcription time. A small barcode label maker has been provided to help with DNA sample tracing. Plans are in place to extend the barcoding system to the food quality laboratory.

Setting up a central database and collating historical data,

Prior to this project the EIAR sorghum team had no central storage of field trial data with the exception of hard copies. As part of the project, the sorghum program data from 2007 to 2015 has been collated and cleaned and stored in a Katmandoo database on the server. New systems have been developed or formalized for pedigrees, seed sources and trial names. As of 2016 more than 500 trials have been stored and are available for retrieval and analysis. EIAR has chosen the BMS database as their plant breeding database as part of the MERCI project (a follow on project funded by the Bill and Melinda Gates Foundation). We will facilitate transfer of data to the new system in our role as consultants to the MERCI project.

Improved statistical methods

Improved statistical methods play a critical role in modern plant breeding programs both by improving the accuracy of the estimates of variety performance and by permitting more individuals to be evaluated for the same level of resource. Statistical methods used by EIAR were poorly implemented and used methods that were developed more than 40 years ago. In this project we trained EIAR staff to implement a range of new methods including spatial analysis, partially replicated trials, pedigree analysis and multi-environment trial analysis. These methods enabled trials with many more entries to be run and greatly improved the accuracy of the estimates of genotype performance (heritability). While this technology had a major impact, the high staff turnover in EIAR has meant that we are unable to retain the key staff member who was trained in these methods. Luckily this activity is a major focus of the follow-on project MERCI which is being supported by the Bill and Melinda Gates Foundation. In this project we aim to have a larger group of statisticians supporting multiple breeding programs which should be much more stable to staff changes.

Introduction of molecular marker technology

Molecular marker technology was implemented in the program in 2014, starting with a preliminary diversity analysis of 192 selected landrace lines, that enabled the genetic characterisation of key groups of germplasm being used in the breeding program. The marker genotyping was outsourced to Diversity Array Technology in Australia, and a functional sample preparation system to enable outsourced genotyping was developed.Capital items purchased for EIAR to support the molecular marker work were installed by UQ and DAF project team members in October 2015 to support leaf tissues collection, storage, freeze-drying and grinding. A larger diversity analysis of 718 genotypes was conducted in 2015, leading to a marker data set of ~1000 lines and a total of >25M data –points. Pair-wise genetic distcnaces have been calculated between all entries for use in parental line selection within the breeding program. The whole genome profile marker data generated was also used to design customised KASP SNP assays for markers flanking the lgs gene associated with striga resistance and also flanking five key stay-green QTL identified previously (stg1, stg2, stg3a, stg3b and stg4). In 2015, a total of 359 F2 progeny from 48 families were screened with 3 KASP assays flanking lgs (service outsourced to LGC) and a total of 62 progeny homozygous for the lgs donor allele were identified in addition to 179 progeny heterozygous for the lgs donor allele. The lines identified with the lgs donor alleles were crossed back to the recurrent parent resulting in a total of 16 BC1F1 families generated from a cross with a homozygous F2 plant and 60 BC1F1 families from a cross with a heterozygous F2 plant. In the 2016 season, up to 8 plants per family were be sampled to a) confirm the lgs status, in the case of the homozygous F2 plant derived BC1F1 families and b) identify segregating lgs donors, in the case of the heterozygous F2 derived BC1F1 families. A total of 131 progeny were identified for progression to the next generation based on the lgs SNP assays in 2016. Further, in 2016, 317 progeny from 19 families were screened with 10 KASP assays flanking 5 stay-green QTL regions. A total of 171 progeny with beneficial stay-green alleles at a minimum of 3 of the 5 stay-green QTL regions were identified for progression to the next generation in 2017.

Introduction of NIR technology

Sorghum's main use in Ethiopia is for human consumption. However, end-product evaluation is labor intensive and time consuming, which prevents its implementation in early generations of breeding programs. This causes considerable inefficiencies for breeding programs if varieties are progressed through the program to the release stage only to be discarded due to failure to meet quality standards (waste of effort, lack of acceptance, lack of improvement in quality). NIR and other technologies provide methods for rapidly screening large numbers of lines for a number of quality parameters, allowing selection early in the breeding program. As well as ensuring that varieties that do not meet quality standards are not released it also provides the opportunity for forward selection for improved quality. In 2014 a Perten Inframatic 9500 NIR machine was purchased and deployed in Melkassa. Training courses were run for 20 participants. NIR calibrations were developed based on samples from the breeding program for moisture, protein, ash, iron, zinc and tannin in grain and flour. In 2016 new NIR calibrations were developed from ~160 samples for total starch and amylose in grain and flour. More than 1000 samples from the preliminary yield testing (PYT) trials in 2013 and 2014 were scanned and trait values predicted for the existing calibrations. Injera quality remains the limiting factor due to the time taken for sensory evaluation using human panels. In 2016/17 we developed and calibrated image analysis, including customised software, of injera eye parameters to quantify both the number and the size of the eyes over time (in fresh injera and then over a course of days to assess staling and the associated change in texture). These new screening technologies will be implemented at different stages of the breeding program, with the NIR screening being conducted on the larger early generation populations to exclude low quality samples, followed by the automated injera texture/image analysis at the PVT stage and finally the injera sensory analysis at the NVT stage. The full implementation of these quality screens into the product concept pipelines is continuing in the MERCI project.

*Crop model based environment characterization and cropping system (Genotype*Management*Environment – G*M*E) simulation*

This activity aimed to characterise the nature of water limitation in production environments in Ethiopia in a manner suitable to enhance genetic gain in breeding, and to quantify the possibilities for yield improvement via G*M*E simulation studies in target environments in Ethiopia. Environment characterisation (envirotyping) involves quantifying the type and frequency of water stress environments experienced by sorghum grown in key locations within the target environments. It required the collection of historical environment and weather data, characterisation of local genotypes for modelling and running of simulation models. Large experiments were conducted measuring biomass and flowering on multiple check genotypes. The data from these experiments was of very high quality and was used for model validation. Developmental patterns of Ethiopian germplasm have now been quantified and a paper is being drafted as part Ethiopian PhD students program. The experiments provided interesting insights into the differences in performance between Ethiopian and Australian sorghum genotypes, potentially indicating lower base temperatures for Ethiopian material compared to Australian material. There was also an absence of any photoperiodic response of relevance to conditions in Ethiopia. This is starkly different from the phenological characteristics of West African sorghum germplasm. Growth and yield predictions on all available data from growth experiments indicate the sorghum model is performing credibly.

Available long term daily weather files for sites in the dry lowlands sorghum producing regions have now been collated and edited for gaps and quality. Daily radiation data was added using robust weather generation procedures. Soil attribute files were constructed for all sites based on best available information. Ethiopian scientis visited Toowoomba for training and Australian scientists conducted APSIM training on 2 occasions in Ethiopia. A comprehensive environment characterisation for dry lowlands sorghum was conducted by simulating stress patterns experienced at each site with available long-term weather data and soil information. Two systems were simulated – a traditional, late-maturing land-race sown early and an early-maturing type sown late. The phenology model for each genotype was derived from analysis of phenology field experiments in Ethiopia. Five environment types, which differed in the level of drought stress experienced by the crop, were identified in each of the situations. There was a higher frequency of types with stress around flowering with the early sown case. The breeding trial at Miesso in 2015 was sampled and instrumented so that the environment type experienced by the check in that trial could be quantified. The simulation indicated a severe terminal stress type with onset of water stress just prior to flowering. Automated weather stations are being installed at other key breeding trial sites and sampling protocols being put in place for trials during 2016. This will enable envirotyping across the breeding trials and facilitate use of this information in genetic analyses and selection.

In undertaking the envirotyping simulations across seasons, it was observed that the extent of carry-over of stored soil water from one season to the next (due to late rains during grain filling) was an important factor in the stress level experienced in the subsequent season. This provides opportunity for prediction of risk of crop failure as well opportunity for adjusting G*M to suit the specific circumstance. This possibility will be further explored in the G*M*E simulation analysis planned for the coming year.

Objective 3

The rationale of this objective was to underpin the development and deployment of sorghum cultivars with improved yield in environments where water stress is likely to occur, such as the environments identified and used in objective 2. The focus of this objective was to understand the physiological and genetic basis of trait complexes that influence water capture (root traits) and water use (transpiration efficiency). Molecular markers and screening methodologies were developed that can be used by the enhanced breeding program in Ethiopia as well as sorghum breeding programs targeting water limited environments world-wide.

For each of the trait complexes, we employed a broadly similar strategy that integrates physiological and genetic dissection. First, we identified sources of genetic variability in the two key drought tolerance component traits relating to water capture and water use. Due to the complex nature of these traits and their significant G*E*M interactions, we also employed physiological dissection to identify the processes that determine genotypic differences for these traits, in order to identify relevant genotypic differences in underpinning component traits using our large nested association mapping population.

Genetic resource development

Whole genome profiles (Diversity Arrays, www.diversityarrays.com) have been generated for 2180 NAM progeny from 35 families, representing a data set of >100M data-points. Seed from these progeny has been increased and subsets of seed have been distributed to project team members for key trait dissection activities. Whole genome resequencing data is available for a total of 20 of the parental lines of the genotyped populations, which has enabled sequence imputation methodologies to be applied in order to impute whole genome sequence data for the progeny. Additionally, high density GBS data has been generated for a further 904 diverse lines from the sorghum conversion program, representing broader genetic diversity across the cultivated gene-pool. Information from these populations can be transferred to Ethiopian germplasm by identifying shared haplotypes in genomic regions containing QTLs for the trait in question.

Trait dissection: transpiration efficiency (TE)

Simulation modelling suggests that TE would have a large impact on genotype performance in water limited environments in Australia (and potentially in Ethiopia). Genotypic differences in transpiration efficiency (TE) can be associated with differences in photosynthetic capacity (which determines plant growth) and leaf conductance (which determines water use). Two experiments were conducted to quantify the role these two components play in the determination of genotypic differences in TE, with the results indicating that genotypic differences in TE are predominantly driven by differences in leaf conductance, although photosynthetic rates can explain a significant proportion of the residual variation.

TE is difficult to measure in the field we set up a high-throughput phenotyping for TE, a fully automated lysimetry platform with a capacity of 560 small (4 litre) pots was commissioned and used it to estimate TE in 871 lines from the NAM populations and subsequently mapped 21 QTL for this trait. A smaller scale lysimetric experiment was conducted in Ethiopia and showed similar ranking so common genotypes and diversity in TE within local landraces. The analysis of this data is ongoing but is expected to be published in 2019.

Trait dissection: Root architecture

Previous research conducted by UQ has shown that the angle of nodal roots in seedlings is correlated with root angle in adult plants and is associated with variation in the timing and spatial distribution of water uptake. As with TE this is a difficult trait to evaluate in the field so a high throughput system was developed which could measure root angle on 500 plants per run. Ten runs of 500 plants each have been conducted, with the first two runs focusing on phenotyping of advanced hybrids, and six runs on phenotyping NAM populations, and the last two runs on screening the large diversity panel. Across individual runs, root angle typically ranged from a minimum of 16-20˚ to a maximum of 36-42˚ importantly, the wide-sense heritability exceeded 80% in six of the runs, and repeatability of results across runs was generally high. This indicates that the system provides a suitable phenotyping platform for root angle. A similar system has been shipped to Ethiopia and is now operational at Jimma University as part of the PEARL project (a small BMGF funded project).

~1300 NAM progeny, 900 diverse lines were screened for nodal root angle in the root chambers. QTL analysis was conducted and identified ~30 common genomic regions associated with root angle, with an average QTL effect size of approximately 2 degrees and a maximum QTL effect of 3.6 degrees. Additionally a set of 564 unique hybrids from the advanced yield testing stage of the sorghum breeding program in Queensland were screened for nodal root angle which identified 24 QTL for root angle, of which half (13) were in common with the QTL identified in the NAM population. QTL will be identified on the diverse set of Ethiopian landraces being screened in a second identical root chamber setup at Jimma University in Ethiopia as part of the associated BMGF PEARL project there.

8 Impacts

8.1 Scientific impacts – now and in 5 years

The main science impacts arising from this project are as follows:

- Identification of germplasm source lines and QTLs for transpiration efficiency and root angle which can be used for conventional breeding and marker assisted selection in Ethiopia and Australia. In the longer term this should result in sorghum varieties being developed that are higher yielding and more robust to the impact of drought.
- Development of NIR calibrations and automated image analysis for key quality characteristics influencing injera quality of Ethiopian lines which will result in more efficient selection and an improvement in product quality. In the longer term this should result in improved end-product quality for people consuming sorghum products.
- Development of an understanding of the types and frequency of water stress environments for sorghum grown in the dry lowlands of Ethiopia. In the longer term this should enable more appropriate varieties and management systems to be developed which should in turn increase yield and reduce risk for small holder farmers in Ethiopia.

8.2 Capacity impacts – now and in 5 years

Capacity building was the main focus of this project with the major capacities developed including:

- Development of the capacity for EIAR scientists to use the APSIM sorghum model. This will enable improved capacity to develop new varieties and management systems in future and potentially to develop systems to estimate yield and risk.
- Development of the capacity of EIAR sorghum researchers to analyze the quality of grain. In the future this will contribute to a variety of activities around improved varieties and product quality.
- Development of the capacity of the EIAR sorghum breeding program. The changes in this project will result in a large increase in the rate of genetic gain achieved by the Ethiopian national sorghum breeding program. In the longer term this will result in better varieties (eg higher yields, better quality, improved drought and pest resistance) being available to small holder farmers more quickly potentially increasing productivity, food security and incomes.

8.3 Community impacts – now and in 5 years

The project is somewhat upstream so most of the benefits for communities will come when new varieties from the breeding program are released and have impacts on the productivity of smallholder farmers and the quality of the products they produce. Economic impacts

The first products of the breeding program will be released in 2019 or 2020 with benefits scaling with adoption. The main benefits will be via economic improvements and improvements in the quality and reliability of production of sorghum foods. Increases in incomes of smallholder farmers are likely to result from greater productivity and quality associated with increased demand for grains from urban populations

8.3.1 Social impacts

Potentially increased productivity will allow small holder farmers to have greater surpluses to trade. Women play the major role in the production and sale of sorghum so it is likely that an increase in surpluses will improve cash flow in farm families and will be more likely used for the benefit of children.

8.3.2 Environmental impacts

Ethiopian farming has substantial environmental impacts due to the loss of soil through erosion resulting from intensive land use, over cultivation and free grazing. Potentially more productive varieties are one way that more sustainable land management practices could be made feasible.

8.4 Communication and dissemination activities

Within Ethiopia there have been a number of communication and dissemination activities. During the project the activity provided multiple training activities each year attended by breeders and scientists from EIAR and beyond. For example more than 100 staff have been trained in the use of hand held data capture devices. Others have been trained in the use of NIR and cereal chemistry methods.

A large workshop was held at the end of the project over 2 days in Addis Ababa. The meeting was expanded thanks to additional funding from ACIAR which was used to invite additional guests from outside of the project team. The meeting was opened by the Ethiopian Agriculture Minister with remarks by the Australian Ambassador and was attended by more than 90 researchers, funders and managers from more than 11 countries. The attendees fell into the following groups; EIAR researchers and managers (44), other Ethiopian researchers (13), sorghum scientists from other African countries including ICRISAT researchers (13), funding body representatives (4) and Australian scientists (11). The EIAR attendees included members of the sorghum team as well as key members of the breeding teams of other crops including those that form part of the MERCI project. Upper management of EIAR was represented by the DDG of EIAR Dr Adugna Wakijira, the Crop Director Dr Eshetu Derso and Dr Alemayehu Aseffa who is the coordinator of the BMGF funded MERCI project.

12+ presentations have been given at international meetings including the global sorghum conference. Results of the project have influenced funders such as the Bill and Melinda Gates Foundation and organizations such as ICRISAT.

13 scientific papers have been published with 8 more in preparation.

9 Conclusions and recommendations

The integrated combination of plant breeding and agronomic research has a long track record of generating increased crop productivity and food security. However this type of approach tends to be context dependent and requires crop improvement in the target environment. Despite having a well trained workforce and a strong government commitment to agricultural R&D, the crop improvement programs at EIAR were in a poor state, with a lack of critical equipment and strategic direction. As result they were not making a major contribution to improving the lives of the people they served. This project demonstrates the capacity of national agricultural research agencies to modernize and take up new technologies when properly supported and funded.

9.1 Conclusions

This project demonstrates that at least in some cases with relatively modest investment and good mentoring it is possible to improve the capacity of plant breeding programs in research agencies like EIAR to a level at or near world's best practice. This project also demonstrated that the use of genomics tools and common phenotyping platforms can greatly enhance the synergistic outcomes of crop breeding research across countries with similar breeding targets such as Australia and Ethiopia. Crop simulation modeling can provide insight into changes that could be made to genetics and farming systems to increase yields and manage risk in developing country agriculture systems

9.2 Recommendations

Further investment in capacity within EIAR building on this and other projects is likely to be beneficial. In particular investment areas such as seed systems and the application of crop modelling would build on and enhance the work done in this project. In addition consideration should be given to investing in the improvement of agricultural research management within EIAR which is also in need of modernization.

10 References

10.1 References cited in report

Enter text

10.2 List of publications produced by project

Joshi DC, Singh V, Hunt C, Mace ES, van Oosterom E, Sulman R, Jordan DR, Hammer GL (2017). Development of a phenotyping platform for high throughput screening of nodal root angle in sorghum. Plant Methods. 13:56. DOI: 10.1186/s13007-017-0206-2.

Mindaye TT, Mace ES, Godwin ID, Jordan DR (2016) Heterosis in locally adapted sorghum genotypes and potential of hybrids for increased productivity in contrasting environments in Ethiopia. The Crop Journal 4: 479-489; doi: 10.1016/j.cj.2016.06.020

Mindaye TT, Mace ES, Godwin ID, Jordan DR (2015). Genetic differentiation analysis for the identification of complementary parental pools for sorghum hybrid breeding in Ethiopia. Theor Appl Genet. 128: 1765-1775. doi: 10.1007/s00122-015-2545-6.

Chenu K, Van Oosterom EJ, McLean G, Deifel KS, Fletcher A, Geetika G, Tirfessa A, Mace ES, Jordan DR, Sulman R, Hammer GL (2018). Integrating modelling and phenotyping approaches to identify and screen complex traits: transpiration efficiency in cereals. Journal of Experimental Botany 69, 3181-3194.

Partial contribution from iMashilla

Hammer G, Messina C, van Oosterom E, Chapman S, Singh V, Borrell A, Jordan D, Cooper M 2016. Molecular breeding for complex adaptive traits: how integrating crop ecophysiology and modelling can enhance efficiency. Crop Systems Biology, 147-162. DOI: 10.1007/978-3-319-20562-5_7

Luo H, Zhao W, Wang Y, Xia Y, Wu X, Zhang L, Tang B, Zhu J, Fang L, Du Z, Bekele W, Tai S, Jordan DR, Godwin ID, Snowdon RJ, Mace ES, Jing H-C, Luo J (2016). SorGSD: a sorghum genome SNP database. Biotechnol Biofuels 9:6; **doi:** 10.1186/s13068-015-0415-8.

Alam MM, Mace ES, van Oosterom EJ, Cruickshank A, Hunt CH, Hammer GL, Jordan DR. (2014) QTL analysis in multiple sorghum populations facilitates the dissection of the genetic and physiological control of tillering. Theor Appl Genet 127: 2253-2266. DOI: 10.1007/s00122-014-2377-9.

Mace ES, Singh V, van Oosterom EJ, Hammer GL, Hunt CH, Jordan DR., 2012. QTL for nodal root angle in sorghum (*Sorghum bicolor* L. Moench) co-locate with QTL for traits associated with drought adaptation. Theor. Appl Genet. 124: 97-109. DOI 10.1007/s00122-011-1690-9.

Alam MM, EJ van Oosterom, AW Cruickshank, DR Jordan, GL Hammer (2016). Predicting Tillering of Diverse Sorghum Germplasm across Environments. Crop Science. 57: 78-87. DOI: http://dx.doi.org/10.2135/cropsci2016.04.0262

Alam MM, GL Hammer, EJ Oosterom, AW Cruickshank, CH Hunt, Jordan DR (2014) A physiological framework to explain genetic and environmental regulation of tillering in sorghum New Phytologist 203 (1), 155-167. DOI: 10.1111/nph.12767

Alam MM, van Oosterom EJ, Cruickshank AW, Jordan DR, Hammer GL (2016). Predicting Tillering of Diverse Sorghum Germplasm across Environments. Crop Science. doi:10.2135/cropsci2016.04.0262

Alam MM, Hammer GL, Van Oosterom EJ, Cruickshank A, Hunt CH, Jordan DR (2014). A physiological framework to explain genetic and environmental regulation of tillering in sorghum. New Phytologist 203 (1), 155-167. doi: 10.1111/nph.12767.

11 Appendixes

11.1 Appendix 1:

Enter text