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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Art direction: Eliot Sánchez P, CIMMYT
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Acronyms

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<th>Acronym</th>
<th>Description</th>
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<tr>
<td>CIMMYT</td>
<td>Centro Internacional de Mejoramiento de Maíz y Trigo</td>
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<tr>
<td>CSIRO</td>
<td>Commonwealth Scientific and Industrial Research Organization (Australia)</td>
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<tr>
<td>DArT</td>
<td>diversity array technology</td>
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<tr>
<td>EIAR</td>
<td>Ethiopia Institute for Agricultural Research</td>
</tr>
<tr>
<td>GY</td>
<td>grain yield</td>
</tr>
<tr>
<td>HAAS</td>
<td>Hebei Academy of Agricultural Sciences (China)</td>
</tr>
<tr>
<td>IARI</td>
<td>Indian Agricultural Research Institute</td>
</tr>
<tr>
<td>ICARDA</td>
<td>International Center for Agricultural Research in the Dry Areas</td>
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<tr>
<td>ICIS</td>
<td>international crop information system</td>
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<tr>
<td>INRA</td>
<td>Institut National de la Recherche Agronomique (Morocco)</td>
</tr>
<tr>
<td>JNKVV</td>
<td>Jawaharlal Nehru Krishi Vishwavidyalaya (India)</td>
</tr>
<tr>
<td>MABC</td>
<td>marker assisted backcrossing</td>
</tr>
<tr>
<td>MARS</td>
<td>marker assisted recurrent selection</td>
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<tr>
<td>MAS</td>
<td>marker assisted selection</td>
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<tr>
<td>NRCPB</td>
<td>National Research Centre for Plant Biotechnology (India)</td>
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<tr>
<td>QTL</td>
<td>quantitative trait locus</td>
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<tr>
<td>SAAS</td>
<td>Shanxi Academy of Agricultural Sciences (China)</td>
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<tr>
<td>SHW</td>
<td>synthetic hexaploid wheat</td>
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<tr>
<td>SNP</td>
<td>single nucleotide polymorphism</td>
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<tr>
<td>SSR</td>
<td>simple sequence repeat (microsatellite)</td>
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<tr>
<td>WSC</td>
<td>water soluble carbohydrates</td>
</tr>
<tr>
<td>WUE</td>
<td>water use efficiency</td>
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<tr>
<td>XAAS</td>
<td>Xinjiang Academy of Agricultural Sciences (China)</td>
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Wheat Research Initiative

Introduction

Globally, wheat is the world’s second largest contributor to calorie intake, but its productivity over large parts of its cultivated area falls well below its potential. A major cause for this shortfall is the yield constraint imposed by drought and high temperature, stresses which are set to become more severe as the climate changes. Bread (hexaploid) wheat is a relatively newly evolved species, having been formed scarcely 10,000 years ago. Its rather recent origin has left it with a notably narrow genetic base. Nevertheless, the species exhibits remarkable plasticity, enabling it to be grown almost from the Arctic Circle to the Equator (albeit, with respect to the latter, only at high altitudes). The core activity in this Research Initiative is to elucidate the genetic basis of the genetic variation for tolerance to abiotic stress present in adapted Indian and Chinese germplasm, with a view to assembling the relevant quantitative trait locus (QTL) into elite materials via a marker assisted selection (MAS) and a major marker assisted recurrent selection (MARS) approach. The scale of the latter programmes is quite unprecedented in public sector breeding efforts, large enough to have the potential to deliver a substantial pay-back for the investment. A second possible avenue to be explored is to widen the genetic base of the crop by accessing its immediate progenitors, the tetraploids emmer and durum wheat (A and B genomes) and the diploid goatgrass (D genome). The introgression of novel allelesgenes from these donors into bread wheat is in principle relatively straightforward and considerable progress has been made in using such materials to improve levels of disease resistance and even the capacity to sustain grain yield (GY) in drought-prone environments. The Research Initiative finally includes a project seeking to identify plant traits which are key for drought adaptation, and to use this knowledge to develop and validate field-based, practical and relevant phenotyping methods.
A first step, a substantial collection of emmer wheat (tetraploid wheat, genomes A and B) was assembled and its genetic diversity sampled both genotypically, using simple sequence repeat (SSR) and diversity array technology (DArT) markers, and phenotypically by growing the material under Indian conditions. The genotypic characterization allowed the collection to be reduced to a reference set of 108 accessions which captured 80% of the SSR alleles represented in the collection. In all, 115 fertile SHWs were generated, involving three different goatgrass (diploid, genome D) accessions. In an attempt to sample further diversity in the A and B genomes, 50 combinations of emmer and hexaploid wheat were combined by crossing, and these hybrids were backcrossed to the bread wheat parent. Over 1,000 doubled haploid progeny were obtained from the hexaploid BC₁F₁ plants, which at the same time were forwarded to F₅; this set of homozygous or near homozygous derivatives was transferred for field testing in India and Australia. A further 53 emmer x bread wheat combinations were forwarded to BC₁F₄ at CIMMYT. A set of 102 durum- or emmer-based SHWs made by CIMMYT were crossed with emmer, generating 137 successful hybrids. Additionally, there was a programme involving the intercrossing of durum- and emmer-based SHWs which generated 176 lines from 30 crosses, and these have been advanced to F₆ in preparation for phenotyping. Some of the earlier generation material has been crossed with elite Indian bread wheat cultivars. A 2013 field trial showed that some of the emmer-based hexaploids out-yielded an established local elite Australian cultivar both when sown at the normal time and when sown late. The yield of these materials will be determined in India during 2014. The data will include genotypic (SSRs, DArTs), germplasm passports and morpho-physiological evaluation, covering emmer wheat and SHWs and derivatives from crosses with bread wheat. These data will be lodged in the GCP Central Registry during early 2014.

**Achievements**

The Final Technical Report for this project was submitted in 2013. The aim of the project was establish a range of new synthetic hexaploid wheat (SHW) lines and AB genome recombinants by hybridizing well characterized emmer wheat accessions acquired from various sources with either goatgrass (to generate SHWs), or directly with hexaploid wheats (to introduce diversity into the A and B genomes); either way, the focus was to access genes able to improve the tolerance of bread wheat to high temperature and drought. As a first step, a substantial collection of emmer wheat (tetraploid wheat, genomes A and B) was assembled and its genetic diversity sampled both genotypically, using simple sequence repeat (SSR) and diversity array technology (DArT) markers, and phenotypically by growing the material under Indian conditions. The genotypic characterization allowed the collection to be reduced to a reference set of 108 accessions which captured 80% of the SSR alleles represented in the collection. In all, 115 fertile SHWs were generated, involving three different goatgrass (diploid, genome D) accessions. In an attempt to sample further diversity in the A and B genomes, 50 combinations of emmer and hexaploid wheat were combined by crossing, and these hybrids were backcrossed to the bread wheat parent. Over 1,000 doubled haploid progeny were obtained from the hexaploid BC₁F₁ plants, which at the same time were forwarded to F₅; this set of homozygous or near homozygous derivatives was transferred for field testing in India and Australia. A further 53 emmer x bread wheat combinations were forwarded to BC₁F₄ at CIMMYT. A set of 102 durum- or emmer-based SHWs made by CIMMYT were crossed with emmer, generating 137 successful hybrids. Additionally, there was a programme involving the intercrossing of durum- and emmer-based SHWs which generated 176 lines from 30 crosses, and these have been advanced to F₆ in preparation for phenotyping.
Achievements

The Final Technical Report for this project was submitted in 2013. Its objectives were first to identify a set of key traits underlying drought adaptation, and then to build on this knowledge to develop a field-based, high throughput relevant phenotyping methodology. For this purpose, a common germplasm panel was raised in 38 field trials placed in locations representing three contrasting mega-environments. The panel comprised an elite set of ICARDA bread wheat germplasm adapted to drought (200 lines) and a training set based on contrasting performance with respect to a selection of important physiological characters (transpiration efficiency, tillering capacity, stem water soluble carbohydrates (WSC), early vigour and flowering). Reflecting the variation between the chosen trial sites, the mean yield of the material varied from under 0.5 to 6.5 t/ha. Under the Mediterranean-type climate, typified by Morocco, a prolonged life cycle and a maximal production of fertile spikes per plant were both identified as desirable plant traits; in this situation, manipulating photoperiod sensitivity could help to fine-tune flowering and thereby increase the length of the stem elongation period. In the terminal drought type environment (Ethiopia), the earliest maturing lines were the best performers with respect to GY. High carbon isotope discrimination ability was correlated with performance. An array of field remote sensing methodologies was tested. These included digital imaging to quantify the development over time of ground cover by the crop, and hyperspectral reflectance to track stem WSC, leaf area index and canopy water content. Linking remote sensing data to crop simulation as a means of predicting performance with respect to complex traits proved to be a promising research avenue. Phenotypic and marker data associated with the lines used in this study will be made available after the six month embargo period.

G7010.02.01: Wheat breeding and selection strategies to combine and validate QTL for WUE and heat tolerance in China

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Achievements

This programme aims to characterize the genetic basis of water use efficiency (WUE) and high temperature tolerance in Chinese wheat germplasm, with a view to developing lines with improved drought and high temperature tolerance. The approach has been based on MAS and MARS. The MARS approach has targeted five populations, genotyped using a single nucleotide polymorphism (SNP) platform, and tested under a diverse set of temperature and moisture regimes. A total of 30 additive QTL and 41 pairs of epistatic QTL has been shown to underlie variation in grain
weight. Seven of the most consistently detected of these loci were involved in seedling root development under both well-watered or moisture stress conditions. One genetic interval on chromosome 3B was found to harbour nine QTL affecting root traits, and so is a prime target for MAS-based breeding. A set of 70 markers of QTL involving chlorophyll fluorescence, canopy temperature depression, WSC and chlorophyll content have been applied in the MARS scheme and recombination is well under way. With respect to the genetic basis of drought tolerance, a QTL discovery programme employed 207 recombinant inbred lines developed from the cross Jingdong8 x Aikang58, which was genotyped with SSRs and phenotyped at two locations under both irrigated and moisture deficient conditions. The analysis identified 16 GY QTL and six for a drought tolerance index. QTL hot spots were detected on chromosomes 3B, 4D and 7A. Progeny from this population are also being recombined in a MARS approach targeting the above markers and traits. The “WPHYSGP” (Wheat Physiological Germplasm Screening Nursery) set of germplasm has been phenotyped at multiple sites across two years, and has been exploited in the form of a large number of crosses, of which 17 have been advanced to F$_2$ and BC$_2$F$_2$; 278 lines have been selected from this material to enter the next round of genotyping and selection. Eleven elite selections have been entered into formal yield testing, and one of these, Zhongmai 36, has moved into its second year of national trials, while seven other selections have been submitted for yield trials at the Province level. The archived data relate to phenotypic and genotypic descriptions of 100 core wheat accessions, along with QTL associated with drought/heat tolerance and the outcomes of MARS breeding. These data will be lodged in GCP Central Registry and uploaded to the International Crop Information System (ICIS) as they are generated.

**Achievements**

A standardized drought and high temperature set of phenotyping protocols has been applied to a core germplasm panel (The Wheat Physiological Germplasm Screening Nursery, supplied by CIMMYT) consisting of 162 entries. The accessions were field evaluated under both irrigated and rainfed conditions at four locations in India. A number of traits related to WUE and high temperature tolerance have been recorded, and superior performers identified as potential parental material. Drought stress was generated by manipulating irrigation, and post anthesis high temperature stress by varying the crop’s sowing date. Entries showing a higher level of stomatal conductance and relatively cooler canopies were identified. Chlorophyll fluorescence proved to be an effective indicator of high temperature stress during the grain filling period. Some stay green types were observed under rainfed conditions. To initiate a MARS strategy, four biparental populations (DBW43 x HI1500, HUW510 x HI1500, BW7203 x BW9149 and PBW442 x BWL0056) have been bred to the F$_5$ generation and phenotyped at four locations, both under rainfed and irrigation conditions; genotyping is being carried out.

**G7010.02.02: Molecular breeding and selection strategies to combine and validate QTL for improving water use efficiency and heat tolerance in India**

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out at IARI. A number of favourable alleles at genes/QTL for WUE and high temperature stress have been identified, and these are being stacked into single lines via a further round of complex crossing. The various progenies will need to be tested for genetic homogeneity and enhanced WUE and/or high temperature tolerance as appropriate, bulked in preparation for the subsequent round of MARS. Genotyping of the MARS populations so far has relied on SSR assays, but SNPs are now to be incorporated. The tagging of known QTL associated with abiotic stress tolerance is being exploited to improve key Indian cultivars (HD 2967, DBW 17, HD 2733 and GW 322, which together cover about 75% of Indian wheat acreage) using marker assisted backcrossing (MABC), with an investment in background, as well as foreground selection. Up to three chromosomes are involved in each MABC stream, and the programme has now reached the BC$_2$F$_1$ generation. Lines which are homozygous for the target QTL and have inherited a high (>90%) proportion of recurrent parent as background are currently being multiplied for field testing in the forthcoming season. The ICIS platform has been used to manage pedigrees, phenotypic and genotypic data. A stand-alone version of ICIS has been established at both Delhi and Ludhiana, and all data generated at these locations will be uploaded to the GCP Central Registry.

**Capacity building**

Two workshops were held during the lifetime of the G3008.08 project, one at ICARDA in May 2010, attended by 12 participants, and the second in Morocco in 2013 attended by nine participants. The topics covered related to the theory and practice of field experiments, traits which are important for water use efficiency, non-invasive high throughput phenotyping, the “focused identification of germplasm strategy” and various breeding methodologies. Within the context of the G7010.02.01 project, six trainee scientists participated in Year 2 of the Integrated Breeding Multi-Year Course held during 2013 in Zaragoza (Spain). One of these, the PhD student F Azam (from Pakistan), who had also attended Year 1 of this course, was awarded his doctorate in Plant Genetics and Breeding in 2013 from the Institute of Crop Sciences, CAAS, winning an “Outstanding Student” award. Y Xiao gave an introduction to the Integrated Breeding Platform and the Integrated Breeding Workbench to a group of 20 staff and students of the Northwest A & F University in December, 2012, and to a group of 12 breeders with the Shandong Academy of Agricultural Sciences in March 2013. Three young breeders (J Yan, A Zhao and Q Li) were instructed in genotyping in wheat using SSRs at CAAS in 2013. Various project personnel co-operated to translate Application of Physiology in Wheat Breeding (edited by M Reynolds et al.) into Mandarin, and this was published by Science Press in January 2013. Within the frame of the G7010.02.02 project, a group of five students from Delhi and two from Ludhiana have benefitted since 2010 from training acquired during their research activities.
Major accomplishments, challenges & lessons learnt

While there is no doubt about the presence of intraspecific variation in the wheat plant’s ability to withstand drought and/or high temperature stress, exploiting this in a breeding situation remains a major challenge. The realization that the genetic basis of tolerance can lie in the presence of several to many (rather than just a small number) modest effect QTL (such as the 30 additive and 41 pairs of epistatic QTL for grain weight and 29 QTL for seedling root traits uncovered in the large MAS/MARS project carried out in China) raises problems not just of logistics but also of selection accuracy. Nevertheless it is encouraging that a single genetic interval on chromosome 3B has been identified as a potential target for MAS. Where smaller numbers of QTL can be identified, progress has been much more rapid: in the Indian MAS/MARS project, favourable alleles at a small number of QTL underlying WUE and high temperature stress have been identified, and the stacking of these into single lines has reached an advanced stage. An issue which confronts almost every QTL programme is that a large proportion of the overall variation present cannot be ascribed to any QTL at all. As an example, the only significant GY QTL identified in the Hanxuan 10 × Lumai 14 cross explained just 13% of the phenotypic variance present under well watered conditions, and hardly 10% under moisture deficient conditions. A part of the problem lies in the imprecision of phenotyping when perforce plants are grown in a heterogeneous environment (notwithstanding attempts to limit this using rotation, soil mapping etc.) under uncontrollable weather. This is of course the driver behind efforts to develop novel phenotyping platforms, such as digital imaging and hyperspectral reflectance, which if successful, can be expected to have a large impact on breeding practice, not just in wheat, but in all arable crops grown under conditions of abiotic stress. On the genetic side, a substantial contribution of this Research Initiative has been the production and evaluation of SHWs and AB genome recombinants, technology. Despite challenges, this effort and the progress that has been made with the MARS research demonstrate that there still remains many opportunities for wheat improvement and that can be conducted directly in developing countries themselves.

Conclusions & perspectives

The focus on new molecular breeding strategies in the Wheat Research Initiative is both timely and appropriate. It is clear from both this and other explorations of diversity within the cultivated wheat gene pool that genetic variation for abiotic stress tolerance is there to be found. The challenge is how to exploit it to best effect, given that few of the individual QTL exert a very large effect. Conventional breeding over many years has succeeded in adapting wheat to an enormous range of environments, including some which were at one time thought too dry and/or too hot for the crop to be viable. The promise of QTL discovery is that the genes involved in this adaptation can be tagged in such a way that will allow them to be moved predictably from one genetic background to another. Fortunately, unlike most, if not all, genes for disease resistance, those determining abiotic stress tolerance are not liable to breakdown, since the environment, unlike the pathogens, is relatively static. Further, there could much to be gained from accessing the secondary gene pool represented by the tetraploid wheats and the D genome donor goatgrass. Probably their biggest contribution will be felt in wheat growing areas where the major constraints to production are a lack of adequate water and a greater risk of experiencing overly high temperatures, scenarios which are of particular relevance if global warming leads to the predicted patterns of climate change across such currently important wheat production areas as northern India and southern Australia. Nevertheless, explorations of diversity within the cultivated wheat gene pool, genetic variation for abiotic stress tolerance was found, target genetic regions identified and elite alleles stacked in elite germplasm in the MARS projects of India and China. These two projects are considered highlights of GCP’s research portfolio and might result in the first successful MARS experiments reported in developing countries.
Hosted by CIMMYT
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