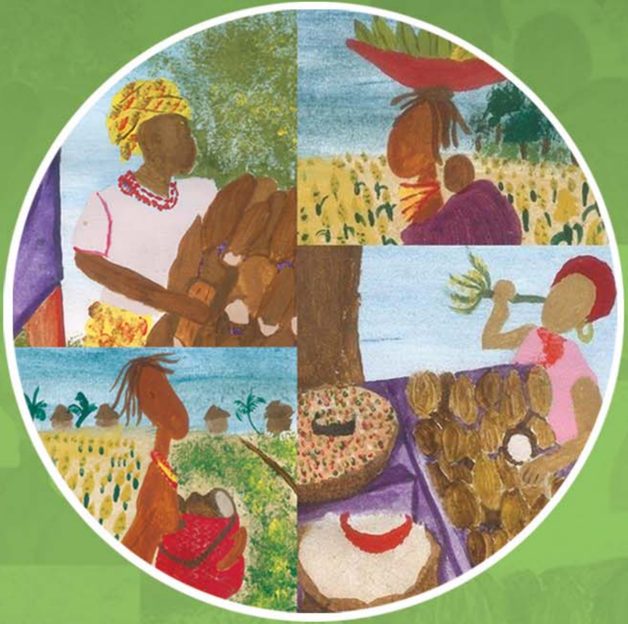

Poster abstracts

General Research Meeting • 27–30 September 2013 • Lisbon, Portugal

Generation Challenge Programme

Partnerships in modern crop breeding for food security

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CGIAR Generation Challenge Programme

General Research Meeting
27–30 September 2013
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Poster abstracts

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Mailing address:
c/o CIMMYT, Apdo Postal 6-641
06600 México, DF México

Physical address:
c/o CIMMYT, Km 45 Carretera México-Veracruz
El Batán, Texcoco, México, CP 56130

Tel: +52 55 5804 2004
Fax: +52 55 5804 7558

Email: generationcp@cgiar.org or info@generationcp.org
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1. Cassava

1.1: Analysis of inbreeding depression in five S_1 cassava families of African varieties

Lydia Ezenwaka, Emmanuel Okogbenin, Chiedozie Egesi, Ugochukwu Ikeogu, Eunice Ekaette, Kenneth Eluwa, Alex Ogbonna and Favour Ewa*

* *National Roots Crops Research Institute (NRCRI), Umudike, Nigeria; e-mail: eokogbenin@yahoo.com*

Cassava is an out-crossing, highly heterozygous plant but is reported to suffer from inbreeding depression (ID). The need to unravel recessive traits, and explore additive genes in cassava would require some limited level of inbreeding in genetic improvement of cassava. In this study, S_1 progenies from five African cassava varieties were evaluated in the seedling nursery (SN) and clonal evaluation trial (CET) stages for disease, morphological/architectural and agronomic traits. SNP markers were used to estimate the level of heterozygosity in the population. Results indicate ID was higher at SN than at CET. Cassava shows superior performance with stem cuttings as planting materials hence the lower ID at CET. No significant ID were observed for the major cassava diseases with the highest being 9.14% for cassava bacterial blight. Considerable variations in ID were observed among S1 progenies for morphological/architectural traits with highest ID ranging from 0.56% in plant height to 46.47% for vigor. Agronomic traits result revealed high ID with for fresh root yield being the highest (53.05%). ID observed for other agronomic traits were 38% for fresh foliage yield and 22% for harvest index. The effects of ID tended to be relatively higher for the much more complex traits...

Related GCP project–G4008.26/G7010.01.05: A cassava breeding community of practice in Africa: for accelerated production and dissemination of farmer-preferred cassava varieties resistant to pests and diseases (Phase II)

Notes:

1.2: Genetic variability of six cassava traits across three locations in Ghana

Peprah Bright Boakye, Agyeman Adelaide and Elizabeth Yaa Parkes*

* *Crops Research Institute, Fumesua, Kumasi, P. O. Box 3785, Ghana; e-mail: brightpeprah@yahoo.com*

A study was conducted to assess the extent of genetic variability, broad-sense heritability and correlations for fresh root weight, root number, top weight, vigour, cassava mosac disease and cassava green mite of eight marker assisted selected cassava genotypes across three locations in 2 years in Ghana. Combined analysis of variance revealed highly significant genotypic effect for all the traits except root number which was just significant. Genotype x environment interaction was also significant for root number, top weight, cassava mosaic disease and vigour indicating considerable but, varying response of the genotypes to the environments. High broad-sense heritability values were observed for all the traits. High broad- sense heritability and genetic advance as percent of the mean were observed for cassava mosaic disease, suggesting that the trait is primarily under genetic control and that a simple recurrent phenotypic selection scheme would be rewarding. Phenotypic coefficients of variation values were larger than their corresponding genotypic coefficient of variation values for all traits. Correlations between root number, root weight and top weight were highly significant and positive indicating that simultaneous progress for the three traits is feasible.

Related GCP project: Not applicable

Notes:

2. Legumes

2.2 Beans

2.2.1: SNP marker development to improve marker assisted selection at CIAT bean breeding program

*Alvaro Soler, Beat Keller, Juanita Bedoya, Bodo Raatz**
** CIAT Colombia; e-mail: b.raatz@cgiar.org*

Common bean is an important food legume particularly for smallholder farmers in developing countries, where it is an essential due to its high protein and micronutrient contents. Breeding at CIAT aims to develop improved varieties with superior resistance to abiotic and biotic stresses and higher micronutrient levels. Marker assisted selection (MAS) is utilized to accelerate the breeding process and to increase efficiency. SNP markers are developed that can be analyzed in a gel-free system to replace SSR markers. Marker conversions have been achieved for markers for BCMV, ALS, CBB and bruchid resistance. Fine mapping approaches are employed to further improve markers. In case of the major ALS resistance locus from genotype G5686, the position of the resistance gene could be mapped to a 400 KB region. A protocol for seed DNA extraction is being improved to be able to genotype plants before bringing them to the field. As genotyping is getting ever cheaper and easier, while field phenotyping becomes the most resource limited activity, seed DNA extraction has a big potential to improve breeding in future. MAS is now routinely used in bean breeding and efforts are directed at further improving the process and developing more high quality markers.

Related GCP project– G6010.03: Tropical Legumes I: Improving tropical legume productivity for marginal environments in sub-Saharan Africa.

Notes:

2.3 Chickpeas

2.3.1: Improve chickpea productivity for marginal environments in Sub-Saharan Africa and Asia- Phase II

Rajeev Varshney, Pooran Gaur, L Krishnamurthy, Mahendar Thudi, Trushar Shah, NVPR Ganga Rao, Paul Kimurto, Asnake Fikre, Shailesh Tripati, N Nadarajan*

* *International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, 502324, India and CGIAR Generation Challenge Programme, c/o CIMMYT, 06600, Mexico DF, Mexico; e-mail: r.k.varshney@cgiar.org*

Notes:

TLI Phase II aims at harnessing the resources developed during Phase I for chickpea crop improvement. Towards this direction, 38 pre-breeding populations and MAGIC population comprising 1200 lines were developed. A genome-wide physical map was developed spanning 574 Mb that contributed to sequencing of the chickpea genome. Using GBS approach, 49 SNP markers were integrated in the QTL region; as a result, the QTL interval is narrowed down from 35 cM to 14 cM. Several lines with > 10% increase in yield under rainfed and irrigated conditions were identified on evaluating 20 BC_3F_5 lines at ICRISAT-Patancheru and by TL-II partners in India. NARS partners as leaders initiated MABC activities in Kenya and Ethiopia and completed three backcrosses for enhancing drought tolerance. Using OptiMAS, eight superior lines were selected from the cross JG 130 × ICCV05107 and true F_1s from first recombination were chosen and second recombination cycle is in progress. One PhD and three MSc students from NARS obtained their degree and two more PhD students from NARS have been working at ICRISAT-India as well as in Kenya and Ethiopia. Data generated during TLI Phase I were curated into the Integrated Breeding System workflow.

Related GCP Projects–
G4011.08: Harnessing the potential of multi parent advanced generation inter cross (MAGIC) populations for gene discovery and breeding applications in chickpeas
G4009.07.03: Marker-assisted back crossing (MABC) for drought tolerance in chickpea-students for analysis of drought tolerance in chickpea (TLI- Kenyan student)
G7010.06.01: Accelerating development of genomic resources and strengthening NARS partner capacities for enhancing adoption of molecular breeding for drought tolerance in chickpea

2.3.2: Harnessing the potential of multi parent advanced generation inter cross (MAGIC) populations for gene discovery and breeding applications in chickpeas

Rajeev Varshney, Pooran Gaur, Arun Sama, Mahendar Thudi, Srinivasan Samineni, Abhishek Rathore*

* *International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, 502324, India and CGIAR Generation Challenge Program, C/O CIMMYT, 06600, Mexico DF, Mexico; e-mail: r.k.varshney@cgiar.org*

For harnessing the genetic diversity present in the elite germplasm collection a Multi-parent Advanced Generation Inter-Cross (MAGIC) lines are being developed in chickpea using eight cultivars/promising germplasm lines (ICC 4958, ICCV 10, JAKI 9218, JG 11, JG 130, JG 16, ICCV 97105 and ICCV 00108) from South Asia and sub-Saharan Africa. Towards this direction, 28 two-way, 14 four-way and 7 eight-way crosses were made to develop this MAGIC population. Over 1200 F2 plants were advanced to subsequent generations through a single seed descent (SSD) method. The bulk F_4 seeds of eight-way crosses have been supplied to several NARS partners in India for direct use in breeding program. The eight parents were genotyped using 70 SSR and 747 SNP markers. In addition, to large-scale sequence data using restriction site associated DNA (RAD) sequencing and whole-genome re-sequencing (WGRS), the parental lines were also sequenced using Illumina Miseq and detailed data analysis is in progress. The F_6 progenies were grown in the field during Oct 2012 to Feb 2013 and DNA was isolated from all 1200 lines. These lines will be genotyped using SNP markers for identification of haplotype groups for multilocation evaluation of the selected haplotype groups from F6-derived F7 progenies.

Related GCP project–G6010.4: Objective 4: Improve chickpea productivity for marginal environments in Sub-Saharan Africa and Asia- Phase II

Notes:

2.3.3: Use of marker-assisted breeding to improve drought tolerance in chickpea

Paul Kimurto, Moses Oyier, Richard Mulwa, Bernard Towett, Alice Kosgei, Serah Songok Gangarao NV Rao, Said Silim, Pooran Gaur, Mahendar Thudi, and Rajeev K Varshney*
** Egerton University, P.O. Box 536, Egerton 20115, Kenya*

Chickpea (*Cicer arietinum* L.) is gaining importance in semi-arid tropics of Africa as a major protein source for the poor in ASALs. Since it is generally grown under rained on residual soil moisture after the rainy season as rotational crop, it experiences terminal drought which is a major constraint to its productivity. Productivity can be improved if drought tolerance can be enhanced. Root traits, particularly rooting depth and root biomass, are known to play an important role in drought avoidance through more efficient extraction of available soil moisture. Previous studies identified hot spot in the chickpea genome of two parents ICCV 8261 and ICCV 4958 that contained QTLs for several drought tolerance related traits contributing to up to 36% phenotypic variation with genomic region flanked by two SSR markers TAA 170 and ICCM 0249. This genomic resources were used to improve Kenyan elite line ICCV 97105 (Chania Desi 1) using marker assisted backcrossing (MABC). A set of 4 markers including TAA 170 and ICCM 0249 were used for foreground selection. Subsequent backcrosses were conducted until 17 BC_3F_4 progenies were obtained. These were evaluated along with donor and recipient parent in both irrigated and rainfed conditions in ASALS of Kenya…

Related GCP project–G6010.4: Objective 4: Improve chickpea productivity for marginal environments in Sub-Saharan Africa and Asia- Phase II

Notes:

2.4 Cowpeas

2.4.1: Cowpea diversity for modern breeding in sub-Saharan Africa

Bao-Lam Huynh, Timothy J. Close, Issa Drabo, Jean-Baptiste Tignegre De La Salle, Ousmane Boukar, Christian Fatokun, Ndiaga Cissé, Rogério Marcos Chiulele, Batieno T. Benoît Joseph, Steve Wanamaker, Mitchell R. Lucas, Arsenio Ndeve, Ndeye Ndack Diop, Xavier Delannay, and Philip A. Roberts*

* *University of California, Riverside, California, CA 92521, USA*
Corresponding author: philip.roberts@ucr.edu

Cowpea (*Vigna unguiculata* L. Walp.) is an important protein-rich grain legume and fodder crop grown across the semi-arid zones of the tropics below the Saharan desert and similar agro-ecological zones of eastern and southern Africa. Drought, heat, low fertility soils, pests and diseases are key factors causing traditional varieties in Africa to yield up to 5-fold lower than their potential. Using new knowledge of cowpea gene-pools and the genetic architecture of domesticated cowpea from diversity studies and quantitative trait loci (QTL) for target traits, collaborative breeding programs are being aimed to develop improved cowpea cultivars for Africa. Marker-assisted recurrent selection is being evaluated using several populations, each derived from a cross between elite parents carrying traits relevant to each target environment. Following QTL discovery at F_3 - F_4 generations, members of highest QTL-index families were genotyped, selected and inter-crossed to recombine favorable alleles. Marker-assisted backcrossing is being applied to accelerate introgression of known resistance genes into local cultivars, including resistance to *Striga* and several fungal and bacterial diseases. These activities are enabled by high-density genetic maps and out-sourced SNP genotyping, and by the application of Generation Challenge Programme Integrated Breeding Platform (https://www.integratedbreeding.net/) decision support tools.

Related GCP project–G7010.07.01: Tropical Legumes 1 Objective 2: Improve cowpea productivity for marginal environments in sub-Saharan Africa

Notes:

2.5 Groundnuts

2.5.1: Three elite peanut cultivars improved for rust resistance by introgressing a QTL genomic region through marker-assisted backcrossing (MABC) approach

Rajeev K Varshney, Manish K Pandey, Pasupuleti Janila, Shyam N Nigam, Hari Sudhini, MVC Gowda, Manda Sriswathi, T Radhakrishnan, P Nagesh*

* *International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, 502324, India and CGIAR Generation Challenge Programme (GCP), c/o CIMMYT, 06600 Mexico DF, Mexico; e-mail: r.k.varshney@cgiar.org*

Leaf rust, caused by *Puccinia arachidis,* is one of the major devastating diseases in peanut (*Arachis hypogaea* L.). After validating a major QTL (82.62% phenotypic variation) for resistance to rust, it was introgressed in three susceptible varieties namely ICGV 91114, JL 24 and TAG 24 using GPBD 4 variety as donor through MABC approach. A total of four markers (IPAHM103, GM2079, GM1536, and GM2301) were used to select target QTL genomic region. A total of 81 introgression lines developed from 2 to 3 backcrosses with high level of rust resistance were selected with disease score of <2.0 on 1.0-9.0 scale as par the donor were selected. Screening of 43 promising lines with 13 markers present on the carrier linkage group showed introgression of only target genomic region from resistant donor in 11 lines. Multi-location field evaluation of most promising lines should provide entries for possible release of the improved varieties with enhanced disease resistance that will eventually provide better yield and higher income to resource poor farmers of the semi-arid regions of the world. Further, this study highlights the utility of four markers for improving rust resistance in any peanut molecular breeding programme of the world.

Related GCP project–G6007.01, Objective 1: Groundnut- Improving tropical legume productivity for marginal environments in sub-Saharan Africa and South Asia

Notes:

2.5.2: Development and application of cost-effective genotyping assays for genetic diversity analysis in the reference set of peanut (*Arachis* spp.)

Rajeev K Varshney, Pawan Khera, Hari D Upadhyaya, Manish K Pandey, Manish Roorkiwal, Manda Sriswathi, Pasupuleti Janila, Yufang Guo, Michael R McKain, Ervin D Nagy, Steven J Knapp, James Leebens-Mack, Joann A Conner, Peggy Ozias-Akins*

* *International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, 502324, India and CGIAR Generation Challenge Programme (GCP), c/o CIMMYT, 06600 Mexico DF, Mexico; e-mail: r.k.varshney@cgiar.org*

With an objective to develop cost-effective marker assays, a set of 96 informative SNPs was used to develop competitive allele-specific PCR (KASPar) assays (GKAMs: Groundnut KASPar Assay Markers) in peanut. All 96 GKAMs were screened on a validation set comprised of 94 genotypes including parental lines of 27 mapping populations, 7 synthetic autotetraploid/amphidiploid lines and 19 wild accessions. As a result, 90 GKAMs could be validated and 73 GKAMs showed polymorphism across validation set. Furthermore, the validated GKAMs were screened on a subset of the reference set (280 diverse genotypes) for estimating diversity features and elucidating genetic relationships. Cluster analysis of marker allelic data grouped accessions according to their genome type, subspecies and botanical variety. The subspecies *fastigiata* and *hypogaea* formed distinct cluster, however, some overlaps were found indicating their frequent inter-crossing during the course of evolution. The wild species, having diploid genomes were grouped into a single cluster. The average polymorphism information content (PIC) value for polymorphic GKAMs was 0.32 in the validation set and 0.31 in the reference set. These validated and highly informative GKAMs may be deployed in genetic and breeding applications in peanut.

Related GCP project–G6007.01, Objective 1: Groundnut-Improving tropical legume productivity for marginal environments in sub-Saharan Africa and South Asia & GCP-Theme Leader Discretionary Grant.

Notes:

2.5.3: Widening the gene pool of cultivated peanut using wild relatives: AB-QTL and CSSL development

Daniel Fonceka, Hodo-Abalo Tossim, Issa Faye, David Bertioli, Soraya Leal-Bertioli, Vincent Vadez, Jean-Christophe Glaszmann, Brigitte Courtois and Jean-François Rami*

* *CIRAD UMR AGAP, Centre d'Etude Régional pour l'Amélioration de l'adaptation à la Sécheresse (CERAAS), Thiès, Senegal; e-mail: daniel.fonceka@cirad.fr*

Cultivated peanut is a recent allotetraploid with limited genetic diversity. Therefore, capturing the genetic diversity from peanut wild relatives is an important objective. Through an international initiative, which started in 2004, interspecific QTL mapping populations with high resolution are being developed using several wild synthetic tetraploids as donors. As part of this initiative, Advanced-Backcross QTL (AB-QTL) and Chromosome Segment Substitution Line (CSSL) populations derived from the cross between the cultivated variety Fleur11 and the wild synthetic tetraploid (*A. duranensis* x *A. ipaensis*)^{4}x were developed using a marker assisted backcross strategy. These populations have proven efficiency for QTL mapping and for deciphering the molecular basis of traits variations. For example, 95 QTLs involved in plant, pod and seed morphology as well as in yield components were mapped under two water regimes, using the AB-QTL population. The CSSL population allowed shedding new light on the complex inheritance of the peanut growth habit. The CSSL population is of particular interest as it is a permanent population that has already been shared with different countries and is being evaluated for various traits in different environments. This study is

Notes:

a compelling example of the utilization of wild genetic resources for genetic analysis and peanut breeding.

Related GCP projects–
G6010.01: Improve groundnut productivity for marginal environments in sub-Saharan Africa
G3005.05: Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools
G4008.49: Enhancing groundnut (Arachis hypogaea L) genetic diversity and speeding its utilisation in breeding for improving drought tolerance
G4007.13.03: Capacity-building à la carte 2007 – Application of molecular tools for controlled wild introgression into peanut cultivated germplasm in Senegal

Notes:

2.5.4: Identification of Quantitative Trait Loci for yield and yield related traits of peanut (*Arachis hypogaea* L.) using a recombinant inbred lines population

I Faye, H Falalou, V Vadez, A Rathore, MK Pandey, RK Varshney*

* *Institut Sénégalais de Recherches Agricoles-Centre National de Recherches Agronomiques, BP 53 Bambey, Senegal; e-mail: issafaye2001@yahoo.fr*

Drought is a paramount constraint for peanut production across the world and particularly in semi-arid tropical zone. A population of 284 recombinant inbred lines derived from the cross TAG 24 x ICGV 86031 was evaluated was evaluated under well water and water stress conditions in three different trials, one at ISRA-CNRA (Bambey, Senegal) and two at ICRISAT Sahelian Centre (Sadore, Niger). A standard protocol was used in the different trials for the water stress imposition. Phenotypic data of nine traits (pod yield, haulm yield, SPAD chlorophyll meter reading, harvest index, shelling percentage, percentage of pod maturity, 100 Kernel weight, number of primarily branches and plant height) were analyzed to evaluate the magnitude of correlation between yield and these traits. A QTLs analysis was also carried out for detecting main effects QTLs using WinQTL Cartographer 2.5 and QTLNetwork 2.0 and epistasic interactions using QTL Network 2.0 and GMM 2.1. The results showed a positive correlation between pod yield and harvest index, with a greater magnitude under water stress conditions. In addition, its broad sense heritability (*H*2) was medium to high (0.23 - 0.59) in the different trials. These results are in agreement with previous studies for the correlation between yield and harvest index and its heritability...

Related GCP project–G6010.01: Improve groundnut productivity for marginal environments in sub-Saharan Africa

Notes:

2.5.5: Improving groundnut productivity through resilience to the biotic and abiotic stresses: progress under TLI Phase II

P Okori, E Monyo, A Chamango and V Vadez*

* *ICRISAT Malawi P.O. Box 1096 Lilongwe, Malawi; e-mail: p.okori@cgiar.org*

The purpose of Tropical legumes 1 (TL I) which is now in its second phase is to deploy genetic resources, and tools to improve resilience and production performance of targeted legumes their cropping systems. Groundnut is one of the selected crops covering about 18 million ha with over 10 M ha in Africa and about 7 M ha in South East Asia. In both regions, biotic and abiotic factors reduce production performance of the crop with complete yield loss under severe stress. TL I project, being implemented by a network of scientists from international and national agricultural research systems is underpinned by genetic resources and genomic tools developed under Phase 1 of the project. To date, good momentum has been gained in the groundnut objective of the project with all six activities of (Diversity, Molecular Tools, Diseases, Breeding, Training and Data management). A highlight of products developed or under development under activities 3, 4, 6 are presented. The rest are presented separately. New products developed in east and southern Africa included; validated sources of resistance to GRD, Rust and ELS, a multiplex PCR technique for detection of GRD pathogens and CSSL materials are still being multiplied for multi- agro-ecological testing to endemic stresses…

Related GCP project–G6010.05: Cross-cutting crop activities (drought phenotyping, data management and capacity building) (TLI project, Objective 5)

Notes:

2.5.6: Groundnut improvement in Uganda

DK Okello, M Biruma P Okori and CM Deom*

* *Groundnut breeding Department, National Semi-Arid Research Resources Institute, P.O Box Soroti, Uganda; e-mail: kod142@gmail.com*

The Groundnut Department at National Semi-Arid Research Resources Institute (NaSARRI) is mandated to conduct research on groundnuts (*Arachis hypogaea* L) in Uganda aimed at cultivar development, maintenance and conservation. Groundnut is a staple food and fast becoming a cash crop. Most traditional cultivars are landraces adapted more for survival. Onfarm yields averages 800 kg/ha of dry pods compared to potential onstation yields of 3,000kg/ha. The yield gaps are attributed to a combination of factors such as unreliable rains, mostly non-irrigated cultures, traditional small-scale farming with little mechanization, outbreaks of pest infestations and diseases, the use of low-yielding seed varieties and increased and/or continued cultivation on marginal land, Political instability, unsupportive oilseed policies and weak extension services. Research efforts have, since the 1920s released 24 varieties, the most recent being Serenut 1-14 series. These varieties have helped to alleviate some of the production problems listed above. However, the market and field stability of those varieties, in light of emerging stresses, calls for continuous research while at the same time keeping crop improvement, quality and safety linked to practical applications. Emerging stresses like aflatoxin, leafminer, late leafspots, rosette, oil quality, drought and biotechnology forms the current research agenda.

Related GCP project: Not applicable

Notes:

2.5.7: Marker assisted backcrossing (MABC) to improve oil quality in peanut

Janila Pasupuleti, Rajeev K Varshney, Manish K Pandey, HD Upadhyaya, Nagesh P, Murali TV and Shyam N Nigam*

* *International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru – 502324, Andhra Pradesh, India; email p.janila@cgiar.org*

Peanut kernels contain 48-50% oil, and Oleic (O) and Linoleic (L) fatty acids constitute about 80% of the oil. The O/L (Oleic to Linoleic acid) ratio in normal peanut is about 2, however, in case of FAD (Fatty Acid Desaturase) gene mutants it can go as high as >20. High O/L ratio has benefits to consumer's health as well as food processing industry. Allele specific and CPAS markers were validated for mutant alleles of FADA and FADB genes. MABC was initiated at ICRISAT and four other national centers in India to enhance O/L ratio of six elite genotypes that have >50% of seed oil content. Allele-specific markers differentiated the genotypes possessing mutations in A and B genomes and are used for confirmation of F_1 plants as well as for foreground selection to select heterozygotes among backcrossed BC1F1, BC2F1 and BC3F1 plants. CAPS are co-dominant in nature and clearly differentiated the homozygotes and heterozygotes at both the loci in BC2F2 populations. A three step-strategy has been proposed to identify homozygotes in BC2/3F2 populations for optimization of the resources.

The work is supported by Department of Agriculture and Cooperation, Ministry of Agriculture, Government of India
Related GCP project: Not applicable

Notes:

2.6 Other legumes/crosscutting

2.6.1: Harnessing genome sequence information for pigeonpea (*Cajanus cajan*) improvement

Rajeev K Varshney, Rachit K Saxena, Vikas Singh, Vinay Kumar, Kishan Patel, Jimmy Obala, Swathi Parupalli, Seleman R Koneka, KB Saxena, Sameerkumar V Chanda, Hari D Upadhyaya, Mamta Sharma, Abhishek Rathore, Anuradha Ghanta, PS Dharmaraj, KN Yamini, S Muniswamy*

* *International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, 502324, India and CGIAR Generation Challenge Programme (GCP), c/o CIMMYT, 06600 Mexico DF, Mexico; e-mail: r.k.varshney@cgiar.org*

Pigeonpea is the sixth most important legume crop and grown in 4.75 M ha. Pigeonpea crop productivity is challenged by several biotic (*Fusarium* wilt and sterility mosaic disease) and abiotic (water logging and soil salinity) stresses. Molecular breeding could not be deployed mainly due to low level of genetic diversity present in the primary gene pool and non-availability of marker-trait information. With the availability of recently decoded pigeonpea genome, significant amount of genomic information is now available that can be applied for crop improvement. In order to harness genome sequence information we are developing one nested association mapping (NAM) population of 2000 F_2s derived from 10 elite crossing combinations. In addition, multi-parent advanced generation inter-cross (MAGIC) population with 500 lines and introgression libraries (ILs) are being developed for enhancing genetic diversity in cultivated gene pool from landraces and wild species. Reference set of 300 lines is also being utilized for genome-wide association study (GWAS) for mapping genetic diversity of economically important traits. Multi-location phenotyping for targeted traits is being conducted under field conditions. Detailed analysis of both genotyping and phenotyping data will provide useful information on marker(s)/ gene(s)/ haplotype(s) - trait association that can be used in future molecular breeding programmes.

Related GCP project–GCP-Theme Leader Discretionary grant

Notes:

2.6.2: Integrated agronomy, physiology, and crop modelling approaches to improve drought tolerance phenotyping across legumes in the semi-arid tropics

Nouhoun Belko, Ndiaga Cisse, Thomas R. Sinclair, Vincent Vadez*

* *Centre d'Étude Régional pour l'Amélioration de l'Adaptation à la Sécheresse, Thies, Senegal; e-mail: nouhoun.belko@yahoo.fr or nouhoun.belko@gmail.com*

Drought stress is a major limitation of crop yields under rain-fed conditions in the semi-arid tropics. Phenotyping of complex traits such as drought tolerance is difficult in the field because of the large genotype-by-environment interactions. An integrated approach is therefore needed for traits dissection and better understanding of stress tolerance mechanisms to revitalize the development of drought-adapted cultivars. In this poster, we describe relevant methodologies for the assessment of legumes for drought tolerance and present results from different studies. Several early and medium maturing terminal drought-tolerant and high-yielding cowpea genotypes were identified using stress tolerance indices in field station. Gravimetric method and infrared thermography were adapted for precise evaluation of legumes genotypic differences of plant transpiration rate in response to vapor pressure deficit. A lysimetric platform was designed for accurate and high throughput measurement of plant water budget and transpiration efficiency throughout the crop cycle, and timely evaluation of root traits, harvest index and grain yield under drought and irrigated conditions. A legume crop model is under development for predicting the effects of plant traits or trait combinations on grain yield and determining their probability of success across drought scenarios and environments.

Related GCP project: G6007.02: Cowpea - Improving productivity in Sub-Saharan Africa

Notes:

2.6.3: Using mini core collection to identify new sources of variations for breeding and genomics of chickpea, groundnut, and pigeonpea

Hari D Upadhyaya, Sangam L Dwivedi, Vincent Vadez, L Krishnamurthy, J Kashiwagi, Sube Singh, Rajeev K Varshney, and KN Reddy*

* *International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru PO, 502324, AP, India; e-mail: h.upadhyaya@cgiar.org*

Notes:

Grain legumes contribute significantly to world food production, and primary source of dietary proteins in developing countries, where hunger and malnutrition are widespread. Generation Challenge Program supported the development of composite collections, which was molecularly profiled to form genotype-based reference sets in food crops. Chickpea, groundnut and pigeonpea reference sets contain 300 accessions each and represented 78% to 95% allelic diversity discovered in composite collection of these crops. Mini core collections (10% of core or 1% of entire collection) that were part of reference sets were evaluated for agronomic traits, including abiotic and biotic stresses. A number of genetically diverse accessions possessing agronomically beneficial traits, ICCs 440, 637, 1098, 3325, 3362, 4872, 7441, 8621, 9586, 10399, 12307, 14402, 15680, and 15686 in chickpea; ICGs 442, 2381, 6022, 7963, 8285, 11088, 11426, 12625, 12672, 12697, 14710, and 15419 in groundnut; and ICPs 6739, 8860, 11015, 13304, and 14819 in pigeonpea have been identified. Many of these identified accessions had combination of resistance to abiotic and biotic stresses, some with specific adaptation and nutritionally dense types. These accessions are ideal genetic resources which may be used to develop agronomically superior and nutritionally enhanced cultivars with multiple resistances to abiotic and biotic stress.

Related GCP projects–
G4005.01.04: Completing genotyping of composite germplasm set of chickpea
G4006.32: Molecular characterization of pigeonpea (Cajanus cajan) composite collection
G4005.03.06: Molecular characterization of tier 2 (orphan) crops - groundnut

2.6.4: From fingerprinting to quality control in breeding programmes – Introduction and implementation of the forensic (QA/QC) project

Chunlin He, Ndeye Ndack Diop, and Xavier Delannay*
* *Generation Challenge Programme, c/o CIMMYT, Texcoco, Mexico; e-mail: c.he@cgiar.org*

The forensic project involving fingerprinting, quality assurance (QA) and quality control (QC) was firstly introduced by GCP to the NARS partners at TL1 meeting in Ethiopia in May 2012. This project aimed to enhance the breeding efficiency through molecular genotyping using SNP markers and increase legume productivity and profitability in sub-Saharan Africa and India for the key tropical legume crops including cowpea, chickpeas, pigeonpeas, common bean, soybean and groundnut. In order to facilitate the QA/QC activities, 1000-2000 KASP SNPs have been developed at KBioscience/LGC, and a set of about 200 elite germplasm has been fingerprinted with these KASP SNPs for each of the legume crops. These genotypic data have been maintained in the GDMS databases for access by all users. Currently, there are a total of 1,091,579 SNP data points generated from the SNP conversion projects and about 955,531 SNP data points generated from the fingerprinting projects that can be used for QA/QC activities for the breeding pipelines. In addition, the main QA/QC activities have been suggested and scheduled for the participating programs including: (1) identity confirmation of breeding lines; (2) identity confirmation of F1 and BC1 materials; (3) line-finishing assistance (verification of parentage, residual heterozygosity and duplications).

Related GCP project–G6010.06: Forensic marker service activities at GCP (including 6 tropical legume crops)

Notes:

3. Maize

3.1: Incorporation of maize streak virus resistance genes in a Mozambican adapted maize inbred line LP23, mediated by use of SSR and SNP markers

John Derera, Nothando Mafu, Pedro Fato, Sharmane Naidoo and Mark Laing*

* *School of Agricultural, Earth and Environmental Sciences, University of KwaZulu-Natal, South Africa; P Bag X01, Scottsville, South Africa 3209; e-mail: dereraj@ukzn.ac.za*

The maize inbred line LP23 is an important parent of hybrids in Mozambique due to its high productivity and its resistance to downy mildew disease (DM). Its productivity, however, is compromised by its susceptibility to maize streak virus disease (MSV). Therefore CML509 and CML505 were used as donor parents for incorporating MSV resistance genes in LP23. A total of 118 F3 families derived from F2 crosses (LP23 x CML505 and LP23 x CML509) were genotyped using two SSR markers (bnlg1811 and umc2228) and HRM analysis. Background selection was facilitated by 400 Panzea SNPs with an even distribution across the 10 chromosomes of maize and a call rate of 98%. Eventually 35 MSV and DM resistant families were identified for advancement in the program. The Jaccard similarity coefficients data ranged from 52% to 88%. The progeny lines with LP23 as a common parent were placed in two clusters, with those lines derived from CML509 x LP23 clustering with LP23, and those from CML505 x LP23 clustering with CML505. There are at least 13 new progeny lines with ≥80% similarity with the common parent LP23, qualifying them as suitable candidates for use to create new hybrids in lieu of LP23.

Related GCP project–G4008.19: Incorporation of MSV resistance gene in Mozambican maize varieties, mediated by use of MAS

Notes:

3.2: Combining genotypic with phenotypic selection gives higher genetic gains than phenotypic-only selection for drought tolerance in maize (*Zea mays* L.).

BS Vivek, Girish Kumar Krishna, V. Vengadessan, PH Zaidi, Le Quy Kha, P Grudloyma, IS Singh, R Babu, Eureka M Ocampo, Dang Ngoc Ha, F Xingming, M Azrai, RP Singh*

* *CIMMYT, c/o ICRISAT, Patancheru-502324, Hyderabad, INDIA;*
e-mail: bvivek@cgiar.org

Over 80% of the 19 million hectares of maize in South and South-East Asia is rainfed and prone to drought. Drought tolerance is a highly polygenic trait. Marker-Assisted Recurrent Selection applied with Genome Wide Selection (MARS-GWS) is designed to increase the frequency of favourable alleles in breeding populations. Two bi-parental populations (AMDROUT1 and AMDROUT2) were generated by crossing elite Asian adapted yellow inbreds (CML470 and VL1012767, respectively) with an African white drought tolerant line (CML444). Marker effects of polymorphic SNPs were determined from F3 test crosses. Cycle 1 was formed by recombining superior F3 families based on test cross data. C1F2 was subsequently derived by recombining phenotypically superior c1 plants (thus resulting in two rounds of phenotypic-only selection). C2 was derived by recombining superior c1 plants (determined from marker effects). All generations of both populations were evaluated under drought in the dry season of 2012. Per se performance of c1F2 of each population was 40% better while that of c2 was 60-80% better than the respective F2. More interestingly, C2s of both populations showed superiority (16.5 and 25%) over c1F2s of respective populations. Thus, phenotypic selection followed by genotypic selection gave higher gains compared to two rounds of phenotypic-only selection.

Related GCP project–G4008.56: Asian Maize Drought Tolerance (AMDROUT) Project

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3.3: Breeding for drought tolerant maize in Indonesia

M. Azrai, R. Effendi and H. Subagio*
* *Indonesian Cereals Research Institute, Jl. Dr. Ratulangi, No. 274, Maros, South Sulawesi, Indonesia; e-mail: azraimuh@yahoo.com*

Maize in Indonesia are the second most important cereal crop after rice, and is a promising option because the strong demand and good domestic prices had been attracting farmers to grow maize and its acreage will keep increasing in future. However, the major problem that often arises is drought, particularly in the dry season. Farmers usually left their land for bare during dry season due to the lack of water. Besides, downy mildew is also a limiting factor in the development of maize in Indonesia. This disease is very dangerous because it can cause yield losses of up to 100% in the maize develop development central in Indonesia. Development of early maturity, drought tolerant and downy mildew resistance of maize is a challenge in order to optimize more bare lands during the dry season. Under AMROUT program, we develop new populations using recurrent selection and formation of new high yielding inbred lines. We used 6 recombination as a basic population i.e. Ki3/VL062692, Ki3/ VL06386, Ki3/ ZM523B-29-2-1-1-B*4, Ki3/ ZM309, Ki3/VL062718, Ki3/VL062701. The Ki3 inbred lines is yellow color, tolerant to downy mildew and early maturity, then six inbred lines as the donor of drought tolerant and also early maturity derived from CIMMYT-Kenya…

Related GCP project–G4008.56: Improving drought tolerance for maize in Asia
AMDROUT: Asian Maize Drought-Tolerance Project
(PI:Bindiganavile S Vivek, CIMMYT)

Notes:

3.4: The genetic diversity and aluminium toxicity tolerance of selected Kenyan maize breeding lines

Matonyei KT, Ouma EO, Kisinyo PO, Too EJ, Were BA, Onkware AO, Ligeyo DO, Agalo J, Magalhães, JV, Guimarães CT, Gudu S*

* *University of Eldoret-Kenya, P. o Box 1125 – 30100 Eldoret – Kenya. Corresponding author: samgudu2002@yahoo.com*

Maize (*Zea mays* L.) genotypes exhibit significant variation in response to aluminium (Al) stress and phosphorus (P) deficiency. Selection and breeding for tolerance to both problems has been going on in Kenya using both local and exotic maize genotypes. The relative net root growth of 235 maize lines was assessed in the standard Maganavaca nutrient solution without or with Al stress activity at 39 µM Al3+. The Scott and Knott's test grouped the 235 breeding lines into 10 clusters. The top 20 most tolerant lines were dominated by derivatives of the Kenyan 203B or CATETO. The Kenyan inbred line 203B-14, a derivative of 203B, was ranked as the most tolerant. 40 breeding lines derived either from Brazilian CATETO or Kenyan sources were used to determine Al induced ZmMATE1 expression using quantitative real-time PCR. The ZmMATE1 expression levels were very high in the accession SYN AL × R12C10 – 8 and other lines that had CATETO background, but very low in the accession MUL 89, which is sensitive to Al. Most of the Kenya lines including those that exhibited high Al tolerance in solution culture exhibited exceptionally low activities of the gene. Therefore, a different gene from ZmMATE1 could be responsible for their Al tolerance…

Related GCP project–G4005.20: Optimising marker-assisted breeding systems for drought tolerance in cereals through linkage of physiological and genetic models

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3.5: Initial results on application of the tropically adapted inducer lines in DH maize lines development in Vietnam

Le Quy Kha, Nguyen Duc Thanh, Luong Thai Ha, Nguyen Thi Phuong Thao*

** The Institute of Agricultural Sciences for Southern Vietnam, Vietnam Academy of Agricultural Sciences (VAAS); e-mail:Kha.lq@iasvn.org*

During 2012, three staff from Maize Research Institute, Vietnam (NMRI) got training for DH technology in CIMMYT and many other NMRI's researchers were transferred for protocol of DH line development by CIMMYT experts. By September 2012, NMRI received license to use tropically adapted inducer lines (TAILs) P1, P2 and P1 x P2 developed by CIMMYT and UHo for commercial purposes. In spring 2013, TAILs were agronomically tested in 2 regions in Vietnam, one in Red river delta, 10 m above sea level and the other in Son La province, about 600 -1000 m asl. These TAILs were crossed with commercial single crosses, bulk of several single crosses of the same kernel types and QPM synthesis for evaluation of induction rates. TAIL P1 x P2 did not showed heterosis compared to TAIL P1, TAIL P2 in both regions. In Son La, plant height of both TAILs and crosses were 1.8 – 2.0 m and they were 1.1 – 1.5 m in Red river delta. All of TAILs produced good number of seeds per plant. Induction rate when TAILs crossed with single crosses and QPM synthesis was 6 – 8 % but it was about 3 % when crossed with bulk of several single crosses.

Related GCP project: Not applicable

Notes:

4. Rice

4.1: Rice root phenotyping of the OryzaSNP panel: associated genomic regions and environmental effects

Amelia Henry, Len Wade, Adam Price, Akira Yamauchi, R Chandra Babu, V Shenoy, S Mande, R Mauleon, Kenneth McNally*

** International Rice Research Institute (IRRI), Los Baños, Philippines; e-mail: A.Henry@irri.org*

Although there is a strong case for the role of roots in plant performance under drought stress, appropriate methods for evaluating them in relation to performance under drought (particularly in rice) are less clear-cut. There is also a strong need for advances in phenotyping to match the rapid progress in genotyping of rice. This project focused on rice root phenotyping of genetic diversity in response to drought on the OryzaSNP panel, which is a set of 20 diverse genotypes that has been mapped for over 170,000 SNP markers. Phenotyping was achieved through root studies from eight different sites or screening methods conducted in Australia, India, Japan, Nigeria, the UK, and the Philippines. The data are now undergoing collective analysis for GxE effects to understand conditions that affected different root traits, and to relate root growth in controlled studies with that in field studies. Phenotype/genotype association analysis is underway, which has revealed several hot spots in the genome where multiple root traits and grain yield aligned. This project was conducted to provide recommendations on efficient ways to measure roots, in order to realize the huge genetic potential of rice for root traits that can be effective for drought resistance.

Related GCP project–G3008.06: Targeting drought-avoidance root traits to enhance rice productivity under water-limited environments

Notes:

4.2: Genotypic performance under various drought screening methods and multilocation trials in rainfed lowland rice in Lao PDR

P. Xangsayasane, B Jongdee, G Pantuwan, S Fukai, J Mitchell, P Inthapaya1 and Darunee Jothityangkoon*

* *Agriculture Research Center, NAFRI, Laos, KhonKaen University, Faculty of Agriculture, Thailand; e-mail: phetmanyseng@gmail.com*

Lowland rice is the staple food crop in Lao PDR. In the rainfed lowlands, drought is considered to be the main constraint to rice production and drought resistant varieties will stabilize yield. The current drought screening method utilizes late planting to impose a prolonged terminal drought in wet season. The aim of the current experiments was to determine whether screening for drought resistance could be achieved via an aerobic (intermittent stress) screening method. The performance of 25 genotypes was tested under traditional flooded and terminal drought conditions and compared to performance under aerobic conditions for two years in both wet and dry seasons at research stations (10 experiments). The same genotypes were also tested in 12 multi-location on-farm experiments across two years. Mean yield reduction in intermittent and terminal drought was 19 and 37% respectively in wet season and 43 and 64% respectively in dry season, indicating the magnitude of drought severity would be appropriate for screening. Genotypes shown to be drought tolerant, based on the drought response index (DRI), were consistent in intermittent and terminal drought. Genotypic variation was explained by variation in potential yield and drought tolerance. This wet season aerobic screening is considered a promising alternative to late planting terminal drought screening for the development of widely adapted rice varieties for rainfed lowlands.

Related GCP project–G3008.09: Breeding drought tolerance for rainfed lowland rice in the Mekong region

Notes:

4.3: Identification of novel QTL for salinity tolerance in rice from the landrace Kutipatnai

Armin Bhuiya, Abdelbagi M Ismail*

* *International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines; e-mail: a.bhuiya@irri.org*

Salinity is one of the major abiotic stresses affecting rice production worldwide; however, substantial genetic variability is present in local rice landraces that can be exploited for breeding salt tolerant varieties. Identifying major QTLs for tolerance will help speed the development of these tolerant varieties through molecular breeding. A population of 288 F2 progenies developed from the Bangladeshi landrace Kutipatnai and the salt-sensitive Azucena was genotyped using 106 SSR markers polymorphic between the two parents. A linkage map was developed that covers 1396.6 cM with an average distance of 13.18 cM between loci. The F2:3 families were phenotyped under salt stress of 12 dS m1, for several traits associated with salinity tolerance. A total of 14 QTLs were identified using Composite Interval Mapping. Two large effect QTLs each with a phenotypic variance of 11% were identified on chromosome 1, one for shoot K+ concentration (qSKC1.1) and the other (qSL1.1) for shoot length. Additional QTLs with phenotypic variances in the range of 5.1 – 11% were also identified. The positive QTL alleles for all QTLs were contributed by the tolerant parent Kutipatnai. Some of these QTLs will be important for marker assisted breeding of salt tolerant varieties.

Related GCP project–G4010.04/G4010.01.01: Identification of novel QTLs for salinity tolerance and pyramiding with submergence tolerance to develop improved rice varieties for Bangladesh.

Notes:

4.4: Molecular breeding for drought tolerance: is rice different from other cereals?

Arvind Kumar, Shalabh Dixit and Anshuman Singh*
* *International Rice Research Institute, DAPO BOX 7777, Metro Manila, Philippines; e-mail: a.kumar@irri.org*

Systematic research at International Rice Research Institute (IRRI), Philippines during 2004-2012 has led to the identification of fourteen major QTLs for grain yield under drought. Many of the identified QTLs showed effect against single genetic background. QTLs qDTY1.1, qDTY2.2, qDTY3.1, qDTY3.2, qDTY6.1, qDTY12.1 showed large effect on grain yield under drought against two or more genetic backgrounds. qDTY1.1, qDTY3.2, qDTY12.1 showed effect across direct seeded upland and transplanted lowland situations. Consistent large effect of qDTY1.1, qDTY3.2, qDTY12.1 across genetic backgrounds and ecosystems make them appropriate candidates for use in marker assisted breeding to develop high yielding drought tolerant rice varieties. The identified QTLs with effect against individual or multiple backgrounds have been introgressed in popular high yielding varieties IR64, Vandna, Swarna and Sambha Mahsuri following marker assisted backcross breeding approach. Drought tolerant versions of IR64, Vandna, Swarna and Sambha Mahsuri showed yield advantage of 0.5 – 1.2 tha-1 under drought with 4-10% increased yield under irrigated situation. Existence of loci contributing to large effect on grain yield under drought in rice most probably due to its cultivation across diverse ecosystems provides unique advantage to rice for yield gain under drought. With the success achieved in increasing the yield under drought, pyramiding of genes/QTLs for two abiotic stresses was undertaken…

Related GCP project–G4011.04: Dissemination and community of practice for newly developed drought-tolerant QTLs pyramided breeding lines

Notes:

4.5: MAGIC Rice: harnessing genetic recombination for trait improvement

Hei Leung, Nonoy Bandillo, Chitra Raghavan, Emma Huang, Ramil Mauleon, Mike Thomson, Ed Redona, RK Singh, Glenn Gregorio*

* *International Rice Research Institute, Los Banos, Laguna, Philippines; e-mail: h.leung@irri.org*

MAGIC (Multi-parent Advanced Generation Inter-Crosses) is an experimental method to create highly recombined germplasm for direct use as breeding lines and for fine mapping of QTL. The increased recombination in MAGIC populations can lead to novel rearrangements of alleles and greater genotypic diversity with broader adaption. Using 16 founder parents with desirable agronomic traits, we have developed 4 multi-parent populations: indica MAGIC (8 indica); MAGIC plus (2 additional rounds of inter-crossing); japonica MAGIC (8 japonica); and Global MAGIC (intercross between 8-way F1s of the indica and japonica MAGIC). Genotyping-by-sequencing was used to generate ~17,000 SNP markers for genome-wide association analysis of QTL for blast and bacterial blight resistance, salinity and submergence tolerance, and grain quality. Depending on genomic regions, QTL were mapped with a resolution of 6 to 0.13 Mb. Linkage blocks of Indica MAGIC and MAGIC PLUS lines are being compared to determine whether extra inter-crossings lead to increased recombination. Field evaluation of indica MAGIC lines at 5 locations in the Philippines (3), Tanzania (1), and Vietnam (1) showed transgressive segregation in yield, leading to the identification of lines with stable high yield across locations. The new genetic resource holds promise as breeding-ready materials for rice breeding programs.

Related GCP Project–G4011.07:Rice Multi-parent Advanced Generation Inter-Crosses (MAGIC) Phase II

Notes:

4.6: Effect of water deficit on a bi-parental population derived from IR64 x Kogoni 91-1: agro-morpho-physiological evaluation and identification of QTLs involved in drought tolerance

Sangaré J, Sow M, Futakuchi K, Sanni A, Cissé F, Ndjiondjop MN.*

* *Africa Rice Center (AfricaRice), 01 BP 2031, Cotonou- Benin,*
Tel: 229 6418 1313/6418; e-mail: J.Sangare@cgiar.org

Rice is one of the most cultivated cereals in the world. It is the main source of energy for more than half the world's population. The global paddy production was expected to reach a record level of 666 million tons in 2008. However, production in sub-Saharan Africa is very far from reaching the required growth rate, due to various constraints. Drought is considered as the major constraint, among the various abiotic and biotic factors limiting rice yield in West Africa. Several studies have proven that direct screening and selection for yield is possible under drought. Furthermore, with the advent of molecular biology, progress has been made in the identification of quantitative trait locus (QTL) involved in drought tolerance. The current study aims at evaluating the agronomic performance of 230 lines derived from a cross between IR64 and Kogoni91-1 (an elite rice variety in Mali), and 10 checks under both drought stress and full irrigation, and to identify genomic regions involved under drought and normal conditions. Thus, two adjacent trials have been conducted with two water regimes (irrigated and drought stress), and 2 replications each. The irrigated trial remains flooded till harvest, while cyclical drought stress is imposed in the stressed trial at 45 days after sowing (DAS) till leaf rolling of the resistant check variety…

Related GCP Project–G7010.04.01: Improving rice productivity in the lowland ecosystems of Burkina Faso, Mali and Nigeria through marker-assisted recurrent selection (MARS) for drought tolerance and yield potential

Notes:

4.7: Generation of a phenotyping strategy in the selection of tolerant rice to drought in rainfed lowland

Konaté KA, Ndjiondjop MN, Sow M, Futakuchi K, Sanni A, Audebert A*

* *Africa Rice Center (AfricaRice), Cotonou, 01 BP 2031 Benin; e-mail: K.Konate@cgiar.org*

Drought is one of the serious constraints for the production of rice grown in rainfed lowland. AfricaRice leads a GCP supported project to develop rice varieties for rainfed lowland with high yield potential and tolerance to drought using marker-assisted recurrent selection (MARS) in collaboration with national partners in Burkina Faso, Mali and Nigeria. The main target trait for selection is yield under drought. Additionally, several other traits—leaf temperature by infrared thermography, chlorophyll fluorescence, morphological traits (plant height, number of tillers, drought sensitivity scores and yield component)—have also been measured in both drought and well-watered conditions during the phenotyping of the developed populations in controlled environments under the rainout shelter of AfricaRice's station in Cotonou, Benin. Besides the selection, we attempt to generate a strategy for further effective phenotyping for tolerance to lowland drought by examining the relationship of these determined traits under both drought and well-watered conditions. 230 lines derived from a cross between IR64 and B6144F X-MR-6-0-0 were tested with the parents and 2 tolerant and 2 susceptive checks in 2012 and the 62 lines best lines for yield were retested in the same conditions in 2013. Preliminary results showed that drought increased leaf temperature and created disruption in the status of photosystem II…

Related GCP Project–G7010.04.01: Improving rice productivity in the lowland ecosystems of Burkina Faso, Mali and Nigeria through marker-assisted recurrent selection (MARS) for drought tolerance and yield potential

Notes:

4.8: Exploitation of *Oryza glaberrima* lines for drought tolerance rice breeding in lowland ecosystem in Africa

*AA Shaibu, MI Uguru, AT Maji, MN Ndjiondjop, and R Venuprasad**

* *Africa Rice Center Regional Station, P.M.B 5320, Oyo Road, Ibadan, Nigeria; e-mail: r.venuprasad@cgiar.org*

About 70% of total rice area in Africa is rainfed and drought is an important production constraint. Periodic drought caused by irregular and erratic rainfall pattern in Africa often results in unpredictable midseason drought, the consequence of which is poor rice yield in this region. Yield losses due to drought are estimated to be around 50% or more in sub Saharan Africa. Consistent efforts are requisite to breed for improved drought-tolerant and high-yielding rice varieties. More than 1700 accessions of *O. glaberrimas* obtained from AfricaRice Genebank were previously screen for drought tolerance and yield under drought stress in lowland ecosystem. Subsequently, 485 lines along with standard checks were evaluated in replicated trial in Alpha Lattice Design for drought tolerance and yield during the 2013 dry season. The analysis of variance show significance differences between genotypes at (P = 0.05, 0.01 and 0.001) respectively. The mixed model analysis using REML option of the SAS MIXED procedure showed high heritability for most traits measured; specially yield, indicating a lower environmental influence. A total of eighty lines, were identified as good performers under stress. This set will be further evaluated to identify the most promising lines that could be used as donors in breeding for drought tolerance.

Related GCP Project–G7010.04.01: Improving rice productivity in the lowland ecosystems of Burkina Faso, Mali and Nigeria through marker-assisted recurrent selection (MARS) for drought tolerance and yield potential

Notes:

4.9: Stengthening rice breeding in Mekong Region

Jonaliza Lanceras-Siangliw, Theerayut Toojinda, Khin Soe,*
Bounthong Bouahom, Ouk Makara
** Rice Gene Discovery Unit (RGDU), National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand; e-mail: jsiangliw@gmail.com*

Notes:

Countries around the Mekong River rely on rice as the main food in the region. Rice production in the region is facing constraints that threaten food security. RGDU of BIOTEC initiated a program which includes Department of Agricultural Research (DAR), National Agriculture and Forestry Research Institute (NAFRI) and Cambodian Agricultural Research and Development Institute (CARDI) as partners. Marker-assisted selection (MAS) hastened the improvement of Mekong mega varieties in terms of biotic and abiotic stresses. Rice in the region is marked by good eating and cooking qualities and these characters were also improved. To further strengthen the rice breeding program in the region, phenotyping facilities were developed in participating institutes to validate MAS-developed lines. Moreover, human resource was developed through training and scholarship together with financial aid from BIOTEC, Kasetsart University, Rajamankala University and Ubon Ratchatani University. Since the start of the project, this project has trained 22 researchers from participating institutes and provided 10 graduate scholarships. Advance lines of aromatic Manawthukha, salinity tolerant Sin Thwe Latt, aromatic TDK1 and IR57514 with good eating qualities will be released as new varieties as a result of the combined effort in strengthening breeding procedures, phenotyping facilities and human resources in our partner institutes.

Related GCP project–G4009.09: Community of Practice: Strengthening rice breeding program using genotyping building strategy and improving phenotyping capacity for biotic and abiotic stresses in Mekong region

5. Sorghum

5.1: Discovery and development of alleles contributing to sorghum drought tolerance

AH Paterson, IDK Atokple, C Tom Hash, S Deshpande, SP Mehtre*
** Plant Genome Mapping Laboratory, University of Georgia; e-mail: paterson@uga.edu*

Fine-scale characterization of qualitative factors related to sustained photosynthetic output under drought stress will yield improved understanding of the structure and functions of genomic regions of importance to sorghum improvement, advancing genetic dissection and molecular cloning of genes conferring the phenotypic effects mapped to these regions. Empirical testing of key combinations of stay-green QTLs is revealing the comparative efficacy of various combinations under stress conditions in Ghana and India, also providing for obtaining additional recombinants needed to reduce linkage drag. About 30 sorghum genome and 40 transcriptome sequences provide the means to design comparative DNA markers suitable for utilization both in sorghum and in many additional cereals, and are supporting development of hypotheses about roles of specific genes and pathways in drought response. We are testing these and other hypotheses using breeding populations in which drought tolerance is being combined with other traits addressing production constraints in West and Central Africa, Eastern and Southern Africa, and South Asia.

Related GCP project–G3008.05: Discovery and development of alleles contributing to sorghum drought tolerance

Notes:

5.2: Multi-traits and multi-environments sorghum breeding in Mali through marker assisted recurrent selection

Baptiste Guitton, Dramane Sako, Korotimi Thera, Diarah Guindo, Mohamed Tekete, Mamoutou Kouressy, Michel Vaksmann, Denis Lespinasse, Michel Ragot, Niaba Teme, Jean-Francois Rami*

* *CIRAD UMR AGAP, TA 108/03, Av Agropolis, 34398 Montpellier, CEDEX 5, France; e-mail: baptiste.guitton@cirad.fr*

Marker assisted recurrent selection (MARS) is a recent approach that integrates molecular markers all along of the breeding process. The approach combines an exhaustive multi-environment bi-parental populations based QTL analysis, for all the traits that define the breeder's target, with genotypic index definition, and several generations of intercrossing monitored by markers. The genetic material produced by this approach corresponds to one or several ideal genotypes defined based on the QTL results and their variation in different environments. This approach aims at getting the most out of breeding populations, and finally of resources allocated to the breeding program. MARS can be seen as a pipeline of genetic material improvement through enrichment in good alleles for target traits and corresponding identified QTLs.

Since 2008, two populations developed from the crosses of Tiandougou with Keninkeni and Tiandougou with Lata3 have been evaluated in 2010 and 2011 respectively in 6 environments. QTLs have been detected for both populations for a large number of traits (grain productivity, flowering time, plant morphology, grain quality, etc.) in the 6 environments and MARS cycles are ongoing. The evaluation of material generated through the first MARS cycle showed lines with superior and stable performance as compared to elite checks.

Related GCP projects–G4008.48: Improve sorghum productivity in semi-arid environments of Mali through integrated MARS

Notes:

5.3: Evaluation of sorghum grain quality for QTL analysis and marker assisted recurrent selection (MARS)

Diarah Guindo, Andre Kapitan Gnimdu, Baptiste Guitton, Geneviève Fliedel, Fabrice Davrieux, Michel Vaksmann, Niaba Teme, Jean-Francois Rami*

* *CIRAD UMR AGAP, TA 108/03, Av Agropolis, 34398 Montpellier, CEDEX 5, France; e-mail: diarah.guindo@cirad.fr*

Sorghum breeding in Mali mostly focuses on varieties for human consumption. Even if most of breeding efforts concentrate on productivity and adaptation, grain quality is a very important aspect to consider for improved material to be adopted and successful. One major traditional use of sorghum in West-Africa is the tô, a thick porridge prepared from sorghum flour, but grain quality is also important for emerging applications incorporating sorghum in food industry.

We present in this poster the methodological developments that have been achieved to better characterize sorghum grain quality in two MARS breeding populations. Several technological traits have been measured on grain (pericarp thickness, dehulling yield, endosperm texture, grain roundness, size, and color) and on mini-tô preparations (consistency, color). Biochemical characteristics (protein, lipid and amylose content) have also been assessed on the sorghum flour. Near infrared reflectance spectroscopy (NIRS) has been investigated as an indirect, fast, and non-destructive method to access all these traits on sorghum grain directly. These results are being used together with many other traits for grain yield, flowering time, plant and panicle morphology, to select varieties combining productivity and grain quality through integrated marker assisted recurrent selection.

Related GCP project–G4008.48: Improve sorghum productivity in semi-arid environments of Mali through integrated MARS

Notes:

5.4: QTL analysis of panicle architecture traits and yield components in sorghum

Dramane Sako, Baptiste Guitton, Michel Vaksmann, Niaba Teme, Jean-Francois Rami*

* *Institut d'Économie Rurale, BP258, Rue Mohamed V, Bamako, Mali. e-mail: dramanesako@yahoo.fr*

Sorghum is the fifth most important cereal in the world founding uses in both human consumption and forage. This crop has a predominant role in food security for millions of rural families in arid and semi-arid regions of the world and particularly in West-Africa. It appears thus primordial to develop new varieties adapted to these dry environments that combine high yield performance with grain quality adapted to local uses. The agronomic performance of cereals is significantly influenced by panicle architecture organization. Introducing panicle architectural traits in breeding programs could thus lead to select new varieties with high yield performance. In the context of a MARS breeding program, we investigated the genetic determinism of panicle architectural traits in sorghum, studying an F3 population derived from a cross between contrasted parents for panicle habit. Exhaustive descriptions of panicle were performed for branching, branch elongation and grain number traits along the rachis, primary and secondary branches. Panicle architecture was decomposed in quantitative traits and studied in relation to plant growth and yield traits to propose a list of architectural traits associated with a phenotyping strategy that can be used by breeders to improve grain yield.

Related GCP project–G4008.48: Improve sorghum productivity in semi-arid environments of Mali through integrated MARS

Notes:

5.5: Development and evaluation of drought-adapted sorghum germplasm for Africa and Australia – Phase II

Andrew Borrell, Sidi Bekaye Coulibaly, Niaba Teme, Barbara George-Jaeggli, Simon Hamlet, Peter George, David Jordan*

* *Queensland Alliance for Agriculture and Food Innovation, Australia; e-mail: Andrew.Borrell@daff.qld.gov.au*

In Phase I of this project, stay-green, a trait that has been very important in providing post-anthesis drought tolerance to Australian sorghum hybrids, was introgressed into elite sorghum lines from Mali. A Recombinant Inbred Line (RIL) mapping population was also developed and should be a valuable resource for sorghum breeders in Africa. Seed from the introgression lines was sent to Mali and Ethiopia for seed increase in 2012. Two African scientists visited Australia in 2012 to train in plant breeding, molecular breeding, crop physiology, simulation modeling and bioinformatics. In Phase II of the project, the stay-green enriched lines will be grown and phenotyped at two sites per country in West Africa (Burkina Faso, Mali, Niger) and East Africa (Ethiopia, Kenya, Sudan). The collaboration between Australia and the six African countries provides an opportunity to enhance the sorghum community of practice in Africa. Four more African researchers will be trained in crop improvement technologies in Australia during February 2014.

Related GCP project–G7009.04: Development and evaluation of drought-adapted sorghum germplasm for Africa and Australia-Phase II

Notes:

5.6: Selecting sorghum for adaptation to low phosphorus soils in West Africa

Willmar L Leiser, H Frederick W Rattunde, Eva Weltzien, Bettina IG Haussmann*

* *Institute of Plant Breeding, Seed Science and Population Genetics, University of Hohenheim, 70593 Stuttgart, Germany*
International Crops Research Institute for the Semi-Arid Tropics, BP 320 Bamako, Mali; e-mail: willmar_leiser@uni-hohenheim.de

Limited soil-phosphorus (P) availability is a serious and frequent constraint to sorghum production across the range of rainfall zones in West Africa. We assessed grain yields and P uptake and P use efficiency traits of 70 diverse West African sorghum genotypes under –P (no P fertilization) and +P conditions at two locations in Mali (2006 – 2010). The –P fields showed relative yield reductions of 2-59% compared to the +P fields. We could show that sorghum germplasm from West Africa is overall well adapted to low P soils, with a generally strong relationship between performance under +P and –P. However genotype-by-phosphorus cross over type interaction was observed among some of the best yielding genotypes. Direct selection under –P conditions was predicted to give 12% more yield gain for P-limited conditions, relative to indirect selection under +P conditions. There was a large genetic diversity for P uptake and P utilization traits. Guinea landraces as a group showed slightly better adaptation towards –P, and included those genotypes with specific adaptation to –P conditions. Although P uptake traits were better at predicting grain yield across –P conditions than P use efficiency traits, selection for high yielding genotypes with a high P use efficiency is possible.

Related GCP project–G7010.03.03: Establishing a molecular breeding program based on the aluminum tolerance gene Alt_{SB} and the P efficiency QTL, Pup-1, for increasing sorghum production in Sub-Saharan Africa

Notes:

5.7: Enhancing sorghum grain yield and quality for the Sudano-Sahelian zone of West Africa using the Backcross Nested Association Mapping (BCNAM) approach

Niaba Teme, E Weltzien, Michel Vaksmann, JF Rami, F Rattunde, C Diallo, M Tekete, M Kouressy, Sidi B Coulibaly*

* *Institut d'Économie Rurale, BP258, Rue Mohamed V, Bamako, Mali; e-mail: niabateme@gmail.com*

The sorghum breeding programs of IER and ICRISAT in Mali are jointly implementing a backcross-nested association mapping (BCNAM) design since 2010. This multi-parental design combines high-resolution population development for genetic analysis of complex traits, genetic basis enlargement and enrichment and direct breeding application thanks to the use of advanced-backcross populations with adapted elite recurrent parents (RPs). This complex multi-parental crossing scheme involved three elite varieties, obtained from participatory breeding in Mali (Lata3, Grinkan and Keninkeni), as recurrent parents and 29 donor parents which are either specific or common to one or several of the RPs. A total of 50 BC1F3 populations of 70 to 200 families each were developed, representing approximately 6300 families. These populations were evaluated in multi-year and multi-site trials in 2012 and will be evaluated in 2013 and 2014. The genetic diversity and polymorphism of recurrent and donor parents assessed with the ca. 1400 SNPs available through the IBP provides a medium density genotyping framework for the analysis of the populations. Phenotyping in multi-location with various sowing dates, in high and low P environments of 33 populations in 2012 showed a wide range of agronomic and phenologic variation within and across populations.

Related GCP project–G7010.05.01: Enhancing sorghum grain yield and quality for the Sudano-Sahelian zone of West Africa using the backcross nested association mapping (BCNAM) approach

Notes:

6. Wheat

6.1: Exploiting AB genome diversity to create new hexaploid wheat germplasm with enhanced drought/heat tolerance

Misra S, Tetali S, Bagwan J, Tamhankar S, Bonnett D, Zaharieva M, Desai AS and Trethowan R*

* *Agharkar Research Institute, Pune, Maharashtra, India; e-mail: satishmisra@yahoo.com, or scmisra@gmail.com*

Many potentially beneficial alleles have been lost in wheat due to bottlenecks imposed by domestication coupled with intensive selection. We are also facing new challenges of biotic and abiotic stresses and new diversity is needed. We propose using new sources of genetic diversity to create wheat germplasm with superior drought and heat tolerance. A subset of 108 genetically diverse emmer wheat accessions were identified from a large collection originating from 35 countries based on agronomic traits and genetic diversity assessed using SSR and DArT markers. These selected emmers were crossed to three Ae. tauschii accessions to produce new emmer based synthetic hexaploid wheat at CIMMYT, Mexico. At PBI, Sydney, approximately 1000 double haploids were made on hexaploid progeny derived from emmer x hexaploid crosses; the hexaploid parents included durum and emmer based synthetics and drought tolerant Indian and CIMMYT lines. At ARI, Pune and UAS, Dharwad, synthetic back cross lines were developed based on 176 F6 families generated from 30 crosses between durum and emmer based synthetics and elite Indian bread wheat varieties. New hexaploid wheat germplasm with enhanced genetic diversity and drought and heat tolerance is now available for use in breeding programmes.

Related GCP project–G3008.01: Generating new wheat germplasm with enhanced drought/heat tolerance using AB genomes genetic diversity

Notes:

6.2: Assessment of the relative impact of key physiological traits on adaptation to drought in different mega-environments

M Fernanda Dreccer, Tony G Condon, Farid Makdis, Laura Barnes, Hassan Ouabbou, Firdissa Eticha, Matthew Reynolds, M Gabriela Borgognone, Greg Rebetzke, Francis C Ogbonnaya*

* *CSIRO Plant Industry, Cooper Laboratory, P.O. Box 863, University of Queensland, Warrego Highway, Gatton, QLD 4343 Australia; e-mail: fernanda.dreccer@csiro.au*

In wheat, traits with successful impact under drought have the ability to increase water use, shift water use to critical crop periods, increase water use efficiency and/or influence biomass partitioning to the grains. To prioritise traits between regions and decide which ones would be most useful to combine, a comparative appraisal of their effects is required under contrasting water availability patterns. Given the changing nature of drought, its timing and intensity, different patterns of water use are ultimately required to maximise yield. This study aimed to quantify the relative impact of key physiological traits and the performance of some ICARDA germplasm in regions of contrasting drought patterns, representative of the main wheat growing mega-environments. A set of trials were grown in locations around the world representing summer dominant environments with terminal drought (Ethiopia, Mexico and Northern Australia), Mediterranean type winter rainfall distribution (Syria, Lebanon, Morocco), and even winter rainfall (Southern Australia). A set of germplasm, consisting of related lines contrasting in trait value for transpiration efficiency, tillering, stem water soluble carbohydrates, early vigour and flowering, were assessed. In addition, a set of globally important checks and ca. 200 elite ICARDA's germplasm were tested. Performance was measured as yield and yield components, early cover, phenology, canopy temperature and stay-green…

Related GCP project–G3008.08: Breeder-friendly high-throughput phenotyping tools to select for wheat adaptive traits in drought environments

Notes:

6.3: Breeding of new varieties with drought-resistant, high and stable yield of wheat using Cross Selecting method in irrigated and dry field

Meirong Sun, Junling Zhang, Dongxu Zhang, Jinlong Yan, Shuzhen Shen*

* *Institute of Millet, Shangxi Academy of Agricultural Science (SAAS), Changzhi; e-mail: gzssmr@163.com*

The target traits were effectively combined using asymptotic hybridization methods integrating the excellent genes from the two major wheat growing areas including the northern China and Huang-Huai winter wheat areas in the breeding of new varieties of wheat. Hybrid generations were selected using Cross Selecting method in irrigated and dry field, namely: F1 and F2 generations were selected in irrigated field, F2 and subsequent generations were simultaneously selected both in irrigated and dry conditions, so that the various traits of every generations can be fully expressed both in natural and man-created environmental conditions. The approach made natural selection, artificial selection and orientation cultivate closely together, and increased the selection pressure and frequency, and improved the generations selection quality and efficiency. This method not only created the diverse breeding environmental conditions, but also provided a new idea for different ecotypes varieties breeding. In recent years, we had bred 13 new varieties with drought-resistant, wide adaptability, high and stable yield including Jinmai 63, Chang 6878, etc. using the approach. These new varieties have been applied to production in large scale and Chang 6878 has been determined as the drought area test check (CK) in the northern China winter wheat areas since 2004.

Related GCP project–G7010.02.01: Wheat breeding and selection strategies to combine and validate QTLs for WUE and wheat tolerance in China

Notes:

6.4: High throughput assessment, favourable allele detection and pyramiding of stem water-soluble carbohydrates in wheat

Ruilian Jing, Zhenghang Wang, Weiyu Li, Bin Zhang, Xiaoping Chang, Xinguo Mao, Ang Li, Matthew Reynolds, Richard Trethowan*

* *Institute of Crop Science, Chinese Academy of Agricultural Science (CAAS), Beijing 100081, China; e-mail: jingrl@caas.net.cn*

Stem water-soluble carbohydrates (WSC), a useful trait for predicting terminal drought and heat tolerance, can buffer wheat grain yields against conditions unfavorable for photosynthesis during the grain filling stage in wheat. We developed a mixed NIRS (near-infrared reflectance spectroscopy) model for WSC quantitative analysis of the wheat sample, which allows rapid and high throughput assessments and selections of WSC contents in wheat genetics and breeding programs. Two hundred and sixty-two winter wheat accessions with different drought responses were collected to detect favorable alleles for WSC and grain yield component traits under various water regimes. The WSC in lower internodes showed close genetic relationships with grain weight, especially at grain filling stage under drought stress. Based on the association analysis, 16 WSC-favorable alleles were identified, and five of them contributed to significantly higher grain weight. They are being used in the molecular marker assisted recurrent selection in five genetic populations to accumulate superior alleles for target traits. Our results showed a high potential approach for improving the drought and heat tolerance, and grain yield by using the NIRS model for WSC quantitative analysis and pyramiding WSC favorable alleles in wheat.

Related GCP project–G7010.02.01: Wheat breeding and selection strategies to combine and validate QTLs for WUE and heat tolerance in China

Notes:

6.5: Molecular breeding for selecting drought-tolerant and high yield winter wheat

Xiumin Chen and Qiang Li
Dry-Land Farming Institute of Hebei Academy of Agricultural and Forestry Sciences (DFI); e-mail: chenxiumin168@163.com or sdshengqishi@163.com

Drought-tolerant and high yield Winter wheat should be semi-dwarf with low canopy temperature, resistant to many diseases. Two parent lines were used: Hengguan35, a variety with dwarf genes (Rht1, Rht2, Rht4, Rht8) powdery mildew resistant genes (Pm4, Pm16 yellow rust genes (YrTp2), and photoperiod insensitive gene (Ppd-D1a); Jifeng703, which has low canopy temperature and resistance to fusarium blight. Nine of F4 lines which is semi-dwarf with dwarf genes, resistance genes, drought-tolerant related gene locus (e.g. with low canopy temperature, high content of chlorophyll) has been selected. These lines will be further selected by molecular detection and object trait identification.

Related GCP project G7010.02.01: Wheat breeding and selection strategies to combine and validate QTLs for WUE and heat tolerance in China

Notes:

6.6: Breeding wheat for drought-resistance and heat-tolerance of higher yielding potentials with the ecological-adaptation-oriented selection strategy

XiuRong Li, YongFeng Chai, ZhiYong Zhao, LaiHu Sun*

* *Cotton Research Institute, Shanxi Agricultural Science Academy, Yuncheng, Shanxi, 044000, P.R.China; e-mail: sxlixiurong@sina.com*

Located at the southeast end of the Loess Plateau, Yuncheng prefecture belongs to the Huang-Huai-wheat-growing region in China. According to the data of the 13 weather stations in Yuncheng prefecture, the mean annual precipitation was 470~630 mm (1950~2012), in which 200~300 mm was in wheat growth season.The main climate problems are: short of water, winter hardness damage, spring frost damage,and dry-hot-wind during ripening. We rain-fed wheat breeding group, emphasized the Breeding Wheat for Drought-resistance and Heat-tolerance of Higher Yielding Potentials with ecological-adaptation-oriented selection strategy, focused on the developing pattern of SLOWLY during tillering and rooting, STEADILY during stem extension, QUICKLY during ripening, focused on the phenotypic model of organs with high photosynthetic efficiency and deep rooting capacity, focused on the yielding structure of moderate ears/m2 and grains/ear with higher TKW potential. We grew the early generations of the selected crosses in both irrigated and rain-fed nurseries for selections. Our group has had 6 and 5 cultivars registered by the national and provincial governments respectively. Of them JinMai 47 covered more than 6.7 million hm2 in the last 18 years, and has been the CK in both the national and provincial Wheat Performance Test Nurseries since 1996.

Related GCP project–G7010.02.01: Wheat breeding and selection strategies to combine and validate QTLs for WUE and heat tolerance in China

Notes:

6.7: Evaluating and phenotyping a set of CIMMYT nursery WPHYSGP and local varieties in two irrigation regimes in three years

Yueqiang Zhang, Zheru Fan, Jianfeng Li, Zhong Wang, Zhenlu Wu, Qi Zhao, Hongzhi Zhang, Ruilian Jing*

* *Institute of Nuclear and Biological Technologies, Xinjiang Academy of Agricultural Sciences(XAAS), Xinjiang, Urumqi 830091, China; e-mail: zhangyqyhm@163.com*

Accurate field evaluation of yield related physiological traits is critical for selecting high yield and drought resistance in wheat (*Triticum aestivum* L.). A set of CIMMYT nursery WPHYSGP comprising 145 entries and 25 local varieties and elite lines were evaluated and phenotyped in two irrigation regimes in 2010, 2011 and 2012 growing seasons. Our study showed that plant height, thousand kernel weight, grain per spike, grain weight per spike and NDVI Index were significant positive correlation with yield and canopy temperature was significant negative correlation with yield across normal irrigation and limited irrigation. Days to heading, spikelet per spike, grain plumpness were significant positive correlation with yield across normal irrigation, but not in drought. Genotypes were classified based on yield performance across different irrigation regimes. High yield genotypes are entry 9650, 9637, 9638, 9646, 9611, 9625 from CIMMYT and local variety Xinchun 6, Xinchun 10, Xinchun 17, Xinchun 23, Xinchun 29 in both normal and limited irrigations. Grain per spike, grain weight per spike, grain plumpness, thousand kernel weight, NDVI, and canopy temperature can be used effectively as selecting criteria for spring breeding. High yield of those genotypes was contributed by good performance of those morphological and physiological traits.

Related GCP project–G7010.02.01: Wheat breeding and selection strategies to combine and validate QTLs for WUE and heat tolerance in China

Notes:

6.8: MARS and MABC for improvement of drought tolerance in spring wheat

GP Singh, KV Prabhu, Neelu Jain, Ramya P, P K Singh , PC Mishra, S C Mishra, V S Sohu, G S Mavi, Parveen Chunneja, Hari Krishna, Shweta Umar, Biswajeet Mondal, Neha Rai, Priyanka Vijay, Jyoti Jha, Arun Gangawar and Manoj Kumar Pandey*

* *Indian Agricultural Research Institute, New Delhi-110012, India; e-mail: gyanendrapsingh@hotmail.com*

Notes:

The project aims to implement drought phenotyping protocols integrated with the marker assisted recurrent selection (MARS) and marker assisted back cross breeding (MABC) to combine QTLs contributing to drought tolerance imparting with significant phenotypic effect of drought tolerance to the progenies derived from biparental crosses. The within population inter-family crosses selected among four different F5 populations were developed under multi-locational phenotyping under two environmental variants of drought and irrigation regimes, for carrying out MARS strategy. Superior progenies were selected on the basis of the traits including early ground cover, DH, FLE, SPAD values, CT, NDVI, GY and component traits. AMMI analysis for genotype X location interactions indicated that Delhi and Pune locations represented stable environments to effect MARS integrating phenotype data for decision making along with QTLs in the population DBW43 X HI1500 and Ludhiana and Powarkheda were ranked as the best location in the population HUW510 X HI1500. Delhi and Powarkheda locations were the best under drought conditions. In the MABC approach, five backcross BC2F1 populations comprising 300-700 individuals each were targeted for introgression of previously reported QTLs (foreground selection) governing physiological traits to recover background genomes of HD2733, HD2967 and GW322 using background selection.

Related GCP project–G7010.02.02: Molecular breeding and selection strategies to combine and validate quantitative trait loci for improving water-use efficiency and heat tolerance of wheat in India (PI: K Vinod Prabhu, IARI-ICAR)

6.9: Transfer of drought tolerance QTL to elite Indian wheats through molecular breeding

Parveen Chhuneja, VS Sohu, GS Mavi, Urmila, GP Singh, KV Prabhu*

* *School of Agricultural Biotechnology, Punjab Agricultural University, Ludhiana-141004 (Punjab) India; email: pchhuneja@pau.edu*

The present study was aimed at the developing drought tolerant wheat using marker assisted backcross breeding. Three drought tolerant genotypes, viz. Excalibur, Krichauff and Babax were crossed with two elite Indian wheat genotypes, viz. HD2967 and PBW 343+Lr24-Lr28-Yr10-Yr15. However, most of the markers, reported to be linked with drought tolerance QTL, were found to be monomorphic in parental combinations. So backcross populations were screened for target regions. Major QTL has been reported on 4A, 3B and 1B. Total of 77 SSR markers from target regions were evaluated, but only 17 markers were polymorphic for these parental combinations. Eleven of these markers showed introgression in BC1F1 plants. Foreground selection was conducted in BC2F1 using markers for target regions. For identifying additional markers for the target regions on 4A, 52 SSR markers developed from survey sequence data of 4A were analyzed and 16 were found polymorphic and surveyed on BC2F1. Very good plant type was recovered in BC2F1s and selections were made for tiller number, grains per spike and grain weight. The seeds of the selected BC2F1 plants are being multiplied at off season nursery at Keylong which will be used for small scale trials during 2013-14 under drought conditions.

Related GCP project: Not applicable

Notes:

6.10: Genetic analysis for screening high temperature and moisture stress tolerance traits in bread wheat

PC Mishra, Niharika Shukla and RS Shukla*

** Wheat Improvement Project, Department of Planr breeding and genetics JNKVV, Powarkheda-461110(M.P.); e-mail: pc_mishra@rediffmail.com*

Genetic analysis for 25 diverse genotypes in bread wheat were studied for high temperature and moisture stress tolerant characters under laboratory and field condition (two dates of sowing). The data from laboratory studies for different temperature regimes revealed that the existence of high amount genetic variability for vigor index and coleoptile length while germination percentage was the lowest. It indicated that the germination was least affected by temperature regimes as compared to seedling length and vigor. Similarly field observation indicated that number of grains per ear, grains yield per plant, total biomass per plant, straw weight per plant and spike weight per plant had high heritability coupled with genetic advance in both date of sowing. The adverse effects of heat stress can be mitigated by developing crop plants with improved thermo tolerance using various genetic approaches. For instance, during seed germination, high temperature may slow down or totally inhibit germination, depending on plant species and the intensity of the stress. At later stages, high temperature may adversely affect photosynthesis, respiration, water relations and membrane stability. Damage caused by heat/temperature extremes could be minimized by framing strategy to screen and develop such a variety which would tolerate high temperature.

Related GCP project: Not applicable

Notes:

7. Comparative Genomics

7.1: Validation of *ZmMATEs* as genes underlying major Al tolerance QTLs in maize

Claudia T Guimarães, Lyza G Maron, Maria M Pastina, Thomas Matonyei, Jurandir V. Magalhães, Lauro JM Guimarães, Ubiraci GP Lana, Roberto W Noda, Sidney N Parentoni, Dickson Ligeyo, Vera MC Alves, Leon V Kochian, Samuel Gudu*

* *Embrapa Milho e Sorgo, Sete Lagoas, Brazil; e-mail: claudia.guimaraes@embrapa.br*

In this study, we identified a major Al tolerance QTL on chromosome 6 (qALT6), which was co-localized with ZmMATE1, and with its expression QTL (eQTL). Near-isogenic lines developed for qALT6 showed a two-fold increase in Al tolerance that resulted in a significantly higher grain yield on acid soils, maintaining a similar yield performance under corrected soil in comparison to the recurrent line L53. qALT6 also increased grain yield in near-isogenic hybrids. In addition to validate ZmMATE1 as a functional gene underling the major Al tolerance qALT6, we identified another candidate gene, ZmNrat1, located close to qALT5. ZmNrat1 shares a high amino acid sequence identity and an expression up-regulated by Al with OsNrat1, a specific transporter for Al3+ associated with Al tolerance in rice. A further characterization of Kenyan maize lines indicated that ZmMATE1 was not present in these Al tolerant lines. However, we identified three adapted Kenyan showing high expression of ZmMATE1, which were derived from crosses with Brazilian germplasm. These lines and two SNPs flanking qALT6 can be used for marker-assisted selection in Kenyan lines. Thus, molecular tools were developed and can be applied to improve maize adaptation to acidic soils.

Related GCP project–G7010.03.02: Cloning, characterisation and validation of $\mathit{Alt}_{SB/Al}$ *tolerance in maize*

Notes:

7.2: Improving phosphorus efficiency in sorghum by the identification and validation of sorghum homologs for Pstol1, a major QTL underlying phosphorus uptake in rice (SorghumPup1)

Jurandir Magalhães, Barbara Maciel, Gabriel Azevedo, Robert Schaffert, Claudia Guimarães, Vera Alves, Sylvia Morais de Souza, Alvaro Resende, João Herbert Viana, Leon Kochian, Jiping Liu, Randy Clark, Zhangjun Fei, Steve Kresovich, Martha Hamblin, Sharon Mitchell, Theresa Fulton, Soumana Souley, Sam Gudu, Eva Weltzien, Fred Rattunde, Willmar Leiser, Matthias Wissuwa, Sigrid Heuer*

* *Embrapa Maize and Sorghum, Brazil; e-mail: jurandir.magalhaes@embrapa.br*

Low productivity due to soil constraints and a lack of properly adapted crop cultivars is a serious problem in many parts of Africa, where sorghum is a staple food supporting millions of the rural poor. JIRCAS and IRRI have cloned the gene encoding Pstol1, which encodes a protein kinase that enhances early root growth and P acquisition. This project aims at the identification of sorghum Pstol1 homologs and their validation as bona fide genes underlying tolerance to P deficiency in sorghum. A sorghum association panel was phenotyped for agronomic performance under low P in the field and for root morphology traits. SNPs within sorghum Pstol1 homologs were identified and converted into the KASPar system. Our data suggests that SNPs within Pstol1 homologs are associated with both root morphology and traits related to P acquisition. Validation is being conducted in a large recombinant inbred line population that was genotyped by sequencing. Our preliminary results indicate that some Pstol1 homologs co-localize with QTLs controlling root morphology traits and shoot dry weight. We are currently finalizing QTL mapping and are also phenotyping the sorghum association panel for root architecture. The final step will be the selection of markers for sorghum genotyping.

Related GCP project–G7010.03.06: Improving phosphorus efficiency in sorghum by the identification and validation of sorghum homologs for Pup1, a major QTL underlying phosphorus uptake in rice, and identification of other P efficiency QTLs

Notes:

8. Integrated Breeding Platform (IBP)

8.1: The Crop Ontology for annotation and interoperability of crop phenotypic data

Elizabeth Arnaud, Luca Matteis, Milko Skofic, Tom Hazekamp, Alberto Fabio Guerrero, Rosemary Shrestha , Simon Reinhard , Jean Francois Rami, Peter Kulakow, Moshood Bakare, Antonio Lopez-Montes , Sam Ofodile, Ousmane Boukare, Praveen Reddy T., Ibrahima Sissoko, Prasad Peteti, Suyash Patil, Trushar Shah, Nikki Frances Borja, Mauleon Ramil, Inge van den Bergh, Rhiannon Chrichton, Arlett Portugal, Pierre Yves Chibon, Naama Menda, Rex Nelson, Cyril Pommier, Glenn Hyman, Herlin Espinosa, Graham McLaren*

* *Bioversity International, Parc Scientifique Agropolis II, 34394 Montpellier Cedex 5, France; e-mail: e.arnaud@cgiar.org*

The Crop Ontology (CO) is published online (www.cropontology.org) and currently includes breeders'traits, with measurement methods and scales, for cassava, banana, chickpea, common bean, cowpea, groundnut, maize, pearl millet, pigeon pea, potato, rice, sorghum, wheat and yam. The IBFieldbook uses these reference lists of traits for the capture and annotation of breeders' data. A Programmatic Application Interface (API) enables the direct use of the CO concepts by third- party web sites like: the international cassava database (http://www.cassavabase.org/), the Global Agricultural Trial Repository (http://agtrials.org/), Eu-Solanaceae at University of Wageningen, NDL (https://www.eu-sol.wur.nl/), the Phenomics Ontology Driven Database (PODD: http://150.229.2.236/podd/about) of the Australian Plant Phenomics Facility (APPF) and the Australian Phenomics Network (APN). CO concepts are cross referenced to Plant Ontology (PO) and Trait Ontology (TO). CO will be aligned with the AGROVOC thesaurus (FAO) to integrate crop data into OpenAgris (http://aims.fao.org/openagris) using semantic web technologies like Linked Open Data (LOD). An environmental and experimental design ontology group will be formed with experts of GIS, phenotyping and

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crop modelling projects. A vision is now emerging of a consortium contributing to an international semantic framework for the integration of phenotypic and genotypic data in which CO will be a key resource.

> *Related GCP project–G4009.03/G4010.06/G4011.01/ G4011.10: Enhancement and implementation of the Crop Ontology for data integration and data interoperability, and expanding its use within communities of practice and to partners to integrate datasets for GCP priority crops through the IBP*

Notes:

8.2: Towards enhancing ISMU pipeline with genomic slection modules for facilitating molecular breeding

*Abhishek Rathore, Sarwar Azam, Roma Rani Das, Manish Roorkiwal, Dadakhalandar Doddamani, Mohan Telluri, David Marshall, Trushar Shah, A Bhanu Prakash, Dave Edwards, Alain Charcosset, Mark Sorrells, John M Hickey, Jean-Luc Jannink, Rajeev K Varshney**

* *International crops Research institute for the Semi –Arid Tropics (ICRISAT), Patancheru 502 324, Andhra Pradesh, India. Email: r.k.varshney@cgiar.org*

Integrated SNPs mining and utilization (ISMU 1.0) pipeline was developed to analyze the next generation sequencing (NGS) data for variant analysis. ISMU 1.0 is a GUI based pipeline which offers a complete range of tools required for SNP analysis including data processing, alignment, mapping and variant detection. To utilize the genotyping information from the ISMU 1.0 together with available phenotypic information, ISMU 2.0 is being developed. Several data processing capabilities and genomic selection (GS) modules are being integrated in the existing pipeline. Several R and Fortran scripts including Ridge Regression Best Linear Unbiased Predictor (RR-BLUP), Kinship Gauss, Bayesian Ridge Regression, Bayesian LASSO, BayesA, BayesB, BayesCπ and Random Forest are being customised and integrated in to pipeline. Most of these scripts have been tested successfully on simulated datasets and now are in a process of being layered with a JAVA wrapper. Some scrtipts based on RR-BLUP integrated in GUI are being tested on real datasets from ICRISAT. Additionally, the pipeline has a module to check quality and different features of marker datasets such as % missing data, minor allele frequency (MAF) and polymorphism information content (PIC). The pipeline has been developed to run on 64-bit Linux, server edition is being written in CGI Perl and standalone version is being developed in Java. The pipeline is regularly tested on CentOS and Ubuntu platforms.

Related GCP project–G4011.05: Integration of MARS and GWS modules in the ISMU pipeline for facilitating molecular breading for complex traits

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8.3: Genotyping services for crop improvement in the developing countries

Chunlin He, Ndeye Ndack Diop, and Xavier Delannay*
* *Generation Challenge Programme, c/o CIMMYT, Texcoco, Mexico; e-mail: c.he@cgiar.org*

Marker-assisted breeding (MAB) can greatly increase the breeding efficiency compared with conventional breeding without using markers, and molecular genotyping with DNA markers, mainly SNPs and SSRs, is currently a prerequisite for generating genotypic data for marker-assisted selection (MAS). The Genotyping Support Service (GSS) at GCP was created to facilitate the access by breeders in developing countries and support their breeding programs not only by collaborating with service providers worldwide but also by providing training for data analysis. Since August 2007, GCP has launched several types of calls for research grant applications of GSS projects. Hundreds of applications have been received and about 200 of them have been awarded for genotyping with SNPs and SSRs. The awarded projects with topics from genetic diversity to MAS to improve yield, quality and stress tolerance have covered 14 major field crops from 25 countries. Currently, GCP has focused on SNP marker genotyping and created GDMS databases which are accessible to customers through the integrated breeding platform (IBP) for MAB. With available SNP marker data, GCP/IBP will provide the users from developing countries with easier access to more convenient genotyping services to support molecular breeding schemes including MAS, MABC, MARS and GWS.

Related GCP projects–G8009.05: Provide access to critical molecular breeding services, and G8009.06: Provide assistance with a range of molecular breeding support

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8.4: QTL IciMapping: Integrated software for building genetic linkage maps and mapping quantitative trait genes

Jiankang Wang, Huihui Li, Luyan Zhang, Lei Meng*

* *Institute of Crop Sciences and CIMMYT China, Chinese Academy of Agricultural Sciences, No. 12 Zhongguancun South Street, Beijing 100081, China; e-mail: wangjiankang@caas.cn*

QTL IciMapping is freely-available public software, capable of building high-density genetic linkage maps and mapping quantitative trait loci (QTL). Seven functionalities are fully implemented in QTL IciMapping v3.2 (accessed from http://www.isbreeding.net). (1) MAP: Construction of genetic linkage maps in biparental populations. (2) BIP: Mapping of additive and digenic epistasis genes in biparental populations. (3) CSL: Mapping of additive and digenic epistasis genes with chromosome segment substitution lines. (4) MET: QTL by environment interaction in biparental populations. (5) NAM: QTL mapping in nested association mapping populations. (6) SDL: Mapping of segregation distortion loci in biparental populations. (7) CMP: Integration of multiple maps sharing common markers. The latest released version has the following new features compared with previous versions. (1) Dominant/recessive markers are considered in recombination frequency estimation, map construction and QTL mapping. (2) A new functionality called CMP is implemented, which can be used to build the consensus map from multiple genetic linkage maps sharing common markers. (3) A new tool called 2pointREC is implemented, which can be used to estimate the pair-wise recombination frequency in biparental population. (4) Much more markers can be handled in the software. (5) Figures of linkage maps are improved.

Related GCP project–G8009.10: Computing system for planning molecular breeding and genetic analysis for multi-parental populations

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8.5: Agricultural Genomics Network (AGN): a much needed platform for the genomics research!

Rajeev K Varshney, Manish Roorkiwal, Dadakhalandar Doddamani, Abhishek Rathore, Antonia Okono, Fredrick Okono*

* *International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, 502324, India and CGIAR Generation Challenge Programme (GCP), c/o CIMMYT, 06600 Mexico DF, Mexico; e-mail: r.k.varshney@cgiar.org*

With the advancement in technology, several molecular breeding approaches like marker-assisted backcrossing (MABC), genotyping-by-sequencing (GBS), and genomic selection (GS) have been gaining popularity and are being adopted by researchers. In general researchers do not get clear idea which technology and/or which service provider will be cost-effective for the intended purpose. As a part of CGIAR Generation Challenge Programme (GCP)'s community-building efforts, a Linkedin group named, GCP-Agricultural Genomics Network (GCP-AGN) (http://www.linkedin.com/groups/GCPAgricultural-Genomics-Network-4919729) has been established to facilitate discussion in modern genomics areas. The group is offering a suitable platform to researchers for interactions, discussions, activity planning and exchange of ideas to the genomics and breeding communities. In addition, explore and harness plant genetic diversity using genomics tools to advance the breeding has been one of the key focuses of GCP. The GCP network has led to generation a range of genomic resources. With an objective to make the use of these resources and make them easily available for breeders and researchers a Genomics page has been developed at Integrated Breeding Platform (IBP) (https://www.integratedbreeding.net/agricultural-genomics). In order to avoid the redundant efforts mining of the existing, scattered data have been initiated and links to databases are being added on the genomics page.

Related GCP project–G8009.11: Developing and implementing the genomic component of the IBP

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8.6: Statistics, software and training for plant breeders working with multi-environment and multi-trait data

Marcos Malosetti and Fred A. van Eeuwijk*
** Biometris, Department of Applied Statistics Wageningen University, Wageningen; e-mail: marcos.malosetti@wur.nl*

Repeated measures in space (locations) and time (years, seasons) are the norm in applied plant breeding. Besides yield (in terms of whichever plant product), quality-related traits, disease and pest resistance, and others are also part of the breeding target, and so part of the breeders' equation. Therefore almost inevitably a breeder has to work with multi-trait data, so being able to extract the main patterns in such data sets is of main interest for making informed breeding decisions. In this poster, we discuss different statistical methodologies to handle multi-trait and multi-environment data in plant breeding. Those range from the determination of homogeneous sets of environments (megaenvironments) in a network of trials, characterization of stability of genotypic performance, the understanding of the genetic causes underpinning differential adaptation of genotypes across environments (QTLxE), mapping QTLs for multipletraits, and summarizing QTL information for several traits and environments using selection index theory. This has been complemented by the development of dedicated userfriendly software (Breeding View) and training courses. To be continued in the poster…

Related GCP projects–
Subactivity 2.2.5.2: Develop a Phenotypic data Analysis Application,
Subactivity 2.2.5.3: Develop a Molecular Genetic Analysis Application,
G8009.06.04/Activity 3.2.4: Design & analysis

Notes:

9. Capacity building

9.1: Genotyping services and capacity building activities at ICRISAT to enhance adoption of molecular breeding in developing countries

Rajeev K. Varshney, Mahendar Thudi, Annapurna Chitikineni, Abhishek Rathore, Senapthy Senthilvel, Trushar Shah and Stefania Grando*

* *International crops Research institute for the Semi –Arid Tropics (ICRISAT), Patancheru 502 324, Andhra Pradesh, India. E-mail: r.k.varshney@cgiar.org (author for correspondence)*

Molecular breeding is being successfully deployed by ARIs or private sectors in developed countries or by some CGIAR centres in developing countries. Although adequate genomic information is available in almost all crop species, NARS partners in developing countries seem to be lagging behind in practicing molecular breeding due to mainly lack of physical infrastructure and limited expertise in molecular breeding. The Center of Excellence in Genomics (CEG, http://www.icrisat.org/ceg) at ICRISAT, therefore, is engaged to address above mentioned issues by offering marker genotyping services on cost-to-cost basis as well as conducting training courses in modern breeding. With state-of-art marker genotyping platforms like ABI 3730 DNA Genetic analyzer (SSR genotyping), diversity array technology (DArT) platform (DArT genotyping), Illumina Beadxpress (SNP genotyping) and Illumina MiSeq (genotyping-by-sequencing), CEG-ICRISAT has provided genotyping services to a range of partners including NARS, ARIs, small & medium enterprises (SMEs) and CGIAR centrers in many countries. Similarly after organizing 10 training courses using a range of tools from Integrated Breeding Platform and other Open Access programmes, 257 scientists from several countries of sub-Saharan Africa and South Asia have been trained. Such efforts of CEG-ICRISAT are expected to enhance adoption of molecular breeding in developing countries.

Related GCP project: Not applicable

Notes:

10. Other

10.1: Molecular characterization of ripening-specific MADS-box genes and its application in varietal improvement for delayed ripening trait in Philippine bananas

*Laarni Grace Corrales, Jean Claude Balingit, Evelyn Mae Tecson-Mendoza and Eureka Teresa Ocampo**

* *Institute of Plant Breeding, Crop Science Cluster, College of Agriculture, University of the Philippines Los Baños, College, Laguna, Philippines; email: eteresaocampo@yahoo.com, or etmocampo@uplb.edu.ph*

The fruit-specific MADS-box gene, MaMADS2, encodes a transcription factor that regulates the developmental competence of climacteric fruits to ripen. Four isoforms of MaMADS2 gene from Lakatan (Musa acuminata, AAA), and two isoforms from Saba (M. balbisiana, BBB) were isolated from climacteric fruit cDNA. The isoforms differed in their 3'UTR regions, showing a strong regulation of the ripening process. Sequence analysis of the promoters for the dominant MaMADS2 isoforms showed the presence of light responsive elements, and control elements for salicylic acid production. Specific primers were designed from the promoter and 3' UTR and then utilized to isolate a 1.2 kb fragment of the genomic DNA that putatively codes for MaMADS2 of the Saba cultivar. Additional primers were designed and used to screen for changes along the MaMADS2 coding and promoter regions of Saba mutant seedlings developed through gamma irradiation of shoot tips and grown in tissue culture. Melt curve analysis verified the PCR results. Selected mutants will be grown to full maturity. At fruiting stage, the development, and postharvest traits of banana fruits will be closely monitored. This approach will hopefully produce new varieties of Saba, which is the major source of processed products such as banana chips and flour.

Related GCP project: Not applicable

Notes:

10.2: Development of molecular markers for the assessment of drought stress tolerance in eggplant

*Sarah Jane Manaday, Alma Canama, Eureka Teresa Ocampo, Rodel Maghirang and Evelyn Delfin**

** Institute of Plant Breeding, Crop Science Cluster, College of Agriculture, University of the Philippines Los Baños, College, Laguna, Philippines; email: efdelfin@yahoo.com*

Unexpected and prolonged drought adversely limit yield in eggplant, the number one vegetable in terms of production value in the Philippines. With only a few select eggplant cultivars grown, there is a need to identify genotypes that can be used in a breeding program for drought tolerance. One hundred eggplant genotypes consisting of Solanum melongena, S. linociera, S. nigrum, S. aculeatissima, S. sisymbriifolium, S. parkinsonii, S. stramonifolium, S. ferox, and S. nodiflorum collected from the Philippines and other countries were evaluated for growth responses under well-watered and drought stress conditions. Under drought, increases in root dry weight, and total dry matter yield were observed in 25% and 13% of the entries, respectively. One susceptible cultivar and several drought tolerant wild accessions were identified as putative parentals for developing drought tolerant populations. QTL mapping for drought tolerance in eggplant will be carried out using SSR markers. Two hundred SSR primers that were di-repeats and derived from ESTs were chosen based on their uniform coverage of the eggplant genome, and PCR product size. Initial screening of 60 primers showed that 19 showed polymorphic bands among the tolerant and susceptible eggplant genotypes. Further optimization and polymorphism analysis of additional 140 primers is underway.

Related GCP project: Not applicable

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(Centro Internacional de Mejoramiento de Maíz y Trigo;
the International Maize and Wheat Improvement Center)

Mailing address:
Apdo Postal 6–641
06600 México, DF, México

Physical address:
Km 45 Carretera México-Veracruz
El Batán, Texcoco, México, CP 56130

Tel: +52 55 5804 2004 | **Fax:** +52 55 5804 7558

Email: generationcp@cgiar.org or info@generationcp.org
www.generationcp.org