Poster abstracts

2011 General Research Meeting • 21–25 September 2011 • Hyderabad, India

Generation Challenge Programme

CGIAR Generation Challenge Programme

General Research Meeting
21–25 September 2011
Hyderabad, India

Poster abstracts

Editorial note: Abstracts are published as presented by the authors, except for abstracts that extend beyond the pre-established word limit communicated to authors. Text beyond the word limit has been omitted, and this omission is indicated by suspension marks (...)

TABLE OF CONTENTS

Theme 1:
Comparative and applied genomics

Cassava

1.1: Development of a genetic resource base for drought and biotic stress improvement in cassava

Morag Ferguson*, Luis Augusto Becerra Lopez-Lavalle, Jorge Franco, Dominique Dumet, Daniel Debouck, Peter Kulakow, Hernan Ceballos, Geoffrey Mkamilo, Elizabeth Parkes, Chiedozie Egesie, Melaku Gedil, Ismail Rabbi, Edward Kanju and Clair Hershey

*International Institute of Tropical Agriculture (IITA), c/o International Livestock Research Institute (ILRI), P.O. Box 30709, Nairobi 00100, Kenya; email: m.ferguson@cgiar.org

It can be argued that for a germplasm reference set to be broadly useful to plant breeders it should not only represent diversity but also encompass germplasm with a range of responses to traits of interest. The objectives of this project are to (1) define a reference set in cassava that incorporates diversity as well as germplasm with specific traits of interest to breeders (2) to characterise this germplasm with 1,536 SNPs using an Illumina GoldenGate assay (Illumina Inc., San Diego, CA), and (3) make the reference set available to collaborating NARS breeding programs. Initially approximately 550 cassava varieties will be genotyped using SNPs. This will consist of 100 varieties from southern, eastern and central Africa, 200 IITA and CIAT breeder-preferred germplasm lines and 250 IITA and CIAT diverse germplasm lines based on 30 SSR markers. From the SNP results a set of about 200 genotypes will be selected that reflect both diversity and breeder preferred traits to form the GCP reference set. This reference set will be dynamic and should be reviewed and updated on a regular basis as new gene combinations become available. Cassava varieties in the GCP reference set will be placed *in vitro* and, as far as phytosanitary regulations allow, will be available for distribution under SMTA, but initially through this...

Related GCP project– G7010.01.01: Improvement and evaluation of the existing cassava reference set for Africa (PI: Morag Ferguson, IITA)

Notes:

Maize

1.2: QTLs and genes for aluminium tolerance in maize

CT Guimarães,* CC Simões, CFS Tinoco, RCC Vasconcellos, JV Magalhães, LJM Guimarães, LG Maron and LV Kochian

*Embrapa Maize and Sorghum, Sete Lagoas, Brazil; email: claudia@cnpms.embrapa.br

Al toxicity is one of the major constrictive factors of plant root growth in acid soils, leading to limitations in agricultural production. These soils are present in close to 50% of global arable land. Development of Al tolerant germplasm is of the main sustainable solution to overcome this limitation. Al tolerance is a quantitatively inherited trait in maize, a crop that displays considerable variation for this trait, as well a highly complex genome organization. Taking advantage of the Al tolerance gene cloned in sorghum (Alt_{SB}) and findings from our recent research in maize, where two major Al tolerance QTLs were co-localized with Alt_{SB} homologues (*ZmMATE* genes), we will characterize and validate functional *ZmMATE* genes or QTLs conferring superior Al tolerance in maize. In our current work, we mapped the expression of both *ZmMATE* genes, and validated one major Al tolerance QTL located at maize chromosome 6. This QTL harbor the *ZmMATE1* candidate gene, and its expression, which proved to increase the Al tolerance in a set of near-isogenic lines. For the *ZmMATE2*, a candidate gene mapped within the Al tolerance QTL5.1, its expression was mapped in the maize chromosome 3 and was not able to affect the Al tolerance in NILs, compared to the recurrent Al sensitive line…

Related GCP project–G7010.03.02: Cloning, characterisation and validation of AltSB/Al tolerance in maize (PI: Claudia Guimarães, EMBRAPA)

Notes:

3

Pigeonpea

1.3: Single-nucleotide polymorphisms (SNPs) for diversity analysis and linkage mapping in pigeonpea (*Cajanus cajan* L.)

Rachit K Saxena,* Serah Songok, Anuja Dubey, R Varma Penmetsa, Hari Upadhyaya, KB Saxena, Paul Kimurto, Doug Cook, Greg May, Rajeev K Varshney

*International crops research institute for the semi-arid tropics (ICRISAT), Patancheru, Hyderabad, India;
email: r.k.varshney@cgiar.org; r.saxena@cgiar.org

Pigeonpea is one of the most important legume crops for human and livestock feed. However, the paucity of the genomic resources coupled with low genetic diversity in cultivars has hindered the application of molecular-assisted breeding programmes. A crucial step in the successful application of molecular assisted breeding programmes is the development of high-throughput and cost-effective molecular markers, such as single-nucleotide polymorphisms (SNPs). Here, we describe the development of KASPar assays for 1,834 SNPs. A set of 184 pigeonpea genotypes comprising of parental lines of mapping populations, breeding lines and wild relatives representing 10 different countries around the globe, were chosen for genotyping with the developed SNP markers. As a result 1,226 SNPs showed polymorphisms in the germplasms analyzed. Less genetic variation was observed within cultivated species; however, phenetic analysis clearly distinguished all wild species genotypes from each other and from the cultivated genotypes. The close relationships of *C. cajanifolius* with cultivated pigeonpea (*C. cajan*) has been verified in this study. By using 188 F2 lines from ICP 28 × ICPW 94 cross, a linkage map comprising 875 SNP loci has been developed that should be useful for accelerating molecular genetics and breeding applications in pigeonpea.

Related GCP project–G4008.47: Genomic resources (ESTs, markers and maps) developed for pigeonpea to enable trait/gene identification (PI: Gregory D May, NCGR)

Notes:

4

Rice

1.4: Genetic architecture of aluminium tolerance in rice (*O. sativa*) determined through genome-wide association analysis and QTL mapping

Leon Kochian,* Adam Famoso, and Susan McCouch

*Robert Holley Center for Agriculture and Health, USDA-ARS, Cornell University, Ithaca, NY 14853;
e-mail: lvk1@cornell.edu

Aluminium (Al) toxicity is a primary limitation to crop productivity on acid soils and rice has been demonstrated to be significantly more Al tolerant than other cereal crops. However, the mechanisms rice employs to tolerate Al in acid soils are largely unknown and no genes underlying natural variation have been identified to date. In this study, we screened 374 diverse rice accessions, conducted a genome-wide association (GWA) study, and carried out QTL mapping in two bi-parental populations for rice Al tolerance. Subpopulation structure explained 57% of the phenotypic variation and the mean Al tolerance in *Japonica* was twice that of *Indica*. Forty-seven regions associated with Al tolerance were identified by GWA analysis, most of which were subpopulation-specific. Nine of these regions co-localized with *a priori* candidate genes and ten co-localized with previously identified QTLs. Three regions corresponding to Al sensitive rice mutants (*ART1, STAR2, Nrat1*) were identified through bi-parental QTL mapping or GWA to be involved in natural variation of rice Al tolerance. Haplotype analysis around the *Nrat1* gene identified susceptible and tolerant haplotypes explaining 40% of the Al tolerance variation within the *aus* subpopulation. Sequence analysis of the *Nrat1* gene identified two non-synonymous mutations specific to Al sensitive *aus* accessions…

Notes:

....
....
....
....
....
....
....
....
....
....
....
....
....
....
....
....

Sorghum

1.5:   Improving phosphorus efficiency in sorghum by the identification and validation of sorghum homologues for *Pup1*, a major QTL underlying phosphorus uptake in rice

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

*EMBRAPA Maize and Sorghum, Sete Lagoas, Brazil; email: jurandir@ cnpms.embrapa.br

Low productivity due to soil constraints is a serious problem in many parts of Africa, where sorghum is a staple food supporting millions of the rural poor. *Pup1* is a major QTL located on rice chromosome 12 that underlies phosphorus uptake. The aluminium tolerance gene, Alt_{SB}, is an Al-induced root citrate efflux transporter and citrate can mobilize P that is fixed in the soil clay. Association analysis is being used to identify significant associations between allelic variation at $Pup1/Alt_{SB}$ and P efficiency. A sorghum panel was phenotyped for P-efficiency traits in the field in 2010 and a second experiment is now underway both at EMBRAPA and JIRCAS. Root traits were assessed in controlled conditions. Sequence similarity analysis identified 7 *Pup1* candidate genes in sorghum and Sb07g00284, located on chromosome 7, was the top hit. Using Primer-blast, we designed primers specific to each gene family member. We are now sequencing amplicons for SNP discovery and association analysis will follow with both field and root morphology data. Primers for quantitative analysis of gene expression were also designed and optimized to assess *Pup1* candidate gene expression in 6 sorghum accessions. This approach is expected to identify functional homologues of *Pup1* in sorghum.

> *Related to GCP project–G7010.03.06: Improving phosphorus efficiency in sorghum by the identification and validation of sorghum homologues for Pup1, a major QTL underlying phosphorus uptake in rice, and identification of other P efficiency QTLs (PI: Jurandir Magalhaes, EMBRAPA)*

Notes:

6

Theme 2:
Integrated crop breeding

Beans

2.1: Improving drought adaptation in Pinto bean for the semiarid highlands of Mexico

Jorge A. Acosta-Gallegos* and Edgar Espinoza-Trujillo

*Bajio Experimental Station of the National Research Institute for Forestry, Agriculture and Livestock (INIFAP), Mexico; e-mail: acosta.jorge@inifap.gob.mx

This project aims to improve drought adaptation and productivity by crossing two drought resistant cultivars, Pinto Villa and Pinto Saltillo. Trials were conducted on 289 F_5 families under irrigation and terminal drought during 2010 and 2011 at two locations in Guanajuato, Mexico. Data from the 2010 trials were used to conduct a stepwise multiple regression analysis. Traits that showed to be significant in the model were, biomass, HI, length of the reproductive stage, days to flowering and 100-seed weight. From these, biomass and HI contributed largely to the observed variation in yield (53 and 33%). The yield of both parents under stress was similar to the highest yielding families. In 2011 data were taken on leaf temperature (LT) and leaf water content (LWC) at the pod elongation stage among other traits. Under both moisture conditions families displayed large variation for all recorded traits (data to be presented). Under stress, plants displayed higher average LT, 23.6 vs 22.4; lower temperature differential, 9.8 vs 11.0 and lower LWC, 3.6 vs 4.2 A 't' test at p≤0.01 indicated highly significant differences between moisture conditions. A low relationship between LT and LWC was observed. The genotyping of this population is being conducted.

> *Related GCP project–G4008.11: Dry bean improvement and marker-assisted breeding for diseases and abiotic stresses in Central America and the Caribbean (PI: Jorge A Acosta-Gallegos, INIFAP)*

Notes:

2.2: Improving common bean productivity for marginal environments in sub-Saharan Africa

S Beebe,* M Blair, F Alemayehu, A Asfaw, R Chirwa, L Kalolokesya, P Kimani, S Kweka, G Makunde, E Mazuma, P Okwiri, F Waweru

*Centro Internacional de Agricultura Tropical (CIAT), Colombia; e-mail: s.beebe@cgiar.org

Drought is a serious risk factor of smallholder bean farmers in Africa and Latin America. Breeding through phenotypic evaluation under field conditions is occurring in several countries, but combining tolerance with a range of other agronomic traits including resistance to biotic constraints is a challenge. Furthermore, more efficient selection criteria, either trait based or with DNA markers, would facilitate progress. The GCP has administered a project, Tropical Legumes-I or TL-1, to develop tools for the improvement of drought tolerance in four legume crops including common bean. Major outputs from this project to date include: refinement of the genetic structure of common bean gene pools; improvement and testing of markers for the selection of resistance to bruchid storage insects and common bacterial blight; collaboration in the establishment of a SNP platform for common bean; development of populations for testing of MARS in common bean; in conjunction with G4009.07.01, training of 2 M.Sc. and 2 Ph.D. candidates, and the initiation of a third Ph.D. candidate in his program of studies.

Related GCP projects–G6007.03/G6010.03: Improve common bean (Phaseolus vulgaris L) productivity for marginal environments in sub-Saharan Africa (PI: Steve Beebe, effective October 2010; previous PI: Matthew Blair (CIAT)

Notes:

Cassava

2.3: Participatory clonal evaluation of introduced cassava genotypes in agro-ecological zones of Ghana

Elizabeth Yaa Parkes*, Bright Boakye Peprah, Edem Lotsu and John Asafu Agyei

** CSIR- Crops Research Institute, Kumasi ,Ghana;
   e-mail: ey.parkes@yahoo.co.uk*

A major staple in Ghana and contributing 22% of Agricultural GDP, cassava has assumed industrial and cash crop status in the country. However, this good and reliable cheap source of carbohydrates is susceptible to cassava mosaic virus (CMD) and other devastating diseases and pests, as well as post harvest physiological deterioration. Cassava improvement in Ghana, with the support of the International Institute of Tropical Agriculture (IITA), has yielded several varieties. Adoption challenges and susceptibility of some varieties to diseases and pests necessitated this study. New improved varieties are needed to feed the growing cassava-based industry. Marker assisted selected genotypes resistant to pests and diseases developed by the International Center of Tropical Agriculture (CIAT) and evaluated by the Crops Research Institute (CRI) together with farmers and end-users, identified outstanding clones CR52A-31 and CR52A-25 with starch levels between 26-30% and root yields of 50 to 62 t/ha. Genotype CR 42-4 recorded the highest yield of 101.2 t/ha at Ejura location but the second highest yield across all locations. Farmers preferred two other genotypes CR52A-4 and AR14-10. The materials have been crossed to local varieties with unique characteristics for further evaluation. Participatory testing and the use of MAS has accelerated the improvement of cassava and promise to ensure enhance adaptation and adoption.

Notes:

2.4: Integrated breeding strategies for disease resistant and nutritious cassava varieties in Africa

Chiedozie Egesi,* E Okogbenin, J Onyeka, B Olasanmi, O Akinbo and M Fregene

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

Improved cassava varieties should have high stable yields, resistance to major diseases and drought, as well as meet end-use qualities. Integrated breeding strategies are being used by cassava breeders in Africa to develop genetic stocks that will meet end-user preferences. Traditional breeding complemented with tools of modern biotechnology (molecular markers and transgenic approaches) are currently being applied as a mix to achieve set goals for cassava improvement. In the last one decade, such efforts in Nigeria have yielded sixteen improved varieties of cassava thereby strengthening cassava agro-business. Of special importance is UMUCASS 33 a variety developed from molecular breeding with *CMD2* resistance gene, high yields and dry matter, good plant architecture and tolerance to acidic soils. Other molecular breeding activities initiated in Africa include QTL analysis for drought tolerance, post-harvest physiological deterioration, carotene content, protein content, tagging of more genes for resistance to various biotic stresses. Also in the mix is the incorporation of transgenic technologies to enhance nutritional traits in cassava particularly pro-vitamin A and iron. One critical aspect in the entire cassava improvement value chain is the development of capacity by NARS to use new tools to solve old problems and address emerging threats to production.

> *Related GCP project–G7010.01.02: Improving and deploying markers for biotic stresses in cassava (PI: Chiedozie Egesi, NRCRI)*

Notes:

2.5: Drought tolerance performance of cassava genotypes in the savannah ecological zone of Ghana

Kwabena Acheremu, Joseph Adjebeng-Danquah, Samuel Kwadwo Asante, Bright Boakye-Peprah and Elizabeth Yaa Parkes*

*CSIR-Savannah Agricultural Research Institute (SARI), Nyankpala, Ghana;
e-mail Acheremukwabena@yahoo.com

Eighteen cassava genotypes, introduced from IITA, CIAT and landraces were evaluated for two seasons for physiological traits that contributed to tolerance to drought conditions in Northern Region of Ghana. The location used for the study falls within, the savannah ecological zone, that is noted for its inherent long dry spell and great variability in the distribution and amount of precipitation that could result in the reduction in cassava root yield of 30-60% and even 100% when the crop fails completely. The cassava genotypes were studied for drought tolerant attributes such as; leaf retention, plant height, canopy spread, stem diameter and yield parameters. The genotype CTSIA 48 recorded the highest leaf retention with an average leaf number of 160, and CTSIA 8, the highest canopy spread of 1.134m. The genotype 96/409 recorded the highest root yield of 12.50 t/ha. The genotype 96/409 showed stability in terms of performance in the drought environment for both seasons. The average amount of rainfall during the period of study was 250mm. The genotypes would be used in the improvement of the farmer preferred landraces, to introgress the drought tolerance trait.

Related GCP project: Not applicable

Notes:

Chickpeas

2.6: Deployment of molecular markers for developing high yielding wilt resistance chickpea genotypes

Bharadwaj Chellapilla,* Shailesh Tripathi, Rajeev Varshney and Kumar Jitendra.

*Division of Genetics, Indian Agricultural Research Institute Pusa, New Delhi 110 01;
email: drchbharadwaj@gmail.com

Development of breeding material through the deployment of MABC and MARS is urgently required to develop high yielding wilt resistant lines in chickpea, the most important pulse crop of India. At IARI, New Delhi a core set of markers for *fusarium* wilt (TA 96, TA 110) and yield QTLs (TR 56, TA 78, TR 29, TA 47) have been identified through mapping related activities. The strategy being adopted involves in summary, crossing the selected parental genotype Pusa 372 (high yielding, wilt susceptible) with WR 315 (wilt tolerant donor parent) and F1 generated will be backcrossed with the recurrent genotype. The BC1F1 generated will be screened with targeted polymorphic markers to identify heterozygote plants carrying the targeted alleles. The selected BC1F1 plants will be backcrossed with the recurrent genotypes. As per planned schedule of this proposal, the BC3F1 plants will be screened with the markers and the selected plants will be selfed to generate the BC3F2. These plants will be screened to select the homozygous BC3F2 plants carrying the wilt resistance allele (foreground selection) and high yielding QTLs (background selection). These selected plants will be selfed to generate BC3F3 progenies.

Related GCP project: Not applicable

Notes:

2.7: Improving drought tolerance of Kenyan chickpea variety by introgressing root QTL traits using Marker Assisted Backcross Crossing (MABC)

Paul Kimurto,* Moses Oyier, Richard Mulwa, Sarah Songok, Bernard Towett, Erick Cheruiyot, Rajeev Varshney, Pooran Gaur, Thudi Mahender, Gangarao Rao and Said Silim

*Egerton University, Dept of Crop & Soil sciences Institute of Crop Science, Kenya;
email: kimurtopk@gmail.com

Drought is the leading constraint in chickpea production in Semi arid tropics. Previous efforts to improve drought tolerance have been hindered due to its quantitative nature. Recent research efforts have availed the genetic resources especially molecular markers and root QTL traits conferring resistance to drought. This study introgressed these QTL root traits identified in ICRISAT donor parent genotype ICCV 4958 into Kenyan cultivar ICCV 97105 (recurrent parent) through MABC. Four markers STMS11, GA24, ICCM0249 and TAA170 were used to track QTL traits from one generation to the next. Crosses (ICCV 97105 x ICCV 4958) were made to introgress the drought QTL traits to obtain F1 and planted; DNA extracted and analyzed for QTL presence as heterozygote and backcrossed to the recurrent parent to obtain BC1F1 seeds and process was repeated to finally obtain BC3F1. These will be selfed to obtain BC3F2 and BC2F2, which will be planted in the field and compared with the RP ICCV97105 to confirm the presence of root QTL; determine the improvement in drought tolerance and confirm the agronomic performances of the RP in comparison with newly developed progenies. The seeds will be increased and preserved for further research.

> *Related GCP project–TLI-Improving Tropical Legume Productivity for marginal environments in sub-Saharan Africa and South Asia: Phase II [G6010.04: Improve chickpea productivity for marginal environments in sub-Saharan Africa and South Asia (PI: Rajeev K Varshney, ICRISAT)]*

Notes:

2.8: Integrated chickpea breeding approach to enhance crop responses to climate change in Ethiopia

Asnake Fikre,* Musa Jarso, Million Eshete, Tebikew Damite, Nigusse Girma, Tsigereda Wubshet, Rajeev Varshney

*Ethiopian Institute of Agricultural Research, Debre Zeit Center, POBox 32,
e-mail:fikreasnake@yahoo.com

Chickpea is one of the principal legumes both for home consumption and marketing. Its importance is progressively increasing, particularly with the introduction of kabuli type that seem to have got more societal acceptance. Integrating both molecular and conventional breeding techniques to improve the tolerance level of the crop to climate change (drought) is being undertaken. With this objective a donor parent ICC 4958, identified for enriched drought tolerance genes, was crossed to two recipient Ethiopian supper cultivars (cvs) FLIP 97-263C (Ejere) and FLIP 89-84C(Arerti). Identification of true crosses at F1 was easily identified by blue flower color as expressed at F1 over the white colors of both recipients. F_1BC_1 is generated. Molecular characterization will be employed using SSR markers in detecting the level of drought resistance conferring gene integration into the target. These will be supported by phenotyping techniques at field level. The envisaged outcome of this integrated approach would be 1. Improving the drought tolerance level through molecular integration for otherwise the superior cvs. 2. Widening the adaptation zone of the modified cvs with enhanced use by economic and social and climatic change measures. The molecular and conventional breeding approach could have element of synergy for efficient, effective and resource sensitive chickpea improvement approach.

> *Related GCP project–G6007.04/6010.04: Improve chickpea (Cicer arietinum L) productivity for marginal environments in sub-Saharan Africa (PI: Rajeev Varshney, GCP/ICRISAT) (Ethiopian program)*

Notes:

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

2.9: Development and implementation of genomic and genetic resources for improving chickpea productivity for marginal environments in Sub-Saharan Africa and Asia

Rajeev K Varshney,* Pooran Gaur, Mahendar Thudi, L Krishnamurthy, NVPR Gangarao, Hari Sharma, Rachit Saxena, Aravindkumar Jukanti, Paul Kimurto, Serah Songok, Richard Mulwa, Asnake Fikre, Shailesh Triapthi, Ch Bharadwaj, Subhojit Datta, SK Chaturvedi, N Nadarajan, MS Sheshashayee, Reyazul Rouf Mir, Pavana Hiremath, Himabindu Kudapa, Sabhyata Bhatia, Abhishek Rathore, Trushar Shah, Hari Upadhyaya, Andrzej Kilian, Akhilesh Tyagi, Mingcheng Luo and Doug Cook

*International crops research institute for the semi-arid tropics (ICRISAT), Patancheru, Hyderabad, India; Email: r.k.varshney@cgiar.org; t.mahendar@cgiar.org

Significant progress has been made to develop and utilize large-scale genomic and genetic resources in chickpea breeding programmes. Large-scale genomic resources including >1600 SSRs, DArT array (>15,000 features), GoldenGate Assay (768 SNPs), KASPar assays (>2000 SNPs), a high-density reference genetic map and several intra-specific genetic and QTL maps have become available. BAC-fingerprinting based whole-genome physical map is also being developed. Several superior lines with improved drought tolerance and insect resistance for Ethiopia, Kenya and India were identified based on phenotyping of the reference set. Employing these lines, development of >70 pre-breeding populations and MAGIC populations is in progress. A genomic region harboring several QTLs for drought tolerance traits contributing >30% phenotypic variation was introgressed into three elite cultivars and >20 promising BC_3F_3 lines have been identified.

Notes:

2.9:   Development and implementation of (cont'd....)

MARS approach is being used to accumulate superior alleles for drought tolerance. Molecular breeding skills have been imparted to sixteen scientists from Africa and Asia by organizing a workshop on "Modern Breeding Technologies for Chickpea Improvement" (25th Oct- 19th Nov 2010) and three PhD and four MSc students from NARS are pursuing their research in molecular chickpea breeding. A variety of datasets have been assembled and curated in databases for disseminating them with community.

Related GCP projects–
G4009.07.03: Marker-assisted backcrossing (MABC) for drought tolerance in chickpea: support to students for analysis of drought tolerance in chickpea (TLI – Kenyan student) (PI: Rajeev Varshney, ICRISAT)
G6007.04/6010.04: Improve chickpea (Cicer arietinum L) productivity for marginal environments in sub-Saharan Africa (PI: Rajeev Varshney, GCP/ICRISAT)
G7009.02: Validation of QTLs associated with drought tolerance traits in chickpea (PI: Pooran M Gaur, ICRISAT)
G7010.06.01 Accelerating development of genomic resources and strengthening NARS partner capacities for enhancing adoption of molecular breeding for drought tolerance in chickpea (PI: Rajeev K Varshney, ICRISAT)

Notes:

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

Cowpeas

2.10: Application of Marker-Assisted Selection for *Striga* Resistance in Cowpea (*Vigna unguiculata* L. WALP)

JB Tignegre,* JT Ouedraogo, I Drabo, B Bationo, S Ouramatou, M Satoru, O Boukar, M Toure

* Institut de l'environnement et de recherches agricoles (INERA), Burkina Faso;
email: racinetignegre@yahoo.com

A collaborative research between INERA, Burkina Faso and IITA funded by Generation Challenge Programme aims at increasing the speed for developing adapted cowpea varieties containing pyramided agronomic productivity traits and sustainable resistance to diseases and pest, especially the resistance to *Striga gesnerioides*. This project intends to show the potential benefit of MAS for *Striga* resistance to NARS breeding programmes. The methodology consisted of (i) implementing a Participatory Rural appraisal (PRA) were used for identifying breeding priorities, (ii) Introgressing Striga resistance genes into farmers preferred varieties (MAS and backcrossing), (iii) developing and adjusting a convenient MAS protocol for breeding adapted and Striga resistant lines by combining the use of FTA cards, SSR and AFLP-SCAR markers and backcross breeding. The genetic materials comprised 108 screening lines, MAS parents, F1s, BC1F1s to BC4F2s. F2s were used as base-populations for the allelic relationship study of Striga-resistant genes. As results, Two markers were validated for MAS in cowpea resistance to *Striga gesnerioides*. The allelic relationship study showed that gene *Rsg3* for resistance to *S. gesnerioides SG1* was singly inherited and dominant and confirmed previous results. Adapted and *Striga*-resistant cowpea lines were identified and new improved lines with farmer's preferred traits will be released during 2012 humid season...

Notes:

Groundnuts

2.11: Pattern of flowering and yield components under water stress imposed during reproductive phase in groundnut (*Arachis hypogaea* L.)

Halilou Oumarou*, Falalou Hamidou, Vincent Vadez

*University Abdou Moumouni of Niamey /Niger (UAM), Faculty of Science, department of biology/International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Sahelian center Niamey; email: omarhalilou2000@yahoo.fr

Groundnut typically experiences a range of water stress with a dramatic negative impact on yield when it occurs at reproductive phase. This work investigated the effect of water stress imposed progressively at early flowering stage of ten genotypes of groundnut under glasshouse conditions and contrasting for drought tolerance. Three water regime were imposed: A well-watered treatment where plants were maintained at field capacity, a water stress imposed by reducing the soil water content by 120g daily until the fraction of transpirable soil water (FTSW) was depleted, before re-watering at field capacity, and a water stress imposed until the FTSW dropped to 20%, maintained at these FTSW level for 15 days before rewatering at field capacity. Transpiration, flowering pattern, yield and its components were measured. During 30 days after starting flowering, no significant genotypic variation for transpiration was observed, and tolerant genotypes produced more flowers (61) than the sensitive (17) except JL24 (56). After water stress was released, sensitive genotypes produced more flowers. Under water stress conditions, the flowers abortion in sensitive genotypes (47%) was less than in tolerant (61%) but the pods and seeds weight were significantly ($P < 0.001$) higher in tolerant than in sensitive. This study showed also that the yield and its components were more affected by stress1 than stress2.

Related GCP project–G6010.01: Improve groundnut productivity for marginal environments in sub-Saharan Africa (PI: Vincent Vadez, ICRISAT)

Notes:

2.12: Consensus genetic maps for drought tolerance related traits and foliar diseases resistance traits in cultivated groundnut (*Arachis hypogaea* L.)

Manish Pandey,*, Rajeev Varshney, Bhimana Gautami, Vanhi Sujay, MVC Gowda, T Radhakrishnan, Vincent Vadez, Shyam Nigam, Trushar Shah, Hari Upadhyaya, Sachiko Isobe, Guohao He, David Bertioli, Steven Knapp and Douglas Cook

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

The realized yield in groundnut in the semi-arid region remains low due to its exposure to drought and foliar diseases. With an objective to identify genomic regions for drought tolerance and foliar disease resistance, two consensus maps were developed using five individual genetic maps based on populations segregating for drought tolerance (TAG 24 × ICGV 86031, ICGS 44 × ICGS 76 and ICGS 76 × CSMG 84-1) and foliar diseases (TAG 24 × GPBD 4 and TG 26 × GPBD 4). These maps are comprised of 293 loci (drought tolerance) 225 loci (foliar disease resistance). A comprehensive QTL analysis for drought tolerance has identified 153 main effect QTLs (M-QTLs) and 25 epistatic QTLs (E-QTLs) that are scattered throughout the genome that indicates non-applicability of MABC approach for molecular breeding for drought tolerance. On the other hand, 43 M-QTLs have been identified for resistance to foliar diseases and one genomic region contains major QTL each for late leaf spot and rust resistance with a high phenotypic variation (68-83%). Therefore, MABC approach is being used for molecular breeding for rust resistance and genomic selection approach is being explored for molecular breeding for drought tolerance.

Notes:

....
....
....
....
....
....
....
....
....
....
....
....
....
....
....
....
....

Maize

2.13: Maize genetic analysis of gray leaf spot resistance

Xingming Fan *, Wei Chen, Lijuan Yu, Jing Tan, and Li Liu

*Institute of Food Crops, Yunnan Academy of Agricultural Sciences, (YAAS), Yunnan Kunming, China; email:xingmingfan@163.com

Gray leaf spot is a disease severely reducing maize yield, which is popular in southwest of China including Yunnan. And, breeding new varieties with high resistance is urgent, however, this depends on understanding the genetic mechanism of resistance. Here, YML32 and Q1 which have contrasting resistance to gray leaf spot were used to generate F1 and F2:3 progenies. Resistance of these materials were evaluated with Huidan 4 as control in Baoshan and Dehong. First, it was found that YML32 was consistent with a high level of resistance, Q11 and Huidan 4 were highly susceptible, all F1s were resistant, and F2:3 familes segregated for resistance under natural infection in both locations. Moreover, it was shown that resistance of F2:3 families followed a continuous normal distribution in both locations. These suggested maize gray leaf spot disease resistance is a quantitative trait. Moreover, it was found that the additive effects for maize gray leaf spot disease resistance was 3.0186, dominant effects was 0.0642, broad sense heritability was 89.45%, and narrow sense heritability was 87.59%, these indicated that maize gray leaf spot disease resistance is controlled by additive genes and highly heritable. These results are important in guiding breeding new varieties with high resistance.

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

Notes:

2.14: Development of Maize Drought Tolerance in Indonesia: Status and Progress

Azrai Muhammad* and Roy Efendy

*Indonesian Cereals Research Institute (ICERI), Maros, Indonesia; email: azraimuh@yahoo.com

Maize is very important crop in Indonesia as second staple food crop after rice. Prime varieties and advance technology is required to overcome the climate change, since maize crop is cultivated at dry and acid land in Indonesia. 79% maize crop in Indonesia is cultivated in the dry land; therefore it is required drought tolerant (DT) varieties. Asian maize drought tolerance (AMROUT) is joint project between CIMMYT and GCP facilitate Indonesian researcher to interact with other Asian countries producer, member of AMROUT. The establishment of maize producer network enables Indonesia to exchange the genetic material, experience, and transfer technology in order to accelerate the development of drought tolerant varieties. The aim of the research are to develop new hybrid maize varieties which is early maturity ≤ 90 days, high yielding potency (> 10 t/ha) and tolerant to drought. The research project consisted of two activities: First: Phenotyping of AMROUT hybrids and lines under drought tolerant and normal irrigation in Indonesian. We evaluated of 09-DRT-CAGCP-24 population on 2009. The results of evaluation showing that crosses of (CA00310/AMATLC0HS71-1-1-2-1-1-1-B*6-B- B-B-B)/CML442; (CA14517/P145C4MH7-1-B-1-1-B-1-1-BBBB-B-B-B-B-B)/CML488; (PT963216-B-B-B-B-B-B-B-B-B-B)/DRB-F2-60-1-1-1-BBB and CML429/CML470 have get yield > 8 t/ha, better than the best local check variety. For this year, we evaluate of AMROUT trial under drought condition in ICERI Experimental station at Bajeng, South Sulawesi…

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

Notes:

2.15: Screening for tolerance to Al toxicity and P-efficiency in Kenyan maize germplasm

Samuel Gudu,* Evans Ouma,* Beatrice Were,* Dickson Ligeyo

* Moi University: PO Box 3900-30100 Eldoret, Kenya;
 email: samgudu2002@yahoo.com

In acid soils, maize productivity is limited by aluminium (Al) toxicity and phosphorus (P) deficiency. The objective was to identify Al tolerant and P-efficient germpalsm for use in acid soils. One hundred and seventy five diverse maize inbred lines were evaluated in nutrient culture at 222μm Al stress and 100 of them in low P stress (2.0mgP/Kg soil) acid soils at Sega and Chepkoilel sites in Kenya. Root growth inhibition measured after 3 days of growth in solution culture occurred in 95% of the inbreds although in the most tolerant inbreds, Al treatment induced minimal root growth. The line 203B was the most Al tolerant having relative net root growth (RNRG) of 119% while SCH 3 was the most sensitive line with RNRG of only 17%. Fifty eight percent (58%) of the F1 single crosses hybrids developed from these inbred lines were heterotic for tolerance to Al toxicity based on mid-parent heterosis. In terms of P efficiency, 10% of the inbred lines and 62% of the single crosses were P-efficient exceeding a threshold of 3t/ha grain yield under low P condition. CON 5 and few other inbred lines were found to be both Al tolerant and P-efficient and could be useful in the development of maize varieties adapted to acid soils.

Related GCP project–G7010.03.05: Marker-assisted backcrossing for improving phosphorous-use efficiency and tolerance to aluminium toxicity via Pup-1 and Alt$_{SB}$ genes in maize (PI: Samuel Gudu, MU/KARI)

Notes:

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

2.16: Exploiting the genetic diversity of available maize germplasm using markers to cluster inbred lines collection at KARI Katumani

James G. Gethi* and Humberto Gomez Paniagua

*Kenya Agricultural Research Institute (KARI), Machakos; jgethi@wananchi.com

Maize is very prone to water stress especially during the flowering stage, and enormous efforts have gone towards developing varieties that can provide reasonable yield in water stress environments. To achieve this, scientists have explored various avenues such as studying the physiology of drought in tropical materials, screening for earliness and search for markers linked to drought QTLs. In the drylands of Kenya, efforts have been directed towards development of drought tolerant materials that flower early to maximize on available moisture and better survive when moisture is limiting. To achieve this, 407 inbred lines developed at KARI and obtained from GCP Project #13, #15 and CIMMYT were genotyped using 46 Simple Sequence Repeat (SSR) markers. The objective was to classify the inbred lines into genetically related groups and help structure the breeding program to take advantage of possible heterotic combinations for drought stress tolerance and therefore develop better products.

The inbred lines were genotyped under the GCP Genotyping Support Service. The SSR markers used covered the whole of the maize genome. The mean Polymorphic Information Content (PIC) of the SSR markers was 0.6115. The mean allele frequency was 0.4651 with a mean allele number of 7. The gene diversity ranged from 0.2270 to 0.9014...

Related GCP Project–G8009.06.06/Activity 3.2.6: Genotying Support Service (excludes 3rd call, whose implementation will begin in 2011) (PI: Chunlin He, effective October 2010/Humberto Gómez-Paniagua, GCP) (This project follows on from G4007.21, which ended in 2008, and G4009.01,which ended in 2009)

Notes:

2.17: AMDROUT: Perspective and Progress

Bindiganavile Vivek,* Vedachalam Vengadessan and Girish Krishna

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

Over 80% of maize area in Asia is grown under rain-fed conditions and prone to drought stress. Addressing the problem of drought can provide the highest technical returns to rain-fed maize. Drought tolerance is a highly polygenic trait with significant proportion of additive effects. Marker-assisted recurrent selection (MARS) enables the doubling of breeding gains of complex polygenic traits by increasing the frequency of favorable alleles. Traditionally, MARS was practiced using a set of significant QTLs; however African maize populations (DTMA project) have not shown significant major QTLs for yield under drought, to use in MARS. Alternatively, genome-wide selection (GWS) is promising to explain the total genetic variance of a polygenic trait and could be effective for MARS. GWS analyzes all marker effects across the entire genome of a population to predict genomic estimated breeding values (GEBV) of individuals. The approach of MARS based on GWS is being explored in the AMDROUT project. The project identified CML444 as the best donor for drought tolerance and CML470, VL1012767, VL108733, VL108729, VL1012764, and CML472 as recipient lines. Initially, F2:3 progenies derived from CML470 and VL1012767 with donor CML 444 were genotyped with 350 polymorphic SNPs using KASPar assay at KBioscience. Testcrosses of $F_{2:3}$ progenies were made with CML 474, and are being evaluated under drought and optimal conditions...

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

Notes:

Rice

2.18: The use of crop growth performance data for characterization and mapping of variability in soil water holding capacity

Alhassan Tswako Maji,* Emmanuel Myimaorga Abo, Mark Nwoye Ukwungwu, Samuel Oladele Bakare, Abraham Attah Shaibu, Marie Noelle Ndjiondjop, and Mohammed.Bashiru

*National Cereals Research Institute (NCRI) Badeggi, PMB 8, Bida, Niger State, Nigeria;
email: tswakoma@gmail.com

Understanding and managing spatial variability in soils has become one of the main strategies to optimize rice production. The test of uniformity was conducted on 0.68 ha of land divided into 4x4 (16m2) main plots, and each main plot sub-divided into 4 sub-plots of 2x2m from which representative plant height, number of tillers, plant fresh weight and dry weight were sampled and measured. The average value of the 4 plants from the main plot was used as the plot value. These values were further transformed to return a maximum value of 1 by dividing all scores by the highest value. The results showed significant variation in soil water holding capacity as a factor of crop growth variation. Of the four growth parameters measured, tiller count gave the list coefficient variation of 3.2%, plant height, 10.8%, plant dry matter, 37.5% and plant fresh weight had the highest coefficient of variation of 147.1. Combined transformed data was used to physically classify and map the plots. The classes have scores of 0.9-1.0, most favourable, 0.7-0.8, favourable, 0.5-0.6, dry and 0.3-0.4, very dry. The results provide rice breeders and agronomist awareness to develop protocol and management practices for drought tolerance phenotyping.

> *Related GCP project–G7010.04.01: Improving rice productivity in lowland ecosystems of Burkina Faso, Mali and Nigeria through marker-assisted recurrent selection for drought tolerance and yield potential (PI: Marie Noëlle Ndjiondjop, AfricaRice)*

Notes:

2.19: Pyramiding of resistance QTL/gene into Mekong mega varieties using marker-assisted backcrossing

Jonaliza Lanceras-Siangliw,* Theerayut Toojinda, Khin Soe, Bounthong Bouahom, Ouk Makara

*Rice Gene Discovery Unit, National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand; e-mail: jsiangliw@gmail.com

Mekong mega varieties were improved in terms of biotic and abiotic stresses using marker-assisted backcrossing (MAB). During phases I and II (2004 – 2009), single trait was added to each variety. Myanmar varieties namely Manawthukha (MNT) and Sin Thwe Latt (STL) were improved in terms of grain quality and aroma and salinity tolerance, respectively. Promising lines of MNT and STL are soon to be released to Myanmar farmers. Grain quality and aroma of Thadokkham 1 (TDK1) and CAR3 from Laos and Cambodia, respectively was the main target for improvement during phases I and II. The aromatic lines of TDK1 and CAR3 will be planted in farmer's field this wet season 2011. In phase III, new traits are now being added to lines that were advanced in the previous phases of the Mekong project. Bacterial blight (BB) resistance and submergence tolerance are also improved in MNT and STL, respectively. Fixed lines of aromatic MNT with BB resistance will be completed this year while salinity and submergence tolerant STL will be available at the end of 2012. On the other hand Laos and Cambodia will plant aromatic TDK1 and CAR3 in farmer's field this year. Blast resistance (BL) and submergence tolerance (Sub) will be added to aromatic TDK1 and the fixed homozygous lines will be selected in wet season 2011…

> *Related GCP project–G4009.09: CoPs – Strengthening rice breeding programmes using genotyping and improving phenotyping capacity for biotic and abiotic stresses in the Mekong region (PI: Jonaliza Lanceras-Siangliw, RGDU–BIOTEC)*

Notes:

2.20: Root phenotyping for drought tolerance: evaluation of the OryzaSNP panel using a range of methods

Amelia Henry,* Adam Price, Akira Yamauchi, R Chandra Babu, Len Wade, Kenneth McNally

*International Rice Research Institute (IRRI), Los Baños, Philippines;
email: A.Henry@cgiar.org

Rice is highly susceptible to drought stress compared to other crops, which is thought to be attributable in part to a shallow root system. By linking genetic polymorphism to root growth at depth, molecular markers could be identified to improve drought tolerance in rice. In this project, root phenotyping was conducted on the OryzaSNP panel, a collection of 20 diverse cultivars and landraces within the aus, indica, and japonica groups that have been genotyped with over 160,00 SNP markers. Each root phenotyping method was refined for studying rice roots under drought, in order to characterize rice genetic diversity for drought response and root growth at depth. Phenotyping systems included field conditions, 1-m depth lysimeters, 1-m tall transparent-walled rhizotrons, containers with herbicide placement at depth, pinboard root boxes, line-source greenhouse studies, and containers with wax-layers. All studies focused on evaluating deep root growth, but other parameters including water uptake, root branching, and penetration of compacted layers were assessed in some systems. Initial results point to aus lines as promising root trait donors for drought. A collective analysis of these results will be provided to geneticists for identification of molecular markers for deep root growth.

Related GCP project–G3008.06: Targeting drought-avoidance root traits to enhance rice productivity under water-limited environments (PI: K McNally, IRRI, effective June 2010; previous PI, Rachid Serraj, IRRI)

Notes:

2.21: Is drought screening in dry season reliable for genotype selection for rainfed lowland rice- a case study in Laos?

Phetmaniseng Xangsayasane,* Sipaseuth, Boonrat Jongdee, Grienggrai Pantuwan, Phoumi Inthapanya, and Shu Fukai

* Rice&Cash Crop Research Center, National Agriculture & Forestry   Research Institute, P.O. box 7170, Vientiane, Lao PDR;
e-mail: phetmanyseng@gmail.com

An objective of our project was to develop new effective breeding strategies for selection of adapted genotypes for rainfed lowland rice. There was doubt about the effectiveness of selecting genotypes under dry season screening for rainfed lowland rice in wet season. In order to prove this, results from 13 field experiments conducted in wet season 2009 and 2010 and dry season 2010 in Laos were utilized. The reason for using the results from Laos was that the genotypes used were mostly none or weakly photoperiod sensitive. The 13 field experiments include 3 artificially manipulated conditions; flood, aerobic and drought in research station in each of dry and wet season and 7 multi-location trials in wet season 2010. Results from cluster analysis showed that site grain yield varied from 1503 to 4086 kg/ha. The sites were grouped to 4 groups. All 3 conditions (flood, aerobic and drought) in dry season screening were grouped together whereas wet season screening and multi-location trials were grouped together. The results suggested that dry season screening appears not contributing to the selection of lines that perform well under rainfed lowland conditions. However, the results need further analysis and confirmation.

> *Related GCP project–G3008.09: Breeding drought tolerance for rainfed lowland rice in the Mekong region (PI: Boonrat Jongdee, BRRD)*

Notes:

……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..

2.22: MAGIC Rice: production, characterization, and its use in breeding networks

Hei Leung,* Nonoy Bandillo, Pauline Andrea Muyco, Chitra Raghavan, Anna Sevilla, Irish Lobina, Michael Thomson, Ramil Mauleon, Rakesh Kumar Singh, Glenn Gregorio and Edilberto Redoña

**Plant Breeding, Genetics and Biotechnology Division, International Rice Research Institute, DAPO 7777, Metro Manila, Philippines
email: h.leung@cgiar.org*

Breeding populations produced through *multi-parent advanced generation inter-crosses* (MAGIC) can be used directly as source materials for development of varieties adapted to different environments. We have developed two MAGIC populations using indica and japonica ecotypes of rice. Each population is comprised of 8 founders that include elite and modern varieties known to exhibit tolerance to a range of biotic and abiotic stresses, high yield potential, and good grain quality. We made additional cycles of intercrossing to increase the level of recombination and expand the diversity (indica x japonica mating). The size of the MAGIC populations ranges from 600 to 2,000 lines. The most advanced population is indica MAGIC with 1,439 S4 lines being advanced to RIL. We will select 400 S2:4 bulk lines for multi-location evaluation in breeding networks in southeast Asia and Africa. Early generation (S3) selection has yielded individuals with tolerance to salinity and drought. Disease screening also suggests transmission of blast resistance from the resistant founder to a majority of the progeny, showing expected pattern of trait transmission. We will apply genotyping-by-sequencing to characterize the RIL. The finely mapped population will provide SNP markers for MAS in future deployment of the MAGIC populations.

Notes:

2.23: Development of drought-tolerant rice varieties adapted to West Africa lowland agrosystem

Ibnou Dieng,* Hema Drissa, Fousseyni Cisse, Alhassan Maji, Mounirou Sow and Marie-Noëlle Ndjiondjop

*Africa Rice Center (AfricaRice), 01 BP 2031 Cotonou, Benin; email: i.dieng@cgiar.org

This project aims to use marker-assisted recurrent selection (MARS), toward combining drought-tolerance ability, and good yield-potential, into progenies derived from bi-parental varieties crosses, involving elite rice varieties from Burkina Faso, Mali and Nigeria. Cultivars BW348-1, B6144F-MR-6-0-0, FARO35, WAB638-1, IRAT104, and KOGONI91-1 were crossed with IR64 leading to six cross combinations ARC1, ARC2, ARC3, ARC4, ARC5 and ARC6 and a single seed descent (SSD) scheme was implemented. The evaluation of 1882 F_3 families by partners for general adaptability revealed a high phenotypic variability. The variability was confirmed at F_4 generation, and the population IR64 x B6144F-MR-6-0-0 (ARC2) was selected for MARS. Two additional populations, IR64 x IRAT104 (ARC5) and IR64 x FAR035 (ARC3) were selected for QTLs detection. The International Rice Information System (IRIS) was used at each step for data management: (i) an IRIS - RiceCI database was created, nomenclature and standard established for crosses, and also for 220 families of the MARS population (ARC2); (ii) workbooks were generated for phenotyping experiments. Furthermore, traits of interests and drought profiles for target populations of environments (TPE) are being generated. Finally, a total of 805 informative SNP markers were identified between parents of MARS populations BW348-1, B6144F-MR-6-0-0, FARO 35, WAB638-1, and IR64.

Related GCP project–G7010.04.01: Improving rice productivity in lowland ecosystems of Burkina Faso, Mali and Nigeria through marker-assisted recurrent selection for drought tolerance and yield potential (PI: Marie Noëlle Ndjiondjop, AfricaRice)

Notes:

Sorghum

2.24: Variability for post-flowering drought tolerance in sorghum reference set

Hari Deo Upadhyaya,* Vincent Vadez, Shivali Sharma, CTom Hash, Lakshmanan Krishnamurthy, Seetharam Kaliyamoorthy, Eva Weltzien-Rattunde, Sangam Lal Dwivedi, Mary A Mgonja, Prakash Mrutyunjaya Salimath, Clement K Karari, Lourance Njopilai David Mapunda, Sidi Bekaye Coulibaly and Ndiaga Cisse

*International Crops Research Institute for the Semi-arid Tropcs (ICRISAT), Patancheru-502324, Andhra Pradesh, India; e-mail: h.upadhyaya@cgiar.org

Sorghum reference set (384 accessions) (http://www.generationcp. org), selected from composite collection (using 41 SSR loci data on 3372 accessions), was evaluated for post-flowering drought tolerance. A large variation was observed for SPAD chlorophyll meter reading (SCMR) both at flowering and 30 days after flowering (DAF) under well watered (WW) and water stressed (WS) conditions. Four accessions 393 (411) 659, 452 (484) 510, IS 3963, and IS 24009 had higher SCMR at both stages and under both conditions. Some of the reference set accessions and stay green QTL introgression lines (QTL-IL) when evaluated for transpiration efficiency (TE) and for water extraction (WE) under WW and WS conditions, showed higher TE than recurrent parent lines R 16 and S 35. The lysimetric study revealed a range of variation for WE under terminal drought conditions, and that some staygreen QTL introgression lines increased WE in S35 background only. A number of stay-green QTL-IL in R 16 background showed higher TE under WS. Significant variation for Iron and Zinc contents was noticed in reference set under WW and WS conditions. Further studies are in progress.

Related GCP project–G4008.02: Phenotyping sorghum reference set for drought tolerance (PI: HD Upadhyaya, ICRISAT)

Notes:

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

2.25: Development of sorghum isogenic male sterile and restorer lines and isogenic hybrids for use as a tool in field validation of the effect of the gene for aluminium tolerance - Alt_{SB}

Robert E. Schaffert* and Jurandir V. Magalhães

*Embrapa Maize and Sorghum, Sete Lagoas, MG, Brazil; email: schaffer@cnpms.embrapa.br; reschaffert@hotmail.com

Two pairs of isogenic cytoplasmic male sterile lines were derived from a segregating F_5 progeny derived from the cross of an elite B line, BR007B and an Al tolerant line SC283. Four isogenic restorer lines were developed by marker assisted back crossing (MABC) using an elite R line, BR012R and three sources of Al tolerance; SC549, CMSXS225 and SC566-14. The isogenic R lines derived from SC549 and CMSXS225 were developed with six backcrosses to BR012R with selection in nutrient solution with 27µM Al. The isogenic line R line developed from SC566-14 was developed with three backcrosses using molecular markers for Alt_{SB}. The eight lines and eight resulting isogenic hybrids (3 dwarf grain sorghum hybrids) were characterized in nutrient solution with 0, 11, 20, 27 and 39 µM Al. The results of 3, 5, and 7 day seminal root growth of these isogenic lines and hybrids in nutrient solution validated that these isogenic lines and hybrids can be used as a tool to field validate the effect of zero, one or two Al tolerant alleles on the effect of productivity and stability in environments with acid soils and subsoils with Al toxicity very common in the tropics. These lines were included...

Related GCP project–G4008.10: Assessment of the breeding value of superior haplotypes for AltSB, a major Al tolerance gene in sorghum: linking upstream genomics to acid soil breeding in Niger and Mali (ALTFIELD) (PI: Robert Schaffert, EMBRAPA)

Notes:

2.26: Phenotyping of panicle characteristics in a sorghum mapping population in Mali

Dramane Sako,* Sidy Bekaye Coulibaly, Denis Lespinasse, Michel Ragot, Michel Vaksmann, Jean-Francois Rami, Niaba Témé

*Institut d'Economie Rurale, Mali and GCP sponsored PhD student at WACCI of Ghana;
e mail: dramanesako@yahoo.fr

Sorghum shows striking variation in panicle architecture such as branch number and branch length. The number and growth of branches affects directly grain yield. To analyze the implication of panicle architecture in grain yield, a bi-parental population, composed of 401 F_4 families derived from the crossing between Tiandougou and Keninkeni was developed. The whole population was evaluated together with the two parents during the 2010 cropping season at Sotuba research station. One panicle per entry was used to measure panicle traits like panicle length, number of nodes, average number of branches per nodes, number of primary branches, average primary branches length, average number of secondary branches and seed weight per panicle. A t test was used to compare the mean of the families to the mean of the two parents and correlation among panicle traits were analyzed. Seed weight was positively and significantly correlated to the number of primary and secondary branches. Increasing the number of nodes decreases the number of branch per nodes. Primary branch length was negatively correlated to the number of primary branches. This information will be used for QTL detection together with yield and grain quality components in marker assisted recurrent selection (MARS).

Related GCP project–G4008.48: Improve sorghum productivity in semi-arid environments of Mali through integrated MARS (PI: Jean-François Rami, Agropolis–CIRAD)

Notes:

2.27: Development and evaluation of drought-adapted sorghum germplasm for Africa and Australia

Andrew Kenneth Borrell,* David Robert Jordan, Barbara George-Jaeggli

*The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Hermitage Research Facility, Warwick QLD 4370, Australia;
email: a.borrell@uq.edu.au

This project aims to improve drought adaptation and productivity by combining traits from Australian and Malian sorghums. One such trait is stay-green. Stay-green enhances grain yield under post-anthesis drought in 3-dwarf sorghums used in Australia. To evaluate whether this trait is also effective in taller sorghum typically grown in Mali, experiments with isogenic 2-dwarf versus 3-dwarf pair comparisons in a stay-green and senescent background were conducted at a rain-out shelter facility in north-eastern Australia (2009 & 2010). The stay-green pair maintained grain yields even under stressed conditions, while yield in the senescent pair was reduced under stress. Height did not counteract the benefits of stay-green. On the contrary, the tall version of the stay-green pair yielded more than the short version under stress. While this yield advantage was independent of lodging, stem mass during grain filling increased in the stay-green pair and decreased in the senescent pair, highlighting the role of stay-green in lodging resistance. In a further study (2011), crop water use was assessed in two tall genotypes varying in stay-green. Preliminary analysis of this data indicates that the tall stay-green line extracted more water during grain filling compared with the tall senescent line. F2-populations from crosses between Malian...

Related GCP project–G7009.04: Development and evaluation of drought-adapted sorghum germplasm for Africa and Australia (PIs: David Jordan and Andrew Borrell, DPI&F)

Notes:

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

Wheat

2.28: Exploiting AB genome diversity for creating new wheat germplasm for enhanced drought/heat tolerance

S Misra,* S Tetali, S Tamhankar, D Bonnett, M Zaharieva, RR Hanchinal, AS Desai, I Kalappanwar and R Trethowan

**Agharkar Research Institute, Pune, Maharashtra, India;
    satishmisra@yahoo.com,
    email: scmisra@gmail.com*

Higher genetic diversity and allelic richness in cultivated emmer wheat, as revealed by microsatellite markers (SSRs), coupled with high drought and heat tolerance suggests that this species could be used to improve hexaploid bread wheat. A collection of emmer wheat accessions originating from 35 countries has been established. The genetic diversity structure is described using morphological traits, SSR and DArT markers, and drought and heat tolerance related traits assessed. Around 108 genetically diverse emmer wheat accessions capturing 376 (80%) of the 470 total alleles from the original set were then used to create new AB-genome diversity in hexaploid wheat using various strategies. The strategies are: (i) the emmer reference set was crossed to three Ae. tauschii accessions to produce new emmer based synthetic wheat (SHW) and new synthetic back-cross lines (SBL) are being generated by crossing SHW to elite bread wheat; (ii) crosses between emmer wheat and hexaploid bread wheat were made to develop new hexaploid materials with recombined A and B genomes; (iii) durum wheat based SHW were crossed to emmer wheat and emmer based SHW to produce AB-genome recombinants; (iv) durum based synthetics were crossed to and emmer based synthetics. This newly developed diversity is excellent pre-breeding material.

Related GCP project–G3008.01: New wheat germplasm generated with broadened AB genome diversity (PI: SC Misra, ARI–ICAR)

Notes:

2.29: Association mapping of dynamic developmental plant height in common wheat

Ruilian Jing,* Jianan Zhang, Ang Li, Xiaoping Chang, Xinguo Mao, Matthew Reynolds, Richard Trethowan

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

Drought as a major abiotic stress often occurs from stem elongation to the grain filling stage of wheat in northern China. Plant height (PH) is a suitable trait to model the dissection of drought tolerance. The purposes of the present study were to validate molecular markers for PH developmental behavior and identify elite alleles of molecular markers. After the phenotyping of 154 accessions for PH dynamic development under well-watered (WW) and drought stressed (DS) conditions, and the genotyping of 60 SSR markers from six candidate chromosome regions related to PH found in our previous linkage mapping studies, both parameters PH and drought tolerance coefficient (DTC) calculated by the conditional analysis were used for association mapping. A total of 46 significant association signals (P<0.01) were identified in 23 markers, and phenotypic variation ranged from 7 to 50%. Among them, four markers Xgwm261-2D, Xgwm495-4B, Xbarc109-4B and Xcfd23-4D were detected under both water regimes. Furthermore, 10 markers were associated with DTC, and four with both parameters PH and DTC at the same plant development stage. The results revealed different allelic effects of associated markers; for example, the 155 bp Xgwm495-4B allele was associated with a reduced height of 11.2 cm under DS and...

Related GCP project–G7010.02.01 Breeding and selection strategies to combine and validate quantitative trait loci for water-use efficiency and heat tolerance in China (PI: Ruilian Jing, CAAS, China)

Notes:

2.30: Physiological trait based phenotyping of International core set for drought tolerance in wheat

KV Prabhu,* GP Singh, Neelu Jain, SC Mishra, PC Mishra, N K Singh, TR Sharma, Praveen Chuneja, VS Sohu, GS Mavi, Biswajeet Mondal, Neha Rai, Shweta Umar, Dnyaneshwar Kadam, Lokesh Thawait and AC Pandey

*Indian Agricultural Research Institute, New Delhi, India; email: kvinodprabhu@rediffmail.com

India is the world's second largest producer of wheat and Indian wheat production is of critical importance to global food security. Climate change is projected to reduce the amount of water available for irrigated wheat production. It is therefore vitally important that more water-use-efficient farming systems and wheat cultivars are identified. To identify QTLs in wheat to enable wheat to tolerate water deficiency and heat without losing much of productivity, an attempt is made using MARS in Indian locations. A trial comprising 145 entries was evaluated and phenotyping was carried out. Data on germination, days to heading, yield, thousand kernel weight, days to maturity, canopy temperature depression, NDVI and SPAD was taken. Significant correlations were observed between DH and DM, yield and DH (negative), TKW with DH, DM and yield, CT with DM and yield (negative) and canopy CTD with DH and yield and negative correlation with CT.

> *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: Vinod Prabhu, IARI–ICAR)*

Notes:

……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..
……………………………………………………………………………………..

Theme 3:
Crop information systems

3.1: Construction of Genetic Linkage Maps and Mapping of Quantitative Trait Loci in the Integrated Software Package QTL IciMapping v3.1

Jiankang Wang

Institute of Crop Science and CIMMYT China Office, Chinese Academy of Agricultural Science (CAAS), No. 12 Zhongguancun South Street, Beijing 100081, China; e-mail: wangjk@caas.net.cn; jkwang@cgiar.org

Linkage maps construction and QTL mapping were once two separate procedures. Some software are available for linkage map construction, whereas others for QTL mapping. Now we have one integrated software package that can do both, i.e., QTL IciMapping v3.1, freely-available from http://www.isbreeding.net. Core computing modules in QTL IciMapping were written by Fortran 90/95, and the interface was written by C#. The software runs on Windows XP/Vista/7, with .NET Framework 2.0(x86)/3.0/3.5. To our knowledge, this is the first software which integrates the linkage map construction and QTL mapping, saving researchers a lot of time when they are using QTL mapping to identify the genes of important traits. Four general steps are involved in map construction: Grouping, Ordering, Rippling, and Outputting. Grouping can be based on (i) anchored marker information, (ii) a threshold of LOD score to test linkage relationship, and (iii) a threshold of marker distance. Three ordering algorithms are (i) SER: SERiation, (ii) RECORD: REcombination Counting and ORDering, and (iii) MF: Multi-Fragment heuristic algorithm. Five rippling criteria are (i) SARF (Sum of Adjacent Recombination Frequencies), (ii) SAD (Sum of Adjacent Distances), (iii) SALOD (Sum of Adjacent LOD scores), (iv) COUNT (number of recombination events), and (v) LogL (Logarithm Likelihood of the marker sequence)...

Related GCP project–G4008.14: Breeding for drought tolerance with known gene information (PI: Jiankang Wang, CIMMYT)

Notes:

3.2: Molecular characterisation of Burkina Faso rice landraces using 22 microsatellite markers and establishment of a core collection

Honoré Kam*, Marie-Noëlle Ndjiondjop, Mark D. Laing, Julien Froin, and Nourollah Ahmadi

*University of KwaZulu Natal, South Africa and Institut de l'Environnement et de Recherches Agricoles, Burkina Faso; e-mail: kamhonore@yahoo.fr

Understanding the genetic diversity of rice and its population structure is a key to the sustainable *in situ* and *ex situ* management. In this study, the molecular analysis of 243 rice accessions collected in the four main rice cropping regions of Burkina Faso was undertaken, using 22 microsatellite markers. Thus, two subsets were identified in *O. glaberrima* following regional subdivision: the flooded *O. glaberrima* with long culm and long cycle was encountered in the Cascades Region, while lowland *O. glaberrima* early maturing with a short culm was grown in the three other regions. In *O. sativa* samples, three sub-sets were identified. The sub-set Sg2 has long cycle varieties with a long culm, and included flooded *O. sativa indica* as per the check ASD1. B6144 and IR64 were clustered in the sub-set Sg1-1, incorporating *O. s. indica* plants with short culms, which are grown in the lowland cropping system. The *O. sativa* group Sg1-2 have different traits, and incorporate the *O. s. japonica* checks (Moroberekan and Nipponbare) and an *O. s. indica* variety, Gambiaka. Using, the molecular data and the framework it provided a core collection of 52 accessions was established that represents the diversity of rice in Burkina Faso.

> *Related GCP project–G4009.02.01: Study of Burkina Faso rice landraces diversity and breeding for resistance to RYMV (Honore Kam, INERA, UKZN)*

Notes:

………………………………………………………………………………

………………………………………………………………………………

………………………………………………………………………………

………………………………………………………………………………

………………………………………………………………………………

………………………………………………………………………………

………………………………………………………………………………

………………………………………………………………………………

………………………………………………………………………………

………………………………………………………………………………

………………………………………………………………………………

………………………………………………………………………………

………………………………………………………………………………

………………………………………………………………………………

………………………………………………………………………………

………………………………………………………………………………

3.3: Coverage based consensus calling (CbCC) of short sequence reads and comparison of CbCC-results for the identification of SNPs in chickpea, a crop species without a reference genome

Trushar Shah,* Sarwar Azam, Vivek Thakur, R. Pradeep, B. Jayashree, A. BhanuPrakash, Andrew D. Farmer, David J. Studholme, Greg D. May, David Edwards, Jonathan D. G. Jones and Rajeev K. Varshney

*International Crops Research Institute for the Semi Arid Tropics (ICRISAT), Patancheru 502324, Andhra Pradesh, India; e-mail: r.k.varshney@cgiar.org; tm.shah@cgiar.org

In crop species such as chickpea (*Cicer arietinum* L.) that lacks a reference genome sequence, next generation sequencing (NGS)-based SNP discovery is a challenge with commonly used SNP discovery methods. Therefore, a coverage based consensus calling (CbCC) approach was used with four short reads alignment tools (Maq, Bowtie, Novoalign and SOAP2). By using this approach on 15.7 and 22.1 million Illumina reads for two chickpea genotypes ICC 4958 and ICC 1882, together with the chickpea transcriptome assembly (CaTA), a non-redundant set of 4543 SNPs was identified. Experimental validation of 224 randomly selected SNPs showed the superiority of Maq as 50.0% of SNPs predicted by Maq were true SNPs. Using combinations of two tools, the greatest accuracy (55.7%) was reported for Maq and Bowtie, with a combination of Bowtie, Maq and Novoalign identifying 61.5% true SNPs. SNP prediction accuracy generally increased with increasing reads depth, however, in case of Maq, SNPs predicted at lower read depths (<10) showed greatest accuracy. In addition to identification of large number of SNPs in chickpea, this study provides a benchmark comparison of read depths as well as prediction accuracy of four commonly used tools.

> *Related GCP project–G4010.05 Development of integrated SNP mining and utilisation (ISMU) pipeline based on next-generation sequencing (NGS) and high-throughput (HTP) genotyping technologies for facilitating molecular breeding (PIs: Rajeev Varshney/ Trushar Shah, ICRISAT)*

Notes:

3.4: ISMU: An easy-to-use pipeline for identification of SNPs based on next generation sequencing (NGS) data

Abhishek Rathore,* Rajeev Varshney, Trushar Shah, A. BhanuPrakash, R. Pradeep, David Edwards and David Marshall

*International Crops Research Institute for the Semi Arid Tropics (ICRISAT), Patancheru 502324, Andhra Pradesh, India; e-mail: r.k.varshney@cgiar.org; a.rathore@cgiar.org

SNP identification based on NGS data requires complex bioinformatics analysis including mapping/alignment of short reads, consensus calling and detection of variants. These steps require one to either use some commercial softwares or to identify appropriate open-source tools, understand their command line options and also their host operating system. To overcome these difficulties and provide the biologists an easy-to-use integrated platform for identification of SNPs based on NGS data, ISMU (Integrated SNP Mining and Utilization) pipeline has been developed. This pipeline encompasses powerful open-source mapping softwares like Maq, NovoAlign and SOAP and offers the options to the users to modify/select appropriate parameters for SNP discovery. The ISMU pipeline requires the users to feed only raw sequences reads from any NGS platform and a reference genome/transcriptome. As a result of analysis, the pipeline generates alignment file of NGS reads for genotypes, list of SNPs between genotypes in text and gff3 format and analysis results are automatically visualized in popular assembly visualization software Tablet. The pipeline has been developed in perl-cgi for 64 bit linux/unix based system and has been tested on RHEL 5 and Fedora 13. The current version of the pipeline is available at http://hpc.icrisat.cgiar.org/ngs/ as well as a standalone tool.

> *Related GCP project–G4010.05 Development of integrated SNP mining and utilisation (ISMU) pipeline based on next-generation sequencing (NGS) and high-throughput (HTP) genotyping technologies for facilitating molecular breeding (PIs: Rajeev Varshney/Trushar Shah, ICRISAT)*

Notes:

3.5 & 3.6: Expansion of the crop ontology by adding cassava (3.5) and *Musa* (3.6) trait ontologies

Peter Arthur Kulakow,* Moshood Agba Bakare, Stephanie Channeliere, Jean-Pierre Horry, Rosemary Shrestha and Elizabeth Arnaud

*International Institute of Tropical Agriculture, IITA, PMB 5320, Ibadan NIGERIA
e-mail: p.kulakow@cgiar.org

The Crop Ontology describes traits, methods and scales of several economically important plants (http://www.cropontology-curationtool. org). Cassava (*Manihot esculenta* Crantz) and banana (*Musa* sp.) ontologies were added to Crop Ontology in 2010. Simultaneously, the cassava team is developing an ontology-driven cassava database called ICASS for researchers to record and annotate measurements linked to genotypes with defined pedigrees. The cassava crop ontology currently describes over 125 traits representing important trait groups (agronomic, biotic and abiotic stress, morphological, physiological and quality traits).

These traits describe phenotypic variability for characteristics needed for crop improvement. The cassava ontology will facilitate information sharing and collaboration among researchers from CIAT, IITA, national programs and other collaborators. The Crop Ontology also added the *Musa* trait ontology to describe about 173 traits representing agronomic, biotic and abiotic stress and morphology related trait groups. This ontology will be useful for annotating phenotypic and genotypic data produced by banana researchers at Bioversity, IITA and other *Musa* programs. *Musa* trait names have been submitted to Plant Ontology with some already integrated while others need discussion with experts. New ontology-based online curation and annotation tools allow crop curators to provide standard protocols explaining scale, scale value, scoring guidelines and growth stages for scoring traits.

Related GCP project–G4010.06: Enhancement and implementation of the crop ontology for data integration and data interoperability (PI: E Arnaud, Bioversity)

Notes:

3.7: To contribute crop traits lists using the new online Crop Ontology Curation and Annotation tool

Luca Matteis, Milko Skofic, Hector Sanchez, Rosemary Shrestha, and Elizabeth Arnaud*

** Bioversity International;
    e-mail: l.matteis@cgair.org; e.arnaud@cgiar.org*

The Crop Ontology (http://cropontology.org/) provides validated names, definitions and relationships for traits of cassava, chickpea, maize, *Musa*, potato, rice, sorghum and wheat. These lists were developed by Bioversity, CIMMYT, CIP, ICRISAT, IITA, IRRI. The sources of breeders' trait names were the International Crop Information System (ICIS), the Bioversity key crop descriptors and the Trait dictionaries developed by the GCP crop communities. An online tool is now available (http://cropontology-curationtool.org) for the crop communities to share trait lists, contribute new trait names and download concepts for annotating data. The tool allows users to display and print the lists. By using a login, curators of crop trait lists can comment any term or add online attribute information (e.g. photos). A full ontology can be directly uploaded or created online using the current OBO upload service. The system will support other standard formats like OWL. The ICIS teams will synchronize their Trait Templates with the ontology using the web service API. Any application can send to and receive data from the Curation Tool using this API that provides the ability to create, read, update and delete terms. The site is hosted on Google App Engine and the versioned code is hosted on GitHub.

> *Related GCP project–G4011.01: Development, maintenance and use of trait dictionaries and a Crop Ontology to facilitate the annotation of phenotypic data by crop communities (PI: Elizabeth Arnaud, Bioversity)*

Notes:

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

3.8: **QuMARS: A QU-GENE application module to simulate marker assisted recurrent selection and genomic selection**

Jiankang Wang*, Scott Chapman and Mark Dieters

*Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing, China;
e-mail: wangjk@caas.net.cn; jkwang@cgiar.org

The QU-GENE application module QuMARS has been developed to simulate marker assisted recurrent selection (MARS) and genomic selection (GS) in plant breeding. For MARS, selection uses a prediction of molecular markers with significant effects based on the linear regression models. For GS, a BLUP prediction marker effect (without significance test) is used for selection. QuMARS can simulate the three major stages in a MARS or GS breeding program. Stage I: Building a training population and the genotype to phenotype (GP) prediction model. In plants, the training population is normally derived from two fixed parental lines, for example, it can be a doubled haploids population, F2, or F3. Both genotyping and phenotyping need to be conducted in the training population. Phenotyping can be the line per se performance where the breeding objective is to select elite advanced lines, such as in wheat and bean, or the testcross performance where the breeding objective is to select elite hybrids, such as in maize and sorghum. Stage II: Recurrent selection from the training population. (i) To select individuals in the training population, either based on the available phenotypic data or the GP model built in Stage I. (ii) To inter-mate the selected individual to form a new population, grow and genotype the new population...

Related GCP project–G8009.03.03/ Activity 2.2.3: Develop and deploy simulation tools for complex G–E systems (Activity Leader: Mark Dieters, UQ)

Notes:

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

3.9: A new web interface for rice germplasm and breeding data: integrated data browser and StudyMart

Chengzhi Liang, Mylah Rystie Anacleto, Jeffrey Morales, Jack Lagare and Ruaraidh Sackville Hamilton

International Rice Research Institute (IRRI), DAPO 7777, Metro Manila, Philippines;
e-mail: c.liang@cgiar.org.

The IRIS database developed at IRRI held several types of rice data such as germplasm passport and field evaluation data. To give users a better browsing experience, we re-developed a web interface using combination of Apache Wicket and Google Web Toolkit (GWT). This new web interface provides users with basic search functions and browsers for germplasm and phenotypic data, which integrates with a previous developed germplasm pedigree viewer. A query tool (StudyMart) with multi-trait value filtering function for experimental or field trial data is also integrated. The major improvement comparing to the previous web interface is the summary statistics and charts for each data types. A testing version is available at http://webtools.cropinfo.org:8380/WCIMS/.

Related GCP project– G8009.04.01: Integrated GCP informatics platform created (PI: C Liang, IRRI, effective July 2010; previous PI: Guy Davenport [up to August 2010], CIMMYT)

Notes:

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

....

3.10: Molecular Breeding Services at IBP/GCP

Chunlin He* and Xavier Delannay

**Generation Challenge Programme, c/o CIMMYT, Texcoco,
    Mexico;
    e-mail: c.he@cgiar.org*

SSRs and SNPs have become the preferred markers for marker assisted selection in crop breeding but they are not easily accessible in developing countries. The Genotyping Support Service (GSS) at GCP was created to support breeding programs not only by collaborating with service providers worldwide but also by providing training for data analysis. Since August 2007, GCP has launched a total of 3 calls for research grant applications of GSS projects. A total of 174 applications have been received and 73 of them have been awarded as molecular genotyping projects with SSRs and SNPs as well as DArT markers. The awarded research projects with topics from genetic diversity studies to marker-assisted selections have covered 14 crops from 25 countries. GCP is currently transitioning the marker services from SSR to SNP markers which will be accessible to customers through GDMS at IBP. So far, 1000-2000 SNPs have been converted into KASPar system for SNP genotyping for 7 crops of critical importance to developing countries. With available markers at IBP, the GCP will provide the developing country breeding programs with easier access to more convenient genotyping services to support molecular breeding schemes such as MAS, MABC, MARS, and GWS.

> *Related GCP projects–G8009.05 Objective 3.1: Provide access to critical molecular breeding services (PI: X Delannay, GCP) G8009.06 Objective 3.2: Provide assistance with a range of molecular breeding support services (PI: C de Vicente, GCP [up to October 2010])*

Notes:

3.11: Generation Atlas

Glenn Hyman* and Ernesto Giron

*International Center for Tropical Agriculture (CIAT), Cali, Colombia; email: g.hyman@cgiar.org

Geographic information science supports crop improvement in a number of ways and scientists are increasingly taking advantage of the technology. Yet the technology remains beyond the reach of many professionals who have not had the opportunity to master GIS software programs and the methodologies employed. Generation Atlas seeks to bring spatial information and analysis to a broader group of crop improvement specialists working in the Generation Challenge Program. The tool provides data and some simple analysis capabilities aimed at evaluating the geographic context within which crop improvement takes place. The Atlas is an online map server built on ESRI technology. It includes map layers related to GCP focus crops, countries and farming systems. Available information emphasizes production constraints that are the focus of GCP research, such as drought, soil properties and socioeconomic conditions. Several tools support simple queries of drought conditions at a site and across the globe. Tools are available to evaluate conditions at sites or trials sites that are part of phenotyping networks. The data sets are all publicly available for use in standard GIS software packages.

Related GCP project–G8009.06.05/ Activity 3.2.5: Phenotyping sites and screening protocols (Activity Leader: Xavier Delannay, GCP)

Notes:

………………………………………………………………………………..

………………………………………………………………………………..

………………………………………………………………………………..

………………………………………………………………………………..

………………………………………………………………………………..

………………………………………………………………………………..

………………………………………………………………………………..

………………………………………………………………………………..

………………………………………………………………………………..

………………………………………………………………………………..

………………………………………………………………………………..

………………………………………………………………………………..

………………………………………………………………………………..

………………………………………………………………………………..

………………………………………………………………………………..

………………………………………………………………………………..

3.12: Information management and data curation support services of IBP/GCP

Arllet Portugal,* Clarissa Pimentel and Graham McLaren

*Generation Challenge Programme, c/o CIMMYT, El Batan, Texcoco, Mexico,
e-mail: a.portugal@cgiar.org

Quality information system is an integral component of molecular breeding. Lack of information systems is one bottleneck in adoption of molecular breeding in developing countries. The Information Management Support Service of GCP was created to provide assistance in installing, configuring the Integrated Breeding (IBP) platform information system for use by specific breeding programmes and for global crop improvement databases. The Data Curation Support Service was created to assist in curating data into the platform information system of these breeding projects and to establish global crop improvement databases that integrate pedigree and genotype data from publicly available sources. Seven workshops and trainings were coordinated from April 2010 to February 2011 through these Services targeting the nine use cases supported by IBP. Details about these workshops are available at http://ibp.generationcp.org/confluence/display/MBP/ Activity+3.2.2+and+3.2.3 Trait Dictionaries and Fieldbook templates are outputs of these workshops and accessible in the said site. Use of handheld device for fast data collection was introduced. Four Honeywell and nine HP iPaq handheld units were distributed. The Information Management Support Service will make the informatics tools developed through IBP available to developing countries and the Data Curation Support Service will facilitate management of quality data for accurate predictive breeding.

Related GCP projects–G8009.06.02/Activity 3.2.2: Information Management and G8009.06.03/Activity 3.2.3 Data curation (Activity Leader: Arllet Portugal, GCP)

Notes:

Theme 4:
Capacity building and Product delivery

4.1: Exploiting the benefits of sharing knowledge and technology among research partners towards a cassava MAB-based program: experiences from Uganda

Anthony Pariyo,* Yona Baguma, Titus Alicai, Chritopher Omongo, Williams Esuma, Emmanuel Okogbenin and Anton Bua

National Crops Resources Research Institute, P.O. Box, 7084 Kampala, Uganda.
Email: tkakau@yahoo.co.uk; apariyo@agric.mak.ac.ug

Sharing of research facilities and information are fundamental considerations for sustainable research and development among resource constrained programs. This approach is becoming increasingly important as crop research embraces biotechnology techniques with limited available capacity. The approach by cassava breeders' community of practice (CoP) in Africa, in which Uganda participates, involves sharing of facilities, information and technologies among the partners at continental level. We report some of the key successful approaches in Uganda: using the breeder-to-breeder exchange visit approach, seven (7) CBSD tolerant genotypes were introduced from Tanzania and information on field screening for resistance to the disease was discussed. Three international workshops held in which at least three (3) plant breeders were trained on molecular tools for accelerating cassava breeding. Beyond training, efforts were made to expand the genetic base and nutritional content of cassava through shipment of germplasm comprising 25, 6 and 109 genotypes with Protein/Pro-vitamin and delayed PPD genes and carotene-rich genes respectively were introduced from Latin America. One plant breeder with a uniquely rich international exposure compared to his peers has been trained. Additionally, Genotyping Support Services was engaged to share costs of research. The next phase of this research will be to operationalize the MAB scheme.

> *Related GCP project–G4008.26: A cassava breeding community of practice in Africa for accelerated production and dissemination of farmer-preferred cassava varieties resistant to pests and diseases (PI: Emmanuel Okogbenin, NRCRI)*

Notes:

4.2: TLI students for analysis of drought tolerance in common bean

S Beebe,* M Blair, F Alemayehu, A Asfaw, R Chirwa, L Kalolokesya, P Kimani, G Makunde, F Waweru

*Centro Internacional de Agricultura Tropical (CIAT), Colombia; e-mail: s.beebe@cgiar.org

The GCP has administered a project, Tropical Legumes-I or TL-1, to develop tools for the improvement of drought tolerance in four legume crops including common bean. TL-1 is closely aligned with a sister project, Tropical Legumes-II (TL-2), which focuses on breeding. Both projects have had a significant capacity building component, and coordination between the two projects has allowed training both in field management under TL-2, and formal degree training in TL-1. Thesis projects contribute directly to the common goals of the two projects, and cover topics of: QTL analysis for drought tolerance traits; participatory evaluation in drought prone areas; association mapping for drought tolerance QTL; marker assisted selection for resistance to common bacterial blight. A project on marker assisted recurrent selection is currently underway. Students benefiting from this project proceed from Ethiopia, Kenya, Malawi and Zimbabwe.

> *Related GCP project G4009.07.01: TLI students for analysis of drought tolerance in common bean (PI: Steve Beebe, effective October 2010/ Matthew Blair, CIAT)*

Notes:

4.3: Introgression of *Saltol* and fine-mapping of reproductive stage QTLs to develop rice varieties highly tolerant of salt stress

M. Sazzadur Rahman*, Michael J. Thomson, Zeba I. Seraj and Abdelbagi M. Ismail

*University of Dhaka, Bangladesh; and Crop & Environmental Sciences Division, International Rice Research Institute (IRRI), Philippines;
e-mail: s.rahman@irri.org

Salinity is a major problem for rice production in South Bangladesh, and is being aggravated by natural and human activities, such as the increasing frequencies of cyclones and storms, and the excessive withdrawal of water at the upstream of major rivers. Developing high yielding varieties with greater tolerance of salt stress will help in adapting to these adverse conditions, and to sustain food security. *Saltol* introgression lines developed through the previous GCP projects are being evaluated in field trials, however, and because of the complexity of the tolerance trait, this QTL provides moderate to high tolerance only at the seedling stage. Multiple tolerance genes were also recognized in the *Saltol* region, and to identify the optimum introgression size, varying segments of the *Saltol* locus are being introgressed into BRRI dhan28 from the donor FL378. BC_3F_2 progenies with segments of four different sizes (1.3, 2.4, 3.3 and 3.7 Mb) were developed, with a clean or minimum donor background. Furthermore, two novel QTLs associated with tolerance at the reproductive stages (Chr 1L and Chr 5S) from Boilam, a salt tolerant landrace from South Bangladesh, were identified and are being fine-mapped to be combined with *Saltol* using marker assisted backcrossing.

> *Related GCP project– G4010.04 Enhancing capacity for use of advance genotyping for fine-mapping and pyramiding of major salt tolerant QTLs through MABC for the development of durable saline tolerant rice varieties.(PI: Zeba I Seraj, UoD)*

Notes:

4.4: Communities of Practice Generation Challenge Initiative for Rice in West Africa

Andrew A. Efisue* and Marie-Noelle Ndjiondjop

*Department of Crop & Soil Science, University of Port Harcourt, P.M.B.5323, Choba, Port Harcourt, Nigeria, e-mail: andyefisue@yahoo.com

Rice is one of the major food staples in Sub Sahara Africa (SSA). It contributes more than 40 % of gross domestic product (GDP) and 70% of the labour force. The demand for rice surpasses production rate, which create a wide gap being filled by importation that drains the scarce foreign reserve of these nations. Generation Challenge Program (GCP) established a program called "challenge initiative" to address the aforementioned problems using Communities of Practice (CoP) approach in three West African countries (Burkina Faso, Mali and Nigeria) as pilot study. Major activities of CoP are capacity building and support for the implementation of markers assisted selections in the breeding programs of NARS. To achieve these, CoP will provide training for genotyping, data management and analyses among others. Communities of Practice essentially are interactive forum for collaboration and exchange of ideas. This will be led by a coordinator whose responsibility is to facilitate project activities and provide technical support in modern breeding techniques and is assisted by a mentor from each member countries. CoP will hold regular meetings and workshops to discuss joint research activities and share information to strengthen the NARS breeding program. CoP members comprised scientists at senior and junior level of the national research institutions as well, voluntary individual scientists...

> *Related GCP project–G7010.04.01: Improving rice productivity in lowland ecosystems of Burkina Faso, Mali and Nigeria through marker-assisted recurrent selection for drought tolerance and yield potential (PI: Marie Noëlle Ndjiondjop, AfricaRice)*

Notes: