2009 Annual Research Meeting

20–23 September 2009
Bamako, Mali

Poster abstracts

Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE-POOR

Generation
Cultivating Plant Diversity for the Resource-Poor

CGIAR Generation Challenge Programme

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Poster abstracts

Generation Challenge Programme (GCP)

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

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Theme 1:
Exploiting allelic diversity

1.1: Genetic studies of yield components in early generations of interspecific rice populations

Andrew Efisue and Bartholomew Nwija*

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Notes:

Yield is an important agronomic trait in rice production. Yield components become important where absolute yield measurement is difficult. Five *O. glaberrima* genotypes and four inbred interspecific lines were used as female parents and crossed with two improved *O. sativa* L. subsp. *japonica*, and two inbred interspecfic lines as pollen parents in a North Carolina Design II mating. Significant negative correlation (r = 0.83***) was observed between yield and spikelet sterility in F_2 and F_3 populations and 1000 grain-weight significantly correlated with yield components like effective panicle per plant and panicles per m^2. Significant correlations were observed with other traits of yield components. Harvest index showed significant positive correlation with grain to straw ratio and negative correlation with spikelet sterility. Panicle exsertion showed significant positive correlations with days to 50% flowering and panicle length. Heritability estimates for 1000 grain-weight and spikelet sterility were estimated by regressing F_3 populations means on F_2 parents' values. Significant (h^2 = -0.41**) and (h^2 = -0.32*) for WBK 35 and WBK 40, respectively was observed for spikelet sterility. Understanding the genetics of yield components could be a way of assessing the performance of population in the early generation of the breeding cycle.

Related GCP project–CI-1: Improving drought tolerance in rice for Africa (Project Delivery Coordinator: Nourollah Ahmadi, Agropolis–CIRAD)

1.2: Study of Burkina Faso rice landraces diversity and breeding for resistance to Rice Yellow Mottle Virus (RYMV)

Kam Honoré, Mark Laing, Laurence Alba, Dakouo Dona, Séré Yacouba, Onasanya Amos, Sow Mounirou, Alain Ghesquiere, Nourollah Ahmadi and Marie Noelle Ndjiondjop*

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In Burkina Faso, rice is cultivated in three main agro-ecosystems: lowland, upland, and irrigated ecosystem. To establish a core collection of rice genetic resources used by farmers and researchers in breeding programmes, a broad collection of 512 rice seed samples were collected in 59 villages during January and May 2008. The collection was characterised using agromorphological characters and is currently being genotyping with 26 SSR markers in order to study the genetic diversity and determine the population structure. The collection is also in use to breed for durable resistance to RYMV. Four hundred and twenty five accessions comprising 50 *O. glaberrima* were screened with three strains. Four checks have been used and the inoculation was done at 14 days after sowing. The disease symptoms were recorded from 14 until 42 days after inoculation, and the plant height and panicle fertility taken at maturity. Only 26 accessions comprising 22 *O. glaberrima* and 4 *O. sativa* displayed resistant or tolerant features. The resistant accessions are currently being screened with molecular markers from the *rymv-1* gene to further the study and to check whether it is already known genes and search for new genes or alleles.

Related GCP project–SP5 Commissioned G4009.02: Fellowships and travel grants 2009–'Study of Burkina Faso rice landraces diversity and breeding for resistance to Rice Yellow Mottle Virus (RYMV)' (Fellow: Kam Honoré)

Notes:

1.3: Phenotyping maize inbred lines for the maximum utilisation of drought tolerance in maize

James Gethi, Maria Zaharieva, Claude Welcker and Andreas Hund*

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Notes:

Lack of detailed characterisation of available materials to allow for direct use in product development has severely limited the use of this trait. Phenotyping of the maize reference set was carried out at KARI and CIMMYT (field), INRA (Leaf Growth) and ETH Switzerland (Root Growth). 180 inbred lines were phenotyped under well watered and stressed conditions at Kiboko. 225 inbred lines and 220 hybrids were phenotyped at CIMMYT. The early lines seem to escape the stress at flowering as the yield was not depressed by withdrawal of water. Vegetative stress had severe impact on grain yield for the three sets of materials. The 100 kernel weight was not severely affected. Characterisation of leaf growth rate revealed that a large variation exists for biomass accumulation under water deficit within the panel. 224 lines from the reference set were phenotyped in growth pouches and 33 genotypes from another panel were phenotyped in growth columns for root traits that determine the root depth and distribution in soil important for efficient water and nutrient acquisition. Three independent experiments, comprising of three harvest dates per genotype were conducted. The data were used to characterize the genotypes for their heterotrophic development during the early autotrophic growth.

Related GCP Project–SP3 Commissioned G4008.33: 'Drought tolerance phenotyping of the GCP maize inbred line reference set' (PI: James Gethi, KARI)

1.4: A whole genome scan of cultivated sorghum (Sorghum *bicolor* L. Moench): evolving diversity in the light of different marker systems

Jean Christophe Glaszmann, Sophie Bouchet, Monique Deu, Jean-Francois Rami, Claire Billot, Ronan Rivallan, Laeticia Gardes, Ling Xia and Andrej Kilian*

**Agricultural Research Centre for Developing Countries (Agropolis–CIRAD), France; email: jean-christophe.glaszmann@cirad.fr*

Sorghum diversity has been characterised over time with various generations of molecular markers. The first assessments of the extent of linkage disequilibrium place it between that of maize and that of Arabidopsis thaliana, making whole-genome scans realistic. We developed and characterised DArT markers for this purpose. A well documented Core Collection was genotyped and its structure compared according to various available data sets: 713 DArTs, 60 RFLPs and 40 SSRs. The three marker systems revealed similar patterns of diversity. The information retrieved by DArT appeared much closer to saturation than the other two systems. Compared to DArT and RFLP, SSR yielded lower stability across simulations and lower differentiation between the groups with higher residual diversity within the groups. The proportion of 'unclassified' accessions appeared consistently higher with DArT markers, suggesting that higher genome coverage reveals higher admixture, and pointing out recombination as a major source of sorghum germplasm diversity. Taking into consideration the structure level of the collection, linkage disequilibrium was weak, with a decrease within one Mb. Our DArT markers represent thus a significant contribution in search for adaptive variation in the sorghum genome.

Related GCP project–SP1Discretionary 'Linkage disequilibrium and patterns of selection in the genome of sorghum used for mapping useful genes' (PI: Jean Christophe Glaszmann, Agropolis–CIRAD/GCP)

Notes:

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1.5: HaploPhyle: a graphical haplotype network in the light of external data

Claire Billot, Nour Ahmadi, Brigitte Courtois, Gaetan Droc, Gerard Second, FuMin Zhang, Dominique Brunel, Mark Lathrop and Kenneth McNally*

**Agricultural Research Centre for Developing Countries, (Agropolis–CIRAD), France; email:claire.billot@cirad.f*

Asian cultivated rice occurs as two major types, indica and japonica that appear to have arisen from independent domestication events. Even though rice is a predominantly self-pollinated crop, both types can frequently be found within the same region allowing the prospect for genetic exchanges between them. Since whole genome sequences are available for each type, we have the opportunity to identify single nucleotide polymorphism (SNP) suitable for determining the extent of linkage disequilibrium and haplotype structure that is indicative of their differentiation. Japonica Nipponbare (IRGSP) and indica 93-11 (Beijing Genomics Institute) sequences were compared to identify a set of 1536 SNPs suitable for undertaking genome scans. These were chosen for a whole genome LD scan (1 SNP for every 320 kb) and for a closer look at specific regions (1 SNP per 50 kb). 900 accessions, finalised from the GCP composite collection (492 accessions) and from accessions at CIRAD that are likely to contain introgressions between the indica and japonica groups as well as wild species (408 accessions) were genotyped. Analyses enable to discriminate perfectly between *japonica* and *indica* accessions, as well as decipher the genetic structure of wild species in comparison to *indica* and *japonica* and identify introgression patterns.

Related GCP project–SP1 Commissioned G4006.03: 'SNP analysis and the genetic diversity along the rice genome (HaplOryza)' (PI: Kenneth McNally, IRRI)

Notes:

1.6: Generating new wheat germplasm with enhanced drought/heat tolerance using AB genomes

Satish Chandra Misra, Maria Zaharieva, S Dreisigacker, J Crossa, T Payne, RR Hanchinal, MY Mujahid, R Trethowan and Tetali Sujata*

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Synthetic hexaploid wheats (SHW) obtained by crossing durum wheat (*Triticum turgidum* subsp. durum) with *Aegilops tauschii* (donor of the D genome of hexaploid wheat) significantly increased genetic diversity among hexaploid wheats. Synthetic backcross lines (SBL) generated by crossing SHW to adapted bread wheats are now widely used in wheat breeding.

Higher genetic diversity and allelic richness in cultivated emmer wheat (*T. turgidum* subsp. dicoccon) than in durum wheat, as revealed by microsatellite markers (SSRs) suggests to use this species to develop new SHW. Cultivated emmer wheat exhibits drought and heat tolerance as well as resistance to various pests and diseases.

A collection of emmer wheat accessions originated 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 have been assessed. Around 100 genetically diverse emmer wheat accessions with good agronomical performance are crossed to three *Ae. tauschii* accessions identified as having high crossability with AB-genome to produce new emmer based SHW. New synthetic backcross lines (SBL) will be generated by crossing SHW to elite bread wheats. Durum wheat based SHW will be crossed to emmer wheat and emmer based SHW to produce AB-genome recombinants.

Related GCP project–SP1 Competitive G3008.01: 'Generating new wheat germplasm with enhanced drought/heat tolerance using AB genomes genetic diversity' (PI: Satish Chandra Misra, ARI)

Notes:

1.7: The genotyping validation of GCP reference sets

*Sarah McGrath**

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Global genetic characterisation of 21 species was undertaken under the SP1 umbrella. Identification of reference samples has been completed or is ongoing for most species. Altogether, these reference samples constitute a key product of the GCP and a public good, which will be widely distributed. However, firstly the genotypic information on these reference sets has to be validated. The validation consists of re-genotyping the reference set of samples with a subset of top quality and most discriminant markers (approximately 20) by a single non-consortium member lab (service provider). Genotyping has been completed for 7 species and is ongoing or scheduled for 7 additional species. Automatic dataset comparison between the reference set and the original dataset for several species was conducted and different sources of variation were detected. For example, marker specific variation, such as non-linear shift between independent experiments due to difficulties in SSR binning and accession specific variation due to errors during seed management or DNA extraction. Discovery of such variation between both datasets reinforces the need for genotypic validation of the GCP reference sets.

Related GCP project–SP1 Commissioned G4007.01: 'Genotyping validation of the GCP reference sets' (PI: Jean-Francois Rami, Agropolis–CIRAD).

Notes:

1.8: A genetic model for the female sterility barrier between Asian and African cultivated rice species

Andrea Garavito, Romain Guyot, Jaime Lozano, Frédérick Gavory, Sylvie Samain, Olivier Panaud, Joe Tohme, Alain Ghesquière and Mathias Lorieux*

**Plant Genome and Development Laboratory (UMR 5096, CNRS, IRD, UPVD), Institut de Recherche pour le Développement (Agropolis–IRD), 911 Av. Agropolis, 34394 Montpellier Cedex 5, France/ Agrobiodiversity and Biotechnology Project, International Center for Tropical Agriculture (CIAT), A.A. 6713, Cali, Colombia*

S1 is the most important locus of the reproductive barrier between *Oryza sativa* and *O. glaberrima*. It is a complex locus that affects differently male and female fertility. We developed a new mapping approach based on the evaluation of the degree of Transmission Ratio Distortion (TRD) of markers in order to fine map the factor of the S1 locus affecting female fertility. By the implementation of this methodology in four *O. sativa* x *O. glaberrima* crosses we were able to map the female component of the locus into a 27.8 kb region in the O. sativa genome. Moreover, evidence of the presence of additional factors that interact epistatically with S1 was also found. Based in our data, a model that explains the female sterility and TRD mediated by S1 was developed.

Related GCP project–G3007.01: 'Ibridges: Interspecific bridges that give full access to the African rice allele pool for enhancing drought tolerance of Asian rice' (PI: Alain Ghesquière, Agropolis–IRD)

Notes:

1.9: Developing multiparent advanced generation inter-cross (MAGIC) populations using diverse genotypes to facilitate gene discovery for multiple traits in rice (*Oryza Sativa* L.)

*Hei Leung *, Edilberto Redoña, Rakesh Kumar Singh, Marcelino Laza, Andy Godwin Sajise, Nonoy Bandillo, Pauline Andrea Muyco and Cesar Caspillo*

**Plant Breeding, Genetics and Biotechnology Division (PBGB), International Rice Research Institute (IRRI), Manila, Philippines; e-mail: h.leung@cgiar.org*

Sixteen diverse lines, eight each from indica and japonica rice subspecies, were used to develop two MAGIC populations. The founder lines were initially genotyped using 50 simple sequence repeat (SSR) markers to characterise their diversity before initiating the intermating cycles and are now being genotyped with 1536 single nucleotide polymorphism (SNP) markers to assess genome-wide variation. The lines were phenotyped for highly-heritable traits under different non-stress and stress (drought, salinity, and iron toxicity) conditions for two seasons. In the first crossing cycle for each population, 28 crosses were made using a half-diallel approach. The single crosses were intermated to generate 70 out of 210 possible four-way crosses that were then used to undertake 35 out of 105 possible eight-way crosses during 2009, with each founder line being genetically represented in each eight-way cross. At least 1000 recombinant inbred lines (RILs) will be produced by single-seed descent for each population. These populations will be further intercrossed for at least two generations to ensure rapid and uniform decay of linkage disequilibrium across the whole genome. The overall goal is to generate permanent mapping populations for localizing multiple quantitative trait loci (QTL) for multiple traits to regions of 3 cM or less.

Related GCP project–SP1 Commissioned G4008.01: 'Population development through Multiparent Advanced Generation Inter-crosses (MAGIC) among diverse genotypes to facilitate gene discovery for various traits in rice' (PI: Hei Leung, IRRI)

Notes:

1.10: Phenotyping sorghum reference set for post-flowering drought tolerance

Hari Deo Upadhyaya, Sangam Lal Dwivedi, Vincent Vadez, Lakshmanan Krishnamurthy, B Clerget, Eva Weltzein-Rattunde, MA Mgonja, PM Salimath, W Ntundu, M Diourte and N Cisse*

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

Drought is one of the most important yield reducing abiotic constraint worldwide. Sorghum reference set accessions (375) and/or stay-green QTL introgression lines were screened for stay-green, chlorophyll content, water uptake and transpiration efficiency (TE) under post-flowering drought stress conditions. Preliminary results revealed several accessions with stay-green trait under post-flowering drought stress conditions. The accessions revealed large variation in water extraction under water stress (10.2 kg plant^{-1} to 15.3 kg plant^{-1}) and well watered (10.5 kg to 42.3 kg plant^{-1}) conditions. Several accessions with either high or low water-extraction ability under water stress as well as under well watered conditions were identified. The TE value varied between 2.44 g kg^{-1} to 6.09 g kg^{-1} water transpired. Few stay-green QTL introgression lines either in S35 or R16 backgrounds showed higher TE than S35 or R16. Some of the sorghum reference set accessions had higher TE than the highest TE of the stay-green introgression lines. Furthermore, seven subsets (two weeks difference in flowering) of reference set accessions were also characterised under water stress and well watered conditions for morphological and agronomic diversity, which revealed significant differences for most of the traits studied.

Related GCP project–SP1 Commissioned G4008.02: 'Phenotyping sorghum reference set for drought tolerance' (PI: Hari Upadhyaya, ICRISAT)

Notes:

Theme 2:
Genomic resources and gene/pathway discovery

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

AH Paterson, IDK Atokple, C Tom Hash, SP Mehtre, A Mohamed and N Seetharama*

**Plant Genome Mapping Laboratory, University of Georgia (UGA), 111 Riverbend Road, Rm 228, Athens, GA 30602; Phone 1-706-583-0162; Fax 1-706-583-0160; URL: www.plantgenome.uga.edu; email: paterson@uga.edu*

Fine-scale characterisation of qualitative factors related to sustained photosynthetic output under drought stress will yield improved understanding of the structure and functions of genomic regions of importance to sorghum improvement, advancing genetic dissection and molecular cloning of genes conferring the phenotypic effects mapped to these regions. Empirical testing of key combinations of *stay-green* QTLs will reveal the comparative efficacy of various combinations under stress conditions in Ghana and India, also providing for obtaining additional recombinants needed to reduce linkage drag. The sorghum sequence will provide us with the means to design comparative DNA markers that are suitable for utilisation both in sorghum and in many additional cereals. Transcriptome profiling of a diverse sampling of field-proven germplasm will support development of hypotheses about roles of specific genes and pathways in drought response. We will begin to test these and other hypotheses based on analysis of the sorghum sequence, using breeding populations in which drought tolerance will be combined with other traits addressing production constraints in West and Central Africa, Eastern and Southern Africa, and South Asia.

Related GCP project–SP2 Competitive G3008.05: 'Discovery and development of alleles contributing to sorghum drought tolerance' (PI: Andrew H Paterson, UGA)

Notes:

2.2: Dissecting the role of root traits in water uptake, maintenance of plant growth and dehydration avoidance mechanisms in rice

Rachid Serraj, Amelia Henry, Veeresh Gowda, Ken McNally and Arvind Kumar*

**International Rice Research Institute (IRRI), DAPO Box 7777, Metro Manila, Philippines; email: r.serraj@cgiar.org*

Notes:

The relationships between root architecture and plant water uptake during progressive soil drying were investigated using sets of rice varieties, germplasm accessions (*OryzaSNP*) and NILs contrasting for yield response to drought. Genotypic differences in dehydration avoidance and crop growth under stress were measured together with root growth parameters, ability to penetrate compact soil layers at depth, and water uptake under water deficit and well-watered conditions. Root growth at depth varied substantially among genotypes under drought, and the growth patterns were significantly correlated with plant water uptake and the reduction in soil moisture at depth. In the field, large differences in soil water uptake, canopy development and plant water status were observed among genotypes, contrasting in their sensitivity to drought stress. Although rooting depth was found to be the key trait for plant water uptake, variation in other root characteristics such as root hydraulic conductance may also be critical under water deficits. The initial results confirm the importance of genetic variation in root growth at depth for conferring drought avoidance through improved water uptake under drought. The integration of root architecture parameters, root growth plasticity and root hydraulic properties will allow better understanding of dehydration avoidance mechanisms in rice.

Related GCP project–SP2 Competitive G3008.06: 'Drought-avoidance root traits to enhance rice productivity under water-limited environments' (PI: Rachid Serraj, IRRI)

2.3: GreenPhylDB V2.0: An improved database for plant functional genomics

MG Conte, MA Laporte, C Aluome, C Perin and M Rouard*

**Bioversity International (Bioversity), Parc Scientifique Agropolis II, 34397, Montpellier, France; email: m.conte@cgiar.org or m.rouard@cgiar.org*

Rapid progress in sequencing and annotation projects has enabled us to work now on 16 full-plant genomes, including socio-economically important crops like rice, sorghum and maize. Our objective is to identify orthologous genes that share the same molecular function in different species and then transfer this information from model-plants to crops. This database provides to molecular biologists a facility for making interesting links between genomic and functional information.

We have developed methods to:

1. **Maintain and improve data sources present in the database**
   Why?: Bioinformatics tools and databases need to be regularly improved and maintained to remain in phase with other databases available on the web and then offer efficient cross-linkages for bio-analysis.
2. **Allow identification and annotation of plant genes' families**
   Why?: Identify a complete catalogue of homeomorphic gene families - genes that evolved from a common ancestor - would be a valuable resource for evolution studies, future gene annotation, and orthologs' inference.
3. **Link ortholog predictions to molecular function**
   Why?: To help biologists with this functional validation, we linked our orthologs' identification to *Genevestigator* a reference expression database allowing the study of gene-regulation in a wide variety of contexts, such as plants under stress.

Related GCP project–SP4 Commissioned G4008.21: 'Large scale phylogenomic analyses to gene function prediction for GCP crops' (PI: Mathieu Rouard, Bioversity).

Notes:

2.4: Improving tools for pearl millet marker-assisted breeding – it's a struggle

C Tom Hash, V Rajaram, Rajeev K Varshney, Vincent Vadez, S Senthilvel and T Nepolean*

**International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad 502 324, Andhra Pradesh, India; e-mail: c.hash@cgiar.org*

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Pearl millet (*Pennisetum glaucum*), a highly cross-pollinated C4 diploid grass, is a staple cereal grown in crop-livestock production systems of the world's hottest, driest cultivated regions. It was among the first cereals with a marker-assisted breeding product adopted by developing country farmers. However, its marker-assisted breeding tool kit is poor, restricting further application. This project strengthens this tool kit. >200 EST-SSR primer pairs mined from large libraries of short ESTs (from 454 sequencing of root and leaf cDNA libraries) were tested for amplification and polymorphism detection ability using parents of 3 RIL populations. Mapping polymorphic SSRs with good amplification characteristics is underway. We anticipate doubling the number of mapped SSRs in each of these 3 RIL populations. Transfer of SSR-based skeleton linkage maps from F2:4 progeny sets to "finished" F7 RIL populations has confirmed anticipated difficulties in developing RIL sets in this normally wind-pollinated species—slower than theoretical advance to homozygosity, severe segregation distortion and unacceptably high out-crossing rates during inbreeding—as a result of the robust nature of pearl millet pollen combined with selection for seedling vigor (inadvertent) and for selfed seed set (required), resulting in loss of >20% of progenies due to either "non-paternal" alleles or inbreeding depression.

Related GCP project–SP2 Commissioned G4008.07: 'Improving molecular tools for pearl millet' (PI: Tom C Hash, ICRISAT)

2.5: Phenotyping tools to select for adaptive traits in drought environments

Francis C Ogbonnaya, Fernanda Dreccer, Osman Abdalla, Tony Condon, Hassan Ouabbou, Sripada M Udupa, Solomon Gelacha, Matthew Reynolds and David Bonnett*

**International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo, Syria; e-mail: F.Ogbonnaya@cgiar.org*

Drought continues to be a major limiting factor to wheat crop production worldwide, with often devastating consequences especially in developing countries. This project proposes to facilitate plant breeding for drought adaptation by developing a package of high-throughput non-invasive techniques to detect genetic variation for single and combined or complex (water use) drought adaptive traits under field conditions. We are also assessing the value of different plant characteristics/traits (e.g. transpiration efficiency, storage of sugars in the stem and tillering) on yield performance under different types of drought in Central and West Asia and North Africa, sub-Saharan Africa, Syria, Mexico and Australia, using germplasm contrasting for known drought adaptive traits from diverse sources. In the same environments, we are growing ICARDA's elite wheat cultivars to find out more about the combination of traits underpinning their performance. The project also aims to build capability in phenotyping for drought tolerance for wheat in the CWANA and sub-Saharan African regions.

Related GCP project–SP3 Competitive G3008.08: 'Breeder-friendly high-throughput phenotyping tools to select for adaptive traits in drought environments' (PI: Francis C Ogbonnaya, ICARDA)

Notes:

2.6: *Musa*: importance, progress and perspectives

Nicolas Roux, Takuji Sasaki and Members of the Global Musa Genomics Consortium*

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Bananas and plantains (*Musa spp*.) are key crops targeted by the GCP which has already supported projects during its first phase. The GCP promoted the development of genomic resources and integrated them with ongoing trait-based *Musa* research. It also supported targeted comparative genomic between *Musa* and rice genomes. The approach was based on utilizing existing *Musa* germplasm resources,and maps and genomic resources. The outputs are publicly available resources and markers for exploiting breeding-relevant genetic variation within *Musa*.

In the context the Global *Musa* Genomics Consortium (GMGC), the development of these resources enabled the French National Research Agency (ANR) to consider *Musa* as the next crop genome to be fully sequenced. The full sequencing of the *Musa* genome by 2011 will strongly influence crop comparative genomics studies and will facilitate gene discovery to benefit breeders.

Although *Musa* is no longer considered as a priority crop in the second phase of GCP, this poster stresses its importance in many countries especially Sub Saharan Africa, where experiments on drought tolerance are being conducted. 150 *Musa* researchers will meet prior to GCP ARM to help optimise genomics tools use in breeding programmes.

This should open collaborative opportunities between the Banana research community and GCP.

Related GCP project–SP2 G4005.15 (terminated): 'Targeted Musa genome sequencing and frame map construction' (PI: Takuji Sasaki, NIAS).

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2.7: Improving grain yield on acid soils by the identification of genetic factors underlying drought and aluminium tolerance in maize and sorghum

Leon Kochian, Jurandir Magalhaes, Steve Kresovich and Sam Gudu*

**Robert W. Holley Center for Agriculture and Health, USDA–ARS/ Cornell University, Ithaca, NY 1485; email: LVK1@cornell.edu or Loen.Kochian@ars.usda.gov*

We have recently cloned a major sorghum aluminium tolerance gene, identified major maize Al tolerance QTL, and are close to identifying the genes responsible for these QTL. Hence we are poised to advance our programme on improving maize/sorghum acid soil tolerance. We are also beginning to investigate the molecular determinants for drought tolerance, in order to improve agronomic performance of crops whose root systems are severely restricted by Al toxicity and more susceptible to yield reductions from drought stress on acid soils. Thus, in this project, we will use near-isogenic lines, biparental mapping, and association analysis together with physiological and molecular/ genomic investigations to:

1) Develop a SNP genotyping platform for high density genotyping in sorghum; 2) Identify polymorphisms associated with maize Al and drought tolerance; 3) Use recently developed computer-based image analysis tools to identify root architecture traits in maize and sorghum associated with drought tolerance; 4) Determine the genetic architecture of very Al tolerant maize and improve maize Al tolerance by introgressing Al tolerance QTLs and/or genes into maize tropical breeding lines; and, 5) Assess the yield advantage of Al tolerant maize and sorghum in Kenyan environments and begin to investigate the contribution of Al tolerance to drought tolerance.

Related GCP project–SP1 Competitive G3008.02 'Improving grain yield on acid soils by the identification of genetic factors underlying drought and aluminium tolerance in maize and sorghum' (PI: Leon Kochian, USDA–ARS/Cornell University)

Notes:

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

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

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Notes:

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, a preliminary experiment with isogenic 2-dwarf versus 3-dwarf pair comparisons in a stay-green and senescent background was conducted at a rain-out shelter facility in north-eastern Australia. 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.

F2-populations from crosses between Malian and Australian lines have also been grown and evaluated with the aim of introgressing the stay-green trait into photoperiod sensitive Malian lines. In addition, a photoperiod-sensitive, tall mapping population is being developed to identify the most important QTL for grain yield and stay-green in a background relevant to sorghum that is adapted to Mali.

Related GCP project–SP2 Commissioned G7009.04: 'Development and evaluation of drought-adapted sorghum germplasm for Africa and Australia' (PIs: David Jordan and Andrew Borrell, DEEDI)

2.9: Cytokinin-dependent delayed leaf senescence and the drought tolerance in rice

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Notes:

The expression of a stress- and maturation-activated promoter (*SARK*, senescence-associated receptor protein kinase) to an isopenthyltransferase (*IPT*) gene promoted cytokinin synthesis and protected leaf photosynthesis during stress. Rice cv. Kitaake was used to produce transformed homozygous lines expressing *pSARK-IPT*. Transgenic, wild-type (wt) and null plants, were tested under two water-stress treatments at different developmental stages: (***i***) *pre-anthesis* (booting) stage and (***ii***) *post-anthesis* stage (two weeks after panicle initiation), by slowly drying water-logged pots until visual stress symptoms (~12 days) appeared. Pots were then re-watered and plant productivity and other parameters were collected from plants after maturation. Under the *pre-anthesis* treatment, the transgenic plants produced up to 80% of grain yield (GY) and 98% of 1000-grain weight (TGW) as compared to the wt grown under well-watered conditions, whereas the wt plants showed a dramatic reduction in GY (26%) or TGW (85%). Water stress during panicle initiation (*pre-anthesis*) caused severe reduction in fertility in the wt plants (60% reduction in grain number), while only a 20% reduction was seen in the transgenic plants. At the later stage (*post-anthesis*), water stress predominantly affected assimilate translocation to the developing grain, reducing GY, the transgenic rice plants showed significantly greater GY than the wt.

Related GCP project–SP2 Competitive project G3008.03: 'Delayed senescence and drought-tolerance in rice' (PI: Eduardo Blumwald, UoC–Davis)

2.10: Transcriptome analysis revealed substantial differences between smoke-water and butenolide mode of action

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Smoke released from burning vegetation functions as an important environmental signal promoting the germination of many plant species following a fire. It not only promotes the germination of species from fire-prone habitats, but several species from non-fire-prone areas also respond, including some crops. Bioactivity-guided fractionation of smoke-water led to the identification of a highly active butenolide compound. Contrary to the efforts to unravel the mode of action of smoke, the mechanism is still largely unknown. We demonstrated that although smoke-water and butenolide treatment of maize kernels results in a similar physiological response, the gene and protein expression patterns are quite different. Treatment with smoke-water enhanced the ubiquitination of proteins and activated protein-degradation-related genes. This effect was completely absent from butenolide-treated kernels, in which a specific aquaporin gene was distinctly upregulated. These findings indicate that other bioactive compounds present in smoke-water may act together, leading to accelerated protein turnover. The results highlight the importance of protein degradation and aquaporins in the seed germination process. Besides their obvious use in the sustainable agricultural practice, smoke and butenolide can be used in studies to gain further insight into the transcriptional changes during germination.

Related GCP project–SP3 Commissioned G4007.24: 'Seed smoke treatment to favour germination under water stressed conditions' (PI: Ervin Balazs, ARI–HAS)

Notes:

2.11: A 1000 marker loci genetic map of chickpea

Spurthi Nayak, Nicy Varghese, Hongyan Zhu, Ralf Horres, T Nepolean, Gudipati Srivani, Ruth Jungmann, Hong-Kyu Choi, Subhojit Datta, Pooran Gaur, PB Kavi Kishor, Guenter Kahl, Dave Hoisington, Andrzej Kilian, Peter Winter, Doug Cook and Rajeev K Varshney*

**International Institute for the Semi-Arid Tropics (ICRISAT), Patancheru 502 324, India*

In order to increase the genomic resources in chickpea, novel molecular markers namely, microsatellite and Diversity Array Technology (DArT) markers were developed. A total of 1,655 microsatellite markers from mining SSR-enriched library (311) and BAC-end sequences (1,344) and a DArT array comprising of 15,360 features were developed. Newly developed SSR and DArT markers were tested for polymorphism on parental genotypes of an interspecific mapping population (*Cicer arietinum* ICC 4958 × *C. reticulatum* PI 489777) comprising of 131 RILs. A total of 305 SSR markers (52 from enriched library and 253 markers from BAC-end sequences) and 675 DArT markers were found polymorphic and segregation data have been obtained. In addition, genotyping data for several hundred published markers from University of Frankfurt as well as novel gene based SNP markers from UC-Davis were assembled. In total, genotyping information has become available for about 1,650 markers on this interspecific mapping population. MAPMAKER/EXP was used to calculate map and we anticipate the presentation of a comprehensive genetic map of chickpea comprising more than 1000 marker loci, which can be used in trait mapping and the markers can be used as anchors for linking with (future) physical map.

Related GCP project–Focus G6007.04: TL1 Objective 4: 'Improved chickpea productivity for marginal environments in South Asia and sub-Saharan Africa' (PI: Rajeev K Varshney, ICRISAT)

Notes:

2.12: A QTL study on late leaf spot and rust revealed a major QTL and candidate marker for rust resistance to deploy in molecular breeding of groundnut (*Arachis hypogaea* L.)

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Late Leaf Spot (LLS) and rust are the major foliar diseases of groundnut that often occur together leading to 50-70% yield loss in the crop. A RIL population (TAG 24 × GPBD 4) was phenotyped for late leaf spot (LLS) for three seasons and rust for five seasons under artificial disease epiphytotics and genotyped with 67 SSR markers. A partial linkage map with 56 SSR markers on 14 linkage groups with 364.40 cM genome coverage was prepared. Composite interval mapping (CIM) showed 12 QTLs for LLS (1.2 to 5.6%) in three different environments. In case of rust, 14 QTLs were detected in five different environments with phenotypic variation ranged upto 54.4%. Furthermore, a major QTL associated with rust was identified by both CIM and single marker analysis (SMA) that contributed 17.6 to 54.4% phenotypic variation. One marker linked with this QTL was validated using a wide range of resistant / susceptible breeding lines as well as progeny lines of another mapping population (TG 26 × GPBD 4). This study provides the first set of molecular tools to the groundnut community to undertake molecular breeding for rust resistance.

Related GCP project: Focus G6007.01–TL1 Objective 1: 'Improved groundnut productivity for marginal environments in South Asia and sub-Saharan Africa' (PI: Vincent Vadez, ICRISAT)

Notes:

2.13: A consensus genetic map of cowpea [*Vigna unguiculata* (L) *Walp*.] and synteny based on EST-derived SNPs and six RIL populations

Wellington Muchero, Ndeye N Diop, Prasanna R Bhat, Raymond D Fenton, Steve Wanamaker, Marti Pottorff, Sarah Hearne, Ndiaga Cisse, Christian Fatokun, Jeffrey D Ehlers, Philip A Roberts and Timothy J Close*

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Consensus genetic maps provide a genomic framework that facilitate genetic studies and applied breeding in marker-assisted selection schemes. Among "orphan crops" with limited genomic resources such as cowpea [*Vigna unguiculata* (L.) Walp.] (2n=2x=22), use of transcript-derived single nucleotide polymorphisms (SNPs) in genetic maps provides opportunities for automated genotyping and estimation of genome structure based on synteny. Here we report the development of a high-throughput EST-derived SNP assay for cowpea, its application in consensus map building, and determination of synteny to reference genomes. SNP mining from 183,118 ESTs sequenced from 17 cDNA libraries yielded approximately 10,000 high-confidence SNPs from which an Illumina 1,536-SNP GoldenGate genotyping assay was developed and applied to 741 recombinant inbred lines from six populations. 1,375 SNPs (90%) were technically successful. Of these, 928 were incorporated into a consensus genetic map spanning 680 cM with 11 linkage groups and an average marker distance of 0.73 cM. Comparison to reference legumes, soybean (*Glycine max*) and *Medicago truncatula* revealed extensive macrosynteny encompassing 85 and 77% respectively, of the cowpea map. Regions of soybean genome duplication were evident relative to the diploid cowpea. The aggregate EST, SNP, genetic map, and synteny information is publicly available from http://harvest.ucr.edu via the HarvEST:Cowpea browser.

Related GCP project: G6007.02–TL1 Objective 2: 'Improved cowpea productivity for marginal environments in South Asia and sub-Saharan Africa' (PI: Jeff Ehlers, UoC–Riverside)

Notes:

2.14: Rapid transcriptome sequencing of sweetpotato

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Breeding of improved and well adapted sweetpotato (*Ipomoea batatas* L. (Lam)) with increased stress tolerance is limited by the crop's genetic complexity - sweetpotato is an allohexaploid highly heterozygous plant - and by the lack of available genetic resources. Until recently sweetpotato genomic data were restricted to around 22 000 ESTs and to ~1500 gene sequences. To increase the available sequence information, we have sequenced two normalized sweetpotato cDNA libraries derived from leaves and stems using the 454 technology. Two 454 quarter runs yielded 523.914 expressed sequence tags, which were assembled *de novo* together with 22.094 publically available ESTs from storage roots into 31.165 contigs and 29 080 singletons. BLASTx comparisons indicated the presence of at least 6450 unique genes, along with 39 201 sequences, most of them singletons, with no match to protein sequences of the manually curated UniProtKB database. The average sequencing depth was 14.1-fold and 29.6-fold for the longest 8011 contigs (>1000 bp in length), which revealed sufficient for SNP identification. 514 potential microsatellite markers have been identified in the assembly and for 220 new SSRs primers have been designed and tested. The successful amplification of most SSR loci corroborated the quality of the assembly.

Related GCP project–SP2 Commissioned G4008.09: 'Development of genetic and genomic resources for breeding improved sweetpotato' (PI: Roland Schafleitner, CIP)

Notes:

2.15: Diversity and distribution of single feature polymorphisms in food crop legumes

R Varma Penmetsa, Andrew D Farmer, Noelia Carrasquilla-Garcia, Birinchi K Sarma, Subhojit Datta, Sally L Vail, Bert Vandenberg, Jimmy Woodward, Gregory D May, George E Bruening, Rajeev K Varshney and Douglas R Cook*

**Department of Plant Pathology, University of California–Davis (UoC–Davis), CA, USA*

Using a set of 1440 low degeneracy oligonucleotide pairs developed for comparative mapping across crop legumes, we amplified and Sanger sequenced gene orthologs from the food legumes chickpea (*Cicer arietinum*), lentil (*Lens culinaris*), pigeonpea (*Cajanus cajan*), cowpea (*Vigna unguiculata*), common bean (*Phaseolus vulgaris*) and peanut (*Arachis hypogaea*). 1043 to 1251 high quality sequences were obtained and aligned for 2-4 parents of mapping populations in each species. We validated 22,827 single nucleotide (SNPs) and indel polymorphisms, within 503 to 691 orthologous genes in each crop legume at an average rate of 6.6 SNPs/locus. High throughput Goldengate OPA assays are being used for genotyping to generate genetic maps in each crop, and comparative maps between crops.

Additionally we are working to develop protocols to define the diversity and distribution of SNPs in the large (>10K accessions) germplasm collections in each food legume via next generation sequencing technologies. This will establish high-throughput genotyping systems for marker-assisted selection, and characterize the genetic structure of crop species in terms of allele frequency, haplotype structure and linkage disequilibrium. Results from these ongoing studies and implications for association mapping and allele mining will be described.

Related GCP project–G6007.05: TL1 Objective 5:' Developing cross-species resources for comparative genomics in tropical crop legumes' (PI: Doug Cook, UoC–Davis)

Notes:

Theme 3:
Marker development and breeding applications

3.1: Marker assisted backcrossing of *Saltol* and mapping novel QTLs associated with salinity tolerance in rice by selective genotyping

M Akhlasur Rahman, Michael J Thomson, Marjorie de Ocampo, James Egdane and Abdelbagi M Ismail*

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Notes:

Salt stress commonly affects one million hectares of rice lands in coastal Bangladesh. A major QTL for salinity tolerance on chromosome 1, *Saltol*, provided the opportunity to apply marker-assisted backcrossing to precisely introduce tolerance into popular, but salt-sensitive Bangladeshi mega-varieties. Using FL478 as a donor, we introgressed *Saltol* into BRRI dhan28, a popular dry season Bangladeshi variety. A BC_3F_2 homozygous individual was identified using marker selection with a 1.4 Mb Pokkali introgression at the *Saltol* region (10.8-12.2 Mb) with 99% recurrent parent content across the rest of the genome. Seeds of the fixed BR28-*Saltol* line were amplified and will be distributed to NARES partners for field trials. In addition, Capsule, a salt tolerant, widely adapted Bangladeshi *indica* landrace, was used to identify new QTLs for salinity tolerance. An $F_{2:3}$ mapping population was evaluated for 9 physiological and agronomic traits. Using 104 SSR markers, QTLs were identified on the long arm of chromosome 1 (different than Saltol) for Na^+ uptake, Na/K ratio and survival; on chromosome 3 for Na^+ uptake, survival and SES; and chromosome 5 for K uptake and SES. Thus Capsule provides an alternative source of salinity tolerance aside from Pokkali, which may be useful for future QTL pyramiding.

Related GCP project–SP3 Commissioned G4008.16: 'Speeding the development of salt-tolerant rice varieties through marker-assisted selection and their dissemination in salt-affected areas of Bangladesh' (PI: Abdelbagi M Ismail, IRRI)

3.2: Use of identified QTL to improve the efficiency of breeding for long coleoptile length of wheat (*Triticum aestivum* L.)

Jiankang Wang, Scott Chapman, David G Bonnett and Greg J Rebetzke*

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How QTL mapping results can be used to pyramid desired alleles at various loci has only been rarely addressed in the literature. In this study we applied computer simulation to investigate the simultaneous selection for alleles at both major and minor gene (as QTL) loci in breeding populations of two wheat parental lines, HM14BS and Sunstate. Loci targeted for selection included six major genes affecting plant height, disease resistance, and grain quality, plus 6 known and 11 "unidentified" QTL affecting coleoptile length (CL). Parental line HM14BS contributed the target alleles at two major gene loci, while parental line Sunstate contributed target alleles at four loci. The parents have similar plant height, but HM14BS has a longer coleoptile, a desirable attribute for deep sowing in rainfed environments. Including the wild type allele at the major reduced-height locus *Rht-D1*, HM14BS was assumed to have 13 QTL for increased CL, and Sunstate four. Simulation indicated that a single biparental F1 cross produced the highest frequency of target genotypes. An average of 2.4 individuals with the target genotype were present in unselected F_1-derived doubled haploid (DH) or recombinant inbred line (RIL) populations of size 200. A selection scheme for the six major genes increased the number of target individuals to 19.1, and additional marker-assisted selection (MAS) for CL increased the number to 23.0...

Related GCP project–SP3 Commissioned G4008.04: 'Breeding for drought tolerance with known gene information' (PI: Jiankang Wang, CAAS and CIMMYT–China)

Notes:

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3.3: Application of marker-assisted backcrossing in line development of popular rice varieties in the Mekong Region

Theerayut Toojinda, Jonaliza L Siangliw, Toe Aung, Monthathip Chanphengsay, Men Sarom and Sureeporn Katengam*

**National Center for Genetic Engineering and Biotechnoligy (BIOTEC), Thailand; e-mail: theerayut@dna.kps.ku.ac.th*

Training on line conversions, trait validations and field trials initiated by BIOTEC and Rice Gene Discovery Unit (RGDU) was started in January 2007. Marker-assisted backcrossing method was used in line development. Department of Agricultural Research (DAR), Myanmar improved salinity tolerance in BC3F5-IR53936 and grain quality of BC4F2-Manawthukha. After trait validation, the materials were planted in Myanmar at target locations at which these materials are usually planted. Fourteen BC3F5-IR53936 and 12 BC4F3-Manawthukha were selected based on trait validation and preliminary field trials. Cambodian Agricultural Research and Development Institute (CARDI) improved aroma and grain quality of drought tolerant CAR3. The validated BC3F3 were planted in CARDI under irrigated and stress conditions to assess the potential of improved lines in both conditions and 15 lines were selected. Twenty-one Aromatic BC3F2-TDK1 lines were developed by National Agriculture and Forestry Research Institute (NAFRI), Laos and were planted for agronomic and plant type characterisation. Lastly, Ubon Ratchatani University (UBU), Thailand improved aroma and grain quality of IR57514. BC3F5 were planted for submergence, drought and preliminary yield trials and 10 lines were selected. All materials had been developed and field trials will be repeated with farmer's participation in selection before varietal release.

Related GCP project–SP5 Commissioned G4007.03: '"Community of Practice" concept applied to rice production in the Mekong Region: Quick conversion of popular rice varieties with emphasis on drought, salinity and grain quality improvement' (PI: Theerayut Toojinda, BIOTEC)

Notes:

3.4: Identification of association between microsatellite markers and downy mildew resistance in elite maize inbred lines in Thailand

Chalermpol Phumichai, Julapark Chunwongse, Sansern Jampatong and Pichet Grudloyma*

**National Centre for Genetic Engineering and Biotechnology (BIOTEC), Department of Agronomy Faculty of Agriculture Kasetsart University; e-mail: chalermpol.ph@gmail.com, agrcpp@ku.ac.th*

Association study is an alternative to linkage mapping in traditional biparental populations which relied on the variation and extent of linkage disequilibrium contrast with variation in the two parents of the mapping population. The objective of this research was investigating genetic diversity within germplasm of maize inbred lines in Thailand and identifies SSR markers associated with downy mildew resistance. Mini core set of 60 maize inbred lines were grown at two locations. The analysis of variance show significant variation among entries. There was a significant location effect as well as a significant entry by location effect. The analysis of variance results were used to measure broad sense heritability. The value was 0.50. All of 48 SSR markers produced a total of 489 alleles among 60 entries. A dendrogram was generating using the UPGMA algorithm with GD matrix that all of the entries could be group in to three clusters. Population structure was estimated using the software programme STRUCTURE. The number of subpopulation (K) was difficult to determine the optimal number of subgroups, since the posterior or probabilities for the number of clusters increased steadily. Association analysis identified marker trait association (P-adj < 0.05). Three significant SSR/trait associations were detected.

Related GCP project–SP3 Commissioned G4007.04: 'Association mapping of downy mildew resistance in elite maize inbred lines in Thailand' (PI: Chalermpol Phumichai, BIOTEC)

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3.5: Incorporation of an MSV resistance gene in Mozambican maize varieties mediated by use of MAS

Jedidah W Danson, John Derera, Pedro Fato, David Mariotte and Mark Laing*

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Maize streak virus is a serious disease of maize which can cause loses of up to 100% yield loss in severe occurrences. Molecular markers have since been developed for gene introgression into elite materials used in different African countries for hybrid development. The main objective of this project was to use MAS technology to accelerate the introgression of Mozambican elite germplasm resistant to *Phaeosporia* leaf spot (PLS), downy mildew with some relative degree of drought tolerance but highly susceptible to maize streak virus disease using CIMMYT lines carrying the MSV1 gene and the backcross breeding scheme. **Outline:** Planting and analysis for polymorphism between parents: Selection for MSV-R using polymorphic SSRs: Corsses perfomed at UKZN: Planting F3s in Mozambique for mildew screening, early maturity and MSV-R: **Mozambican germplasm:** Zm 621- 4 lines, Zm 521-1 lines, Zm 421- 2 lines, P501-1 line, LP19, LP21, LP23, LP37D, LP37F. **Donor Lines (11):** CML 505, CML 509, CML 440, CML 442, CML 444, CML 445, OSU23i—1, OSU23i—2, OSU23i—3, OSU23i—4, OSU23i-JD. **Checks:** Hybrid 1: Olipa (QS7707), Hybrid 2: Hluvukani, OPV1: Changalana, OPV2: Susuma. One hundred and fifty crosses of different combinations according to nicking dates were performed at UKZN and the materials have been harvested.

Related GCP project–SP3 Commissioned G4008.19: 'Incorporation of an MSV resistance gene in Mozambican maize varieties mediated by use of MAS' (PI: Mark Laing, UKZN)

Notes:

3.6: Breeders Tool Kit: A cheap and convenient high throughput method optimised for the sampling and detection of polymorphism using FTA cards and real-time PCR

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The main objective was to develop a cheap and convenient molecular breeding toolkit for conventional breeders for use in various countries of Africa. Secondly, take into consideration a high throughput application that is cost effective. The use of microsatellites in gene introgression of important traits and marker assisted breeding is becoming increasing popular. DNA markers are stable and highly polymorphic. However, analyses are conducted on agarose gels, or the relatively expensive automated sequencers. Furthermore DNA preparation for marker analysis can also be expensive and time consuming requiring special sampling environments such as liquid nitrogen, ice, lyophilisation among others. We optimised the FTA card technology for sampling thousands (4000) of samples from a breeder's field. DNA extraction was done directly into the well plates using a modified FTA. The PCR products were investigated using a high resolution amplicon melting analysis (HRM) and SYBR Green-based real-time PCR. Of the 8 DNA different parental samples analysed for polymorphism using agarose gels, only 5 were found to be polymorphic. However, using the real-time PCR melting curves, it was possible to detect polymorphism for all the samples using the melting curves.

Related GCP project–SP5 Commissioned G4006.36: 'Capacity-building and research project' (PI: Mark Laing, UKZN)

Notes:

3.7: Marker assisted and farmer participatory breeding for the development of farmer preferred cassava lines resistant to pest and disease

Ruth Thompson, Emmanuel Okogbenin, Elizabeth Yaa Parkes, Marian Dorcas Quain, Priscilla Adofo Boateng*

**CSIR–Crops Research Institute (CRI), P. O. BOX 3785, Kumasi, Ghana; email: ginathompsongh@yahoo.com*

The production of cassava is hampered by biotic and abiotic factors which result in low yields. Cassava farmers, lose 48 million tonnes of fresh root, valued at US$1.4billion every year to pests, diseases and Post harvest Physiological Deterioration. Over the years, molecular markers for pest/disease resistance have been developed. It is therefore very important to use these markers in breeding programmes. The objective of the study is to identify molecular markers and use them to develop cassava lines resistant to pest and disease. The methodology includes the importation of germplasm (resistant to pest/disease) from CIAT. These would be established and evaluated. Selected materials will be planted and used in crosses with local varieties. They will also be used in participatory plant breeding in multi-locational trials. F1 populations will be used for MAS for Cassava Mosaic Disease (CMD) and Cassava Green Mite (CGM) to select elite clones for use in the breeding programme which will then be analysed for other important traits for farmers in Ghana. It is expected that, at the end of this study molecular markers for disease/pest resistance identified and cassava varieties resistant to CMD and CGM developed using MAS.

Related GCP project–SP3 Commissioned G4008.26: 'Cassava breeding Community of Practice in Africa for accelerated production and dissemination of farmer preferred cassava varieties resistant to pest and disease' (PI: Emmanuel Okogbenin, NRCRI/ CIAT)

Notes:

3.8: Genotypic variability of cowpea drought tolerance

RM Chiulele, JD Ehlers, T Close and P Roberts*

**Eduardo Mondlane University (EMU), P.O. Box 257, Maputo, Mozambique; email: rchiulele@uem.mz*

A drought experiment was conducted under field conditions during the main cropping season in 2009 (February to May) in Maputo, Mozambique to determine the variability of drought tolerance in 30 genotypes. Drought stress was applied from flowering to physiological maturity by withholding water to stressed treatment whereas the non-stressed treatment was watered regularly to field water capacity. General analysis of variance was performed on yield, yield components (number of pods per plant, number of seeds per pod and 100-seed weight) and drought tolerance indices, namely, tolerance index (TOL), mean productivity (MP), geometric mean productivity (GMP), stress intensity (SI), stress susceptibility index (SSI) and stress tolerance index (STI) followed by multivariate analysis of yield and drought tolerance indices. The results indicate that the intensity of stress was moderate (SI=0.48). However, there was significant effect of water regime, genotype and interaction between genotype and water regime for yield and yield components indicating the existence of genotypic variability of drought tolerance amongst the tested genotypes. Mean yield varied from 0.4 and 1.5t/ha with Monteiro registering the lowest yield and INIA-19F the highest yield. The genotypes FN-2-9-04, Maputo, Tete-2 e Var3A were the most tolerant to drought whereas FN-1-13-04, IT18, Bambey-21, IT82E-18 and INIA-19F were the most susceptible. Stress tolerance index seemed to be the best index for selecting genotypes regarding their drought tolerance. As a result of the study three drought tolerant and two drought susceptible genotypes were crossed in all possible combination for studying the inheritance of drought tolerance and for developing breeding populations suitable for the drought prone areas of the country and for maker-assisted selection.

Related GCP project–SP5 Commissioned G4008.43: 'Improve cowpea productivity for marginal environments in Mozambique' (PI: Rogério Chiulele, EMU)

Notes:

3.9: Evaluation of cassava F1 genotypes and progenitors resistant to Cassava Mosaic Disease (CMD) for the putative presence of the CMD2 resistant gene using molecular markers

Elizabeth Parkes, Bright Boakye Peprah, Edem Lotsu, Priscilla Boateng, Ruth Thompson and Marian Dorcas Quain*

**Crops Research Institute, P. O. Box 3785, Kumasi, Ghana*

A total of 61 F1 families for improved adaptation and CMD resistance generated from crosses of four farmer preferred cassava landraces and eight CIAT elite CMD resistant material introgressed for the CMD2 gene were evaluated for CMD resistance using four markers associated with the CMD2 gene. Four markers associated with CMD2 gene; SCAR marker RME1 (4.5cM) and three SSR markers (SSRY 28 (13.0cM), NS158 (7.1cM) and NS 169 (70cM) were used to identify genotypes with CMD2 based resistance and to assess the presence of new source of CMD resistance in the progenies. Phenotypic evaluation for CMD severity was assessed for all genotpyes. Nineteen genotypes had no marker allele associated with CMD gene. Progenies of "Dabodabo" and TME II showed resistant not conferred by CMD2 gene. Crosses with CMD susceptible parents and bulk segregant analysis may be used to identify the new gene (s) to confirm the landrace "Dabodabo" as possible new source for CMD resistance. Ranking of the F1 population based on disease scores, yield and vigour showed progenies of CR52A-25, CR 52A-4, TME11 and "Dabodabo" with best performance. The second year evaluation will confirm these preliminary results.

Related GCP project–SP5 Commissioned 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, NCRI/CIAT)

Notes:

3.10: Combining marker-assisted and farmer variety selections for *Striga* resistance in cowpea (*Vigna unguiculata* (L.) WALP)

Jean Baptiste S Tignegre, Muranaka Satoru, Jeremy T Ouedraogo, Issa Drabo, Ousmane Boukar N Moutari and Mamadou Toure*

**Institut de l'environnement et de recherches agricoles (INERA), Burkina Faso*

The research being initiated in that project aims at applying available AFLP-SCAR markers for selecting *Striga gesnerioides*-resistant sources in cowpea. To achieve this, the most prevailing two Striga races in Burkina Faso and/or Niger and Nigeria were targeted as major damaging constraints. Participatory variety selection, including farmers, researchers, and developers were conducted. Adapted cowpea resistant-lines were implemented in Burkina Faso and Nigeria in 2007 and 2008. The farmer's cowpea ideotypes were selected in field-screening and then involved in a series of backcrosses associsted with MAS to combine both *Striga* resistance and farmer's desirable traits. An attempt to validate sets of AFLP and SSR markers shows that some polymorphisms are mostly specific to the crosses genetic back ground. No marker showed polymorphisms to all combinations of crosses. Back cross populations varying from BC2F1 to BC4F4 generations and F4 self pollinated populations are being screened for further selection.

Related GCP project–SP3 Commissioned G4008.17: 'Application of marker-assisted selection for Striga resistance in cowpea (Vigna unguiculata (L.) WALP' (PI: Jean Baptiste Tignegre, INERA–Burkina Faso)

Notes:

3.11: Introgression of enhanced micronutrients and other important traits from Latin American germplasm into elite Nigerian cassava cultivars

CN Egesi, E Okogbenin, A Mbanaso, N Eke-Okoro, K Shuaibu, O Ogundapo, S Baiyeri and M Fregene*

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Cassava enriched with micronutrients presents a sustainable avenue for alleviation of the chronic condition in impoverished populations who depend on the staple. One hundred and thirty eight cassava genotypes of Latin American origin with enhanced levels of beta carotene and high protein contents were introduced introduced into Nigeria. Ninety of the introduced genotypes were micro-propagated, hardened and transferred to the field for preliminary assessment at NRCRI. The genotypes were evaluated for resistance to cassava mosaic disease (CMD) and other foliar diseases. A total of 95% of the genotypes were found to be resistant or tolerant to CMD. Selected germplasm have been used as parents in crosses with elite local Nigerian germplasm with the aim of combining useful traits in the gene pools. Two NRCRI research assistants are being supported for M.Sc. degrees and are carrying out degree – research projects in cassava molecular breeding related to project activities. The enhancement of manpower for molecular breeding in relevant breeding programmes in African NARs is very critical for the application of modern tools in agriculture for poverty alleviation.

Related GCP project–SP5 Commissioned G4007.13.02: 'Marker-aided development of nutritionally enhanced cassava for Nigeria' (PI: Chiedozie Egesi, NRCRI)

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3.12: Screening for drought tolerance in selected chickpea (*Cicer Arietinum* L.) germplasm in semi-arid areas of Kenya

PK Kimurto, BK, RK Mulwa, EK Cheruiyot, R Gangarao, S Silim, RK Varshney, and P Gaur*

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Semi arid tropics of Eastern and Southern Africa (ESA) are increasingly facing food shortages associated with frequent droughts. Growing of drought tolerant crop varieties could provide reliable solution to reducing the adverse effects caused by drought stress. Chickpea is a good alternative food-security legume crop that can since it is more drought tolerant and able to escape the effects of terminal stress common in ASAL of ESA. This study aimed at evaluating adaptability and yield performance of drought tolerant chickpea genotypes to be grown in marginal rainfall areas of Kenya. The study was conducted in two dryland sites in Kenya for one season each during the short rains (October 2008-March 2009). The trial evaluated 289 lines for drought tolerance, harvest index and yield in a lattice design with 2 replicates, spaced at 40x10cm 2m long. Results showed significant difference ($P<0.05$) in measured traits among the test genotypes. Overall, days to flowering and maturity ranged between 44-74 and 82-144 days, respectively. Mean harvest index (HI) ranged from 0.18-0.69, with mean of 0.45. Genotypes ICCV10, ICCV7272, ICCV92311, ICC3362, ICC14595 had greatest HI (0.63-0.69) and moderate grain yields (>3 tons ha-1) except ICC 3362 which had yields of 2.3 tons ha-1, which could have been associated with low 100-seed weight (14.7 gm).

Related GCP project: Focus G6007.04–TLI Objective 4: 'Improving drought tolerance in chickpeas for Africa and Asia' (PI: Rajeev Varshney, ICRISAT/GCP)

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3.13: Selection of drought-tolerant cowpea lines under several environments in Burkina Faso

Issa Drabo and Alidou Sawadogo*

**Institute de l'environnement et de recherches agricoles (INERA), Ouqgqdougou, Burkina Faso; e-mail: idrabo@yahoo.fr*

Yield losses in cowpea, Vigna unguiculata (L.) Walp due to drought and heat stress can be high despite of the fact that it is one of the most drought tolerant crop. This work aims to assess drought tolerance of early and medium cowpea varieties and to screen for drought resistance. The varieties were evaluated at Pobe-Mengao during main season at two dates of planting and at Saria during off-season under controlled irrigation. The results sow that 8 early and 8 medium lines were the most drought resistant entries at Pobé-Mengao and Saria. Correlation analysis indicated strong relationships of harvest index (IR), Threshing ratio (TR), and grains number per pod (NG/G) to yield in the terminal stress at Saria. Physiological responses to water deficit using SPAD values measurement indicate two responses of cowpea under drought stress. The first group where SPAD values remains stable under drought stress and under non stress condition. The second group where SPAD values decreases under drought stress. Results indicate specific and general adaptation of some cowpea lines.

Related GCP projects: Focus G6007.02–TLI Objective 2:'Improving cowpea productivity for marginal environment in Sub-Saharan Africa'; SP3 Commissioned: G4008.13 'Improving drought tolerance phenotyping in cowpea' (PI for both projects: Jeff Ehlers, University of California–Riverside, USA)

Notes:

3.14: Basal root architecture traits for drought and low phosphorus tolerance in common bean

Jonathan Lynch, Kathleen Brown, Stephen Beebe, Matthew Blair, Idupulapati Rao, Magalhaes Miguel, Celestina Jochua, Rowland Chirwa, James Burridge and Katy Barlow*

**Department of Horticulture, Penn State University (PSU), University Park, PA 16803, USA; e-mail: JPL4@psu.edu*

Genetic variation for root architecture has important effects on nutrient and water acquisition in stressful environments. We are investigating two root architectural traits of common bean (*Phaseolus vulgaris*); basal root whorl number (BRWN) and basal root growth angle plasticity (BRGA). Evaluating the relative utility and tradeoffs of BRWN and BRGA plasticity for water and nutrient acquisition will be useful for ideotype development. A second goal is to understand genetic control of these traits to facilitate breeding and molecular marker development. Progress to date includes field trails to assess the value of these traits for low P and drought conditions, phenotypic profiling of bean germplasm, and QTL analysis of BRWN in 2 bean RILs. The project is in early stages by results so far support the potential value f these traits in bean breeding.

Related GCP project–SP3 Competitive G3008.07: 'Basal root architecture and drought tolerance in common bean' (PI: Jonathan Lynch, PSU).

Notes:

3.15: QTL validation in introgression line populations of common wheat

Ruilian Jing, Wenliang Chen, Qian Ren, Xiaoping Chang and Xinguo Mao*

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

One of the challenges for marker assisted selection (MAS) is that majority of QTL involved significant additive and epistatic effects with the interactions of QTLs and genetic backgrounds, which badly impact the MAS effect. Seven introgression line (IL) populations (BC3F4) derived from a common recurrent parent Jinmai 47, an elite Chinese common wheat cultivar, and seven donor parents, including five Chinese DT cultivars and two European cultivars with DT and good quality were used to validate the DT QTL identified from a doubled haploid (DH) population, which was derived from a cross of two Chinese cultivars Hanxuan 10 and Lumai 14. A total of four QTL hot regions for yield components and developmental dynamics of plant height were detected on chromosome 2B, 3B, 4B and 6A in all seven introgression line populations, respectively. All four regions are consistent with that detected in the DH population, but more than half of the QTL flanking markers differ from that in DH, moreover most QTL hot regions identified in the DH population could be only confirmed in one or several IL populations. The QTL hot regions shared by multi-populations with different genetic backgrounds are helpful for using MAS in wheat molecular breeding.

Related GCP project–SP3 Commissioned G4007.06: 'Integrating marker-assisted selection into the conventional breeding procedure for improvement of wheat (Triticum aestivum L.) in the drought-prone areas of Northern China' (PI: Ruilian Jing, CAAS).

Notes:

3.16: Linking genetic diversity with phenotype for drought tolerance traits through molecular and physiological characterisation of a diverse reference collection of chickpea

Lakshmanan Krishnamurthy, Junichi Kashiwagi, Rajeev Kumar Varshney, Hari D Upadhyaya, Satoshi Tobita, Osamu Ito and MS Sheshshayee*

**International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India; e-mail: L.Krishnamurthy@cgiar.org*

Drought is one of the major constraints to the productivity of chickpea. The productivity under drought is determined by transpiration, transpiration efficiency (TE) and harvest index. This research project is aimed at enhancing the productivity of chickpea under drought by improving the component TE through $\Delta^{13}C$ while improvement efforts on other components are already in progress. The objective of this project is to improve the drought tolerance of chickpea via marker assisted selection for TE.

Field experiments were conducted both at ICRISAT, Patancheru and UAS, Bangalore for assessing the variation in phenology, yield and its components, $\Delta^{13}C$, SLA and SCMR of the reference set of chickpea germplasm. The yield and yield components data as well as major part of the $\Delta^{13}C$ from ICRISAT, Patancheru is available now, but such data collection is once again being planned during Oct 2009- Feb 2010 at UAS, Bangalore. The DArT array developed by DArT Pty. Ltd., turned out to be monomorphic for the cultivated chickpea germplasm, leading to the array being further expanded with 7680 new clones. The genotyping result is expected soon. Understanding the relationship of TE with drought yield and identification of DArT markers for drought-related traits would remain as the ultimate goals of this project.

Related GCP project–SP3 Commissioned G4008.12: 'Linking genetic diversity with phenotype for drought tolerance traits through molecular and physiological characterisation of a diverse reference collection of chickpea' (PI: L Krishnamurthy, ICRISAT).

Notes:

3.17: Molecular breeding of Pup1-rice varieties and candidate gene characterisation

Sigrid Heuer, Matthias Wissuwa and Masdiar Bustamam*

**International Rice Research Institute (IRRI), Philippines;*
e-mail: sheuer@cgiar.org

The major QTL *Phosphate Uptake 1* (*Pup1*) confers tolerance of P deficiency by a yet unidentified mechanism. The *Pup1* genomic region was sequenced in the tolerant donor parent Kasalath and six putative genes (fatty acid α-dioxygenase, unknown protein, dirigent, hypothetical protein, protein kinase, Zn-knuckle) have been short listed for in-depth analyses including transgenic approaches (35S; RNAi). In the centre of attention is currently the protein kinase gene *PupK46* which is specifically conserved in upland rice and might be involved in P signaling. Allelic sequencing revealed a tolerant-specific allele for the dirigent gene (*PupK20*). The putative function of *PupK20* was addressed by quantifying the lignin content in drought-stressed roots showing that lignification is a ubiquitous drought response which is absent in plants grown hydroponically with PEG-induced water deficit. Based on the *Pup1* sequence information, molecular markers were developed that target genes that are partially conserved in the Nipponbare reference genome (co-dominant markers) as well as Kasalath-specific genes that are located in a large insertion-deletion (INDEL) region that is not present in Nipponbare genome (dominant markers). The development of *Pup1* rice varieties by marker assisted backcrossing (MABC) is at an advanced stage and first field data are being analysed.

Related projects–SP2 Competitive G3008.04: 'Drought from different perspective: Improved tolerance through phosphorus acquisition'; SP3 Commissioned G4008.41: 'Application and validation of the major QTL Phosphate uptake 1 (Pup1)'; (PI for both projects: Sigrid Heuer, IRRI).

Notes:

3.18: Field drought screening technique for rainfed lowland rice

Boonrat Jongdee, Grienggrai Pantuwan, Shu Fukai, Phoumi Inthapanya and Ouk Makara*

**Bureau of Rice Research and Development (BRRD), Rice Department, Thailand; e-mail: boonrat@brrd.in.th*

Previously, the field phenotyping technique was mostly conducted under 2 conditions, irrigated flood and drought conditions. For drought condition, rice was grown under flooded condition then water was drained out when drought stress was to be imposed. We now consider there are 3 growing conditions; 1) irrigated flooded condition where soil is anaerobic, 2) irrigated un-flooded aerobic soil conditions, and 3) drought conditions. The key point is that growing condition changes from anaerobic to aerobic conditions causing changes in soil chemical properties such as decrease in soil pH and reduced available phosphorus in the soil. Genotypes with well adaptation to flooded (anaerobic) condition may not adapt well to aerobic condition. Thus, poor performance of this type of genotypes under drought condition may be because of their specific adaptation to anaerobic soil condition and lack of adaptation to aerobic conditions rather than the lack of adaptation to drought conditions as such. Thus, one of our hypotheses for this work is that well adapted genotypes in drought-prone rainfed lowland rice require traits that contribute to well adaptation to both anaerobic and aerobic soil conditions as well as possessing appropriate drought tolerance characters.

Related GCP project–SP4 Competitive G3008.09: 'Breeding drought tolerance for rainfed lowland rice in the Mekong region' (PI: Boonrat Jongdee, BRRD).

Notes:

3.19: Validation of the effect of the gene for tolerance to Al toxicity in sorghum, *Alt*$_{SB}$, using isogenic lines and hybrids in field and nutrient solution experiments

Robert E Schaffert, Lidianne A Silva, Vera MC Alves and Jurandir V Magalhaes*

**Embrapa Maize and Sorghum reschaffert@hotmail.com and jurandir@cnpms.embrapa.br*

Experiments were conducted where near isogenic genotypes of sorghum were evaluated as seedlings in nutrient solution and at an aluminium phenotyping site to quantify the effect of the *Alt*$_{SB}$ gene. The experiment consisted of two pair of cytoplasmic male sterile female near isogenic lines (NILs) contrasting for *Alt*$_{SB}$ and four tester restorer R-lines, three susceptible to aluminium toxicity and one tolerant to aluminium toxicity. The seven lines and sixteen hybrids were evaluated as seedlings in nutrient solution with five levels of aluminium toxicity (0. 11, 20, 27 and 39 µM active aluminium). All sources of Al tolerance were from the sorghum line SC283 with the *Alt*$_{SB}$ gene. Root growth was recorded at zero, three, five and seven days in nutrient solution with Al. The same genotypes were evaluated in replicated field trials with three levels of aluminium saturation in the top 20 cm of the soil; 0, 40, and 60%. Significant differences were observed between the NILs and near isogenic hybrids (NIHs) for the seedling root parameters in nutrient solution and grain yield in field trials. Yield advantages of more than one ton per hectare were observed for the NIHs indicating the significant impact of the gene *Alt*$_{SB}$.

Related GCP project–SP3 Commissioned 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:

3.20: Molecular cytogenetic identification, physical mapping and drought tolerance of wheat-barley introgression lines

Márta Molnár-Láng, Éva Szakács, István Molnár, András Cseh, Adél Sepsi, Klaudia Kruppa, Sándor Dulai, Borbála Hoffman and Ruilian Jing*

Agricultural Research Institute of the Hungarian Academy of Sciences (ARI–HAS), 2462 Martonvásár, Brunszvik u. 2, Hungary; molnarm@mail.mgki.hu

Barley is a potential gene source for wheat improvement, because of its good drought tolerance, earliness and nutritional parameters. Wheat-barley introgression lines were developed in Martonvásár, and these are used to determine how the added barley chromosomes (segments) influence various agronomic traits in wheat. New wheat/barley disomic addition line set was developed from the Asakaze komugi (Japanese wheat) × Manas (Ukrainan six-rowed winter barley) hybrid combination. The presence of the barley chromosomes in wheat background was demonstrated using genomic in situ hybridization (GISH). Identification of the individual chromosomes were carried out by fluorescence in situ hybridization (FISH) with the help of repetitive DNA probes (HvT01, GAA, Afa family, pTa71, pSc119.2) and with SSR markers. New wheat-barley translocation lines were detected with GISH. Physical mapping of wheat and barley SSR markers was carried out on wheat 7D and barley 7H chromosomes with the help of wheat/barley translocation lines. The drought tolerance of the wheat-barley introgression lines was studied under rain shelter in the field in three different locations (Martonvásár, Keszthely, Hungary; Beijing, China). Conclusions abut the drought tolerance of the different lines can be made after several years observations.

Related GCP project: SP3 Commissioned G4007.23: 'Field evaluation of wheat-barley introgression lines under different water regimes' (PI: Márta Molnár-Láng, ARI–HAS)

Notes:

Theme 4:
Support services and enabling delivery

4.1: Statistical support for the design and data analysis of GCP projects

Marcos Malosetti, Joost van Heerwaarden, Hans Jansen and Fred van Eeuwijk*

**Biometris, Wageningen University and Research Centre (WUR), Wageningen, The Netherlands; email: marcos.malosetti@wur.nl*

This project aims to provide statistical support to GCP scientists on issues that ranges from experimental design to different types of data analyses (field and lab data analysis, diversity analysis, QTL mapping, and association mapping). Project's major activities are: 1) development of training material, 2) delivery of training courses, and 3) consultancy with GCP researchers on a one-to-one basis. Two workshops were delivered in 2009; the first one held at CIAT headquarters in Cali, Colombia (January 26-30, 2009), was organised to provide statistical support to beneficiaries of the Genotyping Support Services (GSS). The second workshop was organised by SP5 to provide statistical support to researchers working within the framework of the project *Improving tropical legume productivity for marginal environments in Africa* (venue: IAMZ, Mediterranean Agronomic Institute of Zaragoza, Spain, June 29th to July 3rd, 2009). Training material has been compiled from these events, including issues on data quality control, experimental design, diversity analysis, molecular maps construction, and theory on QTL mapping and association mapping. This material plus further elaborated material is (and will be) available in internet. With respect to consultancy, we have been addressed with questions related to genetic map construction, QTL and association mapping.

Related GCP project–SP4 Commissioned G4006.35: 'Statistical support for the design and data analysis of GCP projects' (PI: Marcos Malosetti, WUR).

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4.2: Drought stress profiling for improved phenotyping: characterising cultivar trial sites

Nirman Shrestha, Sam Geerts, Glenn Hyman and Dirk Raes*

**Faculty of Bioscience Engineering, Division Soil and Water Management, Katholieke Universiteit Leuven (KUL), Celestijnenlaan 200 E, 3001 Heverlee, Belgium; email: Nirman.shrestha@gmail.com*

For an improved phenotyping of the crop varieties that perform under drought, improved drought stress profiling for specific crops is necessary. Monthly climatic data of different locations around the world were extracted using the CLIMWAT and FAOClim2 software developed by FAO. Frequency analysis was performed on the extracted climatic data for each location using RAINBOW software and monthly rainfall and reference evapotranspiration was calculated for dry, normal and wet years. Using the statistically analysed climatic data, simulations were performed for different crops common to the region to calculate the soil water balance during the crop growing period using the BUDGET soil water balance software. The crop specific simulations were performed for three time frames each starting two weeks apart within the season. 1 - ETa/ETc was used as indicator of water stress, where ETa is the actual evapotranspiration and ETc is the crop evapotranspiration under the same conditions but for non-limiting water conditions. The water stress profiles were calculated for 9 different crops and 17 different regions around the world and sites were categorised based on similarity in mid season drought stress. They can be the basis for testing promising drought tolerant varieties in developing countries.

Related GCP project SP3 Commissioned G4008.34: 'Environmental assessment for phenotyping network' (PI: Glenn Hyman, CIAT)

Notes:

4.3: Agropolis Resource Center for Crop Conservation, Adaptation and Diversity (ARCAD): a new open multi-function platform devoted to plant agrobiodiversity

Jean-Louis Pham, Jean-Pierre Labouisse, Nour Ahmadi, Jacques David, Florent Engelmann, Alain Ghesquière, Sylvain Glémin, Christian Leclerc, Jean-Louis Noyer, Jean-Marie Prosperi, Ange-Marie Risterucci, Joëlle Ronfort, Pierre Roumet, Manuel Ruiz, Sylvain Santoni, Marc Seguin, Patrice This, Anne-Céline Thuillet and Yves Vigouroux*

**Agropolis Foundation, Montpellier, France; e-mail: arcad@agropolis.fr*

ARCAD is an initiative supported by Agropolis Fondation and the Region Languedoc Roussillon (France). ARCAD aims at setting up a new open multi-function (conservation, research and training) platform devoted to the assessment and better use of plant agrobiodiversity in Mediterranean and tropical regions. The programme's scientific agenda will prioritise the study of history and patterns of crop domestication and adaptation as well as the analysis of key parameters underpinning adaptation and diversity structure, at various time scales, through studies of evolutionary genomics, population genetics and social sciences. The research will focus on Population comparative genomics, Crop adaptation to climate change and Cereal crops in Africa. These activities will be complemented with technological and methodological components for the conservation (DNA bank, cryopreservation) and analysis (bioinformatics, linkage disequilibrium) of crop diversity. A major objective of the programme is also to set up a demand-oriented capacity building platform, based upon the educational facilities offered by universities in Montpellier and the development of specific training modules. The ARCAD programme is jointly developed by CIRAD, INRA, IRD, Montpellier SupAgro and University of Montpellier 2, in partnership with numerous South and international institutions. As an open platform, ARCAD will continuously seek the involvement of interested partners.

Related GCP project: Not applicable

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4.4: The GCP phenotyping template wizard

Robert Koebner and Warren Vincent E Constantino*

**CropGen International (www.cropgeninternational.com);*
email: mockbeggars@gmail.com

We are presenting a working version of the phenotyping data template. The purpose of the template is to establish a platform to store phenotypic data emerging from GCP projects. We wish to both encourage the standardisation of phenotyping methods (without seeking to restrict the initiative of any individual project team), and to house the resulting data in a way which will facilitate meta-analyses. We are aiming to provide a simple way for PIs to capture their phenotypic observations along with all associated environmental data and experimental methods required to make them interpretable, whilst assuring compatibility with the GCP domain models and crop information systems such as ICIS. The wizard will be presented both in the form of this poster and verbally through the aid of an animated video.

> *Related GCP project–SP4 Commissioned G4008.31: 'Upgrading the quality and utility of GCP phenotyping data through the development of a data input template to facilitate the storage of data' (PI: Robert Koebner, CropGen International).*

Notes:

4.5: Organisation of a workshop entitled 'Reference sets of food crop germplasm for international collaboration', organised in Montpellier, November 13–17, 2008

Jean-Christophe Glaszmann, M Carmen de Vicente and Claire Billot*

**Agropolis–CIRAD, France; email: jean-christophe.glaszmann@cirad.fr*

Notes:

71 participants from 28 countries, including crop specialists, breeders and germplasm managers have exchanged their background in term of definition and use of crop reference germplasm, through oral presentations and/or posters, and structured as communications and brainstorming sessions (http://www.generationcp.org/sp5/?da=08137827). The main conclusions are:

- The GCP approach was affirmed in exploring, evaluating and using germplasm diversity, in defining reference sets on the principles that all GCP products must be delivered to users.
- The expectation extends to related initiatives in the System-Wide Genetic Resources Program (SGRP) of the CGIAR, the Global Crop Diversity Trust and the Global Partnership Initiative for Plant Breeding Capacity Building (GIPB). GCP-derived reference sets can play a prominent role provided that there is clarity on political availability of the resource and the attached data by placing them under the Multi-Lateral System (web system being put in place by the SGRP and Bioversity), and that research continues on their use as an entry to broader collections.
- Information has been shared about the availability of reference sets, their compilation and status, exhibiting the broad diversity of situations and limitations that need to be overcome (representation, choice and justification of methodology, data quality, traceability, availability of information…)

Related GCP project–SP1/SP5 Commissioned G4008.40: 'Workshop on "Reference sets of food crop germplasm for international collaboration"' (PIs: MC de Vicente and JC Glaszmann, GCP and Agropolis–CIRAD/GCP, respectively)

4.6: HaploPhyle: a graphical haplotype network in the light of external data

Claire Billot, Manuel Ruiz*, Xavier Perrier, Jean-François Rami and Reinhard Simon*

**Agropolis–CIRAD, France; email:claire.billot@cirad.fr; manuel.ruiz@cirad.fr*

Genetic diversity assessment through genotyping is gaining much resolution and currently produces now large quantity of DNA sequences or chains of tightly linked markers. The close linkage between the polymorphisms observed is likely to leave the patterns little affected by recombination. Therefore patterns evolve less quickly (than with unlinked or loosely linked makers) and better reflect past situations. In the particular context of crops, the past comprises a major event, domestication, which generally involved strong genetic bottlenecks. Pattern analysis of polymorphisms can lead to identification of predominant haplotypes, and inference of ancestral haplotypes vs recombinant haplotypes. Haplotype analysis is likely to enable breakthroughs in crop germplasm analysis. This project provides the community with new software for analysis of genotyping data, HaploPhyle (pipeline version 1.0, haplophyle.cirad.fr, code source freely available). This Web based pipeline includes haplotype definition, haplotype network analysis and connexion with external data, such as geographic origin, evolutionary history or genetic group assessment. Visualisation at once of the haplotypes ordered according to a tree can be performed with a R function.

Related GCP project–SP4 Commissioned G4008.22: 'Methodology development for reconstruction of Genealogies based on Haplotypes related to geographic patterns (HaploPhyle: graphical haplotype network in the light of external data)' (PIs: Claire Billot and Manuel Ruiz, Agropolis–CIRAD)

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4.7: Extension of the GCP stress gene catalogue using the maize genome sequence information

Genevieve Mae Aquino, Trushar Shah, Ramil Mauleon, Victor Jun Ulat, Samart Wanchana, Supat Thongjeau, Jeffrey Detras, Frances Nikki Borja, Franjel Consolacion, Carlos Ortiz and Guy Davenport*

**IRRI–CIMMYT Crop Research Informatics Laboratory (CRIL), Philippines; email: g.aquino@cgiar.org*

The Generation Challenge Programme comparative plant stress-responsive gene catalogue (http://dayhoff.generationcp.org) allows scientists to elucidate orthologous and paralogous relationships between plant genes that may be involved in abiotic stresses. With the availability of the accessioned golden path (AGP) and the filtered gene sets of the maize genome sequence (http://www.maizesequence.org), we have extended the existing catalogue to include the maize sequence information by using the analysis pipeline outlined in the original study. In the process, we have identified around 500 of the original Uniprot seed sequences that have been updated. This work identifies orthologues of evidence-based stress genes in maize, updates the original Dayhoff database based on current Uniprot gene structural and functional annotation, and improves the web interface of the online resource.

Related GCP project–SP4 Commissioned G4008.32: 'Promotion of Data Quality Management in genotyping laboratories, development of crop ontologies, comparative genomics for drought tolerance and evaluation and promotion of selection indices' (PI: Guy Davenport, CIMMYT).

Notes:

4.8: Future sustainable HPC Grid Computing platforms

*Anthony Collins**

**International Potato Center (CIP), Lima, Peru;*
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HPC application support within the GCP Informatics Platform is focusing on:

- Sustainable HPC options beyond the existing GCP systems - BOINC and EELA Grid systems.
- Porting of R and Structure ported to alternative platforms
- An upgraded HPC website providing
  - o Improved documentation and use case support for the GCP community applications
  - o New processing options beyond the GCP systems: BOINC and EELA Grids.
  - o Improved HPC task performance for collaborators performing data analysis on SP1, 2 and 3.
- Development of a programmatic access to the programme ***Structure***, running as a Grid resource, integrated and complying with existing GCP Platform APIs.

Related GCP project–SP4 Commissioned G4005.27: 'High Performance Computing facilities for the GenerationCP' (PI: Anthony Collins, CIP), now included within G4006.16: 'Development of an Integrated GCP Informatics Platform' (PI: Martin Senger, IRRI).

Notes:

4.9: The Crop Ontology: the source for maize, wheat, chickpea, sorghum, *Musa*, potato and rice trait information

Rosemary Shrestha, Ramil Mauleon, Reinhard Simon, Jayashree Balaji, Stephanie Channelière, Adriana Alercia, Martin Senger, Kevin Manansala, Thomas Metz, Guy Davenport, Richard Bruskiewich, Graham McLaren and Elizabeth Arnaud*

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The Crop Ontology (CO) developed by crop teams scientists can be browsed using the new GCP ontology browser (http://ontology.grinfo.net/ontology-lookup/). The current version of the CO describes traits for chickpea, maize, Musa, potato, rice, sorghum and wheat at http://cropforge.org/projects/gcpontology/. To advance knowledge of the data-curation process using a controlled vocabulary, the CO team organised a meeting at Bioversity, Italy. Collaboration was identified with experts from FAO and Cornell University for AGROVOC, Thai Rice Ontology, Plant Ontology Consortium and Maize GDB. This phase of the project is examining the application of the crop ontology and integration into the International Crop Information System (ICIS) and other crop databases. New trait names for chickpea and sorghum were submitted to the Plant Ontology Consortium. The *Musa* ontology for plant structure was validated by botanists. The CIP team is interacting with SOL Genomics on potato ontology. The wheat and maize team has begun curation and annotation using the International Wheat Information System (IWIS) and International Maize Information System (IMIS). The rice team is working along with the software team on other applications such as ontology mining using the MS Word 2007 ontology add-in and Terminizer, software for assisted detection of ontological terms (http://terminizer.org/).

Related GCP project–S4 Commissioned G4009.03: 'Development of data standards and community of practice enabling the capture of and access to Generation Challenge Programme quality data sets' (PI: Elizabeth Arnaud, Bioversity).

Notes:

4.10: Development of an integrated informatics platform

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The GCP platform was developed to meet the challenges of data, computational resource, and software interoperability and integration across a globally distributed consortium of partners; hosting a diversity of legacy databases; generating large, diverse high throughput data sets; and applying a diversity of analytical tools and methodology to answer GCP research questions. The platform consists of the independent domain model, ontology, and software components that together provide end-user oriented environment. The poster shows several applications and integrating tools, such as GCP web query and display application ("Zeus"), GCP Ontology browser, standalone molecular breeding components MBDT and MOSEL, GCP Central Registry accession passport data and registry metadata browser, GenDiversity web application, and tools accessing computational grid resources.

Related GCP project–SP4 Commissioned G4006.16: 'Development of an Integrated GCP Informatics Platform' (PI: Martin Senger, IRRI)

Notes:

4.11: Further development and support for use of iMAS by NARS and the other user communities

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The identification and application of trait-linked markers involves several computational processes that normally need to be executed through a number of different software. The iMAS system integrates a number of such open-source computing tools for marker-aided research and breeding.

In the present stable release (v.1.8) several GUI modifications within phenotyping, linkage mapping and QTL analysis modules were carried out to make several analyses easier. Phenotyping module was redesigned to enable user to summarise biometric analysis in a much easier fashion. Linkage Map building module was extended to use multiple populations to build consensus map.

QTL mapping module now works with multi-environment data. Integration of simulation system QUGene with iMAS is also under progress, in which the creation of input file for simulation system is being discussed. Integration with CMTV has been implemented successfully and accordingly, online decision guidelines and user manual has been updated.

iMAS setup file has also been modified for easier installation with less dependencies . iMAS has been used in several training programmes to NARS and other partners. In addition to this a final debugging workshop has been scheduled in August, 2009, which will be followed by a final release workshop in December.

Related GCP project–SP4 Commissioned G4007.11: 'Further development and support for use of iMAS by NARS and other user communities' (PI: Jayashree Balaji, ICRISAT, until October 2008; Abhishek Rathore, ICRISAT, effective October 2008).

Notes:

4.12: Support to GCP scientists regarding issues related to bioinformatics and data handling

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In 2009 the SP4 helpdesk facility, as being set up in 2008 to support GCP scientist regarding issues related to bioinformatics, biometry and data handling, continued its operation. The expert database, functioning as the backbone of the helpdesk, allowing targeted identification of experts, was updated. This helpdesk can be reached at sp4helpdesk@generationcp.org

The SP4 bioinformatics portal was restructured to offer easier access to, and more information on GCP SP4 products and services. It aims at guiding users via short texts to the information they are looking for. For this purpose it is organised in thematic areas:

- Access to high quality data, including the GCP web services and the Central Registry, complemented with data quality subjects such as quality assurance and improvement, quality management and standardisation
- Analytical tools and facilities, including products and services in the field of genomics, breeding and diversity studies. This section also includes information of interest for SP4 software developers.
- Support to GCP scientists, giving an overview on where to get help, and where to find courses and training materials.

The portal is accessible via the SP4 section of GCP website.

Related GCP project–SP4 Commissioned G4006.17: 'GCP quality management and data quality improvement' (PI: Theo van Hintum, WUR).

Notes:

4.13: The Generation Challenge Programme Central Registry and its Helpdesk

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The Central Registry, operational since November 2005, provides the GCP with a facility where datasets can be registered, stored and shared with the entire GCP community and beyond. An extensive set of quality checks were ran for template, a quantification of the quality of the data and a process is to be defined for interaction with the Central Registry and the PIs. The helpdesk has a new mail address to collect the reports on automatic validation is: gcpcr.validation@generationcp.org. 33 Principal Investigators of the five Subprogrammes were contacted in the process of data chasing. Researchers were assisted to select the correct data templates, and received personalised guidance through the data set upload procedure on the Central Registry. An overview of the validation reports was created. Datasets will be made available via web-services allowing GCP middleware applications to search the registry using metadata.

> *Related GCP project–S4 Commissioned G4009.03: 'Development of data standards and community of practice enabling the capture of and access to Generation Challenge Programme quality data sets' (PI: Elizabeth Arnaud, Bioversity).*

Notes:

4.14: Assessment of NGS assembly/analysis tools for SNP discovery

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Next generation sequencing (NGS) methods have the capacity to accelerate acquisition of genomic resources through the generation of gigabases of sequence information in an exceedingly short time. Several SP2 projects are beginning to use NGS technologies in several (also in so called orphan) crops to generate EST and SNP marker resources to facilitate molecular breeding in these crops. NGS methods however generate a deluge of data; the shorter read lengths require considerable bioinformatics effort in assembly. With an objective of identification and optimization of analytical tools and approaches, as an example, Solexa datasets generated from two genotypes was used with three NGS analysis tools namely Alpheus, MAQ and NOVOAlign. A varying number of SNPs (922 to 1632) were identified, of which only 176 SNPs (in 163 contigs) were common while several hundred SNPs identified were specific to a particular tool. SNPs identified uniquely to a tool or common to two or all three tools are presently being validated to assess the potential as well as methodology of tools for SNP discovery from NGS data in the species without a reference genome. In parallel, a NGS Analysis pipeline is being developed so that multiple applications can be executed at a single platform.

Related GCP project–SP4 Commissioned G4009.04: 'Data analysis support for existing projects in sp2 with emphasis on analysis of next generation sequencing data' (PI: Rajeev Varshney, ICRISAT).

Notes:

4.15: Interactive Resource Center & Helpdesk – now on Facebook!

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The Interactive Resource Center (http://irc.igd.cornell.edu/) is a support tool for scientists worldwide, with a particular focus on marker assisted plant breeding and genetic diversity assessment. It includes resources such as protocols, tutorials, funding opportunities, learning modules, literature, news, etc. Contact lists of sorghum and millet researchers are available (others underway). Also posted are links to journals, the African Molecular Marker Network, and GCP resources. A 'helpdesk' answers scientists' questions with the help of a volunteer team (specializing in molecular markers, plant breeding, genetic diversity, etc.). Recently added is a list of sources of laboratory supplies (with links to regional representatives), FAQ, info about the Helpdesk Team, and a DNA extraction troubleshooting page. The number of visitors to the site has increased every year, with more than 4,000 unique visitors to the site this year. Site visitors have been from all around the globe but particularly from Africa. The IRC is now on Facebook! Facebook is an online social networking site. Register (free) and look for the Resource Center for Global Plant Scientists group. This will complement the Resource Center website and enable members to have discussions, post notes, and more.

Related GCP project: G4005.63: 'Interactive Resource Center & Helpdesk' (PI: Theresa Fulton, Cornell University).

Notes:

4.16: Assessment of the capacity to develop and adopt GCP technologies in five case study countries

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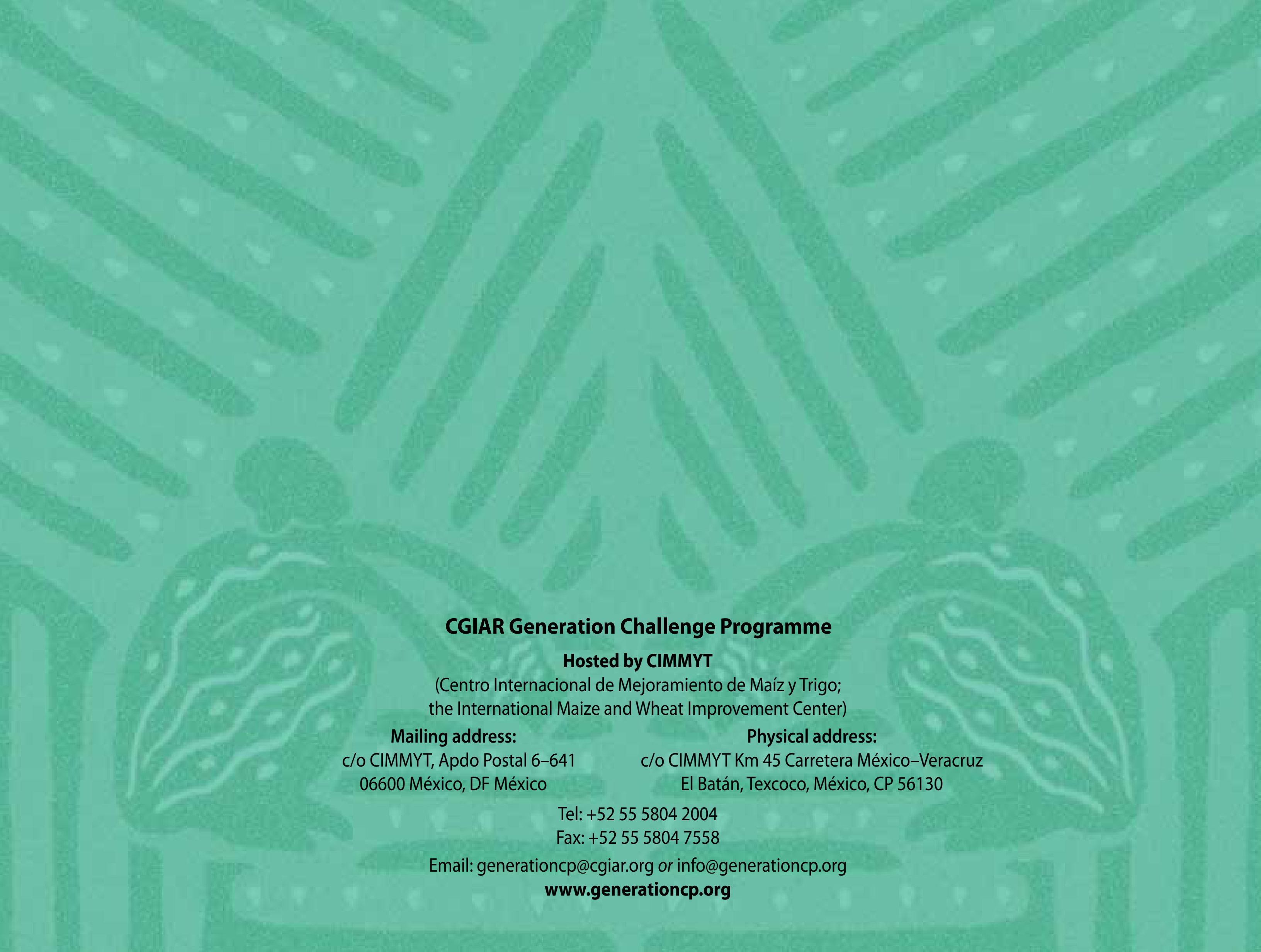
Notes:

Surveys are currently being implemented in five case study countries of relevance to GCP (Burkina Faso, Mali, Nigeria, Tanzania, and Indonesia). While drought resistance is the primary focus, GCP is also targeting soil fertility in Indonesia. The surveys involve participation by NARS, seed companies, ministries of agriculture, universities, farmer associations, and NGOs. Three survey instruments (including 50 indicators) were designed during a planning design workshop held in Toronto, Canada from June 8th – 10th, 2009. The survey instruments will be completed through research, expert sources, and focus groups, in order to provide evidence of the capacities of: crop breeding programmes to take on and further develop GCP technologies; seed systems and extension services to facilitate the multiplication, and dissemination of improved varieties; and households and enabling environments to facilitate widespread, successful adoption of locally-adapted GCP-based varieties. The findings of the survey will be cross-checked with other country and commodity data sources including, among others, value of production (IFPRI), agricultural research investments and human resources statistics (ASTI), and GIS data and maps (CIAT), with the aim of providing new methods, databases and tools to support future capacity assessments in other countries of where GCP technologies might be further developed and applied.

Related GCP project–SP5 Commissioned G4008.24: 'From attractiveness to feasibility: a strategic assessment of the capacity to develop and adopt GCP technologies' (PI: Stanley Wood, IFPRI)



CGIAR Generation Challenge Programme

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