2008 Annual Research Meeting
16–20 September 2008
Bangkok, Thailand

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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Correct Citation: CGIAR Generation Challenge Programme, 2008. 2008 Annual Research Meeting poster abstracts. Texcoco, Mexico: Generation Challenge Programme.

Editorial note: Abstracts are published as presented by the authors, except for abstracts that extended beyond the set word limit where text beyond this point has been omitted, indicated by continuation dots/suspension points (...)

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Theme 1:

Exploiting allelic diversity

1.1: Comparing the GCP SSR data sets regarding the ability to describe population structure: some methodological aspects

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Notes:

The quality of the SSR data sets as available on the GCP Central Registry has many aspects. Apart from obvious elements, such as interpretability and endorsement (confirmation to the expected format) there is the complicated aspect of the ability of the dataset to describe the structure of the population genotyped. This ability is determined by a number of factors such as the number of markers, the reliability of the scores and finally the level of population structure. The resultant is quantified with the Data Resolution (DR).

Comparison of the DR of the GCP SSR data sets showed that the DR varied widely, also when the number of markers is taken into account. The population structure was quantified based on the standard deviation of all pair wise distances. This value appeared, as expected, to be associated with the value of DR. It appeared that often resolution was lost due to poor binning of the bands. To resolve this issue a new distance measure was created that allowed some degree of error in the size estimation of the bands, and thus the binning. Use of this measure appeared to improve the DR of datasets only in case of low to intermediate DR.

Related GCP project: SP4 Commissioned G4006.17—GCP quality management and data quality improvement

1.2: Comparison of the DR of the GCP SSR data sets showed that the DR varied widely, also when the number of markers is taken into account

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Notes:

The ADOC project aims to characterise allelic diversity at orthologous loci of candidate genes for drought tolerance in seven GCP crops (rice, barley, sorghum, bean, chickpea, cassava and potato), working on reference collections of around 300 accessions. Six gene families (ERECTA, DREB, SS, SPS, ASR and VIN) were selected as an initial subset. From 7 (bean) to 20 (rice) different genes were targeted per crop, and from 6 (DREB) to 24 (SuSy) genes across species in each gene family. In all crops, population structure influence partially haplotype patterns. Different patterns and intensity of sequence diversity have been found, within gene families and between crops, but in some cases orthologous genes presented similar diversity patterns. For a few genes, computation of a sequence-based neutrality test suggests selection events acting at the species and/or subgroup level. Getting hold of allelic differences in candidate genes of our target crops, will allow researchers and breeders to investigate correlations between phenotypic data and the SNP data obtained by this project. Furthermore, the SNP database produced by this project will serve as resource for designing markers for favorable candidate gene alleles, and use relevant SNPs in selection programmes.

Related GCP project—SP1 Commissioned G4006.02: A dataset on allele diversity at orthologous candidate genes in GCP crops (ADOC)

1.3: A drought phenotyping network in contrasting Brazilian environment targets

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A good environment characterisation is necessary for the drought process studies, requiring registration and acquisition of soil, water, plants, and atmosphere factors and understanding how these factors interact with plants genotypes performance under water constraint condition. Embrapa's researchers have established and described the procedures and practices to develop a "drought phenotyping network" in contrasting brazilian environment targets for drought tolerance investigation in cereals and legumes, by means of selecting, installing, and characterizing seven "Drought Tolerance Phenotyping Centers", according to geographical coordinates, elevation, climatic condition, and soil physical and chemical properties. The work emphasised the protocols, methods, and techniques for water stress levels control and management, the description of genetic materials and traits selected and evaluated, the structure and maintenance of a database, and the modelling to better understand the effects of plants genetic and environmental (GxE) interactions for grain yield, identifying and establishing the causes which will result ultimately on genotypes yield reduction due to a controlled water stress pressure selection. Genetic and environmental interactions are largely a result of phenotypic plasticity in terms of adaptive morphogenesis, physiology, and phenology, resulted from the different water regimes utilised, taking into account soils, plants, and canopy surface atmosphere water dynamics status.

Related GCP project—SP1 Commissioned G4005.06: Supporting emergence or reference drought tolerance phenotyping centers - Drought phenotyping network (DPN)

Notes:

1.4: Phenotyping reference sets for tracking drought tolerance alleles from large collections: application to maize

Maria Zaharieva, Ciro Sanchez, Hugo Lopez, Mijail Javier, Claudia Bedoya, Marilyn Warburton, Suketoshi Taba, Mateo Vargas, Jose-Luis Araus, Peter Stamp, Andreas Hund, Rainer Messmer, François Tardieu, Claude Welcker and James Gethi*

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A more efficient use of genetic diversity is essential to address the challenges faced by maize production in developing countries. New beneficial genetic variation may be identified using molecular markers and precise phenotyping, allowing priority traits to be introgressed into local background. A reference set of 240 maize inbred lines, established from a composite collection of 987 lines was sown in winter 2007-2008 at the Tlaltizapan CIMMYT station (Mexico) for seed multiplication and preliminary observations. 60 un-adapted accessions did not produce seeds. The remaining 180 accessions were characterised for earliness to facilitate further drought phenotyping. Leaf tissue was collected from one plant of each accession for DNA extraction. Seeds and DNA of the «founder» plants will be made available for further research activities. In summer 2008, single hybrids were generated by crossing the lines with CML 312, a tester with high combining ability. Inbred lines and hybrids will be phenotyped in field conditions at Tlaltizapan and Kiboko (Kenya) using drought tolerance secondary traits. Variation in root morphology and leaf elongation rate will be also assessed under controlled conditions. Integration of accumulated information will allow the detection of associations between molecular polymorphisms and important agronomic features.

Related GCP project—SP1 Commissioned G4008.33: Drought tolerance phenotyping of the GCP maize inbred line reference set

Notes:

1.5: Molecular characterisation of a sub-collection of African rice (*Oryza glaberrima*)

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Notes:

Oryza glaberrima constitutes a great reservoir of useful genes for the improvement of elite lines. A tangible example is the development of NERICA rice from glaberrima accessions. WARDA's germplasm collection consisting of *O. glaberrima* is about 1,200 accessions. To fully exploit the natural genetic variation of this collection, the genetic diversity of the material needs to be assessed. From germplasm selected in the project, a subset of *O. glaberrima* accessions was constituted based on the availability of full passport data and seeds. Thirty labeled SSR markers well dispersed on the rice genetic map were used to genotype the accessions including a few sativa and wild outgroup. The analysis showed a total of 256 alleles and a mean PIC value of 0.5. On average, 8.5 alleles/locus were detected ranging from 3 to 19 alleles/locus. Three main genetic groups were identified. One consisted in a mixture of sativas, glaberrimas and the wild longistaminata accession. The second is constituted exclusively of glaberrimas. The third one represented glaberrimas plus the wild barthii accession. These results confirmed the usefulness of microsatellites to assess genetic diversity in African rice and the existence of intermediates or admixtures between the two cultivated species, *O. sativa* and *O. glaberrima*.

Related GCP project—SP3 Commissioned G4007.08: Integration of genomic tools with conventional screening for developing NERICA rice cultivars for West Africa

1.6: Identification of sources of resistance to drought, rice yellow mottle virus and African bacterial leaf blight (*Xanthomonas oryzae pv. Oryzae*) in African rice (*O. glaberrima*) and interspecific lines

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The NERICA varieties, bridging O. sativa and O. glaberrima, have shown potential in Africa. However, additional effort to develop drought-tolerant NERICAs, resistant to RYMV and BLB is needed.

Two upland trials were carried out using 324 rice germplasm comprising O. glaberrima and interspecific lines. Drought stress and full irrigation were applied respectively at vegetative stage and during vegetative untill flowering stage. Agronomic traits, drought related characters and yield components measured showed drought effects in the two trials. Average yield loss was 34.1%, ranging from 9.8% to 72.1%. Five O. glaberrima and two interspecific lines were selected as drought tolerant.

255 accessions were also screened against RYMV S1 strain through visual and Elisa scoring. Of the 104 accessions found resistant, 21 were confirmed highly resistant by the more virulent S2. PCR-specific markers of the Rymv1 gene identified accessions bearing new Rymv1-3 and Rymv1-4 alleles. Rymv1 sequencing showed most resistant lines harbouring the susceptible allele suggesting a resistant gene different from Rymv1.

Finally, 47 O. glaberrima accessions were screened with four BLB Xoo strains including BAI3 (race1), BAI4 (race2) and MAI1 (race3) from Africa and PXO86 (race2) from Asia as control. Nine and 12 accessions were resistant to MAI1 and PXO86 respectively.

Related GCP project—SP3 Commissioned G4007.08: Integration of genomic tools with conventional screening for developing NERICA rice cultivars for West Africa

Notes:

1.7: Ready to go into phenotyping: The wheat reference samples

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CIMMYT and its partners have committed to collect and complete the structural characterisation of diversity of the composite set in wheat. The genotypic data production of the composite set was completed in 2007 for up to 44 SSRs on a total number of 2932 entries. In order to streamline the process of evaluating genetic diversity, international reference samples of 372 spring bread wheat entries, 96 winter wheat entries, and 96 durum wheat entries were assembled based on the neutral marker information. To build the reference samples the D strategy was applied. The D-strategy has proven to maximise the representativeness of the genetic diversity in subsets of entries by including “generalists” alleles giving the advantage of minimizing population structure. The reference samples will be useful for genetic diversity studies such as SNP discovery and phenotyping agronomic traits in wheat germplasm and for analyzing the linkage disequilibrium and the association of complex traits. Single plant seed of each accession has been collected and will be deposited in the CIMMYT Wellhausen Genetic Resource Centre and are available upon request and for collaborative projects. In this poster we want to introduce the three reference samples, present their population structure and genetic diversity.

Related GCP project—SP1 Commissioned G4005.01: Genotyping of composite germplasm set

Notes:

1.8: Phenotyping reference set of chickpea (*Cicer arietinum*) for agronomic traits including resistance to legume pod borer (*Helicoverpa armigera*)

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Chickpea is an important grain legume crop. A composite collection of 3000 accessions was developed (http://www.generationcp.org), molecularly profiled using 48 SSRs, and extracted a reference set of 300 accessions representing 78% (1315 of the 1683 alleles) allelic diversity in composite collection. This reference set has been evaluated for agronomic traits during 2006/07 postrainy season at Patancheru, India. The best five highest-yielding desi accessions were ICC# 1180, 2263, 6802, 13892, and 15868 (seed yield 3.7 t ha-1) as against Annigeri (3.03 t ha-1), while ICC# 6905, 8155, 12328, and 16654, among kabuli types, showed higher yield (2.4 to 3.5 t ha-1) and 100-seed weight (39-44 g) than L550 (seed yield 2.1 t ha-1, seed weight 20.5 g). Accessions with high seed protein contents (26-27%) were ICC# 9418, 11903, 12654, and 69974 than controls (18%-20%). The promising accessions for pod borer were ICC# 3218 and 15294 and IG# 6067, 6905, and 73074, all scored 2 to 2.5, on 1 to 9 scale, as compared to controls (3 in ICC 506 and 5 in G 130). Further studies are in progress to add 100 markers on this reference set, phenotype for drought and salinity tolerance, and establish marker-trait association using linkage disequilibrium mapping.

Related GCP project—SP1 Commissioned G4005.01.04 (1d): Completing genotyping of composite germplasm set of chickpea

Notes:

1.9: Phenotyping reference set of finger millet [*Eleusine coracana (L.) Gaertn*] for agronomic traits

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Finger millet is widely grown as cereal in the arid areas of Africa and Asia. A composite collection of 1000 accessions was developed (http://www.generationcp.org) and molecularly profiled using 20 SSRs. A reference set of 300 accessions representing 89% (206 of the 231 alleles) allelic diversity of the composite collection was developed. Biologically, this reference set predominantly represented by Vulgaris, Plana, Compacta, and Elongata races; geographically predominantly from Asia and Africa regions. Spontanea and Africana races were represented by few accessions. When evaluated for 18 agronomic traits for two seasons, it showed wide spectrum of diversity: IE# 501, 600, 2093, 2158, 3537, 3543, and 4442 flowered earlier than VR 708 (43 days ± 1.84), IE# 897, 2333, 2691, 2765, and 5066 had more tillers than VR 708 (6.51± 0.912), and IE# 2340, 2498, 2587, 2773, 2903, 2983, 2992, 3194, 3790, 3802, and 4600 produced significantly higher grain yield than VR 708 (2150 kgha-1 ± 112.56). Accessions with higher Fe and Zn contents than VL 149 (Fe 26.6 mg/g and Zn 29.5mg/g) were IE# 2217, 2572, and 3045. Further studies are in progress to access the usefulness of this reference set for identifying new sources of variation for biotic and abiotic stresses.

Related GCP project—SP1 Commissioned G4006.06: Genotyping of composite collection of finger millet [Eleusine coracana (L.) Gaertn]

Notes:

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1.10: Phenotyping reference set of foxtail millet [*Seteria italica (L.).Beauv*] for agronomic traits

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Foxtail millet is one of the oldest cereals in Eurasia. A composite collection of 500 accessions was developed (http://www.generationcp.org) and molecularly profiled using 21 SSRs. A reference set of 200 accessions capturing 87% (316 of 362 alleles) allelic diversity of the composite collection was established. It is predominantly represented by accessions from Indica, Moharia, Maxima, and Pumila races, while geographically from South Asia. Other regions were represented by 12 to 21 accessions from West Asia, Central Asia, East Asia, Europe, and Africa. This reference set has been evaluated for agronomic traits for two rainy seasons at Patancheru, India. Accessions ISe# 1575, 1581, 1593, and 1647 flowered earlier than control ISe 1468 (25 days ± 0.73), while ISe# 769, 792, 821, 1059, and 1575 produced significantly higher grain yield than the best yielding control ISe 1468 (1650 kg ha-1 ± 68.94). Inflorescence length and width are related to grain yield. Accessions ISe # 969, 1668, 1789, and 1851 showed higher inflorescence length and width than the control ISe 1541 (length 250±10.01 mm, width 45±7.85 mm). Further studies are in progress to access the usefulness of this reference set for identifying new sources of variation for biotic and abiotic stresses.

Related GCP project—SP1 Commissioned G4006.30: Genotyping of composite collection of foxtail millet [Seteria italica (L.).Beauv]

Notes:

1.11: Sweet sorghum a promising bioenergy crop - phenotyping reference set for sugar content

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Worldwide sorghum has been recognised as a promising bio-energy crop. Sweet sorghum is similar to grain sorghum but with a sugar-rich stalk. A composite collection of 3367 accessions was developed (http://www.generationcp.org) and molecularly profiled using 41 SSRs. A reference set of 384 accessions representing 78% (615 of the 789 alleles) allelic diversity of the composite collection was developed. We evaluated 375 accessions of this reference set and controls (IS# 33844, 2205, and 18758) for sugar content during the 2007/2008 postrainy season at Patancheru, India. Main sorghum-stalk at 40 days after anthesis was sampled (4rth internode), juice extracted, and sugar content determined. The sugar content in the reference set ranged from 3.8% to 21.0%, averaged 11.2%. The average sugar content for the controls was 9% for IS 33844, 10.4% for IS2205, and 14.7% for IS18758. Forty-three lines showed sugar content similar or greater (14.8 to 21%) than the best control IS 18758. Biologically, accessions represent diversity from five basic races (Bicolor, Guinea, Caudatum, Kafir, and Durra) and three intermediate races (Caudatum-bicolor, Durra-bicolor, and Guninea-Caudatum); geographically predominantly from Africa. Further work is in progress to evaluating this reference set for sugar content during the 2008 rainy season at Patancheru, India.

Related GCP project—SP1 Commissioned G4005.01.03: Completing genotyping of composite germplasm set of sorghum

Notes:

1.12: Genetic diversity of maize landraces at SSR and adaptative loci: First inferences on worldwide migration

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Maize originated from the domestication of a teosinte in Mexico ~ 9000 years ago. Its progressive spread over all continents resulted from complicated patterns of introductions linked to trading and colonisation. This expansion and the increasing use of maize have favored the differentiation of thousands of local farmers' varieties (landraces) worldwide, adapted to local environmental conditions and uses. Our study aims i) to establish a global picture of maize landrace diversity to aid in its effective maintenance and use by breeding programmes, and ii) to compare genetic and historical data to better understand how maize has migrated globally over time. A total of 12,270 individuals (818 landraces populations) from America (including teosintes), Europe, Asia and Africa were genotyped for 28 SSR markers and vgt 1 (a flowering time marker) by using a bulked DNA method. PCA based on SSR frequencies highlights the important diversification of landraces in America, Europe, Africa, and, to a lesser extent, Asia. In agreement with cluster analysis, the geographical representations of vgt1 polymorphism and of the first PCA components suggest different scenarios of introduction in Western and Eastern Asia, probably linked Spanish and Portuguese trading routes, and a multiple and complex origin of African maize.

Related GCP project—SP1 Competitive G3005.14: Characterisation of genetic diversity of maize populations: Documenting global maize migration from the center of origin

Notes:

1.13: Diversity analysis of the sorghum global composite collection and reference set

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The GCP global composite collection of 3372 wild and cultivated sorghum accessions was initially genotyped with 41 SSRs to dissect the diversity and structure of genetic resources available for sorghum improvement. A reference set of 384 accessions was then selected representing global germplasm diversity. Population structure of this reference germplasm set was largely validated when independently assessed using a set of 40 EST-SSR primer pairs developed at ICRISAT from public EST sequence information. Cultivated accessions are grouped primarily by race within geographic origin. Within the guinea race, the margaritiferum group clusters with wild accessions, suggesting its independent domestication. Race kafir (largely from Southern Africa) is distinct. Durra, caudatum and guinea race accessions form distinct geographic subgroups. Race bicolor exhibits two clusters of East African origin, one grouping with bicolor accessions having passport data indicating a North American origin (which suggests the latter are originally from East Africa). The GCP sorghum reference germplasm set is sufficiently diverse to serve as a panel for linkage disequilibrium mapping, and/or as an entry to global sorghum germplasm collections when seeking variation in any trait of interest, provided that phenological diversity present is not so great that it interferes with phenotyping of other traits.

Related GCP project—SP1 Commissioned G4005.01.03: Completing genotyping of composite germplasm set of sorghum

Notes:

1.14: Genetic diversity assessment of cassava landraces and elite cultivars in Nigeria with simple sequence repeats (SSR)

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Cassava landraces and improved varieties which are widely grown and well adapted in Nigeria are being utilised in cassava breeding in the National Root Crops Research Institute (NRCRI), Nigeria. Genetic diversity study is important in facilitating the efficient utilisation of such valuable germplasm in breeding activities. Twenty seven SSR markers were used to analyze 54 Nigerian accessions comprising landraces, and elite cultivars from NRCRI and the international Institute of Tropical Agriculture (IITA). Additional 26 Latin American accessions from the International center of Tropical Agriculture (CIAT), Colombia were also evaluated. Except for one, all other SSR markers were polymorphic. The polymorphism information content ranged from 0.24 to 0.81. The number of alleles identified per locus ranged from 3 to 14. Heterozygousity varied from 0.01 to 0.79 with an. average gene diversity of 0.66. Cluster analysis produced two broad groups of Nigeria and Latin American germplasm indicating genetic differentiation based on geographical origin. Genetic diversity differentiated the sub-groups (landraces, NRCRI and IITA) in the Nigerian germplasm, possibly reflecting pedigree differences and breeding history while genetic relatedness was found high within each sub-group. The various sources of germplasm studied therefore represent important genetic variation that could be explored in cassava improvement in Nigeria.

Related GCP project—SP5 Commissioned new GCP TSG05 grant: SSR marker based analysis of genetic diversity of cassava landraces and elite cultivars in Nigeria.

Notes:

1.15: Deciphering the code: identifying alleles linked to performance in drought-prone environments through genotype-phenotype associations

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While many genomic regions associated with drought response have been identified, understanding specific alleles that influence performance under drought stress will help improve yields in drought-prone environments. Association studies offer great potential to identify key alleles by linking phenotypes to single polymorphisms within key genes or genomic regions. This approach has been successfully applied using eight candidate genes linked to performance under drought stress in rice. Associations were established between secondary traits related to performance under drought stress and haplotypes of drought responsive genes. Recent advances in genome-wide SNP arrays allow this approach to be upscaled to thousands of candidate genes/regions. Twenty rice accessions have been genotyped using this technology, with a further 2000 accessions to be genotyped. To exploit this information for drought research, detailed physiological information on the performance of genotyped accessions across drought environments is required. Phenotyping will be conducted under reproductive stage drought stress, the most sensitive stage to drought, across six drought environments. This dataset will be a valuable resource for association studies, allowing the identification of key genes and alleles associated with yield stability under water deficits.

Notes:

1.16: Variation in drought candidate genes in rice and association with vegetative drought tolerance

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EcoTILLING was employed to survey variation in a panel of Oryza germplasm consisting of 1536 O. sativa accessions. These accessions were screened by agarose-based ecotilling for the drought candidate genes TPP, ERF3, DREB2, ADF2a, ADF2b, MAPk2, BZIP, SUC, and 14-3-3 using contrasts to japonica (Nipponbare) and indica (IR64). Haplotypes were generated based on the contrast patterns and verified by confirmatory sequencing of representative accessions. The samples showed an average of 10 haplotypes per gene, largely supported by sequence data with the number of SNPs ranging from 6 (ADF2a) to 17 (TPP) for areas covering the coding region. SNPs were mostly transitions (68%) or transversions (28%) while indels were observed only in the SUC and TPP loci. Confirmatory sequencing verified 4 SNPs for BZIP, 7 for ERF3, and 12 for MAPk2. O. sativa accessions were screened over three consecutive dry seasons for performance under vegetative-stage drought stress with large phenotypic variation observed within each variety group. Our results indicate that several polymorphims of key drought responsive genes are associated with differences in response to water deficits. Continuous phenotypic variation was observed within many haplotype groups for each candidate gene; however, several haplotypes were associated with lower tolerance to vegetative drought stress.

Related GCP project—SP1 Commissioned G4005.05: Assessing Eco-tilling as a methodology for targeted genotyping and SNP discovery

Notes:

Theme 2:
Genomic resources and gene/pathway discovery

2.1: Development of genetic and genomic resources for breeding improved sweetpotato

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Notes:

The present project aims at developing genetic and genomic resources for sweetpotato improvement and will stimulate the use of these tools in ongoing breeding programmes at CG Centers and NARS. We have started to develop a Composite Genotype Set consisting of 480 sweetpotato accessions including landraces, breeding clones, mapping parents, a drought tolerant selection and wild germplasm, which reflects sweetpotato diversity and contains useful traits for sweetpotato improvement. 120 Ipomoea trifida individuals derived from a cross between CIP-4653.22 and CIP-4597.1 that exhibit large genetic distance and a high degree of heterozygosity have been produced. This population is used to develop a diploid reference map. Normalised EST libraries were produced from tissues harvested from drought-exposed sweetpotato plants. Actually the ESTs are sequenced using the 454 pyrosequencing technology. A sweetpotato gene index follows. New markers for sweetpotato will be made available. Based on geographical origin and SSR diversity data, 94 sweetpotato accessions have been chosen by CIP, NAARI Uganda and INIA Urugay for the production of a DArT array produced by DArT/Pl. Additionally we will mine the newly available EST library for SSRs and test COS markers for their application on sweetpotato.

Related GCP project—SP2 Commissioned G4008.09: Development of genetic and genomic resources for breeding improved sweetpotato

2.2: Evaluation of allelic diversity of the Hungarian maize and bean germplasm

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Notes:

Both of our studies aimed to assess the Hungarian collections by characterizing a subset of maize and bean accessions and comparing their allelic diversity with the diversity present in GCP's reference sets. Selections of the accessions were based on known pedigrees, phenotypic traits and geographic locations to represent a broad range of diversity of the maize and bean germplasm available in the Hungarian collection.

Hungarian maize inbred lines and populations were scored with the same SSR markers (27 SSRs for 32 inbred lines and 45 SSRs for 26 populations) as has been used in the GCP. Control maize lines and populations, included in the characterisation, ensured comparability with previously obtained data.

100 Hungarian bean accessions and 2-2 controls, to identify both Mesoamerican and Andean gene pools, were characterised by 52 SSR markers. The majority of genotypes were clustered with either the Mesoamerican or the Andean controls but their relationships indicated diverged allelic compositions in the Hungarian genotypes.

Analyses of the marker data revealed that both the Hungarian maize and bean germplasm contain substantial diversity, which could support national programme's breeding objectives as well as allow participation in international programmes aiming at maize and bean improvement and conservation.

Related GCP projects—SP5 Commissioned G4008.28 'Characterisation of maize diversity in Central Europe' and G4008.29 'Characterisation of bean diversity in Central Europe'

2.3: EST-SSR Marker resources for groundnut

Sameer Khanal, Shunxue Tang, Ervin Nagy, Yufang Guo, Yan Li, Vadim Beilinson, Phillip San Miguel, Baozhu Guo, Niels Nielsen, Thomas Stalker, Marie-Michele Cordonnier-Pratt, Lee H Pratt, Virgil Ed Johnson, Christopher A Taylor, Graham B Wiley, Simone L. Macmil, Bruce Roe, Koppolu Ravi, Gautami Naidu, David Hoisington, Rajeev Varshney, and Steven J Knapp*

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Narrow genetic diversity and a deficiency of polymorphic DNA markers have hindered genetic mapping and the application of translational genomics approaches and marker-assisted selection in groundnut (*Arachis hypogaea*). We developed and mined a groundnut EST database for simple sequence repeats (SSRs), assessed the frequency of polymorphic SSRs in ESTs, and developed 2,054 EST-SSR markers. We assembled 71,448 long-read (Sanger) ESTs and 304,215 short-read (454) ESTs into 37,914 unigenes, identified 7,413 perfect repeats, designed and tested primers for 80 EST-SSRs sampled from broad spectrum of motifs and repeat lengths, and screened 58 EST-SSR markers for polymorphisms among elite and exotic germplasm accessions. Of the 58 EST-SSR markers, 55 were polymorphic, 32 were polymorphic among elite lines (mean heterozygosity = 0.18), 27 were polymorphic among four elite x elite mapping populations, and 48 were polymorphic in two diploid mapping populations. The frequency of polymorphic EST-SSRs seems to be sufficient for developing the critical mass of DNA markers needed for routine genetic mapping and marker-assisted selection applications in groundnut. The EST-SSR markers described here are currently being screened for polymorphisms and mapped in multiple diploid and tetraploid mapping populations and could play an important role in breaking the DNA marker bottleneck in groundnut.

Related GCP project—SP2 Commissioned G4008.06: SNP discovery, validation, and mapping in groundnut

Notes:

2.4: Discovery and genetic mapping of NBS-LRR encoding resistance gene candidates linked to a root knot nematode resistance gene (*Rma*) introgressed from a wild diploid donor in groundnut

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Root knot nematode (*Meloidogyne arenaria*) is a devastating pathogen of groundnut (*Arachis hypogaea*). Resistant cultivars have been developed through the introgression of a dominant resistance gene (*Rma*) from a synthetic allotetraploid donor (TxAG-6). The genomic segment harboring *Rma* has not been genetically mapped and candidates for the gene encoded by *Rma* have not been identified. We describe the development and screening of DNA markers for nucleotide binding site leucine rich repeat (NBS-LRR) encoding resistance gene candidates (RGCs), genetic mapping of the genomic segment carrying the *Rma*-locus introgression, and RGCs for *Rma*. We mined a tetraploid EST database for NBS-LRR cDNA sequences, developed 403 SSCP markers for 318 partial NBS-LRR genomic or cDNA sequences identified in public databases and the EST database, screened 556 SSR and 403 SSCP markers for polymorphisms between nematode susceptible and resistant near-isogenic lines, and mapped the *Rma* introgression in two tetraploid populations (NemaTAM x WS14 and Tifguard x Gregory). Several NBS-LRR loci cosegregated with *Rma*. We developed a NemaTAM fosmid library and are currently isolating full-length sequences for NBS-LRR encoding genes linked to *Rma* to facilitate more in-depth analyses and discovery of the gene encoded by *Rma*.

Related GCP project—SP2 Commissioned G4008.06: SNP discovery, validation, and mapping in groundnut

Notes:

2.5: Strengthening pearl millet genomics tools

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This new project is intended to strengthen genomic resources for pearl millet (*Pennisetum glaucum*), developing EST libraries from parents (841B-P3 and 863B-P2) of a mapping population that is well-characterised for drought tolerance, identifying EST sequence polymorphisms between these parental lines, and mapping these polymorphisms using the 150 RIL progenies. This augmented linkage map, combined with information on positions on the sorghum and rice genome sequences of homologues of the pearl millet ESTs from which these newly mapped markers are derived, then will be used to refine the rice-pearl millet comparative map and to develop a sorghum-pearl millet comparative map. In addition, we will use STS and SSR markers to skeleton map two new conventional biparental pearl millet RIL mapping populations, and conduct initial testcross hybrid evaluations of these populations for terminal drought stress tolerance (measured in terms of grain and stover yield maintenance under stress conditions) and grain and stover nutritional value (measured in terms of digestibility and metabolizable energy content). Finally, we will advance eight additional pearl millet RIL populations to F7 inbred lines suitable for map saturation with DArT markers in a future project, which would permit development of a high density pearl millet consensus map.

Related GCP project—SP2 Commissioned G4008.07: Improving molecular tools for pearl millet

Notes:

2.6: Identification of orthologous regions associated with tissue growth under water-limited conditions

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Leaf expansion is one of the most sensitive processes to water deficit, and an important parameter in determining plant ability to intercept light and convert it into biomass. To identify orthologous genetic regions controlling tissue growth under water-limited conditions, a series of QTL mapping and microarray gene expression studies were conducted in both maize and rice. QTLs associated with ASI, leaf extension rate, and gradients of leaf expansion response to evaporative demand and water deficits were identified in maize under controlled and field conditions. In rice, QTLs associated with leaf growth were identified under water deficit over three field seasons. Large scale gene profiling on tissue from the expanding zone of leaves under water deficits in both species was used to identify groups of genes whose expression patterns correlated with plant growth maintenance. Results of differentially expressed genes from microarray experiments, QTLs and candidate genes related to growth in the different species are compared on consensus maps (within the species) and then on synteny maps (between species), to identify common genetic regions between maize and rice.

Related GCP project—SP2 Competitive G3005.15 Determination of a common genetic basis for tissue growth under water-limited conditions across plant organs and genomes

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2.7: Gene expression profile, physiological and morphological characterisation of wild Arachis spp. under drought stress

PM Guimarães, AC Brasileiro, C Santos, CV Morgante, MC Moretzsohn, FR da Silva, ACG Araujo, PIT Silva, V Vadez, RCS Castro, DJ Bertioli, SCM Leal-Bertioli*

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Wild *Arachis* species are a rich source of alleles for peanut improvement, and have enough polymorphisms for their genetic characterisation. An integrated approach is underway to identify drought tolerant species.

For that, the responses to progressive water deficit in wild, amphidiploids and cultivated peanut were investigated. Although the transpiration behavior of amphidiploids was observed as being distinct from their wild parentals, transpiration efficiency (TE) was similar, showing that direct screening of wild species for desirable drought responses may be feasible. The effects of polyploidisation in the amphidiploids were also evaluated through the analysis of leaf anatomy: stomata type, length, stomata index and epidermis thickness and structure. Large variations of anatomy and transpiration response were found between different wild and cultivated species was observed.

An Arachis magna accession with high TE was chosen for transcriptome analysis. Subtractive libraries were constructed and sequenced, producing 273 clusters with 32.8% novelty Several genes differentially expressed in stressed or control conditions were identified which relate to biotic and abiotic stress. The expression profile and functionality of these candidate genes are being validated using qRT-PCR, in situ hybridisation and VIGs. These sequences will also be used for development of molecular markers (SSRs and SNPs).

Related GCP project—Focus project G4006: Improving tropical legume productivity in sub-Saharan Africa (TLI)

Notes:

2.8: Analysis of qEt8.06, a major QTL for resistance to northern leaf blight of maize

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Northern Leaf Blight (NLB), one of the most important diseases affecting maize production worldwide, is a resurgent problem in Africa. Maize bin 8.06 is associated with resistance to NLB and several other diseases. In response to recurrent selection for NLB, significant changes in allele frequencies occurred at markers in bin 8.06. Evaluation of a subset of the nested association mapping (NAM) population, consisting of ~3000 recombinant inbred lines developed from 25 diverse maize lines, identified a major QTL in bin 8.06 (designated qEt8.06) conditioning increased incubation period and decreased disease severity of NLB. Estimated allele effects varied among NAM subpopulations. To dissect the apparently complex qEt8.06 region, near-isogenic line (NIL) pairs contrasting for this locus were developed from heterogeneous inbred families derived from S11/DK888. Phenotypic analysis indicated that qEt8.06DK888 confers race-specific quantitative resistance to NLB, but not to several other diseases. Trait-marker association among ~200 F9 recombinants delimited the resistance locus to a region of ~5 Mb. Mapping in the NAM population localised qEt8.06 to a 7 Mb region, narrowing the region to ~3 Mb. This region could be transferred using marker-assisted selection in breeding programmes. On-going work focuses on isolating the gene(s) underlying this major QTL.

Related GCP project—SP2 Competitive G3005.08: Targeted discovery of superior disease QTL alleles in the maize and rice genomes

Notes:

2.9: Cowpea breeding for improved drought tolerance in Mozambique: A need for ensuring food security in drought–prone environments

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Cowpea is the most important source of vegetable protein for resource-poor households in Mozambique. The crop is grown countrywide by smallholder farmers for its fresh and dry grain, fresh and dried young leaves, and immature green pods. Drought stress, caused by low, erratic and short duration of rainfall, is a major yield and quality reducing factor. Despite its importance to the country, little has been done in terms of research and breeding activities on drought tolerance in cowpea. This poster presents our planned research activities to improve drought tolerance being conducted by Eduardo Mondlane University in collaboration with the University of California Riverside under the GCP SP5 sub-programme under a project entitled "Improve Cowpea Productivity for Marginal Environments in Mozambique". This project has three specific objectives: (1) provide baseline drought tolerance information for early and medium cycle cowpea varieties and assess the importance of genotype x environment interactions for grain yield under drought in Mozambique; (2) assess genetic variability for drought tolerance in a set of 300 Mozambique cowpea landrace accessions; and (3) develop breeding populations suitable for application of marker-assisted selection (MAS) and marker assisted recurrent selection (MARS) using SNP-based markers developed under an associated GCP Tropical Legume 1 (GCP-TL I) project (….)

Related GCP project—Focus project G4006.02 TLI Objective 2: Improve cowpea productivity for marginal environments in sub-Saharan Africa

Notes:

2.10: Improvement of Indonesian modern upland rice varieties for P– deficiency tolerance using marker assisted backcrossing methods

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Indonesia has 45.794.000 ha acid soils (24% of total area), mostly Ultisol and Oxisol, with high Al and P deficient. Fertilizers and amendments are too expensive for farmers, but developing varieties tolerant of P-deficiency will help solve this problem. Improved varieties tolerant of drought and Al toxicity were developed, but so far no variety with high P-deficiency tolerance is available. Developing such varieties is now feasible after the discovery of Pup1, a major QTL for high P-uptake from P-fixing soils. Three modern varieties (Dodokan, Situ Bagendit, Batur) were used as recipient parents and two lines (Kasalath and NIL-C443) as donors for Pup1 QTL. Marker assisted backcrossing using foreground, recombinant, and background markers, was applied on F1, BC1F1, BC2F1, and BC2F2 generations. Most of recipient parents' genome was recovered in BC2F1, especially with NIL-C443 crosses, and fewer loci carry the donor segments. Twenty out of 300 BC2F2 plants of each cross were being advanced to produce BC2F3 seed for field testing. Moreover, a phenotyping procedure was developed using P-deficient soil from hot spot areas. A minimal dosage of P_2O_5 for -P treatment in this soil is 2 kg /ha and the optimum dosage for +P-treatment is 25 kg kg/ha.

Related GCP project: SP2 Competitive G3005.02: Revitalising marginal lands: Discovery of genes for tolerance of saline and phosphorus-deficient soils to enhance and sustain productivity

Notes:

2.11: Changes in the transcriptome of the smoke – treated germinating maize kernels

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The aims of the project are to investigate the physiological effect of smoke extract, the mode through which the active compound of smoke affects seed dormancy and germination under stressed conditions, using state-of the-art technology. The transcriptome of the smoke - treated imbibed maize kernels and young seedlings were recorded using 48K microarray slides. Global changes in gene expression pattern were detected in germinating maize embryos and maize embryo axes in the early postgermination phase. The corresponding genes were GO annotated and the results were filtered against germination-responsive genes using rice and Arabidopsis microarray data. The up-, and downregulated genes were then clustered into functional groups. The promoter regions of the most pronounced genes were extracted in silico from maize BAC library databases. We found that smoke induced the rapid decay of mRNAs present in mature and desiccated embryos. The most highly affected genes are involved in the 26S proteasome regulation, RING-domain containing E3 ligases and LRR-receptor like kinase mediated signal transduction. Smoke induces the expression of phytochrome P450 and many genes involved in ABA signalling; most of them are a positive regulators of the ABA response. This phenomena was particularly prominent in young seedlings.

Related GCP project: SP3 Commissioned G4007.24: Seed smoke treatment to favour germination under water stressed conditions

Notes:

Theme 3:
Marker development and breeding applications

3.1: Designing crossing and selection strategies to combine diagnostic markers and quantitative traits

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Diagnostic molecular markers are now available for more than 20 traits in wheat. The challenge is to combine these markers with phenotypic selection in creating new parental lines and progeny (target genotypes). Based on previous simulation work, we considered six diagnostic markers related to height, grain quality and disease. The objective was to integrate diagnostic selection (including Rht-8, a major gene to increase coleoptile length) with selection for an additional six minor QTL for this quantitative trait.

From 1000 simulations of a cross between a conventional semi-dwarf wheat (Sunstate) and a long coleoptile donor (HM14BS) carrying the Rht8 allele, the creation of 1000 doubled haploid lines only resulted in 2.2 target genotypes, i.e. with desired alleles for six major genes and with coleoptiles >120 mm. As alternatives, we created from the F1, an F2 of either 100 (option 2) or 200 (option 3) lines, and pre-screened these (F2 enhancement) for the six major genes before production of DH lines and final screening. Option 2 (900 DH lines) and 3 (800 DH lines) delivered 13 or 19 DH target genotypes respectively for each 1000 lines screened. New simulations aim to multi-plex markers and integrate with phenotypic screening of coleoptile length.

Related GCP project—SP3 Commissioned G4005.20: Optimising marker-assisted breeding systems for drought tolerance in cereals through linkage of physiological and genetic models

Notes:

3.2: Simulating yield impact of QTL controlling leaf and silk expansion under drought in maize

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Notes:

Part of the impact of drought on maize yield arises from reduction in leaf expansion that affects light interception and from reduction in silk growth that affects grain set. Recently, genome regions (QTL) have been associated with the sensitivities of leaf expansion to soil water status and evaporative demand. Half of them also contribute to silk growth (ASI). In this study, we combined (i) a short-term model (hourly) of maize leaf expansion that captures the effects of genetic and environmental variations, with (ii) a new model co-ordinating the developments of all leaves of a plant, and (iii) the APSIM crop model which works at the canopy level. The integrated model adequately predicted leaf area, biomass accumulation and yield in fields with contrasting evaporative demand and soil water conditions. The model was then used to quantify the impact on yield of combinations of QTLs involved in leaf and silk expansions, under a range of drought scenarios. QTLs for leaf growth maintenance had a positive effect on yield in most scenarios. Their effect on yield was still increased if their contribution to silk growth was taken into account. This study exemplifies the potential for modelling in bridging the gene-to-phenotype gap.

Related GCP project: SP2 Competitive—G3005.15: Determination of a common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes

3.3: Identification of additive and epistatic genes in maize *(Zea mays L.)*

Jiankang Wang, Huihui Li, and Jean-Marcel Ribaut*

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Notes:

Epistasis makes a substantial contribution to the genetic control and evolution of quantitative traits. A novel QTL mapping method called inclusive composite interval mapping (ICIM) was recently proposed to identify both additive and digenic epistatic QTL in biparental mapping populations. In an RIL population derived from two maize inbreds and phenotyped under various water stressed scenarios, a total of 20 additive QTL were detected by ICIM on eight of the 10 maize chromosomes with significant effects on female flowering time (FFLW). qFFLW4-2 was detected in five environments, qFLW1-1 and qFFLW8-1 were detected in four environments, and other QTL were detected in one to three environments. Though no QTL was repeatedly detected in all environments, QTL detected in more than one environment have similar additive genetic effects on FFLW, indicating their relative stability. Unlike the additive QTL, one pair of two interacting QTL was hardly detected in more than one environment. But some hot positions could repeatly interact with many other positions in different environments. The position 120 cM on chromosome 10 interacted with other 10 positions for FFLW, and it was not detected with significant additive effects on FFLW (Table 2). The position 155 cM on chromosome 2 interacted with other 5 positions for FFLW, and it could represent the additive QTL qFFLW2 as well. In general, interacting genes are less repeatable and stable than additive genes in maize.

Related GCP project—SP3 Commissioned G4008.14: Breeding for drought tolerance with known gene information

3.4: Genetic dissection of quantitative trait loci for plant height in common wheat

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Plant height (PH) is a crucial agronomic trait related to plant architecture and yield potential. Developmental behavior of PH in wheat was assessed using 150 lines of a doubled haploid population (Hanxuan 10 ′ Lumai 14) planted in ten environments (year ′ location ′ water regime combinations) by unconditional and conditional mapping. The results showed that QTLs associated with PH development were detected on all chromosomes except 6D. Additive main effect was the major genetic effect for PH, which expressed greatly at jointing stage. QTLs with additive and epistatic effects were the important genetic component for PH, most of them acted in QTL networks. Drought stress coefficient of PH (DS|WWph) during ontogeny was mainly affected by environment components. Drought resistance index of PH (DRIph) was primarily controlled by additive main effect QTLs, most of them also expressed at jointing stage. QTLs for heightening plant height, such as QPh.cgb-2D.1, QPh.cgb-4D.1, QPh.cgb-6B.5 and QPh.cgb-7A.3 specially expressed under well-watered conditions, QPh.cgb-5A.7 and QPh.cgb-6B.7 specially under drought stress conditions, the later might be beneficial for drought-tolerant improvement. We are verifying the functions of the given QTLs in the drought tolerance introgression lines with elite Chinese wheat backgrounds using molecular marker assisted selection.

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

Notes:

3.5: Identification of quantitative trait loci for salinity tolerance to rice in an advanced backcross population derived from two indica varieties, Boilam and BRRI Dhan 27

*HB Shozib, MJ Thomson, MS Rahman, MA Salam, AM Ismail and ZI Seraj**

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Boilam is photoperiod insensitive and early maturing, unlike the salt tolerant rice landrace rice, Pokkali. Pokkali also shows poor heritability of salt tolerance traits in innumerous breeding efforts in SE Asia. This investigation was designed to identify novel Quantitative Trait Loci (QTL) linked to salt tolerance traits of a Bangladeshi Aus landrace, Boilam extensively grown in the mid South for possible introgression into modern rice varieties. BC2F2 progenies from a cross between Boilam and farmer popular rice variety BR27 were developed. A total of 200 tolerant and sensitive BC2F2 seedlings were genotyped by 108 SSR markers across the 12 rice chromosomes. QTLs were identified using single-point analysis and interval mapping using QGene. A total of 4 QTLs were detected on chromosome 1, 9, and 12 using LOD > 3 as threshold. The range of R value of the 4 QTLs was 19.57% – 25.81 %. Salt tolerant BC2F3 having the background genotype of BR27 will be developed further for release or use as parents in breeding programmes with the help of the markers-linked to the salt tolerance QTLs. QTL analysis for reproductive stage salt tolerance with 200 more BC2F2 is now being conducted to establish Boilam as a donor of novel salt tolerance traits.

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.

Notes:

3.6: Improvement of mega rice varieties BR11 and BRRI dhan28 by introgression of the Saltol loci using marker-assisted backcrossing

Zeba I Seraj, M Sazzadur Rahman, M. Rafiqul Islam, Taslima Haque, Suhaila Rahman and Noorjahan Begum*

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This project was undertaken to improve the performance of the two mega rice varieties of Bangladesh, BR11 (T. Aman, monsoon) and BR28 (Boro, dry, winter) by introgression of the major salinity tolerance QTL Saltol on rice chromosome 1. Four markers were found significantly associated with the trait by fine mapping of the Saltol QTL region. These markers were used to locate the QTL in the backcross populations. Similarly two markers were found loosely associated and were used to delineate the QTL and reduce negative linkage drag. For introgression of the Saltol QTL, crossing was done with the donor FL378 (a near isogenic line with the Saltol loci) and repeated backcrossing with either BR11 or BRRI dhan28. For the BR11 programme, two double recombinants and 136 single recombinants were selected by genotyping of 342 BC2F1 using foreground and recombinant markers. 35 BC2F1 are currently being genotyped with background markers. For improvement of BRRI dhan28, a total of >13000 BC1F1 were developed for introgression of Saltol. It is expected that some advanced BR11 Saltol lines will be sent for trial in saline fields for evaluation in the wet season of 2009 (July-December) and BRRI dhan28 Saltol for dry season of 2010 (December-May).

Related GCP project—SP2 Competitive G3005.02: Revitalizing marginal lands: Discovery of genes for tolerance of saline and phosphorus-deficient soil to enhance and sustain productivity

Notes:

3.7: Molecular marker development and genome mapping in coconut in Sri Lanka

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or chandrikaperera2003@yahoo.com

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Coconut is an economically and socially important crop in Sri Lanka. Breeding of coconut is difficult mainly due to heterogeneity of populations and the long vegetative phase. Molecular markers can assist coconut breeding by becoming tools in germplasm characterisation, genome mapping etc. Although about 300 SSRs have been developed for coconut the low density of molecular marker coverage of the genome is a limitation. Therefore validation of the Diversity Arrays Technology (DArT) was completed as a GCP fellowship awarded to Sri Lanka. Three libraries containing cloned restriction fragments were produced. The library Pst1/BstN1 was expanded to include 6144 clones. Genotyping of 224 coconut accessions with Pst1/BstN1 library revealed 347 polymorphic markers validating DArT for coconut and resulting in an expanded DArT library for future usage. A segregating mapping population consisting of 339 individuals was developed in Sri Lanka by crossing 26 Sri Lanka red dwarfs with a single Sri Lanka tall male parent. The individuals were genotyped with SSRs to confirm the parentage of the progeny resulting in 298 legitimate individuals. The progeny is now being genotyped with 70 SSR markers under GSS of the GCP. The framework map for this population is to be developed by the end 2008.

Related GCP project: Not applicable

3.8: Field evaluation of wheat-barley introgression lines under different water regimes

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The present project aims to use the wheat/barley addition, substitution and translocation lines developed in Martonvásár to determine how the added barley chromosome (segments) influence various agronomic traits (drought, salt and Al tolerance) in wheat. It is planned to confirm the results achieved by earlier mapping data or to find new chromosome regions responsible for parameters connected with drought-, salt and Al-tolerance.

The following genetic materials developed in Martonvásár will be used in this project:
New disomic winter wheat/winter barley addition lines (2H, 3H, 4H, 1HS, 7H) from the Mv9 kr1 × Igri (German two-rowed winter barley) combination, Disomic (4H, 6H, 7H) and monosomic (2H, 3H) addition lines from the Asakaze komugi × Manas (Ukrainan six-rowed winter barley) combination, Wheat/barley substitution line 4H(4D), Wheat/barley translocation lines (3HS.3BL, 2DS.2DL-1HS, 6BS.6BL-4HL, 4D-5HS, 7DL.7DS-5HS) carrying Betzes barley chromosome segments in a Mv9 kr1 background.

The multiplication and cytological checking of these lines is in progress in Martonvasar.
The drought tolerance of the lines is currently being tested under laboratory conditions and in the field under a rain shelter in Martonvásár. Aluminium toxicity tests have been carried out under laboratory conditions (....)

Related GCP project—SP3 Commissioned G4007.23 Field evaluation of wheat-barley introgression lines under different water regimes

Notes:

3.9: Marker−assited selection for drought tolerance rice in Vietnam

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Environment degradation and climatic change become global problem. Drought cover our VIETNAM s surface that estimates from one millilion hectares . Improving the drought tolerance in rice is one of the most important objectives of rice breeding programmes Drought is a major yield- limiting factor in rice production. .Two hundred twenty nine (BC2F2) derived from the cross between OM 1490 / WAB880-1-38-18-20-P1-HB were evaluated. BC lines were evaluated for drought at flowering (Drf) , dry root weigh (DR), root length (RL) . Microsetellite map of this population were used with 232 markers to detect the linkage to target traits. A linkage map was constructed from 12-linkage groups based on the population. The map covers 2,553.7 cM with an average interval of 10.97 cM between marker loci. Markers associated withdrought t tolerance were located mostly on chromosomes 2, 3, ,4,8,9,10 and 12 . Quantitative trait loci (QTL) mapping was used to determine effects of QTLs associated with drought tolerance traits. We also mapped QTLs for morphological attributes drought tolerance. Chi-square tests (χ^2), single maker analysis (SMA), interval mapping (IM) were combined in QTL analysis procedure. All approaches are similar to QTL detection result. Fine QTLs were identified for DRR , two QTL for length root , two QTLs for dry root weight (....)

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3.10: Application and validation of the major QTL phosphate uptake 1 (*Pup1*).

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The major rice QTL Phosphate Uptake 1 (*Pup1*) confers tolerance to phosphorus (P) deficiency in soil. The *Pup1* locus has recently been fine mapped to a 272 kb region on rice Chr.12 and was sequenced in the tolerant donor landrace Kasalath. Sequence analyses revealed that *Pup1* is a hot spot of transposon integration leading to a complex and highly dynamic structure. Due to this complexity, prediction of candidate genes and development of *Pup1* specific molecular markers required extensive in silico analyses. The validation of short listed candidate genes is now ongoing at IRRI and JIRCAS.

For the development of P-deficiency tolerant rice varieties, highly specific PCR based markers were designed based on the *Pup1* sequence. These markers are now being used to (i) assess the haplotype of *Pup1* in diverse rice germplasm, (ii) identify recipient parents for *Pup1* introgression, and (iii) select for *Pup1* in the breeding process. The development of *Pup1* introgression lines is ongoing at IRRI and ICABIGRAD and first field screenings will be conducted next year. In parallel, we are working on the development of a *Pup1* phenotyping system that facilitates functional analyses of *Pup1* and selection of tolerant plants at an early seedling stage.

Related GCP project—SP3 Commissioned G4008.41: Application and validation of the major QTL phosphate uptake 1 (Pup1).

Notes:

3.11: Enhancing efficiency of hybrid pigeonpea breeding through genomics

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Notes:

Pigeonpea [*Cajanus cajan (L.) Millspaugh*] is an important food legume crop of sustainable agriculture system in the semi-arid tropics (SAT) of Africa and Asia. In spite of breeding a number of pure line varieties, the productivity of pigeonpea for the last five decades has remained low at around 700 kg ha-1. To achieve a breakthrough in the productivity of pigeonpea, ICRISAT scientists successfully developed a hybrid breeding technology based on a cytoplasmic-nuclear male-sterility system and partial (25 - 30%) natural out-crossing. For wider adoption of hybrid breeding technologies by seed companies, it is mandatory that the hybrid seed is of highest genetic purity. Therefore, efforts have been initiated to establish hybridity test based on molecular (microsatellite) markers. Furthermore, to address the breeding constraints such as narrow genetic diversity among hybrid parents, expansion of limited heterosis and narrow adaptation, we are in process of mapping of fertility restorer gene(s) as well as identifying genes conferring male- sterility through characterisation of mitochondrial genomes. Thus, integrated breeding and genomics activities are expected to help in enhancing the progress of developing new improved pigeonpea hybrids to improving the livelihoods of SAT farmers in Asia and Africa.

Related GCP project: Developing genomics resources for pigeonpea using next generation sequencing technologies.

3.12: Marker–assisted backcrossing for improved salt tolerance in rice

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In Bangladesh salt-affected areas cover 1 million hectares and pose a serious problem for resource-poor farmers who depend on rice production for their livelihoods. Our goal is to precisely transfer QTLs conferring salinity tolerance into modern varieties to enable higher and more stable yields for farmers living off these marginal lands. This project is employing a precise marker-assisted backcrossing (MAB) approach to introgress Saltol, a major QTL for salinity tolerance, into several varieties that will subsequently be tested in partnership with farmers. At IRRI, progress has been made in developing a BC3F2 line with the Pokkali Saltol allele in the background of the popular variety BRRI dhan28, which is an important cultivar for the dry season or "boro" rice in Bangladesh. Subsequent steps will confirm the clean background, test the level of salinity tolerance, and amplify seeds for field testing in South Bangladesh. Additional populations are being advanced in collaboration with Dhaka University and the Bangladesh Rice Research Institute (BRRI) to transfer additional tolerance alleles into BRRI dhan 28 and BR11. Through SP5, the project is also building a molecular marker laboratory in the BRRI Plant Breeding Division to incorporate MAB in their breeding programmes for agronomically important traits.

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

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3.13: Development of chromosome segment substitution lines from a cross between cultivated peanut and a wild synthetic amphidiploid

Daniel Foncéka, Hodo-Abalo Tossim, Issa Faye, Ousmane Ndoye, Jean-Francois Rami*

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A synthetic amphidiploid obtained from the cross between two diploid wild species *A. ipaensis* and *A. duranensis* was crossed with the Fleur11 cultivated *A. hypogaea* variety. 88 BC1 plants obtained from the cross between the resulting F1 and Fleur11 as recurrent parent were grown and DNA was extracted. This BC1 population was used to build a SSR genetic map comprising 231 loci into 21 linkage groups and spanning a total distance of 1793 cM. This map showed good colinearity with the existing maps of the A and B genomes developed on diploid mapping populations. Using genotypic information and the genetic map, a set of 22 BC2 families representing optimal genome coverage of chromosome segments from the donor genome was selected to be advanced to the BC3 generation. It is expected that a collection of about 100 chromosome segments substitution lines, targeting an average introgression size of 20 cM, will be available in the coming year. Once fixed and increased, this material can be characterised in different environments for different traits of interest involved in biotic or abiotic stress response. Moreover, these lines can be used as a starting point toward gene cloning through deriving near isogenic lines in QTL regions.

Related GCP project—SP5 Commissioned Capacity-building à la carte G4007.13.03: Application of molecular tools for controlled wild introgression into peanut cultivated germplasm in Senegal

Notes:

3.14: Tailoring superior alleles for abiotic stress genes for deployment into breeding programmes: A case study based on association analysis of Altsb, a major aluminum tolerance gene in sorghum (Altsorghum)

Jurandir Magalhaes, Fernanda Caniato, Leon Kochian, Stephen Kresovich, Sharon Mitchell, Theresa Fulton, Claudia Guimaraes, Robert Schaffert, Vera Alves, Owen Hoekenga, Jiping Liu, Alexandra Casa, Antonio Marcos Coelho, Soumana Souley, Maman Nouri, Magagi Abdou, Adam Kiari, Fatouma Beidari*

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Aluminum toxicity represents a major agricultural constraint in large regions of acid soils throughout the world. Based on the isolation of AltSB, a major aluminum tolerance gene in sorghum, we are applying association analysis as a bridge to integrate our findings to acid soil breeding programs. Operationally, we are looking for superior AltSB haplotypes in diverse association panels, isolating their allelic effects in near-isogenic lines, and defining elite haplotypes using SNPs and indels associated with Al tolerance, which will be used for allele mining in breeding panels. We have found that high Al tolerance is extremely rare in sorghum as only 6% of the accessions in the panel, which belonged largely to the Guineae race, were highly tolerant to Al toxicity. Our preliminary data allowed us to identify 7 polymorphisms associated with Al tolerance with apparently variable linkage disequilibrium among sites. Two low frequency alleles at two loci can discriminate ~80% of the elite haplotypes, which would otherwise require extensive phenotyping to be identified since those are found at a rather low frequency in the association panel. Our association results suggest an important role for regulatory regions controlling differences in gene expression and leading to strong allelic effects at AltSB.

Related GCP project—SP3 Competitive G3007.04: Tailoring superior alleles for abiotic stress genes for deployment into breeding programmes: A case study based on association analysis of Altsb, a major aluminum tolerance gene in sorghum

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3.15: A participatory "cowpea production appraisal": A reliable frame to building up a marker assisted selection for *Striga* resistance in cowpea

Jean Baptiste Tignegre, Jeremy T Ouedraogo, Issa Drabo, Ilboudo Dieudonne, Neya B James, Ba Malick, Diasso Gabriel, Satoru Muranaka, Boukar Ousmane Moutari N, Mamadou Toure*

** Institut de l'Environnement et des Recherches Agricoles (INERA),CREAF de Kamboinse 01 BP 476 Ouagadougou 01 Burkina Faso; Tel (Off.): +226 50 31 31 92 02/08; (Hom): +226 50 38 27 70; Cell.: +226 76 02 49 50 Cell.:+226 70 04 92 72, racinetignegre@yahoo.com*

Cowpea is well adapted to semi-arid areas and an affordable source of protein, and income for poor resource people of sahelian zones. However, in Striga hot-spots, Striga causes complete yield losses. The objective of this research is to identify breeding priorities in a participatory approach, to determine the ideotype of cowpea variety. The constraints, causes and solutions associated with Striga problem were determined by using participatory rural appraisal tools. As results, farmers were aware that Striga problem arises from combined effects of both soil degradation and climate (drought). They have also ranked Striga in cowpea among the major constraints. Farmer's desirable traits were oriented towards grain quality. No available cowpea genotype combined all farmer and other user's desirable traits. In conclusion, achieving food security and poverty reduction, with cowpea as staple would consist of speeding the development of Striga-resistant varieties. This supposes including end-user's (farmer, trader, food processor's) preferences, to fast breed suitable varieties through a combined back-cross/marker-assisted selection.

Related GCP project—SP3 Commissioned G4008.17: Application of marker-assisted selection for Striga resistance in cowpea

Notes:

3.16: A lysimetric system to simultaneously assess T, TE and HI in peanut (*Arachis hypogaea L.*)

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The component of the yield architecture T, TE and HI were measured simultaneously in a lysimetric system (PVC tubes of 1.2m length, 20cm diameter, filled with soil), in nine peanut genotypes (Chico, ICGS 44, ICGV 00350, ICGV 86015, ICGV 86031, ICGV 91114, JL 24, TAG 24 and TMV 2) under well-watered and intermittent drought conditions. The transpiration was measured by regular weighing of the lysimeters with surface mulched with 4-cm thick polythene beads to avoid evaporation. Variation in water extraction from the tubes was found. TE varied from 1.4 to 2.9 g kg-1 under well watered and 1.7 to 2.9 g kg-1 under drought conditions. Highest TE was found in ICGV 86031 and lowest TE in TAG-24, across water regimes. HI was severely reduced under drought and varied from 0.07 to 0.22 across genotypes. Highest HI under drought was found in Chico and ICGV86015. Transpiration efficiency and HI were significantly correlated with pod weight under drought (r2 = 0.48 and r2 = 0.78 respectively). By contrast, there was only a loose relation between the total water extracted and pod dry weight. The system is being used to evaluate T and TE in a large set of germplasm.

Related GCP project—G4006.01 TLI Objective 1 project - Improve groundnut productivity in marginal environments of sub-Saharan Africa

Notes:

3.17: Correlating yield stability under drought with genome introgression through graphical genotyping

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Notes:

Drought stress is uniquely characteristic to specific environments that searching for generalised genomic solutions for drought resistance has impacted little so far. A native landrace, Norungan, considered the most drought resistant rice variety in Tamil Nadu, India was targeted for selective genome exploitation. Advanced backcross progenies of IR642 x Norungan beyond BC2F5 generation were tested under GCP-RF-IRRI funded India- Drought Breeding Network (DBN) since 2005. One line, CB001524 was one of the best potentially drought resistant genotype based on pooled analysis. This line was whole-genome assayed with microsatellite markers and introgressed regions from Norungan putatively responsible for yield stability under stress were located. The randomly introgressed segments possessed QTLs responsible for several component traits. One such region in chromosome 9 at 20 Mb site was bioinformatically characterised to understand the genetic polymorphism of the key drought responsive transcription factors DREB1A and DREB1B. Attempts to study the allelic diversity at this locus between IR64 and Norungan indicated the existence of sequence polymorphism (a small deletion in Norungan and a few bp duplication in IR64). A set of homozygous lines of similar morphology and phenology was phenotyped under drought and the Dreb1 allele variation was associated with the performance.

Related GCP project—SP3 Competitive G4007.05: Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-aided breeding

3.18: Marker–assisted multiple traits pyramiding of root QTLs, water–use efficiency, seedling vigour and grain yield for semi irrigated aerobic and drought tolerance in rice

*MG Vaishali, NS Rudresh, Venkatesh Gandhi R, Pavana Hiremath, Hanamareddy Biradar, Keshavamurthy B C, Grace Arul Selvi, Ahmad Farid Rahmani, Sheshashayee M, Nagabhushana K and Shailaja Hittalmani**

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Drought tolerance and Roots are related intrinsically as they are the main structures that come into contact with soil and water and directly associated with water uptake from the soil. Introgression lines obtained from IRRI were back crossed for other traits and selected for two generations and pyramided for 4-9 QTLs on four of the rice chromosomes for grain yield, water use efficiency and seedling vigour QTLs. The NILs with weed competitiveness- high seedling vigour and water use efficiency and high grain yield were crossed and NILs with the two-three-four traits plants were identified. 60 SSR markers for the four chromosomes, 10 candidate genes were used to identify and test multiple traits pyramids. QTL pyramids accounted for 65 percent phenotypic variation. The combinations of two, three and four QTLs along with check varieties and one QTL were evaluated under severe stress, aerobic situation and control for WUE along with other traits. Under stress, QTL combination on chromosome 9 +2 for roots with others trait combination performed superior for both water use efficiency and grain yield and seedling vigour.

The pyramids had both additive and epistatic effects for root morphological characters, seedling vigour and water use efficiency.

Related GCP project—SP3 Competitive G3007.05: Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker– aided breeding

Notes:

3.19: Response of multiple-trait QTL pyramids for drought tolerance and aerobic situation in India by farmer participatory selection and evaluation

Shailaja Hittalmani, Ramachandrappa BK, Nanjappa HV, Ramakrishna Parama VR, Shivamurthy M, Rudresh NS, Sanathkumar VB, Venkatesh Gandhi R, Hanamareddy Biradar, Keshavamurthy BC and Nagabhushana K*

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Notes:

Multiple traits-QTL pyramids were evaluated in farmer's field and experimental fields for three years. Field selection was Southern Dry Zone of Karnataka, India. Selected 81 genotypes–pyramids of four traits of root morphology, water use efficiency, weed competitiveness and grain yield were evaluated. Genotypes were developed by pyramiding from donor genotypes identified by marker assisted selection. The QTL-traits pyramids exhibited additive and epistatic effects for traits. Two–trait- QTLs were superior for drought stress.

In mother baby trials across 65 locations MAS 26 and MAS 946-1 were found superior for grain yield under aerobic conditions. These genotypes were much liked by farmers and did well in experimental fields too. In moisture stress trials MAS109, MAS229 produced 4.8 tons perha of grain yield and 7. 50 tons of fodder yield. MAS868 gave maximum grain and fodder yield but was not liked by farmers due coarse grains. Under severe moisture stress, MAS109 was liked by 75 percent of farmers for its short duration and fine grain quality and high grain yield.

MAS946-1 and MAS26 are officially released by UAS, Bangalore for aerobic situation and the rest of the advanced selections by farmers are in pre-release State and All India Co-ordinated Trials.

Related GCP project—SP3 Competitive G3007.05: Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker - aided breeding

3.20: Advances in bridging small grain cereals genetic resources, genomics and breeding work in Morocco

Nsarellah N, Udupa S, Abbad FA., Jlibene M, , Tuberosa R, Labhillili M, Ouabbou H, Amamou A, Rhrib K Taghouti M, Ramdani A Lhaloui S and El-Yousfi B, El-Haddoury J and D Ghizlane.*

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A successful integration of modern and conventional approaches to plant improvement is key element in order to show impact of modern biotechnology research on the livelihood of end users. In this project, the integration of genomics, genetic resources use and plant breeding is sought thru several components: a) Enhanced utilisation of germplasm , b) Development of segregating/mapping populations, c) Development of lines through application of genomics tools in conventional breeding programme, d) Generation of new markers including candidate gene/allele-based molecular markers for enhancing the breeding strategies, e) Mining the novel genes and alleles and e) Empower Moroccan researchers to implement new tools of genomics. As the integration of these components and the ability and commitment to collaboration is what should bring tangible results, this project aimed to start and help Moroccan wheat and barley scientists towards this direction. This poster cites some of the advances made in this respect in Morocco in collaboration with GCP. During the 2007-08 season, several genetic resources were identified as valuable for biotic and abiotic stresses common in the dry areas. Several genomic tools are being developed and applied in currently used material by the breeders. Training and disciplinary integration activities were also being undertaken.

Related GCP project—SP3 Commissioned G4007.05: Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco

Notes:

3.21: Cassava wild relatives utilisation at Embrapa

Alfredo Alves, Rui Mendes; Paulo Cézar de Carvalho; Ivo Costa; Miguel Dita; Alba Farias; Alineaurea Silva; Leônidas Tavares Filho; Carlos Ledo; Martin Fregene*

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A collection of Manihot species has been field established at Embrapa/CNPMF, obtained from different sources: 1) wild accessions from CENARGEN and other institutions; and 2) collection expeditions accomplished in semi-arid ("caatinga") and savanna ("cerrado") ecosystems. Currently, the collection has around 920 accessions of 18 cassava wild relatives. The crossing compatibity was assessed in crosses involving cultivars of *M. esculenta* and accessions of 13 wild species: *M. anomala*, *M. flabellifolia*, *M. jacobinensis*, *M. peruviana*, *M. tomentosa*, '*Pornúncia*', *M. caerulescens*, *M. cecropiaefolia*, *M. dichotoma*, *M. glaziovii*, *M. irwinii*, '*Maniçoba*' and cassava 'Sete Anos'. The average rates of fertilised flowers, fruit set, and seed production were significantly different among species and dependent of both donor and receptor of the pollen grains. A total of 158 hybrid seeds were produced from 972 pollinated flowers. Interspecific hybrids between elite cassava varieties and *M. tristis*, *M. flabellifollia* and *M. peruviana* were evaluated for pests resistance in different regions of Brazil. Most of genotypes with high levels of resistance to anthracnose and brown leaf spot were found in progenies involving *M. tristis*. For rust, higher numbers of resistant hybrids had *M. flabellifollia* or *M. peruviana* as parent. Resistance to cassava mealybugs and green mites were found in hybrids of *M. flabellifolia*.

Related GCP project—SP3 Competitive G3005.09: Development of low-cost technologies for pyramiding useful genes from wild relatives of cassava into elite progenitors

Notes:

3.22: Traits related to drought tolerance mechanisms in cassava

Alfredo Alves; Tim Setter; Martin Fregene; Morag Ferguson; Luis Duque; Rosemary Mutegi; Geoffrey Mkamilo*

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Contrasting cassava varieties were screened in semi-arid environments to characterise genotypes for drought tolerance traits. The following hypotheses were supported: 1) genotypes that accumulate substantial stem starch reserves may be more able to sustain meristems and other respiring organs during a prolonged stress; 2) genotypes that maintain deep fibrous root growth perform better in drought; 3) genotypes that maintain partitioning to storage roots and have high harvest index yield better in drought; and 4) genotypes that are more effective in closing stomata are more able to maintain water status and retain leaves. Leaf conductance, leaf retention, leaf size, harvest index, ABA, sugars and starch accumulation in the leaves and stems were differentially affected in the cassava varieties and highly correlated to yield performance under water deficit. The different responses to water deficit for some parameters has helped us to better discriminate varieties as tolerant or susceptible to drought and to define the best traits for selecting in breeding programmes.Three segregating populations with a total of 370 individuals were produced. A genotypic parental screen has revealed 168 polymorphic SSRs in COL1734 x VEN77 and 147 in COL 1468 x BRA 255, from 307 SSRs screened. Genotyping and phenotyping of the mapping populations are underway.

Related GCP project—SP3 Competitive G3005.03: Identifying the physiological and genetic traits that make cassava one of the most drought tolerant crops

Notes:

3.23: Field evaluation of cassava varieties under drought stress in Kenya, Tanzania and Ghana

R Mutegi, M Ferguson, BL Maass., G Mkamilo, J Kamau, J., Adjebeng-Danquah, A Alves, T Setter, T., and M Fregene*

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Notes:

A collaborative project is underway between IITA, CIAT, EMBRAPA, Cornell University and the NARS of Tanzania, Kenya and Ghana to identify the physiological and genetic traits that make cassava one of the most drought tolerant crops. This involves firstly the evaluation under drought stress conditions in Tanzania (Hombolo), Kenya (Kiboko) and Ghana (Tamale) of local varieties and a selection of genotypes from IITA, with contrasting responses to drought stress; and secondly the phenotyping, at the same sites, of two mapping populations (MCOL 1734 x VEN 77; MCOL 1468 x BRA 255) and self progeny (MCOL 1734) developed at CIAT. Currently 31 genotypes are being evaluated in a replicated trial with irrigated and non-irrigated treatments in Kenya, and ten local varieties are being evaluated in a similar experiment in Tanzania. Methodologies for physiological evaluation are being tested, and include stomatal conductance, leaf retention, stem, leaf and petiole starch content, ABA and yield parameters. The in vitro mapping populations are being hardened in Kenya, Tanzania and Ghana. The project has a large capacity building component, both for evaluating the response to drought, and in receiving and hardening in vitro cassava plantlets. Protocols for hardening and rapid micro-propagation of in vitro cassava plantlets have been developed. Genotyping of the mapping populations is underway using approximately 200 polymorphic SSR markers.

Related GCP project—SP3 Competitive G3005.03: Identifying the physiological and genetic traits that make cassava one of the most drought tolerant crops

Theme 4:

Support services and enabling delivery

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

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There is a new facility called the SP4 helpdesk, giving support to GCP scientists regarding issues related to bioinformatics, biometry and data handling. This helpdesk aims to be the entry point for any GCP scientist with questions in these fields. To reach the SP4 helpdesk send a mail to sp4helpdesk@generationcp.org

Current and past SP4 PIs have been approached and an expert database, for internal use, was created. This database will allow easy identification of experts and is used to direct questions received via the helpdesk to the proper expert.

A first start was made to document SP4 products and to rearrange the information on the SP4 web pages. In this way, the visibility and the accessibility of facilities and products, generated over the last years in the GCP Subprogramme 4 is improved.
At present the bioinformatics portal offers an overview of, and links to the bioinformatics products funded by the GCP, or to which GCP has contributed. Also a link to the page of the SP4 helpdesk on bioinformatics and biometrics is available there; Google on 'generation cp bioinformatics' and you'll find the new GCP bioinformatics portal.

Related GCP Project—SP4 Commissioned G4007.10: Support to GCP scientists regarding issues related to bioinformatics and data handling

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4.2: Further development of iMAS for use by NARS and other user communities

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The iMAS system integrates a number of open-source computing tools for marker-aided research and breeding. User feedback on the beta-version of the software called for further enhancements, including multi-environment QTL analyses, comparative QTL mapping through integration of CMTV, linkage with Qu-Gene for modeling MABC and integration of the application with the GCP platform. In its latest release (v1.3), the data validation module incorporates added functionality in validating multiple location phenotypic and multiple population mapping datasets. User interfaces allow the use of multiple data files/sheets for IRRISTAT, GMendel and PlabQTL The IRRISTAT tool has now been extended for multi-environment data analysis. In the linkage map and QTL analysis modules, incorporation of selective viewing and printing options enhance ease of use. Linkage map outputs from GMendel can be exported in formats that are compatible for viewing with the CMTV tool. The current version of iMAS is being distributed as an easy to install Microsoft installer (.msi) file. The software has been used in three training courses in 2008 and over 60 CDs of ver. 1.1 distributed. The user community has provided vital feedback for the improvement of the software, with further training courses schedule later in the year.

Related GCP project—SP4 Commissioned G4007.11: Further development and support for use of iMAS by NARS and other user communities.

Notes:

4.3: Assessing production constraints and opportunities for GCP priority food crops and farming systems

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Notes:

To generate information to support existing projects and identify areas for future investment, the GCP is funding a study of production constraints and opportunities for important food crops in priority farming systems with high degrees of poverty. The study includes wheat, rice, sorghum, cassava, cowpea and chickpea for 15 broad farming systems with large numbers of stunted children (up to 28 million) and large production areas of food crops; mainly in south and east Asia, and sub Saharan Africa. Applying a modified Delphi method, three rounds of surveys will identify and quantify important constraints, and propose opportunities for solutions, especially those that may guide GCP investments. The expert knowledge of around 450 panellists familiar with the crop and region is being sought, including plant breeders, agronomists and other researchers; extensionists, NGO staff and input suppliers. Preliminary results described many important abiotic, biotic, socio-economic and management-related constraints. For example, 'heat during grain filling' (average loss 153 kg/ha grain), the related 'late planting of crop' (150 kg/ha loss), and 'weed competition' (155 kg/ha loss) were the initial main constraints for wheat in the rice-wheat system of south Asia. A comprehensive report and journal article of findings will guide GCP priority setting.

Related GCP project—SP5 Commissioned G4008.36: Getting the focus right: Food crops and smallholder constraints

4.4: Marker-assisted selection on rice and cassava: What is it worth?

George W Norton, Vida Alpuerto, Ndrem Rudi, Abdelbagi Ismail, Martin Fregene, Emmanuel Ikogbenin, and Chiedozie Egesi*

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Economic benefits were projected for GCP supported research aimed at (a) discovering genes for tolerance to saline and phosphorous–deficient soils to enhance rice productivity and (b) developing low cost technologies for pyramiding genes from wild relatives into elite progenitors of cassava. Economic benefits were projected based on the situation with and without the new traits. Benefits considered (a) area planted to crops affected by target stresses and production in specific countries, (b) nature of markets, (c) projected yield and cost changes, (d) time to develop and deploy the DNA marker technologies, (e) time to develop and disseminate new cultivars, and (f) the discount rate. Marker-assisted breeding (MAB) in rice is estimated to save 3-6 years compared to conventional breeding (CB) and result in significant incremental benefits in the range of $50 to $500 million depending on the country, abiotic stress, and lag for CB under base assumptions. Benefits almost double if the 3 year time advantage for MAB over CB is assumed to be 6 years. For cassava, benefits for MAB to incorporate resistance to cassava mosaic disease, green mites, white flies, and post harvest deterioration vary from $34 to $817 million depending on the country.

Related GCP project—SP5 Commissioned G4006.14: Ex Ante impact analysis of marker-assisted selection technologies supported by the Generation Challenge Programme (GCP)

Notes:

4.5: Progress on HPC sustainability options beyond 2008

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HPC hardware funded by the GCP SP4 is approaching its limit of processing capacity, thus a key goal for 2008 is to review and test sustainability options for the GCP Grid beyond 2008, involving external Grid collaborators. The most promising option being explored to date is "plugging in" the GCP grid to resources in Europe via the **EELA**[1] project.

Rationale

GCP HPCs are now aging in terms of a typical 3-5 year life cycle for IT infrastructure, so the goal is to

- define a profile of future processing requirements, using consolidated GCP grid and HPC site usage reports that demonstrate impact and relevance to the GCP SP1, 2 and 3 programmes
- analyse options to support high power GCP bioinformatics computing demands and applications beyond 2008, in the absence of capital investment by centres for replacement or upgrade of existing HPC sites.
- present alternative scenarios to maintain adequate HPC processing capacity at the service of GCP bioinformatics researchers, based on the profile of user requirements with realistic projections for the future.

[1]: E-infrastructure shared between Europe and Latin America project, coordinated via RAAP in Peru. (where RAAP is the Peruvian Internet2 organisation)

Related GCP project—SP4 Commissioned G4005.27: High performance computing facilities for the GCP platform

Notes:

4.6: The 'Community of Practices' concept applied to rice production in the Mekong Region: Quick conversion of popular rice varieties with emphasis on drought, salinity and grain quality improvement

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Line conversion using MAS of target varieties started in May 2007 and was followed up in November 2007 and May 2008. DAR (Myanmar) converted IR53936 to have salinity tolerance and Manawthuka to be aromatic. Homozygous F2s are validated for target traits and will be planted in 4 provinces in Myanmar for yield trial. CARDI (Cambodia) developed drought tolerant line CAR3 to be aromatic with good eating quality. BC3F2-CAR3 selected lines are now evaluated for aroma and other quality traits and observation yield trial will be conducted in CARDI this wet season. NAFRI (Laos) improved the aroma of glutinous rice TDK1 by transferring aroma gene from Homnangnouane (HMN). Twenty-six BC3F2-TDK1 were found carrying HMN allele in all markers and the selected BC3F2 will be planted in NAFRI in 2008 wet season for seed increase before testing in target locations. RGDU and UBN (Thailand) work together in developing aromatic IR57514 with good eating and cooking qualities as well as tolerance to submergence and drought and resistance to bacterial leaf blight. BC3F4-IR57514 lines (236) are screened for submergence and drought tolerance this wet season as well as aroma and grain qualities at RGDU. Observation trial will also be conducted at RGDU.

Related GCP project—SP5 Commissioned G4007.03: The 'Community of Practices' concept applied to rice production in the Mekong region: Quick conversion of popular rice varieties with emphasis on drought, salinity and grain quality improvement

Notes:

4.7: Development of a toolbox of available molecular markers useful for marker assisted selection in GCP crops

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As information on molecular markers for marker assisted selection is often scattered in numerous, expensive peer-reviewed journals and in several databases, some of unknown existence to many, the development of a GCP toolbox made by and for breeders has been initiated. The final product will concentrate on information directly useful for breeding, avoiding that of limited value. The toolbox will providing free and easy access to information on all publicly available molecular markers (SSR, SCAR, SNP, STS) for simply inherited traits and QTLs useful in marker assisted selection for 19 food security crops, i.e. Musa spp., barley, bean, cassava, chickpea, coconut, cowpea, faba bean, groundnut, lentil, maize, millet, pigeonpea, potato, rice, sorghum, sweet potato, wheat and yam. The toolbox will include validated markers as well as markers in process of validation, the latter to avoid duplication of research among scientists. If no markers useful for marker assisted selection are currently available for a specific crop this will be indicated as well. The information provided for each marker includes general information (trait identified by this marker, marker code, marker type…), the lab protocol, the validation process, the most relevant references, and the name of corresponding experts.

Related GCP project—SP5 Commissioned G4008.35: Toolbox of available molecular markers useful for marker assisted selection in GCP crops

Notes:

4.8: Improving capacity for phenotyping cowpea for abiotic and biotic stress tolerance in Senegal

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Cowpea yield is low at farm level in Senegal due to drought, diseases and pests. Biomass production, harvest index and number of pods per plant are important traits for adaptation to drought. Capacities are being developed to properly phenotype these characteristics and physiological parameters for identifying drought tolerant germplasm. In 2007 – 2008, we screened 500 germplasm lines and RILs in the field. Terminal drought stress was achieved by planting at the end of the rainy season. Irrigation was applied during the first 20 days after emergence afterward no water was supplied. Agronomic and physiological parameters were measured,. Based on visual scoring, yield potential and pod number, some accessions were promising across these 3 parameters, including UCR830; IT98K-128-4, IT97K-1479 and IT99K-1245. Five more had a great potential of pod production: IT98K-428-3, IT99K-718-6, IT95K-1093-5, Early Scarlet and 1393-1-2-3. Another five had the ability to resist drought by regulating the loss in pod production: CB46, IT90K-284-2, Big Buff, Sasaque and IT86F-2014. Funds provided by the GCP are being used to improve the irrigation system and screen house facilities at Bambey station allowing us to confirm these results and improve our phenotyping for ashy stem blight bacterial blight and aphids.

Related GCP project—SP5 Commissioned Capacity-building a la carte G4008.39.03 Improving capacity for phenotyping for abiotic and biotic stress in Senegal

Notes:

4.9: Molecular breeding application for the management and visualisation of information from MAB programmes–SP3 use case

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The design and development of a tracking and visualisation system for marker assisted breeding (MAB) is in progress. Development is driven by user requirements gathered and documented through frequent interactions with breeders from ICRISAT, CIMMYT and national programmes. The application will provide users with four major functional components:

a) Query and visual selection tool that facilitates choice of promising lines in a cross.
b) Visual design of target genotype after analyzing compatibility between donor and recurrent parents.
c) Tracking system that functions as a LIMS for MAB.
d) Data loading component that commits useful data to a central database.

The first and second components provide generic functionality that can be used across different breeding programmes and crops, and is being developed in collaboration with ICRISAT and IRRI-CIMMYT CRIL. These components rely on genotyping, phenotyping, QTL and genetic map data available in files or through the GCP Informatics Platform (Bruskiewich, et al. 2008). The third and fourth components are laboratory specific and will be developed independently. To provide the user with the benefits of a standalone application with a rich user interface, the tool is being built using Eclipse RCP technology (http://www.eclipse.org; http://www.bioclipse.net). A prototype has been developed that allows a user to view linkage and QTL maps with graphical genotypes of potential parents, analyze compatibility between donor and recurrent for the design of a target genotype.

Related GCP project—SP4 Commissioned G4006.16: Development of an integrated GCP platform

Notes:

4.10: Marker-aided development of nutritionally-enhanced cassava for Nigeria

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Micronutrient deficiency among children under five years and nursing mothers is prevalent in developing countries. Crosses were made at CIAT to generate populations with combined enhanced beta carotene and high protein contents in cassava roots. The parents were known to have cream or deep yellow coloured-roots and crude protein contents of 3-8%. A total of 1555 seeds were derived from 17 parents in different combinations. The number of plants successfully established in vitro from embryo axes was 981 (68%). Marker-assisted selection (MAS) for resistance to cassava mosaic disease (CMD) was conducted using one SSR marker, NS158 and a SCAR marker, RME 1. Fourteen percent of the plants (138) were selected and micro-propagated to generate 8-10 plants each. The selected CMD-resistant genotypes (687) were shipped as in-vitro materials to Nigeria for evaluations. Two NRCRI scientists were trained at CIAT in MAS for these nutritionally-enhanced germplasm. Also, 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 Capacity-building à la carte G4007.13.02: Marker-aided development of nutritionally-enhanced cassava for Nigeria

Notes:

4.11: HaploPhyle: Graphical Haplotype network in the light of external data

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The HaploPhyle project intends to provide the community with a pipeline of genotyping data (sequences or SNPs) analysis which will include haplotypes definition, haplotype network analysis and connection with external data such as geographic origin or genetic group. The haplotyping part will reuse existing software like Haplotyper or Gevalt. The pipeline will define the haplotype network. This part will be done via a java library implementing for now the Minimum Spanning Network algorithm. In the future, more algorithms, like Median Joining Network, will be added enabling more choices to the users. In the graphical representation, nodes sizes will be proportional to the numbers of germplasms sharing a haplotype and edges length will be proportional to the differences between haplotypes. Nodes of the network will include pie-charts representing the repartition of external information (set by the user) among germplasms owning this haplotype. Users may also wish to compare the different haplotypes, and outline their differences, by comparison to reference haplotypes. This can be added to the haplotype graphical representation. Analyzing haplotype networks and relating them to geographic patterns allows development of phylogeographic analyses and has a great power for resolving crop domestication and understanding further crop adaptation.

Related GCP project—SP4 Commissioned G4008.22: Methodology development for reconstruction of Genealogies based on Haplotypes related to geographic pattern (Haplophyle: graphical haplotype network in the light of external data)

Notes:

4.12: Software for data analysis and integration of gene expression microarray and QTL data

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The major goal of this project is to further elucidate genes, alleles, mechanisms and other factors related to abiotic and biotic stress response across multiple crops. This will be achieved through the analysis of available crop gene expression, genomic sequence, phenotype, genotype and QTL mapping data sets from GCP projects. Extensions to the Maxd software for supporting genomic expression analysis have been made to allow this software to be fully Plant-MIAME compliant and to take advantage of the ontologies in development by the GCP. Other extensions include those for the EASE software for gene enrichment in gene expression analysis and MAPMAN for displaying gene expression data in relation to pathways. These plant specific extensions will allow GCP researchers to use these tools, which were not developed originally for crop species. The RiCES: Rice Cis-Element Searcher, a cis-element searching tool optimised for rice genome and MAANOVA software for microarray gene expression analysis are available on the HPC. QTL data, publicly available sequence data, microarray data, and genetic and physical maps have been integrated using CMAP, a comparative map viewer. Links to software and documentation developed and used by this project can be found on the GCP Bioinformatics Portal (http://www.generationcp.org/bioinformatics).

Related GCP project—SP4 Commissioned G4006.08: Data analysis support for existing projects in SP2 with emphasis on integrating results from microarray and mapping experiments

Notes:

4.13: Evaluation of the GCP Central Registry and data templates

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Established in 2005, the Generation Challenge Programme (GCP) Central Registry provides an overview of all available data resources generated by the different GCP projects. In tandem to this resource, data templates were developed to facilitate the storage of various data types within the Central Registry. To increase the availability of GCP data templates, enhance data validation results, further extend the collection of resources managed by the Central Registry and improve access to the data held therein, the status of both was evaluated for 2008. Statistics were collected to determine the availability and use of the GCP Data Templates and of the data sets within the GCP Central Registry. Feedback from principal investigators and other project collaborators was surveyed to evaluate the quality of both resources and the expected needs of users. Results were used for priority setting to devise a combined action plan for the future use and development of both resources. Links to Central Registry and GCP data templates can be found on the GCP Bioinformatics Portal (http://www.generationcp.org/bioinformatics).

Related GCP project—SP4 Commissioned G4008.20: Management of the GCP Central Registry and the creation and maintenance of templates for data storage in repositories

Notes:

4.14: Development of Generation CP domain models and ontology management embedded in the GCP Platform

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To maintain semantic flexibility and extensibility, Generation CP domain models (DM) were designed to be heavily parameterised by diverse context-specific ontology within the Generation Challenge Programme (GCP). The maintenance of the DM is continued and has generated the current version 1.18.0 of the Demeter ontology. GCP compliant ontology data source is made with the description and use cases at http://pantheon.generationcp.org for embedding ontology management in the GCP platform. The GCP data template with ontology integration is part of phase II at http://www.generationcp.org/bioinformatics.php?da=0650728. Initial sources of ontology terms for crop-specific ontologies are identified such as the ICIS for rice, wheat and maize and the Bioversity germplasm descriptors. Draft releases of the OBO formatted ontology files for rice, wheat and maize traits are available at http://cropforge.org/projects/gcpontology/. In addition, collaborators are developing initial draft of the OBO formatted ontology files for the crops musa, chickpea, groundnut and potato. The validation of GCP ontologies will be made through representative datasets from the GCP Central Registry (http://gcpcr.grinfo.net/) and the ontologies will be annotated with the available datasets. The training materials for co-PIs have been posted at the pantheon website. Aside from the Pantheon website, a project was made specifically for GCP ontology at CropForge (http://cropforge.org/projects/gcpontology/).

Related GCP project—SP4 Commissioned G4005.22: Development of Generation CP domain models and ontology

Notes:

4.15: Indicators of attractiveness and feasibility of GCP technologies

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This project assesses the capacity for development and adoption of GCP technologies. Building on an existing evaluation of high priority geographic areas and cropping systems, the assessment identifies local capacities for technology adoption. The study develops and evaluates indicators according to combinations of priority traits and crops of the GCP. First, 36 unique combinations of farming systems and countries were ranked according to their levels of drought and crop production. Next, GCP research was inventoried according to country, crop and trait combinations, allowing us to delineate the extent of GCP activities in developing countries. An analysis of adoption capacity at country level was initiated using the Agricultural Science and Technology Indicators (ASTI) database. The next step is to develop case studies of the feasibility of technology adoption for key combinations of crops and traits that are high priority for the GCP. The case studies will explore local scientific and institutional capacities, and other local conditions necessary for farmers to adopt GCP technology.

Related GCP project—SP5 Commissioned G4008.24: From attractiveness to feasibility: a strategic assessment of the capacity to develop and adopt GCP technologies

Notes:

4.16: Provision of Genotyping Support Services (GSS): An IRRI perspective

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Notes:

The GCP-Genotyping Support Services assists developing country institutes apply molecular marker technology for crop improvement. GCP engaged IRRI as an expert genotyping services provider responsible for legal and phytosanitary requirements for shipment of rice DNA, for genotyping of samples, and for providing the client institution and GCP with the data generated from the services described in each work order. As host agent for GCP, CIMMYT provides information on the client institution and the marker data for use in genotyping. Two work orders from the China National Rice Research Institute and Crops Research Institute in Ghana, respectively, are currently in place - screening of a population for Xa7 and Xa21 bacterial blight resistance genes and Rf3 and Rf4 fertility restorer genes and genetic diversity analyses of African rice germplasm. In the pipeline is the work order for genotyping of CBSN-derived indica x indica lines from India. These initial work orders will provide GCP with feedback on the logistics needed to complete each work order efficiently and effectively – from getting the good quality DNA to IRRI, and the data back to the client and GCP.

Related GCP project—SP5 Commissioned G4007.21: Genotyping Support Service

4.17: Environmental assessment for phenotyping network

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To assess performance of genotypes, crop improvement programmes require evaluation of materials under different environmental conditions. Testing programmes have an opportunity to be more efficient by carefully selecting testing sites that permit evaluation over a broad range of environments. What methods and tools can be used to guide the selection of testing sites for the evaluation of genotypes? This project demonstrates the use of agronomic and environmental modeling of possible locations for assessing genotypes within a phenotyping network. Conditions at more than fifty candidate testing sites were evaluated using data on climate, soils, crop production and other variables. For each candidate site, climate information was developed to get a sense of the water balance and the seasonal variation in rainfall, evapotranspiration, temperature and length of the growing season. Crop production, soil characteristics and climatic conditions surrounding each candidate site were derived from digital maps using overlay techniques. A set of existing climate analysis tools and a research atlas have been adapted and modified for use by GCP researchers. The information derived from this study will be used to support decisions on the deployment and testing of genotypes in crop improvement programmes.

*Related GCP project—SP5 Commissioned G4008.34:
Environmental assessment for phenotyping network*

Notes:

4.18: Development of salt tolerance in rice through marker–assisted selection

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Sinthwelatt (IR 53936-60-3-2-3-1) is popular rice variety in Myanmar. It has high yielding and good eating quality. It is sensitive to salinity. It was improved for salinity tolerance through marker assisted selection (MAS) and conventional backcrossing. Pokkali was used as donor for salinity tolerance and Sinthwelatt was used as recurrent parent. Up to BC3F4 progenies were selected by using 2 markers linked to salt tolerance, including SalT and RM 472 (chromosome 1). Homozygous lines for Pokkali allele were selected and 10 lines were backcrossed to generate BC4F1. The rests were selfed to produce BC3F5. In BC4F1 49 homozygous were identified for Pokkali allele and these were selfed to produce BC4F2. BC3F5 plants and BC4F2 plants were selected by using salt markers, salT, RM 10720, RM 3412, RM 1287and RM 10772 (on chromosome 1) and RM 411 (chromosome 3). All plants were checked for Sinthwelatt allele by using quality markers (waxy, RM 21, RM 5349 and RM 457 locating on chromosome 11) linked to amylose content and gelatinisation temperature. Near isogenic lines containing the targeted QTLs were obtained by visual selection for agronomic traits and yield performance under normal soil condition. Some promising introgression lines will be tested in salt affected area.

Related GCP project—SP5 Commissioned G4007.03: The 'Community of Practices' concept applied to rice production in the Mekong region: Quick conversion of popular rice varieties with emphasis on drought, salinity and grain quality improvement

Notes:

4.19: Preliminary results in phenotyping cowpea for drought tolerance in Burkina Faso using two dates of planting

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Terminal drought occurring around mid-September is one of the constraints that reduce cowpea production in Burkina Faso. Two series of trials, UCR core and UCR RIL's composed respectively of 100 entries and 125 entries have been conducted in 2007 at Kamboinse research station in order to select the best entries for further screenings. Each trial has been planted twice (Early and mid-August) in order to submit the entries to drought stress in September during flowering period. Seed production was significantly reduced by drought in the second date of planting compared to the first date while 100 seed weight was generally higher in the second date of planting. Characteristics of the top 25% of the entries of each trial are presented in this paper.

Related GCP project—SP5 Commissioned Capacity-building à la carte G4008.39.02: Improving capacity for phenotyping for abiotic and biotic stress in Burkina Faso

Notes:

4.20: Query, visualisation and analysis workbench for genetic diversity studies and for functional genomics research

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The GCP Informatics Platform seeks to alleviate the problem of integrating dispersed data sources for analysis by diverse tools by providing an informatics platform using consensus domain models and software standards.

Here, we describe GCP platform efforts to further develop and more extensively cross-link two web components designed to facilitate, respectively, the analysis of genetic diversity and functional genomics research.

The first component is a genetic diversity module, GenDiversity, to combine, query and analyze decentralised genotyping data from different databases and convert outputs to different file formats for further diversity analysis by DARwin, Convert, Structure, Haploview. Such data may be queried by passport data, computation of allelic frequencies, computation of LD, and checking for duplicates.

The second component is the GCP domain model driven web search engine ("Koios"). This engine cross-links structural and functional genomics data, including gene annotation linked to phylogenomic information, gene expression, with linkage to sample information in germplasm databases, and QTL mapping data.

In 2009, these two components will share a common Joomla! based web portal cross links between them are being established through the shared standards of the GCP domain model, GCP application programming interfaces and use of common Koios search engine software libraries.

Related GCP Project—SP4 Commissioned G4006.16: Integrated GCP Informatics Platform

Notes:

4.21: Characterising cassava germplasm in seven African NARS breeding programmes

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To efficiently manipulate germplasm within a breeding programme, plant breeders need to understand the extent, nature and structure of the diversity of their germplasm, and how this relates to diversity available internationally. This project aims at characterising and assessing diversity at the phenotypic and genotypic levels in cassava used by seven NARS breeding programs in Africa, namely DR Congo, Rwanda, Kenya, Uganda, Tanzania, Mozambique and Madagascar. The assembled cassava set for study includes local varieties, breeders’ germplasm, germplasm resources within national genebanks and international nurseries. The principle outputs will include: (1) development of standardised cassava phenotypic characterisation methodologies; (2) generation of qualitative, quantitative and genotypic data on cassava germplasm available in the NARS; 3) development of a central database with passport data, farmer-knowledge, pedigrees, phenotyping and genotyping data of accessions used by NARS; (4) seven NARS scientists trained in SSR genotyping at IITA-Nairobi; and (5) an assessment of diversity at the national and regional levels in relation to that at the global level through comparison with GCP diversity studies. The project was funded by GCP in collaboration with the Rockefeller Foundation and BioSciences eastern and central Africa (BecA), and runs in parallel with a similar project on sorghum, coordinated by ICRISAT. Data will become available following a final data analysis workshop in October 2008.

Related GCP project—Focus (GCP/RF) G4005.70.02 (CB20b): Tapping crop biodiversity for the resource–poor in East and Central Africa

Notes:

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