Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE-POOR

2008 Project briefs

GCP's five Subprogrammes

Subprogramme 1: Crop genetic diversity – Characterises the diversity of crop germplasm collections in the custody of the CGIAR and national programmes in terms of genetic structure and associated phenotypic variation

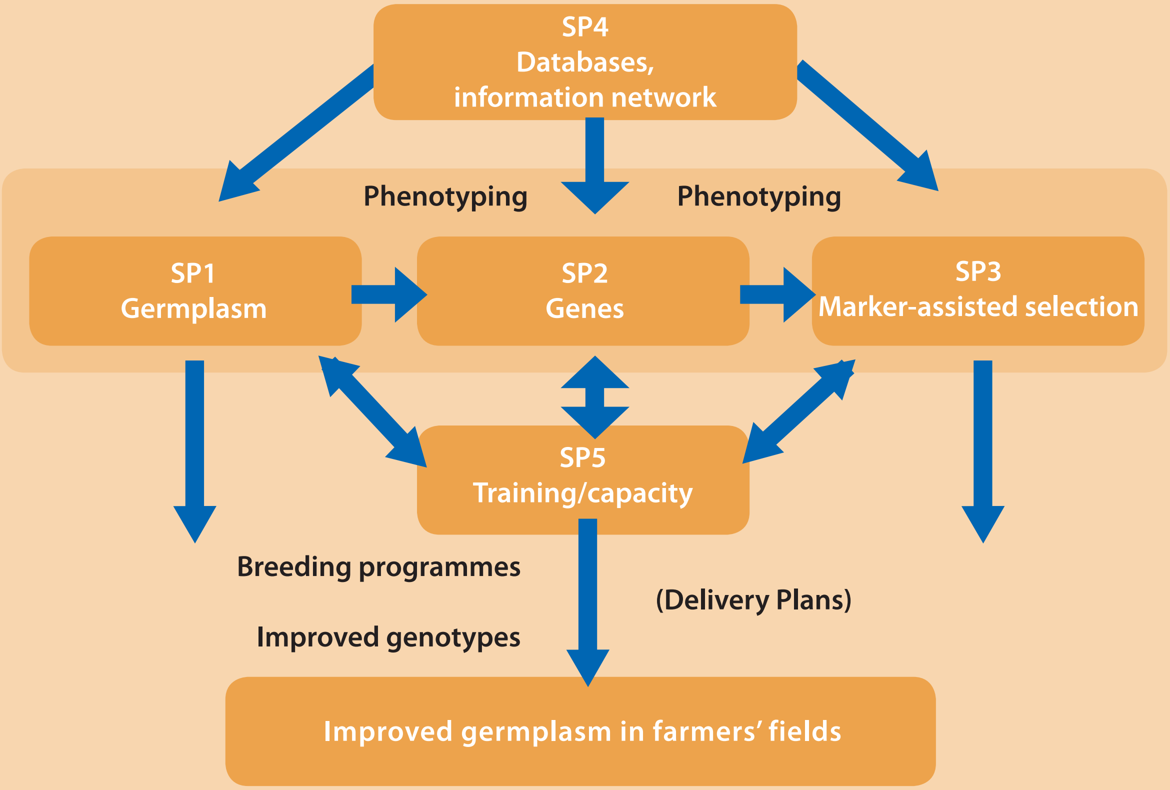
Subprogramme 2: Genomics towards gene discovery – Uses and designs genomic tools and technologies and evaluates interdisciplinary approaches to better understand gene function and interaction, in order to improve knowledge of gene systems across crops

Subprogramme 3: Trait capture for crop improvement – Validates gene function and refines molecular breeding systems and the resulting enhanced germplasm, so as to increase the efficiency, speed and scope of plant breeding

Subprogramme 4: Bioinformatics and crop information systems – Integrates GCP information components and analysis tools into a coherent information gateway and provides support for data analysis to the other GCP Subprogrammes

Subprogramme 5: Capacity-building and enabling delivery – Empowers scientists in developing country agricultural research programmes to use modern breeding approaches. SP5 also coordinates the design and implementation of project Delivery Plans and is responsible for intellectual property issues, and research in policy and impact assessment.

GCP's five Subprogrammes



Generation Challenge programme

2008 Project briefs

July 2010

The project briefs are extracted from the original, or – where applicable – updated project proposals. Partners are listed based on the most recent submissions received from project Principal Investigators. Budget figures are extracted from project proposals.

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Acronyms

ABC	Agricultural Biotechnology Center, Gödöllö, Hungary
ABRII	Agricultural Biotechnology Research Institute of Iran
ACCI	African Centre for Crop Improvement, South Africa
ACGT	African Centre for Gene Technologies, South Africa
ACPFG	Australian Centre for Plant Functional Genomics Pty Ltd
Agropolis–CIRAD	Centre de coopération internationale en recherche agronomique pour le développement, France
Agropolis–INRA	Institut national de la recherche agronomique, France
Agropolis–IRD	Institut de recherche pour le développement, France
AICPMIP	All India Coordinated Pearl Millet Improvement Project
ARC–Sudan	The Agricultural Research Corporation, Sudan
ARI–HAS	Agricultural Research Institute of the Hungarian Academy of Sciences, Hungary
ARI–Naliendele	Agricultural Research Institute–Naliendele Research Station, Tanzania
ARI–India	Agharkar Research Institute, India
ARTC	Agricultural Research and Technology Corporation, Sudan
BAU	Birsa Agricultural University, India
BF	Barwale Foundation
BGBM	Botanic Garden and Botanical Museum Berlin–Dahlem, Germany
BINA	Bangladesh Institute of Nuclear Agriculture
BIOSS	Biomathematics and Statistics Scotland Research Institution, UK
BIOTEC	National Center for Genetic Engineering and Biotechnology, Thailand
Bioversity	Bioversity International
BRRD	Bureau of Rice Research and Development, Rice Department, Thailand
BRRI	Bangladesh Rice Research Institute
CARDI	Cambodia Agricultural Research and Development Institute
CAAS	Chinese Academy of Agricultural Sciences
CARBAP	Centre Africain de recherche sur bananas et plantains, Cameroon
CAS–IP	CGIAR Central Advisory Service for Intellectual Property
CAZRI	Central Arid Zone Research Institute, India
CERAAS	Centre d'Etude Régional pour l'Amélioration de l'Adaptation à la Sécheresse, Senegal
ChSU	Charles Sturt University, Australia
CIAT	International Center for Tropical Agriculture
CIHEAM–IAMM	Institut Agronomique Mediterranéan de Montpellier, France
CIMMYT	Centro Internacional de Mejoramiento de Maíz y Trigo; the International Maize and Wheat Improvement Center
CIMS	Centro de Inteligencia sobre Mercados Sostenibles, Costa Rica
CINVESTAV	Centro de Investigación y de Estudios Avanzados
CIP	International Potato Center
CNG	Centre National de Génotypage, France
CRI	Crop Research Institute, Ghana
CRIL	(CIMMYT–IRRI) Crop Research Informatics Laboratory
CRRI	Central Rice Research Institute, India
CRURRS	Central Rainfed Upland Rice Research Station, India
CSIR	Council for Scientific and Industrial Research, Ghana
CSIRO	Commonwealth Scientific and Industrial Research Organisation, Australia
CSU	Carolina State University, USA
CU	Cornell University, USA
DAR	Department of Agricultural Research, Myanmar
DARS	Department of Agricultural Research & Technical Services, Malawi
DArT P/L	Diversity Arrays Technology Pty Ltd
DPSPP–EKC	Department of Plant Sciences and Plant Physiology, Eszterházy Károly College, Eger, Hungary
DMR	Directorate of Maize Research, India
DOA	Department of Agriculture, Thailand
DWR	Directorate of Wheat Research, India
EARO	Ethiopian Agricultural Research Organization
EBI	European Bioinformatics Institute, United Kingdom
EIAR	Ethiopia Institute for Agricultural Research
EMBRAPA	Empresa Brasileira de Pesquisa Agropecuária, Brazil
ETH–Zurich	Eidgenössische Technische Hochschule, (Swiss Federal Institute ofTechnology), Zürich
FABI	Forestry and Agricultural Biotechnology Institute, South Africa
Fedearroz	Federación Nacional de Arroceros, Colombia
GIPB	Global Partnership Initiative for Plant Breeding Capacity Building
HAAS	Institute of Dry Farming, Hebei Academy of Agricultural Sciences, China
HAKI	Research Institute for Fisheries, Aquaculture and Irrigation, Hungary
HUAZ	Huazhong Agricultural University, China
IA–Tápiószele	Institute for Agrobotany, Tápiószele, Hungary
IAO	Instituto Agronomico per l'Oltremare, Italy
IARI	Indian Agriculture Research Institute
IBONE	Instituto de Botánica del Nordeste, Argentina
ICABIOGRAD	Indonesian Centre for Agricultural Biotechnology and Genetic Resources and Research Development
ICAR	Indian Council of Agricultural Research
ICARDA	International Center for Agricultural Research in the Dry Areas
ICL	Imperial College London, UK
ICERI	Indonesian Cereals Research Institute
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
IER	Institut d'Economie Rurale, Mali
IGAU	Indira Gandhi Agricultural University
IGD	Institute for Genomic Diversity, Cornell University, USA
IGKV	Indira Gandhi Krishi Vishwa Vidyalaya (Indira Gandhi Agricultural University), India
IIAM	Institute of Agricultural Research of Mozambique
ILRI	International Livestock Research Institute
IITA	International Institute of Tropical Agriculture
INCA	Instituto Nacional de Ciencias Agricolas, Cuba
INIA–Chile	Instituto de Investigaciones Agropecuarias, Chile

INIA–Uruguay	Instituto Nacional de Investigación Agropecuaria, Uruguay
INERA–Burkina Faso	Institut de l'Environnement et de Recherches Agricoles, Burkina Faso
INERA–DRC	Institut national pour létude et la recherche agronomique, Democratic Republic of Congo
INRA–Morocco	Institut National de la Recherche Agronomique, Morocco
INRAN	Institut National de Recherches Agronomiques du Niger
INTA	Instituto Nacional de Tecnologia Agropecuaria, Nicaragua
IPB	Centre Research for Biotechnology, Bogor Agriculture University, Indonesia
IPK	Institute for Plant Genetics and Crop Plant Research, Germany
IRRI	International Rice Research Institute
ISABU	Institut des sciences agronomiques du Burundi
ISAR	Institut des sciences agronomiques du Rwanda
ISRA	Institut Sénégalais de Recherches Agricoles
JIC	John Innes Centre, UK
JIRCAS	Japan International Research Center for Agricultural Sciences
JNKV	Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur, India
KARI	Kenya Agriculture Research Institute
KUL	Katholieke Universiteit Leuven, Belgium
LAAS	Luoyang Academy of Agricultural Sciences, China
LGDP	Laboratoire génome et développement des plantes, Agropolis, France
LUMC	Leiden University Medical Center, The Netherlands
MAU	Marathwada Agricultural University, India
MPUAT	Maharana Pratap University of Agriculture and Technology, India
MMRI	Maize and Millets Research Institute, Pakistan
MU	Moi University, Kenya
NAARI	Namulonge Agricultural and Animal Production Research Institute, Uganda
NACRRI	National Crops Resources Research Institute, Uganda
NagU	Nagoya University, Japan
NARC	Nepal Agricultural Research Centre
NAFRI	National Agricultural and Forestry Research Institute, Laos
NARI	National Agricultural Research Institute, Eritrea
NAU	Nanjing Agricultural University, China
NCGR	National Center for Genomics Resources, USA
NCSU	North Carolina State University, USA
NDUAT	Narendra Dev University of Agriculture and Technology, Faizabad, India
NIAB	National Institute of Agricultural Biology, UK
NIAS	National Institute of Agrobiological Sciences, Japan
NMRI	National Maize Research Institute, Vietnam
NPGRC	National Plant Genetic Resources Centre, Tanzania
NRCPB	National Research Centre on Plant Biotechnology
NRCRI	National Root Crops Research Institute, Nigeria
NRCS	National Research Centre for Sorghum, India
NSFCRC	Nakhon Sawan Fields Crop Research Centre, Thailand
NWSUAF	University of Agriculture and Forestry, China
OSU	Oregon State University, USA
PARC	Pakistani Agricultural Research Council
PAU	Punjab Agricultural University, India
PBI–UoS	Plant Breeding Institute, University of Sydney, Australia
PDKV	Dr Panjabrao Deshmukh Krishi Vidyapeeth, (Dr Panjabrao Deshmukh Agricultural University) India
PEU	Peking University, China
PhilRice	Philippine Rice Research Institute
PROINPA	Promoción e Investigación de Productos Andinos, Bolivia
PSU	Pennsylvania State University, USA
RCB–IPB	Research Center for Biotechnology, Bogor Agricultural University, Indonesia
RGDU	Rice Gene Discovery Unit, Thailand
SAAS	Shanxi Academy of Agricultural Sciences, China
SAARI	Serere Agricultural and Animal Production Research Institute, Uganda
SABRN	Southern Africa Bean Research Network
SARI	Savannah Agricultural Research Institute, Ghana
SCRI	Scottish Crop Research Institute, UK
SGRP	System-wide Genetic Resource Programme
SIRDC	Scientific and Industrial Research and Development Centre, Zimbabwe
SUA	SUA Sokoine University of Agriculture, Tanzania
TAMU	Texas A&M University, USA
TNAU	Tamil Nadu Agricultural University, India
TU	Tishreen University, Syria
UBU	Ubon Ratchatani University, Thailand
UCB	Universidade Católica de Brasilia, Brazil
UdB	Università di Bologna, Italy
UdlR	Universidad de la Republica, Uruguay
UdU	Università di Udine, Italy
UKZN	University of KwaZulu–Natal, South Africa
UAS	University of Agricultural Sciences, India
UoC	University of California, USA
UdT	Universidad de Talca, Chile
UEM	Universidade Eduardo Mondlane, Mozambique
USDA–ARS	United States Department of Agriculture–Agricultural Research Service
UoA	University of Arizona, USA
UoAlb	University of Alberta, Canada
UoAb	University of Aberdeen, UK
UoAa	University of Aarhus, Denmark
UoAd	University of Adelaide, Australia
UAC	Universidad Autónoma Chapingo, Mexico
UoC–Davis	University of California–Davis, USA
UoC–Riverside	University of California–Rivdserside, USA
UoD	University of Dhaka, Bangladesh
UoG	University of Georgia, USA
UoGh	University of Ghana
UoH	University of Hohenheim, Germany
UKZN	University of KwaZulu–Natal, South Africa
UoM	University of Maryland, USA
UoMi	University of Missouri, USA
UoP	University of Perpignan, France
UoPd	University of Potsdam, Germany
UoQ	The University of Queensland, Australia
UoV	University of Virginia, USA
VPI	Virginia Polytechnic Institute and State University, USA
WARDA	Africa Rice Center
WUR	Wageningen University and Research Centre, The Netherlands
YAAS	Yunnan Academy of Agricultural Sciences, China
YU	Yale University, USA
ZU	Zhejiang University, China

I. COMPETITIVE PROJECTS

Subprogramme 1: Crop genetic diversity

Current projects

1. Project No G3005.10: Exploring natural genetic variation: developing genomic resources and introgression lines for four AA genome rice relatives

- *Duration: Jan 2005–Dec 2008*
- *Budget by year: $331,700 (2005), $337,800 (2006), $325,200 (2007), $80,200 (2008); Total budget: $1,074,900*

Rice/Drought tolerance/Various regions

Lead institute
Agropolis–IRD/CIAT (Mathias Lorieux, Joe Tohme)
Collaborating institutes and scientists

- CU (Susan R. McCouch)
- EMBRAPA (Claudio Brondani)
- WARDA (Baboucarr Manneh, Marie Noelle Ndjiondjop)
- CIAT (César P. Martinez)
- Fedearroz (Miguel Diago Ramirez)

Cereals provide the majority of calories consumed by humans. Cereal production faces growing challenges due to increasing human population, changing nutritional requirements and variable environmental conditions that require new approaches to crop production. Wild relatives of modern crop species have survived for millions of years using natural genetic defenses to endure biotic and abiotic aggressions. These wild relatives represent a valuable source of under-utilised genetic variation that is available to plant breeders and represent an invaluable source of genetic information for modern genomics research initiatives. A systematic approach is required to identify and characterise genes from wild species that can be used to enhance crop productivity in a range of environments and under diverse cultural conditions. Using rice as a model, we propose to (1) develop four libraries of interspecific lines called Chromosome Segment Substitution Lines (CSSLs), targeting chromosomal introgressions from different rice relatives, (2) develop a set of 140 molecular markers (called SNPs) identified in genes associated with tolerance to abiotic stress (drought, acid soils, mineral deficiencies or toxicities), (3) validate the utility of the SNPs by using them in the development of the CSSLs in this project and exploring their value in breeding programmes for other cereals (4) analyse a set of advanced CSSLs generated from Asian x African rice crosses for their phenotypic response to drought stress. Generating such resources and knowledge will contribute to the objectives of Subprogrammes 1 and 3 by (i) utilising *natural genetic diversity* to develop whole-genome libraries of CSSLs as a permanent genetic resource for both breeding and genomics-based research (ii) producing high-throughput, cost-effective markers to *facilitate access* to genetic diversity in a range of different cereal species (iii) making the CSSLs available to breeders and geneticists so that the intersection of their efforts will continue to generate new knowledge.

2. Project No G3007.01: Interspecific bridges that give full access to the African rice allele pool for enhancing drought tolerance of Asian rice

- *Duration: Aug 2007–Jul 2009*
- *Budget by year: $340,000 (2007), $329,000 (2008); Total budget: $669,000*

Rice/Drought tolerance/Africa and Asia

Lead institute
Agropolis–IRD (Alain Ghesquière)
Collaborating institutes and scientists

- PhilRice (A Alfonso)
- IER (Fousseyni Cissé)
- Fedearroz (M Diago)
- INERA–Burkina Faso (H Drissa)
- UoA (DW Galbraith)
- Agropolis–IRD/CIAT (M Lorieux)
- CIAT (CP Martinez, J Tohme)
- WARDA (MN Ndjiondjop, M Semon, M Sié)
- UoP/Agropolis–LGDP/IRD (O Panaud, R Guyot)
- PAU (JS Sidhu)

This project aims to overcome an important obstacle to rice breeding: the interspecific sterility barrier. While many interesting traits have been introgressed into cultivated rice (*Oryza sativa L.*) from African cultivated rice (*O. glaberrima Steud.*) and other rice relatives, this approach is very tedious and time consuming and breeders generally prefer the simplest path of intra-specific crosses since the sterility barrier is not an issue. We propose to combine the power of the latest genetic marker technologies (Single Feature Polymorphisms, Simple Sequence Repeats), gene discovery techniques, and a specially designed crossing scheme to produce interspecific bridges between the two cultivated species of rice. These interspecific bridges basically comprise *O. sativa* lines, carrying large introgressions of the *O. glaberrima* genome and that are compatible with *O. sativa* in crosses. These would therefore be the materials of choice for large scale introduction of allelic diversity of African rice into Asian cultivated rice germplasm.

Implications and outputs of this project would be substantial with respect to rice breeding: nearly the whole genetic diversity of *O. glaberrima* would become available to breeders for use in classical breeding schemes or marker-aided selection schemes, whether or not combined with recurrent selection.

If successful, this approach could be applied to other AA-genome rice relatives and even to other crops to obtain a full and quick access to the ancestral allele reservoir that was largely lost during the domestication process.

This project involves nine partners: two ARIs (LGDP–IRD/CNRS/Perpignan University, France and the University of Arizona, USA), two CGIAR Centers (CIAT, Colombia and WARDA, Benin), four NARS – from Africa (IER–Mali, INERA–Burkina Faso), South America (Fedearroz–Colombia) and Asia (PhilRice–Philippines) – and the University of Punjab (India).

3. Project No G3007.02: Genomic dissection of tolerance to drought stress in wild barley

- *Duration: Aug 2007–Jul 2009*
- *Budget by year: $343,154 (2007), $224,450 (2008); Total budget: $567,604*

Barley/Drought tolerance/Various regions

Lead institute
SCRI (Robbie Waugh)
Collaborating institutes and scientists

- SCRI (Dave Marshall, Joanne Russell)
- ICRADA (Michael Baum, Stefania Grando, Maria von Korff Schmising, Salvatore Ceccarelli)
- OSU (Patrick M Hayes)
- INIA–Chile (Ivan Matus)
- UdT (Alejandro Del Pozo)
- UoC–Riverside (Timothy J Close)

Through an existing collaboration we have developed a unique segregating population of 140 barley lines composed of an advanced elite genetic background containing introduced chromosomal segments from a wild barley accession that comes from the Fertile Crescent. The wild species, the donor of the introduced genomic segments, is genetically distant from the cultivated line and is both adapted to, and tolerant of, drought and salt stresses. Using genetic tools that allow us to follow the inheritance of the genomic segments from the donor into the recipient line we have been able to show that in this unique population we have representative segments covering the entire genome of the donor in each of the different lines. In genetical terms we call these lines recombinant chromosome substitution lines or **RCSL's**. Evolution by natural selection, domestication and plant breeding has resulted in each of the paired genomic segments from the wild species and elite line having subtly to strikingly different versions of the same genes. This variation will affect the growth and/or performance characteristics of each of the **RCSLs** compared to each other and to their parents. For example, if the introduced segment contained a version of a gene that conferred resistance to salinity that was absent in the elite line, then we expect all of the individual **RCSLs** that contain that segment also to become resistant to salinity. The unique feature of **RCSLs** that is different from standard bi-parental cross populations is that by breaking the donor genome up into many small segments and having these segments in an otherwise identical genetic background, it becomes possible to precisely dissect even complex characteristics into a series of genetically tractable parts. We know that we have been successful in doing this as we have already examined the effects of the introgressed wild species genome segments on a range of phenotypes (Matus et al, 2003). In the interim, we have also developed a technology (we call it an oligo pool assay or **OPA**) that allows us to very precisely characterise the genomes of each of the **RCSLs** and identify the genes that are present on the introduced donor segments. In this project we propose to combine the power of our OPA genome characterisation technology with relevant phenotypic trait information on the unique **RCSL** genetic resource to identify segments of the donor genome that confer increased (or decreased) drought tolerance to the recipient. Although these characteristics are considered to be controlled by many genes, by isolating a small number (sometimes individual) donor genome segments in an identical genetic background, **RCSLs** effectively fragment the genetic contributions of many loci into individual component loci that can be subsequently analysed in detail by simple genetic analysis. Once we have identified specific target regions of the wild species genome that confer increased drought tolerance, for the most clearcut examples, we will use the model rice genome sequence to provide a putative barley regional gene content and a list of candidate stress tolerance genes. We have successfully used this approach in the past for winter hardiness. We will then pursue the objective of characterising the DNA sequence of a selection of the genes in this region from both parents to develop the tools that will allow us to accurately associate the drought tolerant character with specific genes. We will extend these studies to a broad selection of agro-ecologically adapted landraces where we will use both the genes identified in the RCSL studies and, in a pilot study, the genes on the **OPA**, to validate observed, and identify new associations between genes and drought tolerant phenotypes. Finally, we will initiate crosses to mobilise favourable alleles from the landrace germplasm into a common elite genetic background for further testing and validation of their impact on stress tolerance.

4. Project No G3008.01: Generating new wheat germplasm with enhanced drought/heat tolerance using AB genomes genetic diversity

- *Duration: Nov 2008–Oct 2011*
- *Budget by year: $259,940 (2008), $259,940 (2009), $259,940 (2010); Total budget: $779,820*

Wheat/Drought tolerance/Various regions

Lead institute
ARI–India (SC Misra)
Collaborating institutes and scientists

- CIMMYT (M Zaharieva, S Dreisigacker, J Crossa and T Payne)
- PBI–UoS (R Trethowan and P Sharp)
- UAS–Dharwad (RR Hanchinal, A Shreenivas Desai, IK Kalappanavar, KK Math, B Nirmal Yenagi)
- ARI–India (VS Rao)
- PARC (MY Mujahid)

The recent evidence of climatic change (reflected by rises in global temperature and unpredictable rainfall) and the increase in wheat prices have considerably questioned the optimistic food supply scenarios of the past decade. Increasing cereal production in developing countries by enhancing crop resilience under high temperatures and irregular rainfall or water supply is now a tremendous challenge. To address this challenge we propose combining the use of new sources of novel genetic diversity and of molecular markers to create new wheat germplasm as a potential source of drought and heat tolerance. Emmer wheat will constitute the reservoir of new diversity and drought/heat tolerance traits. Highly diverse accessions will be crossed to *Aegilops tauschii* accessions to create synthetic hexaploid wheats (SHW) that will be re-crossed to elite bread wheats to produce a large set of synthetic back-crossed lines (SBL). In addition, some emmer x hexaploid bread wheat crosses will be made to recombine the A and B genomes.

Molecular markers will be used to analyse diversity within a large collection of emmer wheats and to develop a reference set of diverse individuals to be crossed to *Aegilops tauschii* accessions. Markers will help to estimate the genetic diversity within families or populations originating from different regions.

Germplasm generated by this project will be further extensively used by CIMMYT, Agharkar Institute, Dharwad University, Pakistan Agricultural Research Council and Sydney University breeding programmes to improve drought/heat tolerance and will be made available to the entire wheat breeding community. Inter and intra family variation for drought tolerance traits in synthetic back-crossed lines and their association with genomic regions are expected to provide important information for further marker-assisted breeding activities.

5. Project No G3008.02: Improving grain yield on acid soils by the identification of genetic factors underlying drought and aluminium tolerance in maize and sorghum

- *Duration: Nov 2008–Oct 2011*
- *Budget by year: $406,521 (2008), $257,248 (2009), $193,597 (2010); Total budget: $857,366*

Maize; sorghum/Acidity/Sub-Saharan Africa

Lead institute
Robert W. Holley Center for Agriculture and Health, USDA–ARS (Leon Kochian)
Collaborating institutes and scientists

- Embrapa Maize and Sorghum (Jurandir Vieira Magalhaes)
- IGD (Stephen Kresovich, Sharon Mitchell and Martha Hamblin)
- MU (Sam Gudu)
- Embrapa Maize and Sorghum (Claudia Guimaraes, Robert Schaffert, Reinaldo Gomide, Vera Alves, Flavio Tardin as collaborator, Lauro Guimarães as collaborator, Sidney Parentoni as collaborator)
- Robert W. Holley Center for Agriculture and Health, USDA–ARS (Owen Hoekenga, Jiping Liu, and Lyza Maron)

Two of the most important limitations to crop production in sub-Saharan Africa are drought and acid soils. It is estimated that nearly 50% of the soils in this region suffer from insufficient water, while agriculture on nearly a quarter of the lands of sub-Saharan Africa are constrained by aluminum (Al) toxicity on acid soils. Because the primary symptom of Al toxicity is root growth inhibition and damage, resulting in compromised water and nutrient uptake, Al toxicity is a significant however poorly understood component of drought stress in Africa and other developing regions of the world. We already have assembled an effective research consortium that in ongoing GCP projects has identified a major sorghum Al tolerance gene which is now being exploited to improve sorghum Al tolerance in Africa. We also have recently identified several very promising candidate maize Al tolerance genes and QTLs that are poised to enter into a molecular breeding pipeline for assessing/validating their breeding values, and ultimately for generating maize genotypes with superior performance on acid soils. In this proposal, we will build upon this progress to generate maize and sorghum breeding lines with enhanced acid soil tolerance. Using our capability to phenotype maize and sorghum genotypes for drought tolerance in the field and a newly developed platform for high-throughput root imaging analysis, we also will begin to focus on the molecular and genetic determinants of maize and sorghum drought tolerance. This will involve the generation of new genetic resources in sorghum and maize, taking advantage of recent advances in sequencing and association genetics to develop a SNP genotyping array in sorghum and a maize breeding association panel. In particular the sorghum platform should become an useful community resource not only for drought and Al tolerance, but also for many other agronomically important traits. Finally, we will continue our field testing of improved sorghum and maize lines on acid soils in Kenya, and expand that programme to begin assessing the interplay between drought and Al tolerance on soils in Africa.

Projects on NCE into 2008 or beyond

6. Project No G3005.13: Development of informative DNA markers through association mapping in maize to improve drought tolerance in cereals

- *Duration: Jan 2005–Dec 2007 with NCE to Dec 2008*
- *Budget by year: $268,080 (2005), $293,420 (2006), $337,552 (2007); Total budget: $899,052*

Maize/Drought tolerance; low soil fertility/Various regions

Lead institute
CIMMYT (Jianbing Yan, effective June 2008; Previous PI: Marilyn Warburton)
Collaborating institutes and scientists
- CU (Tim Setter, Edward Buckler)
- Agropolis–INRA (Alain Charcosset)
- KARI (James Gethi)
- NSFCRC (Pichet Grudloyma)
- SIRDC (Esther Khosa)
- SAU (Li Wanchen)
- CIMMYT (José Crossa, Xu Yunbi, Magorokosho Cosmos, Jose Luis Araus)

Drought and low soil fertility are the major limiting factors for cereal-crop production in developing countries. The objective of this project is to use the natural variation inherent in the maize genome for the dissection of drought tolerance and for the identification of superior alleles. While maize grows in a wide range of environments and is the most diverse crop in the world, we do not know the genes that are responsible for these adaptations. For phenotypic selection, although allowing genetic progress, crops need to be fully evaluated in every environment, which is costly and time consuming. Association studies, proposed in this project, are based on correlation between a gene sequence and plant performance for target traits, and represent a powerful approach to evaluate candidate genes regulating plant phenotype. This project will focus on evaluating the genes in two major pathways that are involved in drought tolerance. We will build upon previous mapping approaches that have identified genomic regions containing a few hundred genes, and use high resolution approaches that can evaluate individual genes. This high resolution mapping will require combining rapid molecular approaches with careful evaluation of diverse germplasm for drought tolerance and physiological response. Additionally, by screening several hundred diverse lines this project maximises its potential to identify the best alleles in the maize gene pool. The discovery of superior alleles at the gene level will permit the development of molecular markers that can facilitate breeding drought tolerance in a wide range of germplasm. One important benefit of working with the natural variation, it is that any discovery can be rapidly converted to improved breeding materials without the societal and regulatory obstacles of transgenics materials. Because of the genetic and physiological commonalities among cereal crops, this knowledge gathered in maize can be applied to all other cereal crops.

7. Project No G3005.14: Characterisation of genetic diversity of maize populations: Documenting global maize migration from the center of origin

- *Duration: Jan 2005–Dec 2007 with NCE to Dec 2008*
- *Budget by year: $305,620 (2005), $183,490 (2006), $228,035 (2007); Total budget: $717,145*

Maize/Drought tolerance/Various regions

Lead institute
CIMMYT (Marilyn Warburton)
Collaborating institutes and scientists

- CIMMYT (S Taba)
- IITA (Sarah Hearne)
- Agropolis–INRA (Alain Charcosset)
- KARI (Zachary Muthamia)
- CAAS (SH Zhang)
- ICAR (BM Prasanna Sutrisno)
- NSFCRC (Pichet Grudloyma)
- NMRI (Phan Xuan Hao)

Although maize hybrids represent the most economically important portion of the species, maize breeding populations, open pollinated varieties (OPVs), landraces, and wild relatives contain the majority of the diversity found in maize, much of which has never been incorporated into improved varieties. Populations introduced into other countries, originally from the center of origin in Central America but following a complicated pattern of introductions, have become adapted to many new growing conditions and local stresses, including drought. Past studies of maize population diversity have revealed useful clues as to relationships and patterns of diversity; however, a complete, global picture of maize diversity is lacking because analysis of heterogenous populations has been until recently very expensive and time consuming. Phenotypic characterisation of cultivated maize and wild teosinte populations for traits important to breeders and farmers has been done only in a very limited manner, and at the molecular level, essentially not at all. Drought tolerance is a trait of extreme importance to farmers who have access to limited resources, but one that is difficult to phenotype (especially in wild species) and sufficient diversity is lacking in current breeding germplasm, so a great need for new diversity exists.
This study aims to complete the global picture of maize diversity and spread by collecting and analysing maize populations from geographic regions that have been underrepresented in previous studies, and representatives of the wild ancestor of maize (teosinte). Structural characterisation will occur at the molecular level using SSR markers. The populations containing the most unique alleles at the SSR loci will then be characterised for markers associated with drought tolerance, as these are the populations most likely to contain new alleles in general and potentially for drought related loci. The genetic characterisation data will provide useful information for utilising these populations in genomic studies and breeding efforts to create drought tolerant maize.

8. Project No G3005.17: Allele mining based on non-coding regulatory SNPs in barley germplasm

- *Duration: Jan 2005–Dec 2007 with NCE to Jun 2008*
- *Budget by year: $300,000 (2005), $300,000 (2006), $299,000 (2007); Total budget: $899,000*

Barley/Tolerance to drought, frost, cold and salinity stresses/Various regions

Lead institute
ICARDA (Michael Baum)
Collaborating institutes and scientists

- NIAB (Wayne Powell, K Stamati)
- ICARDA (Salvatore Ceccarelli, Stefania Grando, Sripada M Udupa)
- TU (Wafaa Choumane)
- ACPFG (P Langridge, Mark Tester)
- UoAd (JK Eglinton)
- UdU (M Morgante)

In recent years analysis of genetic variation has focused on the study of changes in DNA coding for proteins. It is now becoming increasingly clear that this only accounts for one aspect of heritable variation and for many traits, notably tolerance to environment stresses, the level of gene expression is also likely to be of great importance. If changes in gene expression underlie many evolutionary changes in phenotype, then identifying the genetic variants that regulate gene expression is a significant and important endeavor. One of the key problems in genetics is how to identify this type of variation. We propose a robust, quantitative approach to efficiently identify plant genes that harbor such regulatory variants. The approach is novel and particularly amenable to plants since it is based on monitoring gene expression in experimentally created hybrids. A successful outcome will provide a new mechanism to connect genotype to phenotype based on changes in gene expression rather than changes in the structure of an encoded protein. This approach will be used to characterise a series of genes identified and reveal potential candidates for tolerance to drought, frost, cold and salinity stresses. The approach is generic and widely applicable. The project will also involve training researchers in Developing Countries and create a high quality collaborative network of researchers delivering new knowledge on genetic diversity and translatable outputs for the developing world.

Subprogramme 2: Genomics towards gene discovery

Current projects

9. Project No G3007.03: Development of genomics resources for molecular breeding of drought tolerance in cassava

- *Duration: Aug 2007–Feb 2010*
- *Budget by year: $434,215 (2007), $323,843 (2008); Total budget: $758,058*

Cassava/Drought tolerance/Africa; Asia; Latin America

Lead institute
UoM (Pablo Rabinowicz)
Collaborating institutes and scientists
- ACGT (Jane Morris, Alexander Myburg, Chris Rey)
- UoC–Davis, USA (Ming-Cheng Luo)

Cassava is one of the most important crops in unfavorable environments in developing countries, where poverty is common and severe. Because of its high productivity, even in extreme conditions, cassava constitutes a source of food and income for poor farmers in Africa, Asia and Latin America. Although cassava is fairly resistant to water stress, the molecular basis for this tolerance is poorly understood. Several traits have been associated with its drought tolerance, such as regulation of stomata activity, changing leaf expansion rates due to decrease in cell proliferation, and modifications of photosynthetic pathways to maintain high photosynthetic activity. Improving cassava's tolerance to drought is important to help increasing yields in the semi-arid Sub Saharan African regions where cassava as an essential crop. Cassava's natural stress tolerance can be substantially improved by breeding, especially by marker-assisted selection of key physiological traits associated with drought tolerance. In recognition of the importance of cassava improvement for dry areas in the developing world, the Generation Challenge Programme (GCP) awarded a grant to study drought tolerance traits and develop molecular markers to improve cassava breeding for drought tolerance. This proposal builds on that project by offering to develop single nucleotide polymorphism (SNP) markers throughout the genome to identify favorable alleles related to drought tolerance in these mapping populations. In order to achieve this goal, a physical map of the cassava genome will be generated that will allow the development of SNP markers uniformly distributed around the genome. In this way we will be able to identify quantitative trait loci (QTL) associated with drought tolerance in a high-throughput manner. These markers will be useful for marker-assisted selection of favorable traits.

10. Project No G3007.06: Genetic dissection of drought adaptive mechanisms in bread and durum wheat through large scale phenotyping methodologies

- *Duration: Aug 2007–Jul 2009*
- *Budget by year: $301,000 (2007), $301,000 (2008); Total budget: $602,000*

Wheat/Drought tolerance/Australia; Asia; Latin America

Lead institute
CIMMYT (Matthew Reynolds)
Collaborating institutes and scientists
- CIMMYT (Daniel Mullan, Yann Manes, Jose Crossa)
- ACPFG (Peter Langridge)
- DWR (Jagadish Rane, B Mishra, Ravish Chatrath)
- ARI–India (Satish Mishra)

Declining water resources and unpredictable rainfall are serious threats to crop productivity throughout the world. Although wheat is relatively well adapted to moisture stress, and breeding progress using conventional approaches has resulted in significant improvements in productivity in rain-fed areas, there is considerable scope to improve the scale and pace of progress through exploiting the genetic diversity that exists in wheat genomes. Through a combination of precision phenotyping on well designed populations grown at key field locations in conjunction with deployment of the latest molecular marker technologies, it is anticipated that genetic markers associated with drought adaptive traits will be identified or confirmed. Such markers will then permit targeted molecular screening of genetic resources within wheat and related genomes thus identifying new parental sources and markers for progeny selection. The collaborative model proposed combines partners with expertise in genetics, breeding and physiology thus facilitating the design of agronomic and genetically relevant mapping populations, a realistic and rigorous approach to phenotyping, and application of the most appropriate biotechnologies. The proposed research material (bread wheat and durum wheat mapping populations) offers a unique ability to dissect the genomic effects of drought tolerance (particularly for the D genome). The collaborators work in three major wheat producing countries (India, Mexico and Australia) where the crop is either rain-fed or grown with restricted irrigation. The project will provide selection tools and methodologies including genetic and physiological markers that can be applied in breeding programmes worldwide and well characterised experimental populations that can be used to develop similar tools in other stress prone environments. This proposal also addresses the considerable methodological challenges associated with determining the genetic basis of drought adaptation in that it will validate high throughput screening protocols in controlled environments and develop more optimal parents for a subsequent generation of molecular mapping populations.

11. Project No G3008.03: Delayed senescence and drought tolerance in rice

- *Duration: Nov 2008–Oct 2011*
- *Budget by year: $264,108 (2008), $281,873 (2009), $305,915 (2010); Total budget: $851,896*

Rice/Drought tolerance/Various regions

Lead institute
UoC–Davis, USA (Eduardo Blumwald)
Collaborating institutes and scientists
IRRI (Abdelgabi M Ismail, Rachid Serraj)

Drought is the major constraint to rice production in the drought-prone rainfed environments, and enhanced drought tolerance and crop water productivity are major targets for improving and sustaining food security in these areas. We hypothesised that drought-induced plant senescence is due to a type of cell death programme naturally activated during drought. Down-regulating such programme could therefore enable plants to acquire vigorous acclimation responses to stress, resulting in enhanced drought tolerance with reduced yield losses. We generated plants overexpressing an IPT gene (mediating the synthesis of cytokinins) under the control of SARK, an inducible maturation- and stress-dependent promoter, and demonstrated that the suppression of drought-induced leaf senescence results in significantly enhanced drought-tolerance of the plants. These plants maintained relatively high relative water content, retained photosynthetic activity and survived longer periods without irrigation, Moreover, the plants overexpressing PSARK-IPT were able to grow under restrictive water supply with a lower yield penalty compared to controls and displayed minimal yield losses when watered with only 30% of the amount of water used under control conditions. Based on all previous results, in this proposal we will test the efficacy of stressinduced cytokinin synthesis in conferring drought tolerance in upland and lowland rice varieties overexpressing IPT. The general objective is to identify genes with significant roles in conferring drought tolerance in rice, and the generation of drought-tolerant and water useefficient rice plants in different genetic backgrounds. We will use forward-, reverse-genetics and TILLING to assess and confirm the roles of the identified genes in drought tolerance. The development of drought-tolerant rice varieties able to grow and produce higher biomass and yield under restricted water regimes would considerably minimise drought-related losses and increase food production in water-limited rainfed rice lands.

12. Project No G3008.04: Drought from a different perspective: Improved tolerance through Phosphorous acquisition

- *Duration: Nov 2008–Oct 2011*
- *Budget by year: $300,000 (2008), $300,000 (2009), $300,000 (2010); Total budget: $900,000*

Rice/Drought tolerance; P-deficiency/Various regions

Lead institute
IRRI (Sigrid Heuer)
Collaborating institutes and scientists

- IRRI (Stephan Haefele, Arvind Kumar, Abdelbagi Ismail)
- UoPs and MPI of Molecular Plant Physiology, Germany (Bernd Mueller-Roeber)
- JIRCAS (Matthias Wissuwa)
- ICABIOGGRAD (Masdiar Bustamam)

Partner (without budget)
ZU (Ping Wu)

Almost 50% of rice soils are currently deficient in phosphorous (P), yet resource-poor farmers in upland and drought-prone rainfed lowland environments typically apply little fertilizer. P deficiency therefore often coincides with drought and frequently aggravates its negative effects. Efforts to improve tolerance of either stress have typically been carried out separately without addressing nutrient x drought interactions. We have shown repeatedly that rice lines with the major P uptake QTL *Pup1* maintain higher root growth rates under P deficiency than lines lacking *Pup1*.We thus hypothesised that this effect would enhance drought tolerance. First results from pot experiments confirmed this hypothesis. Lines containing *Pup1* had 5-fold higher yield when P deficiency was combined with drought compared with 3-fold higher yield under P deficiency alone. The *Pup1* locus therefore represents a prime target in improving P deficiency and drought tolerance in rice. Previous analyses of tolerance mechanisms and genes associated with P uptake suggest that *Pup1* confers tolerance via a novel gene of unknown function. One objective of this project is to identify this gene and to understand the underlying physiological mechanisms. An immediate product of these activities will be the development of allele-specific markers for marker-assisted selection (MAS). Understanding how *Pup1* exerts its positive effect will furthermore aid in identifying complementary genes and tolerance mechanisms that should be combined with *Pup1* to further improve dual tolerance of P deficiency and drought. For that purpose, we will evaluate the effect of four additional QTLs known to be associated with root growth, and tolerance of drought and P deficiency, respectively. QTLs that best complement *Pup1* will be pyramided through MAS using markers developed within the project. By this approach, it will be possible to develop tolerant varieties while preserving all important traits (eg. disease resistances, grain quality) of locally adapted varieties.

13. Project No G3008.05: Discovery and development of alleles contributing to sorghum drought tolerance

- *Duration: Nov 2008–Oct 2011*
- *Budget by year: $246,880 (2008), $250,167 (2009), $259,178 (2010); Total budget: $756,225*

Sorghum/Drought tolerance/Africa; Asia

Lead institute

UoG (Andrew H Paterson)

Collaborating institutes and scientists

- SARI (IDK Atokple)
- ICRISAT (C Thomas Hash)
- MAU (SP Mehtre)
- ARC (Abdalla Mohamed)
- NRCS (Nadoor Seetharama)

Sorghum is the most drought-tolerant dual-purpose (grain + straw) cereal crop of the semi-arid tropics and subtropics, where development challenges are the greatest and market failure is most acute. As such, it is both a priority for further improvement and a botanical model from which we might glean information about drought tolerance that might be leveraged in improvement of many other cereals by comparative approaches. Sorghum has recently become only the second cereal (after rice), to have its genome fully sequenced, opening new doors to its improvement and enhancing its value for comparative biology.

In a partnership joining African and Asian sorghum improvement researchers with genomic scientists experienced in crop breeding and germplasm enhancement, we will engage the sorghum sequence in a balanced approach to durably increase rates of sorghum improvement. Toward a pathway joining discovery research of increasing scope and sensitivity with application to the needs of resource-poor farmers living in drought-prone environments, early study of a few genes already known to have qualitative effects on drought tolerance will set the stage for identifying a growing pipeline of additional genes/alleles with more subtle effects, engaging several previously GCP-funded resources. Key to both discovery research and product development/delivery will be our focus on breeding populations in which drought tolerance will be combined with other traits that address production constraints in West and Central Africa, Eastern and Southern Africa, and South Asia. By applying sorghum's fully-sequenced genome to study of these field-proven genetic resources, we will elucidate genotype x environment interactions that render drought tolerance a difficult trait to work with. Improved knowledge of sorghum presents a singularly-promising opportunity to leverage comparative genomics approaches to benefit improvement of many other cereals. NARS scientists are full research partners, and will also benefit from training visits to UGA and/or ICRISAT.

Projects on NCE into 2008 or beyond

14. Project No G3005.01: Identifying genes responsible for failure of grain formation in rice and wheat under drought

- *Duration: Jan 2005–Dec 2007 with NCE to Jun 2009*
- *Budget by year: $305,836 (2005), $295,768 (2006), $298,396 (2007); Total budget: $900,000*

Rice; wheat/Drought tolerance/Asia

Lead institute

IRRI (Rachid Serraj, effective December 2008; Previous PI: John Bennett)

Collaborating institutes and scientists

- CSIRO (Rudy Dolferus)
- IRRI (Kenneth McNally, Xuemei Ji, Muthurajan Raveendran)
- NIAS (Shoshi Kikuchi, Kouji Satoh)
- TNAU (R Chandra Babu)
- NAU (Zhengqiang Ma)

Rice and wheat provide approximately 50% of the calories consumed directly by the human population. The projected increase in this population from 6 billion in 2000 to 9 billion in 2050 requires that production of rice and wheat continue to increase as it has done over the last 40 years, following the introduction of high-yielding modern varieties. Future increases will come principally from further intensification of production in the limited irrigated areas and from improved yields in the larger rainfed areas. Drought is the main cause of yield loss in rainfed rice and wheat, and losses are most severe when drought occurs at the flowering stage. Water-saving strategies for irrigated areas must also deal with the sensitivity of the flowering stage to water deficit. For these reasons, we focus here on a comparative study of drought tolerance in rice and wheat, exploiting on the one hand the greater drought tolerance of wheat and on the other hand the recent explosion of information on the rice genome. The rice genome is approximately one-twentieth the size of the wheat genome, but these two cereals are comparatively closely related, with highly similar genes controlling growth, reproduction, and protection. Our team combines expertise on drought-stress physiology, gene expression, genome structure, biodiversity, and plant breeding. Years of research have produced detailed knowledge of which rice and wheat varieties and mutants show contrasting responses to drought during key steps of flowering such as panicle/spike emergence and pollination. Progeny derived by crossing these contrasting lines provide highly informative comparisons that help scientists to interpret the large data sets emerging from modern studies of gene expression using such techniques as microarrays and proteomics, and to identify and validate genes crucial to drought tolerance. Superior forms (alleles) of these genes can be identified in traditional varieties and other sources. Such alleles can then be efficiently transferred into popular rice and wheat varieties via DNA-assisted backcrossing to enhance drought tolerance in both cereals.

15. Project No G3005.02: Revitalising marginal lands: discovery of genes for tolerance of saline and phosphorus deficient soils to enhance and sustain productivity

- *Duration: Jan 2005–Dec 2007 with NCE to Jun 2008*
- *Budget by year: $312,300 (2005), $342,244 (2006), 245,456 (2007); Total budget: $900,000*

Rice/Salinity and phosphorus deficiency/Asia

Lead institute
IRRI (Abdelbagi M. Ismail)
Collaborating institutes and scientists

- IRRI (David J Mackill, Michael Thomson, Sigrid Heuer, Glenn Gregorio, Rakesh Kumar Singh)
- JIRCAS (Matthias Wissuwa)
- UoC–Davis (Eduardo Blumwald)
- UoD (Zeba I Seraj)
- ICABIORAD (Masdiar Bustamam)
- UoC–Riverside (Timothy J Close)
- ABRII (Ghasem H Salekdeh)
- NIAS (Massahiro Yano)

Soils that contain toxic levels of salts and/or are deficient in essential plant nutrients have low productivity and are commonly associated with poverty. Problems of particular importance in these soils are salinity and phosphorus deficiency. In Asia alone, more than 12 million ha are currently affected by salinity and about 50% of the rice lands are P-deficient. Salt stress often coexists with other abiotic stresses such as drought and P deficiency.

Amendments and management options for these soils are too expensive for the resourcepoor farmers commonly living in these areas; however, solutions through improved germplasm are affordable to farmers and are becoming more feasible with the developments in modern molecular tools that are becoming available to unravel the genetic basis of tolerance. Combining mechanisms underlying tolerance for complex traits such as salt and P-deficiency as well as those for multiple stresses is now feasible once the genetic components or genes for tolerance are tagged to allow them to be traced in the breeding process. We aim to identify and tag the genes for tolerance for salinity and P-deficiency. For both stresses, we have made excellent progress in understanding the biology and in identifying major chromosomal regions that are associated with tolerance. We will further fine-map these regions and use modern molecular approaches to discover the genes that are involved in tolerance using a range of molecular strategies. We will also use biological information and genes discovered from other crops to facilitate the identification of similar genes in rice. Ultimately, we will develop a marker system to allow the efficient incorporation of these genes into popular, yet intolerant, varieties, initiate a marker-assisted breeding system with NARES partners, and provide them with the training needed to carry out these activities.

16. Project No G3005.08: Targeted discovery of superior disease QTL alleles in maize and rice genomes

- *Duration: Jan 2005–Dec 2007 with NCE to Dec 2008*
- *Budget by year: $294,297 (2005), $291,386 (2006), $313,928 (2007); Total budget: $899,611*

Maize; rice/Disease resistance/Various regions

Lead institute
CU (Rebecca Nelson)
Collaborating institutes and scientists

- NCSU (Peter Balint-Kurti)
- IRRI (Darshan Brar, Hei Leung, Casiana Vera Cruz)
- ICABIOGRAD (Masdiar Bustamam)
- KARI (James Gethi, Jedidah Danson, Jane Ininda)
- CSU (Jan Leach)
- CU (Margaret Smith)
- IPB (Utut Suharsono)

We propose to identify, characterise and utilise sections of the rice and maize genomes that provide superior disease resistance to cereal diseases of critical and global importance. Durable, broad-spectrum resistance would be valuable to resource-poor farmers. Although much research has been focused on qualitative (complete, race-specific) resistance, the proposed work will focus on quantitative (incomplete, presumably race non-specific) disease resistance (QDR) because QDR is usually the more durable form or the only form available. At present, the chromosomal regions associated with QDR are defined with very low precision, and germplasm has not been systematically analysed to identify superior alleles at the loci of greatest potential utility. We propose to characterise selected maize and rice germplasm for urgently needed disease resistance. We will initiate development of near-isogenic lines (NILs) capturing useful segments of maize and rice chromosomes in a susceptible background for detailed analysis. We will use a set of complementary strategies in the development of the NILs, including backcrossing of advanced resistant lines derived from rice varieties known for durable resistance; selection of allelic series at loci of outstanding interest based on a summary of all available disease QTL studies in maize; and selection of lines carrying alleles showing increases in frequency under recurrent selection for a maize disease. We will make use of the existing collection of rice mutants to validate the function of candidate QDR genes. The superior chromosomal segments identified in this project will be analysed in detail and utilised in the applied breeding programmes in which improving disease resistance is a high priority.

17. Project No G3005.11: Functional genomics of cross-species resistance to fungal diseases in rice and wheat (Cereal Immunity)

- *Duration: Jan 2005–Dec 2007 with NCE to Oct 2008*
- *Budget by year: $387,000 (2005), $327,000 (2006), $186,000 (2007), Total budget: $900,000*

Rice; wheat/Disease resistance/Various regions

Lead institute
Agropolis–INRA (Jean-Benoit Morel)
Collaborating institutes and scientists

- EMBRAPA (M Ferreira, G de Capdeville, S Scagliusi, A Bonato, Y Mehta, J Maciel, P Scheeren, MS Chaves, S Brammer)
- UoC–Davis (P Ronald, KH Jung)
- CIMMYT (R Sing, M William)
- NIAS (S Kikuchi, K Satoh)
- JIC (L Boyd, H Tufan, G McGrann)
- Agropolis–INRA (C Feuillet, P Sourdille, J Salse, L Miché, M Bousquet, C Michel)

Resistance shown by a plant species to the majority of potentially pathogenic microbes is known as non-host resistance. The events leading to non-host resistance in plants represents one of the least understood phenomena and a remaining challenge in the field of plant-microbe interactions. Comparative genomics is a promising method to identify key genes involved in cross-species interactions and to better understand their regulation at the genetic level and their evolution.

Non-host resistance also represents one promising defence mechanism in developing durable resistance against plant pathogens, namely due to its effectiveness against a broad range of pathogen species and its durability in nature. The proposed project will strengthen and extend ongoing research in rice and wheat and aims at defining the signalling and effector genetic components involved in non-host resistance in cereals to devise novel defence strategies which have the potential to yield durable resistance against host pathogens in cereals.

This project aims at implementing existing breeding programmes for resistance to blast and rust diseases in developing countries taking advantage of the availability of advanced genomic platforms and technologies.

18. Project No G3005.15: Determination of a common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes

- *Duration: Jan 2005–Dec 2007 with NCE to Dec 2008*
- *Budget by year: $297,678 (2005), $302,398 (2006), $298,610 (2007); Total budget: $898,686*

Various crops/Drought tolerance/Various regions

Lead institute
Agropolis–INRA (François Tardieu)
Collaborating institutes and scientists

- Agropolis–INRA (C Welcker, O Turc, B Parent)
- CIMMYT (G Davenport, J-L Araus, M Reynolds, C Bencivenni)
- IRRI (R Serraj, J Cairns, R Bruskiewich, R Mauleon)
- ETH (A Hund, P Stamp, M Liedgens, N Pa-In)
- Biogemma (P Lessard)
- ACPFG (Peter Langridge, T Schnurbusch, U Baumann, A Schreiber)
- ICAR (BM Prasanna)
- KARI (J Gethi)

The effort to minimise the impact of drought on yield needs new approaches for bridging traditional breeding to molecular genetics. Recent advances in comparative genomics allow information to be moved from one genome into another for identifying key genes controlling drought tolerance. However, comparison between species remains difficult because compared processes, organs and conditions differ between species in most published studies. We will undertake a multiple-species, multiple-organ study on a key process: growth maintenance under water deficit. The project combines new approaches of phenotyping (controlled conditions and field), modeling, quantitative genetics, comparative genomics and first steps towards association genetics. It also combines the strengths of research in "advanced" countries, CGIAR centers and developing countries. It is applied to three cereals (wheat, maize and rice) for growth maintenance of leaves and to three organs (leaves, roots and reproductive organs) in maize. The project will adopt the approach of characterising environmental conditions in all experiments (including those for genomics), and analysing germplasm under controlled environment and field conditions using a modeling approach. Common genomic regions and genes important for growth will be identified through existing and new QTL data across the three cereals. Comparison of gene expression in common tissue across and within species will be used to identify candidates for detailed analysis. Questions to be addressed will include: How do identified genes contribute to growth maintenance in different climates over the world and how does that correlate with yields? And, What combinations of alleles optimise the growth of key tissues in droughted rice, wheat and maize under different environments? A comparative study of the three species will generate results that feed into modeling work, thereby interpreting and using (for breeding) the genotype x environment interaction of key traits involved in drought tolerance such as early vigor, high light interception or maintenance of reproductive development.

19. Project No G3005.16: Isolation and characterisation of aluminum tolerance genes in the cereals: An integrated functional genomic, molecular genetic and physiological analysis

- *Duration: Jan 2005–Dec 2007 with NCE to Dec 2008*
- *Budget by year: $300,000 (2005), $300,000 (2006), $300,000 (2007); Total budget: $900,000*

Sorghum; maize; rice; Triticea/Aluminium tolerance/ Various regions

Lead institute
USDA–ARS and CU (Leon V Kochian)
Collaborating institutes and scientists

- EMBRAPA Maize and Sorghum (Jurandir Magalhaes, Claudia Guimarães, Vera Alves, Newton Carneiro, Andrea Carneiro, Robert Schaffert)
- EMBRAPA Wheat (Sandra Brammer, Luciano Consoli, José Pereira da Silva Junior, Euclydes Minella, Eduardo Caierão, Alfredo Nacimento Junior)
- EMBRAPA Rice and Bean (Flavio Breseghello, Pericles Neves)
- MU (Samuel Gudu)
- USDA–ARS and CU (Owen Hoekenga, Ed Buckler, Lyza Maron, Jiping Liu)

One of the most important soil-related factors limiting agriculture in developing countries is acid soil pH (pH < 5). Acid soils occur for both natural and humanity-derived reasons. On acid soils, regardless of their source, toxic levels of aluminum (Al) ions are released into soil solution, where they damage roots and impair their growth and function. This damage results in reduced nutrient and water uptake, with concomitant reductions in crop yield. There is considerable natural variation in Al tolerance both within and between plant species, and we have assembled an interdisciplinary group of scientists to take advantage of this variation to improve crop tolerance to Al toxicity on acid soils. This proposal details an interdisciplinary project that will characterise recently isolated cereal Al tolerance genes as well as identify novel Al tolerance genes and physiological mechanisms in a range of cereal species (sorghum, maize, rice and the *Triticeae*). The research group we have assembled has considerable expertise in the genetics, molecular biology and physiology of aluminum tolerance in these crops, and has available the necessary genetic resources to ensure the success of this project. We will use information from candidate genes identified in wheat and sorghum, as well as ongoing progress from our genetic mapping and cloning programme in maize, to identify and verify candidate Al tolerance genes in several cereals species. The long-term goals of this research are to generate cereal genotypes expressing improved Al tolerance that ultimately can be distributed to farmers who till acid soils in Africa and other developing regions, thus exploiting a wide range of still hidden genetic variation for Al tolerance. Increasing the Al tolerance of staple crops, such as maize and sorghum, will help increase yields and thus food security.

Subprogramme 3: Trait capture for crop improvement

Current projects

20. Project No G3007.04: Tailoring superior alleles for abiotic stress genes for deployment into breeding programmes: a case study based on association analysis of *Alt*$_{sb}$, a major aluminum tolerance gene in sorghum

- *Duration: Aug 2007–Jul 2009*
- *Budget by year: $299,598 (2007), $303,503 (2008); Total budget: $603,101*

Sorghum/Aluminum tolerance/Africa and other developing regions

Lead institute
Embrapa Maize and Sorghum (Jurandir Vieira Magalhaes)
Collaborating institutes and scientists

- USDA–ARS (Leon Kochian, Owen Hoekenga, Jinping Liu)
- IGD (Stephen Kresovich, Alexandra M.Casa, SharonMitchell; Theresa Fulton)
- EMBRAPA (Claudia Guimaraes, Robert Schaffert, Fernanda Caniato, Antonio Marcos Coelho, Vera Alves)
- INRAN (Soumana Souley, Maman Nouri, Magagi Abdou, Adam Kiari, Fatouma Beidari)

One of the most important factors limiting agriculture in developing countries involves the large areas of acid soils found in these countries. On acid soils, toxic levels of aluminum (Al) ions are released into soil solution, where they damage roots and impair their growth and function. This results in reduced nutrient and water uptake, with concomitant reductions in crop yield. There is considerable natural variation in Al tolerance both within and between plant species, and we have assembled an interdisciplinary team of scientists to take advantage of this variation to improve crop tolerance to Al toxicity, building upon our recent success in isolating a novel Al tolerance gene in sorghum. Thus, as we have been able to identify at least one apparently improved version of this gene, we will now apply association mapping to undertake a comprehensive scan for even better versions of this gene for deployment into sorghum breeding programmes. The research group we have assembled has considerable expertise in the genetics, molecular biology and physiology of aluminum tolerance, and has the necessary genetic resources to ensure the success of this project. Through the use of cutting edge genomics and statistical genetics approaches, this research will bridge the gap between basic research on Al tolerance and applied breeding programmes, to develop the tools that plant breeders can use to efficiently and effectively breed for improved acid soil tolerance.
The long-term goals of this research are to generate sorghum genotypes expressing improved Al tolerance that ultimately can be distributed to farmers who till acid soils in Africa and other developing regions, thus exploiting a wide range of still hidden genetic variation for Al tolerance. Increasing the Al tolerance of staple crops, such as sorghum, will help increase yields and thus food security worldwide.

21. Project No G3007.05: Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-aided breeding

- *Duration: Aug 2007–Jul 2009*
- *Budget by year: $284,458 (2007), $314,132 (2008); Total budget: $598,590*

Rice/Drought tolerance/Asia

Lead institute
IRRI (Arvind Kumar)
Collaborating institutes and scientists

- CRRI (ON Singh, P Swain, LK Bose)
- CRURRS (K Sinha, NP Mandal)
- NDUAT (JL Dwivedi)
- UAS–Bangalore (S Hittalmani; Venkatesh Gandhi)
- TNAU (R Chandrababu, A Senthil, S Robin)
- BAU (BN Singh; RL Mahato)
- JNKV (P Perraju)
- BF (HE Shashidhar, Abhinav Jain)
- YAAS (D Tao)
- UoAlb (Dean Spaner)

Rice production losses due to drought are a risk on more than 20 million ha, and primarily affect the poorest communities. Drought risk depresses productivity even in favorable years because risk of crop failure drives farmers to limit investment in fertilizer.

Varieties with improved tolerance could reduce risk and help alleviate poverty, but progress in their development has been slow because few rice breeding programmes screen directly for grain yield under drought stress, assuming that the trait is too complex for conventional breeding approaches. However, research by IRRI and collaborators has shown that, when stress is carefully imposed in the field, large differences in the yield of tolerant and susceptible varieties can be reliably detected. Recent experiments also show that much of the difference between tolerant and susceptible cultivars appears to result from the effects of a small number of genes. Several such genes have been identified at IRRI, but they must be precisely "tagged" by DNA markers to be used in developing improved varieties. The proposed project will tag (or fine-map) four genes that have been shown to reliably affect yield under both artificially imposed and natural drought. The physiological basis for their effects on tolerance will be studied, and their effects in farmers' environments in India and southern China will be confirmed. Many such genes probably exist in rice genebanks, but have not been identified because conventional mapping requires that large populations derived from crosses between tolerant and susceptible parents be subjected to expensive DNA analysis. However, only genes with large effects on stress tolerance are likely to be useful in breeding; these can be detected by "quick and dirty" methods that involve DNA testing of only the most tolerant and susceptible progeny of a cross. This approach, known as selective genotyping, will be optimised for rice drought gene detection. Lines developed by introducing genes that improve drought tolerance into elite varieties will be disseminated in collaboration with NARES partners.

22. Project No G3008.06: Targeting drought-avoidance root traits to enhance rice productivity under water-limited environments

- *Duration: Nov 2008–Oct 2011*
- *Budget by year: $300,000 (2008), $300,000 (2009), $300,000 (2010); Total budget: $900,000*

Rice/Drought tolerance/Asia

Lead institute

IRRI (Rachid Serraj)

Collaborating institutes and scientists

- IRRI (K McNally, A. Kumar, J Cairns, N Kobayashi, R Bruskiewich)
- WARDA: G Gregorio and S Mande (Co-PIs); T Hiroshi (collaborator)
- SUA (A Kijoji)
- TNAU (R Chandra Babu)
- BF (HE Shashidhar)
- UoAb (A Price)
- ChSU (LJ Wade)
- UoMi (RE Sharp and HT Nguyen)
- NagU (A Yamauchi)
- Drought Breeding Network, India
- UAS–Bangalore (S Hittalmani)
- Raipur (S Verulkar)
- CRURRS (PK Sinha)
- NDUAT (JL Dwivedi)
- CRRI (P Swain)

Water shortage is the overarching environmental constraint for the sustainable productivity of rice in rainfed cropping systems, where yields remain low and unstable. Despite various efforts deployed over past decades, the identification and characterisation of drought-resistance traits, which can be transferred into cultivars with high-yielding genetic backgrounds, have been generally unsuccessful. In most agricultural situations, the focus on tolerance traits and plant survival mechanisms has little relevance to increasing/stabilising crop yield. Thus, increasing both crop yields and water-use efficiency requires the optimisation of the physiological processes involved in the most critical stages of plant responses to soil dehydration. The focus of this project will be on dehydration avoidance and the plant's ability to maintain its water status under conditions of soil water deficits, through increased water uptake by the roots. Our research team combining expertise in drought-stress physiology, plant breeding, and molecular genetics will target the understanding and improvement of drought-avoidance root traits to enhance rice productivity under water-limited environments. We will first address the need for highthroughput precision phenotyping protocols for drought-avoidance traits and detailed site environmental characterisation systems. We will develop and refine innovative screening tools and protocols for dehydration avoidance and root traits, and compare the various methods and screening techniques. We will screen large numbers of rice germplasm accessions, cultivars, and breeding lines for drought-avoidance traits. We will also assess the value of these droughtavoidance traits and their relationships with grain yield in the major rainfed lowland target environments. The ultimate targets will be to assist with molecular breeding for drought resistance and to enhance the capacity of NARES researchers in the use of improved tools and methods for the genetic enhancement of drought resistance in rice.

23. Project No G3008.07: Basal root architecture and drought tolerance in common bean

- *Duration: Nov 2008–Oct 2011*
- *Budget: $292,667 (2008), $ 300,667 (2009), $306,666 (2010); Total budget: $900,000*

Beans/Drought tolerance/Africa

Lead institute
PSU (JP Lynch)
Collaborating institutes and scientists

- CIAT (SE Beebe, MW Blair, I Rao)
- PSU (K Brown)
- SABRN, Malawi (R Chirwa)
- IIAM (C Jochua, M Miguel)

Root traits have critical importance for drought tolerance, but have not yet been widely employed in crop breeding programmes. A major reason for this is that root systems are a complex aggregation of poorly understood individual traits that are hard to evaluate in the field. This project will offer bean breeders two new root traits with potential to improve drought tolerance. These traits vary substantially among genotypes and are known to play important roles in rooting depth, which is the most important determinant of drought tolerance in bean. Before these traits can be deployed in bean breeding, we must confirm their value under drought conditions, and because bean producers in developing countries often confront low soil fertility as well as drought, we must be confident that selection for these root traits will not have negative consequences for plant performance in low fertility soil. A major objective of this project is to rigorously determine the utility of these traits for plants under water stress and combined water/phosphorus stress. A second objective is to survey bean germplasm for variation in these traits, to aid breeders in identifying sources and parents. A third objective is to characterise the genetic control of these traits, and to develop molecular markers, which would be especially useful since root traits are difficult to evaluate in the field. These products will be powerful new tools for bean breeders and will also have relevance to the breeding of other crops. Our research team has a long history of successful collaboration, combining the group at Penn State that discovered these traits, bean genetics expertise at CIAT, and bean breeders and researchers in Mozambique where drought and low soil fertility are severe problems. We look forward to this opportunity to develop new tools for the selection of drought tolerant crops.

24. Project No G3008.08: Breeder-friendly high-throughput phenotyping tools to select for adaptive traits in drought environments

- *Duration: Nov 2008–Oct 2011*
- *Budget by year: $300,050 (2008), $303,327 (2009), $293,696 (2010); Total budget: $897,073*

Wheat/Drought tolerance/Africa; Asia

Lead institute
ICARDA (Francis Ogbonnaya)
Collaborating institutes and scientists

- CSIRO (M Fernanda Dreccer)
- Participating scientists
- ICARDA (Osman Abdalla, Mohammed Karrou)
- CSIRO (David Bonnett, Tony Condon)
- CIMMYT (Matthew Reynolds)
- INRA–CRRA, Morocco (Hassan Ouabbou)
- ICARDA–INRA Cooperative Research Program, Morocco (Sripada M Udupa)
- INRA–CRRA, EIAR (Solomon Gelacha)

Drought continues to be a major limiting factor to wheat crop production worldwide, with often devastating consequences especially in developing countries. This project proposes to facilitate plant breeding for drought adaptation by developing a package of high-throughput non-invasive techniques to detect genetic variation for single and combined or complex (water use) drought adaptive traits under field conditions. We will also assess the value of different plant characteristics (transpiration efficiency, early vigour, storage of sugars in the stem, flowering date, tillering and stay green) on performance under different types of drought. Finally, we will investigate the traits or trait combinations behind ICARDA's elite drought adapted material. We believe this new knowledge will help focus breeding programmes in the partner regions, particularly Central and West Asia and North Africa (CWANA). All project lines will be genotyped using markers from the GCP genetic diversity kit and markers related to agronomic and drought adaptive characteristics. The project will be executed by a multidisciplinary team operating from cornerstone centres for wheat breeding located in contrasting drought environments (from summer to winter rainfall), working in contrasting wheat gene pools, and with a wide range of relevant expertise (from genetics to remote sensing). A workshop targeted at mainly breeding programmes in the CWANA region as well as Generation Challenge Programme (GCP) members will be held to demonstrate the breeder-friendly tools, the value of several drought adaptive traits per region and the physiological and genetic knowledge on ICARDA's elite lines.

Projects on NCE into 2008 or beyond

25. Project No G3005.03: Identifying the physiological and genetic traits that make cassava one of the most drought-tolerant crops

- *Duration: Jan 2005–Dec 2007 with NCE to Dec 2008*
- *Budget by year: $298,540 (2005), $294,883 (2006), $273,722 (2007); Total budget: $867,145*

Cassava/Drought tolerance/Latin America; Africa

Lead institute
EMBRAPA (Alfredo Augusto Cunha Alves)
Collaborating institutes and scientists

- CIAT (Martin Fregene, Hernán Ceballos)
- IITA (Morag Ferguson, Rosemary Mutegi)
- CU (Tim Setter, Luis Duque)
- ARI–Naliendele (Geoffrey Mkamilo)
- IITA (Edward Kanju)
- SARI (Joseph Adjebeng)
- EMBRAPA (Antonio Souza, Miguel Angel Dita Rodríguez, Alineaurea Silva)
- KARI (Joseph Kamau)

Cassava is usually cultivated in areas considered marginal for other crops, with soils of low fertilityand long periods of droughts. Cassava's photosynthesis and growth decrease to near zero during episodes of water deficit, and it achieves most of its growth after rainfall resumes. This suggests that a key to cassava's success is its ability to regulate numerous plant processes to rapidly change course as it navigates between episodes of favorable and unfavorable weather. The general objective of the proposed work is to determine the best traits to be used in breeding programmes for drought tolerance by elucidating the mechanisms of cassava's remarkable tolerance to drought and making full use of the expanding body of information on the physiological and molecular bases of drought tolerance in other well studied crops. Contrasting genotypes for several traits related to drought tolerance will be selected for evaluation and segregating progenies will be developed for genetic studies. The effect of water deficit on traits which are related to the probable mechanism(s) for drought tolerance in cassava will be evaluated and compared with other well-studied crops. The selected contrasting genotypes will be crossed to generate segregating populations. In addition, drought tolerant genotypes will be selfed to provide S1 families to study recessive gene action. Evaluations will be conducted on the parental clones and the segregating progenies in semi-arid environments of Brazil, Colombia, Ghana, and Tanzania, to screen phenotypes. Segregating progenies will be analysed using a set of genome-wide molecular markers and candidate genes to identify quantitative trait loci (QTL) of component traits of drought tolerance. To assess the value of enhanced leaf retention during stress, a transgenic cassava in which a cytokinin synthesis gene is over expressed will be field evaluated. Expected outputs of this project include an improved understanding of drought tolerance traits and their biological bases, molecular markers for key drought tolerance traits, and cassava genotypes ready to be introduced into breeding programmes.

26. Project No G3005.05: Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools

- *Duration: Jan 2005–Dec 2007 with NCE to Jun 2008*
- *Budget by year: $390,311 (2005), $277,589 (2006), $230,335 (2007); Total budget: $898,235*

Peanut/Drought tolerance and disease resistance/ Africa and Asia

Lead institute
EMBRAPA (José Valls)
Collaborating institutes and scientists

- UCB (David Bertioli, Wellington Martins)
- CERAAS (Ousmane Ndoye)
- ICRISAT (Vincent Vadez: Rajeev Varshney: Aruna Rupakula)
- UAS–Bangalore (Udaya Kumar)
- Agropolis–CIRAD (Angelique d'Hont)
- IBONE (Guillermo Seijo: Germán Robledo)
- UoAa (Jens Stougaard: Lene Madsen, Niels Sandal)
- TAMU (Consultant; Charles Simpson)

Legumes, unlike other crops, fix nitrogen, need little fertiliser and help maintain the soil productive. Legume seeds are among the most important sources of protein and iron for the poor. Peanut (*A.hypogaea*) is a legume grown throughout the tropics on about 24.8 million ha (>90% cultivated by small farmers). Peanut is particularly important in Africa, where production greatly exceeds that of any other legume, and in Asia, where production is almost as high as soybean. Peanut is sensitive to fungal diseases and drought stress and these factors are important reducers of yield.

Improvement of peanut has been limited by an extreme genetic bottleneck at its origin, which occurred via hybridisation of two wild species followed by a rare spontaneous duplication of chromosomes.

The resultant plant had hybrid vigor, but because of the difference in chromosome number, be reproductively isolated from its wild relatives. Therefore, all peanuts are probably derived from one, or a few plants. This led to low diversity for important agricultural traits and very limited genetic diversity, which has constrained advances in genetics necessary for modern breeding. In contrast, wild *Arachis* species are very diverse and have been selected during evolution by a range of environments and diseases, providing a rich source of variation in agronomically important traits.

Recently, partners in this proposal have artificially recreated the events that gave rise to peanut, using a wide range of diploid species. So far, four viable synthetic hybrids have been created thus bringing to peanut breeding, for the first time, the genetic diversity of the genomes of eight wild *Arachis* species. In parallel, major breakthroughs in genetic mapping have been made using a new strategy that will allow plant breeders to work complex hybrids more efficiently. This proposal aims to build on these advances to enable the creation of peanut varieties resistant to disease and drought. In addition, we propose to include peanut in a single genetic system for legumes, allowing peanut research to benefit from the knowledge of modern "genomics".

27. Project No G3005.06: Marker development and marker-assisted selection for *Striga* resistance in cowpea

- *Duration: Jan 2005–Dec 2007 with NCE to Oct 2008*
- *Budget by year: $300,000 (2005), $300,000 (2006), $300,000 (2007); Total budget: $900,000*

Cowpea/**Striga** ***resistance/Africa***

Lead institute
IITA (Satoru Muranaka)
Collaborating institutes and scientists

- IITA (Christian Fatokun, Adebola Raji, Boukar Ousmane, Dong-Jin Kim)
- UoV (Michael Timko)
- CERAAS (Ndiaga Cissé)
- ISRA (Moctar Wade)

Cowpea is an important food grain legume grown on 9.8 million hectares of small farms in the dry savannah of tropical Africa. Current estimates place world cowpea production at 3 million tons, with 80% of its production in Africa, principally West and Central Africa where the crop productivity is low due to pests and diseases. The parasitic angiosperm *Striga gesnerioides* (Willd.) is one of the major limitations to cowpea productivity. Conventional breeding efforts have helped to alleviate some of the *Striga* problems, but pyramiding resistance to the parasite with other important agronomic and resistance traits is time-consuming and difficult. Modern technologies, such as marker-assisted selection (MAS), in combination with conventional breeding have been successfully used for genetic enhancement of other crop species. The cooperative work proposed here, involving the International Institute of Tropical Agriculture (IITA), the Centre d'Etude Regional pour l'amelioration de l'Adaptation a la Seccheresse (CERAAS), the Institut d'Environnement et de Recherches Agricoles (INERA) of Burkina Faso, and the University of Virginia (UVA), seeks to develop a MAS strategy for cowpea that will allow the rapid, reliable identification of race-specific *Striga* resistance genes in breeding lines and integration of MAS for *Striga* resistance in their breeding programmes. The outcome of this work will be superior-performing, well-adapted cowpea varieties containing pyramided agronomic productivity, disease and pest resistance traits available to farmers. This project will also contribute to the development of human and institutional capacity to fully integrate the use of MAS technologies in cowpea breeding. It is expected that farmers will achieve higher yields of better quality cowpea that would impact favorably on their general livelihoods.

28. Project No G3005.09: Development of low-cost technologies for pyramiding useful genes from wild relatives of cassava into elite progenitors

- *Duration: Jan 2005–Dec 2007 with NCE to Dec 2008*
- *Budget by year: $298,194 (2005), $298,164 (2006), $298,548 (2007); Total budget: $894,906*

Cassava/Disease resistance/Latin America and Africa

Lead institute
CIAT (Anthony Bellotti, Martin Fregene)
Collaborating institutes and scientists

- CIAT–NRCRI (Emmanuel Okogbenin, Chiedozie Egesi)
- EMBRAPA (Alfredo Alves)
- CRI (Elizabeth Okai)
- NAARI (Yona Baguma, Anthony Pariyo)

Cassava (*Manihot esculenta Crantz*) is increasing in importance in the tropics due to its hardy nature but it suffers from a plethora of anthropod pests and diseases as well as post harvest physiological deterioration (PPD). It has been estimated that cassava farmers, typically resource-poor farmers, lose 48 million tons of fresh root, some 30% of total world production, valued at US$1.4billion every year to pests, diseases, and PPD. Wild relatives of cassava are important sources of genes for resistance to pests and diseases and longer shelf life. Dramatically delayed PPD has been identified in inter-specific hybrids from *Manihot walkerae*. The only source of resistance to the cassava hornworm and a widely deployed source of resistance to the cassava mosaic disease (CMD) were identified in 4th backcross derivatives of *M. glaziovii*. Moderate to high levels of resistance to cassava green mites (CGM), white flies and the cassava mealy bug have been found in inter-specific hybrids of *M. esculenta* sub spp *flabellifolia*. *Furthermore, M.glaziovii, M. catingae*, and *M. carthaginensis*, are adapted to semiarid lands and are potential sources of genes for tolerance to drought. But the heterozygous nature and long reproductive cycle of cassava makes introgression and pyramiding of these genes a long-term effort. For several years molecular marker tools and a modified Advanced Back Cross QTL (ABC-QTL) scheme have been tested for cost-effective pyramiding of useful genes from cultivated and wild gene pool through the elimination of phenotypic evaluations in each breeding cycle. This proposal seeks to make marker-assisted introgression of exotic genes into elite cassava progenitors widely available by the development of low cost approaches, expand the gene tagging effort to other traits, and establish a systematic approach of collection, evaluation and use of additional wild germplasm.

Subprogramme 4: Bioinformatics and crop information systems

By its nature, work carried out by Subprogramme 4 on Crop Information Systems and Bioinformatics is applicable across crop, traits and regions. Relative to the other GCP Subprogrammes, SP4 has thus far had less direct interaction with NARS scientists, with bioinformatics tools and methods typically being developed in ARIs and CGIAR Centres. All tools developed however are of direct relevance and benefit to NARSs partners and associates. It should be noted that as SP4 increasingly shifts focus from infrastructure development to infrastructure release and use, NARS participation in SP4 activities is expected to increase

Current projects

29. Project No G3008.09: Breeding drought tolerance for rainfed lowland rice in the Mekong region

- *Duration: Nov 2008–Oct 2011*
- *Budget by year: $269,200 (2008), $287,200 (2009), $291,200 (2010); Total budget: $847,600*

Rice/Drought tolerance/Asia

Lead institute
BRRD (Boonrat Jongdee)
Collaborating institutes and scientists

- BRRD (Grienggrai Pantuwan)
- BIOTEC (Theerayut Toojinda, Jonaliza Lanceras-Singliw)
- UoQ (Shu Fukai)
- NAFRI (Phoumi Inthapanya)
- CARDI (Ouk Makara)

The rainfed lowland rice ecosystem is the major food production system in the Mekong region, covering Northeast Thailand, Laos and Cambodia. Drought is considered to be the main constraint for rice production, and development of drought resistant varieties will stabilise yield in the region.

Over the last 10 years, NARS and BIOTEC of Thailand, CARDI of Cambodia, NAFRI of Laos, and the University of Queensland have had collaborative programmes on drought tolerance improvement, supported by the Rockefeller Foundation and the Australian Center for International Agriculture Research. Field screening for drought tolerance was conducted, more than 20 populations from crosses between parents with drought tolerance and popular varieties have been developed, a few secondary traits such as leaf water potential, have been identified as potentially useful, and QTLs and their linked markers for drought tolerance have been identified and developed. We have adopted a concept that widely acceptable varieties require drought tolerance and high yield potential. However, research is required to improve strategies for selecting for yield potential, to test the identified drought tolerant traits and the genotypes in different drought environments, and to identify drought-prone areas that are suitable for these genotypes.

The objective of this proposed project is to develop strategies and protocol for selection of drought tolerant genotypes by using diverse populations which have been developed by us. This study will be conducted in Thailand, Laos and Cambodia. A strong advantage of our work is that the populations have been developed from popular varieties and donors which have been identified for drought tolerance under field condition. The outcome of this work, in addition to developing strategies for selecting drought tolerance, will be release of drought tolerant genotypes as commercial varieties, identification of traits corresponding to adaptation to aerobic condition, confirmation of putative secondary traits and identification of their genomic regions, and GIS maps that identify drought prone areas.

Projects on NCE into 2008 or beyond

30. Project No G3005.04: An eco-physiological–statistical framework for the analysis of GxE and QTLxE as occurring in abiotic stress trials, with applications to the CIMMYT drought stress programmes in tropical maize and bread wheat

- *Duration: Jan 2005–Dec 2007 with NCE to Jul 2008*
- *Budget by year: $169,550 (2005), $175,050 (2006), $162,550 (2007); Total budget: $507,150*

Maize; wheat/Drought tolerance/Various regions

Lead institute
WUR (Fred van Eeuwijk)
Collaborating institutes and scientists

- CIMMYT (Matthew Reynolds, José Crossa)
- CSIRO (Scott Chapman)
- UoC (Mateo Vargas)
- WUR (Marco Bink)

When breeders try to develop adapted genotypes for abiotic stress conditions, i.e.,plants with on average superior genetic constitution with respect to yield, they are faced with the problem that it is hard to get reliable estimates of genetic superiority under stress conditions. Under stress, the phenotype, that what the breeder can measure and observe, provides little information on the underlying genetics. A traditional solution uses measurements on yield or other, secondary traits in non-stress conditions to predict the performance under stress. The idea is that under non-stress conditions the genetic value can be estimated more precisely, and as long as the genetic basis of the trait observed under non-stress is closely enough related to the genetic basis of yield under stress, or, the genetic correlation high enough, then selection under non-stress is preferable. Recently, the traditional approach was challenged by an alternative approach originating from CIMMYT researchers that was built on physiological understanding of the stress response and relevant environmental characterisation of selection and stress environment. The alternative approach would facilitate a better choice of secondary traits and selection environments. Molecular marker techniques make this alternative even more attractive, because of the possibility of selection at the genetic level. However, the new approach still does not live up to the expectations and we think that one of the important reasons for this partial failure is the use of a less than adequate statistical framework for analysing data from abiotic stress trials. The present statistical approaches do not incorporate any explicit physiological knowledge on the part of the genotype nor the environment. We propose the development of an integrated eco-physiological statistical framework, modeling yield responses on both the phenotypic and genetic level in direct dependence on physiologically relevant environmental factors. Application of this framework to existing CIMMYT data on drought stress in maize and wheat, will significantly add value in the form of deeper insight in the genetic and physiological mechanisms underlying drought stress in those crops. Additional features of our approach include facilities for the analysis of multiple traits and crosses. To make the methodology generally available to students and researchers in developing countries, course material and corresponding software modules will be developed.This teaching material will be presented in one-week courses in Uruguay and Kenya.

II. COMMISSIONED PROJECTS

Subprogramme 1: Genetic diversity of global genetic resources

Current projects

31. Project No G4006.01: Developing strategies for allele mining within large collections

- *Duration: Jan 2006–Jul 2008*
- *Budget by year: $109,386 (2006), $90,614 (2007); Total budget: $200,000*

Lead institute
IRRI (NR Sackville Hamilton)
Collaborating institutes and scientists

- CIAT (M Lorieux)
- ICRISAT (H Upadhyaya)
- ICARDA (M Baum)

GCP SP1 has undertaken new steps towards rationalising the utilisation of germplasm collections. It has assembled a large percentage of the diversity of crop genepools into progressively refined subsets as composite, core and reference collections. These will enable improved understanding of the structure of genetic diversity and its ecogeographic distribution, and discovery of new functional genes and the range of alleles of each gene included in the composite collections.

However, they represent only a small percentage of the larger collections: in the case of rice, the composite collection contains only around 2% of the germplasm held in the genebank at IRRI, and probably less than 0.5% of global holdings in all rice genebanks. Many distinctive alleles, haplotypes and genotypes have not been captured in the composite collections. The next big challenge is to explore this additional diversity.

This project seeks to establish a strategy for efficiently exploring diversity held within the large collections outside the composite collections. The strategy constitutes true "allele mining": "tunnelling" through the collections, sampling and testing accessions as we go, and using the results to determine where to tunnel next.

SP1 results to date will be analysed to identify genetic gaps and boundaries in the composite collection, and to establish relationships between the rich new molecular data and the sparse passport and phenotypic data previously available. Objective functions will be developed to predict which additional accessions are most likely to lie in specified locations of the hyperspace of molecular data. Those accessions will be fingerprinted to test the predictions and thence to refine the objective functions. The efficiency of the approach will be analysed. The output will be a generic strategy for discovering novel diversity without systematically fingerprinting every accession and more efficiently than using random subsets.

32. Project No G4006.02: A dataset on allele diversity at orthologous candidate genes in GCP crops (ADOC)

- *Duration: Jan 2006–Dec 2008 with NCE to Jul 2009*
- *Budget by year: $573,000 (2006), $187,000 (2007), $100,000 (2008); Total: $860,000*

Various crops/Drought tolerance/Various regions

Lead institute
Agropolis (Dominique This)
Collaborating institutes and scientists

- Agropolis–CIRAD (Brigitte Courtois, Claire Billot, Jean François Rami, Romain Philippe, Pierre Mournet)
- CIP (Merideth Bonierbale, Roland Schaftleitner, Reinhart Simon, Percy Rojas)
- ICRISAT (Rajeev Varshney, Tom Hash, Dave Hoisington, Spurthi Nayak, Hari Upadhyaya)
- Agropolis–INRA/CNG (Dominique Brunel, Redouane El Malki)
- IRRI (Ken McNally)
- ICARDA (Michael Baum, Wafaa Choumane)
- CIAT (Matthew Blair, Martin Fregene)

Many candidate genes have been proposed during the last years which could explain some aspects of tolerance to drought stress, for a specific crop and in a specific environment. However, the relation between gene structural polymorphism and functional diversity is seldom clear. Moreover, whether this information may be valuable for different species is poorly investigated. The Generation Challenge Programme is the only initiative that can coordinate a global approach with parallel components in a wide range of crops. Within the SP1 and SP2 sub-programmes, this project proposes to produce and deliver a public dataset of allelic diversity at orthologous candidate genes across seven important GCP crops. A set of 10 to 12 genes corresponding to enzymes involved in sugar metabolism, or regulatory components of drought tolerance / water us efficiency, will be investigated for their orthologous relationships among crops, and their sequence polymorphism will be assessed in a sample of 300 reference accessions for each crop. This reference germplasm, derived from selection after SSR genotyping and meant to be submitted to drought related phenotyping in complementary projects, will allow testing association between observed polymorphism and trait variability. We will thus establish a GCP resource that will be useful to quickly capture the value of results obtained in the most advanced genetic studies with regards to drought tolerance. It will enable production of scientifically coherent sets of (ortho)allelic diversity data with high information content and scope for application and impact. As such, it will facilitate establishment of collaborations with partners who run high-throughput genomics facilities. It is also meant to attract partnership with advanced research groups interested in particular biological processes, metabolic pathways, and gene families. This resource may, then, allow plant breeders to identify specific progenitors in their crops based on gene haplotypes to further improve adaptation to environmental stresses.

33. Project No G4007.01: Genotyping validation of the GCP reference sets

- *Duration: Jan 2007–Dec 2008*
- *Budget by year: $50,000 (2007), $329,280 (2008); Total budget: $379,280*

Various crops, traits and regions

Lead institute
Agropolis–CIRAD (Jean-Francois Rami)
Collaborating institutes and scientists
Validation labs subcontracted by Agropolis–CIRAD

The scientific community involved in the SP1 sub-programme of the Generation Challenge Programme is about to deliver one of the biggest efforts of characterisation of genetic diversity on 21 crop species. This characterisation was based on the utilisation of microsatellite markers, which constitute a powerful marker system for such a purpose. However, this work was by nature composite, involving different species and different partners using different technologies. For each crop, one of the main products of this exercise is a reference set of representative germplasm to serve as a material for international coordination in the future. The present project proposes to assess the different microsatellite datasets produced in SP1 by having a subsample of germplasm accessions re-genotyped by an external genotyping facility (service provider). This subsample will be the reference set, so that the new data will also serve to validate and certify the genotypic information attached to the reference set. This genotyping validation project will be connected to the management of the genetic material constituting the reference sets. As an output, stabilised materials specifically handled as genetic stocks by gene bank curators and associated to validated genetic diversity data will be available.

34. Project No G4008.01: Population development to underpin gene discovery and allele validation in rice: the Multiparent Advanced Generation Inter-Crosses (MAGIC)

- *Duration: Jan 2008–Dec 2009*
- *Budget by year: $56,280 (2008), $57,714 (2009); Total budget: $113,994*

Various crops, traits and regions

Lead institute
IRRI (Hei Leung)
Collaborating institutes and scientists
IRRI (Ed Redona, RK Singh, N Bandillo and PA Muyco)

MAGIC is an experimental method to increase the precision with which genetic markers are linked to quantitative trait loci (locations in the genome which have a quantifiable effect on measured traits). MAGIC involves two extensions to the traditional method of searching for marker-trait correlations in the segregating progeny of crosses between two parents. Firstly, the mapping population is established by intercrossing multiple founder lines. A MAGIC population is therefore genetically diverse and more QTL can be detected. Secondly the population is cycled through several extra generations of crossing. Each extra generation mills the genetic contribution from the founder lines finer. QTL are therefore located with greater accuracy and are of more use in plant breeding and genetical research.

There is an increasing amount of fundamental work in the genomics and molecular genetics of these crops. For the outputs of this research to be transferred to new varieties, our knowledge of the DNA of these crops must be linked to the traits of important to farmers. MAGIC populations provide a means to this end.

IRRI proposes to establish MAGIC populations in rice, in parallel to three other MAGIC projects on sorghum, pearl millet and cowpea sponsored by GCP. Specially, we will establish two populations in rice and initiate development of 2000 inbred lines from the populations. One population will be targeted at agro-ecosystem in Africa and one for south and south-east Asia. Each population will have eight founder lines. We shall also intermate each population in preparation for generation of a second cycle of lines for finer mapping. We will monitor with DNA markers to ensure line purity and progress of the mating cycles. Comprehensive genotyping, phenotyping, and QTL mapping work will be considered in next phase of the project after the initial populations are established.

35. Project No G4008.02: Phenotyping sorghum reference set for drought tolerance

- *Duration: Jan 2008–Dec 2010*
- *Budget by year: $163,950 (2008), $156,550 (2009), $153,150 (2010); Total budget: $473,650*

Sorghum/Drought tolerance/Asia; Africa

Lead institute
ICRISAT (HD Upadhyaya)
Collaborating institutes and scientists

- ICRISAT (V Vadez, CT Hash, L Krishnamurthy, F Rattunde, E Weltzien-Rattunde, MA Mgonja)
- UAS–Dharwad (PM Salimath)
- KARI (CK Karari)
- NPGRC (W Ntundu)
- IER (M Diourte)
- ISRA/CERAAS (N Cissé)

Drought is one of the most important yields reducing abiotic constraint worldwide. It is proposed to evaluate sorghum reference germplasm set (about 360 of the 384 reference set accessions), selected based on the genotyping information of composite collection (41 SSR loci data on 3372 accessions), for post-flowering drought tolerance. In the first year, the reference set will be characterised for morpho-agronomic traits to classify accessions into distinct flowering and plant height groups at ICRISAT locations in India, Mali, and Kenya. In the second year, these subgroups will be evaluated for post-flowering drought tolerant traits at three ICRISAT locations (as above). In addition, they will also be evaluated at ICRISAT Patancheru, India for seed micronutrients (Zn and Fe) under varying water regimes (stressed vs unstressed conditions) to identify seed micronutrient dense lines. In third year, selected reference set accessions and stay-green QTL introgression lines will be evaluated for water uptake under stressed conditions in PVC tubes (2.0-m long and 25-cm diameter), and for the proportion of water used prior/after anthesis. In the same year, the most promising post-flowering drought tolerant reference set accessions and stay-green QTL introgression lines will be multilocationally evaluated for post-flowering drought tolerance at ICRISAT and NARS locations in India and Africa. In addition to evaluating for post-flowering drought tolerance traits, additional data will be collected on grain/stover yield and component traits to identify lines that are better able to maintain normal growth/yield processes under stress. It is proposed to evaluate this select group of materials in the fourth year (subject to GCP provides funds) at NARS locations to generate additional data on the performance of post-flowering drought tolerant lines. At the completion of project, we will have a better understanding of post-flowering drought tolerance in sorghum, the traits associated with post-flowering drought tolerance, and a range of post-flowering drought tolerant sorghum lines for use in crop improvement programmes.

36. Project No G4008.03: Precision phenotyping of the GCP spring wheat reference sample for drought

- *Duration: Jan 2008–Dec 2010*
- *Budget by year: $10,000 (2008), $97,300 (2009), $46,300 (2010); Total budget: $153,600*

Wheat/Various traits and regions

Lead institute
CIMMYT (Susanne Dreisigacker)
Collaborating institutes and scientists

- CIMMYT (Matthew Reynolds, Yann Manes, Tom Payne, Hans-Joachim Braun, Jose Crossa, M Zaharieva)
- INRA–Morocco (Rachid Dahan, Nsarellah Nasrolhaq, Hassan Quabbou)
- CIMMYT–Iran in collaboration with the Dryland Agricultural Research Institute (Jalal Kamali)

Global genetic resources provide a fundamental source for further crop improvement. The GCP Subprogramme 1 aims to characterise the diversity of crop germplasm collections held by the CGIAR and its partners. This characterisation includes an assessment of the genetic structure of the collections as well as the phenotypic variation associated with that structure. The ultimate goal is to provide access to sources of genetic diversity that may supply genes and alleles involved in key agricultural traits, especially stress tolerance. During the last three years, 3000 wheat accessions provided by major germplasm banks were characterised by CIMMYT and collaborators with 50 SSR markers for the development of reference samples including accessions maximising neutral genetic diversity. In the first year of this project we will build up a seed stock for three developed international reference samples in wheat: the spring bread wheat, winter wheat and durum wheat reference samples. Seed will be stored in the CIMMYT wheat germplasm bank and made available for distribution. A drought specific spring bread wheat reference sample will be defined and characterised in multi-location trails for relevant agronomic traits, as well as physiological traits related to the main drivers of yield under drought. The same reference sample will be genotyped with high density DArT markers. This will allow associating the observed trait variation with the genotypic information in order to uncover QTL related to drought tolerance.

37. Project No G4008.05: Connecting performance under drought with genotypes through phenotype associations

- *Duration: Jan 2008–Dec 2010*
- *Budget by year: $193,440 (2008), $187,356 (2009), $86,880 (2010); Total budget: $467,676*

Rice/Drought tolerance/Asia

Lead institute
IRRI (Jill Cairns)
Collaborating institutes and scientists

- IRRI (Ken McNally, Arvind Kumar, Rachid Serraj)
- Agropolis–CIRAD (Michael Dingkuhn, Delphine Luquet, Brigitte Courtois)
- WARDA (Semon Mande)
- CRRI (Padmi Swain)
- TNAU (S Robin, M Raveendran)
- BIOTEC (T Theerayut)
- BAU (BN Singh)

Water stress is frequently the main limitation of rice productivity and yield stability in rainfed systems. Most "mega-varieties" that are grown over vast areas of South and Southeast Asia are highly susceptible to water deficits. Yet, within the primary rice gene pool resides a large amount of genetic diversity for abiotic stress tolerance (Ali et al 2006). Indeed, drought-tolerant landraces are in the parentage of many of the megavarieties. Rapid advances in molecular biology provide great potential to harness this genetic diversity within rice but, to fully exploit this information, by relating allelic variation to agronomic performance, an in-depth phenonomics initiative is necessary. By developing a standardised, high-throughput, precise phenotyping strategy, employed across a range of drought environments, valuable data sets on performance under field drought stress on a large reference set of accessions will be generated. This information can be combined with data obtained from new high-throughput SNP platforms in association studies linking field performance to DNA sequence variation (McNally et al 2006). This project will build on individual partners' phenotyping capabilities to develop a large-scale phenotyping programme incorporating standardised protocols, environmental characterisation, and new analytical tools for rapid phenotypic analysis. Successful application for breeding programmes must target developmental stages during which yield is sensitive to drought. The greatest yield losses occur when drought stress occurs at the same time as irreversible reproductive processes (Cruz and O'Toole 1984, Boyer and Westgate 2004). This project will focus on reproductive-stage stress, with specific emphasis on grain yield and key physiological traits related to grain yield decline caused by stress.

38. Project No G4008.33: Drought tolerance phenotyping of the GCP maize inbred line reference set

- *Duration: Jan 2008–Feb 2011*
- *Budget by year: $128,120 (2008), $83,832 (2009), $45,348 (2010); Total budget: $257,301*

Maize/Drought tolerance/Africa

Principal Investigator
KARI (James Gethi)
Collaborating institutes and scientists

- CIMMYT (M Warburton, M Zaharieva, S Taba, M Vargas, JL Araus, C Sanchez)
- ETH (P Stamp, A Hund, R Messmer)
- Agropolis–INRA (F Tardieu, C Welcker)

Under GCP subprogramme 1, several projects have assessed the genetic structure of crop germplasm collections held by the CG centers and their partners, including maize in which a collection of 987 inbred lines, provided by CAAS, CIMMYT and IITA was characterised by CIMMYT and CAAS with 47 SSR markers. As a product of this study, a subset of 240 reference lines has been chosen to represent a majority of the neutral genetic diversity of the whole collection. The objective of the present project is to characterize the phenotypic variation associated with the reference set, particularly for drought tolerance related traits. The expected output is to ensure a better access to new genes and alleles involved in drought tolerance.

In winter 2007-2008, the reference set will be sown at the Tlaltizapan experimental station (Mexico) under irrigated conditions to ensure seed multiplication of the 240 lines, and identify and discard those that are un-adapted to the local, subtropical growing conditions. Phenological traits will be scored during this growing cycle to improve further phenotyping design by grouping similar individuals (for example by earliness and plant height). At Tlaltizapan, single hybrids will be generated by crossing the lines having produced ears and grain with a tester with high general combining ability and good adaptation to African conditions (i.e., CML 312). Inbred lines and hybrids will be phenotyped at Tlaltizapan and Kiboko (Kenya) using different secondary traits. In addition, variation in growth of main axile and lateral roots under controlled conditions will be assessed at ETH Zűrich using a non-invasive imaging technique, and variation in leaf elongation rate under vegetative drought conditions will be examined at INRA Montpelllier. During the seed multiplication step carried out at CIMMYT, leaf tissue will be collected for DNA extraction. Leaf tissue will be collected from two separate plants presuming that at least one of them will produce grain. This plant will be retained as founder for generating a stock of seeds available for further research activities. Its DNA will be made available to GCP for genotyping the 240 lines (using the 20 most discriminant SSR markers from the 47 used for genotyping the composite set). This will permit a validation of the original genotyping of the reference set. Any lines missing marker data for the 47 SSR markers will be genotyped at CIMMYT to allow a complete data set. The remaining DNA will be made available for further research activities, including high density genotyping using SNP markers in future projects planned by CIMMYT and others.

This project will permit i) a validation of the previous genotyping of the composite set and of the identification of the reference set, ii) a high quality seed multiplication and creation of hybrids, iii) a multi-years and multi-locations phenotyping of the reference set and of the hybrids generated from this set, and iv) a phenotyping of root morphology and leaf elongation rate under drought controlled conditions.

A NARS from Eastern Africa, KARI (Kenyan Agricultural Research Institute) will be PI of the project and play a major role from the very beginning of the phenotyping process. Parts of the drought areas in Kenya (and particularly the Kiboko region) are representative of many areas in Eastern and Southern Africa (ESA).

39. Project No G4008.42: Developing DArT markers for several crops in the GCP

- *Duration: Jan 2008–Dec 2009*
- *Budget: $ 229,200 (2008), $108 400 (2009); Total budget: $337,600*

Various crops, traits and regions

Lead institute

Agropolis–CIRAD (JC Glaszmann)

Collaborating institutes and scientists

- DArT P/L (A Kilian – subcontractor)
- ICRISAT (D Hoisington)
- IITA, Agropolis–IRD, Agropolis–CIRAD, CRI
- *For potato*: INIA–Chile (Boris Sagredo), USDA (David Spooner), CIP (Merideth Bonierbale)

This proposal aims at reinforcing the capacity to genotype large numbers of materials with large numbers of markers at a relatively low cost, one of the objectives of SP1 in order to facilitate the use of markers for monitoring genetic diversity. It builds on the successful commissioned project executed in 2005 by the team substantially overlapping with the list of contributors to the current proposal. It includes expanding arrays developed in the previous project for Musa (banana) and coconut, expanding arrays developed by Diversity Arrays Technology Pty Ltd (chickpea, pigeonpea, potato) and developing new arrays for yams, groundnut and pearl millet. For each case, we will genotype with the arrays developed a set of important germplasm in the process of marker discovery. In the case of coconut, groundnut, yam and pearl millet, additional genotyping will be performed to explore the diversity in particular populations of interest. In the case of banana, this project will support high density genetic mapping as a contribution to genome sequencing in ANR and JGI projects. The libraries generated in this project will be available to the GCP; their sequences will be provided when they are available.

40. Project No G4008.45: A nested association mapping (NAM): Laying the bases for highly efficient QTL characterisation population of rice

- *Duration: Aug 2008–Jul 2010*
- *Budget: $98,620 (2008), $127,390 (2009); Total budget: $226,010*

Rice/Drought tolerance/Various regions

Lead institute

Agropolis–IRD/CIAT (Mathias Lorieux)

Collaborating institutes and scientists

- CIAT (César P. Martinez, Edgar Torres)
- WARDA (Marie-Noelle Ndjiondjop)

Crop improvement is a crucial area of research and development for food stability at the world level. Virtually all crop species have reached a yield plateau, due to various and distinct reasons. In order to generate a real breakthrough in crop yields, technologies able to boost crop breeding efficiency are urgently needed. Modern breeding strategies often fail to include precise genetic information. Marker-Aided Selection (MAS) strategies have proven to be more efficient than conventional selection in several cases, but still suffers of (1) lack of precision in the localisation of the genes of agronomical importance (the so-called QTLs, for Quantitative Trait Loci) and (2) are often limited to the alleles available in the crossing scheme used for QTL detection, i.e., the genetic information obtained from a particular cross between two genotypes (or lines) will not be useful when working with other genotypes. The area of research called Genomics (i.e., the massive and parallel analysis of the thousands of DNA sequences that constitute the genetic code of an organism) has made considerable progress in the last few years. Currently, we have access to the complete genome information for several crops, and rice is the most advanced of them in this sense. However, there is a strong need to bridge the gap between Genomics and Crop Improvement. Rice, as one of the most important cereals for human nutrition, must be considered a priority. In Africa, rice is getting increasing importance as a staple food. It constitutes a major source of calories for the urban and rural poor, with a fast growing demand. At the same time, the germplasm (i.e., cultivated varieties) grown in Africa suffers of low genetic diversity and needs to be enriched in order to develop new varieties, more adaptable to the inherent or new environmental constraints (e.g., drought stress, pests and diseases, low inputs). We propose to develop a new genetic resource, called a Nested Association Mapping population, that would (1) help in linking the genomic tools available for rice, (2) give access to a much higher allelic diversity at the important QTLs than "conventional" mapping approaches do, (3) allow fine mapping of QTLs (i.e., localise them with high precision on the rice genome), thus increasing significantly the efficiency of MAS strategies, and (4) provide interesting and promising genetic materials (advanced lines) for direct introduction in breeding schemes.

41. Project No G4008.46: Sorghum MAGIC: Multiparent advanced generation inter-cross development for gene discovery and allele validation

- *Duration: Aug 2008–Jul 2010*
- *Budget: $31,800 (2008), $60,486 (2009); Total budget: $92,286*

Sorghum/Africa/Various traits

Lead institute
ICRISAT (Tom Hash)
Collaborating institutes and scientists

- NIAB (Ian Mackay)
- ICRISAT (Mary A Mgonja, H Fred W Rattunde, S Senthilvel, SP Deshpande)
- NRCS (R Madhusudhana)

MAGIC is an experimental method to increase the precision with which genetic markers are linked to quantitative trait loci (locations in the genome that have a quantifiable effect on measured traits). MAGIC involves two extensions to traditional methods of searching for marker-trait correlations among segregating progeny of crosses between two parents. First, the mapping population is established by intercrossing multiple founder lines. A MAGIC population is therefore more genetically diverse than a conventional bi-parental mapping population and more QTLs can be detected. Second, the MAGIC population can be cycled through several extra generations of forced intermating. Each extra generation mills the genetic contribution from the founder lines finer. QTLs are therefore located with greater accuracy and flanking markers for QTLs detected are potentially of greater value for use in plant breeding and genetic research.

We will establish several MAGIC-like populations for sorghum, each having 8-16 founder lines, and each targeting a specific tropical agro-ecology where sorghum is an important component of current crop-livestock production systems.

There is an increasing amount of fundamental work in the genomics and molecular genetics of sorghum and the aligned genome sequence for elite sorghum inbred BTx623 is now available. Further, BTx623 is being used as the common parent in a set of nested sorghum RIL populations that are being developed in the USA as a tool for allele mining and association mapping of QTLs for many sorghum traits of economic importance, and has been used as the genetic background for development of a sorghum TILLING population. For outputs of this upstream research to be applied to development of improved crop varieties, our knowledge of the DNA sequence and population structure of the primary genepool of this crop must be linked to the traits of importance to farmers. MAGIC populations provide a means to this end.

We will establish initial cycle intermated bulks of two sorghum MAGIC populations, targeting South Asian rainy season and postrainy season sorghum production environments, respectively. We will then initiate development of 1000 inbred lines from each of these. We will also intermate population bulks of these two MAGIC populations, following the initial cycle of crosses to create a given population, in preparation for generation of second-cycle lines for finer mapping. We will validate the structure and pedigree of these two MAGIC populations targeting South Asia with a small number of SSR markers (one per chromosome arm) drawn from the GCP programme.

We will also introduce sets of proposed founder parents for two additional sorghum MAGIC populations [one each targeting sorghum production environments in Western and Central Africa (WCA) and Eastern and Southern Africa (ESA)] for which all of the proposed founder parents are not currently available at ICRISAT–Patancheru. Following introduction in 2008 of the founder parents of these latter two MAGIC populations, through the Post-Entry Quarantine Isolation Area facility at ICRISAT–Patancheru, cycles of crossing to generate the initial cycle intermated bulks of these two populations will be undertaken in 2009.

Founder parents of all four sorghum MAGIC populations will be fingerprinted with SSR-anchored DArT markers to assess the level of marker variation within each MAGIC population, and the distribution of this variation across the genome, to help us plan the future genotyping of finished inbred line sets from the initial and more advanced generation cycles of these populations.

42. Project No G4008.52: Genetic Resources Support Services (GRSS) Implementation feasibility work programme

- *Duration: Sep 2008–Dec 2008*
- *Total budget: $15,000*

Various crops, traits and regions

Lead institute
GCP (Jean Christophe Glaszmann)

1. Background
The Generation Challenge Programme (GCP) is at the heart of a research and capacity-building network that uses plant genetic diversity, advanced genomic science and comparative biology to develop tools and technologies that help plant breeders in the developing world produce better crop varieties for resource-poor farmers. All GCP activities aim to generate usable products in the form of knowledge and tools for plant breeders. A core mission is to promote and disseminate these products through provision of cost-efficient services worldwide. A suite of plant breeding support services (PBSS) are being developed or are envisaged. These include:

1. Genetic resources support service
2. Genotyping support service
3. Phenotyping support service
4. Analysis and policy support service

Beneficiaries of the PBSS will be partners in GCP projects, but also breeders outside GCP working on crop improvement in marginal environments.
The work programme contained in this document focuses on preparation of options, feasibility and planning for creation and implementation of the Genetic Resources Support Service (GRSS).

Projects on NCE into 2008 or beyond

43. Project No G4005.01.03 Genotyping of composite germplasm set—Sorghum

- *Duration: Jan 2005–Dec 2005 with NCE to Sep 2008*
- *Total budget: $129,000*

Sorghum/Various traits and regions

Lead institute
ICRISAT (Tom Hash)
Collaborating institutes and scientists

- Agropolis–CIRAD (Claire Billot, Monica Deu, Jean-François Rami and Jacques Chantereau)
- CAAS (Yu Li)
- ICRISAT (P Ramu and HD Upadhyaya)
- BECA, ICRISAT–Nairobi (RT Folkertsma)

Sorghum is the fifth most important cereal globally following maize, rice, wheat and barley. It provides staple food grain and stover (used for fodder, fuel and construction material) in semi-arid and sub-humid tropical, sub-tropical and temperate environments too harsh for rainfed production of maize or rice. Sorghum is well known as a drought-tolerant grain and fodder crop, is closely related to maize, and has a much smaller genome than maize or pearl millet. Substantial genetic variability is available in global collections of wild and cultivated sorghum germplasm, but only a very limited fraction of the >40,000 collected accessions have been exploited in applied sorghum breeding programmes. The activities described here are intended to provide a better understanding of the structure of global sorghum genetic resources so that these can be more effectively harnessed for crop improvement—not only of sorghum in the short term, but potentially for other crops as well in a longer time horizon.

The activities proposed for 2005 build upon GENERATION CP activities initiated in 2004, including constitution of a composite germplasm set of 3,000 wild and cultivated (including landraces, elite cultivars and hybrid parents, mapping population parents, trait donors and recurrent parents for current and future marker-assisted breeding programmes) sorghum accessions, assessment of a set of 104 sorghum SSR primer pairs for their ability to consistently detect variation (across Agropolis, CAAS, and ICRISAT labs) among a mini-core of 48 sorghum accessions, and selection of an initial 30 of these primer pairs for genotyping approximately 700 accessions that are included in the sorghum composite germplasm set.

44. Project No G4005.05: Assesing Ecotilling as a methodology for targetted genotyping and SNP discovery

- *Duration: Jan 2005–Dec 2005 with NCE to Sep 2008*
- *Total budget: $150,000*

Rice, sorghum/Various traits and regions

Lead institutes
- IRRI (Kenneth McNally)
- Agropolis–CIRAD (Co-PI) L Claire Billot

Collaborating institutes and scientists
- IRRI (N Ruaraidh Sackville Hamilton)
- Agropolis–CIRAD (M Deu, I Hippolyte, F-C Baurens, J-F Rami)

TILLING (Targeting Induced Local Lesions IN Genomes) is a new technique that can identify polymorphisms in a target gene by heteroduplex analysis. A variation of this technique (EcoTILLING) represents a means to determine the extent of natural variation in selected genes in crops. EcoTILLING may be a cost-effective approach for haplotyping and SNP discovery.

The objectives of the projects are i) to assess Eco-tilling as a reliable and cost-effective method to detect SNP in a large number of accessions, ii) to test for validity in triploid species, and iii) to establish Eco-tilling transfer technology platforms at IRRI and Agropolis–CIRAD. These will be performed through the study of 10 orthologous genes in three related species, two diploid (rice and sorghum) and one presenting different ploidy levels (Musa).

45. Project No G4005.06: Supporting emergence of reference drought tolerance phenotyping centers

- *Duration: Jan 2005–Dec 2007 with NCE to June 2008*
- *Budget by year: $254,730 (2005), $78,430 (2006), $148,430 (2007); Total budget: $581,590*

Cereals (maize, sorghum, rice, and wheat) and legumes (common bean and cowpea)/Drought tolerance/Various regions

Lead institute
Embrapa–National Maize and Sorghum Research Center (Reinaldo L Gomide)
Collaborating institutes and scientists
- EMBRAPA Rice and Beans (Cleber M Guimarães and others)
- EMBRAPA Mid-North (Edson A Bastos and OthersEMBRAPA Wheat and Savannah (Walter Q. Ribeiro Júnior and Others)
- EMBRAPA Semi-Arid (Luiz BMorgado and others)

The development of drought tolerant varieties for crops of economical importance represents a major challenge for the 21st. century, considering that agriculture growth will be limited by world water availability. A first step to be taken in this direction is to select germplasm adapted to water stress conditions through appropriated screening techniques and defined protocols. Thus, the great challenge is the identification and characterisation of drought tolerant genitors to provide material to be used in genetic breeding programmes focused on regions historically known as prone to water deficit during crop growing season. The improvement of drought tolerance relies on the manipulation of the traits that limit yield and their accurate phenotyping under the prevailing field conditions being target. This issue is particularly crucial for the breeding programme and identification of *QTLs* for traits categorised as adaptive as compared to constitutive traits, per each specie. On this purpose it is necessary to amplify an infrastructure to allow plant exposure to water deficit pressure to be used for the evaluation of genotypes and characterisation of plant physiological responses to these stress conditions.

The objectives of this project are to develop and make useful phenotypic evaluation protocols for cereals (maize, sorghum, rice, and wheat) and legume crops (common bean and cowpea), as well as to establish the amplification of the three Phenotyping Center of Excellence for Drought Tolerance Studies composed of phenotyping central laboratories, including controlled environment field and greenhouse and a training unit for researchers and research assistants, and six–eight experimental stations located in regions with facilities and well defined dry season periods to assure total soil moisture control during the drought phenotyping field experiments. In fact, the project seeks to establish a scientific and service net, like a model to drought tolerance phenotyping of cereals and legumes, including national and international genotypes.

Embrapa–National Maize and Sorghum Research Center, as the main coordinating institute, accumulates over 30 years of experience working with the application of phenotyping methodologies, conducting maize and sorghum breeding programmes, and releasing drought tolerant germplasm. Also, all partners have large experience with others crops, as rice and bean, wheat, etc. The innovative character of the present proposal consist in having different crop expertise aggregated in one single project stimulating the exchange of personal experiences, providing simultaneous experiment conduction and data integration, establishing news and futures partnerships for simulation models, and also promoting knowledge diffusion by planning and organising training courses.

46. Project No G4005.07: Whole plant physiology modeling of drought tolerance in cereals

- *Duration: Jan 2005–Dec 2006 with NCE to May 2008*
- *Budget by year: $179,000 (2005), $396,720 (2006); Total budget: $575,720*

Lead institute

Agropolis–CIRAD (Delphine Luquet)

Collaborating institutes and scientists

- Agropolis–CIRAD (M Dingkuhn, JC Combres, Vincent Bonnal, A Clément-Vidal, N Ahmadi)
- Agropolis–CIRAD/INRA (François Tardieu, C Welker, K Chenu)
- IRRI (Renée Lafitte, B Bouman)
- CSIRO (Scott Chapman)
- UoQ (Graeme Hammer)
- CIMMYT (M Bänzinger, M Reynolds, R Trethowan)
- ICRISAT (Eva Weltzien)
- EMBRAPA (Reinaldo Gomide, Cleber Morais, Edson Bastos, Alexandre Bryan Heinemann, Camilo Andrade)
- Pioneer (Mark Cooper)

Close partners

- Agropolis–CIRAD (M Vaksmann)
- IER (M Kouressy)
- IRRI (K Mc Nally)

The present project is a continuation of the GCP phenotyping workshop organised in July in Montpellier, where more than 40 breeders and physiologists from inside and outside the consortium met for a week. Conclusions of the workshop (available on GCP website (www.generationcp.org) stressed the importance modeling in supporting phenotyping processes for drought tolerance by: (i) a quantification of traits and integration of their impact on yield, (ii) a genetic analysis of adaptive traits, and (iii) a characterisation of target population of environments.

The need for better interactions between physiologists, modelers, and breeders to develop a comprehensive approach and improve phenotyping methods and outputs was also stressed during the meeting and must be kept in mind as a main issue of this project.

This project is the only GCP project to develop modeling approaches and deliver new tools. Consequently, it proposes interactions or complements with other initiatives:

- Competitive Project 4 "An ecophysiological-statistical framework for the analysis of G X E and QTL X E," focusing on more statistical concepts, in which some environmental characterisations will be carried out using the same models for wheat and maize as in this project.
- The commissioned project on "Simulation on marker-assisted selection strategies." An attempt will be made to link these two projects on the basis of component 3 activities.
- The commissioned project on "Reference drought tolerance phenotyping centres." A first interaction is planned on environment characterisation of these centres by model use.
- Interaction will be sought with the project on "Modeling alternate drought tolerance strategies on globally important crops" lead by IFPRI on the impact of improved drought tolerance characterisation.

47. Project No G4006.30: Development and genotyping of composite collection of foxtail millet [*Setaria italica* (L.) *Breauv*].

- *Duration: Jan 2006–Dec 2006 with NCE to Jul 2008*
- *Budget by year: $25,016 (2006); Total budget: $25,016*

Foxtail millet/Various traits/Asia; Europe; North America

Lead institute
ICRISAT (HD Upadhyaya)
Collaborating institutes and scientists
ICRISAT (RK Varshney, CT Hash, D Hoisington, CLL Gowda, S Chandra)

The genus *Setaria* is widely distributed in warm and temperate areas, and foxtail millet (*Setaria italica* (L.) Beauv.) is the most economically valuable coarse grain food crop, largely grown in China, India, Russia, and the United States. Globally, the millets are grown in 3.5 million ha, with a total production of 2.9 million tons and productivity of 0.83 t ha-1. Millet grains including foxtail millet are rich in calcium, iron, phosphorous, vitamins, sulphur-containing amino acids, and soluble fiber content. Because of these properties, minor millets have been recently designated as "nutritious millets" for the poor man's diet. There have been very limited crop improvement efforts to boost the production and productivity of this crop in spite of the fact that it is a very hardy crop and its seeds have high biological food value.

The Rajendra S. Prasad gene bank at ICRISAT holds 1,481 cultivated and 54 wild relatives accessions of foxtail millet from 26 countries. These germplasm accessions have been characterised for various morphological and agronomic traits. To facilitate the use of germplasm in breeding, it is important to develop a composite collection capturing most of the genetic variation present in the entire collection. An important goal of the Generation Challenge Programme is to help genebank curators to develop composite collection, representing most of the genetic variation present in the entire collection, for the rational use of genetic resources in crop improvement programmes. It is proposed to develop a composite collection of 500 accessions that will be genotyped using 20 SSR markers to determine the genetic structure of this composite collection.

48. Project No G4006.31: Development and genotyping of composite collection of pearl millet (*Pennisetum glaucum* (L.) R. Br.)

- *Duration: Jan 2006–Dec 2006 with NCE to Jul 2008*
- *Budget by year: $60,042 (2006); Total budget: $60,042*

Pearl millet/Various traits/Africa, Asia and Latin America

Lead institute
ICRISAT (HD Upadhyaya)
Collaborating institutes and scientists
ICRISAT (CT Hash, S Senthilvel, RK Varshney, D Hoisington, KN Rai, RP Thakur, S Chandra)

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] is an important coarse grain food, feed and fuel crop in Africa and South Asia. This hardy C4 cereal can be grown in very diverse environments from sea level to about 1800 meters above sea level. Pearlmillet is grown in over 40 countries, predominantly in Asia and Africa. It is cultivated in 29 m ha, supporting >100 million people. China, India, Pakistan, and Yemen in Asia and Nigeria, Niger, Mali, Senegal, Burkina Faso, Sudan and Tanzania in Africa are the major countries producing pearl millet. In addition, the crop is expanding rapidly in the acid soil savannahs of Latin America, where it finds use as the mulch component in conservation tillage systems of soybean production, and as an annual green fodder crop. The grains of pearl millet are rich in minerals high in fat (3.5-7.0%), and contain 10-14% protein that has high tryptophan, cystine, and methionine contents compared to other major cereal crops such a rice, wheat, and maize. Efforts to boost the production and productivity of this crop have been reasonably successful in India, where average grain yields have more than doubled over the past 40 years due to a combination of genetic improvement and improved crop management. Elsewhere there have been very limited crop improvement efforts to boost the production and productivity of this crop in spite of the fact that it is the hardiest tropical cereal crop, grown in the hottest, driest regions where dryland agriculture is practiced, and its grain have high food and feed value.

The Rajendra S. Prasad gene bank at ICRISAT holds 20,844 cultivated and 750 wild relatives accessions of pearl millet from 50 countries. To make use of germplasm in applied plant breeding, it is important to develop a composite collection capturing most of the genetic variation present in the entire collection. An important goal of the Generation Challenge Programme is to help CGIAR's genebank curators to develop such composite collections, representing most of the genetic variation present in the entire collection for each crop, for the better management of the genetic resources and facilitate their wider use in crop improvement programmes. It is proposed to develop a composite collection of 1,000 pearl millet breeding lines and germplasm accessions that will be genotyped using 20 DNA markers to determine the genetic structure of this composite collection.

Subprogramme 2: Genomics towards gene discovery

Current projects

49. Project No G4007.02: Validation of drought-response/resistance pathway genes by phenotypic analysis of mutants

- *Duration: Aug 2007–Jul 2009*
- *Budget by year: $100,272 (2007), $100,272 (2008); Total budget: $200,543*

Rice/Drought tolerance/Various regions

Lead institute
VBI, VPI (Andy Pereira)
Collaborating institutes and scientists

- IRRI (Hei Leung, Rachid Serraj, Jill Cairns)
- HZAU (Lizhong Xiong)

Research within the GCP and other ongoing research on abiotic stress biology, has provided researchers a number of candidate genes with a potential role in drought response and resistance. These genes have been identified in a number of crops, in response to a variety of environmental stresses and by data derived from breeding, genetics, physiology and genomics. For most of these candidate genes their exact role has not been determined due to lack of high throughput methods of relating the genes to a drought response/resistance phenotype. The analysis of mutants is one of the most reliable and time-proven ways of correlating the genotype to a phenotype. The international research community has generated significant mutant resources in the two sequenced plants rice and Arabidopsis. Systematic mutant analysis of candidate genes for drought response/resistance in these plants, including field testing at critical drought sensitive stages, will provide supporting evidence, and in some cases the definite answers, of the role of the genes in drought resistance that will be available as a knowledge resource for all plants. This project aims to provide drought response phenotypes for an extensive list of about 500 candidate orthologous genes in the two plants selected for their potential role in drought responses and resistance mechanisms. The comparative analysis between the dicot and monocot plants would be applicable across a wide number of crop plants. The mutant phenotypes will be evaluated for important physiological components and at vegetative and reproductive drought stages in relevant field or controlled experimental conditions. Results of this project will support the GCP ADOC project analysing natural variation in a selection of candidate genes, and validate the results of microarray experiments from previous projects, be able to test candidate genes coming from ongoing GCP projects. The results of drought response phenotypes of candidate genes will be curated in a database and made available to all GCP participants and collaborators to aid their research.

50. Project No G4008.06: Single Nucleotide Polymorphism discovery, validation, and mapping in groundnut

- *Duration: Jan 2008–Dec 2008*
- *Budget by year: $152,543 (2008); Total budget: $152,543*

Groundnut/Various traits and regions

Lead institute
UoG (Steven J Knapp)
Collaborating institutes and scientists

- ICRISAT (David Hoisington, Rupakula Aruna, Rajeev Varshney)
- NCGR (Gregory May and Andrew Farmer)
- USDA–ARS (Corley Holbrook and Peggy Ozias-Akins)

DNA marker resources are currently inadequate for routine genomic and molecular breeding applications in cultivated groundnut (*Arachis hypogaea* L.; $2n = 4x = 40$). The proposed research focuses on significantly enhancing the infrastructure for translational genomics and molecular breeding research in groundnut by testing the efficacy of massively parallel DNA sequencing and highly parallel single nucleotide polymorphism (SNP) genotyping strategies for SNP discovery, validation, and mapping. We are specifically proposing to: (i) develop protocols for reduced representation allele sequencing (RRS) in groundnut; (ii) enhance DNA sequence resources for groundnut using a combination of Sanger and Solexa sequencing; (iii) identify 2,000 or more common SNPs in elite lines and cultivars; (iv) develop a 1,536-SNP Illumina GoldenGate SNP genotyping array; and (v) complete the validation and genetic mapping of 1,536 SNPs in two elite recombinant inbred line (RIL) populations using an Illumina GoldenGate SNP genotyping array. The proposed research will dramatically increase DNA sequence resources and the supply of mapped DNA markers in groundnut, should enable the identification and assembly of 20 linkage groups using elite mapping populations, particularly when coupled with genetic mapping of SSR markers, and should identify additional SNPs for genotyping assay development, validation, and mapping.

51. Project No G4008.07: Improving molecular tools for pearl millet

- *Duration: Jan 2008–Dec 2009*
- *Budget by year: $214,037 (2008), $82,392 (2009); Total budget: $296,429*

Pearl millet/Various traits/Africa; Asia; Latin America

Lead institute
ICRISAT (C Tom Hash)
Collaborating institutes and scientists

- ICRISAT (FR Bidinger, V Vadez, RK Varshney, T Nepolean and S Senthilvel)
- AICPMIP (IS Khairwal)
- CAZRI (OP Yadav)
- RAU (PC Gupta)
- ILRI (Michael Blümmel)

Pearl millet (*Pennisetum glaucum*) is a dual-purpose grain and fodder crop that is an essential component of dryland crop-livestock production systems of sub-Saharan Africa (e.g., Nigeria, Niger, Burkina Faso, Mali, Senegal, Sudan, and Chad) and South Asia (e.g., India) in areas that are too hot, too dry, and/or have soils that are too acid or too infertile for reliable production of maize, sorghum or any other cereal crop. The crop is also increasingly used as the mulch component of sustainable minimum tillage crop production systems in the humid tropics (e.g., Brazil) , where its acid soil tolerance, deep root system, and high vegetative growth rates under high temperature conditions often make it the best option for retrieving soil nutrients from depth, smothering weeds, and producing a mulch that protecting the soil surface from erosion by rain drop impact or surface water movement. There are limited genomic tools available for this orphan crop despite pearl millet being the 6th most important cereal crop globally and being likely to be, along with sorghum, an important source of genes and alleles that will enable plant breeders to engineer other crops (e.g., rice, wheat and maize) to better tolerate higher temperatures and increased frequencies of drought stress that are predicted to arise from on-going global warming. This project proposes to strengthen genomic resources for pearl millet, developing cDNA libraries from the parents (841B-P3 and 863B-P2) of a well-characterised pearl millet drought tolerance mapping population, identifying EST sequence polymorphisms between the parents of this population, and mapping these polymorphisms using the 150 RIL progenies of this population. The augmented linkage map of this population, combined with information on the positions in the completed sorghum and rice genome sequences of homologues of the pearl millet ESTs from which these newly mapped markers are derived, be used to refine the rice–pearl millet comparative map and develop at sorghum–pearl millet comparative map. We will then use the additional markers mapping to pearl millet linkage group 2 to better define the position of a major drought tolerance QTL from 863B, using available segmental substitution lines (developed in a DBT-supported project) for this genomic region in the genetic background of elite seed parent maintainer line 841B (using funding from a BBSRC project that will start in April 2008).

In addition, we will use STS and SSR markers to skeleton linkage map two new conventional biparental pearl millet mapping populations of random inbred lines, 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 that will be ready for map saturation with DArT markers in a future project, which would permit development of a high density consensus linkage map for pearl millet.

52. Project No G4008.08: Transcriptome analysis of near-isogenic rice lines to identify expression signatures and gene combinations conferring tolerance to drought stress

- *Duration: Jan 2008–Dec 2009*
- *Budget by year: $177,300 (2008), $128,100 (2009); Total budget: $305,400*

Rice/Drought tolerance/Various regions

Lead institute
NIAS (Shoshi Kikuchi)
Collaborating institutes and scientists
IRRI (Hei Leung, Venuprasad Ramaiah, Arvind Kumar, Rachid Serraj, Ramil Mauleon, Violeta Bartolome)

We propose to make use of two recent advances in gene expression analysis and drought-QTL mapping to test the hypothesis that gene expression patterns in a chromosomal context are causally correlated with manifestation of drought tolerance as detected in near-isogenic lines. We will apply a new comprehensive 44K oligoarray platform to determine the transcriptomes of two pairs of near isogenic lines (NILs) exhibiting large difference in their yield response to drought stress at reproductive stage. Parallel to transcriptome analyses, we will determine the fine-scale genotypes of the NILs to determine whether expression signatures co-segregate with specific regions of the genome. Results from this series of studies will reveal genes or narrow chromosomal regions contributing to drought tolerance. Because the NILs are field-proven genetic stocks that are adapted to the rainfed and upland rice production environment, the results are likely to have high agronomic relevance. Experimental support to a causal relationship between gene expression patterns and QTL is of fundamental and practical interest in understanding the genetic control of a complex trait such as drought tolerance. The proposed project will produce breeding-ready, well-characterised isogenic lines with specific chromosomal regions tagged for their contribution to drought tolerance. The project will also generate expression/QTL mapping datasets that can be further exploited by data mining. The results will be viewed in Genome Browser that will enable consolidation of multiple sources of information anchored to the rice genome.

53. Project No G4008.09: Development of genetic and genomic resources for breeding improved sweetpotato varieties

- *Duration: Jan 2008–Dec 2009*
- *Budget: $192,780 (2008), $106,760 (2009); Total budget: $299,540*

Sweetpotato/Drought and disease resistance/Sub-Saharan Africa

Lead institute
CIP (Roland Schafleitner)
Collaborating institutes and scientists

- IIAM (Nurbibi Cossa)
- NAARI (Robert Mwanga)
- INIA–Uruguay (Francisco Vilaró)
- EMBRAPA (Andre Dusi)
- DArT P/L (Andrzej Kilian)

Production of sweetpotato, an important staple food in Sub-Saharan Africa, is limited by a number of constraints, such as low adaptability of available varieties and landraces, virus diseases, insect pests and drought. Consequently, yields achieved by resource-poor farmers in SSA are typically low and remain, on average, below 5 tons per hectare. Improved and well adapted sweetpotato varieties with increased tolerance to biotic and abiotic stresses can significantly contribute to increasing productivity and will have a large positive impact on food and income security in Sub-Saharan Africa. However, breeding efforts are limited by the crop's genetic complexity and lack of information available about its genetic resources. The development of genetic tools, including populations and markers, and concerted efforts towards understanding the gene pools of sweetpotato would improve access to and targeted use of the allelic diversity for breeding improved varieties.

The basic tools needed to mobilise allelic diversity and to monitor introgression of desirable alleles in breeding populations consist of a well defined Composite Genotype Set and segregating populations for marker development and trait capture. Today, techniques such as DArT that yield a large number of markers for genetic studies and selection should be made accessible for sweetpotato. A diploid reference map will help to synthesise genetic information already available from independent hexaploid populations, and enable comparative genomics among sweetpotato and other crops.

This project aims at developing genetic and genomic resources for sweetpotato and will stimulate the use of these tools in ongoing breeding programmes in CG Centers and NARS.

54. Project No G4008.47: Developing genomic resources for pigeonpea using next generation sequencing technologies

- *Duration: Aug 2008–Jul 2010*
- *Budget: $170,100 (2008), $122,100 (2009); Total budget: $292,200*

Pigeonpea/Drought and disease resistance/Various regions

Lead institute
NCGR (Gregory D May)
Collaborating institutes and scientists

- NCGR (Andrew Farmer)
- ICRISAT (Rajeev Varshney, Kulbhushan Saxena)
- NRCPB (Nagendra K Singh)
- PDKV (Pawan L Kulwal)

Legumes are one of the largest and diverse families of higher plants containing more than 20,000 species, and are second only to cereal crops in world-wide agricultural importance. With the exception of soybean, Medicago and Lotus, legumes have not benefited from the establishment of expanded genomics resources. Pigeonpea (*Cajanus cajan L.*), an important legume crop in Indian subcontinent, ranks sixth in area and production in comparison to other grain legumes such as beans, peas, and chickpeas. It is now widely grown in the Indian subcontinent that accounts for almost 90% of the world's crops. However, the productivity of pigeonpea crop in semi-arid regions is less than 650 kg/ha due to exposure of the crop with several diseases such as fusarium wilt, sterility mosaic and other abiotic stresses. Biotechnological tools especially molecular markers have been proven very useful for improving the breeding efficiency in several major crop species, only about 100 microsatellite or simple sequence repeat (SSR) markers are available for pigeonpea. Furthermore, low level of genetic diversity in pigeonpea germplasm is another bottleneck to varietial improvement. Because of these two reasons, not a single genetic map has become available for pigeonpea to date. The proposed research will develop genomic resources such as expressed sequence tags (ESTs) and single nucleotide polymorphism (SNP) markers by using 454 FLX and Solexa next generation sequencing technologies. High throughput genotyping assay such as GoldenGate assay (Illumina) will enable the development of a pigeonpea genetic map. Genomic resources, to be developed, in the planned project will be of great use for the pigeonpea community in particular, and the legume community in general.

Subprogramme 3: Trait capture for crop improvement

Current projects

55. Project No G4007.04: Association mapping of downy mildew resistance in elite maize inbred lines in Thailand

- *Duration: Aug 2007–Jul 2009*
- *Budget by year: $34,775 (2007), $25,689 (2008); Total budget: $60,464*

Maize/Mildew resistance/Asia

Lead institute
BIOTEC (Chalermpol Phumichai, Julapark Chunwongse)
Collaborating institutes and scientists
NSFCRC (Sansern Jampatong, Pichet Grudloyma)

Maize is one of five major crops grown in the uplands of Thailand, which is predominantly used for animal feed, with 80–100% production being sold to commercial poultry and livestock feed mills. It is a highly commercial crop, handled by an extensive network of merchants. Maize sold as animal feed is mainly used domestically, and only a small fraction is exported. Meanwhile, about 5–20% of all maize grown in Thailand is consumed as food, either as white corn or sweet corn. Downy mildew caused by the fungus *Peronosclerospora sorghi* (Weston & Uppal) C.G. Shaw, is one of the most destructive diseases of maize in Thailand. Genetic resistance is a cost-effective and environmentally safe alternative in controlling the downy mildew disease. The objective of this project is to use the association analysis that is a method relies on linkage disequilibrium to study the relationship between phenotypic variation in maize genome for the dissection of downy mildew resistance and genetic polymorphism (superior alleles). This project will focus on evaluating the loci conferring resistance to downy mildews of maize. We will raise maize inbred lines from public and private sectors and phenotypic evaluation will be conducted by using a spreader-row technique. Haplotypes contributing to a favorable plant phenotype under downy mildew resistance conditions will be identified through association tests. The discovery of superior alleles will permit the development of molecular markers that can facilitate breeding programmes.

56. Project No 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

- *Duration: Aug 2007–Jul 2010*
- *Budget by year: $74,600 (2007), $57,600 (2008), $18,390 (2009); Total budget: $150,590*

Wheat/Drought tolerance/Asia

Lead institute
CAAS (Ruilian Jing)
Collaborating institutes and scientists

- NU (Xing XU)
- NWSUAF (Hui-Min XIE)
- SAAS (Mei-Rong SUN)
- LAAS (Can-Jun ZHANG)
- HAAS (Xiu-Min CHEN)

To implement the general objectives of the proposed project, we will develop the following research activities:

1. To hold training courses for molecular marker assisted (MAS) selection techniques and drought tolerance (DT) phenotyping;
2. To integrate MAS tools into conventional breeding programme and select stable introgression lines (ILs) carrying target genes/markers;
3. To phenotype and genotype the ILs with the elite Chinese wheat genetic backgrounds in diverse environments and select DT ILs;
4. To exchange the information, technology and methodology associated with the molecular breeding for DT, promote interactions among regions, build the capacity of wheat modern breeding in China and other Asian countries.

57. Project No G4007.07: Marker-assisted selection for Sweetpotato Virus Disease (SPVD) Resistance in Sweetpotato Germplasm and Breeding Populations

- *Duration: Aug 2007–Jul 2010*
- *Budget by year: $122,720 (2007), $122,720 (2008), $134,360 (2009); Total budget: $379,800*

Sweetpotato/SPVD Resistance/Various regions

Lead institute
CIP (Wolfgang Grüneberg)
Collaborating institutes and scientists

- CIP (I Barker, S Fuentes, K Huamani, J Espinoza)
- NACRRI (R Mwanga)

Sweetpotato is an important food crop and due to extreme high pro-vitamin A content orange fleshed sweetpotatoes (OFSP) can alleviate vitamin A deficiency in many regions of the world. However, sweetpotato virus disease (SPVD) is often causing serious yield losses, especially in high virus pressure zones within Sub-Saharan Africa, where OFSPs are often not sufficient SPVD virus tolerant. The disease occurs after infection of two viruses: the sweetpotato feathery mottle virus (SPFMV) and the sweetpotato clorotic stunt virus (SPCSV). The SPCSV is the more problematic component of SPVD, because yield losses due to SPFMV - without SPCSV infection – are low and SPFMV resistance of sweetpotato breaks after the plant is infected by SPCSV. There was no SPCSV resistance known until recently in the CIP germplasm one SPCSV resistant clone was found (termed "Resitan"). This resistance is a new option to foster OFSP production, but marker assisted selection (MAS) should be applied. It is nearly certain that this new resistance to SPVD is recessive and inherited by one or two genes. This will be confirmed in the first step of this project by developing the required populations (Resistan x Resitan and OFSP parents x Resistan). Marker associated with the recessive allele(s) conferring SPVD resistance are an ideal tool to identify clones in breeding populations and germplasm, which carry the recessive allele(s) with high frequency. It should be noted, that sweetpotato is hexaploid and highly heterozygous and this makes resistance breeding for a recessive inherited characteristic without MAS very slow. In the second step markers for SPVD will be developed, by using backcross populations, AFLP, and SSR or SNP markers. In a third step OFSP breeding populations and the CIP germplasm will be screened with the marker system to increase the use of parental material segregating for the phenotype "SPVD Resistance".

58. Project No G4007.08: Integration of genomic tools with conventional screening for developing NERICA rice cultivars for West Africa

- *Duration: Aug 2007–Jul 2009*
- *Budget by year: $156,350 (2007), $148,090 (2008); Total budget: $304,440*

Rice/Drought tolerance/Africa

Lead institute
WARDA (Marie Noelle Ndjiondjop)
Collaborating institutes and scientists

- Agropolis–IRD (Alain Ghesquiere, Valerie Verdier)
- Agropolis–IRD/CIAT (Mathias Lorieux)
- IER (Fousseyni Cisse)
- WARDA (Manneh Baboucarr, Dramé K Nani, Sanchez Ines, Tsunematsu Hirochi, Séré Yacouba)

Food security and water shortage are challenges facing Africa today. Rice, which is one of Africa's staple foods, is generally sensitive to drought at different developmental stages from germination to the reproductive stage. However, genetic variation for drought tolerance exists in rice, especially in the African cultivated rice (*Oryza glaberrima*). Different traits are reported to be associated to drought tolerance, including deep and thick roots, osmotic adjustment and recovery ability after water shortage. *O. glaberrima* has good recovery ability after water shortage. Hence, development of drought-tolerant lines with *glaberrima's* good recovery ability would be one of the most effective approaches for enhancing rice yield in drought-prone environments. The overall goal of this project is to develop new rice for West Africa by combining the power of genomic technology with a conventional phenotypic approach. The project consist of two major components: (1) identification of highly promising lines from among various *glaberrima* accessions and interspecific breeding lines that contain trait-improving alleles for drought tolerance as well as for other traits of agronomic importance; (2) detailed characterisation of *O. glaberrima* accessions or interspecific lines already identified as good drought-tolerant materials. For the latter, accessions and interspecific lines selected in relation to drought tolerance will be (i) genotyped using a genome-wide set of 200 SSR markers in order to characterise quantitative trait loci associated with recovery ability; (ii) phenotyped for two major diseases (rice yellow mottle virus and bacterial leaf blight) in West Africa; (iii) studied for the proportion of *O. sativa* and *O. glaberrima* introgressions by using microsatellite markers techniques; and (iv) checked for foreground markers that are associated with rice yellow mottle virus (RYMV) and bacterial leaf blight (BLB) resistance genes. Finally, selected interspecific lines (new NERICA lines) with desirable traits will be supplied to NARS scientists for further evaluation and dissimination in the region. This project will also train a Malian NARS scientist on genomic technology.

59. Project No G4007.25: Development of drought phenotyping network

- *Duration: Dec 2007–Feb 2008*
- *Total budget: $22,500*

Various crops, traits and regions

Lead institute
Consultants (Gregory Edmeades, Abraham Blum)
Collaborating institutes and scientists
- CIAT (Glenn Hyman)
- Gent University, Belgium (Dirk Raes)
- Consultant (Robert Koebner)
- CU (Tim Setter)
- ICRISAT (Vincent Vadez)
- KARI (James Gethi)

The objective of the project is to develop an efficient GCP Phenotyping Network, able to respond to the increasing phenotyping needs of genomic studies and breeding programmes targeting abiotic stress tolerance. The project will focus primarily on drought tolerance and on crops, regions and cropping systems defined as priorities in the GCP Strategic framework.

The GCP Phenotyping Network will support and boost plant breeding by globally improving phenotyping conditions and protocols, focusing on products and traits determined by the Generation Challenge Programme (GCP). It will improve the existing phenotyping capacities in the NARs, facilitate access to accurate and high quality field phenotyping under managed stress conditions, and/or single trait measurements in controlled conditions and analysis of metabolites, and will permit to evaluate the association between those traits and yield under stress. These different components will develop links and synergies between the different GCP partners (NARs, CGs, ARIs), accelerating the use of improved germplasm and, in essence, the breeding of crop varieties that better meet farmer needs.

60. Project No G4008.10: Assessment of the breeding value of superior haplotypes for *Alt*$_{SB}$, a major Al tolerance gene in sorghum: linking upstream genomics to acid soil breeding in Niger and Mali (ALTFIELD)

- *Duration: Jan 2008–Dec 2010*
- *Budget by year: $79,200 (2008), $72,600 (2009), $53,400, (2010); Total budget : $205,200*

Sorghum/Al-tolerance/Africa

Lead institute
Embrapa Maize and Sorghum (Robert Schaffert)
Collaborating institutes and scientists
- INRAN (Maman Nouri: Soumana Souley: Magagi Abdou: Adam Kiari: Fatouma Beidari, Issoufou Kapran)
- ICRISAT (Bettina Haussmann, Eva Weltzien Rattunde, Fred Rattunde)
- EMBRAPA Maize and Sorghum (Jurandir Magalhães: Antônio Marcos Coelho)

Aluminum (Al) toxicity is a major agricultural constraint on acid soils, which comprise over 50% of the world's potentially arable lands, particularly jeopardising food security in the poorest regions of the globe. We have recently cloned a major sorghum Al tolerance gene, *Alt*$_{SB}$, which is a membrane transporter that confers Al tolerance via Al-induced citrate release into the rhizosphere. We have also gathered evidences that a thorough scan into the sorghum genetic diversity can be used to identify improved versions of *Alt*$_{SB}$ that may yield significant agronomic advantages upon crop cultivation on acid soils. Thus, a research project was then designed and funded in the last competitive call from the Generation Challenge Programme to apply association genetics to identify superior haplotypes of *Alt*$_{SB}$, generate pre-breeding near-isogenic lines carrying these haplotypes, develop haplotype-specific markers and identify new Al tolerance genes in sorghum (ALTSORGHUM project). The concept note presented here aims at establishing the connection between the outputs of the ALTSORGHUM project and sorghum breeding programmes from Niger and Mali, ensuring that products will be properly validated in the specifically developed phenotyping sites and effectively used to attain higher and more stable yields in farmer's field on acid, Al toxic African soils.

61. Project No G4008.11: Dry bean improvement and marker assisted selection for diseases and abiotic stresses in Central America and the Caribbean

- *Duration: Jan 2008–Dec 2010*
- *Budget by year: $128,020 (2008), $133,220 (2009), $121,350 (2010); Total budget: $382,590*

Bean/Drought and disease resistance/Latin America and Caribbean

Lead institute
INIFAP (Jorge A Acosta-Gallegos)
Collaborating institutes and scientists

- CIAT (Steve Beebe and Mattew Blair)
- INTA (Aurelio del Llano; Julio Molina)
- INCA (Humberto Rios Labrada and Orlando Chaveco)
- CINVESTAV (Beatriz Xoconostle Cazares)
- INIFAP (Ernesto Lopez Salinas; Raul Rodriguez Guerra; Alejandra Mora Aviles)

Diseases, drought and low soil fertility are the most important constraints to dry bean production in Latin America and the Caribbean. The development of bean cultivars with resistance to these stresses represents a cost-effective and sustainable means to address these constraints. Bean golden yellow mosaic virus (BGYMV) transmitted by the sweetpotato whitefly is an endemic disease threat to production in the region and tends to explode with vector populations that increase during drought years. Root-rot resistance is another important trait that needs to be tackled along with drought, low soil fertility and BGYMV resistance. Two nurseries, in the opaque black and small red seed classes will be formed and established for the main bean growing areas in Cuba, Nicaragua, Mexico and possibly Haiti in 2008. Nurseries will include best lines identified among the partners to conform a drought nursery. In these nurseries disease reaction and productivity will be recorded along with climatic parameters. Segregating populations will be developed at Mexico and CIAT with best local parents from the partners and sources of BGYMV and root-rot resistance genes possessing molecular markers to assist in the selection. In this project we will make use of prior knowledge in the development of bean cultivars better able to resist BGYMV and root-rot to cope with drought and low soil fertility stress. One aim is to explore the available genetic diversity for tolerance to water stress, adaptation to low soil fertility, as well as for BGYMV and root rot resistance. This project will be one of the first to apply molecular breeding on a large scale to common bean improvement for the region and will focus on tolerance to drought stress and diseases that occur under drought and low soil fertility conditions.

62 Project No G4008.12: Linking genetic diversity with phenotype for drought tolerance traits through molecular and physiological characterisation of a diverse reference collection of chickpea

- *Duration: Jan 2008–Dec 2009*
- *Budget: $94,340 (2008), $61,875 (2009); Total budget: $156,215*

Chickpea/Drought tolerance/Various regions

Lead institute
ICRISAT (Junichi Kashiwagi)
Collaborating institutes and scientists

- ICRISAT (Rajeev Varshney, Lekha Pazhamala, Hari Upadhyaya, Subhash Chandra, David Hoisington, L Krishnamurthy)
- JIRCAS (Satoshi Tobita, Osamu Ito)
- UAS (MS Sheshshayee)

Chickpea is the third most important grain legume crop, and drought is one of the major constraints limiting the productivity. This research project is to enhance the productivity of chickpea under drought environments, and comprise three key research components, that is, i) characterising the target drought environments, ii) phenotyping the transpiration efficiency (TE), specific leaf area (SLA) and chlorophyll content (SPAD) by noble idea and sophisticated devices to improve the drought tolerance, and iii) identifying robust molecular markers for marker assisted breeding selection. The component i) is important as the drought environments is not uniform among the arid or semi-arid regions. The target drought environments need to be characterised so that logistic understanding could be obtained on the plant mechanisms and traits to cope with the target drought environments. It will also help us to apply the drought tolerant mechanisms and traits when it is applied to other drought environments to improve the productivity. The component ii) is important as TE, SLA and SPAD are directly contribute to the crop growth under drought environments, viz., TE for improving photosynthetic products per unit water, SLA for maintaining proper chlorophyll concentration for photosynthesis, and SPAD for maintaining the capability of photosynthesis. Since drought stress is a very complex stress, several of these mechanisms and traits need to be brought under a single elite genetic background. To achieve it effectively in terms of the time as well as cost, the component iii) is important because introgressing complex multi-gene regulated physiological mechanisms and traits can be better achieved based on the robust molecular markers linked with QTL conditioning these traits.

The objective of this project is to improve the drought tolerance of chickpea via marker assisted selection for critical characteristics to improve the drought tolerance under proper drought environment characterisation, and to provide training opportunities to share new knowledge and skills for NARS scientists.

63 Project No G4008.13: Improving drought tolerance phenotyping in cowpea

- *Duration: Jan 2008–Dec 2010*
- *Budget by year: $173,802 (2008), $146,874 (2009), $130,160 (2010); Total: $450,836*

Cowpea/Drought tolerance/Africa

Lead institute
UoC–Riverside (Jeff Ehlers)
Collaborating institutes and scientists

- UoC–Riverside (Timothy Close, Philip Roberts)
- TAMU (William Payne, BB Singh)
- ISRA (Ndiaga Cissé)
- INERA–Burkina Faso (Issa Drabo)
- IITA (Satoru Muranaka, Ousmane Boukar)

This proposal seeks to (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 across a range of environments; (2) study the relationship between grain yield under drought and various traits, and select applicable methodologies for practical and efficient indirect measures of drought tolerance, such as thermal imaging, that are relevant to the major cowpea production zones in Africa; and (3) determine the relationship between drought tolerance and shoot and root traits, and select potential drought tolerant genotypes with beneficial root characteristics which contribute higher productivity under drought conditions.

Thirty early maturing and thirty medium maturing cowpea varieties will be compared for grain yield under terminal drought conditions using late plantings at two sites during the main growing season in West Africa and in four controlled irrigation and rain-free environments in West Africa and California. This will provide baseline drought tolerance information that will allow identification of drought tolerant and susceptible 'checks' for future drought studies and provide an estimate of genotype x environment interaction for grain yield under drought, including the degree of correlation between the results of off-season controlled environment screening and results from main-season African growing environments. Information about the importance of genotype x environment interactions will guide future investigators on whether to breed for specific regions separately, or whether region-based and/or off-season drought-screening nurseries can be employed effectively to breed for improved drought tolerance. Identification of efficient indirect selection methods like thermal imaging allows screening of a large number of germplasm lines to help ensure capture of traits that exist in the cowpea germplasm pool, and may also help reveal important component characteristics contributing to grain yield under drought. Thermal imaging is a potentially powerful method for drought tolerance screening that has not be comprehensively evaluated for its ability to discriminate drought tolerant and susceptible cowpea genotypes and this proposal seeks to establish its usefulness in cowpea.

64. Project No G4008.14: Breeding for drought tolerance with known gene information

- Duration: Jan 2008–Dec 2009
- Budget by year: $150,000 (2008), $150,000 (2009); Total budget: $300,000

Various crops/Drought tolerance/Various regions

Lead institute
CIMMYT/CAAS (Jiankang Wang)
Collaborating institutes and scientists

- CSIRO and UoQ (Scott Chapman, David, Mark Dieters Nick Hansen)
- CAAS (Ruilian Jing, Xianchun Xia, Huihui Li, Changbin Yin)
- GCP (Jean-Marcel Ribaut)
- CIMMYT (Gary Atlin, Matthew Reynolds, Yunbi Xu)
- Agropolis–INRA (Francois Tardieu, Claude Welcker)
- ICRISAT (Dave Hoisington, Shyam Nigam, Vincent Vadez)

Despite substantial investment in QTL mapping for many traits important to plant breeders, there are relatively few examples of the effective implementation of QTL in marker-assisted selection (MAS) for polygenic traits, such as drought tolerance. Given that breeders are increasingly able to access genotypic and phenotypic information, the major hurdles are:

(i) QTL for such traits typically account for only a relatively small proportion of genotypic variance and simultaneous selection for multiple QTL will be necessary to make useful genetic gain;

(ii) Breeders need to retain 'known' genes (e.g. of known effects and locations for disease and quality traits) in germplasm that is targeted for improvement in drought adaptation;

(iii) Identification of repeatable QTL across genetic backgrounds and growing environments for use in MAS for drought adaptation is still problematic;

(iv) Lack of adequate tools and training of breeders to optimise the design of breeding schemes based on the best available genetic and genomic information.

To address these issues, methodology, software training courses and technical backstopping during initial implementation phases are needed to assist breeders to design and validate optimal breeding schemes for their specific profile of goals and constraints. Ideally, outputs from QTL analysis should be fully integrated into this process. Prototypes of the required tools were developed and validated in previous GCP-funded projects, and now need to be integrated with databases of QTL mapping data and known gene information. In particular, software tools need to be able to identify 'robust' breeding schemes that tolerate the presence of 'erroneous' QTL, or at least validate those QTL as you go and have the flexibility to be adjusted based on the outcomes of that validation data. This will enable breeders to develop design-led breeding schemes that will great improved the efficiency of their breeding efforts both in terms of pace and impact of progress. This will lead to the development of breeding products for resource-poor farmers in the form of higher yielding, better quality, more disease resistant, and more drought tolerant crop varieties.

65. Project No G4008.15: Developing potato cultivars adapted to Southern Africa countries

- *Duration: Jan 2008–Dec 2009*
- *Budget by year: $103,536 (2008), $106,332 (2009); Total budget: $209,868*

Potato/Various traits/Africa

Lead institute
INIA–Uruguay (F Vilaró)
Collaborating institutes and scientists

- INIA–Chile (J Kalazich)
- INTA–Argentina (M Huarte)
- EMBRAPA (Arione Pereira)
- IIAM (Carolino Martinho)
- DARS (Obed J Mwenye)
- CIP (Paul Demo, Stef de Han)

Potato is one of the highest value crops and provides high nutritious food in a very short growing period. Many developing countries including non Andean South American and in Southern Africa, grow long day adapted *Tuberosum* potatoes, almost year round. Breeding programmes in the northern hemisphere have developed varieties from this same Group, with high commercial quality. However, most of these varieties are mainly adapted to temperate climate and lack resistance to diseases and pests making potato highly dependent on external inputs. They also require well established seed programmes and are mainly adapted just to one crop per year. Adequate planting material is usually expensive and difficult to obtain in appropriate condition for most developing countries. Short day germplasm and landrace varieties from the Andes, have valuable traits but adapt poorly to long days and or high temperature. Genetic resistance sources for various diseases have been incorporated in advanced potato germplasm from participant non Andean South American countries. These countries cover a wide region of environments, from southern temperate Chile to subtropical Brazil, possessing germplasm with a wide range of adaptation. In this region, with the exception of the most southern area, potatoes are grown on a two crop per year regime. Several varieties significantly improved on quality aspects have been released and are being grown in and out of the region. This project will evaluate advanced germplasm from this region, along with CIP improved germplasm on Southern Africa (Malawi and Mozambique). Microarray DaRt technology analysis will be employed to analyse population structure of germplam from participating programmes. Secondarily, easy to use molecular markers will be validated and applied in Latin America helping to characterise degree and stability of disease resistance. GIS site characterisation will be employed to determine potential variety deployment in given locations. It is anticipated that promising germplasm sources and very valuable genotypes adapted to various growing constraints, could be identified and multiplied for releasing new cultivars. This would promote a more sustainable crop for helping resource poor farmers in these countries.

66. Project No G4008.16: Speeding the development of salt-tolerant rice varieties through marker-assisted selection and their dissemination in salt-affected areas of Bangladesh

- *Duration: Jan 2008–Dec 2009*
- *Budget by year: $128,871 (2008), $96,500 (2009); Total budget: $223,768*

Rice/Salt tolerance/Asia

Lead institute
IRRI (Abdelbagi M Ismail)
Collaborating institutes and scientists

- IRRI (Michael J Thomson, David J Mackill, and Thelma Paris)
- BRRI (MA Salam)
- UoD (Zeba I Seraj)
- BINA (Mirza M Islam)

Salt stress is a major constraint across many rice-producing areas because of the high sensitivity of modern rice varieties to salinity, which forces farmers to continue to grow their traditional landraces with low yield and low grain quality. In Bangladesh, salt-affected regions cover about 1 million ha across the southern parts of the country, and pose a serious problem for resource-poor farmers who depend on rice production for their livelihoods where other crops can barely grow during the monsoon season. If modern high-yielding rice varieties were developed that were adapted to these local saline conditions, there would be enormous scope for improving the lives of farmers living on these marginal lands. This project aims to take advantage of modern breeding tools, such as marke-assisted backcrossing (MAB), to develop high-yielding salt-tolerant rice varieties adapted to the conditions in southern Bangladesh. We will build upon the knowledge gained concerning the genetic control of salinity tolerance in rice to increase the speed and efficiency for developing improved varieties. Scientists at the International Rice Research Institute will collaborate closely with their counterparts at the Bangladesh Rice Research Institute, Dhaka University, and the Bangladesh Institute of Nuclear Agriculture to refine and use an MAB approach to introgress *Saltol*, a major QTL for salinity tolerance, into popular varieties adapted to target environments, and test these varieties with farmers through participatory varietal selection trials. Assessment of the potential impact of new salt-tolerant varieties across target areas will be conducted and NARES partners will be trained in relevant technologies, including production and handling of high-quality seeds. Through this unique collaboration, capacity building for improved human resources and research platforms will enable the use of MAB to introgress agronomically useful QTLs/genes into preferred local varieties and breeding lines, even beyond the project time frame.

67. Project No G4008.17: Application of Marker-Assisted Selection for *Striga* resistance in cowpea

- *Duration: Jan 2008–Dec 2009*
- *Budget by year: $99,992 (2008), $99,994 (2009); Total budget: $199,986*

Cowpea/**Striga** ***resistance/Africa***

Lead institute
INERA–Burkina Faso (Jean Baptiste Tignegre)
Collaborating institutes and scientists

- IITA (S Muranaka, Boukar Ousmane)
- INERA (Jeremy T Ouedraogo, Issa Drabo)

In West Africa, cowpea is a strategic edible crop due to it's high protein and micronutrient contents, and therefore grown in a continuous fashion to alleviate poverty and achieve food security. However, biotic and abiotic constraints limit the production, resulting in severe yield reduction at smallholder farmer level (300–700 kg/ha), even though potential productivity of cowpea reaches 4t/ha under well managed field.

Striga gesnerioides (Willd.) is a parasite of cowpea and a major constraint of cowpea production in West and Central Africa. The cowpea infected by *Striga* causing severe chlorosis, wilting, and stunting of susceptible hosts and yield losses is estimated in millions of tons annually.

Conventional breeding efforts have developed some varieties for the *Striga* problems as well as other important agronomic and resistance traits, but it is time-consuming and difficult pyramiding favorable traits. Marker assisted selection (MAS) is a modern and potential tool to fast track the breeding process and increase efficiency of breeding activities. Under GCP project "Marker development and marker-assisted selection for *Striga* resistance in cowpea", MAS methodology for *Striga* resistance is now in the final stage of development. By using the MAS for *Striga* resistance, cowpea breeder can fasten the breeding process and reduce the size of population for field screening.

The cooperative work proposed here, involving the "Institut de l'Environnement et des Recherches Agricoles" (INERA) of Burkina Faso and the International Institute of Tropical Agriculture (IITA), seeks to apply the MAS strategy into cowpea breeding activities for Burkina Faso and Niger to achieve rapid and reliable screening of *Striga* resistant cowpea lines. The outcome of this work will be well-adapted *Striga* resistant cowpea varieties available to farmers in Burkina Faso and Niger Rep. It is expected that farmers will achieve higher yields of better quality cowpea that would impact favorably on their general livelihoods.

68. Project No G4008.19: Incorporation of an MSV resistance gene in Mozambican maize varieties, mediated by use of MAS

- *Duration: Jan 2008–Dec 2010*
- *Budget by year: $76,566 (2008), $80,991 (2009), $82,443 (2010); Total budget: $240,000*

Maize/SVD/Africa

Lead institute
UKZN (Mark Laing)
Collaborating institutes and scientists
- IIAM (David Mariote, Pedro Fato, Calisto Bias)
- UKZN (Tongo Tongoona, John Derera, Greg Watson)

Maize streak virus is a serious disease of maize, which is especially severe in Southern Africa. CIMMYT has done a great job of finding an effective resistance gene, and then developing a molecular marker to track it during breeding steps. This is one of the more effective cases of using marker assisted selection. Our goal is to use this MAS technology to rapidly introgress the MSV resistance gene into Mozambican maize germplasm which has been bred for other characteristics. This will include both key inbred lines for hybrid seed production and important open pollinated lines.

69. Project No G4008.30: Development of a GCP Phenotyping Network

- *Duration: Feb 2008–Feb 2009*
- *Total budget: $117,000*

Various crops, trait and regions

Lead institute
Consultants (Abraham Blum and Greg Edmeades)
Collaborating institutes and scientists
- Consultant (John O'Toole)
- Glenn Hyman (CIAT), and Sam Geerts (University of Leuven) provide inputs to this project but their research is described and costed under the stand-alone Component 2 Project Proposal.

Drought is now being recognised as a major limitation to crop production in the South. While recent developments in genomics have opened new ways to improve crop drought resistance, progress using these methods depends on appropriate field phenotyping of drought resistance in the field. That capacity is not widely available due to limited expertise and logistics. This project aims to establish a strategic network of field drought phenotyping sites for GCP target crops in order to provide the necessary genetic resources for breeders working towards water-limited environments.

This project establishes a strategic network of field phenotyping sites for GCP target crops. In year 1 the project will identify and determine the needs of 10–12 field phenotyping platforms (FPP) that will become centres of excellence in phenotyping for drought tolerance, in environments to which the GCP target crops are well adapted. Methods used in identification will rely on analysis of georeferenced climate data, water balances, target crop distribution and G x E interaction of selected germplasm. These will be combined with site visits and previous experience of requirements to conduct uniform managed stress field trials. Requirements in land, irrigation, field equipment and personnnel needed to conduct precise managed stress drought trials will be determined. A second group of candidate local field phenotyping platforms (LPP) in national programmes and linked to FPPs (3-8 per FPP) will also be identified and later assessed using similar methods. These sites will provide validation of results established at FPP sites, information on local adaptation, and an entry point into national plant breeding and seed systems. Research conducted in Year 2 will be described in a additional project proposal prepared during Year 1. In Year 2 the project will confirm improved performance of FPP sites, and continue to strengthen the phenotyping capacity of the LPP site network.

70. Project No G4008.34: Environmental assessment for phenotyping network

- *Duration: Jan 2008–Dec 2009*
- *Budget by year: $164,304 (2008), $115,098 (2009); Total budget: $279,403*

Various crops, traits and regions

Lead institute
CIAT (Glenn Hyman)
Collaborating institutes and scientists
- KUL (Dirk Raes, Sam Geerts)
- EMBRAPA (Reinaldo Lucio Gomide)
- Waen Associates/CIAT (Peter Jones)

This project aims to support the selection of sites for drought phenotyping and to support decisions about deployment of GCP genotypes for testing. Initially, information on the climatic and soil conditions of proposed testing sites will be developed using environmental data sets and modeling tools. Environmental conditions of the site and its surrounding neighborhood will be assessed using geographic information systems (GIS) software, spatial overlay, and distance and proximity tools. Climate assessment tools will be used to make a rapid appraisal of climatic conditions at proposed "Field Phenotyping Platform" (FPP) sites (phenotyping hubs) of the GCP. These data will be used at the outset of the project to support the selection of FPP sites by the GCP management team. Subsequent analysis will support future decisions on how genotypes developed by GCP researchers will be deployed with the aim of optimising efficiency of testing programs. This work will include site similarity analysis using specialised software for comparing climate and soils of one or more locations. Detailed water budgets will be developed for FPP and "Level 1 Local Phenotyping Platform" (LPP) sites (i.e., locations involved in GCP phenotyping activities for priority crops). All the results and data will be made available to the GCP research community to guide decisions on deployment of genotypes for further phenotyping.

71. Project No G4008.41: Application and Validation of the Major QTL Phosphate Uptake 1 (*Pup1*)

- *Duration: Jan 2008–Dec 2009*
- *Budget by year: $80,931 (2008), $85,619 (2009); Total budget: $166,550*

Rice/Salt tolerance/Asia

Lead institute
IRRI (Sigrid Heuer)
Collaborating institutes and scientists
- IRRI (Abdelbagi Ismail)
- JIRCAS (Matthias Wissuwa)
- ICABIOGRAD (Masdiar Bustamam, Joko Prasetiyono)

The proposed project builds on the GCP project "Revitalising Marginal Lands: Discovery of Genes for Tolerance of Saline and Phosphorus-Deficient Soils to Enhance and Sustain Productivity." Within that project, we have identified rice varieties that are tolerant of phosphorus (P) deficiency. In order to characterise the underlying tolerance mechanisms, a Kasalath (tolerant) × Nipponbare (intolerant) mapping population was developed and a Kasalath region on chromosome 12 was identified that was associated with tolerance. This major quantitative trait locus (QTL) *was named phosphate uptake 1* (*Pup1*). Since extensive analyses of known P-deficiency response mechanisms did not reveal insight into the mode of function of *Pup1*, the locus was sequenced in Kasalath to identify the *Pup1* genes. In agreement with prior data, none of the putative genes is obviously related to known Presponse mechanisms or P uptake, suggesting that *Pup1* represents a novel tolerance mechanism. The finding that *Pup1* overlaps with a major QTL for drought tolerance recently opened new perspectives and indeed we were able to show that *Pup1* is beneficial under drought stress.

Based on molecular marker data that indicated the absence of *Pup1* in conjunction with phenotypic evaluations, we have selected three Indonesian varieties and two IRRI varieties for the development of *Pup1* breeding lines. The Indonesian *Pup1* lines are most advanced and were genotyped last year by an Indonesian student during a visit at IRRI. Within the proposed project, we will further advance these *Pup1* lines and will evaluate them in field experiments in different soil types in Indonesia, Japan, and the Philippines. Seeds will be provided for additional screenings in India and Laos. The effect of *Pup1* under drought stress will be studied in detail to establish whether improved P nutrition confers drought tolerance. The *Pup1* marker technology will be further optimised and training will be provided to NARES scientists.

72. Project No G4008.48: Improve sorghum productivity in semi-arid environments of Mali through integrated MARS

- *Duration: Aug 2008–Jul 2013*
- *Budget by year: $30,600 (2008), $39,600 (2009), $282,000 (2010), $282,000 (2011), $44,400 (2012); Total budget: $678,600*

Sorghum/Drought tolerance/Africa

Lead institute
Agropolis–CIRAD (Jean-Francois Rami)
Collaborating institutes and scientists
- Syngenta (Denis Lespinasse, Michel Ragot)
- IER (Niaba Témé, Sidy Bekaye Coulibaly)
- Agropolis–CIRAD/IER (Michel Vaksmann)

Sorghum is, together with pearl millet, one the most important cereals in West Africa. It is the second most important crop in Africa after maize. However its yield is low and has not really progressed during the past 20 years. The sorghum production in West Africa is principally based on traditional, low harvest index cultivars and the breeding efforts of the past 40 years showed limited impact.

The present project propose to associate recent approaches on sorghum breeding that have been developed at IER and methodologies for marker assisted recurrent selection (MARS) that have proven to provide significant improvement of breeding efficiency for complex traits, especially in the case of maize.

Two populations dedicated to two different environments of sorghum crop in Mali will be developed from the cross of local well characterised advanced breeding cultivars exhibiting complementary traits for the target environment. A multilocal evaluation of the progenies as F4 families, together with genotyping will provide accurate QTL detection for as many traits that have to be considered for breeding. This QTL information will be used in several consecutive cycles of recurrent selection aiming at monitoring recombinations and pyramiding favorable alleles for selected QTLs. All along the recurrent process material will be released for evaluation and selfing to develop new varieties.

This project will illustrate through a private-public partnership the value of the MARS approach for sorghum breeding in Mali.

73. Project No G4008.49: Enhancing groundnut (*Arachis hypogaea L.*) genetic diversity and speeding its utilisation in breeding for improving drought tolerance

- *Duration: Aug 2008–Jul 2009*
- *Budget by year: $81,600 (2008); Total budget: $81,600*

Groundnut/Drought tolerance/Africa; Latin America

Lead institute
ISRA (Ousmane Ndoye)
Collaborating institutes and scientists

- PROINPA (Antonio Gandarillas, Jorge Rojas, Rene Adolfo Maita)
- USDA–ARS (Roy Pittman)
- Agropolis–CIRAD (Jean-François Rami)
- ICRISAT (Vincent Vadez and Hari D Upadhyaya)
- EMBRAPA (Soraya Leal Bertioli)
- UCB (David John Bertioli)

Groundnut (*Arachis hypogaea L.*) is the most largely cultivated legume in Africa, with most of the production originating from drought-prone areas. Drought considerably reduces yield and production. Cultivated groundnut has a narrow genetic basis and the first step for improving drought tolerance in this crop is by enhancing genetic diversity. This can be done either by accessing more effectively the genetic diversity present in the cultivated species or by tapping the genetic diversity from wild related species. The objectives of the present project are i) to characterise and improve access to the genetic diversity present in the center of origin of the cultivated species (South of Bolivia), ii) to develop (from amphidiploids developed previously in the frame work of a GCP competitive project) new sources of genetic diversity (back-cross and introgressions lines), and iii) to develop phenotyping capacities, particularly in Senegal (one of the main groundnut producers in West Africa), that are needed to evaluate further these new sources of variability under drought conditions. An additional aim of the project is to serve as a basis for developing a "groundnut platform" for improving research products management and delivery, contributing to intensify the collaboration between groundnut scientists and breeders worldwide.

74. Project No G4008.55: GCP phenotyping book

- *Duration: Jul 2008–Dec 2008*
- *Total budget: $15,000*

Various crops, traits and regions

Lead institute
GCP (Philippe Monneveux)
Collaborating institutes and scientists
Consultant (Lyndsey Withers, editor)

Terms and references for consultant:
Technical and copy editing of the manuscript for the book above as a first stage. Once the manuscript in MS-Word is completed, the next step will be proofreading of the layout version. ToRs below are for the manuscript stage. For both stages, your main contact person at GCP is Philippe Monneveux and you will work under his direction. An initial four chapters of the manuscript will be sent to you by 25th July 2008, and the remaining chapters as and when they are received from authors, and reviewed by Philippe and Jean-Marcel. Author emails will be sent to you, and an introductory email sent to authors to introduce you to them. You are to submit a layout-ready final version of the manuscript by 31 December 2008. This Stage II-ready version may be accompanied by separate notes for layout as the case may require based on your editorial judgment.

75. Project No G4008.56: Drought tolerant maize for Asia

- *Duration: Nov 2008–Oct 2013*
- *Budget by year: $286,700 (2008), $384,900 (2009), $279,600 (2010), $297,200 (2011), $251,600 (2012); Total budget: $1,500,000*

Maize/Drought tolerance/Asia

Lead institute
CIMMYT (PH Zaidi)
Collaborating institutes and scientists

- YAAS (Fan Xingming)
- DMR (Sain Dass)
- MPUAT (SL Godawat)
- ICERI (M Azra)
- MMRI (Muhammad Saleem Shaheen Yusafwala)
- DOA–Thailand (Pichet Grudloyma)
- NMRI (Phan Xuan Hao)
- BIOSEED, India, Thailand, Philippines, Vietnam; ICI / Syngenta; IFSSA, Hyderabad, India; Monsanto; Pioneer; other APSA members

Maize area in South and South-East Asia has been expanding by 2.2% annually from 16.5 (2001) to 18.0 (2006) million hectares. Over 80% of the maize is grown under rainfed conditions and prone to drought. Addressing the problem of drought has been estimated to provide the highest technical returns to rainfed maize R&D investments in Asia. Based on substantial breeding progress made for drought tolerance in maize in other regions (Central America and eastern and southern Africa), this project proposes to apply marker-assisted selection within pedigree breeding or backcrosses made between drought tolerant source inbreds and a minimum of four elite Asian adapted inbreds, and more through execution of additional self-funded and donor-funded MARS projects by public and private partners. Inbred lines will be extracted from improved populations, using either selfing or doubled haploids, and new drought tolerant Asia-adapted hybrids tested. GCP support will result in a minimum of four Asian adapted drought tolerant inbreds and hybrids, molecular marker information associated with drought tolerance, and NARS and private sector scientists with experience in integrating MARS in applied breeding programmes. The project intends to integrate self-funded public and private sector partners for a larger number of MARS breeding projects (for drought tolerance and other traits) and wider capacity building. This project is expected to become the impetus for significant levels of drought tolerance being introduced into highly relevant Asian maize germplasm with resulting impact in diverse environments and by diverse suppliers, and for a molecular community of practice being established among the Asian maize breeding community.

Projects on NCE into 2008 or beyond

76. Project No G4005.20: Optimising marker-assisted breeding systems for drought tolerance in cereals through linkage of physiological and genetic models

- *Duration: Jan 2005–Dec 2006 with NCE to May 2008*
- *Budget by year: $130,000 (2005), $130,000 (2006); Total budget: $260,000*

Various crops (cereals)/Drought tolerance/Various regions

Lead institute

- CSIRO (Scott Chapman)
- CIMMYT as Co-PI (Jiankang Wang)

Collaborating institutes and scientists

- UoQ (Mark Dieters and Graeme Hammer)
- CIMMYT (Richard Trethowan)
- CSIRO (David Bonnett and Greg J. Rebetzke)
- Agropolis–INRA (Francois Tardieu, Claude Welcker)
- Private sector (Pioneer): Mark Cooper (advisory role)

The dynamic linkage of crop modeling and genetic/breeding simulation allows us to simulate such things as the introgression or marker assisted selection of traits as affected by population genetic structures, selection criteria (e.g. direct or indirect selection for yield) and trait by environment interactions. The aim of this project is to build up the gene to trait information using data from QTL and physiological experiments and to further improve the ability of our crop simulation models to capture the effects of traits and their integration to yield. It will aim to combine these 'gene-to-phenotype' physiological models with existing genetic models for other traits such as disease and quality. Simulating molecular breeding programmes will enable optimisation of MAS strategies and provide a platform for integrating a range of knowledge-based outputs from GCP into breeding programmes.

Subprogramme 4: Bioinformatics and crop information systems

Current projects

77. Project No G4005.22: Development of Generation CP domain models ontology

- *Duration: Jan 2005–Dec 2008*
- *Budget by year: $259,600 (2005), $200,000 (2006), $150,002 (2007), $ 94,572 (2008); Total budget: $704,174*

Lead institute
IRRI (Richard Bruskiewich)
Collaborating institutes and scientists

- IRRI (Thomas Metz, Martin Senger, Graham McLaren)
- Bioversity (Elizabeth Arnaud, Tom Hazekamp, Adriana Alercia)
- CIMMYT (Rosemary Shrestha, Guy Davenport)
- CIP (Reinhard Simon)
- ICRISAT (Jayashree Balaji)

External (self-funded) collaborator
Pankaj Jaiswal (Plant Ontology Consortium, www. plantontology.org

This project is commissioned research continued from a task initiated in 2005 to define semantic standards for data interoperability, so-called domain modeling and ontology (DMO), within the Generation Challenge Programme (GCP).

GCP domain models (DM) are generic sets of scientific concepts blueprinted using an objectoriented computing science formalism Unified Modeling Language (UML). These scientific concepts relate to the domain of discourse of GCP crop r Alves Balazs esearch.

To maintain semantic flexibility and extensibility, these object models are deliberately designed to be heavily parameterised by diverse context-specific ontology. Ontology is basically a dictionary of formally defined terms representing concepts for which interconnecting relationships are explicitly modeled as networks of related terms.

Although many of these ontology are being adapted for GCP use from maturing third party initiatives for ontology development (such as the Gene Ontology and Plant Ontology consortia), there remains additional GCP-pertinent ontology to be formalised.

Project work in 2008 will partly elaborate DMO project outputs initiated in previous years, and partly extend project activities to new GCP partners and crops.

Within the scope of previous work being continued into 2008 is the incremental validation and refinement of the domain model, with further refinement of domain model and ontology management technology, including development of a long term strategy for community-driven extension and application of ontology to efficiently share data across the internet and to undertake integrative data mining on GCP annotated data, using the GCP-compliant platform under development in SP4. This work will primarily be coordinated and undertaken by the lead institution, IRRI. Also carried over from 2007 will be activities planned for, but not initiated, by one partner site, CIMMYT, due to delays in resourcing.

New in 2008 will be the involvement of additional GCP partners in the systematic elaboration of priority plant, trait and phenotype ontology for additional GCP crops.

78. Project No G4005.23: Implementation of web services technology in the Generation Challenge Programme Consortium

- *Duration: Jan 2005–Dec 2008*
- *Budget by year: $180,000 (2005), $140,000 (2006), $120,000 (2007), $67,000 (2008); Total budget: $507,000*

Lead institute
Bioversity (Milko A Škofič)
Collaborating institutes and scientists

- Bioversity (Elisabeth Arnaud, Michael Mackay, Mathieu Rouard)
- IRRI (Martin Senger)
- CIMMYT (Guy Davenport)

Sharing and making data is available to all Generation Challenge Programme Consortium members and partners is crucial for the success of projects in all subprogrammes. Providing access to data via Web Services serves many purposes: it allows data sharing among geographically distant clients; it ensures that data complies with common agreed standards; and it allows software analysis tools to automatically access these resources.

79. Project No G4005.27: High Performance Computing Facilities for the GenerationCP

- *Duration: Jan 2005–Dec 2008*
- *Budget by year: $150,000 (2005), $100,000 (2006), $59,999 (2007), $75,000 (2008); Total budget: $384,000*

Lead institute
CIP (Anthony Collins)
Collaborating institutes and scientists

- CIP (Reinhard Simon)
- ICRISAT (Jayashree B, D Hoisington, Rajeev Varshney)
- IRRI (Richard Bruskiewich, Ramil Mauleon, Martin Senger)
- NIAS (Shoshi Kikuchi, Koji Doi)

The primary goal of this project is to provide high performance computing facilities for the GCP platform, where success is measured by impact on subprogrammes 1, 2 and 3, and reflected by a user community including more GCP collaborators beyond CGIAR. Therefore the HPC support and maintenance programme focuses on this goal to maximise use of HPC facilities, as globally supported by CIP, together with the bioinformatics support teams at each of CIP, ICRISAT, and IRRI working with NIAS. Significant SP1, 2 and 3 use case examples will be highlighted at the ARM in 2008.

As the HPC hardware funded by GCP is approaching the limit of processing capacity, a key new goal is to review and test sustainability options for the GCP Grid beyond 2008 with external Grid collaborators. Ongoing performance, user and load monitoring from CIP will enable a profile of future requirements to be defined.

Thus the primary output of this HPC task in 2008 will be 3 reports targeting:

1. Usage and impact for GCP SPs, updated 6 monthly
2. Collaborators identified for Grid computing capacity expansion experiments in 2008
3. Sustainability options for the GCP Grid beyond 2008
4. Some specific application development.

80. Project No G4006.08: Data analysis support for existing projects in SP2 with emphasis on integrating results across gene expression and QTL mapping experiments

- *Duration: Jan 2005–Dec 2008*
- *Budget by year: $150,000 (2006), $62,500 (2007), $199,800 (2008); Total budget: $412,300*

Lead institute
CIMMYT (Guy Davenport)
Collaborating institutes and scientists

- IRRI (Richard Bruskiewich, Hei Leung)
- CIMMYT (Jose Crossa, Yunbi Xu)
- ICRISAT (Jayashree B, Rajeev Varshney)
- CIP (Simon Reinhard)
- NIAS (Shoshi Kikuchi)
- JIC (Andreas Magusin)

Current GCP projects do not currently support in-depth analyses of data produced by SP2.

- The major goal of this project is to further elucidate genes, alleles, mechanisms and other factors relating to abiotic and biotic stress response across multiple crops through the analysis of available crop gene expression, genomic sequence, phenotype, genotype and QTL mapping data sets and across GCP SP2 commissioned and competitive research projects.
- A dedicated team of expert bioinformatics scientists will pursue the following objectives in collaboration with the providers of the data:
    - Development and integration of tools for the management and analysis of gene expression and QTL data.
    - Support to SP2 projects generating and utilising gene expression, genomic sequence and mapping data
    - To further characterise candidate abiotic and biotic stress responsive genes, pathways and processes by the analysis of consolidated GCP data sets and cross-linkage to other publicly available data
- Consolidated GCP datasets for gene expression and QTL with be fully integrated and annotated with added value from the results of analysis and will be accessible using web browser and service interfaces
- List of candidate abiotic and biotic stress responsive genes will be published
- Online documentation about the methodology, experimental design, analysis software and other pertinent best practice parameters of the data analysis to facilitate the design and analysis of future GCP experiments and projects will be available on the project web site

81. Project No G4006.16: Development of an Integrated GCP Information Platform

- *Duration: Jan 2006–Dec 2008*
- *Budget by year: $150,000 (2006), $150,000 (2007), $ 163,050 (2008); Total: $463,050*

Lead institute
IRRI (Graham McLaren)
Collaborating institutes and scientists

- Agropolis–CIRAD (Manuel Ruiz, Pierre Larmande, Xavier Argout)
- CIMMYT (Guy Davenport)
- EMBRAPA (Marcos Costa)
- ICRISAT (Jayashree B, Senthilvel S)
- IRRI (Richard Bruskiewich)
- EBI/IRRI (Martin Senger)
- NCGR (Andrew Farmer)

A key problem of biological scientists in general and GCP scientists in particular is integration of diverse and dispersed data sources and analysis of data via diverse analytical tools. The GCP Informatics platform seeks to alleviate this problem by providing an informatics platform which allows data integration via an agreed domain model and a workbench of interoperable applications. The domain model and basic architecture are in place and the current stage of the Platform project is to implement biological use cases designed to facilitate analysis of genetic diversity, functional genomics and molecular breeding.

In 2008, the GCP Informatics platform task will implement the following use cases:

- Develop a query, visualisation and analysis workbench for SP1 genetic diversity studies.
- Develop a query, visualisation and analysis workbench for SP2 comparative functional genomics research.
- Develop a query, visualisation and analysis tool for SP3 marker assisted breeding programmes.

The project will also support both GCP and non-GCP scientists in using the platform for the above use cases through training and documentation, and will continue to promote the GCP platform within and outside of the GCP, by providing adequate documentation and support to allow developers to integrate their data sources and applications.

82. Project No G4006.17: GenerationCP data quality improvement and assurance

- *Duration: Jan 2006–Dec 2008*
- *Budget by year: $150,000 (2006), $147,500 (2007), $176,789 (2008); Total budget: $474,289*

Lead institute
IRRI (Thomas Metz)
Collaborating institutes and scientists

- CGN–WUR (Theo Van Hintum)
- ICRISAT (B Jayashree)
- CIP (Reinhard Simon)
- Agropolis–CIRAD (Claire Billot)

In 2008, this project will incorporate the project *GCP Software Engineering and Collaboration Platforms* as an objective. The project will address the following issues that have strong implications on data quality and/or quality management in the GenerationCP:

- Support will be provided to institutes that consider the adoption and adaptation of the ICRISAT LIMS system. This is a continuation of a similar activity in 2007.
- A toolkit will be developed consisting of data quality indicators, best practice manuals, and a customised set of database/informatics and statistical tools applied to the main dataset types of the GCP. This toolkit will allow the routine quality assessment of GCP datasets.The collaboration systems CropForge and CGPWiki will be maintained and supported. This activity is a continuation of the former project *GCP Software Engineering and Collaboration Platforms*.
- A white paper on *Requirements for GCP Projects Producing Primary Data* will be written.This white paper will allow GCP management to specify service level agreements for data-producing projects.

83. Project No G4006.35: Support for existing projects in SP1 on germplasm data analysis (GDA)

- *Duration: Jan 2006–Dec 2008*
- *Budget by year: $50,000 (2006), $75,000 (2007), $80,000 (2008); Total: $205,000*

Lead institute
WUR (Marco Bink)
Collaborating institutes and scientists

- WUR (Hans Jansen, Fred van Eeuwijk, Marcos Malosetti)
- Agropolis–CIRAD (Xavier Perrier, Jean-Francois Rami)
- CIMMYT (Jose Crossa)

Recently, SP1 scientists and NARS scientists that participated in the Genotype Support Service expressed a strong need for support in the proper design, curation and analysis of data sets (e.g., workshops in Zaragoza – Oct 2006, Oct 2007). These requests touch upon the process of experimental design, data description, data quality control and the statistical analyses. In 2006 we (WUR) already successfully started to collaborate with SP1 and NARS scientists and organised in the last 2 years a one-week workshop to provide training and guidance in assessing data quality and performing data analyses. This project targets to continue and expand this support to scientists from all SP's and related NARS via bilateral contacts and consultations, primarily via email but possibly also via on-site visits. The helpdesk facility via a website will be further expanded to touch upon issues more broad than the stepwise procedure guiding the SP1 in their Germplasm data analysis. The need for support on statistical tools is much more widely, i.e., starting at experimental design up to the assessment of Linkage Disequilibria and the marker-trait associations and QTL linkage analysis.

The objective is to support scientists from all SP's to design, curate, and analyse the generated genotypic and phenotypic data in an optimal way, identifying relevant QTLs with appropriate and tailored statistical procedures. This project involves also expert scientists from CIRAD (diversity analysis) and CIMMYT (experimental design). The project will contain consultancy, communication and training components.

84. Project No G4007.09: Design and analysis of marker-trait association studies, with special attention for genetically challenging crops

- *Duration: Aug 2007–Dec 2008*
- *Budget by year: $100,000 (2007), $200,000 (2008); Total budget: $300,000*

Lead institute
WUR (Fred van Eeuwijk)
Collaborating institutes and scientists

- UoH (Hans Peter Piepho, Albrecht Melchinger)
- ICL (David Baldin)
- NIAB (Ian Mackay, Wayne Powell)
- SCRI/BIOSS (Christine Hackett, Dave Marshall)
- ULMC (Hans van Houwelingen, Jeanine Houwing-Duistermaat)
- WUR (Marcos Malosetti, Joao Paulo, Marco Bink, Hans Jansen)

A first step in any marker assisted breeding strategy is the localisation of quantitative trait loci (QTLs). Since the 1990s, the standard methodology for the detection of QTLs in crops is based on a linkage analysis of offspring populations created from crossing two inbred parents. Although successful, a weak point of such linkage analyses is the requirement to create artificial crosses that often are not representative of the germplasm that breeders use in their programmes. As a consequence detected QTLs may have severely reduced effects when translated to real life genetic back grounds. Another weak point concerns the relatively low precision with which QTLs can be located by standard QTL mapping techniques. Precision depends on the number of generative cycles (meioses) since a genetic reference situation, like, for example, a controlled cross between two inbred lines.

A recent attractive alternative to pure linkage based QTL mapping is linkage disequilibrium (LD) mapping, or association mapping. LD approaches can be applied to any pool of selected or arbitrarily structured genotypes, allowing breeders to search for QTLs in relevant genetic back grounds. As LD methods assay the accumulated generative history in the germplasm / population under study, they are often more powerful and precise than standard QTL mapping approaches. LD approaches are appealing within the Generation Challenge Programme (GCP) where inventories of genetic diversity are being made on the basis of molecular markers with the purpose of investigating that genetic diversity in relation to phenotypic variation.

Successful methodology for LD mapping has been proposed for major crops. For smaller crops and genetically more challenging crops, little knowledge and experience is available. For major crops, mixed models are a popular vehicle for LD mapping as they provide various ways to control for spurious associations caused by population structure, i.e., the phenomenon that the whole of the set of genotypes under study falls apart in genetically different groups with group specific allele frequencies. Also for other crops than major crops, mixed models seem a proper choice for LD mapping, but then the mixed models need to be attuned to the requirements of the specific crop.

The current project aims at defining a statistical protocol for the design and analysis of LD strategies in a variety of crop species of importance to the GCP. Design theory for association studies in smaller and genetically complex crops, like polyploids, requires study of the genetic mechanisms causing LD and a proper translation of those mechanisms in statistical parameters. For example, to quantify LD decay with genetic distance on the chromosome in polyploids, first relevant measures for LD need to be defined. This project will bundle the insights of specialists in LD mapping theory to arrive at statistical protocols for conducting LD feasibility studies in crops relevant to the GCP. Such feasibility studies should answer questions on the choice of marker system, marker density, and the type of population in relation to defined phenotypic traits.

For the analysis part of this LD mapping project, we propose to adapt and develop special purpose mixed model strategies focusing on the genetic properties of small and challenging crops. Mixed models are highly suitable for modeling genotype by environment interaction in multi-environment data, data obtained from germplasm evaluations across multiple trials and stress gradients. In the context of the GCP work on stress tolerance, the modeling of genotype by environment interaction has high priority. Mixed models also have good facilities for representing relationships between genotypes, a feature that facilitates correction for population structure in LD studies.

The statistical protocols we develop on design and analysis of LD studies in small and challenging crops will be accompanied by documented software and course material that should open up this methodology to the whole of the GCP.

85. Project No G4007.10: Support to GCP scientists regarding issues related to bioinformatics and data handling

- *Duration: Aug 2007–Jul 2009*
- *Budget by year: $56,640 (2007), $60,600 (2008); Total budget: $116,640*

Lead institute
WUR (Theo van Hintum)
Collaborating institutes and scientists
WUR (Elisabeth van Strien)

The support to GCP scientists regarding issues related to bioinformatics and data handling will be given via a one-stop-shop called the 'SP4 Helpdesk'. The GCP-SP4 helpdesk will be the entry point for any GCP scientist who has questions regarding handling, storing, or analysing his/her data. The helpdesk is responsible for creating transparency in the available expertise and resources in the field of biometry, bioinformatics, and software engineering relevant to GCP scientists, available in the GCP. It will pro-actively improve (or advise on the improvement of) GCP web-sites, create an expert network and act as a point of reference for GCP scientists.

- It will be responsible for restructuring the GCP Bioinformatics portal (http://www.generationcp.org/bioinformatics.php) creating easy access to all GCP-SP4 products and websites.
- It will create resources necessary to answer scientists requests rapidly and effectively, e.g. by creating an expert database with names and contact details and corresponding expertise in SP4 relevant disciplines.
- It will make sure that any email of GCP scientists is handled appropriately, mediating between the one asking and the one with an answer.
- It will advise the SP4 leader in regards funding visits or other means of support that might need funding.

86. Project No G4007.11: Further development and support for use of iMAS by NARS and other user communities

- *Duration: Jan 2007–Dec 2008*
- *Budget by year: $80,000 (2007), $84,000 (2008); Total budget: $164,000*

Lead institute
ICRISAT (Jayashree B, effective June 2008; Previous PIs: Subhash Chandra and Dave Hoisington)
Collaborating institutes and scientists

- ICRISAT (Tom Hash)
- IRRI (Richard Bruskiewich)
- CIMMYT (Guy Davenport)

The iMAS system provides a single unified computing and decision support platform to facilitate marker-aided selection and breeding through integration of a number of freely available open-source quality computing tools. The system frees the user from the painful, time-consuming and error-prone manual preparation of input data files required by a host of computing software involved in the computational process for marker-assisted selection and breeding. The provision of simple-to-use online decision guidelines allows the user to correctly and confidently use the different computing tools and to interpret and use their outputs to facilitate making decisions for marker-aided selection and breeding.

The system comprises of six modules: *Data Validation, Phenotyping, Linkage Map Building, QTL Analysis, Genome Display, and MABC Sample Size*. The *Data Validation* module helps the user to check whether the required initial input data files have been prepared in accordance with the rules required by iMAS. The *Phenotyping* module generates experimental design and undertakes biometric analyses. The *Linkage Map Building* module builds linkage maps. The *QTL Analysis* module undertakes QTL analyses. The *Genome Display* module helps pictorially visualise the genomic content to select genetic material of desired genomic composition. The *MABC Sample Size* module helps determine the optimal sample size for marker-aided backcrossing. Salient features of the system are a seamless integration of different computing tools into one single platform, extensive simple-to-use online decision guidelines and manual, and the provision of a windows interface to all DOS-based programmes, the last one making it easier for a user to correctly, comfortably and confidently use these programmes. The first beta version of iMAS (iMAS 1.0) was released at the ARM in South Africa in September 2007.

During 2008, the system will be further developed to include facilities for (a) construction of consensus genetic linkage maps, (b) multi-environment QTL analyses, (c) comparative QTL mapping through integration of CMTV, and (d) modeling of MABC via inclusion/linkages with Qu-Gene. In addition, the entire iMAS system and/or individual programmes will be integrated into the GCP platform as appropriate. The online decision guidelines and the manual will be accordingly updated and revised. The updated system will be extensively tested on a wide range of different real dataset. A one-week training course on the use of the system will be organised in Africa. The updated system (iMAS 2.0) is expected to be formally released at the ARM 2008, although pre-released versions will be made available as they are finalised.

87. Project No G4007.12: Development of tools and technology to increase the functionality of the GCP Information Platform

- *Duration: Feb 2007–Dec 2008*
- *Budget by year: $100,000 (2007), $86,441 (2008); Total budget: $186,441*

Lead institute
IRRI–CRIL (Martin Senger)
Collaborating institutes and scientists

- IRRI–CRIL (Graham McLaren, Richard Bruskiewich)
- Bioversity (Milko Skovic)

The GCP Platform is a set of collaborating software tools constructed using shared GCPdeveloped semantic and informatic standards. These tools, both web- and stand alone-based, will be able to visualise and analyse data from – normally non-interoperable – data resources from across the GCP partners. The PI is funded by this project to help manage the software development team and participate directly in the development efforts themselves. These efforts include the continued development of the core framework for GCP platform and specific implementations of GCP-compliant platform software tools, internet protocols and data resource wrappers.

88. Project No G4008.20: Management of the GCP Central Registry and the creation and maintenance of templates for data storage in repositories

- *Duration: May 2008–Dec 2008*
- *Total budget: $140,000*

Lead institute
Bioversity (Elizabeth Arnaud)
Collaborating institutes and scientists

- CIMMYT (Guy Davenport)
- CRIL/CIMMYT (Guy Davenport, Genevieve Mae Aquino)
- Bioversity (Milko Skofic, Michael MacKay)

A large amount of data is being generated within the Generation Challenge Programme (GCP). These data must be stored in a form that can be used by GCP Consortium members and the scientific community. In previous years, data templates were developed for the storage of SSR genotyping, passport, mapping, QTL, and phenotype data. In 2008, existing templates will be improved and new ones developed. Data sets are currently being validated and will be reloaded into the templates.

In 2008, GCP data standards for high-throughput (e.g. array-based) technologies such as DArT, gene expression arrays and SNP genotyping will be further developed, and support for uploading data sets, populating the templates and using the software will be provided by a proactive help desk service. Organising and publishing information on the web through a Central Registry provides an overview of all available data resources (a 'yellow pages' directory). This is critical for the successful completion of tasks that require data from different sources. Established in 2005, the GCP Central Registry increased the depth and range of the resources it manages in 2006 and 2007. In 2008, the aim is to strengthen the resource collection managed by the Central Registry, enhance the provision of quality assessment for the data held and improve access to submitted data using web services.

The current project merges the previously separate 'Data Templates' and 'Central Registry' activities into a single project.

89. Project No G4008.21: Large-scale phylogenomic analyses to gene function prediction for GCP crops

- *Duration: Jan 2008–Dec 2009*
- *Budget by year: $119,033 (2008), $121,534 (2009); Total budget by year: $240,567*

Lead institute

Bioversity (Mathieu Rouard)

Collaborating institutes and scientists

- Agropolis–CIRAD (Christophe Périn)
- IRRI (Matthieu Conte, Richard Bruskiewich, Ramil Mauleon, Martin Senger)

With an increasing amount of data provided by Generation Challenge Programme projects on full or partial genome sequencing, there is an urgent need to transfer the information from model species to newly sequenced ones. Orthologous and paralogous gene identification is now a major objective for gene function prediction as orthologous sequences are more likely to share the same function than paralogous sequences. The phylogenomic inference approach has been shown to enable the highest accuracy in predicting protein molecular function, avoiding most false homology inference problems and distinguishing between orthologous and paralogous genes. The GCP has already invested some effort in that strategy and has released promising tools for the plant researcher community. This project's aim is to consolidate and further develop those approaches in order to provide new insights into functional genomics.

90. Project No G4008.22: Methodology development for reconstruction of Genealogies based on Haplotypes related to geographic patterns (HaploPhyle: Graphical haplotype network in the light of external data)

- *Duration: Jan 2008–Dec 2008*
- *Total budget: $152,540*

Lead institute

Agropolis–CIRAD (Claire Billot)

Collaborating institutes and scientists

- Agropolis–CIRAD (Xavier Perrier, Manuel Ruiz, Jean-François Rami)
- CIP (Reinhard Simon)

Genetic diversity assessment gains much sense and power when haplotypes are taken into consideration and linked to evolutionary history. This helps to trace back mutations and their genetic and population environment. This project intends to provide the community with a pipeline of analysis of genotyping data (sequences or SNPs) which will include haplotype definition, haplotype network analysis and connexion with external data, such as geographic origin, evolutionary history or genetic group assessment. It differs from existing projects in the fact that different methods in haplotype definition and haplotype network will be available for users, with tuneable choice criteria, as well as sub-optimal networks. It will be developed and integrated by two research groups: one group at Agropolis–Cirad will take care of the pipeline including haplotyping, haplotype network construction and its illustration by external data, as well as some methodological aspects of network construction. CIP will be more involved into connexion with DIVA-GIS, an already existing tool which manages geographic information, in order to integrate geographic information and enable pertinent modes of graphical representation.

91. Project No G4008.31: Upgrading the quality and utility of GCP phenotyping data through the development of a data input template to facilitate the storage of data in cross-specific databases

- *Duration: Feb 2008–Jan 2009*
- *Total budget: $72,000*

Lead institute

CropGen International (Robert Koebner)

Collaborating institutes and scientists

- CIMMYT–CRIL (Guy Davenport)
- CRIL/IRRI (Warren Vincent E Constantino)

The goals of this proposal are to: (1) create a wizard-driven template ("first generation template") able to store phenotypic data observations and all associated data to make them interpretable, whilst assuring compatibility with the GCP domain models and crop information systems such as ICIS; (2) extend to a "second generation template" which is more crop-specific and prescriptive, via the incorporation of mandatory traits and fields (including drought tolerance indicator traits, experimental designs, environmental indicators etc.), both to facilitate future meta-analyses of the phenotypic data and to improve the homogeneity of experimental protocols across GCP projects; (3) document the use of this template in a user manual; (4) export, as far as possible, the data presently lodged in the GCP Central Registry into the 'first generation' template; (5) monitor the use of the templates and the compliance thereof; and (6) explore the possibility of establishing electronic field data capture technology for the GCP community, as a tool to improve the accuracy of phenotyping.

92. Project No G4008.32: Promotion of Quality Management Procedures in GCP Research Laboratories

- *Duration: Jul 2008–Jun 2009*
- *Total budget: $192,000*

Lead institute
CIMMYT (PIs TBD)
Collaborating institutes and scientists
To be determined

The GCP is a hi-tech scientific programme that depends to a large extent on the quality of the information generated in its research projects. A considerable part of this information is generated in laboratories. The first global impressions of the quality of this information are inconsistent, some data sets appear of appropriate quality and others don't. In an attempt to improve this situation, several activities are being developed in 2008: a more stringent quality testing of produced datasets using quality indicators and increasing the visibility of datasets allowing peer pressure to have a positive influence. However: garbage in - garbage out. This project tries to increase the quality of information generated by the GCP Research Laboratories at the source, by improving the production process. Focused around the document EN ISO/IEC 17025:2005 'General Requirements for the Competence of Testing and Calibration Laboratories' a series of workshops and consultancies will be organised (1) increasing the awareness of the principles of quality management in a laboratory environment (2) proposing changes in the specific workflows seen during the consultancies that will increase the quality (3) produce a 'Best Practices' document for use in a GCP laboratory environment (based on ISO/IEC 17025 and the GCP situation). The result will allow a significant increase of the quality awareness and the output in the laboratories involved in GCP research.

93. Project No G4008.54: Implementation—Molecular Breeding Platform

- *Duration: Sep 2008–Dec 2008*
- *Total budget: $30,000*

Lead institute
GCP (Graham McLaren)

This proposal aims to develop and deploy a functional and sustainable molecular breeding platform providing breeders access to molecular breeding services, an information system and a toolbox of analysis and decision support applications. Such platform will enable breeding programmes in the public and the private sectors to access well-characterised germplasm, modern marker technology and germplasm information in a simple and reliable way, to accelerate variety development in South Asia and sub-Saharan Africa, among other regions.

This project will build on existing MAB projects supported by the Bill & Melinda Gates Foundation and GCP, targeting improved crops for developing countries. The platform will address the needs of these projects in the first instance. Success with these examples will demonstrate the feasibility and effectiveness of the platform, creating incentive for other breeding projects of the same nature to use the platform.

Projects on NCE into 2008 or beyond

94. Project No G4005.24: Application and development of web services technology

- *Duration: Jan 2005–Dec 2007 with NCE to Oct 2008 (continued from Jan 2008 under project G4008.21)*
- *Budget by year: $100,300 (2005), $80,000 (2006), $80,000 (2007); Total budget: $260,300*

Various crops, traits and regions

Lead institute
2005–2006: IRRI (Richard Bruskiewich)
2007 onwards: Bioversity (Mathieu Rouard)
Collaborating institutes and scientists

- IRRI (Martin Senger, Mylah Anacleto)
- Agropolis–CIRAD (Manuel Ruiz, Pierre Larmande, Alexis Dereeper, Matthieu Conte)
- Bioversity (Milko Skofic)
- Agropolis–CIRAD (Manuel Ruiz, Pierre Larmande, Alexis Dereeper, Matthieu Conte)
- EMBRAPA (Natalia Martins, Marcos Costa)
- NIAS (Shoshi Kikuchi, Masaru Takeya, Koji Doi)

In 2005, web services technology was introduced into the Generation Challenge Programme (GCP) with a strong emphasis on BioMOBY (http://www.biomoby.org/). Since then, the GCP has played an active role in further developing this technology, with the aim of increasing its adoption by GCP partners and also becoming a recognised partner of the global bioinformatics community.

Over the past two years, some significant outputs were already produced through this project. For example, a tool kit has been implemented to provide developers with the means to deploy BioMOBY web services more easily. This has been rolled out in different institutes for several crops, and a prototype has been developed for rice functional genomics. In addition, a monitoring system has been set up to ensure that all elements of the service are functional. Further details on those outputs are described on the Moby section of the bioinformatics portal (http: //moby.generationcp.org/).

In 2007, the project aims to develop applications using web services technology on databases and other tools. The objective is to create resources that will be used within the GCP Consortium and that will demonstrate the utility of the technology chosen by the GCP.

95. Project No G4005.25: Creation and maintenance of templates for Generation CP data storage in repositories

- *Duration: January 2005–December 2007 with NCE to October 2008*
- *Total budget: $240,000*

Lead institute
CIMMYT (Guy Davenport)
Collaborating institutes and scientists

- IRRI (Richard Bruskiewich)
- Bioversity (Tom Hazekamp)

GCP projects produce a large amount of data each year. These data must be stored in a form that can be used by GCP consortium members and the scientific community.

In previous years data templates were developed for the storage of SSR genotyping, passport, mapping, QTL, and phenotype data.

This year's project will improve the current templates by allowing users assign control vocabulary or ontology terms to their data.

The Data Editor software will be improved with the inclusion of support for uploading data to databases and converting data to various formats required for visualisation and analytical tools.

GCP data standards for high throughput (e.g. array based) technologies, such as DArT, gene expression arrays and SNP genotyping will be established.

Support for populating the templates and using the software will be provided including a physical help desk at the next Annual Research Meeting.

Subprogramme 5: Capacity-building and enabling delivery

Current projects

96. Project No G4005.53 (CB03): The use of molecular markers in efficient crop improvement: Marker-Assisted Breeding–A learning module

- *Duration: Jan 2005–Dec 2005 and Aug 2007–July 2008*
- *Budget by year: $12,500 (2005), $20,000 (2007); Total budget: $32,500*

Lead institute
2005: WUR (Marja Thijssen)
2007: CU (Theresa Fulton)
Collaborting institutes
ICRISAT (Subhash Chandra)

An IPGRI–IGD collaboration of a learning module CD on molecular marker technologies was very favorably received, generating hundreds of requests from more than 30 countries worldwide (de Vicente and Fulton, 2004). However, while this module describes markers and their uses, it stops short of describing how they are used specifically in crop improvement and marker-assisted breeding. This next step will be the focus of this new learning module.

The topics in this module will include (but not be limited to) genetic linkage, mapping, QTL identification, population types and development, targeted introgression, positive and negative marker-assisted selection, development of near-isogenic lines, etc. Real-life applications will be given as examples, along with limitations and considerations.

Supported by the GCP, iMAS is a new software suite which provides a unified computational platform to facilitate marker-assisted selection. The proposed learning module will provide the conceptual groundwork for potential users of the iMAS platform, as well as serving as a companion guide. This learning module will also be a good complement to the other modules in progress and supported by the GCP, including those on molecular markers in plant diversity, phenotyping, and bioinformatics, creating a "bookshelf" of material available for scientists world-wide.

The targeted audience is plant breeders in developing countries; the modules will be developed in such a way as to be useful either as a self-tutorial, as the basis of a training course, or, as mentioned, as a companion to iMAS. Users will be apprised that the Interactive Resource Center & Helpdesk can answer any follow-up questions they may have.

97. Project No G4005.63 (CB13): The Interactive Resource Center & Helpdesk

- *Duration: Jan 2005–Jul 2009*
- *Budget by year: $50,000 (2005), $0 (2006), $29,621 (2007), $29,966 (2008); Total budget up to 2008: $109,587*

Lead institute
IGD–CU (Theresa Fulton)
Collaborating institutes and scientists
Members of the IGD

The Interactive Resource Center & Helpdesk was developed in 2005 by the Cornell Institute for Genomic Diversity as a support tool for scientists worldwide, with a particular focus on those implementing molecular marker assisted plant breeding and plant genetic diversity assessment programmes.

The IRC now includes a large number of resources, including protocols, tutorials, learning modules, literature and general resources, such as information on writing proposals. Freely available data is also available for download. Also posted are key links, including funding opportunities, journals, the African Molecular Marker Network, and GCP resources. A 'helpdesk,' i.e. a place for scientists ask specific questions, is fully functional. Questions are answered on a same-day basis from a volunteer team of scientists from various fields (specialising in molecular markers, population genetics, plant breeding, genetic diversity, etc.).

Since a statistics counter was added recently, the site has been viewed by approximately 2000 "unique visitors". Pages most frequently 'hit' include the Molecular Marker Modules followed by the Protocols page, and the recently added "Lab Products" page. This page lists vendors and links to regional representatives. This year the new web counter will be used to compile a "world map" of users.

Other upcoming plans for the Resource Center include new learning modules, additional protocols, a list of genotyping services available, contact information to link researchers with similar interests, increasing linkages with the GCP programme, and a more comprehensive survey to assess next priority needs. User information including a "world map" of users will be compiled. A Scientific News wil feature selected articles each month. Increased awareness of the IRC will be prioritised; news articles about the site will be published. For the Helpdesk, a list of "FAQ" will be posted for immediate help to some users, and the team of scientists behind the Helpdesk will be featured.

98. Project No G4006.14: *Ex-ante* impact analysis of marker-assisted selection technologies supported by the Generation Challenge Programme (GCP)

- *Duration: Dec 2006–Dec 2008*
- *Budget by year: $78,430 (2006), $70,188 (2007); Total budget: $148,618*

Lead institute
VPI (George W Norton)
Collaborating institutes and scientists
VPI (Jeffrey Alwang)

The current GCP portfolio includes several research projects with potential near-term "products" that could be subjected to ex ante impact analysis. Impact analysis could help: (a) assist with future prioritisation of research resources, (b) provide early estimates of benefits of the initial GCP investments, and (c) validate an assessment approach that might be employed broadly in the GCP. The proposed project will project impacts of two GCP projects: "Revitalising marginal lands: Discovery of Genes for Tolerance of Saline and Phosphorus Deficient Soils to Enhance and Sustain Productivity," and "Development of Low-Cost Technologies for Pyramiding Useful Genes From Wild Relatives of Cassava into Elite Progenitors." These projects were chosen for the impact assessment because they (a) address significant problems on major crops, and (b) have advanced sufficiently to facilitate the identification of economically useful products. An additional objective for this impact analysis project is to design a useful methodology for reporting progress to GCP donors and identifying possible targets for research and delivery in the 2008–2013 phase of the GCP. The "economic surplus" approach will be used. Total economic benefits of the projects will be projected based on the situation with and without the new technologies (traits). The benefits will be calculated over time, taking into account (a) area planted to crops currently affected by target stresses, projected changes in area under cultivation, and production of the crops in specific countries, (b) the nature of the markets for the crops, (c) projected yield and cost changes due to the new technologies, (d) estimated time for discovery, development, and deployment of the DNA marker technologies and associated germplasm, (e) estimated time required to breed, test and disseminate superior new cultivars, including rates of adoption by farmers, and (f) the discount rate for benefits and costs that occur in the future.

99. Project No G4006.36: Capacity-building and research project

- *Duration: Jan 2007–Dec 2011*
- *Budget by year: $100,132 (2007), $100,098 (2008), $99,987 (2009), $99,987 (2010), $100,108 (2011); Total budget: $500,312*

Lead institute
ACCI/UKZN (Mark Laing)
Collaborating institutes and scientists
We are working in 14 countries in East and Southern Africa, with National Agricultural Research programmes, together with WARDA, CIAT, IITA, CIMMYT, ICRISAT and BECA

In this Project, the University will conduct capacity building and research Activities in sub-Saharan Africa in the disciplines of plant breeding and molecular biology. These Activities shall be conducted with the ultimate aim of enhancing food security and plant genetic diversity for the benefit of resource-poor people within sub-Saharan Africa.

The University shall serve as Lead Institute on this project. Its principal investigator shall be Mark Laing (or a mutually agreed upon substitute for Dr. Laing) of the African Center for Crop Improvement (ACCI) on the University's Pietermaritzburg campus. The principal investigator shall have primary responsibility for ensuring that the University complies with this Agreement.

One of the major capacity building Activities that the University will carry out in this Project is aimed at producing highly-trained Ph.D. scientists from sub-Saharan Africa. In order to accomplish this goal, among other things, the University will use the Grant to recruit and employ a full-time professor of molecular biology, who will teach and mentor Ph.D. students in the discipline of plant breeding and conduct research on food security crops. The University shall direct the Professor to carry out the Activities, and shall be responsible for producing the outputs and products, set forth in this Appendix I.

The University will also identify a "molecular toolbox" – an inventory of molecular tools available for important crops and traits in Africa, and identification of tools that would be particularly useful if developed), to be made broadly available in sub-Saharan Africa. The University will also collaborate with a number of institutes and scientists, including Generation Challenge Programme Consortium Members, Rockefeller Foundation, Bill and Melinda Gates Foundation; University of Illinois, Urbana-Champagne, University of Cape Town, University of the Witwatersrand, RIKEN, Japan; and the University of Kansas. As the lead institution for this project, the University shall have overall responsibility for contracting with, and coordinating the activities of, those other institutes and scientists. The University will also provide support to the implementation of SP5 activities in the region as requested (e.g. assessment of existing and needed capacity at selected NARS institutions, support to training events in the region).

100. Project No 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

- *Duration: Jan 2007–Dec 2008*
- *Budget by year: $65,000 (2007), $55,000 (2008); Total budget: $120,000*

Rice/Drought and salinity tolerance; grain quality/Asia

Lead institute
BIOTEC (Theerayut Toojinda)
Collaborating institutes and scientists

- RGDU (Jonaliza Lanceras-Siangliw)
- UBU (Sureeporn Kate Ngam)
- NAFRI (Monthathip Chang)
- CARDI (Men Sarom)
- DAR (Toe Aung)

Countries in the Mekong region, including Thailand, Laos, Cambodia, Myanmar and Vietnam, are characterised by common problems in relation to rice production. Abiotic stresses such as drought, soil acidity and salinity or nutrient deficiency are commonly encountered in this region, as are biotic stresses such as blast, bacterial leaf blight, brown plant hopper, white back plant hopper, gal midge, to name but a few. Learn about how this team of GCP collaborators are working across the region to take advantage of biotechnology as a means of advancing breeding programmes' efficiency in selecting rice lines containing genes controlling resistance to abiotic and biotic stresses, and focusing particularly on the development of backcross introgression lines via MAS in Thailand, Cambodia, Myanmar and Laos.

Countries bounding the Mekong River include Thailand, Laos, Cambodia, Myanmar and Vietnam. These countries are also known as Mekong Region. Likewise, these countries are also characterised by common problems in relation to agriculture or mainly in rice production. Abiotic stresses such as drought, soil acidity and salinity or nutrient deficiency are commonly encountered in this region. Biotic stresses (diseases and insect pests) such as blast, bacterial leaf blight, brown plant hopper, white back plant hopper, gal midge and a lot more are also commonly encountered in this region and the common strains/races of pathogen and biotype of insect are reported in the region. Collaborative programmes for drought tolerance improvement of varieties from various institutions were and are currently implemented to identify tolerant lines for breeding purposes. Conventional breeding is the most popular way in improving rice in the region. The advent of biotechnology may advance breeding programmes in terms of increasing efficiency of selecting lines that contains gene/s controlling resistance to abiotic and biotic stresses.

In Thailand, the use of biotechnology in agriculture is becoming widespread. Genes/QTL associated with submergence tolerance, salt tolerance, drought tolerance, disease resistance such as blast resistance and bacterial blight resistance, insect resistance such as brown plant hopper, white back plant hopper and stem borer and rice and cooking quality traits such as amylose content, gel consistency, gelatinisation temperature and aroma, were identified in different rice genotypes by BIOTEC at Rice Gene Discovery Unit (RGDU). Marker-assisted selection (MAS) for the traits mentioned has been implemented in Thai rice breeding programmes. Technology transfer of MAS has been done in the last concluded workshop on Molecular Breeding on rice that was held in RGDU, Kasetsart University, Thailand where participants came from Laos, Cambodia, Myanmar and universities and rice institutes in Thailand. Each participating group had their trait/s of interest, which include rice quality traits transferred to rice with drought resistance (Cambodia), salt tolerance traits transferred to rice with good quality (Myanmar), rice quality traits transferred to rice with wide adaptation (Laos), brown plant hopper resistance traits transferred to elite irrigated rice variety (Pisanulok, Thailand), blast resistance traits transferred to popular glutinous rice cultivar (Khon

Khen, Thailand) and rice quality traits transferred to rice with wide adaptation and drought tolerance in the Mekong region (Ubon, Thailand). This workshop was co-funded by the Rockefeller Foundation, BIOTEC and Kasetsart University. Currently, participants had developed backcross lines up to BC3 generation by using their own materials and MAS as selection tool. Two years of hands-on training turn out as a very successful workshop. It not only made them realise the importance of new technologies in breeding but also made them gain knowledge and confidence in implementing MAS in their own rice breeding programmes.

The objective of this proposed project is to continue the development of backcross introgression lines via MAS in which the materials were generated by 4 participating countries from the previous workshop (Thailand, Cambodia, Myanmar and Laos). We will undertake the MAS in Thailand because the participating countries lack DNA laboratory facilities, genomic information, human resource and research budget related to biotechnology. Also, after generating the introgression lines, trait validations in target locations will be followed in Thailand, Cambodia, Myanmar and Laos. Through this, developing lines will be faster and may contribute greatly to the improvement of rice cultivars in which it directly contribute to the welfare of the farmers through increased rice production and cash income and contribute to the economic development of the Mekong region.

101. Project No G4007.13: Capacity-building *à la carte* 2007

- *Duration: Jul 2007–Jul 2008*
- *Budget by year: $400,000, Total budget: $400,000*

Lead institute
GCP (Carmen de Vicente)
Collaborating institutes and scientists
Various (details below)

A new capacity building concept that seeks to identify and provide tailored capacity building to a select group of applied researchers at developing country NARS who will benefit significantly from long-term, personalised training and research support. For each individual selected to participate in this programme, a personalised programme will be developed to train them in the relevant methods, technologies, and approaches, and to provide the necessary equipment to be able to conduct GCP or related projects. The personalised training programme would be comprised of training events in the form of organised training, mini-grants for small equipment, hands-on research opportunities in ARIs, and the *in-situ* assistance of technical experts.

101.1 Project No G4007.13 (01): Capacity-building à la carte *2007–Capacity-building for characterising maize for waterstress tolerance at KARI-Katumani**

- *Duration: Jul 2007–Jul 2009*
- *Budget by year: $41,863 (2007), $7,080 (2008); Total budget: $48,943*

Maize/Water stress tolerance/Africa

Lead institute
KARI (James Gethi)
Collaborating institutes and scientists
Agropolis–INRA (Francois Tardieu, Claude Welcker)

In order to minimise the effects of drought on food production, new varieties that can tolerate water stress are required in drought prone areas. This calls for new approaches, especially those that combine traditional and molecular approaches. In order to maximise the benefits of available molecular tools such as comparative genomics that allow knowledge of one genome being applied to identify genes in another genome accurate data generation, interpretation and application is required. Phenotyping for complex traits such as drought tolerance require methods and equipments to characterise the genotypes and testing environments. We propose to build capacity in equipment, training and mentoring through joint visits to INRA and Katumani.

Katumani is the national dryland research centre that develops technologies to mitigate the effects of water stress on crops. Its capacity to do this work needs to be improved, especially in equipment that monitor water stress related parameters, recording equipments and upgrade of the irrigation at Katumani and Kiboko, our main drought screening sites. Training on how to use and apply the data will be sought from INRA, whom we are already collaborating with in a drought stress related GCP project. This hands-on training, first initiated in July 2006 will be more focused with a major concentration on data collection and analysis on how to link phenotypic data to genotypic data, in-depth design of drought and water stress experiments and genotype panel screening and selection.
This collaboration will involve reciprocal visits in Montpellier and Katunami during experiments and during data analysis.

With this capacity, accurate experimentation for water stress tolerance at KARI–Katumani will be possible. Currently we are developing inbred lines and we are using random drought screening techniques that are at best un-reliable. This has been a problem and progress in identifying drought tolerant genotypes has been slow and erratic.

**Associated GCP Project G3005.15: Determination of a common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes (PI: François Tardieu, Agropolis–INRA)*

101.2 Project No G4007.13 (02): Capacity-building à la carte *2007–Marker-aided development of nutritionally enhanced cassava for Nigeria**

- *Duration: Jul 2007–Jul 2009*
- *Budget by year: $ 48,822 (2007), $ 48,822 (2008); Total budget: $97,644*

Cassava/Various traits/Africa

Lead institute
NRCRI (Chiedozie Egesi)
Collaborating institutes and scientists

- NRCRI (Emmanuel Okogbenin; Ada Mbanaso; Nnamdi Eke-Okoro; Khaya Shuaibu; Oluwakemi Ogundapo; Samuel Baiyeri)
- CIAT (Martin Fregene)

Genomic tools, particularly molecular markers, are expediting cassava breeding by the identification of genotypes with desired traits early in the breeding/evaluation cycle without resort to time-consuming multistage evaluations. The GCP is currently funding the marker-aided introgression of CMD and CGM resistance into valuable Latin American germplasm and deployment to Africa, including the Nigeria. MAS for CMD resistance at CIAT and field evaluations of introductions from Colombia in Nigeria have identified excellent genotypes that combine CMD, CGM resistance with other useful traits; three of these genotypes are in pre-release trials in Nigeria. Cassava is a dietary staple in Africa and its transformation from rural subsistence crop to processed urban staple in Nigeria has necessitated the quest for higher nutritional status for the crop. As a major staple food crop in the country, cassava can serve as a cheap means of deploying protein and vitamins amongst the poor urban population. Besides, enhanced protein content increases its attractiveness in the animal feed industry. The development of varieties with improved nutritional value of increased protein and beta carotene content is therefore of highest priority to the breeding programme at National Root Crop Research Institute (NRCRI), Umudike Nigeria. CIAT has developed beta-carotene and protein rich germplasm that is also resistant to CMD and seeks to share this germplasm with partners in Africa beginning 2007. They will be introduced into Nigeria, evaluated for adaptation, and crossed to local varieties. Molecular marker-aided selection (MAS) will be also be used to identify genotypes with target traits early in evaluation cycle for subsequent on-farm trials and eventual variety release. This proposal is strongly linked to the aforementioned GCP project. It will fast-track the introduction and evaluation of a second generation of improved germplasm by strengthening the capacity of NRCRI staff involved in the project and improving basic facilities.

**Associated GCP Project G3005.09: Development of low-cost technologies for pyramiding useful genes from wild relatives of cassava into elite progenitors genomes (PI: Anthony Bellotti, CIAT)*

101.3 Project No G4007.13 (03): Capacity-building à la carte *2007–Application of molecular tools for controlled wild introgression into peanut cultivated germplasm in Senegal**

- *Duration: Jul 2007–Jul 2009*
- *Budget by year: $69,384 (2007), $64,425 (2008); Total budget: $133,809*

Peanut/Drought and disease resistance/Africa

Lead Institute
ISRA/CERAAS (Ousmane Ndoye)
Collaborating institutes and scientists
Agropolis–CIRAD (Jean-François Rami)
UCB (David John Bertioli)
EMBRAPA (Marcio Moretzsohn)

Groundnut is an important crop of the Sahel zone of Africa. It is a cash crop as well as a major source of dietary proteins and oil, and also a source of stover for animal feeding. Groundnut cultivation in this area faces important constraints, particularly drought stress and diseases, but the narrow genetic basis of the cultivated peanut Arachis hypogaea L. hampers the development of improved varieties through conventional breeding.

The ongoing GCP project "Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools" led by EMBRAPA in collaboration with CERAAS/ISRA in Senegal, and CIRAD in France aims at exploring and exploiting the up to now limitedly used variability of cultivated peanut's wild relatives through the utilisation of amphidiploïds together with molecular tools.

During the first year of the project, two amphidiploïd varieties (A.ipaënsis x A.duranensis from Brazil and TxAg6 from USA) have been transferred to CERAAS/ISRA and each of them have been crossed to four different A. hypogaea cultivars from the national programme to produce backcross populations. Right now, BC1 seeds are available for each of the crosses. Populations derived from crosses of this type segregate strongly for many traits. However, considering the nature of the parentals, and breeder priorities in Senegal, investigation of components of drought tolerance, resistance to leaf spot and seed dormancy will be given top priority.

The main objective of this proposal is to allow the best use of the molecular tools developed in the frame work of the above mentionned project in order to optimise the development of breeding material for these priority traits, from the populations. Since the beginning of the project about 700 microsatellites have been developed and genetic maps have been constructed for both AA and BB genomes. These tools make it possible to develop introgression lines from available material using MAS. This requires the use of integrated genotyping at each step of the breeding process. To achieve this goal, we propose to build on the ISRA/CIRAD/EMBRAPA collaboration to ensure capacity building to PhD students and scientists involved in peanut breeding at ISRA and provide technical backstopping at the key steps of the breeding process for all activities related to MAS.

** Associated GCP Project G3005.05: Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools (PI: José Valls, Embrapa)*

101.4 Project No G4007.13 (04): Capacity-building à la carte *2007–Characterisation of maize germplasm found in Ghana, using the bulking technique**

- *Duration: Jul 2007–Jul 2009*
- *Budget by year: $40,000 (2007), $32,500 (2008); Total budget: $72,500*

Maize/Drought tolerance; streak virus disease/Africa

Lead Institute
CSIR–CRI, Ghana (Allen Oppong)
Collaborating institutes and scientists

- CIMMYT (Marilyn Warburton – now located at USDA–ARS – and Yunbi Xu)
- CSIR (Ruth Thomson, Ewool Manfred, and Maxwell Asante)
- UdlR (Jorge Franco)
- CSIR–CRI, Ghana (Manfred Ewool, Maxwell Darko Asante, Ruth Thompso)

The Pathology Section of the Crops Research Institute of Ghana, together with our maize breeders and partners, are trying to develop drought tolerant maize with resistance to maize streak virus disease using traits found in local germplasm. We would like to use phenotypic screening to characterise drought resistance in the first stage; however, when drought associated molecular markers become available, we hope to be in a position to use these as well for selection gain in our populations. In the first stage, in addition to selecting diverse, drought resistant germplasm for breeding, we will also use molecular markers linked to MSV resistance in our breeding programme in an MAS programme to speed gain from selection for this trait. Maize germplasm in Ghana is not adequately characterised. We hope to collect, conserve, and fingerprint maize populations from Ghana, in addition to known drought tolerant populations from other breeding programmes in Africa, to ensure that the populations we select for our breeding programme are as diverse as possible. In addition to selecting populations for breeding, we hope to create a core subset, that has been adequately characterised morphologically and genetically, that would be used for selection, hybridisation, association studies, etc in our efforts to develop varieties with the desired traits.

The use of bulk fingerprinting will afford us the opportunity to characterise as much as possible most of our stored seed maize germplasm to the DNA. Inbred lines will be selected from the most diverse populations that also show good drought tolerance. Inbred lines will be selected from these populations, using markers linked to MSV to ensure that all of them will be resistant to this disease. These lines will be used for hybrid production, synthetic maize population production, and association mapping of useful traits in the future.

**Associated GCP Project G3005.14: Characterisation of genetic diversity of maize populations:*
Documenting global maize migration from the center of origin (PI: Marilyn Warburton).

101.5 Project No G4007.13 (05): Capacity-building à la carte *2007–An integrated proteomics and genomics approach to discover salt tolerance genes**

- *Duration: Jul 2007–Jul 2009*
- *Budget by year: $25,960 (2007), $23,010 (2008); Total budget: $48,970*

Rice/Salinity resistance/Asia

Lead institute
ABRII (Ghasem Hosseini Salekdeh)
Collaborating institutes and scientists
- IRRI (Abdelbagi M. Ismail)
- IPK (Mohammad-Reza Hajirezaei)

Proteomics showed to be a powerful approach to discover abiotic stress tolerance genes/proteins. In the past few years we used this approach to study rice response to salinity and drought. However, according to these findings and our works in GCP project 2, we learned that:

1. Many important proteins including transcription factors are masked by high abundant proteins and can not be detected on two dimensional electrophoresis gels.
2. It is important to confirm the function of genes as tolerant ones using relevant approaches like RNAi before applying it in marker assisted breeding (MAB) programme.

To address these two important issues, we are going to isolate nucleus from rice tolerant (FL478) and sensitive (IR29) lines and then extract and study their proteome. These will allow us to study low abundant but very important transcription factors. Then, we will further extend our knowledge by analysing metabolome of similar plant samples and combine the information with proteomics data. We will then examine and verify the contribution of most promising candidate proteins in rice tolerance to salinity by applying RNAi approaches and transient expression of candidate genes.

At the end of project, we expect to contribute in increasing rice tolerance to salinity by developing new molecular markers for MAB programme or generating stable transgenic rice of successful RNAi analysis. To reach these objectives, ABRII has enough facilities to grow plants and measure different physiological traits. We also have facilities and expertise to perform 2-DE analysis to identify proteins. However, because of lack of Mass Spectrometry (MS) facilities in Iran, we can not identify proteins or analyse enough metabolome in a high-throughput manner. We think that in collaboration with IPK (Germany), we shall be able to both analyse the samples and train ABRII staff to use MS instrument and analyse data. It will also be possible to use IRRI's facilities and expertise to perform RNAi analysis and train ABRII's staff to apply this very important approach.

**Associated GCP Project G3005.02: Revitalising Marginal Lands: Discovery of Genes for Tolerance of Saline and Phosphorus-Deficient Soils to Enhance and Sustain Productivity(PI: Abdelbagi Ismail)*

101.6 Project No G4007.13 (06): Capacity-building à la carte *2007–Enhancing capacity of ICABIOGRAD in phenotyping and molecular analysis to develop elite rice lines suitable to Indonesian uplands**

- *Duration: Jul 2007–Jul 2009*
- *Budget by year: $39,825 (2007), $39,884 (2008); Total budget: $79,709*

Rice/Blast resistance/Asia

Lead Institute
- ICABIOGRAD, Indonesia (Masdiar Bustamamm)
- Collaborating institutes and scientists
- IRRI (Casiana Vera Cruz)
- RCB/IPB (Utut Widyastuti Suharsono)
- ICABIOGRAD (Kurniawan Rudi Trijatmiko, Wening Enggarini)

As a public research institute involved in Asian Rice Biotechnology Network (ARBN) since 1993, ICABIOGRAD had sent several times its best people to be trained at IRRI, mainly to work on blast resistance in rice. But due to minimal support for research in Indonesia, many of them have left to pursue their careers in nations with more advanced research systems. This brain drain situation has limited the capability of the institute to reach its research target and deliver useful product to poor farmers.

In the past two years, ICABIOGRAD has been involved in two GCP projects working on blast resistance (PI, Rebecca Nelson) and P-deficiency tolerance (PI, Abdelbagi Ismail) in rice. Blast is particularly important for upland sub-ecosystem because the environment favours its proliferation. Upland soils in Indonesia are dominated by highly weathered acid soils, whose phosphorus deficiency is usually a major constraint to crop production. Some useful genes and QTLs have been identified and mapped in these projects. The task remains of incorporating the favourable alleles of these genes and QTLs into an elite upland variety in Indonesia via marker-assisted selection. This task will not be easy to complete through ICABIOGRAD alone due to lack of skills and facilities to do reliable phenotyping and molecular marker analysis. Both phenotypic evaluation and marker-assisted selection of WRxOL5 elite lines for blast resistance and phosphorus deficiency tolerance need to be completed using low-cost marker technology. Training opportunities in advanced research institutes have proven very effective in developing human resources and in reaching targets of research institutes in developing countries. By giving opportunity to get high-quality training for its staff and follow-up research support, ICABIOGRAD will able to complete the research and delivery of GCP products while encouraging its staff to stay and assist in contributing impact to the society in Indonesia.

**Associated GCP Project G3005.08: Targeted discovery of superior disease QTL alleles in the maize and rice genomes (PI: Rebecca Nelson)*

102. Project No G4007.14: Fellowships and travel grants 2007

- *Duration: One year between Jan 2007–Dec 2007 (various start and end dates)*
- *Total budget: $160,000*

Various crops, traits and regions

Lead institute
GCP (Carmen de Vicente)
Collaborators
None

A competitive call for applications for **fellowships** was opened by early December of 2006. The number of applicants for this single annual call was twelve (12), representing 11 countries (Ethiopia, Ivory Coast, China, Benin, Bangladesh, Nigeria, India, Ghana, Philippines, Morocco and Egypt). A total of 5 fellowships were awarded.

As for **Travel Grants** is concerned, a competitive call for travel grants was opened by the end of January 2007.

Unlike previous calls, this one was a single annual call oriented to support hands-on training experiences rather than participation in conferences, seminars, symposiums, etc. A total of 25 applications were received, representing 17 countries (Brazil, Uganda, India, Nigeria, South Africa, Philippines, Tanzania, Iran, Benin, Kenya, Indonesia, Uruguay, Sri Lanka, Egypt, Ghana, Peru and China). 8 Travel Grants were awarded.

SP5 earmarked funds from the Travel Grants programme to support the participation of a number of African scientists in the past Annual Research Meeting, held in Benoni, South Africa, 12 – 16 September 2007. The total number of scientists was 8, representing 7 countries (see table).

In addition, SP5 is supporting the participation of 12 collaborators of GCP rice projects in Asia in the "GCP workshop on product management and delivery in GCP rice research in Asia, Bangkok, Thailand, November 6th and 8th, 2007". The funds to support these collaborators, representing 8 countries, are part of the Travel Grants programme also.

103. Project No G4007.17.02: GCP Project Development Guide–System and implementation

- *Total budget: $7,200*
- *Duration: June 2007–Jan 2008*

Various crops, regions and traits

Lead institute
Consultants (Andreas Idl, Norbert Niederhauser)

Introduction
This paper describes the process to develop a user-friendly version of the web-based Project Delivery Guide (PDG). The final outcome and the approach to establish the application are described in the latter points.

Outcome
At the end of this consultancy a fully functional version of the "Project Delivery Guide" will be handed in. The application includes all necessary features to maintain access and content. In the final version the guide will be integrated in the GCP main webpage.

Methodology
The PDG will be created in short development cycles, each cycle consistent of a development followed by a review and feedback phase. The next cycle than will include the feedback. Due to the distribution of the project members, a first online prototype will be created as a discussion base and feedback will be collected in teleconferences and emails. Moreover the final version will include an online feedback module.

We think that short development cycle gives GCP constant and manageable information to see the progress. Implementations, that do not match user needs, are less probable.

104. Project No G4007.20: Managing the Generation Challenge Programme in a post-International Treaty world: A proposal for a technical training workshop and related materials

- *Duration: Aug 2007–Jul 2008 with NCE to Dec 2008*
- *Total budget: $34,100*

Various crops, traits and regions

Lead institute
Bioversity (Michael Halewood)
Collaborating institutes and scientists

- Bioversity (Gerald Moore)
- CAS–IP, Bioversity (Victoria Henson-Apollonio)
- GCP (Carmen de Vicente)
- EMBRAPA (Maria José Sampaio)
- IRRI (Ruaraidh Sackville-Hamilton)

The multilateral system of access and benefit sharing (MLS), created by the International Treaty on Plant Genetic Resources for Food and Agriculture (known hereafter as the Treaty), could only become operational after the Governing Body of the Treaty adopted the Standard Material Transfer Agreement in June 2006. In the time since June 2006, there has been considerable evidence that researchers working with plant genetic resources for food and agriculture require assistance in coming to terms with the new 'rules of the game'. In this context, it would be appropriate to hold a workshop to document and reflect upon experiences within the Generation Challenge Programme (GCP) concerning the terms and conditions (and related legal instruments) of transfers of materials for use in research and final GCP research products. It would also be useful to raise awareness among research partners in the GCP about the Treaty and the implications of the creation of the MLS, and how to address exchanges of materials that are not covered by the MLS. To make the most out of the documentation and training activities, we propose developing guidelines for best practices for GCP project partners, and finalisation of the training materials (and reference materials used) for future reference by the trainees, and other GCP research partners who could not attend the workshop. Finally, through the workshop, it is anticipated that useful connections will be formed between expert resource people and the GCP research partners, with the result that the latter would contact the former on an as needs basis in

105. Project No G4007.21: Genotyping Support Services 2007

- *Duration: Aug 2007–Feb 2009*
- *Budget by year: $300,000 (2007), $100,000 (2008); Total budget: $400,000*

Lead institute
GCP (Humberto Gómez Paniagua)
Collaborating institutes and scientists
GCP (Carmen de Vicente and Philippe Monneveux)

The Generation Challenge Programme (GCP) researches the genetic diversity of germplasm using genomics to discover the genes and alleles controlling the expression of complex agronomic traits. The results are useful to the biological sciences in general but especially for crop breeding, by allowing a better understanding of traits controlling plant performance. These also allow breeders to create varieties faster and better suited to the crop users' needs. The GCP strives to transfer this new knowledge to crop scientists in the developing countries.

The Genotyping Support Services (GSS) facilitates the access of national agricultural research systems (NARS) in the South to technologies the GCP is developing, bridging the gap between research in advanced facilities and that in the fields of developing countries. With these services, the GCP offers cost-efficient genotyping services worldwide, access to data and support and training in statistics for proper interpretation of genotype and phenotype data. The aim is to raise the researchers' productivity by building their capacity.

In the 2006–7 phase, the GSS (*Genotyping Support Service*) contacted 22 NARS working in cassava, coconut, groundnut, *Musa* and potato. Out of them, eight applications were selected to benefit from the service and test the concept. In this phase, supporting legal documents were designed, consistent with the Consortium Agreement, different options of service providers were tested, in every step different problems or difficulties were faced and solutions devised.

In the 2007–8 phase, the GSS will offer genotyping services to all the mandate crops of the GCP by launching a call for proposals, applying the earned experience of the trial phase. Also, the GSS will start preparing to offer other GCP products and services, as they become available.

106. Project No G4007.22: GCP Workflow and Repository System

- *Duration: Aug 2007–Dec 2008*
- *Budget by year:*
  - Phase I (led by CIAT): ***$20,000***
  - Phase II: (led by Cropster and one consultant): ***$96,980***
  - Total budget: ***$116,980***

Lead institutes
CIAT (Norbert Niederhauser) – Phase I
Cropster GmbH (Norbert Niederhauser) –Phase II
Collaborating institutes and scientists

- Cropster GmbH (Andreas Idl)
- CIAT (Florian Breitwieser)
- Consultant (Sandra Insignares)

Phase I
Until now GCP projects had to be organised by email and phone meetings making processes time consuming. Moreover different applications exist, that cover various parts of the daily routines. There is Axapta for financial purposes, the contact base for contact management and server share repository, where data should be stored centrally. These parts should be connected together. The main aim of the new system is to combine these applications to a single GCP intranet platform, which allows better control of the stored information and reduces management work.

- A single place to store organisation data
- Greater possibilities to backup data
- Worldwide accessible through Internet technology
- Integrate existing technologies
- Manage data with permission management
- Central reporting
- Project management and overview
- Define tasks through milestones in projects
- Get task reminder notification

Phase II
After finishing phase 1 of the workflow and repository system the CGP management team decided to expand and upgrade WF 1's functions in terms of user integration. The new system should be able to:

- Integrate external project collaborators and executors (e.g. PI's) in a more direct manner
- Provide more functionality for collaborative work e.g. online integration of review panels
- Provide traceability for project proposal review process
- Integrate different GCP activities in one place
- Integrate and interchange information about projects amongst different SP

107. Project No G4008.23: Statistical rules for defining characteristic genotype and marker sets

- *Duration: Jan 2008–Dec 2008*
- *Total budget: $30,000*

Various crops, trait and regions

Lead institute
WUR (Fred van Eeuwijk)

Large sets of genotypic score tables for molecular markers have been and are constructed for a wide series of crops within various activities within GCP–SP1. This marker information forms the basis for population genetic studies on domestication, drift, selection, linkage disequilibrium, etc. A next step will consist in using this genotypic information for association mapping purposes.

For easy reference in future population genetic and mapping studies, it is valuable to define crop specific patterns of molecular marker variation. The main objective of this project is to investigate various strategies to arrive at small but informative sets of genotypes and markers. Such reference sets of genotypes and markers should regenerate large part of the relevant genetic variation with relatively little effort. The reference information should be used to connect different population genetic and quantitative genetic studies (including association studies) within the same crop. The choice of the genotypic and marker reference sets should be driven by both statistical and molecular genetic principles. It is obvious that statistical dimension reduction techniques provide guidelines for choosing genotypes and markers. However, for easy use in future, also molecular genetic requirements should be involved in the decision criteria, especially those that determine the ease with which markers can be generated and the quality with which they can be read.

The project asks to support a NARS scientist for a period of 9 months at the department of applied statistics of Wageningen UR. The NARS scientist will there develop rules and protocols for the construction of reference sets of genotypes and markers under supervision of various statisticians and molecular geneticists. The output of the project will consist in 1) rules and protocols to be used in general for all GCP crops and 2) defined reference sets for a number of crops.

108. Project No G4008.24: From attractiveness to feasibility: A strategic assessment of the capacity to develop and adopt GCP technologies

- *Duration: Jan 2008–Dec 2009*
- *Budget by year: $130,643 (2008), $130,469 (2009); Total budget: $261,112*

Various crops, traits and regions

Lead institute
IFPRI (Stanley Wood)
Collaborating institutes and scientists

- CIAT (Glenn Hyman, Scientist)
- Consultant (Carlos Tovar)
- GCP (Carmen de Vicente)
- Virginia Tech, USA (George Norton)
- IFPRI (Nienke Beintema)

Prior studies have identified focus areas for GCP activities based on their potential contribution to the humanitarian and technical goals of GCP. These studies, however, identified priority crops and farming systems for GCP efforts *assuming* that broadly-targeted GCP technologies will be successfully adapted by local breeding efforts and will then be adopted by local smallholders. These are both strong assumptions. It is critical, therefore, that GCP's initial target/focus areas be subjected to a second phase evaluation that makes provision for the likely capacity of local institutions and farmers to realise the projected potential for GCP impact. We can describe this second phase activity as assessing the "feasibility" of achieving desired outcomes in the high-priority (most attractive) focus areas. It is vital to consider attractiveness and feasibility together since in some areas where the potential benefits may be very attractive, the feasibility of achieving them might be quite low; whereas in other cases (e.g., different countries, farming systems, crops, and targeted production constraints) the overall scale of potential benefits may be smaller, but the feasibility of achieving those results might be much higher (and/or may be achieved more quickly). Thus, overall, it is the *combination*, of both attractiveness and feasibility that must be taken into account when fine-tuning the design of a GCP investment portfolio and the targeting of GCP research priorities.

109. Project No G4008.25: Advanced course on 'Applied statistical methods in plant genomics', Zaragoza, 18–29 February 2008

- *Duration: Jan 2008–Dec 2008*
- *Total budget: $25,000*

Various crops, traits and regions

Lead institution
IAMZ–CIHEAM (Manuela Cereza)
Collaborating institutions
WUR (Fred van Eeuwijk)

An advanced course on 'Applied statistical methods in plant genomics' will be conducted in Zaragoza, 18–29 February 2008. The targeted audience consists of plant breeders that want to update their statistical skills to be able to take full benefit of new genomic tools that have been developed over the last decennium. For researchers from NARS within the GCP these genomic tools are gradually becoming available too. For these researchers there is a need to not only update their molecular genetic skills, but also their statistical skills. This proposal is to benefit a limited number of such researchers working in collaboration or close to the GCP goals by attending the course. The project will cover grants for travel, room and board.

110. Project No G4008.26: A cassava breeding Community of Practice in Africa for accelerated production and dissemination of farmer-preferred cassava varieties resistant to pests and diseases

- *Duration: Jan 2008–Dec 2010*
- *Budget by year: $201,900 (2008), $216,975 (2009), $232,650 (2010); Total budget: $651,525*

Cassava/Disease and pest resistance/Africa

Lead institute
CIAT/NRCRI (Emmanuel Okogbenin/Chiedozie Egesi)
Collaborating institutes and scientists

- NRCRI (Chiedozie Egesi)
- CRI (Elizabeth Okai)
- NaCRRI (Yona Baguma)
- ARI–Naliendele, Tanzania (Geoffrey Mkamilo)
- IITA (Alfred Dixon, Melaku Gedil)
- CIAT (Martin Fregene)

Cassava has become a major staple and food security crop in Africa. However, there is an urgent need for improved varieties to stop the rapid spread of pest and diseases, especially the cassava brown streak disease (CBSD) and the cassava mosaic disease (CMD), two resurgent crop diseases that have already caused low-grade famine in parts of Africa. Although National Agricultural Research Systems (NARs) are best suited to breed cassava for local needs, NARs in the past limited their activities mainly to testing and selection of improved germplasm, but more recently NARs breeders have began formal cassava breeding. Several donor funded projects, including a Generation Challenge Programme (GCP) competitive grant to CIAT, Brazil, and 3 African countries – Ghana, Nigeria, and Uganda, and a Rockefeller foundation grant to Tanzania, IITA, and CIAT, are now conducting field-based, Marker Assisted Selection (MAS), and participatory cassava breeding. There is a need to build synergies between these 4 NARS breeding programmes , IITA, and CIAT through exchange of experience and improved germplasm to ensure rapid production of improved varieties and delivery to farmers. We propose setting up of a community of practice (CoP) involving cassava breeders in the 4 target countries that will permit a freeflow of experiences and information on breeding methods, best field practices, and improved varieties amongst the 4 countries. A primary activity of the CoP will be integration of MAS with field-based breeding and pre-breeding strategies. The project will also provide training in MAS as well as field-based and participatory plant breeding for current and a new generation of breeders. MAS is a specialised form of cassava breeding complementary to traditional field-based breeding. The CoP will therefore create and maintain close links with International Institute Tropical Agriculture (IITA) and CIAT, and NARs breeding programmes via sharing of germplasm/information and training that are outcomes of this project. In addition, linkages will be built with primary, secondary, and tertiary users of improved cassava varieties to ensure prompt uptake of improved varieties. Lastly, the CoP will be proactive in developing linkages with existing cassava breeding networks, International breeding programmes, and related GCP projects, including the genotyping support services (GSS), to bring the best expertise and experiences to bear on the breeding goals.

111. Project No G4008.27: Phenotyping course for drought related traits across tropical legumes–Concepts and practices

- *Duration: Jan 2008–Dec 2008*
- *Budget by year: $118,776 (2008); Total budget: $118,776*

Various crops/Drought resistance/Africa

Lead institute

ICRISAT (Vincent Vadez)

Collaborating institutes and scientists

- ICRISAT (Fran Bidinger; L Krishnamurthy, Junichi Kashiwagi, Kesava Rao)
- Agropolis–INRA (Francois Tardieu)
- UAS–Bangalore (MS Sheshshayee)
- UoC–Riverside (Jeff Ehlers)
- CIAT (IN Rao)
- IITA (Satoru Muranaka)

Drought is the most important abiotic factor contributing to yield losses in the semi-arid tropics, particularly in sub-Saharan Africa. Legumes are an important part of the diet of rural populations because they are rich in protein. They are also very important for fertility restoration of infertile lands, and usually fetch good market prices. Increasing their drought tolerance is a must and the use of modern techniques to more efficiently breed drought tolerant cultivars would greatly help. Traits putatively involved in the tolerance to drought are difficult to deal with because the environment in which they are measured is variable, and their value for the crop adaptation to a given environment varies accordingly. So both a good understanding and characterisation of the environment, and established protocols are needed to measure traits with sufficient precision to have a value in research and breeding. Moreover, few traits are known to play a role in drought adaptation, and some are common across crops. This workshop will provide participants: (i) a practical hands-on training in the measurement of drought-related traits and data management, (ii) the key principles about phenotyping, and (iii) opportunities for cross-legume (groundnut, cowpea, bean and chickpea) discussions on key traits involved in their adaptation to drought. The workshop will be organised in two overlapping phases: the first to train technicians and scientists using real experiments and focused on a few key traits; the second involving scientists to cover the conceptual aspects related to the measured traits, to analyse and compute data generated during the course, and to discuss key drought-related traits that matter across crops. We expect from this course to have a group of scientists and technicians well trained to carry out phenotyping at their location, equipped with the conceptual background and necessary knowledge to produce precise and rigorous drought phenotyping data/information.

112. Project No G4008.35: Toolbox of available molecular markers useful for marker assisted selection in GCP crops

- *Duration: March 2008–March 2010*
- *Budget by year: $31,000 (2008), $10,000 (2009); Total budget: $41,000*

Various crops, traits and regions

Lead institute

Veerle Van Damme, Consultant

Collaborating institutes and scientists

GCP (Humberto Gómez Paniagua, M Carmen de Vicente)

Developing countries harbor the majority of the plant genetic resources for food and agriculture. These genetic resources contain numerous genes and alleles possibly useful to overcome most of the challenges of modern agriculture. Genomics has helped in identifying, targeting and deploying useful genes. Molecular markers greatly facilitate the selection of traits that are often difficult and time-consuming to detect based on phenotype. As such, marker assisted selection (MAS) enables speeding up the incorporation of these valuable traits.

Agricultural researchers and plant breeders, in particular in developing countries, face difficulties concerning access to up to date scientific information on useful molecular markers, as the latest discoveries are often scattered in numerous, expensive peer-reviewed journals or in databases of unknown existence to many. If access to information is not a problem, the avalanche of information can be one, as the information offered through digital resources is not always reliable, can be overwhelming and does not provide guidance for its appropriate use.

This project deals with the development of a toolbox providing free and easy access to information of all publicly available molecular markers ready for use for marker assisted selection in 19 food security crops. The activity will compile information available in internet sources, public databases, papers and that gathered through communications with molecular crop breeding experts. Results will be made available via Internet as a global public good and its features described in a peer-reviewed publication. By sharing the latest advances in molecular plant breeding, the toolbox is an important step into supporting modern agriculture for the benefit of the poor in developing countries.

113. Project No G4008.36: Getting the focus right: Food crops and smallholder constraints

- *Duration: Jan 2008–Dec 2009*
- *Budget by year: $115,800 (2008), $30,000 (2009); Total budget: $145, 800*

Various crops, traits and regions

Lead institute
CIMMYT (John Dixon)
Collaborating institutes and scientists
Consultants (Stephen Waddington, Li Xiaoyun)

Drought has been identified as a major priority for food crop improvement programmes in international agricultural research. However, it is generally accepted that a variety of other "secondary" constraints limit productivity in good seasons, as well as in drought years. The well known CABI data base contains comprehensive but rather general information on losses and distribution. However, few of these studies provide sufficient contextual information to extrapolate the results across zones, seasons and years.

In recognition of the complexity of factors which affect the improvement of food crop yields and productivity in under smallholder conditions different farming systems throughout the developing world, the relative importance of abiotic, biotic, crop management and socioeconomic constraints will be assessed in physical and economic terms.

In these circumstances, this proposed study will organise the systematic tapping of the tacit knowledge of experienced research and development practitioners to provide valuable information on the relative importance of different production constraints and traits. The results of this study can be a checklist and guide to those involved in food crop breeding and crop systems research and development by prioritising key traits for the improvement in each of the systems.

114. Project No G4008.37: PhD in plant breeding training at the West Africa Centre for Crop Improvement

- *Duration: March 2008–Feb 2014*
- *Budget by year: $78,750 (2008), $140,560 (2009), $122,878 (2010), $122,005 (2011), $131,690 (2011), $71,170 (2012); Total budget: $667,054*

Various crops, traits and regions

Lead institute
UoGh (EricY Danquah)
Collaborating institutes and scientists
- UoGh (S Kwame Offei)
- CU (Vern Gracen)

It has long been recognised that capacities in plant breeding, including both conventional and modern technologies, in most developing countries are neither sufficient nor properly integrated to fully capture the benefits of the plant genetic resources that are conserved. Today, sub-Saharan Africa remains the only region that may not meet the millennium development goal of eradicating extreme poverty and hunger by

2015. New high-yielding varieties of staple crops with tolerance to biotic and abiotic stresses can help provide food security for increasing populations in the sub-Saharan Africa. A critical mass of a new generation of plant breeders with knowledge in both traditional field based selection methods and emerging laboratory based tools and techniques is needed to develop and provide the necessary high yielding varieties to farmers.

The University of Ghana has received a project support grant of $5.78 from the Alliance for a Green Revolution in Africa to establish a West Africa Centre for Crop Improvement (WACCI). WACCI, a collaboration between the University of Ghana and Cornell University, started operating in the University of Ghana in June 2007 as an autonomous institution in the College of Agriculture and Consumer Sciences. WACCI is dedicated to the training of plant breeders with skills in genetic improvement of the staple crops of the west and central Africa sub-region. Plant breeding is an integrative science that combines the knowledge, information and expertise from a range of disciplines to produce scientists with the capacity to undertake research for germplasm enhancement and development of improved cultivars of the staple crops. The first cohort of eight students enrolled in February 2008. They will undertake two years of course work in the University of Ghana and three years of field research in their local research institutions. WACCI intends to increase its enrollment to ten students a year and to accommodate two additional students in 2009 and 2010 who would be sponsored by Generation Challenge.09.

115. Project No G4008.38: Fellowships and travel grants 2008

- *Duration: Between Jan 2008–Dec 2008 (various end dates)*
- *Total budget: $160,000*

Various crops, traits and regions

Lead institute
GCP (Carmen de Vicente)
Collaborating institutes and scientists
None

Eight **Fellowships** are offered. The maximum award per fellow is up to US$25,000 (travel, living expenses, accommodation, laboratory consumables, and conference participation).

The Fellowship Programme started in 2005 and was based on a call for proposals with the following principles:

1) Proposals should deal with one of the GCP crops
2) They must be linked with ongoing research supported by the GCP, either by competitive or commissioned grants.
3) The proposal should present evidence that the fellowship will be oriented towards training of the candidate and improving capacity at the home institution, *rather than to provide extra funding for ongoing projects* (*).
4) The majority of the proposed research must be done at one of the GCP Consortium centers, or participating institutions in a GCP supported research project.

Invited applications should come from crop science researchers from developing country research institutions (National Agricultural Research Systems at large). Applicants should hold at least a Master of Science degree (MSc), or equivalent, in a relevant subject area.

Applicants should also demonstrate they are engaged in a related ongoing research activity in their home country, and they are expected to return to their home institution and contribute to its research and education programmes.

Priority is given to scientists from National Agricultural Research Systems already involved in GCP research projects.

(*) For 2008, a small twist has been added. Principal Investigators of ongoing GCP projects have been contacted with the request to propose a research subject, already part of the GCP project or complementary to it, for which they are willing to host a fellow for a training experience. If not sufficient subjects are received from PI by November 15th 2007, the Call for Applications to the Fellowship Programme will be opened targeting a selection of research subjects made by the Management Team. The Call will include a description of research subjects, the minimum desired qualifications of the candidate(s), the proposed duration of the fellowship (depending on each subject), among other details. As customary with past calls, an application form plus other supporting documents will be required for the selection of candidates. The applicants will have to present evidence that their ongoing work is related to the subject of choice and that the learning will be used to benefit his research. Once the selection of winners is made, fellows will be requested to prepare a work plan in collaboration with the PI.

The **Travel Grant Programme** is meant to foster linkages within current GCP projects to advance research while providing training opportunities for developing country scientists.

Travel grants and participation in conferences offer new occasions to start collaboration or trigger an interest on a GCP-related research project. As a consequence, the community of skilled and knowledgeable collaborators of the GCP in developing countries increases.
Three types of grants are offered:

Hands-on training opportunities
The grant may be requested to visit a GCP Consortium Institution, a collaborating institution, or an independent advanced research institution to have a **hands-on training** experience related to concepts and/or techniques useful or necessary for the advancement of the GCP research. <u>It is not oriented to support conference participation</u>. The applicant should belong to an institution from a developing country (NARS or Academia) that is either a member of the GCP Consortium or is working in collaboration with a GCP Consortium Institution.

Eight grants are available and the maximum grant award is 5,000 USD, which is intended to cover travel, accommodation, living expenses, and laboratory consumables, if needed.

Participation in GCP organised workshops
The GCP may take advantage of conferences or scientific events to organise workshops for specific purposes, mainly to bring together researchers working in similar subjects, in similar crops or in the same region. The purpose is to promote linkages among researchers at all levels to disseminate the benefits of the science being conducted and simultaneously enhance the number of potential users of GCP products.

Participation in the GCP Annual Research Meeting
These grants are meant to invite selected researchers from National Programmes working in the region where the ARM takes place. Participants should be already engaged with the GCP and may be requested to present results of the research being conducted in the home institution.

116. Project No G4008.39: Capacity-building *à la carte* 2008

- *Duration: April 2008–April 2010*
- *Budget by year: $116,844 (2008), $78,697 (2009); Total budget: $195,541*

Various crops, traits and regions

Lead institute
GCP (Carmen de Vicente)
Collaborating institutes and scientists
None

This project relates to a new capacity building concept, *à la Carte*, that seeks to identify and provide tailored capacity building to a select group of teams of applied researchers at developing country research programmes who will benefit significantly from short-term, personalised training and support. For each team selected to participate in this programme, a customised plan is proposed comprised of training events in the form of formal training at academic institutions or at events organised by the GCP, mini-grants for small equipment, hands-on research opportunities in advanced research institutions, and the *in-situ* assistance of technical experts.

This scheme provides opportunities for researchers to obtain high-quality training and follow-up support, and thereby mobilises a community of well-trained and well-prepared researchers to carry on GCP research.

In practice, the project targets short to medium term support, providing guidance to entice researchers to stay in their countries, hoping they become self-sufficient to attract further support in the long term.

The programme is linked to current GCP research projects and complementary to GCP established activities to strengthen national research institutions.

In 2007, a Call opened with capability to accommodate 10 grants. In the end, six were selected. The plan for 2008 it is to open a Call in December 1st 2007 up to January 31st 2008 aiming again for the selection of 10 winners. The budget though needs to consider that most, if not all, of the grants given in 2007 run for two years.

116.1 Project No G4008.39 (01): Capacity-building à la carte *2008–Enhancing MAS capacity for salt-stress rice breeding in Bangladesh*

- *Duration: April 2008–March 2010*
- *Budget by year: $39,926 (2008), $0 (2009); Total budget: $119,778*

Rice/Salt tolerance/Asia

Lead Institute
BRRI (MA Salam)
Collaborating institutes and scientists

- BRRI (M Alamgir Hossain, M Rafiqul Islam, M Sazzadur Rahman)
- UoD (Zeba I Seraj)
- IRRI (Abdelbagi Ismail, Michael Thomson)

The application of molecular markers to increase the efficiency of breeding for varietal improvement targeted to problem soils is of vital importance for Bangladesh. Gradually increasing salinity levels in the south of Bangladesh is a major concern, particularly because it affects resource poor farmers living in those areas. About one million hectares of land is affected by different levels of salinity in the coastal areas of Bangladesh. BR11 and BRRI dhan28 are two popular varieties cultivated in Bangladesh for rainfed lowland and irrigated ecosystems, respectively, but those are sensitive to salinity. FL378 is an RIL having the Saltol QTL for salinity tolerance but is not well adapted to Bangladesh conditions. To introgress Saltol from FL378 into BR11 and BRRI dhan28, we made backcrosses using BR11 and BRRI dhan28 with FL378. Marker-assisted backcrossing activities are being pursued through a competitive (Project 2) project which is now coming to an end, and a commissioned GCP project just started with collaboration of IRRI and Dhaka University: population development and salinity screening are done at BRRI and molecular selection is being performed at Dhaka University. BRRI has good facilities for population development and phenotyping for salinity tolerance but only partial facilities for molecular analysis and application of MAS. At the same time, BRRI has experienced scientists trained in molecular marker techniques at IRRI, but due to the lack of adequate facilities they cannot contribute their expertise in the current GCP activities. Strengthening BRRI molecular research facilities through acquiring the additional equipments that are currently missing (PCR machine, electrophoresis unit with power pack, centrifuge and electronic pipette) will help equip the laboratory of BRRI to undertake an effective MAB system and deliver the outputs of the ongoing GCP projects more efficiently and, in the long run it will contribute substantially to enhance the capacity of BRRI to incorporate marker assisted breeding in our current breeding programmes using QTLs of agronomic importance. This current capacity building support grant therefore aims to equip the BRRI laboratory for DNA marker technology and to support scientific exchanges between BRRI, DU and IRRI for further training and technical backstopping to support and complement the ongoing GCP funded projects.

116.2 Project No G4008.39 (02): Capacity-building à la carte *2008*–Improving capacity for phenotyping for abiotic and biotic stress in Burkina Faso

- *Duration: April 2008–March 2010*
- *Budget by year: $36,921 (2008), $ 39,462 (2009); Total budget: $76,383*

Cowpea/Various traits/Africa

Lead institute
INERA–Burkina Faso (Issa Drabo)
Collaborating institutes and scientists

- UoC–R (Jeffrey Ehlers,Timothy Close, Philip Roberts)
- IITA (Din-Jong Kim, Satoru Muranaka,Ousmane Boukar)

Cowpea is a major grain and fodder crop in Burkina Faso and one of the few crops adapted to the poor soils, low rainfall and high temperatures found in most of the country. Despite its rustiticity, productivity is decreasing due to drought spells and the pressure from pests. With the recent funding of a large GCP project targeting development of improved genomic resources in tropical legumes including cowpea with emphasis on drought tolerance, it is important that capacity exists to properly phenotype germplasm and genetic populations for drought tolerance.Therefore to meet the goals of the TL1 project and better characterise the 500 genotypes for their responses to abiotic stresses (drought and heat) and biotic ones (thrips, nematodes, Fusarium wilt, and bacterial blight), facilities for phenotyping need to be improved. The background of drought research in Burkina Faso is based on multilocation trials and breeding for agronomical traits. Therefore capabilitites need to be strengthened. Precise and accurate phenotyping will be needed to take advantage of molecular markers being identified under the TL-1 project. Equipment to precisely link the plants physiololical and agronomical responses to water available in the soil is needed.

Objectives

1. Strengthen capacity for drought phenotyping
2. Strengthen capacity for pest control

116.3 Project No G4008.39 (03): Capacity-building à la carte *2008–Improving capacity for phenotyping for abiotic and biotic stress in Senegal*

- *Duration: April 2008–March 2010*
- *Budget by year: $39,997(2008), $39,235 (2009); Total budget: $79,232*

Cowpea/Various traits/Africa

Lead institute
ISRA (Ndiaga Cisse)
Team members
UoC–Riverside (Jeffrey Ehlers)

Cowpea is a major grain and fodder crop in Burkina Faso and one of the few crops adapted to the poor soils, low rainfall and high temperatures found in most of the country. Despite its rustiticity, productivity is decreasing due to drought spells and the pressure from pests. With the recent funding of a large GCP project targeting development of improved genomic resources in tropical legumes including cowpea with emphasis on drought tolerance, it is important that capacity exists to properly phenotype germplasm and genetic populations for drought tolerance.Therefore to meet the goals of the TL1 project and better characterise the 500 genotypes for their responses to abiotic stresses (drought and heat) and biotic ones (thrips, nematodes, Fusarium wilt, and bacterial blight), facilities for phenotyping need to be improved. The background of drought research in Burkina Faso is based on multilocation trials and breeding for agronomical traits. Therefore capabilitites need to be strengthened. Precise and accurate phenotyping will be needed to take advantage of molecular markers being identified under the TLI project. Equipment to precisely link the plants physiololical and agronomical responses to water available in the soil is needed.

Objectives
1. Strengthen capacity for drought phenotyping
2. Strengthen capacity for pest control

117. Project No G4008.40: Workshop on 'Reference sets of food crop germplasm for international collaboration'

- *Duration: Jan 2008–Dec 2008*
- *Total budget: $120,000*

Various crops, traits and regions

Lead institute
Agropolis–CIRAD (MC de Vicente and JC Glaszmann)
Collaborating institutes
- SGRP
- Global Crop Diversity Trust
- GIPB

Access to genetic diversity available in large crop germplasm collections requires identification of representative samples with smaller size to make them suitable for different surveys: screening of traits, evaluation of phenotypic diversity, evaluation of combining ability, assessment of molecular diversity, etc. Moreover, integrating diverse types of characterisation on the same materials makes it possible to assess correlations among traits and investigate gene effects such as epistasis and pleiotropy. Passport data enable selecting based on eco-geographic information; molecular markers offer means to further refine assessment of relatedness and to reduce sample size. Use of standardised methods yields data that can be compared across materials, laboratories and time, providing a durable momentum to enrich global understanding and representativeness.

The first phase of the GCP has yielded massive data sets featuring SSR diversity (12 to 50 loci) among large germplasm samples (300 to 3000 accessions). This has served for identifying reference samples of 50 to 500 accessions. These have been further handled as genetic stocks and data have been ascertained for a subset of high quality SSR markers.

Altogether this led to a major GCP product: germplasm reference samples with validated data of reference markers, accessible as a global public good in a robust form. It is hoped that these samples will be widely shared and used, so that new data can be integrated in order to derive biological understanding useful for germplasm diversity management and use.

This project consists in organising and holding a workshop where all these steps and aspects are described and discussed, as well as the perspectives and the mode of organisation that is necessary for taking full advantage of the initiative. This will be an opportunity for coordination among various players engaged in germplasm management in international programmes. It will take place in Montpellier, France, on November 17–21, 2008.

118. Project No G4008.43: Improve cowpea productivity for marginal environments in Mozambique

- *Duration: Jul 2008–Jun 2010*
- *Budget by year: $34,284 (2008), $34,308 (2009); Total budget: $68,592*

Lead institute
UEM (Rogério Chiulele)
Collaborating institutes and scientists
UoC–Riverside (Jeff Ehlers, Timothy Close, Philip Roberts)

This proposal has three objectives, which will contribute to capacity building. The objective 1 will offer opportunity to build capacity in drought tolerance screening through conducting drought trials and interacting with other groups doing the same type of trials. This will also offer training in analysing data for genotype by environment interaction and presentation of results. Apart from the capacity building this objective will provide baseline information on drought tolerance for early and medium cycle cowpea varieties and assess the importance of genotype x environment interactions for grain yield under drought in Mozambique. The objective 2 will provide experience in larger-scale germplasm screening for drought tolerance by assessing the genetic variability for drought tolerance of a set of 300 Mozambican cowpea landrace accessions. The objective 3 will provide experience on how to design and implement an MAS-based programme, in close collaboration with mentors at UoC–Riverside. This objective will also enable to develop breeding populations suitable for application of marker-assisted selection (MAS) and marker-assisted recurrent selection (MARS) using SNP-based markers developed under the associated GCP Tropical Legume 1 (GCP-TL I) project. In Objective 1, thirty early maturing and thirty medium maturing cowpea varieties will be compared for grain yield under terminal drought conditions using late plantings at two drought-prone sites in Mozambique during the main growing season and in one trial under irrigation during the off-season (dry-season). This will provide baseline drought tolerance information for a wide range of cowpea genotypes in Mozambique and will allow identification of drought tolerant and susceptible 'checks' for future drought studies. By comparing results from identical trials being conducted in West Africa by an associated GCP project "Improving Drought Tolerance Phenotyping in Cowpea" of the SP3, it will be possible to estimate genotype x environment interactions for grain yield under drought across a wide range on conditions, including the degree of correlation between the results of off-season controlled environment screening and results from main-season African growing environments. The effectiveness of a new root screening protocol developed for evaluating drought tolerance and rooting characteristics in common bean (Lynch, 2007) will be evaluated in the Objective 1 trials to determine associations between root ratings and grain yield under drought in cowpea. In Objective 2, 300 landrace accessions from Mozambique will be assessed for tolerance to drought using screening protocols developed for the GCPTL I project and the rapid root screening assay (Lynch, 2007). This will complement assessments of other sets of cowpea germplasm being assessed in the GCP-TL I and ICRISAT Tropical Legume II projects by including unique germplasm not being evaluated in these other projects. In Objective 3, ten breeding populations appropriate for Mozambique and for marker-assisted recurrent selection using SNPbased and SSR markers developed under the GCP-TL I project; targeted training will be conducted in the application of these markers in MAS/MARS through reciprocal two-week visits by UoC–Riverside investigators to EMU and by Mozambique researchers to UoC–Riverside. Overall, the funding will offer opportunities for capacity building on phenotyping for drought tolerance, design and implementation of MAS-based programme. This will also generate useful information on drought tolerance and opportunities for using marker assisted selection in Mozambique.

119. Project No G4008.44: GCP Learning Materials

- *Duration: Jan 2008–Dec 2008*
- *Total budget: $15,000*

Lead institute
GCP (Carmen de Vicente)

GCP learning materials are derived from workshops and/or commissioned at Programme level by GCP's Subprogramme 5, in close collaboration with the technical Subprogrammes. The learning materials cover topics of contemporary relevance to GCP's work and mission, and are offered for free public use. We would however appreciate acknowledgement of the CGIAR Generation Challenge Programme whenever you use or adapt these materials, and we would also appreciate hearing from you on how you have used the material (please send an email to c.devicente@cgiar.org)

You are warmly invited to freely use and/or print any of these materials for educational or other non-commercial purposes without prior permission, provided due credit is attributed.
The materials for the three courses below are accessible via GCP's Capacity-building corner website (http://www.generationcp.org/sp5/) and are also available in CD format. If you would like to receive a copy of the CDs by mail, please contact the GCP Communications Assistant (info@generationcp.org). Another four sets of learning materials are under preparation.

1. Genetic resource policies course (http://www.generationcp.org/distantpolicies/)
A distant learning module for scientists, covering genetic resource policies and implications on freedom to operate. This course material was developed in collaboration with Wageningen University and Research Centre (WUR).

2. The McClintock crop bioinformatics course (http://mcclintock.generationcp.org/)
This self-study introductory online course targets scientists with a reasonable background in germplasm, biology and genetics, and their application in plant and agricultural sciences. Named in honour of Nobel prize winning crop geneticist, Barbara McClintock, this course is a joint project between IRRI and the CGIAR Generation Challenge Programme, designed to demonstrate how basic bioinformatics tools, techniques and resources can help molecular biologists, geneticists and other scientists to effectively manage sequencing projects. This course is a 'living resource' and will be continually updated to attune it with the latest developments in the dynamic field of bioninformatics.

3. Genomics and comparative genomics (http://www.generationcp.org/genomics/)
For use by scientists and advanced students with a strong background in biology and genetics as basic class material or self-tutorial. The principal audience includes plant breeders, molecular biologists and other plant scientists on the fringe of—but not fully engaged in—genomics research. A modular approach accommodates the different backgrounds and needs of users of this material, developed jointly by Cornell University's Institute for Genomic Diversity and the CGIAR Generation Challenge Programme

The following learning materials are under preparation:
1. Genetic diversity
2. Marker-assisted selection
3. Phenotyping
4. Association genetics

120. Project No G4008.50: Delivery Plan Remote Learning Modules

- *Duration: Aug 2008–Jul 2009*
- *Budget by year: $189,980 (2008), $ 56,640 (2009); Total budget: $246,620*

Lead institute
CIMS (Laurence Pratt)
Collaborating institutes and scientists
- CU (Stefan Einarson)
- Various GCP grantees and related NARS, to be determined.

GCP has discovered that agricultural research scientists are clear on how their innovations are expected to benefit resource poor farmers. However, they are very unclear of the process and mechanisms by which their innovations actually get to these farmers. The objective of this project is to develop a series of interactive tools to assist scientists involved in GC programmes to develop high quality "Delivery Plans," based on GCP's current DPKits tool.This project will establish a remote learning strategy to guide GCP grantees through the process of internalising the concept of Delivery Plans and its related objectives. A series of interactive training modules will guide grantees through all the steps of delivery plan development. This effort will directly support the development of well-considered, high quality delivery plans at a very great cost reduction when compared to the costs of bringing groups of grantees together for this purpose.

The project team will apply creative pedagogical design, and best practices in distance learning to achieve the goals of this project. The project includes a design phase, production phase, and finally a testing phase to validate its effectiveness.

Projects on NCE into 2008 or beyond

121. Project No G4006.13: Targeting and impact analysis of Generation Challenge Programme (GCP) technologies

- *Duration: Nov 2006–Oct 2007 with NCE to Dec 2008*
- *Budget by year: $149,742 (2006); $0 (2007); Total budget: $149,742*

Lead institute
CIAT (Glenn Hyman)
Collaborating institutes and scientists
- CIAT (Peter Jones, Sam Fujisaka)
- IFPRI (Stan Wood)
- CIMMYT (John Dixon)

The Generation Challenge Programme (GCP) employs cutting edge crop improvement, microbiology and bioinformatics science and technology to improve livelihoods of resource-poor farmers. The programme has identified the need to geographically target GCP products and to assess ex-ante impact of GCP research. This project will work to fill that need by examining GCP research in the context of the distribution and characteristics of farming systems, drought-prone areas and degrees of risk for specific crops, the geographic distribution of the poor, and potential benefits to the poor from agricultural technology.

The project includes four components. First, the spatial distribution of poverty for small areas within GCP priority farming systems will be assessed using a comprehensive poverty database. Second, climatic variability will be modeled at high spatial resolution to determine the severity and type of crop-specific drought. Third, farming systems will be assessed in the context of crop variety adoption and ways that farmer households can escape poverty. Fourth, the project will conduct an ex-ante impact assessment of the benefits of GCP technologies to the resource-poor. These four components will be synthesised into a comprehensive spatial analysis for geographic targeting and impact assessment of GCP.

FOCUS PROJECTS

Current projects

122. Project No G6007: Tropical Legumes I (TLI): Improving tropical legume productivity for marginal environments in sub-Saharan Africa

Lead institutes

Objective 1:	Improve groundnut (*Arachis hypogaea L.*) productivity for marginal environments in sub-Saharan Africa – **D Hoisington, ICRISAT (September 2007–May 2008)**; **V Vadez (effective June 2008)**
Objective 2:	Improve cowpea (*Vigna unguiculata L*) productivity for marginal environments in Africa – **J Ehlers, UoC–Riverside**
Objective 3:	Improve common bean (*Phaseolus vulgaris L.*) productivity for marginal environments in Africa – **M Blair, CIAT**
Objective 4:	Improve chickpea (*Cicer arietinum L.*) productivity for marginal environments in sub-Saharan Africa – **D Hoisington, ICRISAT (September 2007–May 2008)**; Rajeev Varshney (effective June 2008)
Objective 5:	Develop cross-species resources for comparative biology in tropical crop legumes – **D Cook, UoC–Davis**
Objective 6:	Provide training and capacity-building for SSA scientists - **C de Vicente, GCP**

Activity Leaders

Objective 1

- *Duration: May 2007–April 2010; Budget by year: $1,075,446 (2007), $1,014,030 (2008), $948,036 (2009); Total budget: $3,037,512*

Groundnut/Drought and disease resistance/Sub-Saharan Africa

Activity 1 (Explore diversity – linked to SP1): B Ntare, ICRISAT
Activity 2 (Generate genomic resources – linked to SP2): A Paterson, UGA
Activity 3 (Identify marker development [biotic] – linked to SP2): D Bertioli, UCB
Activity 4 (Identify marker development [abiotic] – linked to SP2): V Vadez, ICRISAT
Activity 5 (Improve germplasm development– linked to SP3): E Monyo, ICRISAT

Objective 2

- *Duration: May 2007–April 2010; Budget by year: $928,623 (2007), $544,374 (2008), $479,011(2009); Total budget: $1,952,008*

Cowpea/Drought and disease resistance/ Sub-Saharan Africa

Activity 1 (Explore diversity – linked to SP1): J Ehlers, UoC–Riverside
Activity 2 (Generate genomic resources – linked to SP2): T Close, UoC–Riverside
Activity 3 (Identify marker development [biotic] – linked to SP2): P Roberts, UoC–Riverside
Activity 4 (Identify marker development [abiotic] – linked to SP2): J Ehlers, UoC–Riverside
Activity 5 (Improve germplasm development– linked to SP3): J Ehlers, UoC–Riverside

Objective 3

- *Duration: May 2007–April 2010; Budget by year: $625,384 (2007), $628,009 (2008), $613,934 (2009); Total budget: $1,867,327*

Bean/Drought and disease resistance/ Sub-Saharan Africa

Activity 1 (Explore diversity – linked to SP1): S Beebe, CIAT
Activity 2 (Generate genomic resources – linked to SP2): M Blair, CIAT
Activity 3 (Identify marker development [biotic] – linked to SP2): M Blair, CIAT
Activity 4 (Identify marker development [abiotic] – linked to SP2): S Beebe, CIAT
Activity 5 (Improve germplasm development– linked to SP3): I Rao, CIAT

Objective 4

- *Duration: May 2007–April 2010; Budget by year: $357,348 (2007), $364,800 (2008), $351,978 (2009); Total budget: $1,074,126*

Chickpea/Drought and disease resistance/Sub-Saharan Africa

Activity 1 (Explore diversity – linked to SP1): E Gwata, ICRISAT
Activity 2 (Generate genomic resources – linked to SP2): R Varshney, ICRISAT

Activity 3 (Identify marker development [biotic] – linked to SP2): H Sharma, ICRISAT
Activity 4 (Identify marker development [abiotic] – linked to SP2): J Kashiwagi, ICRISAT
Activity 5 (Improve germplasm development– linked to SP3): P Gaur, ICRISAT

Objective 5

- *Duration: May 2007–April 2010; Budget by year: $256,402 (2007), $295,166 (2008), $316,120 (2009); Total budget: 867,688*

Various crops (legumes)/Drought and disease resistance/Sub-Saharan Africa

Activity 1 (Explore diversity – linked to SP1): D Cook, UoC–Davis
Activity 2 (Generate genomic resources – linked to SP2): D Bertioli, UCB
Activity 3 (Identify marker development [biotic] – linked to SP2): A Paterson, UGA

Objective 6

- *Duration: May 2007–April 2010; Budget by year: $297,200 (2007), $297,200 (2008), $257,200 (2009); Total budget: $851,600*

Various crops (legumes)/Drought and disease resistance/Sub-Saharan Africa

Activity 1 (Explore diversity – linked to SP1): C de Vicente, GCP
Activity 2 (Generate genomic resources – linked to SP2): C de Vicente, GCP

This proposal focuses on improving the productivity of legume crops of high importance to food security and poverty reduction efforts in sub-Saharan Africa. Modern biotechnologies offer great potential for enhancing the efficiency of plant breeding programmes, but sufficient genomic resources are needed to implement modern breeding. This project will develop the key genomic resources that are currently lacking in legumes (including cross-legume molecular markers for comparative genomics), identify molecular markers for traits of importance to resource-poor farmers (biotic stresses and drought tolerance), and implement breeding capacities in sub-Saharan Africa. The long term objective of this project (10–15 years) is to double grain legume productivity in farmers' fields. Doing so will generate an additional income for farmers of $160/h in cowpea, $370/h in groundnuts, and $220/h in bean per crop cycle in the target countries of the project, where average agricultural population per capita income today is around $120 per year

123. GCP/Rockefeller project G4005.69.01 (CB19a/RF–FS022): Developing and disseminating resilient and productive rice varieties for drought-prone environments in India

- *Duration: March 2005–February 2008*
- *Budget by year: $39,530 (2005), $39,955 (2006), $40,515 (2007); Total budget: $120,000*

Rice/Drought tolerance/Asia

Lead institute
IRRI (Arvind Kumar)
Collaborating institutes and scientists

- IRRI (R Serraj, T Paris, S Haefele, R Anitha, G Atlin)
- IGKV (Satish Verulkar)
- CRRI (ON Singh, P Swain)
- CRURRS (PK Sinha, NP Mandal)
- NDUAT (JL Dwivedi)
- UAS–Bangalore (Shailaja Hittalmani)
- TNAU (R Chandrababu, S Robin)
- BAU (BN Singh, K Prasad)
- BF (HE Shashidhar)

Worldwide, approximately 23 million ha of rainfed rice are frequently affected by drought. Much of this area is in India, where 17 million ha of shallow rainfed lowland and upland rice are grown. Drought is particularly frequent in bunded uplands and shallow rainfed lowland fields in many parts of eastern, southern, and western India. Drought also affects production on about 4 million ha in dry irrigated areas dependent on surface irrigation, where, in drought years, river flows and water impounded in ponds, tanks, and reservoirs may be insufficient to supply the crop (Maclean et al 2002). Variation in rice production in South and Southeast Asia is closely related to total annual rainfall, but, even when the total is adequate, shortages at critical periods greatly reduce productivity. Poverty is particularly severe in communities dependent on rainfed rice. In drought years, food consumption is reduced, indebtedness increases, assets are sold, children are withdrawn from school, and household members migrate. Droughts therefore have long-term destabilising effects. Drought risk reduces productivity even in favorable years because farmers avoid investing in inputs when they fear crop loss. Risk-reducing technologies can therefore lead to increased investment and productivity in rainfed systems. Rice cultivars combining improved drought tolerance with responsiveness to favorable conditions and end-use characteristics favored by farmers are among the most promising and deliverable technologies for alleviating poverty in communities dependent on rainfed agriculture in India.

Significant advances have recently been made in understanding drought physiology and genetics, understanding environmental variability in the production environment, developing effective breeding methods, and understanding the factors that drive the adoption of rainfed rice varieties. A community of researchers with expertise in these areas has been developed in drought-affected areas of India as a result of many years of support from the Rockefeller Foundation. The overall thrust of this project is to integrate this community into an effective breeding programme, and to deliver farmer-preferred varieties with improved drought tolerance and high yield potential within 6 years. In addition to delivering improved varieties, the project will develop new knowledge on the relationship between screening methodologies and on-farm performance, and on the plant characteristics affecting the drought response of cultivars in farmers' fields.

124. GCP/Rockefeller project G5005.69.02 (CB19b/RF–FS029): Pathway dissection and candidate gene identification of drought tolerance in rice by a forward genetics approach

- *Duration: March 2005–February 2008*
- *Budget by year: $40,000 (2005), $40,000 (2006), $40,000 (2007); Total budget: $120,000*

Rice/Drought tolerance/Asia

Lead institute
Institute of Crop Sciences, CAAS (Zhi-Kang Li)
Collaborating institutes and scientists
- PeU and YU (Xing-Wang Deng)
- IRRI (Racid Saraj – replacing R Lafitte)

Developing rice cultivars with drought tolerance (DT) has become a major effort in China to reverse the trend of diminishing rice lands resulting from shrinking water resources. To speed up this process, a full understanding of the genetic, physiological, and molecular mechanisms of DT in rice is required. Accumulated evidence indicates that DT of rice is controlled by large numbers of quantitative trait loci (QTLs) in complex genetic networks, which remain largely uncharacterised at both the molecular and whole-plant physiology levels. With the availability of the whole-rice genome sequences and high-throughput genomic technology, we propose to dissect the metabolic/biochemical pathways of DT in rice by systematically building up and validating related genes and pathways for 26 DT QTLs using 68 QTL near-isogenic lines and high-throughput genomic technology. The objectives are (1) to define 13 important rice DT QTLs in < 3 cM genomic regions using overlapping introgression lines and DNA markers, and determine their positional candidate genes; (2) to characterise the genetic networks involving 26 DT QTLs regarding the physiological and/or morphological traits they affect using whole-plant physiology and trait-based phenotyping; (3) to determine the candidate genes, identified by expression analysis, that underlie the 13 target DT QTLs; (4) to determine the functions of 4–8 key DT QTLs; and (5) to determine the biochemical pathways and involved genes related to the genetic networks underlying DT of rice. The proposed project is expected to provide insights into the genetic, physiological, and molecular mechanisms of DT in the model system of rice and validate a forward genetics strategy and applicable approach for pathway dissection and functional genomic studies of complex phenotypes.

125. GCP/Rockefeller project G4005.70 (CB20a & CB 20b/RF–FS091 & RF—FS092): Tapping crop biodiversity for the resource poor in East and Central Africa (ICRISAT and IITA)

ICRISAT (sorghum)
- *Duration: July 2005–June 2008 with NCE to Oct 2008*
- *Budget by year: $97,750 (2005), $40,250 (2006); $0 (2007); Total budget: $138,000*

IITA (cassava)
- *Duration: July 2005–June 2008*
- *Budget by year: $74,750 (2005), $63,250 (2006), $0 (2007); Total budget: $138,000*

Total budget for entire project: $276,000

CB20a--Partners
Lead institute
ICRISAT (Dave Hoisington)
Collaborating institutes and scientists
- SAARI (Johnnie Ebiyau)
- NARI (Amanuel Mahdere)
- EARO (Tesfaye Teferra Tesso)
- KARI (Ben M Kanyenji)
- ARI (Ambosenigwe Mbwaga)
- ARTC (Abdalla Mohammed)
- ISAR (Theophile Ndacyayisenga)
- ISABU (Espérance Habindavyi)
- ICRISAT (Dan Kiambi, Tom Hash)

CB20b—Partners

Lead institute

IITA (Morag Ferguson)

Collaborating institutes and scientists

- INERA–DRC (Mpansu Bidiaka)
- KARI (James Gichuru Gethi)
- FOFIFA DRA, Madagascar (Isabelle Ralimanana)
- IIAM (Mauricio Francisco)
- ISAR (Gashaka Gervis)
- ARI–Naliendele (Geoffrey Mkamilo)
- NAARI (Robert Kawuki)

General objectives

- To assess and characterise genetic resources available within national genebanks, international nurseries and important breeders germplasm for two crops of primary importance, a cereal and a clonally propagated crop
- To design a database with passport data, farmer-knowledge, pedigrees, phenotyping and genotyping data of accessions present in national genebanks, international nurseries and all accessions analysed
- To provide national breeding programmes with the information, skills, tools and resources to rapidly and efficiently select and utilise appropriate new germplasm
- To promote sustainable utilisation of methodologies and results on a regional basis through inclusion on the crop specific regional networks of ASARECA
- To establish the necessary functional networks to ensure rapid and effective flow of outputs from this project and associated international activities, such as the GCP and Harvest Plus CP, through participatory design, development, testing and deployment of new seed-based technologies
- To foster knowledge and skill flows through BECA from the global genomics community that interfaces with the Generation and Harvest Plus Challenge Programmes for the targeted benefit of NARS scientists
- To establish functional relationships between national breeding programmes across the ASARECA region and the BECA hub for technical backstopping and trouble shooting

Specific objectives

- Compile an inventory of major crop germplasm currently available in national collections, international nurseries and breeding programmes across East and Central Africa for sorghum and cassava, together with farmer-knowledge where appropriate
- Conduct phenotypic characterisation of a subset of the national germplasm for each of these crops
- Determine genetic diversity of a subset of national germplasm for each of the these crops
- Compile a database of all accessions including passport data and pedigrees, and phenotyping and genotyping data of all accessions analysed.
- Identify complementarities between regional genetic diversity and the GCP composite crop collections and identify potentially useful germplasm for NARS breeding programmes
- Define regional populations for association mapping studies and identify potential parental genotypes for mapping populations and marker-assisted selection programmes for major biotic and abiotic stresses in the region
- Identify recurrent parents based on diversity analysis (and agronomic performance and market preference data) for use in marker-assisted backcross programmes
- Provide intensive hands-on training in standardised methodologies for phenotyping and genotyping to visiting scientists associated with selected breeding programmes.
- Develop mechanisms for communicating results and knowledge between NARS partners and the GCP and Harvest Plus CP through BECA
- Provide a complement and conduit for the GCP Molecular Breeding Training Programme enabling a wider range of participants from NARS breeding programmes in a number of countries in the region.

126. Project No G4007.05: Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco

- *Duration: Jan 2007–Dec 2008*
- *Budget by year: $100,000 (2007), $100,000 (2008); Total budget: $200,000*

Wheat; barley/Various traits/Africa

Lead institute

INRA–Morocco (Abbad Andaloussi Fouad)

Collaborating institutes and scientists

- INRA–Morocco (Nsarellah Nasserlehaq, Jlibene Mohammed, Lhaloui Saadia, Labhilili Mustapha, Saidi Seddik)
- ICARDA (Sripada M Udupa)
- UdB (Roberto Tuberosa)
- CU (Mark E Sorrells)
- CIMMYT (Susanne Dreisigacker)
- UoMi (J Perry Gustafson)

INRA Morocco and the GCP have agreed to develop a cooperative research project, based on a combination of financial resources, to support research activities aiming at harnessing the products of genomic revolution for better utilisation of plant genetic resources and improving plant breeding efficiency and effectiveness in INRA research programmes. The project proposal aims to enhance the production of wheat and barley in rain-fed farming systems of Morocco, thus offering an effective mode of enhancing the food security and income of local, resource-poor farming families. The proposed project will focus first on bread and durum wheat and barley improvement with emphasis on developing new high- and stable-yielding wheat and barley germplasm with improved quality and tolerance to various stresses. Additionally, the project will exploit new genomics technologies, tools and germplasm developed in other GCP projects.

127. Project No G4007.23: Field evaluation of wheat-barley introgression lines under different water regimes

- *Duration: Dec 2007–Nov 2010*
- *Budget by year: $48,000 (2007), $48,000 (2008), $48,000 (2009); Total budget: $144,000*

Wheat; barley/Drought, salt and Al tolerance/Various regions

Lead institute
ARI–HAS (Márta Molnár-Láng)
Collaborating institutes and scientists

- CIMMYT (Maria Zaharieva)
- CAAS (Ruilian Jing)
- DPSPP–EKC (Sándor Dulai)
- ARI–HAS (Éva Darkó)

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. It is intended to select lines with better drought, salt and Al-tolerance compared to the wheat parent by screening the genetic materials produced from wheat × barley hybrids in Martonvásár.

It is hoped to obtain new results on barley genome mapping which will increase our knowledge on cereal genetics. In this "prebreeding programme" new genetic stocks with valuable agronomic traits can be selected. New valuable translocation lines can be developed from addition lines, carrying useful genes for drought, salt and Al-tolerance. The wheat × barley derivates can be used in several international cooperations for analysing the effect of various barley chromosome segments on useful agronomic traits under different environmental conditions. The best lines could be used in wheat breeding programmes, especially in dry areas or on salty soils or on soils with high Al-content.

128. G4007.24: Seed smoke treatment to favour germination under water stressed conditions

- *Duration: Dec 2007–Nov 2009*
- *Budget by year: $12,000 (2007), $12,000 (2008); Total budget: $24,000*

Various crops, traits and regions

Lead institute
ARI–HAS (Ervin Balazs)
Collaborating institutes and scientists

- ARI–HAS (Vilmos Soos, Angela Juhasz)
- UKZN (Johannes van Staden, Marnie M Light)

As a major environmental selective force, fire influences plant communities in many parts of the world. Reproductive strategies have evolved as adaptation to the various factors generated by and/or associated with fire. This is particularly true for seeds, in which strategies have evolved that respond to both the physical and chemical germination cues that may be associated with fires. Smoke released from burning vegetation contains a chemical signal triggers germination of both fire climax and non-fire climax species also. It is used in horticulture to stimulate seed germination of wildflower species and can break dormancy and improve germination of vegetable crops. The recent identification of the active compound gives a burst to determine the mechanisms of action. Smoke extracts interact with plant hormones in seeds. However, despite these interactions it remains unclear whether smoke acts via hormones in stimulating seed germination. It became increasingly clear that smoke as a germination or growth regulating cue must have evolved as a consequence of fire, as an evolutionary factor. It could be a very old seedling survival. The aims of the project are to investigate the physiological effect and mode, through which the active compound affects seed dormancy and germination, using tools such as differential display and microarray and characterise the genes and regulatory networks involved in smoke action. These findings largely contribute to the understanding of the smoke effect and could be used for the development of molecular based smoke technology. The agricultural aspects of use this naturally available germination cue are recultivation of native plant species and cultivation of plant species important in horticulture and agriculture. The compound may have a potential in weed control and in the sustainable land also.

129. Project No G4008.28: Characterisation of maize diversity in Central Europe

- *Duration: Jan 2008–Dec 2008*
- *Total budget: $18,000*

Maize/Various traits and regions

Lead institute
ABC (Peter P Papp)
Collaborating institutes and scientists

- IA–Tápiószele (Laszló Holly)
- CIMMYT (Marilyn Warburton, now based at USDA–ARS)

Characterisation of the Hungarian germplasm is planned in the context of global germplasm diversity. Collaborations between the Institutes of Hungarian Ministry of Agriculture (Agricultural Biotechnology Center and Institute for Agrobotany) and GCP affiliated Institute (CIMMYT) have been planned to compare the allelic diversity of the Hungarian maize collection with the diversity present in GCP's reference set. The project will use the allelic calls of SSR markers within a set of reference maize lines and populations generated by the GCP to compare with the alleles found within a set of Hungarian inbred lines and populations when these are scored with the same SSR markers. The project also supports the training of a Hungarian scientist on molecular characterisation, who will work at CIMMYT to complete the characterisation during the training period.

130. Project No G4008.29: Characterisation of bean diversity in Central Europe

- *Duration: Jan 2008–Dec 2008*
- *Total budget: $18,000*

Beans/Various traits and regions

Lead institute
ABC (Peter P Papp)
Collaborating institutes and scientists

- IA–Tápiószele (Laszló Holly)
- CIAT (Matthew Blair)

Characterisation of the Hungarian germplasm is planned in the context of global germplasm diversity. Collaborations between the Institutes of Hungarian Ministry of Agriculture (Agricultural Biotechnology Center and Institute for Agrobotany) and GCP affiliated Institute (CIAT) have been planned to compare the allelic diversity of the Hungarian bean collection with the diversity present in GCP's reference set. The project will use the allelic calls of SSR markers within a set of reference bean populations generated by the GCP to compare with the alleles found within a set of Hungarian populations scored with the same SSR markers. The project also supports the training of a Hungarian scientist on molecular characterisation who will work at CIAT to complete the characterisation during the training period.

131. Project No G4008.51: Use of molecular marker and physiological tests to characterise Hungarian rice diversity and new sources of blast resistance

- *Duration: April 2008–October 2008*
- *Budget by year: $13,500 (2008); Total budget: $13,500*

Rice/Blast resistance/Various regions

Lead institute
HAKI (Ibolya Simon-Kiss)
Collaborating institutes and scientists

- Agropolis–CIRAD (Jean Christophe Glaszmann, Claire Billot, Didier Tharreau)
- HAKI (Mihály Jancsó)

Blast resistance is a major issue for rice breeding in Hungary. The young scientist from the Research Institute for Fisheries Aquaculture and Irrigation (HAKI) will learn about the different screening methodologies for blast resistance in a collection of Hungarian rice, and will relate these physiological tests to the genetic diversity of the host (rice) and the pathogen (Magnaporthe grisea). This will provide some background for the introgression of blast resistance traits into rice Hungarian germplasm.

The HAKI has a well-equipped molecular marker laboratory. The objectives for the young scientist of the Institute are i) to become familiar with the marker technologies available for characterising hungarian rice germplasm and Magnaporthe grisea diversity and ii) to become familiar with blast resistance screening. In order to acquire these skills, the student will spend 3 months at CIRAD, hosted by the Genotyping platform (head Dr. C. Billot) and the Biology and Interaction of Plant and Parasite Unit (head Dr. D. Tharreau).

Projects on NCE into 2008 or beyond

132. GCP/Rockefeller project G4005.69.03 (CB19c/RF–028): Innovative and integrated approaches to improve the tolerance of maize to water–limited environments

- *Duration: April 2005–March 2007 with NCE to June 2008*
- *Budget by year: $40,000 (2005), $40,000 (2006); Total budget: $80,000*

Maize/Drought tolerance/Africa and Asia/

Lead institute
CIMMYT (Yunbi Xu)
Collaborating institutes and scientists

- CIMMYT (Carlos Martinez,, Debra J Skinner, Alan F Krivanek and Jonathan H Crouch)
- SAU (Shibin Gao)
- CAAS (Zhuanfang Hao, Shihuang Zhang, Jiankang Wang)

Capacity building has been identified as one of the key issues that limit the translation of marker-assisted selection (MAS) from academic publications to practical applications in plant breeding (Xu and Crouch, Crop Science, in press). The molecular breeding programme in Drought Tolerance Maize for African (DTMA) project supported by Bill and Melinda Gates Foundation and two GCP projects (GCP13-Development of informative DNA markers through association mapping; GCP18 -Development of low-cost gene-based trait assay technologies) have a specific focus on many of the technical constrains identified in the same review. By taking advantages of currently existing collaborations among breeders and other scientists that have been built up through these projects, a molecular breeding community of practice (CoP) will be established, in coordination with AMMANET, for molecular breeding of drought tolerant maize for Africa. The CoP will initially focus on the MAS introgression of relatively simple adaptive traits into drought tolerant germplasm that are necessary complementary traits to ensure market success of new drought tolerant varieties. In subsequent phases the CoP will add traits directly related to drought tolerance. This project will also take advantage of ground work achieved through ADB-funded Asian Maize Biotechnology Network (AMBIONET) and attempt to reinvigorate that initiative in China and India, as a first stage towards the development of a CoP for molecular breeding of drought tolerant maize for Asia. The model and experience that we will gain from this effort will be valuable for translation to other breeding programmes across the world, including Enhancing Maize Productivity in Drought-prone Environments in East and Southeast Asia Project, supported by ADB, through partnership between ADB and CIMMYT.

Two major activities are proposed for the capacity building: molecular breeding workshop in Mexico and training of visiting scientists from developing countries in Asia. This GCP-funded capacity building activity is associated with RF Drought III FS028. Both activities would leverage benefit from on-going GCP maize drought genomics research projects and the DTMA project. Synergies would also be captured through linkage with the GCP Genotyping Services initiative, AMMANET in Africa and AMBIONET in Asia.

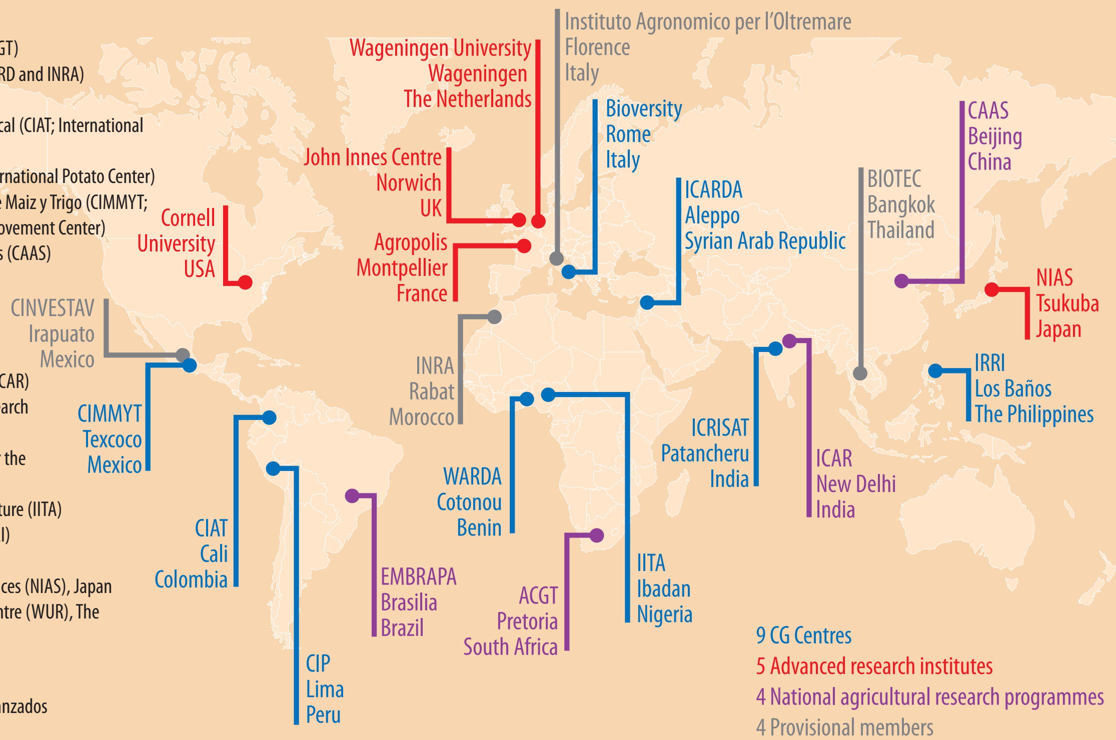
The GCP Consortium

Full members

1. Africa Rice Center (WARDA)
2. African Centre for Gene Technologies (ACGT)
3. Agropolis, France (incorporating CIRAD, IRD and INRA)
4. Bioversity International
5. Centro Internacional de Agricultura Tropical (CIAT; International Center for Tropical Agriculture)
6. Centro Internacional de la Papa (CIP; International Potato Center)
7. Centro Internacional de Mejoramiento de Maiz y Trigo (CIMMYT; The International Maize and Wheat Improvement Center)
8. Chinese Academy of Agricultural Sciences (CAAS)
9. Cornell University, USA
10. Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA; Brazilian Agricultural Research Corporation)
11. Indian Council of Agricultural Research (ICAR)
12. International Center for Agricultural Research in the Dry Areas (ICARDA)
13. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
14. International Institute of Tropical Agriculture (IITA)
15. International Rice Research Institute (IRRI)
16. John Innes Centre (JIC), UK
17. National Institute of Agrobiological Sciences (NIAS), Japan
18. Wageningen University and Research Centre (WUR), The Netherlands

Provisional members

19. Centro de Investigación y de Estudios Avanzados (CINVESTAV), Mexico
20. Institut National de la Recherche Agronomique (INRA), Morocco
21. Istituto Agronomico per l'Oltremare (IAO), Italy
22. National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand



Where in the world is GCP? The GCP network in 2008

In 2008, GCP worked with more than 200 partners spread across 64 countries:

Central and West Asia and North Africa

1. Iran
2. Morocco
3. Syria

Latin America and the Caribbean

4. Argentina
5. Bolivia
6. Brazil
7. Chile
8. Colombia
9. Costa Rica
10. Cuba
11. Haiti
12. Mexico
13. Nicaragua
14. Peru
15. Uruguay

South and Southeast Asia

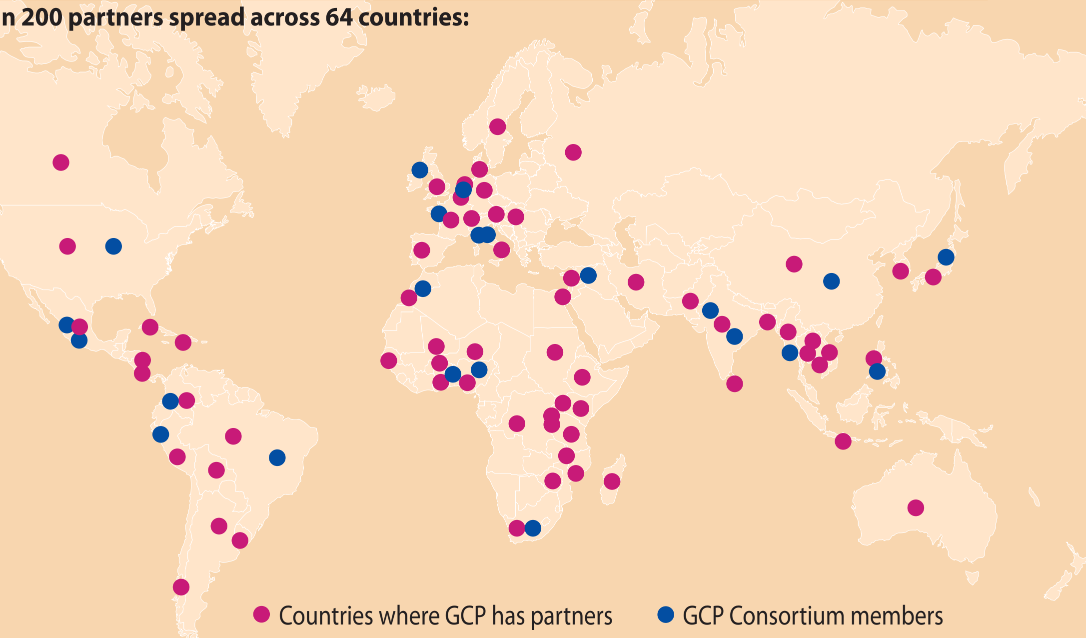
16. Bangladesh
17. Cambodia
18. China
19. India
20. Indonesia
21. Laos
22. Myanmar
23. Pakistan
24. Sri Lanka
25. Thailand
26. The Philippines
27. Vietnam

Sub-Saharan Africa

28. Burkina Faso
29. Burundi
30. Cameroon
31. Democratic Republic of Congo
32. Ethiopia
33. Ghana
34. Kenya
35. Madagascar
36. Malawi
37. Mali
38. Mozambique
39. Niger
40. Nigeria
41. Rwanda
42. Senegal
43. South Africa
44. Sudan
45. Tanzania
46. Uganda
47. Zimbabwe

Others

48. Australia
49. Austria
50. Belgium
51. Canada
52. Denmark
53. France
54. Germany
55. Hungary
56. Italy
57. Japan
58. Russia
59. South Korea
60. Sweden
61. Switzerland
62. The Netherlands
63. UK
64. USA



GCP Annual Research Meeting participants, September 2008, Bangkok, Thailand.

"Perhaps the most important value of GCP thus far, is the opportunities it has provided for people of diverse backgrounds to think collectively about solutions to complex problems, and, in the process, to learn from one another." —*Excerpt from the report of the First External Programme and Management Review, March 2008.*

Generation Challenge programme

Hosted by CIMMYT

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