2009 Project briefs

Generation Challenge programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE-POOR

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GCP's five Subprogrammes

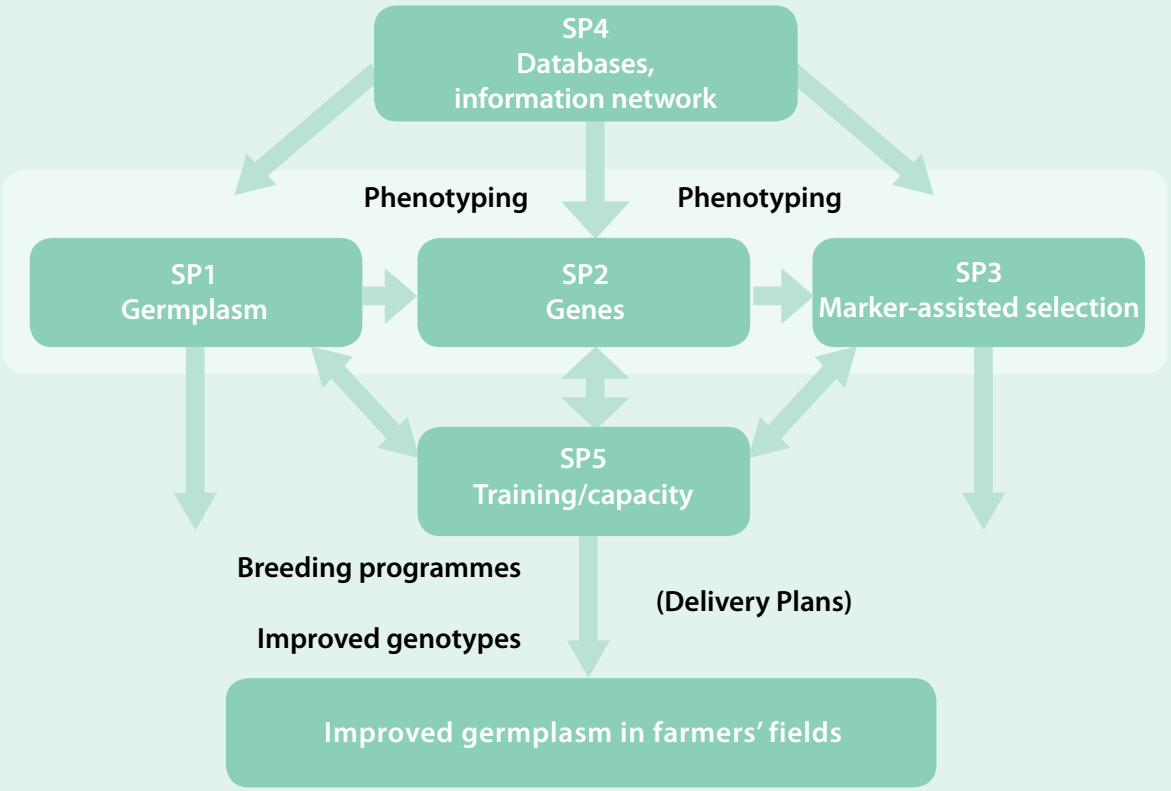
Subprogramme 1: Crop genetic diversity – Characterises the diversity of crop germplasm collections in the custody of the CGIAR and national programmes in terms of genetic structure and associated phenotypic variation

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.



Generation Challenge programme

2009 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.

Correct Citation: Generation Challenge Programme, 2010. 2009 Generation Challenge Programme Project briefs. Texcoco, Mexico: Generation Challenge Programme.

Compiled by: Catherine Durbin
Cover illustration: Recomposition by Miguel Mellado E and Eliot Sánchez P, based on original artwork by Rhoda Okono titled *Autumn in Africa*
Art direction: Miguel Mellado E, CIMMYT
Available online at: http://www.generationcp.org/brochure.php#Exec-summaries_Project-briefs

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Acronyms

AAFC	Agriculture and Agri-Food Canada
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
AfricaRice (formerly WARDA)	Africa Rice Center
Agropolis–CIRAD	Centre de coopération internationale en recherche agronomique pour le développement, France
Agropolis–LGDP	Laboratoire Génome et Développement des Plantes (LGDP)
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
ARI–HAS	Agricultural Research Institute of the Hungarian Academy of Sciences, Hungary
ARI–India	Agharkar Research Institute, India
ARI–Naliendele	Agricultural Research Institute–Naliendele Research Station, Tanzania
ARTC	Agricultural Research and Technology Corporation, Sudan
ASTI	Agricultural Science & Technology Indicators initiative, IFPRI
BAU	Birsa Agricultural University, India
BF	Barwale Foundation
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
CAAS	Chinese Academy of Agricultural Sciences
CARDI	Cambodia Agricultural Research and Development Institute
CAZRI	Central Arid Zone Research Institute, India
CERAAS	Centre d'Etude Régional pour l'Amélioration de l'Adaptation à la Sécheresse, Senegal
CGN–WUR	Centre for Genetic Resources, WUR
ChSU	Charles Sturt University, Australia
CIAT	Centro Internacional de Agricultura Tropical (International Center for Tropical Agriculture)
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
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
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
DOA	Department of Agriculture, Thailand
DPI&F	Department of Primary Industries and Fisheries, Australia
DRC	Democratic Republic of Congo
DR&SS	Department of Research & Specialist Services, Zimbabwe
DWR	Directorate of Wheat Research, India
EARO	Ethiopian Agricultural Research Organization
EgU	Egerton University, Kenya
EIAR	Ethiopia Institute for Agricultural Research
EMBRAPA	Empresa Brasileira de Pesquisa Agropecuária, Brazil
ETH–Zurich	Eidgenössische Technische Hochschule, (Swiss Federal Institute of Technology), Zürich
Fedearroz	Federación Nacional de Arroceros, Colombia
FERA	The Food and Environment Research Agency
FOFIFA–DRA	Foibem-Pirenena Mombra ny Fikarohana Ampiharina Amin'ny Fampandrosoana ny eny Ambanivohitra (National Centre for Applied Research on Rural Development) Département de la recherche agronomique, Madagascar
GCP	The Generation Challenge Programme
GIS	Geographic Information Systsems
HAAS	Institute of Dry Farming, Hebei Academy of Agricultural Sciences, China
HZAU	Huazhong Agricultural University, China
IA–Tápiószele	Institute for Agrobotany, Tápiószele, Hungary
IAMZ	Instituto Agronómico Mediterráneo de Zaragoza
ICABIOGRAD	Indonesian Centre for Agricultural Biotechnology and Genetic Resources and Research Development
ICARDA	International Center for Agricultural Research in the Dry Areas
ICASEPS	Indonesian Center for Agriculture Socio Economic and Policy Studies
ICERI	Indonesian Cereals Research Institute
ICL	Imperial College London, UK
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
IFPRI	International Food Policy Research Institute
ILRI	International Livestock Research Institute
IITA	International Institute of Tropical Agriculture

INERA–Burkina Faso	Institut de l'Environnement et de Recherches Agricoles, Burkina Faso
INIA–Chile	Instituto de Investigaciones Agropecuarias, Chile
INIA–Uruguay	Instituto Nacional de Investigación Agropecuaria, Uruguay
INIFAP Instituto	Nacional de Investigaciones Forestales, Agricolas y Pecuarias, Mexico
INRA–Morocco	Institut National de la Recherche Agronomique, Morocco
INRAN	Institut National de Recherches Agronomiques du Niger
INTA	Instituto Nacional de Tecnologia Agropecuaria, Nicaragua
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
LUMC	Leiden University Medical Center
MAU	Marathwada Agricultural University, India
MPI	Max Planck Institute
MU	Moi University, Kenya
NAARI	Namulonge Agricultural and Animal Production Research Institute, Uganda
NaCRRI	National Crops Resources Research Institute, Uganda
NagU	Nagoya University, Japan
NAFRI	National Agricultural and Forestry Research Institute, Laos
NARI	National Agricultural Research Institute, Eritrea
NARS	National Agricultural Research System
NAU	Nanjing Agricultural University, China
NCGR	National Center for Genomics Resources, USA
NDUAT	Narendra Dev University of Agriculture and Technology, Faizabad, India
NGO	non-governmental organisation
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
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
RAK–CoAg	RAK College of Agriculture, Sehore, Madhya Pradesh, India
RARS–Nandyal	Regional Agricultural Research Station, Nandyal, Andhra Pradesh, India
RGDU	Rice Gene Discovery Unit, Thailand
SAARI	Serere Agricultural and Animal Production Research Institute, Uganda
SAAS	Shanxi Academy of Agricultural Sciences, China
SABRN	Southern Africa Bean Research Network
SARI–Ethiopia	South Agricultural Research Institute, Ethiopia
SARI–Ghana	Savannah Agricultural Research Institute, Ghana
SAU	Sichuan Agricultural University, China
SCRI	Scottish Crop Research Institute, UK
SGRP	System-wide Genetic Resource Programme
SIRDC	Scientific and Industrial Research and Development Centre, Zimbabwe
SUA	Sokoine University of Agriculture, Tanzania
TAMU	Texas A&M University, USA
TNAU	Tamil Nadu Agricultural University, India
TSL	The Sainsbury Laboratory, UK
UAS	University of Agricultural Sciences, India
UBU	Ubon Ratchatani University, Thailand
UCB	Universidade Católica de Brasilia, Brazil
UdB	Università di Bologna, Italy
UdR	Universidad de la República, Uruguay
UdT	Universidad de Talca, Chile
UEM	Universidade Eduardo Mondlane, Mozambique
UGA	University of Georgia, USA
UKZN	University of KwaZulu–Natal, South Africa
UNAM	Universidad Nacional Autónoma de México
UoA	University of Arizona, USA
UoAb	University of Aberdeen, UK
UoAlb	University of Alberta, Canada
UoC	University of California, USA
UoC–Davis	University of California–Davis, USA
UoC–Riverside	University of California–Rivderside, USA
UoD	University of Dhaka, Bangladesh
UoGh	University of Ghana
UoH	University of Hohenheim, Germany
UoM	University of Maryland, USA
UoMi	University of Missouri, USA
UoP	University of Perpignan, France
UoQ	The University of Queensland, Australia
UoZ	The University of Zambia
UPLB	University of the Philippines Los Baños
USDA–ARS	United States Department of Agriculture–Agricultural Research Service
VBI	Virginia Bioinformatics Institute, VPI
VPI	Virginia Polytechnic Institute and State University, USA
WUR	Wageningen University and Research Centre, The Netherlands
YAAS	Yunnan Academy of Agricultural Sciences, China
YU	Yale University, USA
ZU	Zhejiang University, China

COMPETITIVE PROJECTS

Subprogramme 1: Crop genetic diversity

Current projects

1. Project No G3007.01/CI–4: 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)
- AfricaRice (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 AfricaRice, Benin), four NARS – from Africa (IER–Mali, INERA–Burkina Faso), South America (Fedearroz–Colombia) and Asia (PhilRice–Philippines) – and the University of Punjab (India).

2. 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)
- ICARDA (Michael Baum, Stefania Grando, 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.

3. Project No G3008.01/CI–6: 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

- ARI–India: S Tetali
- 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)

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 programme 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.

4. Project No G3008.02/CI–5: 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–CU (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 aluminium (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 2009 or beyond

5. Project No G3005.10/CI–4: Exploring natural genetic variation: developing genomic resources and introgression lines for four AA genome rice relatives

- *Duration: Jan 2005–Dec 2008 with NCE to Sep 2009*
- *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)
- AfricaRice (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.

Subprogramme 2: Genomics towards gene discovery

Current projects

6. Project No G3007.03/CI–1: 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.

7. Project No G3007.06/CI–6: Genetic dissection of drought adaptive mechanisms in bread and durum wheat through large scale phenotyping methodologies

- Duration: Aug 2007–Jul 2009 with NCE to Dec 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.

8. Project No G3008.03/CI–4: 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 droughtinduced 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.

9. Project No G3008.04/CI–7: 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, Slobodan Ruzicic)
- JIRCAS (Matthias Wissuwa)
- ICABIOGGRAD (Masdiar Bustamam, J Prasetiyono)

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.

10. Project No G3008.05/CI–5: 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
UGA (Andrew H Paterson)
Collaborating institutes and scientists

- SARI–Ghana (IDK Atokple)
- ICRISAT (C Thomas Hash)
- MAU (SP Mehtre)
- 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 2009 or beyond

11. 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)
Collaborating institutes and scientists

- CSIRO (Rudy Dolferus)
- IRRI (Kenneth McNally, R Bruskiewich, R Mauleon)
- 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.

Subprogramme 3: Trait capture for crop improvement

Current projects

12. Project No G3007.04/CI–7: Tailoring superior alleles for abiotic stress genes for deployment into breeding programmes: a case study based on association analysis of *Alt_{sb}*, a major aluminium tolerance gene in sorghum

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

Sorghum/Aluminium tolerance/Africa and other developing regions

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

- Robert W. Holley Center, USDA–ARS (Leon Kochian, Jinping Liu)
- IGD–CU (Stephen Kresovich, Alexandra MCasa, Sharon Mitchell, Martha Hamblin, Theresa Fulton)
- EMBRAPA (Claudia Guimaraes, Robert Schaffert, Antonio Marcos Coelho, Vera Alves, Fernanda Caniato (postdoc associate), Barbara Hufnagel (MS student)
- 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 aluminium (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 aluminium 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.

13. Project No G3007.05/CI–4: 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,)
- CRURRS (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)
- IRRI (R. Anitha, R Serraj, D Mackill)
- IGKV (SB Verulkar)

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.

14. Project No G3008.06/CI–4: 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, N Kobayashi)
- AfricaRice: S Mande (Co-PI); 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

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.

15. 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.

16. Project No G3008.08/CI–6: 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 (Tony Condon)
- CIMMYT (Matthew Reynolds, D Bonnett)
- 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.

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

17. 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

- 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.

COMMISSIONED PROJECTS

Subprogramme 1: Genetic diversity of global genetic resources

Current projects

18. Project No G4008.01/CI–4: 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)

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.

19. Project No G4008.02/CI–5: 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, SL Dwivedi, B Clerget)
- UAS–Dharwad (PM Salimath)
- KARI (CK Karari)
- NPGRC (W Ntundu)
- IER (M Diourte)
- ISRA–CNRA (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.

20. Project No G4008.03/CI–6: 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, Jose Crossa, M Zaharieva, H Braun)
- INRA–Morocco (Rachid Dahan, Nsarellah Nasrolhaq, Hassan Quabbou)
- CIMMYT–Iran in collaboration with the Dryland Agricultural Research Institute (Jalal Kamali)
- Seed and Plant Improvement Division, Agriculture and Natural Resources Research Center of Fars Province (SPII), Iran (AR Nikzad, S Tahmasbi, S Sarikhani)

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.

21. Project No G4008.05/CI–4: 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 (Arvind Kumar, effective June 2009; Previous PI: Jill Cairns)

Collaborating institutes and scientists

- IRRI (Ken McNally, Rachid Serraj)
- Agropolis–CIRAD (Michael Dingkuhn, Delphine Luquet, Brigitte Courtois)
- AfricaRice (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.

22. 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 (ie, 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).

23. 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 D 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.

24. Project No G4008.45/CI–4: 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: $226,000*

Rice/Drought tolerance/Various regions

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

- CIAT (César P Martinez, Edgar Torres)
- AfricaRice (M arie-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.

25. Project No G4008.46/CI–5: 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.

Projects on NCE into 2009 or beyond

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

- *Duration: Jan 2006–Jul 2008; NCE to Dec 2009*
- *Budget by year:*

Lead institute
Agropolis (PI: NR Sackville Hamilton, IRRI)
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.

27. Project No G4006.02/CI–2: 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.

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

- *Duration: Jan 2007–Dec 2008 with NCE to Oct 2009*
- *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
- ICRISAT (H D Upadhyaya)
- IRRI (K McNally)
- CIP (M Ghislain)
- CIMMYT (M Zaharieva, S Dreisigacker)
- CIAT (M Fregene, M Blair)
- ICARDA (M Baum)
- Bioversity (N Roux)
- Agropolis–CIRAD (L Baudouin)
- IITA (R Asiedu)
- ICRISAT (T Hash)
- CIP (W Gruneberg)
- UoC–Riverside (J Ehlers)

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.

Subprogramme 2: Genomics towards gene discovery

Current projects

29. Project No G4007.02/CI–4: 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.

30. 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 (V Vadez, RK Varshney, T Nepolean and S Senthilvel)
- AICPMIP (IS Khairwal)
- CAZRI (OP Yadav)
- 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.

31. Project No G4008.08/CI–4: 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.

32. 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

- CIP (Marc Ghislain, L Tincopa, R Simon, D Tay, G Rossel, W Gruneberg, M Bonierbale)
- DArT P/L (Andrzej Kilian)
- INIA–Uruguay (Francisco Vilaró)
- NAARI (Robert Mwanga, G Ssemakula)
- UEM (Ivone Martins Muocha)

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.

33. 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

- ICRISAT (Rajeev Varshney, Kulbhushan Saxena)
- NCGR (Andrew Farmer)
- 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.

34. Project No G4009.06: Illumina genotyping of SNPs in legume mapping populations and germplasm

- *Duration: Nov 2009–Oct 2010*
- *Total budget:$99,828*

Chickpea; cowpea; common bean; groundnut/ Drought and disease resistance/Sub-Saharan Africa

Lead institute
UoC–Davis (Doug Cook)
Collaborating institutes and scientists

- ICRISAT (Rajeev Varshney)
- EMBRAPA (David Bertiloi)
- CIAT (Matthew Blair)

With combined funding from TL1 and the US National Science Foundation, we have completed the identification and validation of single nucleotide polymorphisms in a range of legume crop species, including species of interest to the Generation Challenge Programme. These species are chickpea, cowpea, common bean and groundnut. In total, 22,827 SNPs have been validated and used to design an Illumina GoldenGate genotyping assay that will map ~2,400 loci (averaging 600 loci in each species).

The purpose of this Commissioned Research Project Proposal is to extend the SNP discovery activities, which are now complete, to genotyping SNPs in mapping populations and germplasm from each species. Genotyping represents the last major task of TLI Objective 5, and thus this grant would allow us to complete activities that were described and endorsed in the original TL1 proposal to the Bill and Melinda Gates Foundation.

35. Project No G7009.01/CI–6: Natural variation in the transcriptional regulation of drought responses in wheat

- *Duration: Jan 2009–Dec 2011*
- *Budget: $296,700 (2009), $296,700 (2010), $226,700 (2011); Total budget: $820,100*

Wheat/Drought tolerance/Asia

Lead institute
ACPFG (Peter Langridge)
Collaborating institutes and scientists

- ACPFG (Sergiy Lopato, Serik Eliby)
- ICS/CAAS (Jizeng Jia, Xiuying Kong, Guangyao Zhao, Lifeng Gao)
- CIMMYT (Matthew Reynolds)

Drought stress can affect plants in many ways and plants have evolved complex response pathways that involve the activation or silencing of many genes and many interactions between regulatory proteins or compounds. Despite this complexity, our knowledge of the regulatory pathways is developing rapidly. Key to the drought response is the activity of transcription factors and associated proteins that lead to the activation of multiple pathways. Many of the regulatory sequences that these transcription factors bind to have been described and additional components, such as phosphorylation of the transcription factors are also known. When the expression level of the genes encoding these regulatory proteins is altered, for example in mutants or in transgenic plants, enhanced, or reduced, drought tolerance can be seen in the plants. This project will build on a well established programme to isolate and evaluate these regulatory proteins to screen for natural variation in expression of regulatory genes shown to moderate the drought tolerance response in wheat. Several genes are already available for screening and more will be identified over the life of this project. A wheat germplasm collection assembled to encompass a wide section of variation in cultivated, land race and wild wheat will form the base for the screen. Tissues collected from field grown plants under both well-watered and drought stress conditions will provide the RNA for evaluation. The screen will give preliminary correlation of expression with drought tolerance. These results will be confirmed using introgression lines and other genetic populations. Where expression correlation is validated the germplasm plus diagnostic marker will be made available to breeders for introgression.

36. Project No G7009.02/CI–2: Mapping and validation of QTLs associated with drought tolerance traits in chickpea

- *Duration: January 2009–December 2011*
- *Budget by year: $73,380 (2009), $73,440 (2010), $74,06 (2011); Total budget: $220,880*

Chickpea/Drought tolerance/South Asia; sub-Saharan Africa

Lead institute
ICRISAT (Pooran M Gaur)
Collaborating institutes and scientists

- ICRISAT (Rajeev Varshney, L Krishnamurthy, Vincent Vadez, Shailesh Tripathi)
- UAS–Bangalore (KP Viswanatha, MS Sheshashaye)
- RARS–Nandyal (Veera Jayalakshmi)
- ARS–Durgapura (SJ Singh)
- RAKCA (Md Yasin)

Chickpea (*Cicer arietinum* L.) is globally the third most important food legume mainly grown and consumed in the developing countries. During 2006, chickpea was grown on 10.7 m ha across 51 countries with over 95% of the production and consumption in the developing countries. Chickpea is rich in protein, minerals and vitamins and plays an important role in nutrition of millions of poor, particularly in South Asia and sub-Saharan Africa. Being a leguminous crop, chickpea contributes to improving and maintaining soil fertility and productivity of cropping system when grown in rotation with cereals.

The average global productivity of chickpea continues to be low (~800 kg ha-1), whereas the potential yield is reported to be over 5 t ha-1. Over 90% of chickpea crop is grown rainfed on residual soil moisture stored during the previous rainy season and the crop often experiences drought at the critical stage of pod filling and seed development. Thus drought is the most serious constraint to chickpea production and together with heat stresses accounts for over 40% yield losses annually.

The grain yield under drought environments is the product of Transpiration (T), Transpiration Efficiency (TE) and Harvest index (HI). The root system that can extract water from deeper soils can increase T and contributes to improving the total. biomass productivity and also the HI. A measure of carbon isotope discrimination (δ13C) gives a good estimation of TE as these are positively correlated.

This project builds on Tropical Legume I project, where efforts are being made to map QTLs for root traits. In this project, we propose to map and validate QTLs affecting all three components, T, TE and HI, of the grain yield under drought environments. The root traits will be used for T, carbon discrimination factor for TE and biological and grain yield for HI.

37. Project No G7009.04/CI–5: Development and evaluation of drought-adapted sorghum germplasm for Africa and Australia

- *Duration: Jul 2009–Jun 2012*
- *Budget by year: $82,515 (2009), $118,820 (2010), $14,450 (2011); Total budget: $215,785*

Sorghum/Drought tolerance/Africa; Australia

Lead institute
DPI&F (David Jordan and Andrew Borrell)
Collaborating institutes and scientists

- IER (Sidi Bekaye Coulibaly, Niaba Teme, Mamoutou Kouressy)
- Agropolis–CIRAD, Mali (Michel Vaksmann)

The aim of this project is to improve drought adaptation and productivity in Malian sorghum by integrating three complementary activities:

1. Evaluating the stay-green drought resistance mechanism in plant architectures and genetic backgrounds appropriate to Mali. Stay-green enhances grain yield under post-flowering water stress in the Queensland Primary Industries and Fisheries (QPIF) breeding programme in Australia.
2. Developing sorghum germplasm populations enriched for stay-green genes that also carry genes for adaptation to cropping environments in Mali. The source of the stay-green trait would be an elite line from the QPIF sorghum breeding programme that may carry other useful genes for productive and defensive traits.
3. Carrying out training activities for African sorghum researchers in drought physiology and selection for drought adaptation in sorghum. This would involve detailed training for one or two of our African partner scientists in Australia as part of the project, and sorghum drought breeding/physiology workshops in Africa.

If successful, the project would deliver knowledge of the likely impact of deploying the stay-green trait in Mali, germplasm adapted to Mali containing the trait, and enhanced capacity within Malian sorghum research teams to use this knowledge and germplasm to develop superior varieties with local adaptation. If the results of the project are sufficiently valuable, then the approach would be expanded to other sorghum programmes targeting regions of Africa where post-flowering drought is a major constraint to productivity (eg, Ethiopia and Sudan).

38. Project No G7009.05/CI–3: Improving cowpea productivity for marginal environments in sub-Saharan Africa 2009–2010 'top-off'

- *Duration: Jul 2009–Jun 2010*
- *Total budget: $50,000*

Cowpea/Drought and disease tolerance/Sub-Saharan Africa

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

- UoC–Riverside (Timothy Close, Philip Roberts)
- ISRA (Ndiaga Cisse)
- INERA–Burkina Faso (Issa Drabo)
- IITA (Satoru Muranaka,and Ousmane Boukar, Dong-Jin Kim)

We propose to conduct three activities that build on Phase 1 and initiate/complement Phase 2 TL1 Activities. These include 1) evaluating the cost-effectiveness of two alternative marker platforms for MARS breeding, 2) phenotyping of a RIL set for drought tolerance that is expected to yield unique drought QTL, and 3) beginning development MAGIC populations for future breeding and genetic analyses. For Activity 1, a comparison of marker platforms, we will conduct a tangible small-scale comparison of cost effectiveness of alternative SNP genotyping platforms, based on the Illumina or KBiosciences platforms, in an actual MARS breeding exercise with two 'high x high' MARS populations. This will not only provide platform cost estimates prior to wide adoption of marker-assisted breeding in Phase 2 that is relevant to all GCP crops, but also 'hands-on' experience in MARS breeding for NARS partners. Activity 2 seeks to identify unique drought tolerance QTL by phenotyping the RIL population developed from TVu14676/IT84S-2246. This population appears to be a good population for drought QTL discovery. Genotyping of this population has already been completed using the 1536 Illumina GoldenGate Assay in Phase 1. For Activity 3, we will develop country specific MAGIC populations for Senegal and Burkina, and one for IITA serving sub-Saharan Africa as a whole. These will be a valuable resource for future breeding and genetic investigation. We believe each NARS partner and IITA should develop MAGIC populations composed of locally-adapted elite genotypes. Phenotyping data from TL1 phase 1 has provided new information for selecting new parental combinations. We will initiate development of MAGIC populations now to help ensure quicker results from the genetic analysis and pre-breeding that follow from this approach during Phase 2.

39. Project No G7009.06/CI–2: Development of a SNP platform for molecular breeding in elite material of chickpea

- *Duration: Nov 2009–Oct 2010*
- *Total budget: $66,538*

Chickpea/Drought and disease resistance/Africa; South Asia

Lead institute
UoC–Davis (Douglas Cook)
Collaborating institutes and scientists

- NCGR (Greg May)
- ICRISAT (Rajeev Varshney)

Recent efforts under Tropical Legume 1 (TL1) and allied projects have yielded a significant increase in molecular marker resources for chickpea. Nevertheless, there remains a pressing need to identify polymorphisms that discriminate cultivated accessions, especially the elite germplasm that will form the foundation of phase 2 of TL1 (eg, MARS parents and the focus of current breeding and QTL analyses). The objective of this proposal is to use Next Generation sequencing for deep re-sequencing of cDNA libraries from a select set of elite accessions. This project benefits from earlier efforts funded by the Generation Challenge Programme (SPL-2 discretionary grant) in which the transcriptome of chickpea was sequenced by means of 454 technology. Here we propose to use deep re-sequencing with Solexa technology to develop sequence alignments to these 454 transcript sequences, thereby discovering sequence polymorphisms (SNPs). A subset of 1536 SNPs will be selected to produce an Illumina Golden Gate assay, to ascertain allelic variation in a wider set of breeding and pre-breeding materials.

40. Project No G7009.07/CI–4: Cloning, characterisation and validation of Alt_{SB}/Al tolerance in rice

- *Duration: Oct 2009–Mar 2012*
- *Budget by year: $50,000 (2009), $100,000 (2010), $100,000 (2011); Total budget: $250,000*

Rice/Al tolerance/South-East Asia; Oceania

Lead institute
CU and USDA–ARS (Leon Kochian/Susan McCouch)
Collaborating institutes and scientists

- IRRI (Abdelbagi M Ismail)
- ICABIOGRAD (Sugiono Moeljopawiro)

A primary limitation to crop production on acid soils, which make up as much as 50% of the world's arable lands, is aluminium (Al) toxicity. On acid soils Al toxicity results in rapid damage and growth inhibition of root systems, which leads to significant yield reductions due to inhibited uptake of water and nutrients. Rice is the most Al tolerant cereal, yet Al toxicity is still a major limitation to rice production in both rainfed lowlands and uplands. In this proposal we will take advantage of our recently cloned sorghum Al tolerance gene that is a member of the MATE family of organic solute transporters, to identify rice homologs that are candidate tolerance genes. In rice, we have conducted a computational analysis of the MATE family and have identified 5 MATE genes that are co-localised with previously identified Al tolerance QTL. Here we will test them as candidate Al tolerance genes using T-DNA rice knockout lines. If these homologs are not functional in rice, complementary approaches are already in place. We are poised to fine-scale map and clone a novel major rice Al tolerance QTL. Furthermore, by the fall of 2009, we will have completed whole genome association mapping of rice Al tolerance, which will also identify novel rice genomic regions harboring Al tolerance loci. These will be a resource for the rapid cloning of novel rice Al tolerance genes.

Projects on NCE into 2009 or beyond

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

- *Duration: Jan 2008–Dec 2008 with NCE to Jun 2010*
- *Total budget: $152,543*

Groundnut/Various traits and regions

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

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

Subprogramme 3: Trait capture for crop improvement

Current projects

42. 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.

43. Project No G4007.06/CI–6: 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

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

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.

44. 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".

45. Project No G4007.08/CI–4: Integration of genomic tools with conventional screening for developing NERICA rice cultivars for West Africa

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

Rice/Drought tolerance/Africa

Lead institute
AfricaRice (Marie Noelle Ndjiondjop)
Collaborating institutes and scientists
- Agropolis–IRD (Alain Ghesquiere, Valerie Verdier, M Lorieux)
- IER (Fousseyni Cisse)
- AfricaRice (Manneh Baboucarr, Dramé K Nani, 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.

46. Project No G4008.10/CI–7: 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, FC Santos, J Herbert M Viana)

Aluminium (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 programs 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.

47. 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; Matthew Blair)
- INCA (Humberto Rios Labrada; Orlando Chaveco)
- INIFAP (Ernesto Lopez Salinas; Raul Rodriguez Guerra; Victor Montero)
- INTA (Aurelio del Llano; Julio Molina)

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.

48. Project No G4008.12/CI–2: 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 (Lakshmanan Krishnamurthy, effective March 2009; Previous PI: 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.

49. Project No G4008.13/CI–3: 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)
IITA (S Muranaka)

Collaborating institutes and scientists

- IITA (Ousmane Boukar)
- INERA–Burkina Faso (Issa Drabo)
- ISRA (Ndiaga Cissé)
- TAMU (William Payne)

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.

50. 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

- Agropolis–INRA (Francois Tardieu, Claude Welcker)
- CAAS (Xianchun Xia, Huihui Li, Changbin Yin)
- CIMMYT (Matthew Reynolds, Yunbi Xu)
- CSIRO and UoQ (Scott Chapman, Nick Hansen)
- GCP (Jean-Marcel Ribaut)
- 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.

51. 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

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

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.

52. 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.

53. 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.

54. 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)
- UKZN (John Derera, JW Danson)

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.

55. 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 and Greg Edmeades)
Collaborating institutes and scientists
Participating consultants (John C O'Toole)

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.

56. 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, N Shrestha)
- 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 programmes. 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.

57. Project No G4008.41/CI–7: 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.

58. Project No G4008.48/CI–5: 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.

59. 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*
- *Total budget: $81,600*

Groundnut/Drought tolerance/Africa; Latin America

Lead institute
ISRA (Ousmane Ndoye)
Collaborating institutes and scientists

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

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.

60. 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 (Bindiganavile S Vivek, effective May 2009; Previous PI: PH Zaidi)
Collaborating institutes and scientists

- ICERI (M Azrai)
- Institute of Plant Breeding, UPLB (Eureka Teresa Ocampo)
- Krishidhan Seeds, India (IS Singh)
- NMRI (Dang Ngoc Ha)
- NSFCRC (Pichet Grudloyma)
- YAAS (Fan Xingming)

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.

61. Project No. G7009.09/CI–1: Start up for Cassava Challenge Initiative, project 4: Implement MARS project for drought tolerance

- *Duration: Dec 2009–Feb-2010*
- *Total budget: $2,124*

Cassava/Drought tolerance/Africa

Lead institute
NRCRI (Emmanuel Okogbenin)
Collaborating institutes and scientists

- NRCRI (Chiedozie Egesi)
- CRI–Ghana (Elizabeth Parkes)

Although cassava produces more energy per unit area compared to other crops under marginal conditions of limited annual rain fall (<500mm) or a long dry season (5-6 months), yield potential under drought varies widely in the gene pool. Previous work revealed certain varieties from Africa are tolerant to drought. The afore-mentioned drought tolerant germplasm is the basis of an innovative molecular breeding scheme based on marker assisted recurrent selection (MARS) that seeks to deploy drought tolerance hybrids more widely in cassava gene pools of the major cassava growing agro-ecologies of West Africa.

The scheme employs a two-pronged approach: first, a drought tolerant genotype identified using phenotypic information will be used in crosses with commonly grown elite lines and the progeny used for QTL mapping. Secondly, marker-assisted breeding through MARS will be employed to improve the efficiency of producing elite germplasm with exceptional performance under drought by identifying useful allele (QTL) combinations and pyramiding (and fixing) multiple sources of genes for drought tolerance into a set of new progenitors. Genotypic information will be generated by a high throughput SNP marker genotyping platform based on SNP marker resources currently being developedPartners in the project are two African NARs programmes of Ghana, and Nigeria, Cornell University and an advanced genotyping facility to be identified. Indicators of success of the project include identification of molecular markers for selection of high yield and drought tolerance in breeding schemes. Other indicators are production of new cassava varieties that a) rank high in yield and perform better under drought than any currently available lines, b) are high ranking under non-drought conditions, and c) will serve as improved progenitors for future breeding of drought tolerance in cassava.

62. Project No. G7009.10/CI–1: Start up for Cassava Challenge Initiative, project 2: Improving and deploying markers for biotic traits

- *Duration: Dec 2009–Feb-2010*
- *Total budget: $17,936*

Lead institute
NRCRI (Chiedozie Egesi)
Collaborating institutes and scientists

- NRCRI (Emmanuel Okogbenin)
- CRI–Ghana (Elizabeth Parkes)
- SARI–Ghana (Joseph Adjerbeng)

The genetics of cassava is the least understood of major staple crops in the world. This is largely due in part to its heterozygous nature which makes it difficult to develop appropriate stocks for classical genetic studies. The first genetic map of cassava was published in 1997 using first generation of markers including RFLPs, AFLPs, RAPDs and isozymes. This map was further developed by anchoring SSR markers, which are randomly distributed on the map. The map has been utilized in QTL mapping studies in cassava for various traits including resistance to pests and diseases, yield, morphological and quality traits. While QTLs have been detected for several traits, majority of the markers have yet to be applied in breeding programmes due to poor association with traits in MAS schemes. Only markers associated with the CMD2 gene and CGM have so far been deployed in breeding programmes. Results of MAS conducted so far for CMD2 gene was 68% efficient, while validation studies for markers linked to the CGM resistance was good in East Africa, but response to the CGM for the markers in West Africa was relatively moderate or tolerant to the pest. The lack of strongly linked markers to economic traits of importance necessitated the need for development of over 800 SSR markers for further mapping of the genomic regions controlling traits of interest. While success has been made in improving map saturation, recent efforts indicate that efficient fine mapping has not been successfully attained using SSR markers.

To improve MAS for CMD2 gene, SCAR markers (at 4 cM to the gene) were developed which is now routinely used in breeding programmes. However, the need to accelerate the application of more markers in breeding programmes, means that more efficient marker systems are necessary to efficiently tag genes for MAS schemes. Current initiatives to

develop SNPs for cassava in a GCP funded project and another by the BMGF provides a new vista and array of immense opportunities to identify markers closely linked to new sources of CMD resistance and other biotic constraints. This proposal therefore seeks to develop new mapping populations for QTL mapping for new sources of CMD resistance, and validation studies of the detected QTLs using available SNP markers developed from other GCP and BMGF projects.

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

63. Project No G4006.35: Statistical support for the design and data analysis of GCP projects

- *Duration: Jan 2006–Dec 2009*
- *Budget by year: $50,000 (2006), $75,000 (2007), $80,000 (2008), $40,000 (2009); Total budget: $245,000*

Lead institute
WUR (Marcos Malosetti)
Collaborating institutes and scientists

- WUR (Hans Jansen, Fred van Eeuwijk, Marco Bink)
- UNAM (presently UoC–Davis): Joost van Heerwaarden

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.

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

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

Lead institute
WUR (Theo van Hintum)
Collaborating institute and scientist
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.

65. 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: $240,567*

Lead institute

Bioversity (Mathieu Rouard)

Collaborating institutes and scientists

- Agropolis–CIRAD (Christophe Périn, Gaetan Droc)
- Bioversity (Matthieu Conte)

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.

66. 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 with NCE to Sep 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.

67. 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 (Guy Davenport)

Collaborating institutes and scientists

- CIMMYT (Jose Crossa, Trushar Shah, Rosemary Shrestha)
- FERA (David Galsworthy)

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.

68. Project No. G4009.03: Development of data standards and community of practice enabling the capture of and access to GCP quality data sets

- *Duration: Jan 2009–Dec 2009*
- *Total budget: $148,535*

Lead institute

Bioversity (Elizabeth Arnaud)

Collaborating institutes and scientists

- Bioversity (Adriana Alercia, Elizabeth Arnaud, Stephanie Channelière, Milko Skofic)
- CIMMYT (Rosemary Shrestha, Guy Davenport)
- CIP (Reinhard Simon)
- CU (Chich-Wei Tung)
- ICRISAT (Jayashree Balaji until April 2009; Mike Butterfield, effective May 2009)
- IRRI: Thomas Metz, Ramil Mauleon, Warren Constantino
- OSU, Plant Ontology (Pankaj Jawal)
- Consultant (Robert Koebner)
- WUR (Theo van Hintum, Elizabeth van Strien)

The Generation Challenge Programme (GCP) is reaching the half-way point of its lifespan, and all data sets documenting the released genetic stocks must be made available to Consortium members and the wider scientific community. Ontology, data templates the Central Registry and quality data sets are all inter-related outputs that support the delivery of quality data to the scientific community.

The GCP ontology provides a controlled vocabulary and relationships to enable inter-operability for the retrieval of crop data (both genotypic and phenotypic). A crop-development ontology has already been initiated for chickpea, maize, Musa, potato, rice and wheat traits. In the future, the GCP ontology will allow researchers and end users to query keywords that are related to traits, plant structure, growth stages and molecular functions, and access the associated GCP phenotyping and genotyping data sets such as germplasm, crop physiology, geographic information, genes and quantitative trait loci (QTL). The crop ontology will be integrated into the data-entry user interface or data templates wizard as picklists to facilitate data annotation. In addition, the GCP ontology will be integrated with Plant Ontology (PO) and Gramene (Trait Ontology, TO; Environment Ontology, EO) to develop a common, internationally-shared crop trait and anatomy ontology.

The Central Registry provides an overview of all available data resources from a single viewpoint, similar to a 'yellow pages' directory, which is critical for the successful completion of tasks requiring data from various sources, but also for the visibility of the outputs of the GCP. The Central Registry serves to make GCP data accessible to GCP and other scientists. To increase the access to and use of these data, it is essential to determine and where possible increase the quality of the data. This can involve data checking, correcting and adding metadata, and combining data sets. The 2008 users' online survey emphasised the need to promote awareness among the project PIs regarding use of the templates to load correctly formatted data files loaded into the Central Registry. The current promotion strategy includes a proactive help desk to directly contact project PIs and assist data providers. Central Registry users have also identified data quality as a major concern. The use of data-quality checking tools prior to loading on the Central Registry will be promoted through this project. Once delivered to the Central Registry, the data sets will go through a second data-quality check by experts on both format compliance and their value for secondary use. Feedback from users of data sets will be collected and used to document these data sets.

Finally, to address the need of secondary users to access comprehensive data sets, all versions of the data sets, along with quality reports and corrections, will be indexed by additional metadata, and consolidated packages of data sets will be downloadable from the Central Registry. The Central Registry will remain the single directory of GCP data sets and the repository of data files. Project coordinators will be strongly encouraged to load their data files into it.

69. Project No G4009.04: Data analysis support for existing projects in SP2 with emphasis on analysis of next generation sequencing data

- *Jan 2009–Dec 2009*
- *Total budget: $85,000*

Lead institute

ICRISAT (Rajeev Varshney and – until July 2009 – Jayashree B)

Collaborating institutes and scientists

- ICRISAT (Vivek Thakur)
- NCGR (Greg May, Andrew Farmer)
- TSL (David Studholme, Jonathan Jones)
- IRRI (Ramil P Mauleon)

There is a dearth of genomic resources in crops like pigeonpea, chickpea that could be used for crop improvement. This is partly because of negligible research investment in these crops further compounded by the low levels of genetic diversity in the germplasm of crops like pigeonpea. Next generation sequencing methods have the capacity to accelerate acquisition of genomic resources, through the generation of gigabases of sequence information in an exceedingly short time. SP2 projects using 454 FLX and Solexa sequencing technologies are beginning to generate EST and SNP marker resources in pigeonpea and chickpea that will help overcome a serious bottleneck in the development of these crops – namely shortage of markers and absence of genetic maps. NGS methods however generate a deluge of data; the shorter read lengths require considerable bioinformatics effort in assembly. The choices of methods available to dealing with this kind of data are many and depend on the technology used as well as the biological application.

Since the sequencing itself is being carried out at NCGR and uses the NCGRs computational pipeline; bioinformatics efforts at ICRISAT are related to putting together an open access, open source alternative to the NCGR proprietary pipeline (consisting of Alpheus pipeline for Solexa data and XGI pipeline for EST data). Efforts in 2008 have involved evaluation of available open source NGS data assembly, polymorphism detection and visualisation software and their benchmarking with the NCGR pipeline. Efforts through 2009 will involve developing a protocol for the analysis of NGS data, with the express objective of evaluating differential gene expression in a pair of genotypes. Further, the project also aims to fulfil data submission and software pipeline requirements for public access, data management methods for local analysis, dovetail analysis methods with validation methods for markers generated using Illumina GoldenGate assay on identified mapping populations, development of genetic maps and computational prediction of miRNAs in the transcriptome data.

70. Project No G7009.03/CI–1: Rice Challenge Initiative start-up project

- *Duration: Jun 2009–Aug 2009*
- *Total budget: $40,120*

Rice/Drought tolerance/Africa

Lead institute
GCP (Graham McLaren)
Collaborating institutes and scientists
AfricaRice (Marie Noel Ndjiondjop)

The objective of this project is to establish the Rice Challenge Initiative by convening a project development workshop and commissioning small activities to start the research process in 2009. The main proposal(s) will start in 2010.

71. Project No. G8009.01.01: Establishment of the Molecular Breeding Platform (MBP Activity 1.1.1)

- *Duration: Jul 2009–Jul 2010*
- *Total budget: $77,240*

Lead institute
GCP (Graham McLaren)

Establish Steering Committee terms of reference and activities and appoint members. The Steering Committee will include representation from the private sector, the use case teams, users, and the GCP. Link Use-case requirements to platform development through use-case representation on the steering committee. Develop a platform business plan in collaboration with the steering committee and a communication strategy in collaboration with GCP communication experts.

72. Project No. G8009.01.02: Develop and deploy the Molecular Breeding Portal (MBP Activity 1.1.2)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $215,048 (2009), $157,171 (2010), $153,910 (2011), $156,525 (2012), $159,271 (2013); Total budget: $841,924*

Lead institute
GCP (Graham McLaren)

Work with use-case representatives and portal developers to design develop and test portal elements. Liaise with developers and service providers to ensure updates and access to applications and services.

73. Project No. G8009.01.03: Establish Molecular Breeding Platform Helpdesk and coordinate training and communication activities (MBP Activity 1.1.3)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $171,038 (2009), $190,659 (2010), $204,652 (2011), $195,765 (2012), $198,511 (2013); Total budget: $960,625*

Lead institute
GCP (Graham McLaren)

Establish and implement helpdesk protocols and procedures with use case representatives and partners requiring guidance, training and assistance with applications and services, or who are unable to use the portal. Promote communication between users, service providers, developers and other stakeholders in the platform through an annual meeting and internet-based collaboration tools.

74. Project No G8009.02.01: Identify, deploy and support tools facilitating management of germplasm lists, pedigrees, intellectual property and other passport data (MBP Activity 2.1.1)

- *Duration: Jul 2009–Jun 2012*
- *Budget by year: $75,538 (2009), $50,404 (2010), $54,997 (2011); Total budget: $180,939*

Lead institute
AAFC (Shawn Yates)
Collaborating institutes and scientists

- AAFC (Fran Clarke)
- IRRI (scientists TBD)

This element of the MBP project provides tools to facilitate sample tracking for lists of germplasm to be evaluated in nurseries, trials or laboratory assays. They manage the recording of pedigrees, chronology of breeding processes and naming of germplasm passing through a breeding project. They enable nursery composition and management of breeders' seed inventory.

75. Project No G8009.02.02: Identify, deploy and support tools for management of phenotypic characterisation and evaluation (MBP Activity 2.1.2)

- *Duration: Jul 2009–Jun 2012*
- *Budget by year: $83,410 (2009), $87,285 (2010), $91,930 (2011); Total budget: $262,626*

Lead institute
CIMMYT (Arllet Portugal)
Collaborating institutes and scientists
None

This element of the MBP project provides applications which facilitate the production of electronic fieldbooks for germplasm screening, characterisation and evaluation. Electronic fieldbooks enable randomisation of experimental design, and improve data capture and management reducing overall possible human error. They also facilitate the production of field maps and labels, including barcoding, to ensure traceability of genotypes and samples from the field to the laboratory and back to the field – a critical element of the selection process (see *Critical steps in a high-throughput molecular breeding selection cycle* in Annex 5).

76. Project No G8009.02.03: Identify, deploy and support tools for management of genotypic characterisation (MBP Activity 2.1.3)

- *Duration: Jul 2009–Jun 2012*
- *Budget by year: $ 30,175 (2009), $33,395 (2010), $36,443 (2011); Total budget: $100,013*

Lead institute
ICRISAT (Trushar Shah)

The pedigree information management and electronic fieldbook tools will allow this sample tracking to and from laboratory, and the capture of laboratory output data into local databases. Service laboratories have their own laboratory information management systems (LIMS) in place that are generally compatible with client information systems. For partners who decide to conduct the marker work in their own laboratory, a LIMS developed by ICIRSAT, under an open-source license will be available from the Portal for installation and parameterisation (Jayashree et al 2006). Training on both electronic fieldbook and LIMS will be accessible through the services of the platform.

77. Project No G8009.03.01: Develop and deploy statistical and genetic analysis methodology for molecular breeding (MBP Activity 2.2.1)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $266,750 (2009), $273,942 (2010), $273,244 (2011), $281,300 (2012), $280,283 (2013); Total budget: $1,375,519*

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

This element will provide access to statistical methodologies and applications for appropriate and timely analysis of phenotype and genotype data. It will also provide tools for characterising target populations of environments, weighting the influence of different environment types, analysing GxE, QTLxE and epistatic interactions, mapping molecular markers and detecting marker-trait associations in breeding populations and constructing selection indices from trait and marker data.

78. Project No G8009.03.02: Develop and deploy methodology and tools for molecular breeding (MBP Activity 2.2.2)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $121,136 (2009), $167,654 (2010), $170,657 (2011), $173,882 (2012), $106,595 (2013); Total budget: $739,923*

Lead institute
Agropolis–INRA (Alain Charcosset)

This element will provide analysis models and applications for conducting marker-assisted selection (Bernardo and Charcosset 2006; Bernardo et al 2006), after the analysis of marker trait associations in different types of populations. In addition to classical biparental populations, we will address complex breeding populations involving a broader diversity, such as Multi-Parent Advanced Generation Inter-cross (MAGIC) populations and populations derived from several connected biparental populations as well as large-scale introgression line breeding populations involving different donors.

79. Project No G8009.03.03: Develop and deploy simulation tools for complex G–E systems (MBP Activity 2.2.3)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $326,340 (2009), $569,198 (2010), $555,940 (2011), $516,931 (2012), $357,011 (2013); Total budget: $2,325,420*

Lead institute
UoQ (Mark Dieters)
Collaborating institutes and scientists

- CSIRO (Scott Chapman)
- CAAS (Huihui Li)
- CIMMYT (Jainkang Wang)

This element will see the development of simulation tools and models to test strategic options for molecular breeding and to make tactical decisions relating to selection and crossing of parents. This will build on work already undertaken through GCP projects to develop simulation modules. These quantitative genetics simulation tools will be integrated with eco-physiological models to simulate breeding strategies for complex traits.

80. Project No G8009.04.01 to G8009.04.03: Information Network and Workflow System for Molecular Breeding (MBP Activity 2.3.1 to 2.3.3)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $824,637 (2009), $895,139 (2010), $583,132 (2011), $636,192 (2012), $656,419 (2013); Total budget: $3,595,519*

Lead institute
CIMMYT (Guy Davenport)
Collaborating institutes and scientists

- GCP (Graham McLaren)
- CIMMYT (Arllet Portugal)
- IRRI (Martin Senger)
- IRRI (Guoyou Ye)
- AAFC (Shawn Yates)
- ICRISAT (Trushar Shah)

I*nformation Network Infrastructure*: Given the diversity of data types and the global scope and diversity of potential partnerships, data exchange and information system interoperability is a significant challenge. A cornerstone of this implementation is formulating common standards for data storage by using a precise but flexible data model (Bruskiewich et al 2006). A middleware layer must connect local and remote data sources and transfer data between databases and applications through model-defined data structures (Bruskiewich et al 2008). The Networking Infrastructure is designed to be independent of the database engine and will accommodate whatever database programmes are in use or are demanded by users. Open-source tools such as R and MySQL will be supported, although the applications are designed to be agnostic to the RDBMS and can work with proprietary databases.

Public crop information and integration of external data resources: Information from breeding projects will be managed at two levels: within projects and across partners. At the project level, information must be managed to allow the selection of the most suitable parental lines and to facilitate marker selection at each cycle of the breeding programme dealing with pedigree, genotypic and phenotypic data. Access to public or shared data can be very effective for selecting parents and predicting cross performance (Eagles et al 2006). Project-level data may be submitted to crop-specific central databases hosted by partner institutions and shared through the Platform network (via internet or by mirroring databases).

Visualisation and decision support applications: Results from all the analytical tools and methodologies will be presented in user-friendly interfaces to facilitate the selection decisions that have to be made in each cycle of breeding projects. The first of these decision support tools will be a Molecular Breeding Design Tool (MBDT) to display phenotypic and molecular data for potential parents to facilitate selection of parents and crossing schemes. The second will be a Molecular Selection Tool (MOSEL) to display molecular genotypes and trait data to facilitate selection of lines within breeding populations.

Configurable Workflow System for Molecular Breeding: The logistics applications, analysis and decision support tools and database components defined above will be integrated into a user interface and workflow system to streamline the different steps of breeding experiments.

Projects on NCE into 2009 or beyond

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

- *Duration: Jan 2005–Dec 2008 with NCE to Jun 2009*
- *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

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

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.

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

- *Duration: Jan 2005–Dec 2008 with NCE to Dec 2009*
- *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.

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

- *Duration: Jan 2005–Dec 2008 with NCE to Dec 2009*
- *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, via Mike Butterfield)
- IRRI (Guy Davenport, via Ramil Mauleon)

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 program 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.

84. 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 with NCE to Jun 2009*
- *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

- CIMMYT (Jose Crossa, Yunbi Xu, Trushar Shah)
- CIP (Reinhard Simon)
- IRRI (Richard Bruskiewich, Hei Leung, Ramil Mauleon)
- JIC (Andreas Magusin)
- NIAS (Shoshi Kikuchi, Kouji Satoh, Koji Doi, Masaru Takeya)

- 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

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

- *Duration: Jan 2006–Dec 2008 with NCE to Jun 2009*
- *Budget by year: $150,000 (2006), $150,000 (2007), $163,050 (2008); Total: $463,050*

Lead institute
IRRI (Martin Senger)
Collaborating institutes and scientists

- Agropolis–CIRAD (Manuel Ruiz)
- Bioversity (Milko Skofic)
- CIMMYT (Guy Davenport)
- CIP (Reinhard Simon, Anthony Collins)
- ICRISAT (Jayashree Balaji)
- IRRI (Richard Bruskiewich)

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.

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

- *Duration: Jan 2006–Dec 2008 with NCE to Jun 2009*
- *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
Agropolis–CIRAD (Claire Billot)
CGN–WUR (Theo Van Hintum)
CIP (Reinhard Simon)
ICRISAT (B Jayashree)

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.

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

- *Duration: Aug 2007–Dec 2008 with NCE to Oct 2009*
- *Budget by year: $100,000 (2007), $100,000 (2008); Total budget: $200,000*

Lead institute

WUR (Fred van Eeuwijk)

Collaborating institutes and scientists

- ICL (David Balding)
- LUMC (Hans van Houwelingen, Jeanine Houwing-Duistermaat)
- NIAB (Ian Mackay, Wayne Powell)
- SCRI/BIOSS (Christine Hackett, Dave Marshall)
- UoH (Hans Peter Piepho, Albrecht Melchinger)
- 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.

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

- *Duration: Jan 2007–Dec 2008 with NCE to Dec 2009*
- *Budget by year: $80,000 (2007), $84,000 (2008); Total budget: $164,000*

Lead institute

ICRISAT (Abhishek Rathore)

Collaborating institutes and scientists

- CIMMYT (Guy Davenport)
- ICRISAT (Tom Hash, Mike Butterfield, Jayashree B)
- IRRI (Richard Bruskiewich)

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.

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

- *Duration: Feb 2007–Dec 2008 with NCE to Dec 2009*
- *Budget by year: $100,000 (2007), $86,441 (2008); Total budget: $186,441*

Lead institute

IRRI (Martin Senger)

Collaborating institutes and scientists

- IRRI (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.

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 with NCE to Feb 2009*
- *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 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), $0 (2009); Total budget: $109,587*

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

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.

92. 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

- ACCI/UKZN (Jedidah W Danson)
- 10 countries in east and southern Africa

We are working in 14 countries in East and Southern Africa, with National Agricultural Research programmes, together with AfricaRice, 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).

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

- *Duration: Jul 2007–Jul 2009*
- *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.

93.1 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)*

93.2 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)*

93.3 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)*

93.4 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 (Yunbi Xu, Claudia Bedoya)
- UdR (Jorge Franco)
- USDA–ARS (Marilyn Warburton)

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).*

93.5 *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)

93.6 *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)
- 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 ressearch 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)*

94. Project No G4007.22.04: GCP Workflow and Repository System: Phase III

- *Duration: Jun 2009–Jul 2010*
- *Total budget: $100,000*

Lead institute
Cropster GmbH (Norbert Niederhauser)

Phase III
Details on Phases I and II of this project are available in the 2008 Project briefs (http://www.generationcp.org/brochure.php#Exec-summaries_Project-briefs). Following Cropster's completion of Phase II, GCP identified improvements and additional functionalities and features which it desires to add to the Workflow, hence the necessity for a third phase of the project, which in essence is a contracted service.

95. 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
ASTI (Nienke Beintema)
CIAT (Glenn Hyman, Scientist)
Consultant (Carlos Tovar)
Consultant (Sindi Kasambala)
ICASEPS (Erna Lokollo, Muchjidin Rachmat)
IER (Lamissa Diakite)
INERA–Burkina Faso (Mathieu Ouedraogo)
NRCRI (Godwin Asumugha)
VPI (George Norton)

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.1 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.

96. Project No G4008.26/CI–1: 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
NRCRI (Emmanuel Okogbenin)

Collaborating institutes and scientists

- NRCRI (Chiedozie Egesi)
- CRI (Elizabeth Okai)
- NaCRRI (Yona Baguma)
- ARI–Naliendele, Tanzania (Geoffrey Mkamilo)
- IITA (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.

97. 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.

98. 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, Xiaoyun Li)
- CIAT (Glenn Hyman)
- Food crop breeders, crop management, socio-economics and GIS specialists in CG centers including IRRI, CIMMYT, ICRISAT, CIAT, AfricaRice and IITA
- Numerous NARS and NGO institutions and staff in South and East Asia, Sub-Saharan Africa, Latin America

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.

99. 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.

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

- *Duration: Apr 2008–Apr 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.

100.1 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: $31,940 (2008), $7,986 (2009); Total budget: $39,926*

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.

100.2 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 (Dim-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

100.3 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, N Ndack Diop, Philip Roberts)

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

101. 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)
- Pennsylvania State University (Jonathan Lynch)

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 ll 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.

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

- *Duration: Aug 2008–Jul 2010*
- *Budget by year: $189,980 (2008), $ 56,640 (2009); Total budget: $246,620*

Lead institute

CIMS (Lawrence Pratt)

Collaborating institutes and scientists

CU (Stefan Einarson)

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 develophigh 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 develofpment 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.

103. Project No G4009.01: Genotyping Support Services 2009

- *Duration: Jan 2009–Dec 2009*
- *Total budget: $300,000*

Lead institute
GCP (Humberto Gómez Paniagua)
Collaborating institutes and scientists
GCP Subporgramme Leaders

The GCP mandate rests in unlocking the genetic diversity of crop germplasm by using genomics to discover the genes and alleles responsible for the expression of complex agronomic traits. The results of this research are useful for the biological sciences in general, and in particular for research applied to crop breeding. With better understanding of the traits that condition plant and crop performance, plant breeders may create better varieties at faster rates, and provide the farming communities with more suitable products. The GCP is committed to having impact by ensuring that the discovery work reaches the crop users and the consumers with better harvests due to better cultivars.

The Genotyping Support Service (GSS) facilitates the access of NARS breeding programmes to genotyping technologies, and in turn bridges the gap between the work in the laboratories and that conducted in the field. With this service, the GCP offers cost and time-efficient genotyping services worldwide, access to data and support (local capacity build up) complemented with statistical support for proper interpretation of genotype and phenotype data, and improved experimental design.

This activity helps assess the potential of particular breeding materials with appropriate phenotypic data sets to identify good markers for relevant agronomic traits, and addresses germplasm management needs among other possible services. The GSS provides support for the production of suitable marker data and subsequent data interpretation by funding services with leading genotyping laboratories. It also intends to transfer the knowledge on how to deal with service providers so that the participants learn to do it by them selves and can continue on their own when the GSS is no longer available.

104. Project No. G4009.02: Fellowships and Travel Grants 2009

- *Duration: Jan 2009–Dec 2009*
- *Total budget: $86,000*

Lead institute
Carmen de Vicente, GCP
Collaborating institutes and scientists
None

Fellowships:
Only one Fellowship (Pioneer–GCP) will be ongoing in 2009. The name of the fellow is Honoré Kam, winner of the 2008 call. The contract was signed in February 2009, and research work is underway (start: June 2009, end: December 2009). More details on this project can be found in the brief below.

Travel grants:
Two types of grants are offered in 2009:

Participation in Inter-drought III

The GCP agreed with the organisers of Inter-Drought III (The 3rd International Conference on Integrated Approaches to Improve Crop Production Under Drought Prone Environments, October 11–16, 2009, Shanghai, China) to partially cover the participation of selected young researchers, involved in GCP priority projects focused on drought.
An announcement was made to the GCP communities of the Challenge Initiatives and Tropical Legumes I project to solicit applications. Twelve (12) researchers were selected to participate with a maximum award of 2000 USD to cover travel, registration and accommodation.

Participation in the GCP Annual Research Meeting

These grants are intended 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.

A total of 12 grants were awarded to researchers engaged with GCP projects, emphasising those that will be involved in the new projects of the Challenge Initiatives. Awards cover travel and participation-related expenses at the venue of the ARM (Bamako, Mali).

104.1 2009 Fellowship: Study of Burkina Faso rice landraces diversity and breeding for resistance to rice yellow mottle Virus (RYMV)

- *Duration: June 2009–Dec 2009*
- *Total budget: $36,000*

Rice/RYMV resistance/Sub-Saharan Africa

Fellow

Honoré KAM, INERA–Burkina Faso

Collaborating institutes and scientists

- Agropolis–IRD (Alain Ghesquière)
- AfricaRice–Benin (Marie Noelle Ndjiondjop)
- UKZN (Mark D Laing)

Rice is the staple food in many countries of Africa and constitutes a major part of the diet in many others. A series of abiotic and biotic stresses continue to limit rice productivity. Rice yellow mottle virus (RYMV) is one of the most important rice pathogens in most rice-growing countries of Africa and Madagascar, but not elsewhere. Two types of natural resistance to RYMV have been reported in rice: a partial-resistance in *Oryza sativa* cultivar Azucena and a high-resistance on cultivars Gigante and Tog5681, which represent *Oryza sativa* and *O. glaberrima*, repectively. The high and partial resistances are controlled by a single recessive gene (rymv) and several genes, respectively. IRD in collaboration with The Africa Rice Center (AfricaRice) developed a fine genetic map and the cloning of the high level of resistance and the SNP gene markers tight are used to facilitate the screening of germplasm for their resistance to RYMV. Recently, however, the partial resistance in Azucena has been completely broken down, and high level of resistance in both Gigante and Tog5681 has been overcome by several resistant-breaking-isolates from five countries of the west and central African Sudano-savannah zone. Therefore, there is an urgent need for searching other rice genotypes with high and durable resistance to RYMV in Africa. This project seeks to: (i) genotype 335 accessions collected recently in Burkina Faso with 26 SSR diversity markers used by The Generation Challenge Programme, and (ii) conduct extensive search for durable RYMV resistance among traditional rice accessions from Burkina Faso.

105. Project No. G4009.05: Training workshop on marker-assisted breeding, 29 June–3 July 2009, Zaragoza, Spain

- *Duration: April 2009–Sep 2009*
- *Total budget: $80,000*

Various crops, traits and regions

Lead institute

Carmen de Vicente, GCP

Collaborating institutes

- IAMZ
- WUR

The objective of the course is to introduce the participants to the analysis of single and MET trials using mixed models, and demonstrate how these models can be extended to detect QTL and QEI. The methods will be illustrated both in the context of conventional QTL mapping (i.e. using designed segregating populations) and in the context of LD mapping (i.e. using diverse populations). The course will also touch on the crucial steps of molecular map construction as well as on the analysis of population structure in diverse populations

The course will consist of lecture/discussion sessions in the morning followed by computer practicals in the afternoon where the theory will be demonstrated using actual data sets. We will use the statistical package Genstat for the analyses that has extensive mixed model facilities and its so-called Discovery version is free for non-profit organisations in the developing world (http://www.vsni.co.uk/ products/ discovery/).

Programme contents

Day 1: Introduction to mixed models / Single environment analysis / METs analysis (models for GEI)
Day 2: Genetic map construction from molecular markers
Day 3: Genetic diversity analysis based on molecular markers
Day 4: QTL mapping using mixed models, including the modelling of QEI.
Day 5: LD mapping using mixed models

106. Project No. G4009.07: Capacity building *à la carte* 2009

- *Duration: Oct 2009–Oct 2010*
- *Total budget: $199,992*

Various crops, traits and regions

Lead institute
GCP (Carmen de Vicente)

This project, *à la Carte*, 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 mobilizes 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 2008, the GCP Management Team agreed to make a targeted offer to the Tropical Legumes I teams, in view that the funds for capacity building, as professional development, in TLI were non-existing. Each Principal Investigator of the crop Objectives was requested to present a plan. These ideas were discussed during the TLI Annual Meeting among PI and with their African teams. Afterwards proposals were submitted following the commissioned project template and scheme. A similar budget of 50K was allocated for each crop Objective and the total length of the project was adjusted to one year.

106.1 Project No. G4009.07 (01): Capacity-building à la carte *2009 – TLI students for analysis of drought tolerance in common bean*

- *Duration: Oct 2009–Oct 2010*
- *Total budget: $50,000*

Common bean/Drought tolerance/Sub-Saharan Africa

Lead institute
CIAT (Matthew Blair)
Collaborating institute and scientist

- SARI–Ethiopia (Fitsum Alemayehu)
- DR&SS (Godwill Makunde)
- SABRN/UoZ (Lizzie Kalolokesya)

The project will provide for 1) training for a PhD candidate from Ethiopia (ECABREN region) to engage in marker assisted recurrent selection of common bean for drought tolerance and 2) training at CIAT for current students (SABRN region) in projects that are complementary to the TL1 – bean objective. The candidate identified for Ethiopia is from SARI and is conducting breeding for the southern region of Ethiopia, while the training opportunities are for researchers representing DAR4D (Zimbabwe) and SABRN (Malawi) or EIAR (Ethiopia). The research conducted will support detailed physiological evaluation of the common bean genotypes for drought tolerance and marker assisted selection for common bacterial blight or arcelin-based bruchid resistances which are part of the TL1 project.

106.2 Project No. G4009.07 (02): Capacity-building à la carte *2009 – Capacity-building in modern cowpea breeding*

- *Duration: Oct 2009–Oct 2010*
- *Total budget: 49,800*

Lead institute

UoC–Riverside (Jeffrey D Ehlers)

Collaborating institute and scientist

- UoC–Riverside (Philip A Roberts, Timothy J Close)
- ISRA (Ndiaga Cisse)
- UEM (Rogerio Chiulele)

Cowpea/Drought tolerance/Sub-Saharan Africa

High-throughput genotyping platforms enable new strategies for crop improvement, including more efficient approaches to marker-assisted backcrossing that involve simultaneous selection for flanking markers associated with the target trait(s) and for 'backbone' markers throughout the genome associated with the recurrent parent genetic background. Few if any African plant breeders are trained in the application of this powerful new resource for crop improvement. This Capacity Building Proposal targets training of two African PhD students (from Senegal and Mozambique) in this area, utilizing the new high-throughput SNP genotyping platform we developed for cowpea under Tl-1 Phase I. The students will employ modern breeding tools and a marker-assisted backcrossing strategy to conduct both foreground and background selection to develop an improved version of a preferred local cultivar for each country. QTLs associated with drought tolerance, including the delayed drought-induced senescence trait and drought tolerance candidate genes identified by this and earlier projects will be targeted for introgression, along with markers for resistance to biotic stresses such as diseases caused by Macrophomina phaseolina, which devastates cowpea and other crops when drought is present.

106.3 Project No. G4009.07 (03): Capacity-building à la carte *2009 – Marker-assisted back crossing (MABC) for drought tolerance in chickpea students for analysis of drought tolerance in chickpea (TLI- Kenyan student)*

- *Duration: Dec 2009–Dec 2010*
- *Total budget: 50,160*

Lead institute

- ICRISAT (Rajeev K Varshney)

Collaborating institutes and scientists

- EgU (Paul Kimurto, Richard Mulwa)
- ICRISAT (Pooran Gaur, Mahendar Thudi)

The project will provide a studentship, for a PhD candidate from Egerton University (EU), Kenya for marker assisted introgression of drought tolerance related root trait QTLs into elite Kenyan cultivar of chickpea. Root trait QTLs (a hot spot region) have been identified in the Phase I of TLI. In Phase II, Egerton University Kenya, a collaborative partner, is supposed to take the lead on MABC for introgressing the root trait QTL in the farmers preferred cultivar of Kenya. As a part of TLI, there is a plan to train one PhD student at EU-Kenya and this student has already been identified. This student will undertake the research activities of Activity 5 of TLI- Phase II in Kenya. It is also important to note that this student would be working in close collaboration of ICRISAT and Egerton Uni and would keep on travelling to these places. For instance, majority of crossing and phenotyping work will be carried out at Egerton Uni while genotyping work will be carried out either at ICRISAT or by Molecular Breeding Platform of GCP. Expected costs on genotyping, making crosses and phenotyping etc. has been planned under TLI Phase II proposal. This project will take care of studentship of the student as well as living expenses in Kenya and ICRISAT, India.

106.4 Project No G4009.07 (04): Capacity-building à la carte *2009 – Ensuring 'good' and relevant phenotypic data to feed molecular breeders: the need for long term training of scientists of NARS partners to TLI Objective 1*

- *Duration: Dec 2009–Dec 2010*
- *Total budget: 50,032*

Lead institute

ICRISAT (Vincent Vadez)

Collaborating institute and scientist

- ICRISAT (SN Nigam, Bonny Ntare, Emmanuel Monyo, breeder)
- Intended trainees (Nouhoun Belko, Senegal; Omar, Niger; Philippo Mashamba, Tanzania; Collins Chitawo, Malawi)

The Tropical Legume I project is targeting disease resistance and drought tolerance as the major traits limiting crop production of 4 legumes (groundnut, bean, cowpea, chickpea) in sub-saharian Africa. Skills to phenotype these traits and use the information

in a marker-assisted approach are the key to the future success of breeding in sub-Saharan Africa. For that, there is an urgent need to train a critical mass of plant breeders and technicians to the techniques and protocols that they will need to master in order to usefully assess germplasm and breeding materials and undertake breeding in their locations. In 2008, a training course has been organized at ICRISAT to train a range of scientists and technicians in drought phenotyping. Although very successful, the course did not offer the long term training that is also required to gain full confidence in the skills acquired. In addition, the training was limited to drought phenotyping and had no breeding and disease phenotyping components. Here, we propose a longer term, truly "a la carte" training, where scientists/technicians would receive training over extended stays at ICRISAT's location, and covering all aspects needed for breeding in TLI. The experiments of TLI taking place at ICRISAT would be the learning ground, and those at NARS location would be where trainees would implement the skills acquired, with a close follow up by PI trainers. The objective of the capacity building is to train one scientist or technician, depending on need, at each of the national programmes involved in the Objective 1 (groundnut), although we will also be looking for overlap with objective 2 (cowpea). For the latter reason, the training will be designed to cater specific needs of partners. The training targets are for: (i) Breeding, (ii) drought phenotyping (iii) disease phenotyping (iv) marker use. We want to focus on young scientists already working with the national programme, and through that developing strong linkage CG-NARS.

107. Project No G4009.08: Plant Breeding: concepts & methods – a Learning Module

- *Duration: Nov 2009–Oct 2010*
- *Total budget: 25,058*

Various crops, traits and regions

Lead institute
Cornell University (Theresa Fulton)
Collaborating institute and scientist
CropGen International (Robert Koebner)

A number of new training materials have recently been developed by the GCP, training courses held, and software and bioinformatics tools developed, all directed towards facilitating the use of molecular markers and genomic information by plant breeders. However, all these materials have been based on the assumption that a working knowledge of core plant breeding concepts is already firmly in place. Without this, any positive improvement in plant breeding practice, with or without molecular markers, is unlikely, and much of the effort in exposing trainees to "molecular breeding" will have been wasted. Furthermore, the growing cadre of scientists trained in molecular biology, genetic diversity and other related fields, all too often lack any appreciation or knowledge of basic plant breeding techniques, thereby limiting the potential for fruitful interaction and collaboration between disciplines.

The proposed learning module aims to fill this gap, via the development of a resource covering basic plant breeding concepts and techniques. It seeks, in much the same way as previous SP5 modules have done, to complement, rather than to replace more conventional learning materials; and to supply the content in a way which will be readily accessible for institutions which lack the resources to support comprehensive and up-to-date printed literature. The module will be useful either as a teaching tool or as a self-learning tutorial.

108. Project No G4009.09: The Community of Practices strengthening rice breeding programme using genotyping building strategy and improving phenotyping capacity for biotic and abiotic stresses in the Mekong region

- *Duration: Nov 2009–Oct 2012*
- *Budget by year: $70,800 (2009), $90,270 (2010), $49,560 (2011); Total budget: $210,630*

Lead institute
RGDU (Jonaliza Lanceras-Siangliw)
Collaborating institutes and scientists

- BIOTEC (Theerayut Toojinda)
- NAFRI (Monthathip Chanphengsay)
- CARDI (Ouk Makara)
- DAR (Toe Aung)

Line conversion of popular rice varieties in Laos, Cambodia, Myanmar and Thailand, through the recently concluded project "The Community of Practice: Concept applied to rice production in the Mekong Region: Quick conversion of popular rice varieties with emphasis on drought, salinity and grain quality improvement" proved that working as a community of rice breeders in the region can hasten the development and release of varieties that may answer existing problems affecting rice production in the area. It was also proven that what is useful to one group can be also be beneficial to other groups.

Rainfed lowland areas in Mekong region share common problems in rice production. Drought, soil acidity and salinity or nutrient deficiency are encountered in this region. Diseases and insect pests such as blast, bacterial leaf blight, brown planthopper, white back plant hopper, gal midge and a lot more are also common in the region as well as strains/ races of pathogen and insect biotypes. MAS was introduced to partner institutes and lines that had been developed in the previous project are now ready for more intensive trait validation and field trials. In this proposal, new traits will be added to the improved varieties to be managed by students from each institute through marker-assisted breeding. Proper validation of traits introgressed through efficient phenotyping will strengthen MAS and breeding programmes thus, submergence screening facilities will be established in Laos, Cambodia and Myanmar as well as facilities for bacterial leaf blight, blast and brown planthopper phenotyping.

The objectives of this proposal are to implement research by adding new traits particularly on abiotic and biotic stresses through MAS to the improved varieties from the previous project and to promote phenotyping capacity on abiotic and biotic stresses in order to assess germplasm and developed improved varieties for accurate validation of traits in rice breeding programs of DAR, NAFRI and CARDI.

109. G7009.08/CI–6: Improving drought tolerance in wheat for Asia

- *Duration: Oct 2009–Dec 2009*
- *Total budget: $12,342*

Wheat/Drought tolerance/Asia

Lead institute
CIMMYT (Matthew Reynolds)
Collaborating institutes and scientists

- CAAS (Ruilian Jing)
- IARI (Vinod Prahbu)
- GCP (Carmen de Vicente)

Precise phenotypic data underpins genotyping and much of the breeding process. This project aims to assemble and integrate into breeding programs genetic diversity for WUE and heat tolerance from key sets of genetic resources (including drought-adapted cultivars, advanced lines, landraces, products of inter-specific hybridization and mapping population parents from China, India, CIMMYT, ICARDA, Australia etc.). Many of these materials will be multiplied and provided by CIMMYT. The lines will be shared among the project partners so that analysis of trait and QTL by environment interaction and assessment of genetic gains associated with each trait can be evaluated in target breeding environments. Characterization of target experimental sites will be essential to interpret data, while training in standardized phenotyping protocols for measuring heat and drought adaptive traits and high throughput genotyping will facilitate precise characterization, in all environments, of traits and genotypic variation as well as build human resource capacity (Copied from the Indian project).

The training course on "Phenotyping for drought in wheat" belongs to Objective 1 (Implementation of standardized drought and heat phenotyping protocols to physiologically evaluate genetic populations and germplasm resources in China and India respectively) of each of the two project proposals. It will be conducted at CIMMYT and it is considered a "must" prior to the beginning of other project activities. This background note is submitted to support the disbursement of 2009 start-up funds, as they will be included in the overall project budgets.

110. Project No. G8009.01.04: Establish and support crop molecular breeding Communities of Practice (MBP Activity 1.1.4)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $240,000 (2009), $269,886 (2010), $271,380 (2011), $272,949 (2012), $274,597 (2013); Total budget: $1,328,812*

Lead institute
GCP (Platform Manager)
Collaborating institutes and scientists
None

Establish networks for molecular breeding in regions requiring enhanced support and capacity. Work with communities in these networks by providing tailored capacity in infrastructure, human resource development and technical backstopping. Support the development of Communities of Practice by connecting appropriate groups of crop researchers, mainly breeders, involved in the user cases and willing to share a free flow of experiences and information on modern breeding methods and best field practices.

111. Project No. G8009.05.01: Establishing a Genetic Resource Support service (GRSS) for the plant breeding community (MBP Activity 3.1.1)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $500,000 (2009), $500,000 (2010), $350,000 (2011), $50,000 (2012), $300,000 (2013); Total budget: $2,000,000)*

Various crops, traits and regions

Lead institute
GCP and Agropolis–CIRAD (Jean-Christophe Glaszmann)
Collaborating institutes and scientists

- ICRISAT (Hari Upadhyaya)
- Bioversity International (E Arnaud)
- SGRP, Bioversity (D Williams)
- Agropolis–CIRAD (JF Rami)

The GRSS aims at providing appropriate germplasm to support breeders' activities. It is founded on the idea that any breeding programme needs recurrently or periodically to monitor the genetic base of their programme and possibly decide to broaden it by making use of the most appropriate alternative sources. The GRSS is intended to organise this service in a dedicated manner.

The panel of genetic resource made available will be primarily the product from work conducted by CGIAR centers within the GCP but can also be external products endorsed by the GCP. The potential resources and derived genetic stocks will be inventoried and their quality will be assessed and upgraded in terms of i) accuracy, ii) extent of documentation and iii) availability of seed/plants, so that the service builds on validated genetic stocks that meet high data quality standards.

This process will be followed in close collaboration among actors and will feature ad hoc or more generic workshops which will help share the foundation, the constraints and the opportunities of the GRSS endeavor.

A steering committee representing breeders and germplasm conservation actors, including the main players within the CGIAR, will be established and will monitor quality, demand, and availability of good service providers. It will select the resources and will direct support to the corresponding providers for seed multiplication and distribution. The first service will be established with ICRISAT and will be further expanded in the second year.

The activities of the project will be carried out by a small group at Cirad around the SP1 leader, by the germplasm unit at ICRISAT, by Bioversity and by other groups in germplasm centres to be contracted by GCP headquarters along the project.

The outcomes are a pathway towards a sustainable GRSS, including the concrete implementation on at least two selected cases and its initiation on at least three other cases.

112. Project No G8009.05.02: Marker services (MBP Activity 3.1.2)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $113,788 (2009), $118,056 (2010), $117,939 (2011), $115,746 (2012), $120,690 (2013); Total budget: $586,219*

Lead institute
GCP (Humberto Gomez)
Collaborating institutes and scientists
None

This service will work through the MBP portal to provide a set of options for users to access different marker service laboratories in the public and private sector with clear contractual conditions. Laboratories will be selected on the basis of competitive cost, fit with quality control requirements and expeditious delivery.

Minimum information for accessing private and public service laboratories and respective conditions can be compiled within a few months, based on experience from GSS. This element will however require regular update of information over time as opportunities and conditions might change quite rapidly with the evolution of marker technology. This service will be used by some of the use-case projects by mid-2010.

113. Project No G8009.05.03: Trait and metabolite services (MBP Activity 3.1.3)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $61,463 (2009), $62,886 (2010), $64,380 (2011), $48,699 (2012), $50,346 (2013); Total budget: $287,773*

Lead institute
GCP (Xavier Delannay)

The Portal will provide a set of options for users to access laboratories specialised in the evaluation and analysis of specific traits, such as quality traits, pathology screening or metabolite quantification. Analyses of certain secondary traits or metabolites that are indicative of plant stress tolerance can potentially provide valuable information to be used in breeding. Such analyses are generally prohibitively expensive if done locally, as it is difficult to maintain assay quality and devote the necessary resources for expertise, quality control and specialised facilities.

114. Project No G8009.06.01: Business Plan development (MBP Activity 3.2.1)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $73,713 (2009), $45,636 (2010), $36,380 (2011), $37,949 (2012), $39,596 (2013); Total budet: $233,274*

Lead institute
GCP (Platform Manager)

It is essential to develop a business plan before conducting a multi-cycle MB project. Depending on the nature of the experiment, such a plan may be quite simple or very elaborate, from the transfer of a single region (eg,transgene) to complex selection that can consider the simultaneous transfer of dozens of regions. The critical factor is that the plan must detail all the activities over time, and the costs and benefits of the project to determine if it is worthwhile conducting the experiment. A resource person will be available through the platform for scientists who need support in filling appropriate templates and making decisions. Where necessary, and borrowing from private sector, this person will bridge service providers and breeders, and also follow the evolution of some of the MB projects.

115. Project No G8009.06.02: Information management (MBP Activity 3.2.2)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $86,656 (2009), $63,660 (2010), $64,500 (2011), $65,965 (2012), $68,709 (2013); Total budget: $349,490*

Lead institute
GCP (TBD)

Under this service, assistance will be provided in installing and parameterising the platform information system for use by specific breeding projects. The service to help users to install and parameterise the information system and tools does not need any development per se. Procedures will be developed from user case projects, and the service will be operational when new users join the platform, probably around 2011.

116. Project No G8009.06.03: Data curation (MBP Activity 3.2.3)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $37,619 (2009), $61,560 (2010), $62,901 (2011), $63,366 (2012), $64,963 (2013); Total budget: $290,409*

Lead institute
GCP (Scientist TBD)

This service will assist with capturing and curating current data for particular breeding projects, and in entering them into the integrated information system. This step is absolutely critical for quality control and further sharing of the information. A contact person for each of the user cases will ensure good communication between the platform and the users.

117. Project No G8009.06.04: Design and analysis (MBP Activity 3.2.4)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $187,150 (2009), $187,150 (2010), $180,691 (2011), $177,462 (2012), $177,462 (2013; Total budget: $909,915*

Lead institute
WUR (Fred van Eeuwijk; Marcos Malosetti as collaborator)

This service will provide support on statistics and quantitative genetics. It includes training in data generation, handling, processing and interpretation, as well as experimental design from field planting to MAS and MAB schemes. It provides assistance with the 'translation' of the molecular context to the breeding context and it will take care that the methodology developed for design and analysis of breeding trials is rapidly available to the users.

118. Project No G8009.06.05: Phenotyping sites and screening protocols (MBP Activity 3.2.5)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $702,250 (2009), $702,250 (2010), $431,250 (2011), $285,500 (2012), $162,500 (2013); Total budget: $2,283,750*

Lead institute
GCP (Xavier Delannay)
Collaborating institutes and scientists

- CIAT (Glenn Hyman)
- KUL (Sam Geerts)

Through this service, users will be able to access information on phenotyping sites, protocols and potential collaborators to ensure that selection is carried out under appropriate biotic and abiotic stresses, and that the adaptation of germplasm is well characterised. Some of those sites will be hubs in the GCP phenotyping network: over the next five years, this project proposes to invest in establishing and enhancing phenotyping facilities and expertise at a few key GCP hubs and at other strategic phenotyping sites for NARS. The service for phenotyping sites and screening protocols will build on a current effort to document and implement reference phenotyping sites as well as the development of relevant screening protocols. A large effort will be needed during the early years of the project to have information and protocols at an appropriate level and format, and, where necessary, to improve sites before the first phenotyping of segregating populations will take place (2010–11). Developing this service will continue throughout the entire project cycle.

119. Project No G8009.06.06: Genotying Support Service (MBP Activity 3.2.6)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $400,000 (2009), $400,000 (2010), $400,000 (2011), $401,777 (2012), $398,771 (2013); Total budget: $800,548*

Lead institute
GCP (Humberto Gómez-Paniagua)

The GSS was developed to facilitate NARS access to genotyping technologies, and, in turn, to bridge the gap between lab and field research. This service provides financial and technical support for NARS breeders to access cost-efficient genotyping services worldwide, and supports training activities in experimental design and data analysis for molecular breeding projects.

The GSS is an ongoing GCP initiative. It will be further refined over the first year of the project, in particular to include MAB experiments in addition to the diversity analysis and MAS experiments facilitated so far. There will be regular updates of protocols and technology every few months, and use of this service should increase in both intensity and diversity as new users come on board.

120. Project No G8009.06.07: IP Helpdesk (MBP Activity 3.2.7)

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $100,000 (2009), $50,000 (2010), $50,000 (2011), $25,000 (2012), $25,000 (2013); Total budget: $250,000*

Lead institute
GCP (Humberto Gómez-Paniagua)

This service will provide support on intellectual property rights and freedom to operate in the arena of biotechnology and germplasm use. The nature of this service might need to be reconsidered to address emerging issues of MBP users. The use-case projects will provide good case studies to identify bottlenecks, especially in germplasm exchange.

Projects on NCE into 2009 or beyond

121. 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 with NCE to Dec 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)
Collaborting institutes
Members of the IGD

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.

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

- *Duration: Nov 2006–Oct 2007 with NCE to May 2010*
- *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.

123. 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 with NCE to Apr 2009*
- *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)
- IRRI: Abdelbagi Ismail
- CIAT: Martin Fregene

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.

124. 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 with NCE to Apr 2009*
- *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)
- URU (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.

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

- *Duration: Between Jan 2008–Dec 2008 with NCE to Dec 2009 for some projects*
- *Total budget: $168,320*

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 programs.

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. It is not oriented to support conference participation. 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.

Current projects

126. 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 – V Vadez, ICRISAT (effective June 2008), D Hoisington, ICRISAT (May 2007–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 – R Varshney, ICRISAT (effective June 2008), D Hoisington, ICRISAT (May 2007–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

127. Project No G4007.23/CI–6: 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.

Projects on NCE into 2009 or beyond

129. 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 with NCE to Feb 2009*
- *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)
- IGKV (Satish Verulkar, PR Dongre)
- CRRI (ON Singh, P Swain, L Bose)
- CRURRS (PK Sinha, NP Mandal)
- NDUAT (JL Dwivedi)
- UAS–Bangalore (Shailaja Hittalmani)
- TNAU (R Chandrababu, S Robin)
- BAU (BN Singh, RL Mahato)
- BF (HE Shashidhar, Abhinav Jain)

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.

130. GCP/Rockefeller project G4005.70.02/CI–1: Tapping crop biodiversity for the resource poor in East and Central Africa (IITA)

- *Duration: July 2005–June 2008 with NCE to Jun 2009*
- *Budget by year: $74,750 (2005), $63,250 (2006), $0 (2007); Total budget: $138,000*

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 (Fernando Chitio)
- ISAR (Gashaka Gervis)
- ARI–Naliendele (Geoffrey Mkamilo)
- NaCRRI (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.

131. Project No G4007.05/CI–6: Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco

- *Duration: Jan 2007–Dec 2009 with NCE to Dec 2010*
- *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.

Other projects

132. G8009: A Molecular Breeding Platform

- *Duration: Jul 2009–Jul 2014*
- *Budget by year: $4,693,950 (2009) $4,885,931 (2010), $4,154,326 (2011), $3,805,007 (2012), $3,440,725 (2013); Total: $20,979,939*

Lead institute
GCP (Graham McLaren)
Collaborating institutes and scientists

- GCP (Graham McLaren, Carmen de Vicente, Xavier Delannay, Humberto Gómez-Paniagua, A Okono, others TBD)
- AAFC (Fran Clarke, Shawn Yates)
- ICIS development team (IRRI & CIMMYT)
- CIMMYT (Arllet M Portugal, Jose Crossa, Guy Davenport, SriKalyani P)
- ICRISAT (Trushar Shah)
- WUR (Fred van Eeuwijk, Marcos Malosetti, Hans Jansen, Martin Boer)
- CSIRO (Scott Chapman, X Sirault)
- Agropolis–INRA (Alain Charcosset, Laurence Moreau
- UoQ (Mark Dieters)
- CIMMYYT/CASS (Jiankang Wang)
- CAAS (Huihui Li)
- IRRI (Martin Senger, Thomas Metz, Richard Bruskiewich, R. Serraj, Breeding Informatics Specialist TBD)
- IRRI–CRIL Breeding Informatics Specialist (TBD)
- GCP/Agropolis–CIRAD (JC Glaszmann)
- Bioversity (E Arnaud)
- SGRP (D Williams)
- Consultant (V Anthony)
- ICRISAT (H Upadhyaya, Vincent Vadez)
- Other CGIAR germplasm centres
- CU (Theresa Fulton, T Setter)
- Agropolis (C Welcker)
- GCP Staff
- CIAT (G Hyman)
- KUL (S Geerts)
- EMBRAPA (R Gomide)

Purpose:
Provide access to modern breeding technologies, breeding material and related information in a centralised and functional manner to improve plant breeding efficiency – and therefore crop productivity – in developing countries.

Aim:
Develop and deploy a sustainable web-based Molecular Breeding Platform (MBP) as a one-stop-shop for information, analytical tools and related services to design and efficiently conduct molecular-assisted breeding experiments.

Such a platform will enable breeding programmes in the public and private sector to accelerate variety development for developing countries using marker technologies for various breeding purposes, such as major gene or transgene introgression, gene pyramiding and complex marker-assisted recurrent selection (MARS), and in the near future, genome-wide marker-assisted selection (GWMAS). The platform will also deliver support services to guide and train breeders from national agricultural research systems in accessing and using marker technologies. Critical for the adoption of modern breeding technologies in developing countries will be supporting communities of practice on molecular breeding for the most important food security crops, developing local infrastructure to improve plant phenotyping, and appropriate and targeted capacity building. Through these efforts, the platform will be part of a global strategy on food security and poverty alleviation.

MBP Component 1: Molecular Breeding Portal and Helpdesk

- *Budget by year: $703,326 (2009), $617,716 (2010), $629,942 (2011), $625,239(2012), $632,379(2013); Total budget: $3,208,602*

The structures, policies and procedures for the direction and management of the platform will be established under this component including the Steering Committee, Platform Manager tasks and the business plan. Primary access to the services and applications of the Molecular Breeding Platform will be through a web-based portal which will be established and maintained. A platform helpdesk will also be established to ensure effective communication with users, especially those without adequate internet access and to coordinate human resource development for molecular breeding for food security through crop yield improvement.

Objective 1.1 Establish and Manage the Molecular Breeding Platform
The three aspects of this component, establishment, portal and helpdesk will be achieved through separate activities, as listed below:

1.1.1. Establishment of the molecular breeding platform
1.1.2. Develop and deploy the molecular breeding portal
1.1.3. Establish molecular breeding platform helpdesk and coordinate training and communication activities
1.1.4. Establish and support crop molecular breeding Communities of Practice

MBP Component 2: Information System

- *Budget by year: $1,727,986 (2009), $2,077,017 (2010), $1,766,343 (2011), $1,608,305 (2012), $1,400,308 (2013); Total budget: $8,579,959*

The overall objective of Component 2 of the MBP is the development, deployment and support of a comprehensive information system for molecular plant breeding. This is divided into three modules: 1) Reviewing, deploying and supporting existing tools for information management and logistics of general breeding workflows. These tools need to be modular in nature and allow customisation and integration with existing tools and breeding processes. 2) Reviewing existing applications for statistical and genetic analysis for molecular breeding, adapting those to work with general breeding applications and processes and conducting research and development on new methodology and tools as required. 3) Development of infrastructure to integrate dispersed information resources and, establishing a cyber network connecting these information resources to the statistical and genetic analysis in a configurable workflow.
The development and deployment of these modules will be achieved by the following objectives and activities:

Objective 2.1 Make existing tools for data management and breeding logistics available to molecular breeding projects through the MBP.
Identify, deploy and support tools facilitating management of germplasm lists, pedigrees, intellectual property and other passport data

2.1.2. Identify, deploy and support tools for management of phenotypic characterisation and evaluation
2.1.3. Identify, deploy and support tools for management of genotypic characterisation

Objective 2.2 Develop a suite of analysis, prediction and simulation tools for MAB
2.2.1. Develop and deploy statistical and genetic analysis methodology for molecular breeding
2.2.2. Develop and deploy cross prediction and selection methodology for molecular breeding
2.2.3. Develop and deploy simulation tools for complex G-E systems

Objective 2.3 Develop an information network, decision support applications and a workflow management system for molecular breeding
2.3.1. Establish middleware infrastructure for networking databases and applications
2.3.2. Develop and integrate visualisation and decision support applications
2.2.3. Implement a configurable workflow system for molecular breeding

MBP Component 3: Services

- *Budget by year: $2,262,638 (2009), $2,191,198 (2010), $1,758,041 (2011), $1,571,464 (2012), $1,408,037 (2013); Total budget: $9,191,378*

Component 3 of the Molecular Breeding Platform will provide access and support for a full range of services required to run a successful molecular breeding programme. The objective of the first module, Breeding Services, is to provide access to germplasm and a mechanism for exchange of germplasm, access to validated marker technology and to services for evaluation of specific traits and metabolites. The second component will provide training and support to users lacking expertise in a range of required support functions from planning to deployment.
The goals of the services component will be achieved through the following objectives and activities:

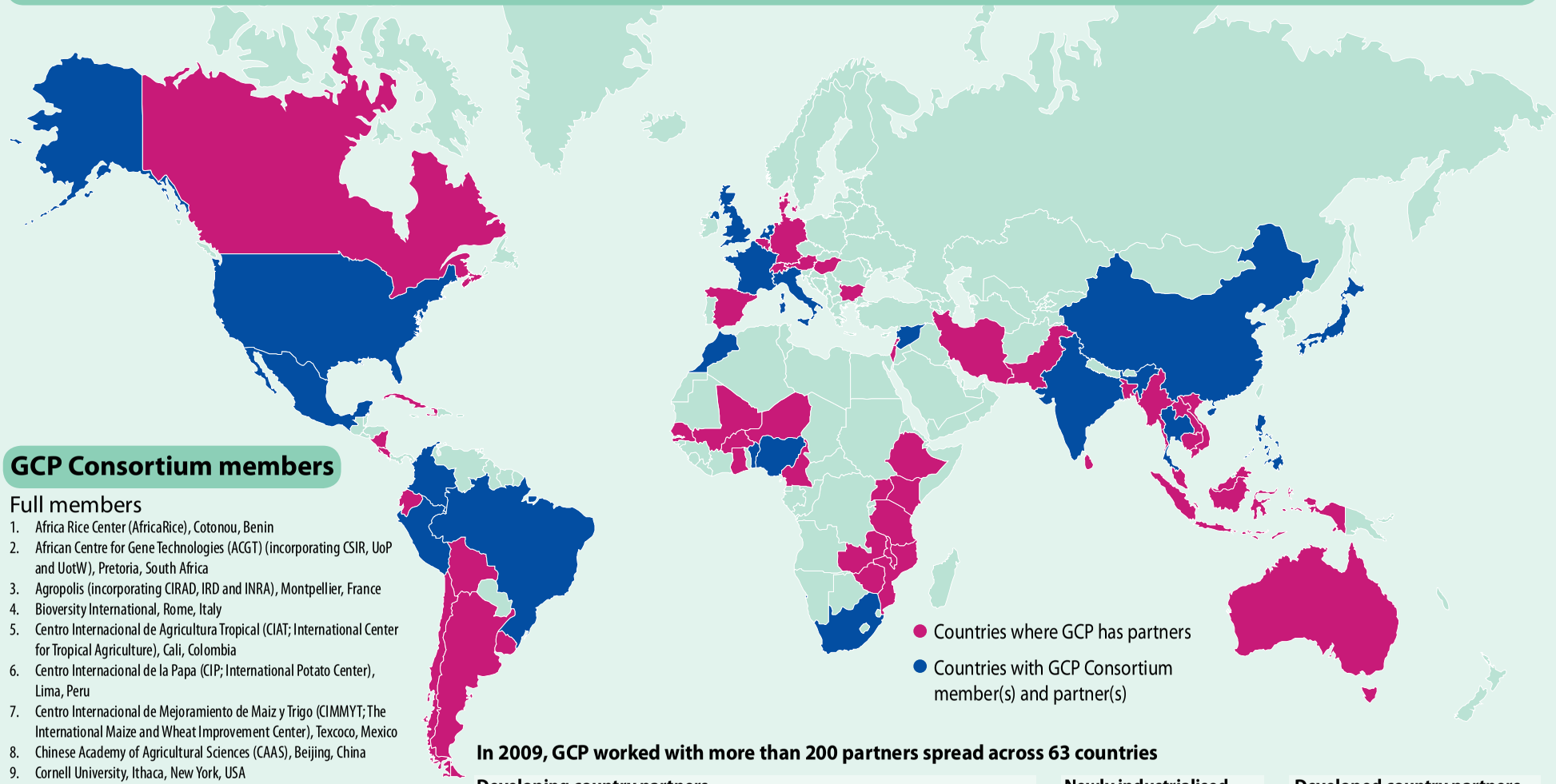
Objective 3.1 Provide access to critical molecular breeding services.
3.1.1. Genetic Resource Support Service
3.1.2. Marker Services
3.1.3. Trait and Metabolite Services

Objective 3.2 Provide assistance with a range of molecular breeding support services.
3.2.1. Business Plan Development
3.2.2. Information Management
3.2.3. Data Curation
3.2.4. Design and Analysis
3.2.5. Phenotyping Sites and Screening Protocols
3.2.6. Genotyping Support Services
3.2.7. 7. IP Helpdesk

MBP activities are reported under their Subprogramme home.

For this start-up year of MBP, details of the various activtities are given within this document in their respective Subprogramme section, and marked 'MBP Activity x.x.x').

Where in the world is GCP? The GCP network in 2009



GCP Consortium members

Full members

1. Africa Rice Center (AfricaRice), Cotonou, Benin
2. African Centre for Gene Technologies (ACGT) (incorporating CSIR, UoP and UotW), Pretoria, South Africa
3. Agropolis (incorporating CIRAD, IRD and INRA), Montpellier, France
4. Bioversity International, Rome, Italy
5. Centro Internacional de Agricultura Tropical (CIAT; International Center for Tropical Agriculture), Cali, Colombia
6. Centro Internacional de la Papa (CIP; International Potato Center), Lima, Peru
7. Centro Internacional de Mejoramiento de Maiz y Trigo (CIMMYT; The International Maize and Wheat Improvement Center), Texcoco, Mexico
8. Chinese Academy of Agricultural Sciences (CAAS), Beijing, China
9. Cornell University, Ithaca, New York, USA
10. Empresa Brasileira de Pesquisa Agropecuària (EMBRAPA; Brazilian Agricultural Research Corporation), Brasilia, Brazil
11. Indian Council of Agricultural Research (ICAR), New Delhi, India
12. International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo, Syria
13. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India
14. International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria
15. International Rice Research Institute (IRRI), Los Baños, The Philippines
16. John Innes Centre (JIC), Norwich, UK
17. National Institute of Agrobiological Sciences (NIAS), Tsukuba, Japan
18. Wageningen University and Research Centre (WUR), Wageningen, The Netherlands

Provisional members

19. Centro de Investigación y de Estudios Avanzados (CINVESTAV), Irapuato, Mexico
20. Institut national de la recherche agronomique (INRA), Rabat, Morocco
21. Istituto Agronomico per l'Oltremare (IAO), Florence, Italy
22. National Center for Genetic Engineering and Biotechnology (BIOTEC), Bangkok, Thailand

In 2009, GCP worked with more than 200 partners spread across 63 countries

Developing country partners

Central and West Asia and North Africa

1. Iran
2. Morocco
3. Syrian Arab Republic

Eastern Europe

4. Bulgaria
5. Hungary

Latin America and the Caribbean

6. Argentina
7. Bolivia
8. Chile
9. Colombia
10. Costa Rica
11. Cuba
12. Ecuador
13. Haiti
14. Nicaragua
15. Peru
16. Uruguay

South and Southeast Asia

17. Bangladesh
18. Cambodia
19. Indonesia
20. Laos
21. Myanmar
22. Pakistan
23. Sri Lanka
24. Vietnam

Sub-Saharan Africa

25. Benin
26. Burkina Faso
27. Cameroon
28. Ethiopia
29. Ghana
30. Kenya
31. Malawi
32. Mali
33. Mozambique
34. Niger
35. Nigeria
36. Senegal
37. Tanzania
38. Uganda
39. Zambia
40. Zimbabwe

Newly industrialised country partners

Latin America and the Caribbean

41. Brazil
42. Mexico

South and Southeast Asia

43. China
44. India
45. Malaysia
46. Thailand
47. The Philippines

Sub-Saharan Africa

48. South Africa

Developed country partners

Asia

49. Israel
50. Japan

Europe

51. Austria
52. Belgium
53. Denmark
54. France
55. Germany
56. Italy
57. Spain
58. Switzerland
59. The Netherlands
60. United Kingdom

North America

61. Canada
62. USA

Oceania

63. Australia

GCP Annual Research Meeting participants, September 2009, Bamako, Mali.

"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 (GCP)
Hosted by CIMMYT

(Centro Internacional de Mejoramiento de Maíz y Trigo;
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Available online at: http://www.generationcp.org/brochure.php#Exec-summaries_Project-briefs