Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE-POOR

2007 Project briefs

GCP's five Subprogrammes

Subprogramme 1 (SP1): 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.

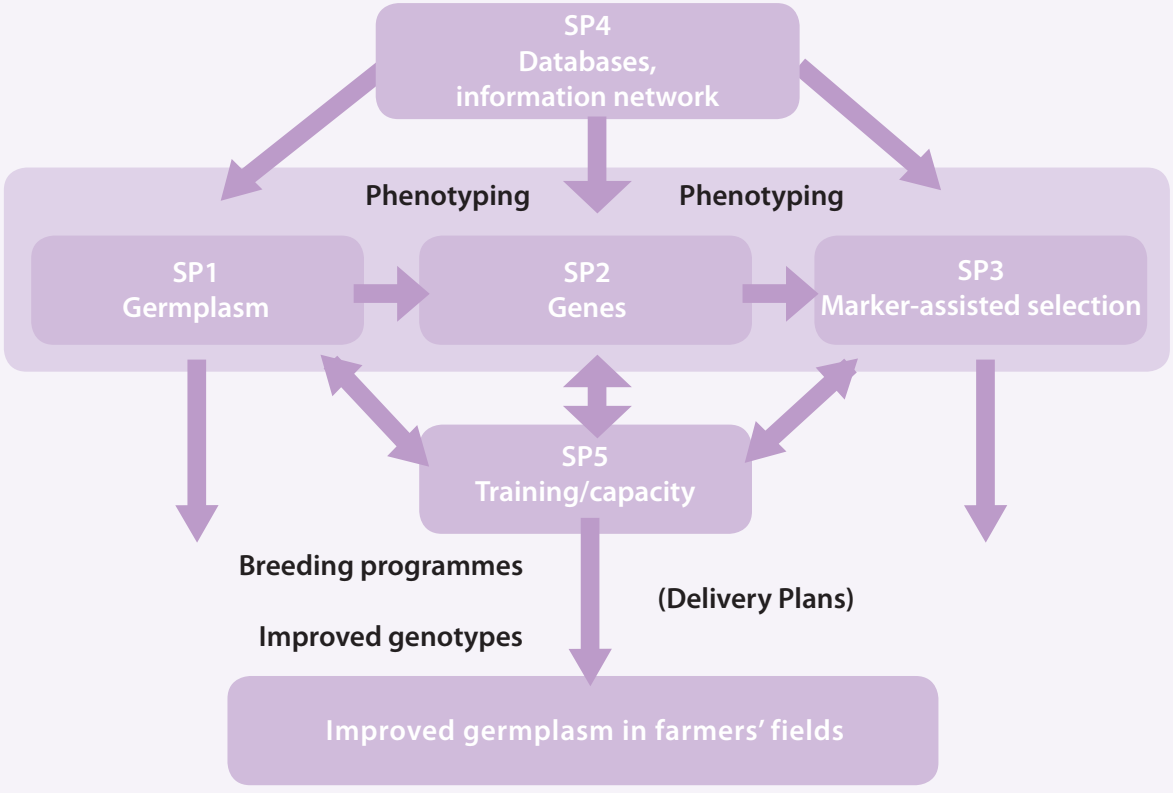
Subprogramme 2 (SP2): Genomics towards gene discovery
Uses or develops genomic tools and technologies and evaluates interdisciplinary approaches to better understand gene function and interaction to improve knowledge of gene systems across crops.

Subprogramme 3 (SP3): 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 (SP4): 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 (SP5): Capacity-building and enabling delivery
Empowers scientists in developing country national programmes to use modern breeding approaches. SP5 also coordinates the development and implementation of project Delivery Plans and is responsible for intellectual property issues, as well as policy and impact assessment research.

GCP's five Subprogrammes



Generation Challenge Programme

2007 Project briefs

October 2008

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Acronyms

ABRII	Agricultural Biotechnology Research Institute of Iran
ACCI at UKZN	African Centre for Crop Improvement , South Africa
ACGT	African Centre for Gene Technologies, South Africa
ACPFG	Australian Centre for Plant Functional Genomics Pty Ltd
ARI	Agricultural Research Institute, Tanzania
ARI—HAS	Agricultural Research Institute of the Hungarian Academy of Sciences
BARI	Bangladesh Agricultural Research Institute
BAU	Birsa Agricultural University, India
BecA	Biosciences Eastern and Central Africa, Kenya
BGBM	Botanic Garden and Botanical Museum Berlin–Dahlem, Germany
BIOTEC	National Center for Genetic Engineering and Biotechnology, Thailand
CARDI	Cambodia Agricultural Research and Development Institute
CAAS	Chinese Academy of Agricultural Sciences
CARBAP	Centre africain de recherche sur bananas et plantains, Cameroon
CAS–IP	CGIAR Central Advisory Service on Intellectual Property
CERAAS	Centre d'Etude Régional pour l'Amélioration de l'Adaptation à la Sécheresse, Senegal
CIAT	International Center for Tropical Agriculture
CIHEAM–IAMM	Institut Agronomique Mediterranéan de Montpellier, France
CIMMYT	International Maize and Wheat Improvement Center
CINVESTAV	Centro de Investigación y de Estudios Avanzados, Mexico
CIP	International Potato Center
CIRAD	Centre de coopération internationale en recherche agronomique pour le développement, France
CNG	Centre National de Génotypage, France
CNRS	Centre National de la Recherche Scientifique, France
CORPOICA	Corporación Colombiana de Investigación Agropecuaria, Colombia
CRI–CSIR	Crop Research Institute, at the Council for Scientific and Industrial Research, Ghana
CRIL	Crop Research Informatics Laboratory
CRRI	Central Rice Research Institute, India
CRURRS	Central Rainfed Upland Rice Research Station, India
CSIRO	Commonwealth Scientific and Industrial Research Organisation, Australia
CSU	Colorado State University, USA
DAR	Department of Agricultural Research, Myanmar
DArT P/L	Diversity Arrays Technology Pty Ltd
DWR	Directorate of Wheat Research, Karnal, India
EBI	European Bioinformatics Institute, United Kingdom
EMBRAPA	Empresa Brasileira de Pesquisa Agropecuária, Brazil
ETH	The Swiss Federal Institute of Technology
FABI	Forestry and Agricultural Biotechnology Institute, South Africa
GCP	Generation Challenge Programme
HAAS	Institute of Dry Farming, Hebei Academy of Agricultural Sciences, China
HZAU	Huazhong Agricultural University, China
IAO	Instituto Agronomico per l'Oltremare, Italy
IARI	Indian Agriculture Research Institute
ICABIOGRAD	Indonesian Centre for Agricultural Biotechnology and Genetic Resources and Research Development
ICAR	Indian Council of Agricultural Research
ICARDA	International Center for Agricultural Research in the Dry Areas
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
ICTA	Instituto de ciencia y technologia agricolas , Guatemala
IEB	Institute of Experimental Botany, Czech Republic
IER	Institut d'Economie Rurale, Mali
IFFIVE—INTA	Argentina and International Fund for Science
IFPRI	International Food Policy Research Institute
IGAU	Indira Gandhi Agricultural University,India
IGD	Institute for Genomic Diversity at Cornell University, USA
IITA	International Institute of Tropical Agriculture
ILRI	International Livestock Research Institute
INCA-Cuba	Instituto Nacional de Ciencias Agricolas, Cuba
INERA	Institut de l'Environnement et de Recherches Agricoles, Burkina Faso
INIA	Instituto de Investigaciones Agropecuarias, Chile
INIA	Instituto Nacional de Investigación Agropecuaria, Uruguay
INIA	Instituto Nacional de Investigación Agropecuaria, Venezuela
INIBAP	The International Network for the Improvement of Banana and Plantain at Bioversity International
INRA	Institut National de la Recherche Agronomique, France
INRA	Institut National de la Recherche Agronomique, Morocco
INRAN	Institut National de Recherches Agronomiques du Niger
IPB	Institut Pertanian Bogor, Bogor Agriculture University, Indonesia
IPK	Institute for Plant Genetics and Crop Plant Research, Germany
IRD	Institut de Recherche pour le Dévelopment,

	France
IRRI	International Rice Research Institute
ISRA	Institut Sénégalais de Recherches Agricoles, Senegal
JIC	John Innes Centre, UK
JIRCAS	Japan International Research Center for Agricultural Sciences
KARI	Kenya Agriculture Research Institute
LAAS	Luoyang Academy of Agricultural Sciences, China
NARC	Nepal Agricultural Research Council
NAARI	Namulonge Agricultural and Animal Production Research Institute, Uganda
NAFRI	National Agricultural and Forestry Research Institute, Laos
NAU	Nanjing Agricultural University, China
NCGR	National Center for Genome Resources, USA
NDUAT	Narendra Deva University of Agriculture and Technology, India
NIAB	National Institute of Agricultural Biology, UK
NIAS	National Institute of Agrobiological Sciences, Japan
NRCRI	National Root Crops Research Institute, Nigeria
NCSU	North Carolina State University, USA
NSFCRC	Nakhon Sawan Field Crops Research Center, Thailand
NWSUAF	University of Agriculture and Forestry, China
PROINPA	Promoción e Investigación de Productos Andinos, Bolivia
RCB	Research Center for Biotechnology, Indonesia
RGDU	Rice Gene Discovery Unit, Thailand
SAAS	Shanxi Academy of Agricultural Sciences, China
SARI	Savannah Agricultural Research Institute, Ghana
SAU	Sichuan Agriculture University, China
SCRI	Scottish Crop Research Institute
SGRP	The System-wide Genetic Resources Programme
SIRDC	Scientific and Industrial Research and Development Centre, Zimbabwe
TIGR	The Institute for Genomic Research, USA (note: TIGR has merged with other institutes to form the J. Craig Venter Institute)
TNAU	Tamil Nadu Agricultural University, India
UAS	University of Agricultural Sciences, India
UBU	Ubon Ratchatani University, Thailand
UCB	Universidade Católica de Brasilia, Brazil
UC–Davis	University of California, Davis
UC–Riverside	University of California, Riverside
UGA	University of Georgia, Athens, USA
UKZN	University of KwaZulu Natal, South Africa
USDA–ARS	United States Department of Agriculture–Agricultural Research Service
VBI	Virginia Bioinformatics Institute
VPKAS	Vivekananda Parvatiya Krishi Anusandhan Sansthan, India (affiliated with ICAR)
WARDA	Africa Rice Center
WUR	Wageningen University and Research Centre
YAAS	Yunnan Academy of Agricultural Sciences, China

I. COMPETITIVE PROJECTS

Subprogramme 1: Genetic diversity of global genetic resources

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

- *Duration: Jan 2005–Dec 2008 with NCE to Sep 2009*
- *Budget by year: $331,700 (2005), $337,800 (2006), $325,100 (2007), $80,200 (2008); Total budget: $1,074,800*

Rice/Various regions/Drought tolerance

Lead institution
Agropolis–IRD/CIAT (Mathias Lorieux)
CIAT (Joe Tohme)
Collaborating institutions

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

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

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

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

Maize/Various regions/Drought tolerance, low soil fertility

Lead institution
CIMMYT (Marilyn Warburton)
Collaborating institutions

- Cornell University (Edward Buckler)
- Agropolis–INRA (Alain Charcosset)
- KARI (James Gethi)
- NSFCRC (Pichet Grudloyma)
- SIRDC (Esther Khosa)
- Cornell University (Tim Setter)
- SAU (Li Wanchen)
- CIMMYT (José Crossa, Xu Yunbi, Magorokosho Cosmos, Jose Luis Araus)

Drought and low soil fertility are the major limiting factors for cereal-crop production in developing countries. The objective of this project is to use the natural variation inherent in the maize genome for the dissection of drought tolerance and for the identification of superior alleles. While maize grows in a wide range of environments and is the most diverse crop in the world, we do not know the genes that are responsible for these adaptations. For phenotypic selection, although allowing genetic progress, crops need to be fully evaluated in every environment, which is costly and time consuming. Association studies, proposed in this project, are based on correlation between a gene sequence and plant performance for target traits, and represent a powerful approach to evaluate candidate genes regulating plant phenotype. This project will focus on evaluating the genes in two major pathways that are involved in drought tolerance. We will build upon previous

mapping approaches that have identified genomic regions containing a few hundred genes, and use high resolution approaches that can evaluate individual genes. This high resolution mapping will require combining rapid molecular approaches with careful evaluation of diverse germplasm for drought tolerance and physiological response. Additionally, by screening several hundred diverse lines this project maximises its potential to identify the best alleles in the maize gene pool. The discovery of superior alleles at the gene level will permit the development of molecular markers that can facilitate breeding drought tolerance in a wide range of germplasm. One important benefit of working with the natural variation, it is that any discovery can be rapidly converted to improved breeding materials without the societal and regulatory obstacles of transgenics materials. Because of the genetic and physiological commonalities among cereal crops, this knowledge gathered in maize can be applied to all other cereal crops.

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

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

Maize/Various regions/Drought tolerance

Lead institution
CIMMYT (Marilyn Warburton)
Collaborating institutions

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

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

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

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

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

Lead institution
ICARDA (Michael Baum)
Collaborating institutions

- NIAB (Wayne Powell, K Stamati)
- ICARDA (Salvatore Ceccarelli, Stefania Grando, Sripada M. Udupa)
- Tishreen University (Wafaa Choumane)
- ACPFG (P Langridge, Mark Tester)
- University of Adelaide (JK Eglinton)

In recent years analysis of genetic variation has focused on the study of changes in DNA coding for proteins. It is now becoming increasingly clear that this only accounts for one aspect of heritable variation and for many traits, notably tolerance to environment stresses, the level of gene expression is also likely to be of great importance. If changes in gene expression underlie many evolutionary changes in phenotype,

then identifying the genetic variants that regulate gene expression is a significant and important endeavor. One of the key problems in genetics is how to identify this type of variation. We propose a robust, quantitative approach to efficiently identify plant genes that harbor such regulatory variants. The approach is novel and particularly amenable to plants since it is based on monitoring gene expression in experimentally created hybrids. A successful outcome will provide a new mechanism to connect genotype to phenotype based on changes in gene expression rather than changes in the structure of an encoded protein. This approach will be used to characterise a series of genes identified and reveal potential candidates for tolerance to drought, frost, cold and salinity stresses. The approach is generic and widely applicable. The project will also involve training researchers in Developing Countries and create a high quality collaborative network of researchers delivering new knowledge on genetic diversity and translatable outputs for the developing world.

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

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

Rice/Africa, Asia/Drought tolerance

Lead institution
Agropolis–LGDP/IRD (Alain Ghesquière)
Collaborating institutions

- Philippine Rice Research Institute (A Alfonso)
- IER (Fousseyni Cissé)
- Fedearroz (M Diago)
- INERA (H. Drissa)
- University of Arizona (DW Galbraith)
- Agropolis–IRD / CIAT (M Lorieux)
- CIAT (C.P Martinez, J Tohme)
- WARDA (MN Ndjiondjop, M Semon)
- Perpignan University (O Panaud)
- Punjab Agricultural University (JS Sidhu)

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

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

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

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

6. 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/Various regions/Drought tolerance

Lead institution
SCRI (Robbie Waugh)
Collaborating institutions

- SCRI (Dave Marshall, Joanne Russell)
- ICRADA (Michael Baum, Stefania Grando, Maria von Korff Schmising, Salvatore Ceccarelli)
- Oregon State University (Patrick M Hayes)
- INIA (Ivan Matus)
- Universidad de Talca (Alejandro Del Pozo)
- UC–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.

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

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

Rice, wheat/Asia/Drought tolerance

Lead institution
IRRI (John Bennett)
Collaborating institutions
- CSIRO (Richard Richards, Tony Condon, Rudy Dolferus, Lynne McIntyre)
- IRRI (Kenneth McNally, Rachid Serraj)
- NIAS (S Kikuchi, Kouji Satoh)
- TNAU (RC 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.

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

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

Rice/Asia/Salinity and phosphorus deficiency

Lead institution
IRRI (Abdelbagi M. Ismail)
Collaborating institutions
- IRRI (David J Mackill, Michael Thomson, Sigrid Heuer, Xiaochun Lu, Glenn Gregorio, Rakesh Kumar Singh)
- JIRCAS (Matthias Wissuwa)
- University of California (Eduardo Blumwald)
- Dhaka University (Zeba I Seraj)
- ICABIORAD (Masdiar Bustamam)
- University of California (Timothy J Close)
- ABRII (Ghasem H Salekdeh)
- NIAS (Massahiro Yano)

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

Amendments and management options for these soils are too expensive for the resourcepoor farmers commonly living in these areas; however, solutions through improved germplasm are affordable to farmers and are becoming more feasible with the developments in modern molecular tools that are becoming available to unravel the genetic basis of tolerance. Combining mechanisms underlying tolerance for complex traits such as salt and P-deficiency as well as those for multiple stresses is now feasible once the genetic components or genes for tolerance are tagged to allow them to be traced in the

breeding process. We aim to identify and tag the genes for tolerance for salinity and P-deficiency. For both stresses, we have made excellent progress in understanding the biology and in identifying major chromosomal regions that are associated with tolerance. We will further fine-map these regions and use modern molecular approaches to discover the genes that are involved in tolerance using a range of molecular strategies. We will also use biological information and genes discovered from other crops to facilitate the identification of similar genes in rice. Ultimately, we will develop a marker system to allow the efficient incorporation of these genes into popular, yet intolerant, varieties, initiate a marker-assisted breeding system with NARES partners, and provide them with the training needed to carry out these activities.

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

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

Maize, rice/Africa, Asia/Disease resistance

Lead institution
Cornell University (Rebecca Nelson)
Collaborating institutions

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

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

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

- *Duration: Jan 2005–Dec 2007 with NCE to Oct 2008*
- *Budget by year: $387,000 (2005), $300,000 (2006), $213,000 (2007), Total budget: $900,000*

Rice, wheat/Asia, Latin America/Disease resistance

Lead institution
Agropolis–INRA (Jean-Benoit Morel)
Collaborating institutions

- Agropolis–CIRAD (D Tharreau, JL Nottéghem, E Guiderdoni)
- EMBRAPA (M Ferreira, G de Capdeville, S Scagliusi, Postdoc, A Bonato, J Maciel, P Scheeren, A Mehta, MS Chaves, S Brammer)
- IAPAR (a state research institute collaborating with EMBRAPA): Y Mehta
- UC–Davis (P Ronald, KH Jung)
- CIMMYT (R Sing, M William)
- NIAS (S Kikuchi, K Satoh)
- JIC (L Boyd, H Tufan)
- Agropolis–INRA (C Feuillet, P Sourdille)

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

Non-host resistance also represents one promising defence mechanism in developing durable resistance against plant pathogens, namely due to its effectiveness against a broad range of pathogen species and its durability in nature. The

proposed project will strengthen and extend ongoing research in rice and wheat and aims at defining the signalling and effector genetic components involved in non-host resistance in cereals to devise novel defence strategies which have the potential to yield durable resistance against host pathogens in cereals.

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

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

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

Various crops/Africa, Asia/Drought tolerance

Lead institution
Agropolis–INRA (François Tardieu)
Collaborating institutions

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

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

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

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

Sorghum, maize, rice, Triticea/Africa, Asia/Aluminium tolerance

Lead institution
USDA/ARS and Cornell University (Leon V Kochian)
Collaborating institutions

- EMBRAPA (Jurandir Magalhaes, Claudia Guimarães, Vera Alves, Newton Carneiro, Robert Schaffert, Sandra Brammer, Pericles Neves, Rosangela Bevitori)
- Moi University, Kenya (Samuel Gudu)
- USDA–ARS and Cornell University (Owen Hoekenga, Ed Buckler)

One of the most important soil-related factors limiting agriculture in developing countries is acid soil pH (pH < 5). Acid soils occur for both natural and humanity-derived reasons. On acid soils, regardless of their source, toxic levels of aluminum (Al) ions are released into soil solution, where they damage roots and impair their growth and function. This damage results in reduced nutrient and water uptake, with concomitant reductions in crop yield.

There is considerable natural variation in Al tolerance both within and between plant species, and we have assembled an interdisciplinary group of scientists to take advantage of this variation to improve crop tolerance to Al toxicity on acid soils. This proposal details an interdisciplinary project that will characterise recently isolated cereal Al tolerance genes as well as identify novel Al tolerance genes and physiological mechanisms in a range of cereal species (sorghum, maize, rice and the *Triticeae*). The research group we have assembled has considerable expertise in the genetics, molecular biology and physiology of aluminum tolerance in these crops, and has available the necessary genetic resources to ensure the success of this project. We will use information from candidate genes identified in wheat and sorghum, as well as ongoing progress from our genetic mapping and cloning programme in maize, to identify and verify candidate Al tolerance genes in several cereals species. The long-term goals of this research are to generate cereal genotypes expressing improved Al tolerance that ultimately can be distributed to farmers who till acid soils in Africa and other developing regions, thus exploiting a wide range of still hidden genetic variation for Al tolerance. Increasing the Al tolerance of staple crops, such as maize and sorghum, will help increase yields and thus food security.

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

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

Cassava/Africa, Asia, Latin America/Drought tolerance

Lead institution
University of Maryland, USA (Pablo Rabinowicz)
Collaborating institutions
- ACGT (Jane Morris, Alexander Myburg, Chris Rey)
- UC–Davis (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.

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

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

Wheat/Australia, Asia, Latin America/Drought tolerance

Lead institution
CIMMYT (Matthew Reynolds)
Collaborating institutions
- CIMMYT (Yann Manes, Jose Crossa, Manilal William)
- ACPFG (Peter Langridge, Thorsten Schnurbusch)
- DWR (Jadadish Rane)

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.

Subprogramme 3: Trait capture for crop improvement

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

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

Cassava /Africa, Latin America/Drought tolerance

Lead institution
EMBRAPA (Alfredo Augusto Cunha Alves)
Collaborating institutions

- CIAT (Martin Fregene, Hernán Ceballos)
- IITA (Morag Ferguson, Edward Kanju
- Cornell University (Tim Setter)
- ARI (Geoffrey Mkamilo)
- SARI (Cecil Osei)
- EMBRAPA (Antonio Souza, Miguel Angel Dita Rodríguez, Alineaurea Silva)

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

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

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

Peanut/Africa, Asia/Drought tolerance, disease resistance

Lead institution
EMBRAPA (José Valls)
Collaborating institutions

- UCB (David Bertioli)
- Universidade Católica de Goiás, Brazil (Wellington Martins)
- CERAAS (Ousmane Ndoye)
- ICRISAT (Vincent Vadez)
- UAS (Udaya Kumar)
- Agropolis–CIRAD (Angelique d'Hont)
- Insituto Botánica del Nordeste (Guillermo Seijo)
- University of Aarhus (Jens Stougaard)
- Texas Agricultural Experiment Station (Charles Simpson)

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

Improvement of peanut has been limited by an extreme genetic bottleneck at its origin, which occurred via hybridisation of two wild species followed by a rare spontaneous duplication of chromosomes. The resultant plant had hybrid vigor, but because of the difference in chromosome

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

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

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

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

Cowpea/Africa/Striga resistance

Lead institution
IITA (Satoru Muranaka)
Collaborating institutions
- IITA (Christian Fatokun, Adebola Raji,Boukar Ousmane, Dong-Jin Kim)
- University of Virginia (Michael Timko)
- CERAAS (Ndiaga Cisse)
- CNRA (Moctar Wade)

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

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

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

Cassava/Africa, Latin America/Disease resistance

Lead institution
CIAT (Martin Fregene)
Collaborating institutions
- EMBRAPA (Alfredo Alves)
- CIAT/NRCRI (Emmanuel Okogbenin)
- CRI (Elizabeth Okai)
- NAARI (Robert Kawuki)

Cassava (*Manihot esculenta* Crantz) is increasing in importance in the tropics due to its hardy nature but it suffers from a plethora of anthropod pests and diseases as well as post harvest physiological deterioration (PPD). It has been estimated that cassava farmers, typically resource-poor farmers, lose 48 million tons of fresh root, some 30% of total world production, valued at US$1.4billion every year to pests, diseases, and PPD. Wild relatives of cassava are important sources of genes for resistance to pests and diseases and longer shelf life. Dramatically delayed PPD has been identified in inter-specific hybrids from *Manihot walkerae*. The only source of resistance to the cassava hornworm and a widely deployed source of resistance to the cassava mosaic disease (CMD)

were identified in 4th backcross derivatives of *M. glaziovii*. Moderate to high levels of resistance to cassava green mites (CGM), white flies and the cassava mealy bug have been found in inter-specific hybrids of *M. esculenta* sub spp f*labellifolia*. Furthermore, *M.glaziovii*, *M. catingae*, and *M. carthaginensis*, are adapted to semiarid lands and are potential sources of genes for tolerance to drought. But the heterozygous nature and long reproductive cycle of cassava makes introgression and pyramiding of these genes a long-term effort. For several years molecular marker tools and a modified Advanced Back Cross QTL (ABC-QTL) scheme have been tested for cost-effective pyramiding of useful genes from cultivated and wild gene pool through the elimination of phenotypic evaluations in each breeding cycle. This proposal seeks to make marker-assisted introgression of exotic genes into elite cassava progenitors widely available by the development of low cost approaches, expand the gene tagging effort to other traits, and establish a systematic approach of collection, evaluation and use of additional wild germplasm.

19. Project No G3005.12: Drought tolerant rice cultivars for North China and South/ Southeast Asia by highly efficient pyramiding of QTLs from diverse origins

- *Duration: Jan 2005–Dec 2007*
- *Budget by year: $296,500 (2005). $296,500 (2006), $296,500 (2007); Total budget: $889,500*

Rice/Asia/Drought tolerance

Lead institution
Institute of Crop Sciences, CAAS (Zhi-Kang Li)
Collaborating institutions
- Liaonin Academy of Agricultural Sciences (Ze-Tian Hua)
- Shenyang Agricultural University (Zheng-Jin Xu)
- CAAS (Yongming Gao)
- IRRI (Arvind Kumar)

Rice is the staple food for most Asian and Chinese people, but rice production uses large amounts of water. Drought has become the single largest factor limiting rice production in North China and the rainfed areas of South/Southeast Asia. Developing drought tolerant (DT) rice cultivars is the most efficient way to stabilise rice production and alleviate food insecurity and poverty in China and Asia. In the proposed project, we propose to develop high yielding and DT rice cultivars for the Northeast/Northwest China and the rainfed areas of South/Southeast Asia by exploiting the rich genetic diversity in the primary gene pool of rice in a large backcross breeding programme integrated with efficient selection and DNA markers. Using molecular markers, linkage disequilibrium mapping and two large sets of introgression lines (ILs) in elite Chinese japonica backgrounds having introgressed DT from 67 diverse germplasm accessions and breeding populations derived from 7 well characterised DT IR64 lines, our goal is to discover and characterise important DT QTLs in the process of breeding for high yielding and DT cultivars for the target environments. The expected outcomes from the project will include four major aspects: (1) important DT QTLs and multiple alleles at many QTLs identified, confirmed and characterised in the elite rice backgrounds; (2) development of superior high yielding and DT rice cultivars for the Northeast/ Northwest China and the rainfed areas of South/Southeast Asia; (3) knowledge, theory and strategy generated for genetic improvement of complex phenotypes; and (4) training of 10 young scientists from China and South/Southeast Asia in molecular breeding. More importantly, information and knowledge generated from the proposed project will allow CAAS to establish its modern breeding systems that fully integrate the molecular tools with the current breeding programmes for genetic improvement of major crops in China.

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

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

Sorghum/Africa/Aluminum tolerance

Lead institution
Embrapa Maize and Sorghum (Jurandir Vieira Magalhaes)
Collaborating institutions
- USDA–ARS (Leon Kochian, Owen Hoekenga, Jinping Liu)
- IGD, Cornell University (Stephen Kresovich, Alexandra M.Casa)
- EMBRAPA (Claudia Guimaraes, Robert Schaffert, Antonio Marcos Coelho, Vera Alves)
- INRAN (Issoufou Kapran, Soumana Souley, Maman Nouri, Magagi Abdou, Adam Kiari, Fatouma Beidari)

One of the most important factors limiting agriculture in developing countries involves the large areas of acid soils found in these countries. On acid soils, toxic levels of aluminum (Al) ions are released into soil solution, where they damage roots and impair their growth and function. This results in reduced nutrient and water uptake, with concomitant reductions in crop yield. There is considerable natural variation in Al tolerance both within and between plant species, and we have assembled an interdisciplinary team of scientists to take advantage of this variation to improve crop tolerance to Al toxicity, building upon our recent success

in isolating a novel Al tolerance gene in sorghum. Thus, as we have been able to identify at least one apparently improved version of this gene, we will now apply association mapping to undertake a comprehensive scan for even better versions of this gene for deployment into sorghum breeding programmes. The research group we have assembled has considerable expertise in the genetics, molecular biology and physiology of aluminum tolerance, and has the necessary genetic resources to ensure the success of this project. Through the use of cutting edge genomics and statistical genetics approaches, this research will bridge the gap between basic research on Al tolerance and applied breeding programmes, to develop the tools that plant breeders can use to efficiently and effectively breed for improved acid soil tolerance. The long-term goals of this research are to generate sorghum genotypes expressing improved Al tolerance that ultimately can be distributed to farmers who till acid soils in Africa and other developing regions, thus exploiting a wide range of still hidden genetic variation for Al tolerance. Increasing the Al tolerance of staple crops, such as sorghum, will help increase yields and thus food security worldwide.

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

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

Rice/Asia/Drought tolerance

Lead institution
IRRI (Arvind Kumar)
Collaborating institutions

- IRRI (D. Mackill, R Serraj)
- TNAU (R. Chandra Babu)
- CRURRS (PK Sinha)
- UAS (HE Shashidhar)
- YAAS (D Tao)
- University of Alberta (D Spaner)

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

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

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

- *Duration: Jan 2005–Dec 2007 with NCE to Jul 2008*
- *Budget by year: $166,100 (2005), $170,500 (2006), $170,550 (2007); Total budget: $507,150*

Maize, wheat/Various regions/Drought tolerance

Lead institution
WUR (Fred van Eeuwijk)
Collaborating institutions

- CIMMYT (Matthew Reynolds, José Crossa)
- CSIRO (Scott Chapman)
- Universidad Autónoma Chapingo, Mexico (Mateo Vargas)
- WUR (Marco Bink)

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

II. COMMISSIONED PROJECTS

Subprogramme 1: Genetic diversity of global genetic resources

23. Project No G4005.01: Genotyping of composite germplasm set

- *Duration: 2005–various end dates*
- *Various sub-budgets*

Barley, sorghum, maize, rice, cowpea, common bean, chickpea, cassava, potato and Musa /Various regions and traits

Lead institutions: ICARDA (barley, wheat, chickpea); CIMMYT (wheat, maize); IITA (maize, cowpea, cassava, *Musa*); CAAS (maize, sorghum, rice, common bean, cowpea); ICRISAT (sorghum, chickpea); Agropolis (sorghum, rice); IRRI (rice); CIAT (rice, common bean, cassava); WARDA (rice); EMBRAPA (rice, common bean, cassava); CIP (potato); INIBAP (*Musa*)

The objective of SP1C1 is to develop a "Composite Germplasm Set" for each of the year1 target crops: wheat, barley, sorghum, maize, rice, cowpea, common bean, chickpea, cassava, potato and *Musa*. These composite collections will form the source of germplasm for all other components of the Challenge Programme.

For *Musa*, this will include all of the non-duplicate accessions currently available. For the other clonally-propagated crops and inbreeding seed-propagated crops, each composite collection will contain not more than 3,000 total entries or no more than 10% of the total number of available accessions, whichever is fewer. For the outbreeding crops (maize), the collection will contain not more than 1,500 accessions, because of the lower ratio of genetic variance between/within accessions and the consequent need to analyse fewer accessions but more genotypes per accession. In addition, a "mini-composite" collection of 80-200 accessions will be formed for cowpea, potato and *Musa*. These mini-composite collections will form the source of germplasm for early pilot studies in SP1C2 to develop appropriate molecular marker systems. Pilot studies are not required for the other crops, since appropriate marker systems are already established.

24. Project No G4005.02: Support and distribution of reference germplasm, *Musa* (Bioversity International)

- *Duration: Jan 2005–Dec 2005 with NCE to Oct 2007*
- *Budget by year: $220,000 (2005); $0 (2006), $0 (2007); Total budget: $220,000*

Musa/Various regions and traits

Lead institution
Bioversity International (Nicolas Roux)
Collaborating institutions

- Agropolis–CIRAD (Isabelle Hippolyte)
- Bioversity International (Mathieu Rouard, Elizabeth Arnaud)
- IEB (Jaroslav Dolezel)

The genotyping activities started in year one end up with the definition of various samples, including a microcore collection of 48 accessions best adapted for allele discovery, and a reference sample of about 500 accessions which will be promoted for use in phenotyping experiments and further molecular characterisation with potential functional markers. Managing, securing, and supplying the corresponding accessions, some of which require controlled selfing, may require a specific effort in the CG germplasm centres in charge. It is proposed that the GCP contributes to this initial effort.

25. Project No G4005.03: Molecular characterisation of tier 2 (orphan) crops

25.1 Project No G4005.03.04: Molecular characterisation of tier 2 (orphan) crops – Yam

- *Duration: Jan 2005–Dec 2005 with NCE to Oct 2007*
- *Budget by year: $30,000 (2005); $0 (2006), $0 (2007); Total budget: $30,000*

Yam/Various regions/Drought tolerance

Lead institution
IITA (PI: M Kolesnikova-Allen, Collaborators: J Obidiegwu, R Asiedu)

Yam, a multi-species, polyploid and vegetatively propagated tuber crop, is cultivated widely in the tropics and subtropics. Over 90% of world yam production occurs in West and Central Africa where white yam (*Dioscorea rotundata* Poir.) is

the most important cultivated species. It is grown in diverse agroecologies including humid forest and lowland/mid-altitude savannas. Early season drought tolerance in varieties adapted to the savannas allows flexibility in planting periods. Identification of germplasm with tolerance to early season stress would provide the needed flexibility in planting. IITA holds over 3000 landrace accessions from 10 African countries of this crop in its ex-situ seed bank. Despite yam's importance in sub Saharan Africa breeding efforts on it and dissemination of improved varieties have been limited and farmers continue to grow local landraces that are low in productivity. Genetic diversity of these landraces can be evaluated using molecular techniques as a first step towards identification of suitable diverse parents for use in breeding programmes. In the past diversity of few of the landraces were assessed with isozymes, AFLP, RAPD or SSRs. Diversity and Genomes of Cultivated Plants" (DGPC), IRD and Cirad is focusing on SSR markers, which were developed jointly (or in collaboration) for yam diversity analysis and 11 microsatellite loci have been used to analyse over 500 accessions from Benin.. Their current objective is to have 20 SSR loci, which would be ideal for diversity analysis under the challenge programme A systematic approach would be to establish a rational collection of this African collection using morphological traits and then to determine the diversity of this collection using SSRs.

25.2 Project No G4005.03.05: Molecular characterisation of tier 2 (orphan) crops – Lentil

- *Duration: Jan 2005–Dec 2005 with NCE to Oct 2007*
- *Budget by year: $30,000 (2005); $0 (2006), $0 (2007); Total budget: $30,000*

Lentil/Africa, Asia/Drought tolerance

Lead institution
ICARDA (PISs: Bonnie Furman, Michael Baum, Collaborators: Christian Jung, Universität Kiel, Aladdin Hamwieh)

Lentil (*Lens culinaris* Medik.) is an important cool-season crop in North Africa, West Asia, the Middle East, the Indian Subcontinent and North America (Erskine 1996). It is an important source of dietary protein (25 percent) in both human and animal diets, second only to soybeans as a source of usable protein (CGIAR). Lentil ranks seventh among grain legumes and is grown on over 3.5 million hectares in over 48 countries with a total production of over 3 million metric tons. The major lentil producing regions are Asia (58 percent of the area) and the West Asia-North Africa region (37 percent of the acreage of developing countries).

The genus *Lens* comprises seven taxa within four species including the cultivated type, *Lens culinaris* spp. *culinaris* (Ferguson and Erskine 2001). Cultivated lentil includes two varietal types: small-seeded microsperma and large-seeded macrosperma. Wild *Lens* species are represented by *L. culinaris* spp. orientalis, *L. odemensis*, *L. nigrican* and *L. ervoides*. All members of *Lens* are self-pollinating diploids (2n = 2x = 14; Sharma et al. 1995). The haploid genome size of the cultivated genome is 4063 Mbp (Arumuganathan and Earle 1991).

The Generation Challenge Programme Subprogramme 1 has the main goal of exploring genetic diversity of global germplasm collections of the Consultative Group of International Agricultural Research (CGIAR). For each crop, a "composite sets" of germplasm, representing the range of diversity of each crop species and its wild relatives, will be identified and characterised with anonymous molecular markers. This molecular characterisation will allow for a study of the diversity across a given genus as well as potentially identify candidate genes involved in resistance to biotic and abiotic stresses, thus providing the base for the research activities of the other 4 subprogrammes.

The International Centre for Agriculture in Dry Areas (ICARDA) has a global mandate for research on lentil improvement. As such, ICARDA houses the world collection of *Lens*, totaling 10,509 accessions. The ICARDA collection includes 8789 accessions of cultivated lentil from 70 different countries, 1146 ICARDA breeding lines, and 574 accessions of 6 wild *Lens* taxa representing 23 countries. From this collection, a composite germplasm set of approximately 1000 accessions will be identified and characterised utilizing molecular microsatellite markers.

Analysis of microsatellite DNA loci is the current method of choice for population analyses (e.g., Morgante and Olivieri. 1993, Vendramin et al. 1998). Microsatellite loci consist of short (2-6 bp) tandemly-repeated nucleotide arrays surrounded by unique flanking sequences (Weber and May 1989). These loci are distributed throughout the genome in high abundance; it is estimated that the mammalian genome may contain in excess of 100,000 to 300,000 such loci, or one locus every 10-30 kilobase pairs (Li 1997). Allelic diversities and heterozygosities are typically extremely high; the presence of 10 or more alleles, and heterozygosities in excess of 0.85, are not uncommon. Microsatellite markers in lentil (about 80) have been developed by ICARDA recently and some of them (30) have already been assigned to linkage groups (Hamwieh et al. 2004, Eujayl et al. 1998).

Microsatellite-DNA markers will be used to obtain baseline data on allelic diversity of a composite germplasm set of lentil. These data will then be used to determine allelic frequency distributions for each locus within the collection as a whole and within source regions, as well as the geographical population genetic structure displayed by these loci among

source regions. The analysis of genetic diversity will help elucidate population structures that influence the analysis of the associations between markers and phenotypes for important traits. Phenotypic data will be collected for the population.

25.3 Project No G4005.03.06: Molecular characterisation of groundnut (Arachis hypogea L.) composite collection

- *Duration: Jan 2005–Dec 2005 with NCE to Oct 2007*
- *Budget by year: $30,000 (2005); $0 (2006), $0 (2007); Total budget: $30,000*

Groundnut/Africa, Asia; Latin America, Oceania/Drought, soil acidity and disease resistance

Lead institution
ICRISAT (HD Upadhyaya)
Collaborating institutions
- ICRISAT (R Bhattacharjee, D Hoisington, S Chandra, RK Varshney)
- EMBRAPA (JFM Valls, MC Moretzsohn, S Leal-Bertioli, P Guimarães)
- UCB (D Bertioli)

Groundnut is one of the major oilseed crops in the world, grown on 26.46 million ha with a total production of 35.66 million t and an average productivity of 1.35 t ha^{-1}. Developing countries contribute about 94% of the world groundnut production, grown mostly in rainfed conditions. Asia and Africa together contribute 92.5% to the world groundnut production, and the remaining 7.5% comes from North and Central America, South America, and Oceania. Abiotic and biotic stresses are the major constraints to world peanut production. The major abiotic stresses include drought, low availability of phosphorous in acidic soils, and non-availability of iron in calcareous soils. Rust, early leaf spot, and late leaf spot are the widely distributed foliar diseases of peanut. Bacterial wilt is restricted in Southeast Asia and Far East.

The world's largest peanut collection of 14,966 accessions of cultivated groundnut and 453 accessions of wild *Arachis* from 93 countries is housed at the ICRISAT genebank, Patancheru, India. This collection represents six botanical varieties that comprised of 45.8% var. *hypogaea* (6838 accessions), 36.6% var. *vulgaris* (5493 accessions), 15.7% var. *fastigiata* (2351 accessions), 0.1% var. *aequatoriana* (14 accessions), 0.13% var. *hirsuta* (19 accessions), and 1.7% var. *peruviana* (251 accessions). Approximately 43% of the collection consists of landrace germplasm, 7% cultivars, 31% breeding lines, and 19% other genetic stocks. CENARGEN at EMBRAPA, have numerous accessions of cultivated and wild *Arachis* species which ICRISAT does not have. The teams at ICRISAT and at EMBRAPA have expertise in genetic mapping. EMBRAPA together with UCB has produced the first PCR-based genetic map of *Arachis*. In addition, this Center has excellent greenhouse facilities, a state-of-the-art genomics laboratory and expertise in biotechnology.

A very small proportion of the groundnut germplasm collection is being used in breeding programmes. At ICRISAT from the available 15,000 accessions of cultivated groundnut and 450 accessions of wild *Arachis*, only 132 cultivated germplasm and 10 wild accessions have been used in developing 8279 breeding lines in 17 years from 1986 to 2002.

An important goal of the Generation Challenge Programme is extensive genetic characterisation, using molecular markers, of the vast genetic resources (including wild relatives, landraces, breeding materials, cultivars and genetic stocks) held by the participating institutions.

26. Project No G4005.04: Assessing DarTs as a genome-wide scanning technology

- *Duration: Jan 2005–Dec 2005 with NCE to Oct 2007*
- *Budget by year: $162,360 (2005); $0 (2006), $0 (2007); Total budget: $162,360*

Various crops, regions and traits

Lead institution
- DArT P/L (Andrzej Kilian)
- GCP (Carmen de Vicente)
- Agropolis–CIRAD (Jean-Christophe Glaszmann)

Associate Investigators
- DArT P/L (Eric Huttner, Peter Wenzl)
- Agropolis–CIRAD (Ange-Marie Risterucci)

Collaborating institutions
- IRRI (Ken McNally)
- Agropolis–CIRAD (Claire Billot, Patricia Lebrun)
- ICARDA (Michael Baum)
- CIAT (M Fregene)
- Bioversity International/INIBAP (Nicolas Roux)
- Coconut Research Institute, Sri Lanka (Chandrika Perera)
- Rayong Field Research Station, Thailand (Prapit Wongtiem)

There are many constraints to the widespread use of molecular markers for diversity analysis of germplasm and the subsequent identification of associations between traits and genes. Limitations include some of the following: theoretical and practical lack of knowledge of the tools, cost of development, low reproducibility, low data yield (limited throughput) of the experiments, restriction of access to proprietary technologies and insufficient resources (laboratory facilities, equipment, chemicals, etc...).

The project proposes to test the usefulness of Diversity Array Technology (DArT) as an alternative for detecting DNA variation in ways that will result to be more effective and resource-efficient. DArT possibly offers the highest throughput available up to date and allows for whole genome scanning in a speedy manner. In addition, the types of polymorphism detected by DArT (single nucleotide polymorphisms, insertion-deletions and methylation changes) may expand the potential of traditionally used markers, increasing the power to ascertain the structure of germplasm collections. Last, the experimental procedures to obtain DArT take into account the complexity of genomes and its effect on the extent of diversity shown by a collection of germplasm. Therefore, a set of different cases will be addressed, using the biological diversity of the crops and the issues, focusing the development of new resources on orphan crops that are not likely to gain much attention elsewhere.

Two additional goals of the project are facilitating DArT technology transfer to members of the Generation CP Consortium (CIAT, Colombia and Agropolis, Europe), and building capacity of NARS scientists through their involvement in technology development at DArT P/L so that they can be a resource for subsequent technology transfer.

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

- *Duration: Jan 2005–Dec 2005 with NCE to Sep 2008*
- *Budget by year: $300,000 (2005); $0 (2006), $0 (2007); Total budget: $300,000*

Rice, sorghum/Various regions and traits

Lead institution
- IRRI (Kenneth McNally)
- Agropolis–CIRAD (Claire Billot asCo-PI)

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

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

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

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

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

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

Lead institution
Embrapa-National Maize and Sorghum Research Center (Frederico Ozanan Machado Durães)

Collaborating scientists (all EMBRAPA)
- Antonio Carlos de Oliveira
- Antonio Marcos Coelho
- Camilo de Lélis Teixeira Andrade
- Elto Eugenio Gomes e Gama
- Fredolino Giacomini dos Santos
- Paulo Emílio P. de Albuquerque
- Manoel Xavier dos Santos
- Reinaldo Lúcio Gomide
- Beatriz da Silveira Pinheiro
- Cleber Morais Guimarães
- Orlando Peixoto de Morais
- Natoniel Franklin de Melo
- Luiz Balbino Morgado
- Hélio Wilson Lemos de Carvalho
- Luciana Marques de Carvalho
- Milton José Cardoso
- Edson Alves Bastos
- Francisco Rodrigues Freire Filho
- Maria da Glória Trindade
- Walter Quadros Ribeiro Jr.

The development of drought tolerant varieties for crops of economical importance represents a major challenge for the 21st. century, considering that agriculture growth will be limited by world water availability. A first step to be taken in this direction is to select germplasm adapted to water stress conditions through appropriated screening techniques and defined protocols. Thus, the great challenge is the identification and characterisation of drought tolerant genitors to provide material to be used in genetic breeding programmes focused on regions historically known as prone to water deficit during crop growing season. The

improvement of drought tolerance relies on the manipulation of the traits that limit yield and their accurate phenotyping under the prevailing field conditions being target. This issue is particularly crucial for the breeding programme and identification of *QTLs* for traits categorised as adaptive as compared to constitutive traits, per each specie. On this purpose it is necessary to amplify an infrastructure to allow plant exposure to water deficit pressure to be used for the evaluation of genotypes and characterisation of plant physiological responses to these stress conditions.

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

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

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

- *Duration: Jan 2005–Dec 2006 with NCE to May 2008*
- *Budget by year: $179,000 (2005), $396,720 (2006), $0 (2007); Total budget: $575,720*

Cereals (various)/Various regions/Drought tolerance

Lead institution
Agropolis–CIRAD (Marcel de Raïssac)

Collaborating institutions
- Agropolis–CIRAD (Delphine Luquet, M Dingkuhn, JC Combres)
- Agropolis–CIRAD/INRA (François Tardieu, C Welker)
- IRRI (Renée Lafitte, B Bouman)
- CSIRO (Scott Chapman)
- University of Queensland, Australia (Graeme Hammer)
- CIMMYT (M Bänzinger, M Reynolds, R Trethowan)
- ICRISAT (Eva Weltzien)
- EMBRAPA (Frederico Duraes)
- Pioneer (Mark Cooper)

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

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

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

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

30. Project No G4005.08: Population structure, phenotypic information and association studies in long-generation crops

- *Duration: Jan 2005–Dec 2005 with NCE to Oct 2007*
- *Budget by year: $277,536 (2005), $0 (2006), $0 (2007); Total budget: $277,536*

Cassava, potato yam, banana, plantain, and coconut/Various regions/Various traits

Lead institution
GCP (M Carmen de Vicente)
Collaborating institutions

- CIAT (Martin Fregene)
- Agropolis–CIRAD (Luc Baudoin, Jean-Louis Noyer)
- CARBAP (Kodjo Tomekpe)
- CIP (Merideth Bonierbale)

Identification of useful genes or chromosome segments involved in traits of agricultural interest rests on the search for co-occurence of molecular tags with desired values for the target traits. This is commonly undertaken by segregation analysis in controlled progenies, where co-occurence will be indicative of linkage on the genome. In such experiments, a particular progeny is generated, planted and evaluated while it is genotyped in the laboratory for markers covering the genetic map of the species. This process has several constraints:

- it requires time for making the crosses and growing the progeny
- it confronts a limited number of alleles at each locus (as many as there are in the few parents)
- it requires specific phenotyping experiments, which usually represent an additional burden to current breeding programmes.

The results generally suffer from several drawbacks. The progeny often represents types that are far from the breeding standards, exhibiting potential interactions between traits that may confound variation for the target features. Phenotyping is often done with limited number of plants, i.e. few repetitions over space and still fewer over time. The use of the materials thus produced and monitored is not easy and they are seldom incorporated in the breeding process.

An alternative option could be to try and make use of materials and evaluation data that are regularly produced in the mainstream of the breeding activities. From the collections of potential parents to the advanced breeding materials going to multilocation trials and to the elite materials close to varietal release, there is a wealth of information produced, which is hardly used for deriving genetic information that can in turn be used to enhance global understanding and mastership. The condition for using these materials is that there be significant linkage disequilibrium (LD) that correlates variation in genetically (recombinationally) linked genes/markers. LD can exist among traditional (modern-pedigree wise unrelated) materials if the germplasm has known significant bottlenecks in the past. For example, LD is actually generated in the breeding materials by the crosses made; in case of a well documented breeding programme, the multi-generation pedigrees can be used to derive linkage information more efficiently. A nice example of such an application has just been described in barley where standard varietal evaluation trials could be used to detect QTLs for yield and yield stability (Kraakman et al, 2004).

Such an approach is especially useful for those crops where refined materials for genetic analysis, such as inbred lines, NILs or sets of substitution lines cannot be produced and for those crops where the generation time is long. Within the CGIAR mandate, these crops include most of the vegetatively propagated crops, which are highly heterozygous, such as cassava, potato (and possibly other Andean roots and tubers), yam, banana and plantain, and the perennial coconut tree. These happen to be mostly "orphan" crops where sequence information (which would allow other strategies to be applied) is scarce and unlikely to develop quickly.

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

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

Various crops, regions and traits

Lead institution
IRRI (NR Sackville Hamilton)
Collaborating institutions

- CIAT (M Lorieux)
- EMBRAPA (C Brondani)
- ICRISAT (H Upadhyaya, R Varshney)
- ICARDA (BJ Furman, S Udupa, M Baum)

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

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

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

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

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

- *Duration: Jan 2006–Dec 2008*
- *Budget by year (as per proposal): $573,000 (2006), $187,000 (2007), $100,000 (2008); Total budget (as per proposal): $860,000*

Various crops and regions/Drought tolerance

Lead institution

Agro-Montpellier, Agropolis-France (Dominique This)

Collaborating institutions

- Agropolis (Brigitte Courtois, Claire Billot, Dominique This)
- CIP (Merideth Bonierbale, Reinhart Simon)
- ICRISAT (Dave Hoisington, Rajeev Varshney)
- INRA-CNG (Dominique Brunel)

Crop partners

- IRRI (Rice): Ken McNally
- ICARDA (Barley): Michael Baum
- ICRISAT (Sorghum): Tom Hash, Rajeev Varshney
- CIAT (Bean): Matthew Blair
- ICRISAT (Chickpea): Rajeev Varshney, Hari Upadhyaya
- CIAT (Cassava): Martin Fregene
- CIP (Potato): Merideth Bonierbale

Gene specialists

- IRRI (Invertases): John Bennett
- Agropolis-Agro-M (Invertases): Dominique This
- Australian National University (ERECTA): Josette Masle
- CNRS (ASR1): Michel Zivy

Advisers

- Sink-source regulation and Sugar metabolism: Michael Dingkuhn, Agropolis-CIRAD, Tim Setter, Cornell University, John Bennett, IRRI, Alex Tiessen, CIMMYT
- Maize (information exchange): Mark Sawkins, CIMMYT

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

33. Project No G4006.03: SNP analysis of the genetic diversity along the rice genome (HAPLORYZA)

- *Duration: Jan 2006–Dec 2006 with NCE to Dec 2007*
- *Budget per year: $150,000 (2006), Total budget: $150,000*

Rice/Asia/Various traits

Lead institution
IRRI (K. McNally)
Collaborating institutions
- Agropolis–CIRAD (C Billot, B Courtois, A-F Abdelkhalik, G Second)
- Agropolis–INRA/CNG (D Brunel)
- CNG (M Lathrop)

Asian cultivated rice occurs as two major types, *indica* and *japonica* that appear to have arisen from independent domestication events. Even though rice is a predominantly selfpollinated crop, both types can frequently be found within the same region allowing the prospect for genetic exchange between them.

Since whole genome sequences are available for each type, we now have the opportunity to identify single nucleotide polymorphism (SNP) suitable for determining the extent of linkage disequilibrium and haplotype structure that is indicative of their differentiation. In this project, the high quality *japonica* Nipponbare sequence (IRGSP) will be compared to the whole genome shotgun *indica* 93-11 (Beijing Genomics Institute) sequence to identify a set of 1536 SNPs suitable for undertaking genome scans. These SNP will be genotyped across 900 types predicted to cover the range of *indica/japonica* diversification and prospective natural hybrids between them. The genotyping platform will consist of single base extension SNP assays implemented on the Illumina BeadArray platform at the National Genotyping Center at Evry.

The outcome of this effort will be a fine scale LD map for common SNP variation among the *indica* and *japonica* types of rice. This will also help to clarify the origin of the peculiar rice varietal groups, such as the aus or basmati types, in relation to *indica* and *japonica*. Analysis of this SNP data with phenotypic data on a range of traits will allow the identification of loci governing the differentiation between the two major types, opening the way for effective manipulation of subtle variation that has hindered the full exploitation of this diversity in hybridisation programmes.

More generally, the *indica-japonica* pattern represents a typical case of diversity derived from admixture. This may reveal patterns of relationships whose existence enables LD-based mapping of genes of agricultural interest and may inspire applications in other breeding species.

34. Project No G4006.04: Phenotyping in the field: global capacity accessible to the GCP – Inventory of phenotyping resources and capacity for the CGP

- *Duration: Jan 2006–Dec 2007*
- *Budget by year: $51,000 (2006), $49,000 (2007); Total budget: $100,000*

Various crops and regions/Drought tolerance

Lead institution
Bioversity International (Jane Toll)
Collaborating institutions
- Plantstress.com (A Blum)
- Consultant (Mahalakshmi Viswanathan)
- Challenge Programme on Water & Food

Plant genetic resources and the knowledge about their resistance to biotic and abiotic stresses is critical for ensuring their usefulness in germplasm enhancement. Marker assisted selection (MAS) in crop breeding programmes are aimed at improving the efficiency and effectiveness of breeding for those traits that are influenced by the environment and therefore have low heritability. Therefore accurate phenotyping is central to the success for the development of MAS breeding programme. As the GCP is currently placing emphasis on drought – this study will initially limit its area to drought but experience gained can be extended to other traits as required. As the emphasis of GCP moves towards other abiotic (salinity, aluminium toxicity etc) stress and biotic stress phenotyping network resources creation will be undertaken.

Drought or improved productivity under limited water conditions is a trait, which has often found limited success in breeding programme. Opportunity for use of linked markers in breeding for performance under drought lies in their use for selection of difficult, low heritability, or expensive to measure traits such as root growth or water soluble carbohydrate content. Many traits are reported to confer drought tolerance in crops e.g., matching phenology to water supply, through photoperiod sensitivity, developmental plasticity, mobilisation of pre-anthesis dry matter, rooting depth and density, low root hydraulic conductance, narrow xylem vessel, early vigour (canopy), leaf area maintenance (´stay-green´), osmotic adjustment, low lethal water status, reduced stomatal conductance, leaf movements, leaf reflectance, heat tolerance, low epidermal conductance and transpiration efficiency. All

this is compounded by the different crops which may have specific drought responses beyond those mentioned above. It is easier to select for traits conferring drought tolerance, which can be related to gene actions than breeding for yield under stress conditions which may be due to many traits pyramiding together to confer the tolerance. Reliable and repeatable phenotyping protocols are therefore central to the development of MAS for drought.

The phenotyping of drought resistance traits employs field or laboratory/screen-house facilities with precision irrigation methods. The traits measured also need special equipments and methods to measure. Breeders have developed their own modifications of physiological testing, which were not always documented Such facilities and methodologies exist among the consortium members and some have developed well co-ordinated drought networks. Some of these facilities and techniques require trained and skilled manpower to operate. This study will collate all the available resources and capacities that are available among the consortium members, suggest ways to optimally use these facilities for crops and regions.

35. Project No G4006.05: Development of a composite collection and the genotyping of faba bean

Duration: Jan 2006–Dec 2006 with NCE to Oct 2007
Budget by year: $35,400 (2006); Total budget: $35,400

Faba bean/Various regions and traits

Lead institution
ICARDA (Bonnie Furman, Michael Baum)
Collaborating institutions
- Agropolis–INRA/UR LEG (G. Duc)
- Instituto de Agricultura Sostenible, Spain (MJ Suso)

The Generation Challenge Programme Subprogramme 1 has the main goal of exploring genetic diversity of global germplasm collections of the Consultative Group of International Agricultural Research (CGIAR). An integral goal of the Generation Challenge Programme is to develop composite collections representing the genetic variation present in the entire collection, for the rational use of genetic resources in crop improvement programmes. Such composite collections with then be characterised with anonymous molecular markers. This molecular characterisation will allow for a study of the diversity across a given genus as well as potentially identify candidate genes involved in resistance to biotic and abiotic stresses. The International Center for Agricultural Research in the Dry Areas (ICARDA) has a global mandate for Faba Bean improvement and as such houses one of the largest collections globally with 10,809 accessions from 69 countries. This collection is maintained in two types of germplasm collections (Robertson 1985). Original germplasm accessions are maintained as heterogeneous composite bulks known as the International Legume Faba Bean (ILB) collection.

This collection contains 5749 accessions. A Faba Bean Pure Line (BPL) collection has been derived from the ILB collection by the creation of single plant progeny rows. This collection contains 5060 accessions. Most of these germplasm accessions have been characterised for various morphological and agronomic traits. In addition, INRA, Dijon, France and INIA, Cordoba, Spain house large collections of European Faba Bean with 1500 and 1150 accessions, respectively. From these collections, we propose here to identify a composite germplasm set of approximately 1000 accessions to be characterised utilizing molecular markers to determine the genetic structure of this composite collection.

36. Project No G4006.06: Genotyping composite collection of finger millet [*Eleusine corcana (L.) Gaertn*]

- *Duration: Jan 2006–Dec 2006 with NCE to Oct 2007*
- *Budget by year: $20,000 (2006); Total budget: $20,000*

Finger millet/Africa, Asia/Various traits

Lead institution
ICRISAT (PI: HD Upadhyaya, Collaborators: RK Varshney, D Hoisington, CLL Gowda, CT Hash, S Chandra)

Finger millet, *Eleusine corcana* (L.) Gaertn., is an important coarse grain food crop in Africa and South Asia. It's a hardy crop that can be grown in very diverse environments from almost at sea level to about 2000 meter above sea level. Globally, millets are grown in 3.5 million ha, with a total production of 4.5 million tons annually. China, India, Myanmar, Nepal, and Srilanka in Asia and Uganda, Rwanda, Zaire, and Kenya in Africa are the major countries producing the finger millet. Finger millet seeds are rich in calcium and iron, and contain 7-14% seed protein that has high tryptophan, cystine, and methionine contents than many cereals. There have been very limited crop improvement efforts to boost the production and productivity of this crop in spite of the fact that it is the hardiest crop and the seeds have high biological food value.

An important goal of the Generation Challenge Programme is to facilitate the extensive genetic characterisation, using molecular markers, of vast genetic resources to identify diverse accessions with beneficial traits for use in molecular genetics and crop improvement programmes. The genebank at ICRISAT holds 5940 accessions of finger millet from 24 countries. Since the entire collection cannot be used for molecular characterisation, it is important to develop a

composite collection representing finger millet germplasm. Using morphological descriptors and characterisation and evaluation data on 5940 accessions, ICRISAT scientists developed a composite collection of 1000 accessions in 2005 that were further grown, a single panicle selfed from each accession that was harvested at maturity, processed, and seed samples kept in gene bank. It is proposed to determine the genetic structure of this composite collection using 20 DNA markers.

37. Project No G4006.29: Preparing IITA-cassava reference germplasm for distribution and association mapping

- *Duration: Jan 2006–Dec 2006 with NCE to Oct 2007*
- *Budget by year: $50,150 (2006); Total budget: $50,150*

Cassava/Africa, Latin America/Drought and disease tolerance

Lead institution
IITA (PI: Dominique Dumet, Collaborators: Morag Ferguson, Odu, Babajide)
Collaborating institutions
- CIAT (Martin Fregene)

IITA, CIAT and EMBRAPA have completed the genotyping of 3000 cassava clones, using 36 primers. A reference set is being selected from this data. It is important that this reference set is made readily accessible to anyone who would like it. The movement of cassava between Africa and South America has been hindered by quarantine restrictions for many years. This is due to Frog Skin Disease in South America and Cassava Mosaic Disease (CMD) in Africa. Within Africa the movement of cassava germplasm has recently been exacerbated by the emergence of different strains of CMD and cassava brown streak virus (CBSV). Cassava plantlets must be *in-vitro* and certified disease free to be distributed.

This project aims at putting the IITA reference cassava germplasm collection, and selected known drought tolerant varieties *in-vitro*, certifying it disease-free, and multiplying it for multi-locational drought tolerance evaluations leading to association mapping studies. In addition, the IITA reference set will be exchanged with that from CIAT.

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

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

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

Lead institution
ICRISAT (PI: HD Upadhyaya, Collaborators: RK Varshney, CT Hash, D Hoisington, CLL Gowda, S Chandra)

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

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

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

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

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

Lead institution
ICRISAT (PI: HD Upadhyaya, Collaborators: CT Hash, S Senthilvel, RK Varshney, D Hoisington, KN Rai, RP Thakur, S Chandra)

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] is an important coarse grain food, feed and fuel crop in Africa and South Asia. This hardy C4 cereal can be grown in very diverse environments from sea level to about 1800 meters above sea level. Pearlmillet is grown in over 40 countries, predominantly

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

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

40. Project No G4006.32: Molecular characterisation of pigeonpea (*Cajanus cajan L.*) composite collection

- *Duration: Jan 2006–Dec 2006 with NCE to Oct 2007*
- *Budget by year: $30,000 (2006); Total budget: $30,000*

Pigeonpea/Africa, Asia, Latin America/Various traits

Lead institution
ICRISAT (PI: HD Upadhyaya, Collaborators: R Bhattacharjee, D Hoisington, S Chandra, RK Varshney, KB Saxena)

Pigeonpea is a major grain legume crop of tropics and subtropics, grown as a field and/or a backyard crop in about 87 countries between 300 N and 300 S latitudes. Of the 25 countries in Asia where pigeonpea is grown, India, Myanmar, and Nepal are the major producers. Kenya, Malawi, Uganda, Mozambique, and Tanzania in southern and eastern Africa, and Dominican Republic, Venezuela, Haiti, and Puerto Rico, in Latin America are the other important pigeonpea growing countries. In India, which accounts for more than 80% world's pigeonpea production, the seed is primarily consumed as *dhal* (decorticated dry split peas) and in Latin America immature seeds are used as vegetable and canned peas. Various parts of pigeonpea plant are put to several other uses such as feed, fodder, and fuel wood, and green manure. It also arrests soil erosion especially in sloping lands, and enriches the soil with organic content and provides nitrogen through symbiotic rhizobia. Therefore, due to these multiple uses, pigeonpea plays an important role in subsistence agriculture.

The genebank at ICRISAT, Patancheru, India, has conserved 13,077 accessions of cultivated pigeonpea and 555 accessions of 41 wild species from 74 countries. However, the use of germplasm in pigeonpea improvement programmes is limited.

41. Project No G4006.33: Development and genotyping of a composite germplasm sample of potato

- *Duration: Jan 2006–Dec 2006*
- *Budget by year: $15,000; Total budget: $15,000*

Potato/Various regions and traits

Lead institution
CIP (PI: Marc Ghislain, Collaborators: Jorge Núñez, Maria del Rosario Herrera, Guillermo Trujillo, Reinhard Simon, Edwin Rojas, One student)

This project aims at completing the work plan established for the "Marker Analysis-Data Analysis-Potato" activity funded by the Generation Challenge Programme (GCP) in 2004. The actual cost of the experiments in our conditions is such that we mobilised in-kind contribution from CIP core budget in 2005, which are now drying out. The earlier experiments achieved very exciting results. Hence, we request an additional US$ 18,500 from the GCP.

The production of the SSR marker data set for potato was initiated after the high throughput genotyping (HTG) facility was established at the end of the first semester of 2004. This facility has been entirely assigned to the GCP activity on a tier 1 crop – Potato. To date we have concluded the identification of 31 new SSR markers to complement the 22 already in use at CIP before the initiation of the GCP activity. Using these 53 SSR markers, 716 landraces of cultivated potato were genotyped on the LI-COR 4300 using the M13 tailing protocol. This large data set was completed at the end of the

first semester of 2005. Genetic analysis has revealed significant structure among and probably within the cultivated potato groups. Samples of two genetic mapping populations have also been included in order to map the new SSR markers. The germplasm analyzed to date comprises just under 80% of the 1083 clonal accessions proposed for CIP's Composite Genotype Set.

A number of landraces were omitted from the 2004-2005 analysis due to delays in obtaining leaf tissue from in vitro plants or acquisition status which is now being clarified. Since phenotyping data are available for these, their genotyping would allow them to be included with germplasm that will be used for association mapping and other activities of the GCP. In addition, no advanced hybrids or improved varieties have been analyzed yet, beyond a small start made for identification purposes in our breeding programme. CIP and NARS breeders have their preferred gene pool which has not been genetically characterised. This germplasm was identified by potato breeders in 2004 and to a large extent included in the composite genotyping set. However, due to limited experience with genotyping large collection and with the new HTG facility, we did not reach our target of genotyping 1083 genotypes with 50 SSR markers. We decided to leave out breeder's material in order to produce a valuable data set which has intrinsic interest. We have now gained significant experience and see that it is essential to genotype the germplasm used by breeders. The objective is to understand what germplasm has been exploited by breeders as well as engage this community in a common research strategy making better use of the tools derived from molecular genetics.

42. Project No G4007.01: SP1 composite sets genotyping data: quality assessment and consolidation

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

Various crops, regions and traits

Lead institution
Agropolis–CIRAD (Jean-Francois Rami)
Collaborating institutions
- ICRISAT (Dave Hoisington)
- CIMMYT (Marylin Warburton)

External validation labs (provisional list)
- CNG
- SCRI

The scientific community involved in the SP1 subprogramme of the Generation Challenge Programme is about to deliver one of the biggest effort 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 purpose. However, this work was by nature composite, involving different species and different partners using different technologies.

The present project proposes to validate the different microsatellites dataset produced in SP1 by re-genotyping of a small percentage of the data by two validation laboratories. This validation effort would provide a global view of genotyping error rate among the entire programme, as well as good practices for diversity genotyping.

43. Project No G4005.09: Systematic evaluation of rice mutant collections for conditional phenotypes with emphasis on stress tolerance

- *Duration: Jan 2005–Dec 2006 with NCE to May 2007*
- *Budget by year: $250,000 (2005), $250,000 (2006), Total budget: $500,000*

Rice/Asia/Various traits

Lead institutions
WUR (Andy Pereira; New Affiliation VBI, Virginia Tech)
Collaborating institutions
- NIAS (Hirohiko Hirochika)
- IRRI (Hei Leung)
- Agropolis (Emmanuel Guiderdoni)
- Agropolis–IRD/CIAT (Mathias Lorieux)
- CIAT (Manabu Ishitani)
- CAAS (Tiegang Lu)
- HZAU (Qifa Zhang/Lizhong Xiong)

Co-Prinicpal Investigators
- Pohang University Science and Technology, Korea (Gyn An)
- Temasek Life Sciences Laboratory, Singapore (Srinivasan Ramachandran)
- CSIRO (Narayana Upadhyaya)
- UC–Davis (Venkatesan Sundaresan)

The rice genome sequence provides the basic framework for the functional analysis of monocot genomes. International efforts have produced rice mutant resources that are a powerful functional genomics tool to identify the function of the sequenced genes. This consortium proposes to create a platform to identify genes that can contribute to a phenotype of resistance/tolerance to abiotic/biotic stresses. Expression analysis of various plant genomes has revealed genes that respond to environmental stresses. In addition, the ongoing functional analysis of Arabidopsis and other model plants identifies genes and associated mechanisms involved in stress tolerance. This comparative genomics information will be integrated to identify a set of candidate rice genes predicted to be associated with drought and other stress responses.

In a reverse genetic strategy, we will use sequence-indexed knockout mutant resources developed by the rice international community to identify insertions in the target stress associated genes. These insertions include rice Tos17 transposons, heterologous Ac-Ds transposons and T-DNA inserts that are identified by available flanking sequences (FSTs), supplemented by PCR based screens for inserts. In addition TILLING will be used to supplement the mutant coverage, and also provide non-transgenic stocks for field testing. To resolve gene redundancy, gain-of-function overexpression lines will be generated by transformation of appropriate constructs, and available activation tag populations will also be accessed for overexpression mutants.

To facilitate novel gene discovery a forward genetics mutant screen will be carried out with random genotypes that have been sequence indexed, thus aiding their further analysis. The mutant genotypes will be phenotyped for drought and disease stress parameters at appropriate growth stages in greenhouse and field-based screens. Genotypes with altered stress tolerance phenotypes will be tested for other abiotic/biotic stresses. Whole genome microarray analysis will be conducted to identify the downstream genes and characterise the stress response mechanism involved. The genes can be utilised directly by transformation to provide stress tolerance, or for cereal comparative genomics studies and allele mining for breeding.

44. Project No G4005.10: Wheat genetic stock assembly and utilisation

- *Duration: Jan 2005–Dec 2006*
- *Budget by year: $60,000 (2005), $60,000 (2006); Total budget: $120,000*

Wheat/Various regions and traits

Lead institutions
CIMMYT (Tom Payne)
Collaborating institutions
- ACPFG/University of Adelaide, Australia (Peter Langridge)
- CAAS (Xueyong Zhang)
- Gatersleben, Germany (Marion Röder)
- Kihara Institute for Biological Research, Japan (Tetsuo Sasakuma)
- Tottori University, Japan (Hitashi Tsujimoto)
- CIMMYT (Maarten van Ginkel, Masahiro Kishii, Hans Braun)
- JIC (John Snape)
- UC–Davis (Jorge Dubcovsky)
- Kansas State University, USA (Bikram Gill and Bernd Friebe)
- USDA–ARS, University of Missouri (Perry Gustafson)
- UC–Riverside (Adam Lukaszewski)
- Cornell University (Mark Sorrells)

Since 1936, a wealth of genetic stocks has been developed in tetraploid (*Triticum turgidum* L.) and hexaploid (*T. aestivum* L.). These genetic stocks include material containing

intervarietal and interspecific translocations, chromosome and chromosome arm additions and deletions, chromosome and alien substitution addition lines, mono- and polysomic series, recombinant doubled haploid populations, mapping populations, NILs, point and other mutations, and synthetics. Hexaploid wheat is allopolyploid in origin, and the homoeology existing between its three component genomes allows for a range of aneuploidy (i.e. additions, substitutions, deletions, etc.) to be tolerated.

These genetic stocks were often developed for specific purposes, e.g. as new source of disease resistance genes, but have seldom been systematically screened for other value-added traits of interest. A few genes introduced from other species, e.g. rye (*Secale cereale* L.), have had a tremendous impact on wheat improvement. It can be assumed that a systematic screening of available genetic stocks will reveal useful genetic variation for many value-added traits of immediate interest to breeders. An important advantage is that any gene characterised in any of the existing or newly created wheat genetic stocks can be transferred to improved wheat cultivars without requiring the utilisation of any biolistic or *Agrobacterium* transformation techniques. And finally, it is anticipated that the distribution of these genetic stocks worldwide will result in many research projects, in particular in the area of gene identification (including across species/genera), marker development, and association mapping, which will greatly increase our knowledge of wheat genetics and breeding efficiency in the future.

It is intended that, to the fullest extent feasible, all genetic stocks within this project will be placed within the Multilateral System of Access and Benefit Sharing to be established under the International Treaty of Plant Genetic Resources for Food and Agriculture ITPGRFA), and that they may be freely distributed under the standard ITPGRFA material transfer agreement (MTA). (FAO has an explanatory page about the Treaty at http://www.fao.org/ag/cgrfa/itpgr.htm, and a video at http://www.fao.org/videocatalogue/index.jsp?lang=EN). It is also intended that, to the fullest extent feasible, results obtained from using these genetic stocks will be considered to be public goods which can be used without restrictions by others. Due to a number of ambiguities in the ITPGRFA that have not yet been resolved, it is not feasible to anticipate all potential implications of the ITPGRFA at this time. Accordingly, to the extent that any germplasm used in this project is protected by intellectual property rights, and to the extent that placing such germplasm within the Multilateral System would be inconsistent with such rights, the parties will endeavor to devise a system for working with and distributing such germplasm that both respects those intellectual property rights and achieves the public goods aims of this project as outlined above.

The preference of this programme, however, shall be for using germplasm that is free of intellectual property rights. Stocks that are initially requested through the proposed central database facilitated CIMMYT website or by normal email to CIMMYT representing the consortium of key genetic research groups listed below, may later actually be sent out from the originator's programme. This may be especially the case for cytogenetic stocks requiring the resident expertise to guarantee quality maintenance of the stocks. CIMMYT would function in that case as a clearing house for routing the requests. The latter routing would allow the material to be shared under the originator's MTA.

45. Project No G4005.11: Legume mutant resource development

- *Duration: Jan 2005–Dec 2006 with NCE to May 2007*
- *Budget by year: $95,000 (2005), $105,000 (2006); Total budget: $200,000*

Common bean/Africa, Latin America/Various traits

Lead institution
CIAT (M. Blair)
Collaborating institutions
- University of Geneva, Switzerland (W Broughton, P Lariguet)

Grain legumes have a paucity of mutant resources compared to Arabidopsis and the cereals. Between the two broad branches of grain legumes, the tropical legumes have fewer mutant stocks compared to the temperate legumes. A well-developed mutant stock, particularly in genotypes of common bean (*Phaseolus vulgaris*), a simple diploid species with a small genome (650 Mb), will serve the broad community involved in tropical legume improvement aiding gene-discovery both in common bean, the most widely consumed grain legume for human consumption and a major protein and mineral source in East Africa and Latin America, as well as in two tropical legume relatives: cowpea (*Vigna unguiculata*), a food crop important in West African agriculture and soybean (*Glycine max*) a major industrial and feedstock crop around the world. Mutant stocks in common bean will allow researchers to conduct both forward (systematic phenotypic screening) and reverse genetics (TILLING or Targeting Induced Local Lesions In Genomes) experiments aimed at understanding the genes involved in abiotic and biotic stress tolerance as well as those genes involved in biological nitrogen fixation in the tropical legumes. Mutations will be sought in common bean genes that have been isolated at CIAT and shown to be associated with drought tolerance. The phenotypic effect of these mutations will be analyzed as a proof of concept for the value of the mutant stocks generated by this project.

46. Project No G4005.12: A saturated potato mutant population for functional genomics among *Solanaceae* and tuber crops

- *Duration: Jan 2005–Dec 2006*
- *Budget by year: $100,300 (2005), $100,300 (2006); Total budget: $200,600*

Potato/Africa, Latin America/Various traits

Lead institution
CIP (Marc Ghislain)
Collaborating institutions
- CIP (Merideth Bonierbale, Alberto Salas, Maria del Rosario Herrera)
- SCRI (Glenn Bryan, Robbie Waugh)
- The Hebrew University of Jerusalem (Dani Zamir, Noa Issman)

Complete sequencing of genomes and transcriptomes provides baseline genetic information, which is increasingly being exploited between related species by comparative genomics. However, the identification of gene function remains one of the most challenging tasks of plant functional genomics. The virtually unlimited number of alleles and allele combinations possible for a single organism makes necessary the development of special tools and genetic stocks designed for functional analyses. Tuber crops, including the potato, generally have limited or poorly accessible genetic stocks. A saturated mutant population of a wild potato species is proposed here as a genetic resource useful for forward and reverse genetics in Solanaceae and other tuber crops. Ethyl methane sulphonate (EMS) mutagenesis will be performed on botanical seed of a diploid self-compatible and near-homozygous accession of the tuber-bearing species *Solanum verrucosum* to produce approximately 400,000 mutant chromosomes in 20,000 M2 seeds. Validation of the mutant population will be conducted for target genes already characterised in tomato and the data will be presented in the Solanaceae Genome Network (SGN).

47. Project No G4005.13: Crop gene expression profiles and stress-gene arrays

- *Duration: Jan 2005–Dec 2006*
- *Budget by year: $99,845 (2005); $99,845 (2006); Total budget: $199,690*

Rice, barley, maize and wheat/Various regions/Drought tolerance

Lead institutions
- Beijing Genomics Institute (Guozhen Liu)
- NIAS (Shoshi Kikuchi)
- CIAT (Manabu Ishitani)

cDNA/oligo microarrays currently provide a robust and accessible platform for genome-wide expression analysis. Whole-genome arrays have been developed for rice, barley, maize, and possibly wheat. The maize and rice chips are being used in Year 1 commissioned research in Generation Challenge Programme (GCP). The identification of stress-tolerance genes by a combination of genome-wide expression and protein-protein interaction analyses has proven promising (Cooper et al. 2003). While gene expression analyses are being pursued in multiple crops, relatively few attempts have been made to integrate experiments to enable cross-species comparison, which will provide opportunities to study the evolution of biological systems (Zhu et al. 2001; Zhou and Gibson, 2004). The GCP has a unique opportunity to generate pan-crop gene expression data for comparative analysis and data mining which allows us to draw evolutionary inferences concerning specific trait(s) and to elucidate the global properties of expression networks in crops.

Drought tolerance is a complex trait in plants. Our challenge is to link molecular phenotype to physiological or morphological trait(s) that have been observed in drought tolerant plants/crops. It will be difficult to comprehend gene expression patterns across crops without knowing physiological phenotype of drought resistance even if existing or developed ortholog arrays are feasible for cross-species comparisons. To address this problem we plan to focus on a common physiological trait found across crops under drought. This will allow us to identify underlying molecular components for a common physiological trait cross crops.

We propose to apply single or multiple microarray platforms to identify candidate genes that are associated with a phenotype of drought resistance across selected crops. The proposed workplan will apply existing rice microarray technology created by NIAS and BGI and test the feasibility of develop ortholog arrays for use in multiple crops. The proposed project will enhance synergy with other projects involved in gene expression studies (maize, millet, wheat) in the GCP toward elucidation of gene function.

48. Project No G4005.14: Stress response-enriched EST resources for targeted species

- *Duration: Jan 2005–Dec 2005 with NCE to May 2007*
- *Budget by year: $99,560 (2005); Total budget: $99,560*

Pearl millet, cowpea/Africa/Various traits

Lead institution
IITA (Sarah Hearne)
Collaborating institutions
- IITA (Morag Ferguson)
- TIGR (Chris Town, Jun Zhuang, Note: TIGR has merged with other institutes to form the J Craig Venter Institute)
- ILRI (Richard Bishop, Jean Hanson)

ESTs are good tools for producing candidate genes as gene-based markers as well as providing the basis for SSR and SNP marker discovery. The GCP is interested in enhancing EST resources in inherently stress-tolerant species that are unlikely to be supported by others. The proponents have been requested to identify target genotypes of a species for which a modest investment will significantly elevate the potential of applying EST resources in the species. Preference will be given to cases that can leverage existing efforts or collaboration.

For this round of commissioned work, the GCP is particularly interested in pearl millet and cowpea because they represent the "hardy" species of each crop group, and progress has already been made. EST resources developed for both crops will be duplicated/deposited at the BioScience Center of East and Central Africa (BECA). Depending upon efficiency considerations, the lead institutions may perform the tasks themselves or coordinate the work (i.e., outsource specific aspects of the EST work to one or more appropriate high-throughput labs or institutions).

49 Project No G4005.15: Targeted *Musa* genome sequencing and frame map construction

- *Duration: Jan 2005–Dec 2006 with NCE to Dec 2007*
- *Budget by year: $200,000 (2005), $200,000 (2006), $19,846 (2007); Total budget: $419,846*

Musa/Asia, Latin America/Various traits

Lead institution
NIAS (Takuji Sasaki)
Collaborating institutions
- NIAS (Takashi Matsumoto)
- Bioversity International (Nicolas Roux, Mathieu Rouard)
- Agropolis–CIRAD (Isabelle Hippolyte, FrancChristophe Baurens, Frederic Bakry)
- EMBRAPA (Manoel Souza)
- University of Leicester, UK (Pat-Heslop–Harrison)
- IEB (Jaroslav Dolezel)

Developing basic genomic tools to assist germplasm exploitation is important for *Musa* (banana), especially in the context of the use of *Musa* genomic diversity. Currently, BAC libraries and germplasm resource collections are available, but EST collections are not publically available and there are no characterised mapping populations available. The development and assembly of publicly accessible EST collections and framework maps anchored with genic markers are top priorities for this species, along with initiation of genomic sequencing to identify genes and regulatory genome regions in this important staple crop of developing countries that involves two different genomes and many triploid cultivars.

The GCP is interested in promoting the development of such genomic resources and integrating them with ongoing traitbased research in *Musa*. The GCP also awaits assessment of the utility of rice-based information for application in *Musa* and other mandate crops The GCP is thus requested to support the development of genomic resources for anchoring of chromosomal regions harbouring valuable traits as well as targeted comparative genomic sequencing relating the A, and B *Musa* genomes and the rice genome. The approach suggested will utilise existing resources of *Musa* germplasm, maps and genomic resources, and the outputs will be publicly available resources and markers for exploiting breeding-relevant genetic variation within *Musa*.

50. Project No G4005.17: Integrative genetic framework for comparative QTL mapping for drought tolerance in beans (CIAT and Agropolis–CIRAD)

- *Duration: Jan 2005–Dec 2006 with NCE to Dec 2007*
- *Budget by year: $117,700 (2005), $82,300 (2006); Total budget: $200,000*

Beans/Africa, Latin America/Drought tolerance

Lead institutions
- CIAT (M Blair)
- Agropolis–CIRAD (N Ahmadi)

Collaborating institutions
- CIAT (M Ishitani)
- Agropolis–CIRAD (B Courtois, J-F Rami)
- Agropolis–IRD (A Ghesquière, C Tranchant)

This project will study the genetics of drought tolerance traits that have been identified in common bean to determine what genes underlay this quantitatively-inherited abiotic stress tolerance and to develop optimal genetic markers for the transfer of quantitative trait loci for drought tolerance. One

area we will focus on specifically is the capacity of common beans to maintain the transport of photosynthetically-fixed carbon into grain under drought stress. This trait has already been shown to be important in several recombinant inbred line populations which have been analyzed under drought conditions for QTLs involved in relative yield, grain filling and photoysynthate accumulation under irrigated vs. non-irrigated treatments in Colombia and Nicaragua. Candidate genes for photosynthate mobilisation and transport will be used as genetic markers in these populations to dissect the most important QTLs by fine mapping and by the creation of isogenic stocks containing individual QTLs. The location of candidate genes will be confirmed on saturated genetic maps for which genomic resources including EST sequences and BAC libraries have been developed. Understanding the genetics of drought tolerance, and having DNA markers linked to drought tolerance genes will help plant breeders to combine drought tolerance with other traits desired by farmers.

51. Project No G4005.35: Sequencing multiple and diverse rice varieties: Connecting whole-genome variation with phenotype

- *Duration: Jan 2005–Dec 2005 with NCE to Dec 2007*
- *Budget by year: $236,000 (2005); Total budget: $236,000*

Rice/Various regions and traits

Lead institution
- IRRI (PI: Kenneth McNally, Collaborators: Dave Mackill, Richard Bruskiewich, Hei Leung)

Collaborating institutions
- Perlegen Sciences, Inc (Renee Stokowski, David Cox, Diana Star)
- Colorado State University (Jan Leach)
- TIGR (C. Robin Buell, Kevin Childs; Note: TIGR has merged with other institutes to form the J. Craig Venter Institute)
- Max Planc, Tubingen (Detlef Weigel)

The overall goal of this project is to apply a cost-efficient re-sequencing technology to generate a multi-varietal, genome-wide SNP database in rice that will allow association between whole-genome variation and phenotypes.

The project cost of re-sequencing 20 rice lines is approximately 2 million dollars. IRRI has committed $0.5 million to initiate this project and is coordinating the International Rice Functional Genomics Consortium to raise funds to complete the task. This proposal seeks support from GCP to contribute towards this goal. The output of this project will be a public SNP database for about 20 rice lines, representing the most comprehensive SNP database for a plant species. It will serve as the platform for SNP-enabled gene discovery not only in rice but in other plant species.

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

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

Rice/Asia/Drought tolerance

Lead institution
VBI, Virginia Tech (Andy Pereira)

Collaborating institutions 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 analyzing 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.

53. Project No G4005.18: Development of low-cost gene-based trait assay technologies in cereals

- *Duration: Jan 2005–Dec 2006 with NCE to Oct 2007*
- *Budget per year: $150,000 (2005); $150,000 (2006); Total budget: $300,000*

Maize, rice/Africa, Asia/Disease resistance

Lead institution
IRRI (Casiana M. Vera Cruz)
Co-Principal Investigator
- CIMMYT (Manilal Williams)

Collaborating institutions
- China National Rice Research Institute (Jianli Wu)
- Philippine Rice Research Institute (Eduardo Redoña)
- Indonesian Agricultural Biotechnology and Genetic Resources Research Institute (Masdiar Bustamam)
- Mahyco Research Foundation, India (Usha Barwale-Zehr)
- Agropolis–IRD (Valerie Verdier)
- VPKAS, India (E. Raman Babu)
- National Agricultural Research Centre, Pakistan (Chughtaisajjad Ur Rehman)
- Field Crops Research & Development Institute, Sri Lanka (K.M. Karunaratne)
- BARI, Bangladesh (Bhuiyan Safiful Alam)
- NARC, Nepal (Dil Prasad Sherchan)
- SME breeding companies
- ICTA, Guatemala
- INIA, Venezuela
- KARI

The Generation Challenge Programme (GCP) has a primary focus on the development of gene-based markers for drought tolerance using comparative genomics and comparative biology. These efforts aim to drive rapid progress across three main crop groups (cereals, legumes, and clonal crops) through comparative analysis with model systems. The development of effective gene-based molecular breeding systems for drought tolerance is clearly a long-term goal in most crops. However, it is fundamentally important that the GCP works with end-users from an early stage to foster the integration of successful, low cost applications of gene-based MAS technologies. Most importantly, we must build champions for these new technologies among breeding programmes of national agricultural research systems (NARS) and small-to-medium-sized enterprise (SME) breeding companies across the major regions of the developing world. Clearly, gene-based technologies for abiotic stress tolerances are only just emerging. Thus, other target traits must be focused upon for this initial pilot project concerning the proof-of-concept for technology product delivery pathways associated with gene-based marker-assisted selection tools. This also offers the added advantage for this preliminary project of being able to target traits with a somewhat simpler genetic basis than drought tolerance. In this context, we envisage two very different models for helping NARS and SME breeders establish their own molecular breeding success stories:

(i) low cost (both in terms of capital investment and assay unit costs), low tech (to save time and offer scalable options) assay technologies that can be used by anyone anywhere;
(ii) low cost (most critically with respect to assay unit costs), high throughput (in terms of millions of samples per year) assay technologies that can be used in shuttle genotyping/MAS service labs.

54. Project No G4005.19: Evaluation and deployment of transgenic drought-tolerant varieties

- *Duration: Jan 2005–Dec 2006 with NCE to Oct 2007*
- *Budget per year: $182,590 (2005); $119,180 (2006); Total budget: $301,770*

Various crops and regions/Drought tolerance

Lead institution
IRRI (John Bennett)
Collaborating institutions
- CIAT (Idupulapati Rao)
- CIMMYT (Matthew Reynolds)
- ICRISAT (Vincent Vadez)
- CIP (Enrique Chujoy)
- JIRCAS (Kazuko Yamaguchi-Shinozaki)
- University of Tsukuba, Japan (Kazuo Watanabe)

Drought is an important limitation on productivity for all of the mandated crops of the CGIAR system. While land and water resource management improves water harvesting and water use efficiency at the field, community, and regional levels, progress in breeding for enhanced drought tolerance is essential for achieving improved crop water productivity and greater food security for hundreds of millions of the rural poor who depend on rainfed agriculture. Water savings in irrigated agroecosystems will also require breeding for tolerance of water deficit.

Although lines of several mandated crops are now available with shorter duration (drought escape) and DNA markers are being identified for deeper and more penetrating roots (drought avoidance), there is also a considerable potential for deploying drought tolerance genes that enable plants to survive and recover from unavoidable periods of low plant water status, especially at the sensitive reproductive stage.

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

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

Maize, wheat/Various regions/Various traits

Lead institution
CSIRO (Scott Chapman)
CIMMYT–China (Jiankang Wang as Co-PI)
Collaborating institutions

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

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

56. Project No G4005.21: Planning for effective product development, delivery, and use

- *Duration: Jan 2005–Dec 2006*
- *Budget by year: $67,850 (2005), $67,850 (2006); Total budget: $135,700*

Various crops, regions and traits

Lead institution
Bioversity International (Victoria Henson-Apollonio)
Collaborating institutions

- Consultant (Lawyer), Costa Rica (Silvia Salazar)
- Consultant (Lawyer), Colombia (Maria Ines Mendosa)
- Consultant (Lawyer), USA (Shawn Sullivan)
- Bioversity International (Zenete Franca)
- University of Capetown, South Africa (Rosemary Wolson)
- AfricaBio (Jocelyn Webster)

Through competitive and commissioned research projects, the Generation Challenge Programme (GCP) is building an extensive number and range of research outputs targeted at the identification of useful germplasm, traits, genes, and alleles for use in enhancing drought tolerance in cereal, legume, and clonal crops. The GCP is also generating knowledge and tools to help plant breeders manipulate those genetic factors. It is well accepted that these resources, tools, and knowledge can be used to improve the food, nutritional, and economic security of small-holder farmers and their families in drought-prone areas. However, uptake of research outputs and seed-based technologies has been patchy and often disappointing. It is, therefore, essential for biotechnologists to consider the entire innovation-to-impact pathway whilst designing and carrying out their research programmes. This type of holistic approach is a highly complex multidisciplinary and multisector endeavour. Yet this is the way to increase the rate of uptake of GCP research outputs by ensuring the development of products that provide end-users with practical, user-friendly, appropriate technology packages that meet their needs, capabilities, and capacities.

Emphasis on using an explicit end-user orientated mapping and planning process to improve product development and delivery is a new approach for many of the scientists involved in GCP research projects. Current strategic biotechnology research projects often define indicators for their outputs in terms such as "publication of the results in…". However, the GCP Subprogramme 3 is committed to populating the intellectual space between conventional academic research outputs and the deployment of research-based products that can have tangible impacts on primary agricultural development parameters. Historically, this is a hugely neglected research domain in the public sector and is surely a major reason for the sub-optimum uptake of research outputs. For this reason, the GCP wishes to move far beyond traditional technology hand-over and training models. Instead, tangible product development and deployment plans must include information on how outputs will serve the end-users, why those end-users would favour transfer/adoption of these new technologies, where the critical linkages for product testing, refinement, and delivery are embedded in the plans, and who or what may be the rate limiting steps for product

development and deployment. It is fundamentally important that these issues are considered at the project design phase by adequate representation and decision-making influence by stakeholders from across the entire innovation-to-impact pathway.

Adoption of a more holistic and product-driven approach requires substantial changes in institutional policies and processes, in the perspectives of individual scientists. Many consortium member institutions are already advancing towards these general goals. To complement this, the GCP is committed to fostering targeted progress by creating resources, tools, and case studies for assisting current and future projects. It is envisaged that ultimately the GCP will establish a framework of criteria and guidelines in support of mandatory inclusion of product development and deployment activities in all competitive and commissioned projects. Initially we propose to pilot this approach in a facilitated mode during 2006 and autonomously from 2007 (with assistance from GCP Helpdesk support services). Thus, this project proposes to collaborate with project scientists to develop a number of diverse case studies from fundamentally important areas of the current competitive and commissioned programmes. These case studies will be used to develop specific product development and delivery pathways, generic process templates, resources and guidelines for pathway analysis, and defining policy statements. In this way, not only will the most immediate concerns be dealt with but resources and patterns of behaviour will also be established for use in the development of future project proposals.

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

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

Maize/Asia/Mildew resistance

Lead institution
BIOTEC (Chalermpol Phumichai, Julapark Chunwongse)
Collaborating institutions and scientists

- National Corn and Sorghum Research Center (Sansern Jampatong)
- Nakhon Sawan Field Crop Research Center (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.

58. Project No G4007.06: Integrating marker-assisted selection into the conventional breeding procedure for improvement of wheat (*Triticum aestivum* L.) in the drought-prone areas of Northern China

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

Wheat/Asia/Drought tolerance

Lead institution
CAAS (PI: Ruilian Jing, Collaborators: Xin-Guo MAO, Xiao-Ping CHANG)
Collaborating institutions

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

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

1. To hold training courses for molecular marker assisted (MAS) selection techniques and drought tolerance (DT) phenotyping;
2. To integrate MAS tools into conventional breeding programme and select stable introgression lines (ILs) carrying target genes/markers;

3. To phenotype and genotype the ILs with the elite Chinese wheat genetic backgrounds in diverse environments and select DT ILs;
4. To exchange the information, technology and methodology associated with the molecular breeding for DT, promote interactions among regions, build the capacity of wheat modern breeding in China and other Asian countries.

59. Project No G4007.07: Marker-assisted selection for sweetpotato virus disease (SPVD) resistance in sweetpotato germplasm and breeding populations

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

Sweetpotato/Africa/SPVD resistance

Lead institution
CIP (Wolfgang Grüneberg)
Collaborating institutions
- CIP (Marc Ghislain, Roland Schafleitner)
- NAARI (Robert 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".

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

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

Rice/Africa/Drought tolerance and disease resistance

Lead institution
WARDA (Marie Noelle Ndjiondjop)
Collaborating institutions
- Agropolis–IRD (Alain Ghesquiere, Mathias Lorieux, Valerie Verdier)
- IER (Fousseyni Cisse)
- WARDA (Koichi Futakuchi, Manneh Baboucarr, Sanchez Ines, Semagn Kassa, Sere Yacouba, Semon Mande)

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.

61. Project No G4007.25: Development of a GCP Drought Phenotyping Network

- *Duration: Dec 2007–Feb 2008*
- *Budget per year (as per proposal): $22,500 (2007); Total budget (as per proposal): $22,500*

Various crops/Africa, Asia, Latin America/Drought tolerance

Lead institution
Consultants (Gregory Edmeades, Abraham Blum)
Collaborating institutions

- CIAT (Glenn Hyman)
- Gent University, Belgium (Dirk Raes)
- Robert Koebner (Consultant)
- Cornell University, USA (Tim Setter)
- ICRISAT (Vincent Vadez)
- KARI (James Gethi)

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

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

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.

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

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

Lead institution
IRRI (Richard Bruskiewich)
Collaborating institutions

- IRRI (Thomas Metz, Martin Senger, Graham McLaren)
- Bioversity (Elizabeth Arnaud, Tom Hazekamp, Adriana Alercia)
- CIMMYT (Rosemary Shrestha, Guy Davenport)
- CIP (Reinhard Simon)
- ICRISAT (Jayashree Balaji)
- External (self-funded) collaborator
- Pankaj Jaiswal (Plant Ontology Consortium)

Generation Challenge Programme (GCP) domain models were developed by SP4 editorial teams during 2005 and 2006, and reviewed in Pretoria in by a wider community of scientific experts in March 2006, then put into production use as a blueprint for software and network engineering projects for "platform specific implementations".

The GCP domain models are a set of generic object models encoded using Unified Modeling Language (UML) formalism and representing various biological and biological objects in the system. In order to maintain semantic flexibility and extensibility, these object models are deliberately designed to be heavily parameterised by a large number of context-specific ontology sets. Although many of these ontology are being adapted from maturing third party initiatives of ontology development (such as the Gene Ontology and Plant Ontology consortia), there remains a sizable scope of GCP ontology remaining to be formalised.

In 2007, although incrementally continuing to correct, validate and refine the GCP domain model, the task will primarily focus on the systematic elaboration of priority ontology required for the domain model and strive to put into place tools and a strategy for long-term, community-curated extension and application of domain model ontology, which will empower end users 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.

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

- *Duration: Jan 2005–Dec 2008*
- *Budget per year: $178,910 (2005), $140,000 (2006), $120,000 (2007); $67,000 (2008); Total budget (as per proposal): $505,910*

Lead institution
Bioversity International (Milko A Škofič)
Collaborating institutions

- Bioversity International/SGRP (Samy Gaiji, Rajesh Sood, Tom Hazekamp)
- Bioversity International (Mathieu Rouard)
- IRRI (Martin Senger)

The availability and sharing of data is crucial to the success of the Generation Challenge Programme. To achieve this objective, web services will be deployed as a mechanism to ensure local and remote access to scientific information, its exchange and compliance with common standards.

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

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

Lead institution
Bioversity International (Mathieu Rouard)
Collaborating institutions

- EBI (Martin Senger)
- IRRI (Richard Bruskiewich)
- Agropolis–CIRAD (Manuel Ruiz, Matthieu Conte)

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

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

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

65. Project No G4005.25: Creation and maintenance of templates for GenerationCP data storage in repositories

- *Duration: Jan 2005–Dec 200 (continued to Oct 2008 under project G4008.20)*
- *Budget per year (as per proposal): $80,000 (2005), $80,000 (2006), $80,000 (2007); Total budget (as per proposal): $240,000*

Lead institution
CIMMYT (Guy Davenport)
Collaborating institutions
- IRRI (Richard Bruskiewich)
- Bioversity International (Tom Hazekamp)

- GCP projects produce a large amount of data each year. These data must be stored in a form that can be used by GCP consortium members and the scientific community.
- In previous years data templates were developed for the storage of SSR genotyping, passport, mapping, QTL, and phenotype data.
- This year's project will improve the current templates by allowing users assign control vocabulary or ontology terms to their data.
- The Data Editor software will be improved with the inclusion of support for uploading data to databases and converting data to various formats required for visualisation and analytical tools.
- GCP data standards for high throughput (e.g. array based) technologies, such as DArT, gene expression arrays and SNP genotyping will be established.
- Support for populating the templates and using the software will be provided including a physical help desk at the next Annual Research Meeting.

66. Project No G4005.26: Management of the Generation Challenge Programme Central Registry

- *Duration: Jan 2005–Dec 2007 (to be continued under project G4008.20)*
- *Budget by year (as per proposal): $147,518 (2005); $120,950 (2006); $80,000 (2007); Total budget (as per proposal): $348,468*

Lead institution
Bioversity International/SGRP (Tom Hazekamp)
Collaborating institutions
- CIMMYT (Guy Davenport)
- Bioversity International/SGRP (Samy Gaiji, Milko Skofic, Raj Sood)

A large amount of data is being generated within the Generation Challenge Programme. These data are stored and maintained at different locations using different formats and standards. Organising and publishing information on the web through a Central Registry provides an overview of all available data resources (like a 'yellow pages' directory). This is critical for the successful completion of tasks that require data from different sources. Established in 2005, the Generation Challenge Programme Central Registry increased the depth and range of the resources it manages in 2006. In 2007 the aim is to strengthen and further develop components of the Central Registry, and to continue encouraging partners to register new resources.

The 2007 component of the project focuses on:

- The technical maintenance and management of the Central Registry;
- Strengthening the Central Registry's resource collection through a pro-active approach toward potential providers;
- Further development of the Central Registry with a web services-caching system;
- Content management resulting in more extensively controlled vocabularies and enhanced data validation rules;
- Help-desk support to providers and users; and
- A user survey.

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

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

Lead institution
CIP (Anthony Collins)
Collaborating institutions

- CIP (Mariana Cruz, M Bonierbale, R Quiroz, R Simon, E Rojas, M Schmitt, L Avila, J-C Gonzalez)
- ICRISAT (B Jayashree, D Hoisington, RK Varshney, S Chandra)
- IRRI-CRIL (Richard Bruskiewich)

The principal goal of this project is to consolidate the 3 global High Performance Computer (HPC) sites created by the GCP into a sustainable cluster/grid facility serving the GCP and it's partners with substantial cost benefit, and with specific support for associated GCP goals.

Further use cases are proposed, complementing and extending the achievements to date, as part of the overall suite of facilities available for the GCP community. The 3 sites will target:

CIP:

- Maintenance of HPC operations
- GIS-based site characterisation

ICRISAT:

- Extending the software resources available in the comparative genomics and population genetics toolbox on the ICRISAT HPC

IRRI:

- Embedding HPC analysis invocation into the GCP Platform using a dedicated SoapLab GCP DataSource.
- Deployment of new third party analysis applications into HPC with integration to GCP platform via the SoapLab GCP DataSource.

Consolidation of the facility will continue to extend integration with the larger HPC facility at ILRI. Systems management of the overall global facility will also focus upon client support and usage monitoring to develop a persuasive cost/benefit case leading towards eventual sustainability of the facility beyond the GCP funding umbrella.

68. Project No G4005.31: Development of ortholog-function display tools

- *Duration: Jan 2005–Dec 2007*
- *Budget per year: $100,000 (2005), $100,000 (2006); Total budget: $200,000*

Various crops, regions and traits

Lead institution
IRRI (Richard Bruskiewich)
Collaborating institutions

- UC–Berkeley (Kimmen Sjölander)
- Agropolis–CIRAD (Brigitte Courtois, Manuel Ruiz, Christophe Perin, Mathieu Conte)
- Bioversity International (Mathieu Rouard)
- EMBRAPA (Marcos Costa, Georgios Pappas, Natalia Martins)

Comparative biology across multiple crop species is a key strategy in the GCP for the identification of stress-responsive gene loci and their corresponding alleles of high agronomic value, for application in breeding for stress tolerance.

Critical to the task of comparative biology is the elucidation of evolutionarily conserved gene orthology relationships across species and related paralogy relationships within a gene family. Such orthologous and paralogous gene loci almost invariably share common gene functions, thus important inferences of comparative biology may be possible once such relationships are clearly defined.

This GCP Subprogramme 4 commissioned research project therefore focuses on the task of compiling a catalog of orthologous and paralogous plant genes for GCP target crops and related model plant species. This task also includes the development of useful (graphical) user interfaces to the catalog and provisions for (web services) integration with other GCP project data and tools, such as comparative gene expression experiments.

69. Project No G4005.32: Development of crop gene expression database and data mining tools

- *Duration: Jan 2005–Dec 2006*
- *Budget by year: $100,000 (2005), $100,000 (2006); Total budget: $200,000*

Various crops, regions and traits

Lead institution
NIAS (Shoshi Kikuchi)
Collaborating institutions

- IRRI (Richard Bruskiewich, Hei Leung)
- NIAS (Masaru Takeya)

During the completion of genome sequence analysis in Arabidopsis and rice, many kinds of technologies for comprehensive analysis of gene expression have been developed. Those are microarray, SAGE (Serial Analysis of Gene Expression) and MPSS (Massively Parallel Signature Sequencing) etc. Gene expression data using such technologies have been accumulated and many databases have been opened. But the problem is that the databases have been independently constructed and for the researchers current databases are not easy to access and to obtain the data what they want.

Shoshi Kikuchi's team in NIAS has been contributed to the establishment of rice microarray system since 1999. Starting with 1265 cDNA-based microarray system, 8987 cDNA-based microarray system was finally established in the Rice Microarray Project in Japan (1999~2003) (1). About sixty research groups have joined in the Rice Microarray Project and almost all microarray experiments were performed in the Rice Microarray Center established in NIAS at that time. All gene expression data using 8987 microarray system were deposited and accumulated in the Rice Expression Database (2). Probed cDNA clones are originated from the large scale EST collection of Rice Genome Project (1991~1997). Total gene number of rice has been estimated to 40,000~50,000 and the unique set of EST collection corresponds to 11,000. This means the coverage is only quarter of the whole expressed genes.

To solve the problem and to collect cDNA clones as an intact form of the mRNA, the Rice full-length cDNA project has launched in the beginning of year 2000. In this project, 32,127 unique set of full-length cDNA clones originated from more than 20 different full-length cDNA libraries have been collected, completely sequenced and opened to the public in July 2003 (3,4). Sequence information of 29,100 full-length cDNA clones were used for the establishment of the first version of rice oligoarray system. After several round of validation experiments, rice 22K oligoarray system ver 1 was commercialised to the world in November 2003 from the Agilent Technologies (5). The first paper using this array system with the gene expression analysis of rice calli treated with ABA and GA was also published in Feburary 2004 (6) and many researchers have started to use the array system. Many kinds of gene expression data using this array system have been accumulated and based-on the experience in rice comparison of gene expression data among crops via orthologous genes are currently required.

70. Project No G4005.34: GenerationCP software engineering and collaboration platform

- *Duration: Jan 2005–Dec 2007*
- *Budget by year: $40,120 (2005), $80,000 (2006), $38,940 (2007); Total budget: $159,060*

Lead institution
IRRI (Thomas Metz)
Collaborating institutions
- None

This project is a continuation of the commissioned research project 34 of 2005 and 2006. Two web-based collaborative development environments, one for the development and support of software (http://cropforge.org), and one for the development of textual content (http://cropwiki.irri.org/gcp) were commissioned in 2005 and successfully used by SP4 team members. Currently (12/10/2006) the CropForge server hosts 63 software projects with 126 registered users, and the GCPWiki collaborative web site has 361 content pages, 280 uploaded files, and 149 registered users. The two systems collectively provide a shared workbench for the software developers in SP4, enabling multiple developers from different institutions to develop a common software platform.

The main objectives of this project in 2007 will be maintain its services in terms of hardware, software, connectivity, as well as helpdesk. In addition to the current GCPWiki site which is restricted to GCP members and collaborators, an additional open wiki site will be established to support the wide dissemination and adoption of the software developed in the GenerationCP SP4. Special support in the methodologies and technologies of collaborative open source software development will be provided to individual projects.

71. 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 2006–Dec 2008*
- *Budget per year (as per proposal): $150,000 (2006), $62,500 (2007), Total budget (as per proposal): $412,300*

Various crops, regions and traits

Lead institution
- CIMMYT (Guy Davenport)
- Collaborating institutions
- IRRI (Richard Bruskiewich, Hei Leung)
- NIAS (Shoshi Kikuchi, K. Satoh, Masaru Takeya)
- JIC (Andreas Magusin)
- CIMMYT (Jose Crossa, Yunbi Xu)

- 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, phenotype, genotype and QTL mapping data sets 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:

  - Consolidate and enhance the organisation, annotation quality and accessibility of comparative gene expression, phenotype, genotype and mapping (QTL) from GCP projects.
  - 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.
  - Document on GCP-hosted web sites the analysis results, methodology, experimental design and other pertinent best practice parameters of the analysis to facilitate the design and analysis of future experiments and projects.
  - Build GCP bioinformatics capacity through direct workshop training of SP2 scientists on data analysis and annotation of SP2 data.

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

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

Lead institution
IRRI (Graham McLaren)
Collaborating institutions
- Agropolis–CIRAD (Brigitte Courtois, Manuel Ruiz)
- EMBRAPA (Marcos Costa)
- NIAS (Shoshi Kikuchi, Maseru Takeya)
- IRRI (Richard Bruskiewich)
- CIMMYT (Xu Yunbi, Guy Davenport)
- IRRI/EBI (Martin Senger)
- INIBAP–Bioversity International (Mathieu Rouard)
- ACGT/CSIR (Jane Morris)
- ACGT/FABI (Zander Myburg)

This project continues the work on platform development commissioned during 2005 and 2006. During the earlier phases work concentrated on supporting implementation of LIMS facilities in CGP labs, on defining a model driven architecture for integrating diverse data sources and analytical applications, developing a prototype of the middleware needed to implement the platform (Pantheon) and attaching several data sources, two query interfaces (Genomedium and Koios) and applications into a pilot platform, whose architecture is now well defined (Figure 1). Further development of the basic infrastructure and connectivity for the platform are now housed under two new commissioned projects: Application and Development of Web Services Technology (SP4 2005-24) and Development of Tools and Technology to Increase the Functionality of the GCP Information Platform. The emphasis of this project will focus on elaboration, prioritisation and implementation of biologically motivated use-cases for the platform. This year three use-cases will be developed, one each in support of diversity studies (SP1), functional genomics (SP2) and molecular breeding (SP3).

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

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

Lead institution
IRRI (Thomas Metz)
Collaborating institutions
- WUR (Theo Van Hintum)
- ICRISAT (B Jayashree)
- Bioversity International (F Atieno)
- SCRI (David Marshall)

In 2007, this project will selectively address four issues that have strong implications on data quality in the GenerationCP.

- A workshop on passport data quality assessment and improvement will bring together 4-5 experts and develop a technical documentation on the state of the art in this area. The workshop will draw extensively from the European and CGIAR genebank experiences and projects, e.g. SINGER, EURISCO.
- A workshop on ISO quality certification for genebanks and service laboratories will bring together 10-12 genebank and laboratory managers from the GCP partner institutions, to be trained to prepare their respective genebanks and laboratories for ISO quality certification. This workshop will draw extensively on the recent ISO certification experience of CGN and PRI.
- A workshop will be conducted to build and support a community of adopter and developers around the ICRISAT laboratory information management system (LIMS). The system has already been implemented at IITA, ILRI and the ICRISAT labs based at the Biosciences Eastern and Central Africa (BecA) facilities in Nairobi, Kenya. The workshop participants will be expected to implement and support the ICRISAT LIMS in their respective institution, and become active contributors in a collaborative

software development effort to adopt, improve, and extend the ICRISAT LIMS. The LIMS software will be freely available under the GPL open source license.
- A study on the quality of the genotyping data deposited in the GCP Central Registry as well as GCP-sponsored datasets available by other means will be conducted and the results reported to GCP management and partner institutions. The study will be part of a feedback mechanism to demonstrate data quality assessment methods and procedures, to highlight deficiencies in GCP sponsored datasets, and to focus resources for data quality improvement.

74. Project No G4006.18: Creation of Institutional Bioinformatics Capacity (CIAT)

- *Duration: Jan 2006–Dec 2006*
- *Budget per year: $16,500 (2006); Total budget: $16,500*

Lead institution
CIAT (PI: Joe Tohme, Collaborators: Fernando Rojas, Mathias Lorieux, Martin Fregene, Matthew Blair)

This project aims at upgrading and expanding existing bioinformatics skills, continuing with the process of integration of molecular data and genotypic information and the sharing of this information with the scientific community. To achieve this, we will:
- develop new programmes that help with the management of genotypic information (SSR & SNPs markers) in rice and other crops (bean, cassava) such that it flows in an automatic way to the LIMS
- develop scripts in Perl to establish pipelines for the detection of SNPs (SNP identification pipeline). Some scripts are already available or need to be improved/ installed, other still need to be developed
- complete the molecular markers database in including information for other markers (RAPDs, RFLPs, DARTs) and for other crops (bean, rice)
- increase the use of Web Services technology (BioCase, BioMoby..), and its diffusion and application at CIAT (within the guidelines established in GCP-SP4)
- transfer the knowledge to research assistants and students in the different projects.

75. Project No G4006.19: Creation of Institutional Bioinformatics Capacity (CIMMYT)

- *Duration: Jan 2006–Dec 2006*
- *Budget by year: $16,500 (2006); Total budget: $16,500*

Lead institution
CIMMYT (Guy Davenport)

The Research Informatics Laboratory is now established at CIMMYT. Prototype systems for the management of CIMMYT genomic data will be installed. These systems will used to provide data via web services to the GCP informatics platform. An Access Grid node will be installed at CIMMYT.

CIMMYT has now established a Research Informatics Laboratory, with sufficient capacity and infrastructure to undergo informatics and analysis projects for the benefit of both CIMMYT and the GCP. Projects are now underway to develop integrated databases for genotyping, QTL, and fingerprinting data, funded both by last year's GCP capacity building project and CIMMYT core funding. We propose to continue these projects in 2006, with the installation of prototype systems for the management and analysis of these systems. CIMMYT is also in the process of obtaining internet 2 in order to have high throughput access to biological databases, connection of our HPC to the GCP HPC grid, and multimedia video conferencing for software development across GC centres. In addition we propose to upgrade one of our existing workstations to allow us to set up an Access Grid node that will allow us to have real time developer's meetings between other centres, such as IRRI, CIP, and ICRISAT.

76. Project No G4006.20: Creation of Institutional Bioinformatics Capacity (CIP)

- *Duration: Jan 2006–Dec 2006*
- *Budget by year: $16,500 (2006); Total budget: $16,500*

Lead institution
CIP (Reinhard Simon)
Collaborating institutions
- CIP (Merideth Bonierbale, Roland Schafleitner)
- Virginia Tech (Ruth Grene, Lenwood Heath)

This project will concentrate on making new tools available to the GCP on gene-expression analysis. It will collaborate with Virginia Tech on integrating the EXPRESSO analysis pipeline (http://bioinformatics.cs.vt.edu/~expresso/) into the Generation Challenge Programme Pipeline. It will also add new tools from systems biology (metabolic control analysis, MCA).

During 2005 gene expression data became available at CIP under the GCP that are currently being analysed. Also, in 2006 CIP expects to realise n one or two new projects. Thus, further expertise and tools will be needed to make best use of the generated data. It is anticipated that under a new activity in SP4 (task 23) new expertise (personnel) will become available such that this project intends to complement this by leveraging software tools.

77. Project No G4006.21: Creation of Institutional Bioinformatics Capacity (ICARDA)

- *Duration: Jan 2006–Dec 2006*
- *Budget by year: $16,500 (2006); Total budget: $16,500*

Lead institution
ICARDA (PI: M. Singh, Collaborators: M Baum, K Chabane, G Peiguo, A Akintunde, K El-Shamaa, H Abed)

Bioinformatics support to the GCP activities under SP1- SP3 is critical to ICARDA's commitment. We aim to continue to develop and exploit molecular and phenotypic databases, LIMS, and other specialised software for data analysis and interpretation, and share bioinformatics and biometric tools with in-house scientists and NARS scientists. To meet the need of bioinformatics at ICARDA, we intend to develop our capability further during 2006 by attending training courses, workshops, and conferences, and exploring the possibility of eventually recruiting a full-time bioinformatician. With the limited funds of US$16,500 we present in the following table our workplan, which reflects only a small part of our activities.

78. Project No G4006.22: Creation of Institutional Bioinformatics Capacity (ICRISAT)

- *Duration: Jan 2006–Dec 2006*
- *Budget by year: $16,500 (2006); Total budget: $16,500*

Various crops, regions and traits

Lead institution
ICRISAT (PI: Subhash Chandra, Collaborators: Jayashree B, Dave Hoisington)

For quality genomics research to take place, it is critically important that (a) Genomics researchers are trained in information management, and in the access of publicly available data resources and tools; (b) Advice and support is readily available to them to help organise and analyse data; and (c) Appropriate information systems and analysis tools are developed, maintained, and regularly updated to facilitate proper management, analysis, and use of genomics data. Accordingly, the project during 2006 aims to (1) Conduct bioinformatics training in (a) simple programming for data management for scientists, (b) in-silico marker development, and (c) Association Mapping; (2) Provide advice and support to genomics researchers; and (3) Develop, maintain, and regularly update appropriate information systems and analysis tools. These will be tailored to meet the current and near-future on-the-job needs of genomics researchers at ICRISAT.

79. Project No G4006.23: Creation of Institutional Bioinformatics Capacity (IITA)

- *Duration: Jan 2006–Dec 2006*
- *Budget by year: $16,500 (2006); Total budget: $16,500*

Lead institution
- IITA (Dong-Jin Kim)
- Collaborating institutions
- ILRI/BECA (Trushar Shah)
- NCGR (Andrew Farmer)

Recent progress in genomics research provides tremendous amounts of bioinformation to the individual scientist. In order to utilise these resources, various bioinformatics tools have been developed and many are freely available to the community, but a customised platform is usually necessary for an individual project. This project proposes to hold a three-day workshop for participants from NARS, Universities, and CG Centres in the Nairobi area to assist them to access and utilise the information. In the workshop we will cover basic topics such as downloading sequences from NCBI, Blast analysis, SSR finding, and Primer Design. We will put these tools into a comparative genomics and COS marker development context. A workshop website will provide the communication platform for participating scientists. Public bioinformatics tools for COS marker design will be linked and a message board will provide a mechanism for feedback after the workshop.

80. Project No G4006.24: Creation of Institutional Bioinformatics Capacity (Bioversity International)

- *Duration: Jan 2006–Dec 2006*
- *Budget by year: $16,500 (2006); Total budget: $16,500*

Lead institution
Bioversity International (Samy Gaiji)
Collaborating institution
- Bioversity International (Milko Skofic)

This project is intended to further support the target activities involved in implementing the Subprogramme 4 workplan. Eligible activities include the recruitment of additional bioinformatics staff as well as sustaining existing bioinformatics experts. IPGRI proposed to allocate the funds within this project to support the recruitment of a Bioinformatics Senior Scientist to be based at IPGRI HQ in Rome (Italy). This person would be dedicated to the GenerationCP Bioinformatics activities led by IPGRI as well as to provide leadership and support in the overall GenerationCP Subprogramme 4 platform and implementation design.

81. Project No G4006.25: Creation of Institutional Bioinformatics Capacity (IRRI)

- *Duration: Jan 2006–Dec 2006*
- *Budget by year: $16,500 (2006); Total budget: $16,500*

Lead institution
IRRI (Graham McLaren)

Bioinformatics capacity building for 2006 will continue to fund NRS bioinformatics staff at IRRI to expand the capability of the bioinformatics team. Documentation and software will continue to be added to the libraries of bioinformatics resources available at IRRI. Bioinformatics staff will have the opportunity to attend GCP meetings, bioinformatics training, and international bioinformatics meetings during 2006.

The capacity building project is required to enhance bioinformatics capacity at IRRI by providing staff resources, an effective literature resource, and software required for bioinformatics analysis to support GCP and IRRI research projects.

82. Project No G4006.34: Installation and Implementation of the ICRISAT LIMS at the Biosciences Eastern and Central Africa (BecA) Facility and IITA-Ibadan

- *Duration: Jan 2006–Dec 2006*
- *Budget by year: $33,453 (2006); Total budget: $33,453*

Lead institution
ICRISAT (Dave Hoisington)
Collaborating institutions
- ILRI (Etienne de Villiers)
- IITA (ME Ferguson, Sarah Hearne)
- ICRISAT (Santie de Villiers, Rosemary Mutegi)

SSR genotyping is a major activity in most crop genomics laboratories. The laboratory workflow needs to be organised and the large amounts of data that are produced during high throughput genotyping need to be managed. During 2005, the existing ICRISAT MS-Windows based LIMS has been re-coded as a platform independent, multi–user Laboratory Information Management System (LIMS) that manages workflow and information in the Applied Genomics Laboratory (AGL) at ICRISAT-Patancheru. The AGL-LIMS can be broken into two main functional areas: laboratory management and data management. Laboratory management includes sample tracking –from the time that DNA is extracted to the time that capillary electrophoresis is complete and the output uploaded into the system. Data management includes management of reagents and protocols, storage of sample information, gel images, textual, graphical, and chromatogram files, implementation of data quality measures, and report generation.

The LIMS has been developed as a three-tier application. Our experience with an earlier two-tier system indicated that one of the key challenges lies in coping with constant changes required by the user, since researchers continually refine existing procedures or introduce new ones. The advantage of having a three-layered architecture is that each layer is completely independent of changes introduced in the other. The LIMS was also developed as modules, thus any number of modules may be added depending upon the needs of the laboratory using the application. The current version of the LIMS has functional modules on experiment set-up and sample tracking that includes DNA extraction, quantification, dilution, PCR setup, marker selection for PCR, capillary electrophoresis, file uploading, and checking for allele binning quality. In addition, there are visualisation or display modules, data management, and storage modules. Given its modular structure, the LIMS can be adapted to the needs of almost any genotyping laboratory.

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

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

Lead institution
WUR (Marco Bink)
Collaborating institutions
- WUR (Hans Jansen, Fred van Eeuwijk, Marcos Malosetti)
- Agropolis–CIRAD (Xavier Perrier, Jean-Francois Rami)
- CIMMYT (Jose Crossa)

Within the Generation Challenge Programme (GCP) the sub programme 1 (SP1) scientists expressed strongly a need for support in the proper analysis of data sets (e.g., workshop in Zaragoza – Oct 2006). 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 scientists and also organised a one-week workshop (Zaragoza – Oct 2006) to provide training and guidance in assessing data quality and performing data analyses. This new project targets to continue and expand this support to SP1 scientists via bilaterial contacts and consultations, mostly via email but possibly also via on-site visits. In addition, the helpdesk functionality will become more visual by establishment of a helpdesk facility via a website. This facility should provide easy-understandable explanation of the stepwise procedure guiding the SP1 in their Germplasm Data Analysis (GDA). This GDA comprises not only the selection of useful sub samples from a broad crop germplasm (as initially expected at the start of 2006). Apparently, the need for support on

statistical tools for GDA (choosing, applying, and making inferences) is much more widely, i.e., starting at experimental design up to the assessment of LD and the marker-trait association analysis. (See Figure 1).

Within the GCP, the Genotype Support System (GSS) is a joint initiative of the sub programmes 1 (SP1) and 5 (SP5), focusing on the development of marker based breeding strategies at National Agricultural Research Stations (NARS) for genetically challenging crops. The activities within the present proposed project will supply statistical support to the NARS scientists included in the GSS. This support includes help with the design of field experiments, checking of genotypic and phenotypic data quality, development of appropriate LD mapping strategies, and help with the LD analyses themselves. The objective is to support SP1 scientists to analyze the generated genotypic and phenotypic data in an optimal way, identifying relevant QTLs with correct and tailored statistical procedures. The project contains consultancy, communication and training components.

84. Project No G4007.09: Methodology and software development for marker-trait association analyses

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

Lead institution
WUR (Fred van Eeuwijk)
Collaborating institutions

- University of Hohenheim, Germany (Hans Peter Piepho, Albrecht Melchinger)
- Imperial College London, UK (David Baldin)
- NIAB (Ian Mackay, Wayne Powell)
- SCRI / BIOSS (Christine Hackett, Dave Marshall)
- Leiden University Medical Center, The Netherlands (Hans van Houwelingen, Jeanine Houwing-Duistermaat)
- WUR (Marcos Malosetti, Joao Paulo, Marco Bink, Hans Jansen)

Quantitative trait loci, QTLs, are stretches of chromosomes containing the hereditary basis for agronomically important traits. Localisation of QTLs for specific traits is a first and important step in the development of efficient genotype improvement strategies. Since the 1990s, the standard methodology for the detection of QTLs in crops is based on the analysis of offspring populations created from controlled crosses. When within such populations a phenotypic trait difference is found between individuals having a particular piece of DNA, a marker, and other individuals missing that piece, we conclude that there is an association between marker and trait and that a QTL must be close. Although this methodology has greatly increased the efficiency of selection strategies in plant breeding, it also had some obvious weak points. The first weak point is the requirement to create artificial crosses that often are not representative of the germ plasm that breeders use in their programmes, with the consequence that the detected QTLs have severely reduced positive effects when translated to more interesting genetic back grounds. The second weak point concerns the limited power to detect QTLs and the relatively low precision in the localisation of standard QTL mapping techniques. Power and precision depend on the number of generative cycles (meioses) since a genetic reference situation, like the controlled crossing of two parents.

A recent and attractive alternative to standard QTL mapping is linkage disequilibrium (LD) mapping. LD approaches can be applied to any pool of selected or random 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 typically more powerful and precise than standard QTL mapping approaches. A disadvantage of LD methods is that marker-trait associations can also arise for reasons that make these associations useless for breeding purposes. Various statistical methods to separate spurious from non-spurious associations have been proposed over the last years, but enough controversy remains about which LD mapping strategies to prefer, especially for genetically more challenging crops with deviating genome and reproduction structure. A common denominator in all those methods is the importance given to a reliable representation of the genetic relationships between genotypes, a first requirement in the separation of real from spurious associations.

The current project will develop LD strategies for general use on arbitrarily structured populations, with special attention for genetically challenging crops. We will adopt a mixed model framework that is highly suitable for modeling multi-environment data, data obtained from germplasm evaluations across multiple trials and stress gradients. Mixed models have good facilities for representing relationships between genotypes and thus provide reliable inference on marker-trait associations. The statistical methodology will be accompanied by documented software and course material that should open up the methodology to the whole of the Generation Challenge Programme.

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

- *Duration: Aug 2007–Jul 2009*
- *Budget by year (as per proposal): $56,640 (2007), $60,600 (2008); Total budget (as per proposal): $117,240*

Lead institution
WUR (Theo van Hintum)
Collaborating institutions
- 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 analyzing his/her data. The helpdesk is responsible for creating transparency in the available expertise and resources in the field of biometry, bioinformatics, and software engineering relevant to GCP scientists, available in the GCP. It will pro-actively improve (or advise on the improvement of) GCP web-sites, create an expert network and act as a point of reference for GCP scientists.

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

86. Project No G4007.11: Refinement and distribution of iMAS for use by NARS and other user communities

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

Lead institution
ICRISAT (Subhash Chandra)
Collaborating institutions
- ICRISAT (David Hoisington, Tom Hash, Jayashree Balaji)

The iMAS system intends to provide 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 process of marker-assisted selection and breeding. The provision of simple-to-use online decision guidelines will allow 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 three modules. The *Phenotyping Module* generates experimental design and undertakes biometric analyses. The *Mapping Population Module* builds linkage maps, undertakes QTL analyses, determines sample size for backcross introgression, and pictorially visualises the genomic content to help select genetic material of desired genomic constitution. The *Germplasm Module* facilitates association mapping using representative collections of germplasm and/or breeding lines. Major achievements during 2005-06 have been the successful integration of different computing tools into one single platform and the provision of a windows interface to all DOS-based programmes, the latter making it easier for a user to correctly, comfortably and confidently use these programmes.

During 2007, the system will be further refined and improved by (a) *Revision/preparation of online decision guidelines for IRRISTAT, GMendel, PlabQTL, WinQTLCart, PopMin, GGT and TASSEL in the light of feedback from users;* (b) *Testing of iMAS on a wide range of different real datasets;* (c) *Preparation of a User Manual;* (d) *Organizing a one-week training course on the use of iMAS; and* (e) *Integrating iMAS into the GCP platform.* The completed system is expected to be formally released at the next annual research meeting of the GCP, although pre-released versions will be made available as they are finalised.

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

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

Lead institution
IRRI-CRIL (Martin Senger)
Collaborating institutions
- IRRI–CRIL (Graham McLaren, Richard Bruskiewich)
  - *Relevant objectives:* [PANTHEON], [KOIOS], [DATA-SOURCES], [GUIDANCE], [DOCS]

- Bioversity (Milko Skovic)
  - *Relevant objectives:* [BIOMOBY], [DATA-SOURCES]
- EBI (January 2008): Peter Rice
  - *Relevant objectives:* [SOAPLAB], [TAVERNA]
- NCGR (Andrew Farmer)
  - *Relevant Objectives:* [PANTHEON], [KOIOS]

Project 2006-16 (Development of an Integrated GCP Information Platform) has developed architecture, infrastructure and tools for obtaining GCP data, and converting them into a common GCP shared domain model. This was the first, and necessary, step to create and/or plug-in visualising applications and data transformation tools.

In 2007 GCP development activities need to further elaborate the "plug-in" framework for application tools themselves, in such a manner to exploit available GCP compliant data sources and domain model structured data. This task will host these activities in the same manner as the project PI defined the GCP core application programming interface and data source framework in 2006.

On the basis of the resulting application framework, crop bioinformatics analysis workflows can designed and additional existing third party tools can be incorporated to create high-end applications for use by the GCP scientists. This task will facilitate this effort by specifically integrating a key third party tool, "Taverna", designed for workflow management, into the GCP platform, while elaborating the underlying GCP domain model search engine ("Koios").

88. Project No G4005.51 (CB01): Training programme on genetic diversity analysis of germplasm

- *Duration: Jan 2005–Dec 2006*
- *Total budget (as per proposal): $12,500*

Various crops, regions and traits

Lead institution
Agropolis–CIRAD (Christian Poisson)

Hereafter a proposed two week course curriculum in the field of genetic diversity analysis. For each topic, it is planned to elaborate a support note in French to accompany the slides in Powerpoint format. Each slide is a succinct summary of a topic used as a support for trainers and a guide for trainees. This work will be done by Cirad and IRD scientists with the help of a young scientist with a computer specialization and a scientific archivist.

Proposed agenda

Week -1

Day 1
- General introduction
- Objectives
- Rationale of the two weeks
- Biology of reproduction
- DNA biology, structure, replication, transcription, translation
- nuclear vs cytoplasmic DNA

Day 2
- molecular tools, enzyms, DNA libraries
- markers: phenotypic and molecular polymorphisms
- laboratory practice: DNA extraction, the different steps from plant tissue to DNA

Day 3
- isozymic markers
- molecular markers
- RFLP
- Microsatellites
- RAPD
- AFLP
- others, EST, DArT

Day 4
- laboratory practice: genetic diversity with microsatellite markers

Day 5
- practice: data acquisition: from gel to data files

Week-2

Day 6
- heredity
- population genetics
- allelic frequencies, H.W. equilibrium
- gene flow

Day 7
- population structure
- similarity indices
- genetic distances
- classification: UPGMA, NJtree, multivariate analysis..

Day 8
- practice: data analysis and soft ware use: Genetix, Fstat, Structure, Darwin

Day 9
- implications for the management of genetic resources
- collection establishment and evaluation , conformity, sampling
- collection management (in isolated or network conditions)
- core collection

Day 10
- extracting meaningful associations
- candidate gene polymorphism
- sampling association mapping panels
- admixture mapping
- Workshop evaluation

89. Project No G4005.52 (CB02): Development of training materials for a course in genomics and comparative genomics, and design of course curriculum

- *Duration: Jan 2005–Dec 2006*
- *Budget by year: $12,500 (2005), $2,500 (2006); Total budget: $15,000*

Various crops, regions and traits

Lead institution
Institute for Genomic Diversity (IGD), Cornell University (Theresa Fulton)
Collaborating institutions
- None directly

Comparative genomics is a relatively new field of research that has developed due to increasing technological capabilities, particularly in the area of DNA sequencing, and an increased understanding of the conservation of biology. The potential

benefits of this new field are extensive, not only on the academic level of an increased understanding of biological organisms, but also including many practical applications. In the field of plant breeding and crop improvement the promise of comparative genomics holds special potency as it has implications on global hunger, nutrition, conservation, and environmental protection. Information that once seemed particular to only one species or limited group of species can now often be useful across many species, genera or even further. For example, genes involved in disease resistances often employ similar processes and biochemical pathways across many crops, and are often even located in similar chromosomal positions (R. Nelson, pers. comm.).

One result of comparative genomics has been the increasing speed at which new data, information, discoveries and technologies are now developing. This is exciting and promises many benefits; however, it also means that it has become increasingly difficult to keep abreast of current research and technologies. This is particularly true for researchers in developing countries who have limited access to scientific publications or extended academic communities. Thus, the very researchers who could most benefit from comparative genomics are those least able to, due at least in part to the lack of know-how (together with infrastructure insufficiencies, etc.).

This project aims to begin to solve this problem by creating materials to be used in training global scientists in the use of genomics and comparative genomics. A recent collaboration of IPGRI and the Institute of Genomic Diversity at Cornell University resulted in 2 learning modules, "Volume 1: Using Molecular Marker Technology in Studies on Plant Genetic Diversity" and "Volume 2: Genetic Diversity Analysis with Molecular Marker Data." These learning modules (available as a CD in several languages and downloadable as pdf) were used as the basis of a molecular marker training workshop in Venezuela in 2003, and more than 300 copies have been requested by researchers worldwide. Similar training materials covering genomics and comparative genomics are now in great demand to follow and complement the concepts covered in the previous learning modules.

90. Project No G4005.54 (CB04): Development of training materials for a course in bioinformatics and design of course curriculum

- *Duration: Jan 2005–Dec 2005 with NCE to Dec 2007*
- *Budget by year: $12,509 (2005), $2,502 (2006); Total budget: $15,011*

Various crops, regions and traits

Lead institution
IRRI (Richard Bruskiewich)
Collaborating institutions
- Cornell University, USA (Theresa Fulton)

- Develop a detailed course curriculum for crop bioinformatics scoped for 2 week delivery and packaged as a web based "distance education" course, structured in a modular fashion with incremental lessons cross-referenced to other publicly available training materials.
- Develop a course operational plan following the distance education model of the S* Alliance (www.s-star.org), specifying the design of various internet resources to be used for such a course including the course website providing access to the online learning environment, a discussion forum, chat facilities, and email integrated for communications between students and course facilitator, and between students.

91. Project No G4005.55 (CB05): Development of reference molecular marker kits to analyse diversity of germplasm for the year 1 GCP crops

- *Duration: Jan 2005–various end-dates*
- *Total budget: $56,700*

Barley, maize, rice, sorghum, wheat, chickpea, cowpea, common bean, cassava, potato and Musa/Various regions and traits

Lead institutions: CIMMYT, ICARDA, ICRISAT, IRRI, IITA, CIP, Agropolis, CIAT, CAAS

An important objective of Subprogramme 1 is the molecular marker analysis of the accessions belonging to the core subsets of up to 3000 accessions per crop so that the structural genetic diversity within the subset may be known. This task started with a selection of priority crops that included: Barley, Maize, Rice, Sorghum, Wheat, Chickpea, Cowpea, Common Bean, Cassava, Potato and Musa. These were named "tier 1" crops. Among the criteria to select them were the relevance of the crop for food security worldwide, the degree of genetic/genomic tools already available for the crops as well as their potential as good sources of genes for drought tolerance.

The analysis of genetic diversity will help to find population structures that influence the analysis of the associations between markers and phenotypes, which will be performed further in the CP. In doing so, these results will also help to define a reduced subset of accessions (likely those that are more dissimilar at the markers loci) that will be subject of more detailed analysis for functional diversity at known genes of interest.

As a complement, the present proposal aims at developing and establishing microsatellite (the molecular marker type of choice for most of SP1 work) kits. The plan is to allow the relation of new germplasm to the reference materials analyzed in the context of SP1 and the GCP as a whole. The genetic diversity of this new germplasm might then be compared with the crop reference samples and decisions might be made regarding the convenience of accessing reference germplasm or to add new germplasm to the reference sample to contribute to their representativeness.

The microsatellite kits will include a list of oligonucleotide primers, the laboratory protocols to use them with ensure repeatability (PCR conditions, detection of polymorphisms, etc…) and the description of the polymorphisms in a subset of samples chosen as controls. These controls should be selected to represent a complete (or close to) range of known alleles and to correspond as much as possible to known germplasm, easily accessible by research teams working with the particular crop. In addition, the kits should contain a description of the methods proposed for comparing new to pre-existing data and classification, as well as much extra information deemed necessary for anyone to use them.

92. Project No G4005.58 (CB08): Functional genomics to improve African crops

- *Duration: Jan 2005–Dec 2005*
- *Total budget (as per proposal): 12,300*

Various crops/Africa/Various regions

Lead institution
WUR (Jan-Peter Nap)
Collaborating institutions
- University of Pretoria, South Africa (Dave Berger)

Most research centres in Africa have access to the Internet. However, most African scientists have not been exposed to the opportunities offered by plant genomic sequence database tools freely available through the Internet. The visit of Dr.Vorst from a premier plant science institute in the Netherlands to Africa provides a unique opportunity to build capacity in genomic data mining, especially at a time when an annotated version of the rice genome (a model for cereals) is expected to be released publicly.

93. Project No G4005.59 (CB09): Molecular markers for allele mining

- *Duration: Jan 2005–Dec 2005 with NCE to Oct 2006*
- *Total budget (as per proposal): $150,480*

Lead institution
GCP (Carmen de Vicente)
Collaborating institutions
- Agropolis—CIRAD (Jean Christophe Glaszmann)
- MS Swaminathan Research Foundation, Chennai, India (A Parida)

One of the objectives of Subprogramme 5 (Capacity Building and Enabling Delivery) is to contribute to institutional capacity building in developing countries.The Consortium of the Generation Challenge Programme brings together three sets of partners—the centres of the Consultative Group on International Agricultural Research (CGIAR), advanced research institutes (ARIs), and national agricultural research systems (NARS) in developing countries. Not all CG Centers and just a few NARS are represented by the Consortium.

It is the desire of the GCP that as many CG Centers and NARS are able to effectively manage their genetic resources and apply advances in modern developments (genetics, genomics, bioinformatics) both to be our valuable partners in the aim to create appropriate varieties for the poor but also to become self-sufficient leaders in their fields.

Subprogramme 5 identifies and implements opportunities to ensure that the knowledge used or newly developed through the GCP research programme reach scientists worldwide. The empowerment of as many scientists as possible is one of the mechanisms by which SP5 may succeed in assuring advances in crop-related tools and technology will reach crop improvement programmes and farmers. This is partly fulfilled by the Training Program. However, another way to do so is to derive benefit from the GCP internal specialized research meetings to incorporate participants that are not active members of the research work plan. These participants can be scientists in the CG, which are not engaged directly with the GCP, and in NARS. The activity of this proposal is an example of this type.

94. Project No G4005.61.01 (CB11a): Training course on plant genetic diversity and molecular marker-assisted breeding

- *Duration: Jan 2005–Dec 2005; Budget per year: $100,000 (2005)*
- *Total budget: $100,000*

Various crops/Africa, Asia and Latin America/Various traits

Lead institution
CIMMYT (Marilyn Warburton)
Collaborating institutions

- INIA, Chile (Patricio Hinrichson, Mario Paredes, Viviana Becerra, Boris Sagredo)
- University of Chile (Carlos Magni)
- Universidad de la Republica, Uruguay (Jorge Franco)
- Universidad Peruana Cayetano Heredia, Peru (Gisela Orjeda)
- Oregon State University, USA (Isabel Vales)
- Pontificia Universidad Católica de Valparaíso, Chile (Eduardo Oyanadel)
- Nidera Seeds (Mariano Bulos)
- Horticulture Research International: Phillip White
- GCP: Carmen de Vicente
- IFFIVE-INTA, Argentina: Edith Talesnik

The GCP Training Programme (Subprogramme 5) will offer a series of regional courses (Africa, Asia and Latin America) focusing on the main subjects of each of the Subprogrammes. Subprogramme 3, Trait Capture for Crop Improvement, has as the main goal the increased efficiency of crop breeding, particularly using new tools such as biotechnology. The uptake of new tools depends on the ability of national partner scientists to use the new technologies, which may include the need for capacity building in some cases. Therefore, the training courses offered in the regions for Subprogramme 3, entitled "Plant Genetic Diversity and Molecular Marker Assisted Breeding", is geared towards National Programme scientists with the desire and possibilities to utilise markers (via diversity analyses and Marker Assisted Selection) in their breeding programmes. The course proposed here will be offered in conjunction with a National Programme in the region (Latin America) who has a demonstrated track record in both training and utilisation of biotechnology in crop improvement.

The Instituto Nacional de Investigaciones Agropecuaria (INIA) in Chile is the country's national programme for investigations in agriculture and fisheries, funded by the Ministry of Agriculture. INIA has been in operation for 40 years and has regional offices in all states of the country. The main office is in the capital, Santiago, where they have extensive laboratories in many disciplines, including biotech. INIA's mission is to "generate, adapt, and transfer technologies" to the agriculture sector in Chile, which is completely compatible with what the Generation Challenge Programme is working on worldwide. Located in Santiago, the La Platina Experiment Station is convenient for travel to Chile, and has good accommodation facilities nearby. Laboratories and classrooms are available for the workshop. In addition to INIA staff, several nearby universities could provide resource people for the classes. Resource staff from CIMMYT, CIAT, and CIP (the Latin American CG centers) will be called upon, as necessary to complement the resource people from Universities and NARs from Chile and other countries in Latin America. The identification of resource people has begun already, and should be finished by July 1, 2005.

95. Project No G4005.63 (CB13): The Interactive Resource Center & Helpdesk (http://irc.igd.cornell.edu/)

- *Duration: Jan 2005–Jul 2009*
- *Budget per year: $50,000 (2005), $0 (2006), $29,621 (2007), $29,966 (2008); Total budget as of 2008: $109,587; Budget for 2009: TBD*

Various crops, regions and traits

Lead institution
Institute for Genomic Diversity at Cornell University, USA (Theresa Fulton)
Collaborating institution

- Members of the IGD

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

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

96. Project No G4005.67 (CB17): Reporting for product distribution: An asset inventory system for the Generation Challenge Programme

- *Duration: Jan 2005–Dec 2006*
- *Budget by year: $20,600 (2005), $20,600 (2006); Total budget: $41,200*

Various crops, regions and traits

Lead institution
Bioversity International (Victoria Henson-Apollonio)

The purpose of this project is to develop a practical on-line service that will facilitate the production of a dynamic inventory of 3rd party materials used by GCP scientists and products produced by GCP research. The GCP is a collaboration among researchers, breeders, and social scientists from a wide variety of institutions, serving an equally broad group of potential users. Much of the success of the programme depends upon having GCP assets and products used and taken up by as broad a user-base as possible. This requires that an inventory of GCP products be created and also that 3rd party materials used in the production of these assets be reported as well.

CAS-IP has developed several reporting tools over the past several years that can be used as the basis for developing this GCP reporting system. In addition, a CAS-intern is currently working on a project to make this reporting system more efficient, informative, and easier for the scientist-originators to use.

97. Project No G4005.71 (CB21): Fellowships and travel grants 2005

- *Duration: Jan 2005–Dec 2005; One fellowship postponed, and due to finish Dec 2009*
- *Budget per year: $263,613 (2005); $0; $18,500 (2007); Total budget: $282,113*

Various crops, regions and traits

Lead institution
GCP (M Carmen de Vicente)
Collaborating institution
- N/A

The Generation Fellowship is established to grant awards to carry out innovative research related to the running theme of the Challenge Programme, i.e. unlocking genetic diversity of crops for the resource-poor. It aims at scientists that want to conduct research outside of their home countries for a period of three months to one year. The Generation Fellowship will emphasise the areas of research that compose the four thematic sub-programmes: genetic diversity of global genetic resources, comparative genomics for gene discovery, crop improvement and gene transfer, and genetic resource, genomic and crop information systems.

Four fellowships in Subprogrammes 2, 3, and 4 (the fellowships for Subprogramme 1 have already been filled). The maximum award per fellow will be US$25,000 which is intended to cover travel, stipend, equipment, conference participation and so on. The fellow may be invited to participate in the Annual Meeting of the Generation Challenge Programme.

All proposals should deal at least with one of the crops that ensure worldwide food security according to the FAO (rice, maize, barley, wheat, sorghum, millet, cassava, potato, sweet potato, yam, banana, plantain, chickpea, cowpea, beans, lentil, pigeon pea, soybean, coconut and groundnut) and they should be closely linked with ongoing research in the GCP. In all cases, quality of the research proposed, scientific suitability of the applicant and appropriateness of the host institute will be carefully assessed.

The Generation Travel Grant Programme is established to cover the expenses of participation of developing country NARS scientists (outside the Consortium) to the annual GCP research meeting, to other conferences organised in the context of the GCP, to conferences whose subject is relevant to the work of the GCP, or to visit an Institution member of the Consortium to discuss the advancement of common research. The maximum grant award will be $5,000 USD, which is intended to cover travel, accommodation, and conference participation, if applicable. The grantees might be requested to make a presentation of their own research.

98. Project No G4005.73 (CB23): Genotyping Support Service

- *Duration: November 2005–November 2006 with NCE to May 2007*
- *Budget by year: $200,000 (2005); Total budget: $200,000*

Various crops, regions and traits

Lead institution
Bioversity International (M Carmen de Vicente)
Collaborating institutions
- Agropolis–CIRAD (Jean Christophe Glaszmann)

The Generation Challenge Programme mandate rests very much in advanced agricultural research: unlocking genetic diversity of crop germplasm, using genomics to discover genes and alleles for complex agronomic traits, incorporating them into meaningful breeding programmes and maximizing the use of the great amounts of data generated. In particular, Subprograme 1 deals with the characterisation of germplasm as a means to identify novel and diverse variants of the genes that control complex abiotic stresses.

In spite of the great insignificance that this endeavor may have for the scientific progress per se, and for the enhanced use of germplasm, the GCP is committed to a greater impact by doing its best to ensure that the discovery work will be grabbed by plant breeders, who will use the new technologies to develop better cropo varieties for resource-poor farmers.

This proposal has two general objectives: 1) Converying the knowledge generated in Subpprogramme 1on understanding and managing genetic diversity by means of molecular markers to National Programme partners outside the Generation Consortium and 2) Linking molecular geneticists (laboratory science) to plant breeders (field science). With these objectives, this proposal aims to create a genotyping support service to help assess the potential of breeding materials, with appropriate phenotypic data, for association studies as a means to identify good markers for relevant agronomic traits. Hopefully, expected results will directly translate into successful stories in breeding programmes.

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

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

Various crops, regions and traits

Lead institution
CIAT (Glenn Hyman)
Collaborating institutions
- 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.

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

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

Various crops, regions and traits

Lead institution
Virginia Tech (PI: George W Norton, Collaborator: Jeffrey Alwang)

The current GCP portfolio includes several research projects with potential near-term "products" that could be subjected to ex ante impact analysis. Impact analysis could help: (a) assist with future prioritisation of research resources, (b) provide early estimates of benefits of the initial GCP investments, and (c) validate an assessment approach that might be employed

broadly in the GCP. The proposed project will project impacts of two GCP projects: "Revitalizing 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.

101. Project No G4006.15: Fellowships and travel grants (2006)

- *Duration: Jan 2006–Dec 2006 with NCE to Dec 2007*
- *Budget by year: $280,000 (2006); Total budget: $280,000*

Various crops, regions and traits

Lead institution
GCP (M Carmen de Vicente)
Collaborating institutions
- N/A

The Generation Fellowship awards were established to facilitate innovative research related to the central theme of the Generation Challenge Programme, i.e. unlocking genetic diversity of crops for the resource-poor. The Fellowship programme is aimed at scientists who want to conduct research outside of their home countries/institutions for a period of three months to one year. The Generation Fellowship places primary emphasis on research in the four thematic subprogrammes: 1) genetic diversity of global genetic resources, 2) comparative genomics for gene discovery, 3) trait capture for crop improvement, and 4) genetic resources, genomic, and crop information systems. Up to 8 fellowships per year are awarded, and the maximum award per fellow will be up to US$25,000, which is intended to cover travel, living expenses, laboratory consumables, and conference participation.

Proposals should deal with at least one of the following GCP crops (rice, maize, barley, wheat, sorghum, millet, cassava, chickpea, sweet potato, cowpea, beans, and groundnut). In addition, proposals must be linked with ongoing research supported by the GCP, either by competitive or commissioned grants. (See the GCP Research Page for information on competitive and commissioned grants: (http://www.generationcp.org/reserach.php?da=0634417).
Applications are invited from crop science researchers from developing country research institutions (National Agricultural Research Systems), who hold at least a Master of Science degree (MSc), or equivalent, in a relevant subject area. Applicants should demonstrate they are engaged in a related ongoing research activity in their home country. Priority is given to scientists from National Agricultural Research Systems already involved in GCP research projects. For more information on the Fellowships programme and to access the application materials, please see the GCP Capacity Building Corner:(http://www.generationcp.org/reserach.php?da=0531908).

The Generation Travel Grant Programme is a key component of the GCP Capacity Building Subprogramme (SP5). Sixteen Travel Grants are available per year to cover the expenses of developing country National Programme scientists working at or in collaboration with a GCP Consortium Institution (list of GCP Consortium Institutions: (http://www.generationcp.org/consort.php?da=0781248). The purpose of the Travel Grant Programme is to encourage and promote collaboration between the GCP and NARS institutions, foster linkages within current GCP projects, and provide training opportunities for developing country scientists. The grant may be requested to visit a GCP Consortium Institution or any other Advanced Research Institution to get training in concepts and/or techniques necessary for the advancement of the GCP research (first priority), to participate in any training event organised by the GCP (second priority), to participate in the annual GCP research meeting (limited number of spaces available), or to participate in conferences whose subject is relevant to the work of the GCP. Preference will be given to applicants with links to current GCP projects and for whom the travel grant will be used as a learning experience.

The maximum grant award will be $5,000 USD, which is intended to cover travel, accommodation, and conference participation, if applicable.

The selection criteria to request a GCP Travel Grant are the following: 1) 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. 2) He/She should work in research related to the running theme of the GCP (any of the Subprogrammes) with one of the GCP crops (rice, maize, barley, wheat, sorghum, millet, cassava, potato, sweet potato, yam, Musa, chickpea, cowpea, beans, lentil, pigeon pea, soybean, coconut, and groundnut). 3) The applicant should justify the objectives of the travel and benefits to his/her research and home institution.

A Generation Travel Grant Committee evaluates all applications and selects the recipients. The deadline for travel grant applications is the 20th of each month. Winners are notified early the following month. Applications are evaluated as they are received until all 16 grants are awarded.

102. Project No G4006.28: Regional PGR courses

- *Duration: Jan 2006–Dec 2006*
- *Budget by year: $25,000 (2006); Total budget: $25,000*

Various crops, regions and traits

Lead institution
WUR (Marja Thijssen)
Collaborating institutions
- WUR (Niels Louwaars)
- Consultant to WUR (Walter de Boef)
- CAS–IP/Bioversity International (Victoria Henson-Apollonio)
- EMBRAPA (Zeze Sampaio)

The project creates a curriculum for regional courses on institutional genetic resource policies in order to create awareness, extend relevant knowledge, and share experiences among scientists and science managers, which will allow them to develop or strengthen institutional policies and tools for handling Freedom to Operate on IPR and ABS in partner institutions of the Challenge Programme.

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

- *Duration: Jan 2007–Dec 2011*
- *Budget by year (as per proposal, in SA Rands): ZAR 700,920 (2007), ZAR 700,684 (2008), ZAR 699,915 (2009), ZAR 699,902 (2010), ZAR 700,671 (2011); Total budget in SA Rands (as per proposal): ZAR 3,502,181/USD $500,312*

Various crops/Africa/Various traits

Lead institution
ACCI/University of KwaZulu-Natal (Mark Laing)
Collaborating institutions
- None

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 Institution 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 institutions 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).

104. Project No G4007.03: The "Community of Practices" concept applied to rice production in the Mekong region: Quick conversion of popular rice varieties with emphasis on drought, salinity and grain quality improvement

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

Rice/Asia/Drought and Salinity tolerance, grain quality

Lead institution
BIOTEC (Theerayut Toojinda)
Collaborating institutions
- RGDU (Jonaliza Lanceras-Siangliw)
- UBU (Sureeporn Kate Ngam)
- NAFRI (Monthathip Chanphengsay, National Agricultural and Forestry Research Institute)
- CARDI (Men Sarom)
- DAR (Khin Than New)

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.

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

- *Duration: Jul 2007–Jul 2009*
- *Budget by year: $400,000, Total budget: $400,000*

Various crops, regions and traits

Lead institution
GCP (Carmen de Vicente)
Collaborating institutions
- Various (see 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.

105.1 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 (as per proposal): $41,863 (2007), $7,080 (2008); Total budget (as per proposal): $48,943*

Maize/Africa/Waterstress tolerance

Lead institution: KARI, Kenya (James Gethi)
Team members

- Agropolis–INRA (François Tardieu, C Welcker, B Suard, and S Berthezene)
- KARI (Josephine Malelu, Josephine Syanda, and Lilian Njeri Gichuru)

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.

105.2 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 per year (as per proposal): $ 48,822 (2007), $ 48,822 (2008); Total budget (as per proposal): $97,644*

Cassava/Africa/Various traits

Lead institution: NRCRI, Ghana (C Egesi)
Team members

- CIAT (M Fregene)
- NRCRI/CIAT (E Okogbenin)
- NRCRI (Okechukwu Nnamdi Eke-Okoro, Egbichi Nnenna Adaoha Mbanaso, Shuaibu Suleiman, Esther Adaku Ekwelem, Samuel Olorunfemi Baiyeri, and Oluwakemi Adedamola Ogundapo)

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

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

* Associated GCP Project: Development of low-cost technologies for pyramiding useful genes from wild relatives of cassava into elite progenitors genomes (Competitive Project 9, Round I – PI: Anthony Bellti,CIAT)

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.

105.3 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 per year (as per proposal): $69,384 (2007), $64,425 (2008); Total budget (as per proposal): $133,809*

Peanut/Africa/Drought and disease resistance

Lead institution: ISRA/CERAAS, Senegal (Ousmane Ndoye)
Team members

- Agropolis–CIRAD (Jean-François Rami)
- UCB (David Bertioli)
- EMBRAPA (Marcio Moretzsohn)
- ISRA (Issa Faye)
- EMBRAPA/ICRISAT (Soraya Bertioli)

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.

105.4 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 per year (as per proposal): $40,000 (2007), $32,500 (2008); Total budget (as per proposal): $72,500*

Maize/Africa/Drought tolerance, streak virus disease

* Associated GCP Project: Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools (Competitive Project 5, Round I – PI: José Valls, Embrapa)

* Associated GCP Project: Characterisation of genetic diversity of maize populations: Documenting global maize migration from the center of origin (Competitive Project 14, Round 1 – PI: Marilyn Warburton).

Lead institution: CRI–CSIR (Allen Oppong)
Team members
- CIMMYT (Marilyn Warburton, Yunbi Xu)
- CRI–CSIR (Ruth Thomson, Ewool Manfred, and Maxwell Asante)
- Universidad de la Republica, Uruguay (Jorge Franco)

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.

*105.5 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 per year (as per proposal): $25,960 (2007), $23,010 (2008); Total budget (as per proposal): $48,970*

Rice/Asia/Salinity resistance

Lead insitution: ABRII, Iran (Ghasem Hosseini Salekdeh)
Team members
- IRRI (Abdelbagi 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 analyze enough metabolome in a high-throughput manner. We think that in collaboration with IPK (Germany), we shall be able to both analyze the samples and train ABRII staff to use MS instrument and analyze 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: Revitalizing Marginal Lands: Discovery of Genes for Tolerance of Saline and Phosphorus-Deficient Soils to Enhance and Sustain Productivity(Competitive Project 2, Round I – PI: Abdelbagi Ismail)

105.6 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 per year (as per proposal): $39,825 (2007), $39,884 (2008); Total budget: $79,709*

Rice/Asia/Blast resistance

Lead institution: ICABIOGRAD, Indonesia (Masdiar Bustamamm)
Team members
- IRRI (Casiana Vera Cruz)
- RCB/IPB (Utut Widyastuti Suharsono)
- ICABIOGRAD (Kurniawan Rudi Trijatmiko, Wening Enggarini)

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

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

106. Project No G4007.14: Fellowships and travel grants (2007)

- *Duration: Jan 2007–Dec 2007*
- *Budget by year: $160,000 (2007); Total budget: $160,000*

Various crops, regions and traits

Lead institution
GCP (Carmen de Vicente)
Collaborators
- Various (see below)

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

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

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

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

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

* Associated GCP Project: Targeted discovery of superior disease QTL alleles in the maize and rice genomes (Competitive Project 8, Round I – PI: Rebecca Nelson)

107. Project No G4007.17: GCP Project Development Guide

- *Budget per year: $40,200 (2007); Total budget: 40,200*

107.1: Concept and Design

- *Duration: April 2007–Sep 2007*

Various crops, regions and traits

Lead institution
Consultant (Viv Anthony)

- This paper provides a proposal for development of a project management knowledge-based tool to maximise the delivery of products on time and to budget in the Generation Challenge Programme. It is termed "the Project Delivery Guide"
- It will be prepared as a reference source for a range of key users including the GCP management team (Director and Sub-Program Leaders), Principle Investigators and Project team members, and the review teams (External review panel for competitive grants, the internal Review and Advisory Team, and the External review teams reporting to donors)
- It is proposed that the guide should be web-based, contain a glossary of terms and templates covering the following 7 themes: product and user specifications, project phases and decision milestones, governance of decisions and roles, activity planning, critical path analysis and risk management, functional expertise requirements, project monitoring and reporting requirements and freedom to operate
- Key inputs and validation of content will be required by selected experts from each area and members of the GCP management team. Support will also be required from the GCP communications manager and a web manager
- It is estimated that it will take an intensive work period between mid April and end May (c. 8 weeks) for both Viv Anthony, Sub-Programme Leaders and designated experts. This will be followed by prototype testing by users at end June/early July and a review/launch with the GC/partner community c. 11 September
- The project requires 30 man days of work by Viv Anthony and c. 10 days by Sub-programme Leaders and 10 days from designated experts

107.2: System and implementation

- *Duration: Jun 2007–Oct 2008*

Various crops, regions and traits

Lead institution
Consultants (Andreas Idl, Norbert Niederhauser)

Introduction
This paper describes the process to develop a user-friendly version of the web-based Project Delivery Guide (PDG). The final outcome and the approach to establish the application are described in the latter points.
Outcome
At the end of this consultancy a fully functional version of the "Project Delivery Guide" will be handed in. The application includes all necessary features to maintain access and content. In the final version the guide will be integrated in the GCP main webpage.
Methodology
The PDG will be created in short development cycles, each cycle consistent of a development followed by a review and feedback phase. The next cycle than will include the feedback. Due to the distribution of the project members, a first online prototype will be created as a discussion base and feedback will be collected in teleconferences and emails. Moreover the final version will include an online feedback module.
We think that short development cycle gives GCP constant and manageable information to see the progress. Implementations, that do not match user needs, are less probable.

108. Project No G4007.18: Translation and training materials

- *Duration: Jun 2007–Jul 2007*
- *Budget by year: $1,200; Total budget: $1,200*

Various crops, regions and traits

Lead institution
Consultant (Carlos de Tovar)
Collaborating institutions
- None

Scope of work:

The following activities will be performed for the successful completion of the task:

Adaptation of the learning module to GCP's style and layout.
To review appropriateness of text.
To ensure that the amount of text is suitable for each PowerPoint slide.
To position text and figures in a proper fashion.
To ensure that text and figures are well distributed (consistency of spacing)
Revision of accompanying notes.
To identify lack of information and/or PowerPoint slides.

Timing:

This proposal covers the period of 1 month starting on the date of signature of the consultancy contract.

Personnel:

Mr. Carlos Andrés Tovar will be responsible for carrying out the above described work.

109. Project No G4007.19: Kick-off meeting of the teams involved in the GCP Competitive Call 2006 – August 2007, Texcoco, Mexico

- *Duration: Jan 2007–Dec 2007*
- *Budget by year: $160,000; Total budget: $160,000*

Various crops, regions and traits

Lead institution
GCP (Carmen de Vicente)
Collaborating institutions

- None

During the first meetings of the GCP Stakeholder Committee and the Programme Steering Committee respectively, the GCP Management Team was requested to consider how delivery of the research products was going to be dealt with. Subprogramme 5 was made responsible for the deliberations of delivery and the development of a delivery strategy for the GCP.

After different consultations involving partners and stakeholders of the GCP, knowledgeable in a diversity of related matters (agricultural economics, IPR, plant breeding and genetics, social sciences, rural innovation, among others), a Strategy for Delivery was produced in 2005,presented to the GCP scientific community during the Annual Research Meeting and later on submitted to the approval of the Programme Steering Committee.

The GCP Delivery Strategy elaborates the philosophy that targeted training and capacity building for project partners and intended users in how to access, use, and apply the research products (markers, methodologies, tools, techniques, etc.) is essential to ensure the impact of the GCP. A synthetic final version of the GCP Delivery Strategy can be found here http://www.generationcp.org/UserFiles/File/Final_Delivery_Strategy_NOV%202005.pdf

The implementation of the Delivery Strategy was announced in the GCP 2006 call for proposals for competitive grants, by introducing the key element that is now the cornerstone of capacity building activities oriented to delivery in these projects. The winners of the competitive call for proposals should organise a workshop with the project partners and other potential relevant users of the research products to develop a Delivery Plan. The basis of this Delivery Plan is the Product and Potential Users section in the full proposal approved. From now on, the requirement of a Delivery Plan will be extended to commissioned projects.

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

- *Duration: Aug 2007–Jul 2008*
- *Budget by year: $34,100 (2007), Total budget: $34,100*

Various crops, regions and traits

Lead institution
Bioversity International (PI: Michael Halewood, Collaborator: Gerald Moore)
Collaborating institutions

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

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

expert resource people and the GCP research partners, with the result that the latter would contact the former on an as needs basis in the future.

111. Project No G4007.21: Genotyping Support Service

- *Duration: Aug 2007–Feb 2009*
- *Budget by year: $300,000 (2007); Total budget as of 2007: $300,000; Budget from 2008 onwards: TBD*

Various crops, regions and traits

Lead institution
GCP (Humberto Gómez Paniagua)
Collaborating institutions
- GCP Subprogramme Leaders

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

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

In the 2006-7 phase, the GSS (*Genotyping Support Service*) contacted 22 NARS working in cassava, coconut, groundnut, Musa and potato. Out of them, eight applications were selected to benefit from the service and test the concept. In this phase, supporting legal documents were designed, consistent with the Consortium Agreement, different options of service providers were tested, in every step different problems or difficulties were faced and solutions devised. In the 2007-8 phase, the GSS will offer genotyping services to all the mandate crops of the GCP by launching a call for proposals, applying the earned experience of the trial phase. Also, the GSS will start preparing to offer other GCP products and services, as they become available.

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

- *Duration: Aug 2007–Dec 2008*
- *Budget by year (as per proposal): $20,000 (2007), $71,980 (2008); Total budget (as per proposals): $91,980*

Various crops, regions and traits

Lead institution
CIAT (Norbert Niederhauser)
Collaborating institutions
- Consultant (Andreas Idl)

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

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

III. FOCUS PROJECTS

113. 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; no-cost extension to February 2009*
- *Contribution by year (as per proposal): 2005: $208,131 (RF), $39,530 (GCP); 2006: $210,407 (RF), $39,955 (GCP); 2007: $212,679 (RF), $40,515 (GCP); Total budget (as per proposal): $631,217 (RF), $120,000 (GCP)*

Rice/Asia/Drought tolerance

Lead institution
IRRI (Arvind Kumar)
Collaborating institutions
- IRRI (R Serraj, T Paris, S Haefele, R Anitha, G Atlin)
- IGAU (SB Verulkar, PR Dongre)
- CRRI (ON Singh, P Swain, L Bose)
- CRRI Research Station, Hazaribag: PK Sinha, NP Mandal)
- NDUAT (JL Dwivedi)
- UAS (S Hittalmani)
- TNAU (R Chandrababu, S Robin)
- BAU (BN Singh, RL Mahato)
- Barwale Foundation, Hyderabad (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 destabilizing 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 program, 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.

114. GCP/Rockefeller project G4005.69.02 (CB19b/RF–FS029): Pathway dissection and candidate gene identification of drought tolerance in rice by a forward genetics approach

- *Duration: March 2005–February 2008*
- *Budget by year (as per proposal): 2005: $199,600 (RF), $40,000 (GCP); 2006: $200,100 (RF), $40,000 (GCP); 2007: $202,500 (RF), $40,000 (GCP); Total budget (as per proposal): $602,200 (RF), $120,000 (GCP)*

Rice/Asia/Drought tolerance

Lead institution
Institute of Crop Sciences, CAAS (Zhi-Kang Li)
Collaborating institutions
- Peking University and Yale University (Xing-Wang Deng)
- IRRI (Racid Saraj (replacing R Lafitte)

Developing rice cultivars with drought tolerance (DT) has become a major effort in China to reverse the trend of diminishing rice lands resulting from shrinking water resources. To speed up this process, a full understanding of

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

115. GCP/Rockefeller project G4005.69.03 (CB19c/RF–028): Innovative and integrated approaches to improve the tolerance of maize to water–limited environments

- *Duration: April 2005–March 2007; no-cost extension to June 2008*
- *Budget by year (as per proposal): 2005: $276,000 (RF), $40,000 (GCP); 2006: $284,000 (RF), $40,000 (GCP); Total contribution from RF (as per budget): $560,000; Total contribution from GCP (as per proposal): $80,000; Total budget (as per proposal): $640,000*

Maize/Africa, Asia/Drought tolerance

Lead institution
CIMMYT (Yunbi Xu)
Collaborating institutions

- CIMMYT (Carlos Martinez, Debra J. Skinner, Alan F. Krivanek and Jonathan H. Crouch)
- SAU (Shibin Gao)
- CAAS (Zhuanfang Hao, Shihuang Zhang, Jiankang Wang)

Capacity building has been identified as one of the key issues that limit the translation of marker-assisted selection (MAS) from academic publications to practical applications in plant breeding (Xu and Crouch, Crop Science, in press). The molecular breeding program in Drought Tolerance Maize for African (DTMA) project supported by Bill and Melinda Gates Foundation and two GCP projects (GCP13-Development of informative DNA markers through association mapping; GCP18 -Development of low-cost gene-based trait assay technologies) have a specific focus on many of the technical constrains identified in the same review. By taking advantages of currently existing collaborations among breeders and other scientists that have been built up through these projects, a molecular breeding community of practice (CoP) will be established, in coordination with AMMANET, for molecular breeding of drought tolerant maize for Africa. The CoP will initially focus on the MAS introgression of relatively simple adaptive traits into drought tolerant germplasm that are necessary complementary traits to ensure market success of new drought tolerant varieties. In subsequent phases the CoP will add traits directly related to drought tolerance. This project will also take advantage of ground work achieved through ADB-funded Asian Maize Biotechnology Network (AMBIONET) and attempt to reinvigorate that initiative in China and India, as a first stage towards the development of a CoP for molecular breeding of drought tolerant maize for Asia. The model and experience that we will gain from this effort will be valuable for translation to other breeding programs across the world, including Enhancing Maize Productivity in Drought-prone Environments in East and Southeast Asia Project, supported by ADB, through partnership between ADB and CIMMYT.

Two major activities are proposed for the capacity building: molecular breeding workshop in Mexico and training of visiting scientists from developing countries in Asia. This GCP-funded capacity building activity is associated with RF Drought III FS028. Both activities would leverage benefit from on-going GCP maize drought genomics research projects and the DTMA project. Synergies would also be captured through linkage with the GCP Genotyping Services initiative, AMMANET in Africa and AMBIONET in Asia.

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

- *Duration: July 2005–June 2008; no-cost extension to Jun 2009*
- *Budget by year as per proposal:*

ICRISAT (sorghum): 2005: 62,100 (RF), $97,750 (GCP); 2006: $47,950 (RF), $40,250 (GCP); 2007: $116,450 (RF), $0 (GCP); Total contribution from RF (as per proposal): $226,500; Total contribution from GCP (as per proposal): $138,000

IITA (cassava): 2005: $92,100 (RF), $74,750 (GCP); 2006: $94,100 (RF), $63,250 (GCP); 2007: $87,300 (RF), $0 (GCP); Total contribution from RF (as per proposal): $273,500; Total contribution from GCP (as per proposal): $138,000

Total RF contribution for entire project: $500,000
Total GCP contribution for entire project: $276,000
Grand total for entire project: $776,000

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 programs with the information, skills, tools and resources to rapidly and efficiently select and utilize 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 Programs for the targeted benefit of NARS scientists
- To establish functional relationships between national breeding programs 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 programs across East and Central Africa for sorghum and cassava, together with farmer-knowledge where appropriate
- Conduct phenotypic characterization 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 programs
- Define regional populations for association mapping studies and identify potential parental genotypes for mapping populations and marker-assisted selection programs 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 programs
- Provide intensive hands-on training in standardized methodologies for phenotyping and genotyping to visiting scientists associated with selected breeding programs.
- 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 Program enabling a wider range of participants from NARS breeding programs in a number of countries in the region.

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

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

Wheat, barley/Africa/Various traits

Lead institution
INRA, Morocco (Abbad Andaloussi Fouad)
Collaborating institutions

- INRA, Morocco (Nsarellah Nasserlehaq, Jlibene Mohammed, Lhaloui Saadia, Labhilili Mustapha, Saidi Seddik)
- ICARDA (Sripada M Udupa)
- University of Bologna, Italy (Roberto Tuberosa)
- Cornell University (Mark E Sorrells)
- CIMMYT (Manilal William)
- University of Missouri (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.

118. Tropical Legumes I (TLI): Improving tropical legume productivity for marginal environments in sub-Saharan Africa

Lead institutions

Objective 1: Improve groundnut (*Arachis hypogaea* L) productivity for marginal environments in sub-Saharan Africa–ICRISAT (D Hoisington)

Objective 2: Improve cowpea (*Vigna unguiculata* L) productivity for marginal environments in Africa–UC–Riverside (J Ehlers)

Objective 3: Improve common bean (*Phaseolus vulgaris* L) productivity for marginal environments in Africa–CIAT (M Blair)

Objective 4: Improve chickpea (*Cicer arietinum* L) productivity for marginal environments in sub-Saharan Africa–ICRISAT (D Hoisington)

Objective 5: Develop cross-species resources for comparative biology in tropical crop legumes–UC–Davis (D Cook)

Objective 6: Provide training and capacity-building for SSA scientists–GCP (C de Vicente)

Activity leaders per objective:

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/Africa/Drought and disease resistance

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/Africa/Drought and disease resistance

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

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/Africa/Drought and disease resistance

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/Africa/Drought and disease resistance

Activity 1 (Explore diversity – linked to SP1): D Cook, UC–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/Africa/Drought and disease resistance

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.

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

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

Wheat/Asia/Drought, salt and Al-tolerance

Lead institution
ARI–HAS (Márta Molnár-Láng)
Collaborating institutions

- CIMMYT (Maria Zaharieva)
- CAAS (Ruilian Jing)
- Eszterházy Károly College, Hungary (Sándor Dulai)
- Agricultural Research Institute of the Hungarian Academy of Sciences (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.

120. Project No G4007.24: Seed smoke treatment to favour germination under water-stressed conditions

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

Maize/Africa/Drought tolerance

Lead institution
ARI–HAS (PI: Ervin Balazs, Collaborators: Vilmos Soos, Angela Juhasz)
Collaborating institutions

- Research Centre for Plant Growth &Development, 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.

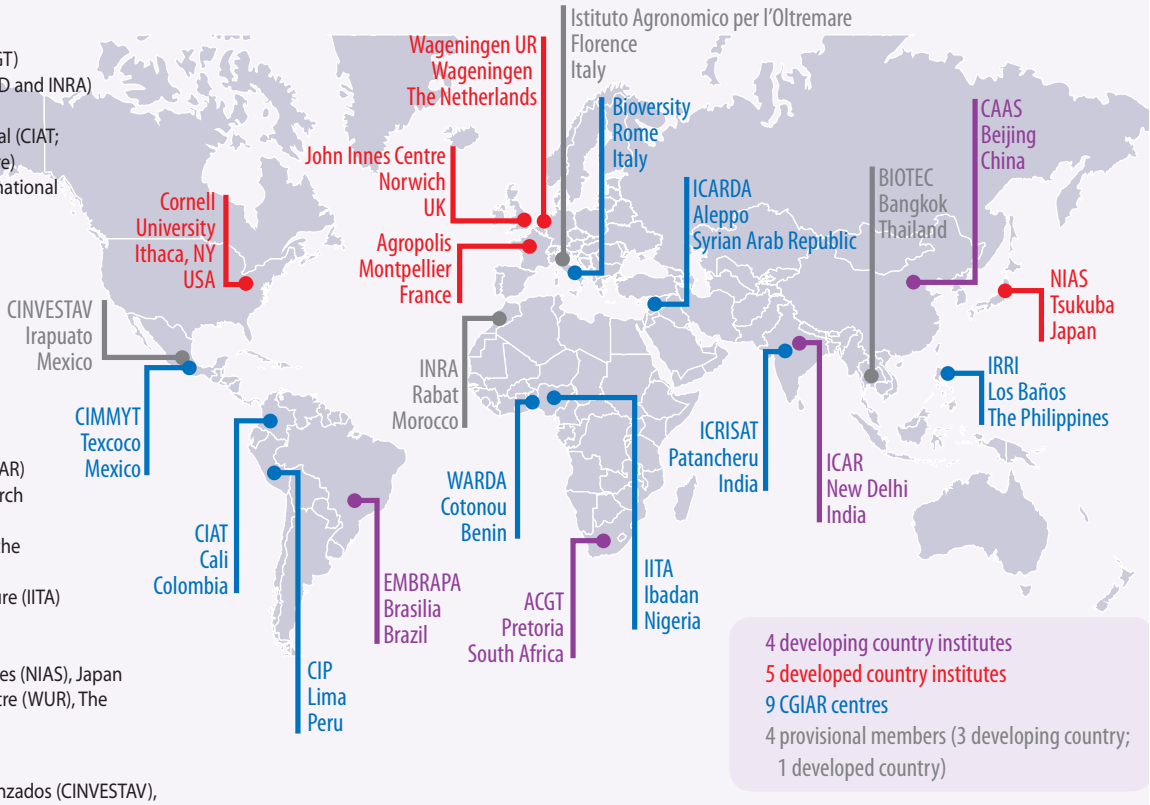
The GCP Consortium

Full members

1. Africa Rice Center (WARDA)
2. African Centre for Gene Technologies (ACGT)
3. Agropolis, France (incorporating CIRAD, IRD and INRA)
4. Bioversity International
5. Centro Internacional de Agricultura Tropical (CIAT; International Center for Tropical Agriculture)
6. Centro Internacional de la Papa (CIP; International Potato Center)
7. Centro Internacional de Mejoramiento de Maiz y Trigo (CIMMYT; The International Maize and Wheat Improvement Center)
8. Chinese Academy of Agricultural Sciences (CAAS)
9. Cornell University, USA
10. Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA; Brazilian Agricultural Research Corporation)
11. Indian Council of Agricultural Research (ICAR)
12. International Center for Agricultural Research in the Dry Areas (ICARDA)
13. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
14. International Institute of Tropical Agriculture (IITA)
15. International Rice Research Institute (IRRI)
16. John Innes Centre (JIC), UK
17. National Institute of Agrobiological Sciences (NIAS), Japan
18. Wageningen University and Research Centre (WUR), The Netherlands

Provisional members

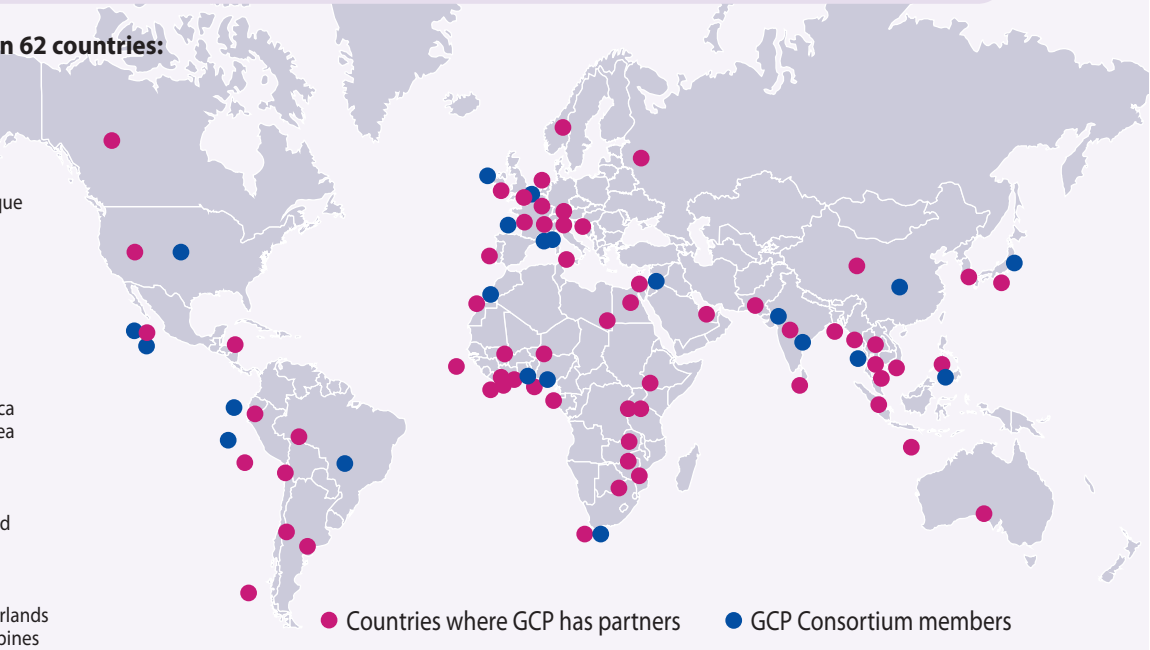
19. Centro de Investigación y de Estudios Avanzados (CINVESTAV), Mexico
20. Institut National de la Recherche Agronomique (INRA), Morocco
21. Istituto Agronomico per l'Oltremare (IAO), Italy
22. National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand



Where in the world is GCP? The GCP network in 2007

In 2007, GCP worked with partners in 62 countries:

1. Argentina
2. Australia
3. Austria
4. Bangladesh
5. Benin
6. Bolivia
7. Brazil
8. Burkina Faso
9. Cambodia
10. Cameroon
11. Canada
12. Chile
13. China
14. Colombia
15. Côte-d'Ivoire
16. Cuba
17. Czech Republic
18. Denmark
19. Egypt
20. Ethiopia
21. France
22. Germany
23. Ghana
24. Hungary
25. India
26. Indonesia
27. Iran
28. Israel
29. Italy
30. Japan
31. Kenya
32. Laos
33. Malawi
34. Mali
35. Mexico
36. Morocco
37. Mozambique
38. Myanmar
39. Niger
40. Nigeria
41. Pakistan
42. Peru
43. Russia
44. Senegal
45. Singapore
46. South Africa
47. South Korea
48. Spain
49. Sri Lanka
50. Sweden
51. Switzerland
52. Syria
53. Tanzania
54. Thailand
55. The Netherlands
56. The Philippines
57. Uganda
58. UK
59. Uruguay
60. USA
61. Vietnam
62. Zimbabwe



Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE-POOR

Hosted by CIMMYT

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