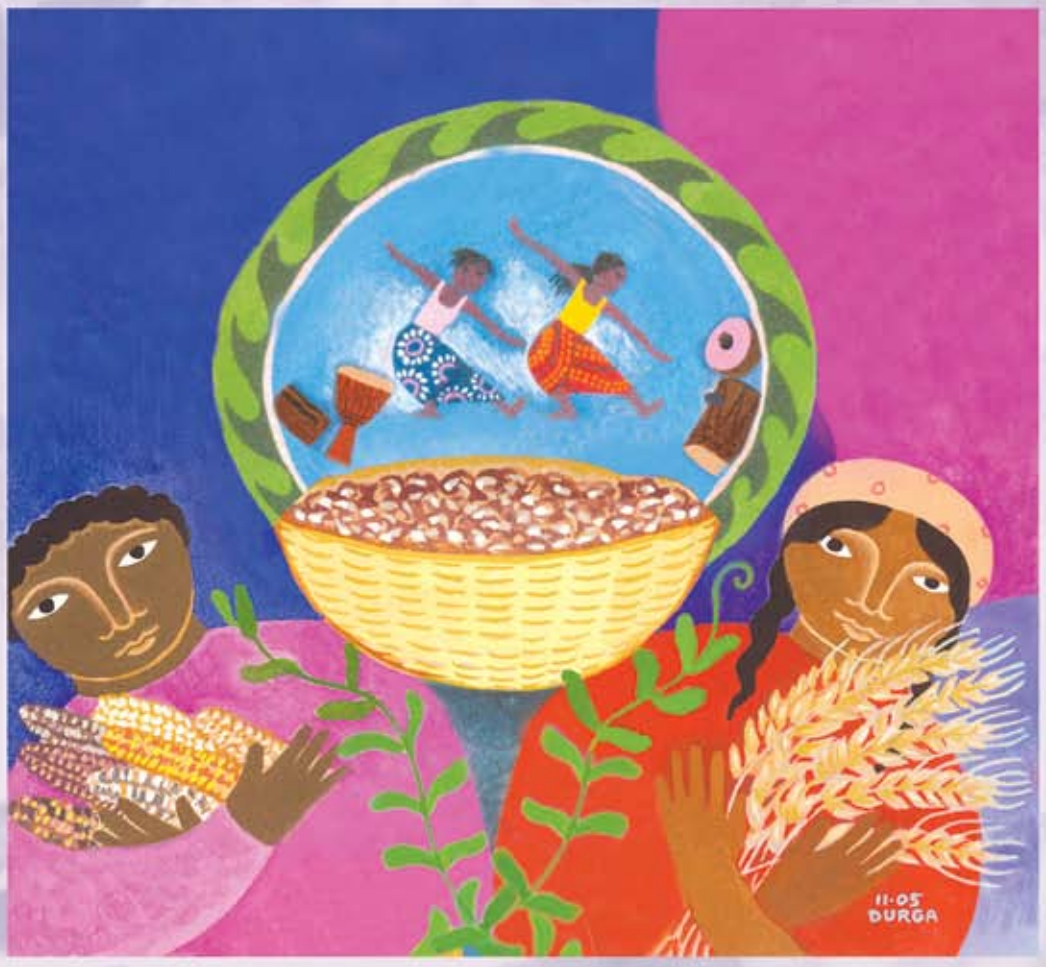


Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE-POOR

2007 Annual report and year five (2008) workplan

GCP's five Subprogrammes

Subprogramme 1 (SP1): Genetic diversity of global genetic resources
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.

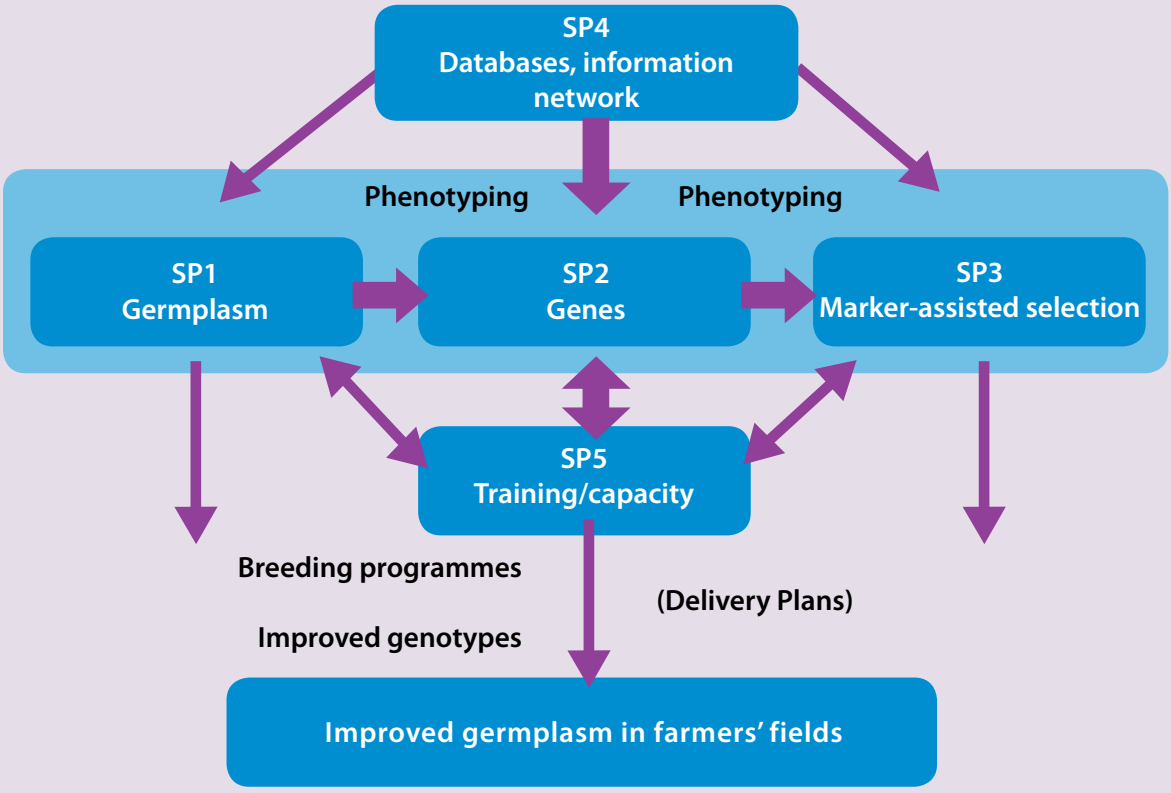
Subprogramme 2 (SP2): Genomics towards gene discovery
Uses or develops genomic tools and technologies and evaluates multidisciplinary approaches to better understand gene function and interaction to improve knowledge of gene systems across crops.

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 and policy and impact assessment research.

GCP's five Subprogrammes



CGIAR Generation Challenge Programme

2007 Annual report and year five (2008) workplan

June 2008

Compiled by the GCP Management Team and Communications Manager

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Acronyms and abbreviations

ABA	abscisic acid
ABA-GE	ABA glucose ester
ABC	Agricultural Biotechnology Center, Gödöllö, Hungary
ABRII	Agriculture Biotechnology Research Institute of Iran
ACCI	African Centre for Crop Improvement, South Africa
ACGT	African Centre for Gene Technologies, South Africa
ACPFG	Australian Centre for Plant Functional Genomics Pty Ltd
aDEG	aggregated differentially expressed gene
ADOC	allelic diversity for orthologous candidate genes
AFLP	amplified fragment length polymorphism
AICMIP	The All-India Coordinated Pearl Millet Improvement Project
Al	aluminium
Alt_{SB}	marker diagnostic for aluminium tolerance
AMMANET	African Molecular Marker Applications Network
APSIM	Agricultural Production Systems Simulator
ARI	Agricultural Research Institute, Tanzania
ARI(s)	advanced research institute(s)
ARI–HAS	Agricultural Research Institute of the Hungarian Academy of Sciences, Hungary
ARI–Naliendele	Agricultural Research Institute–Naliendele Research Station, Tanzania
ARM	GCP Annual Research Meeting
ASI	anthesis-silking interval
ASR	anthracnose stalk rot
BAC	bacterial artificial chromosome
BAU	Birsa Agricultural University, Kanke, Ranchi, India
BecA	Biosciences Eastern and Central Africa, Kenya
BGBM	Botanic Garden and Botanical Museum Berlin–Dahlem, Germany
BIOSS	Biomathematics and Statistics Scotland Research Institution, UK
BIOTEC	National Center for Genetic Engineering and Biotechnology, Thailand
Bioversity	Bioversity International
BMGF	Bill & Melinda Gates Foundation
BRRI	Bangladesh Rice Research Institute
CAAS	Chinese Academy of Agricultural Sciences
CARBAP	Centre africain de recherche sur bananiers et plantains, Cameroon
CARDI	Cambodian Agricultural Research and Development Institute
CAZRI	Central Arid Zone Research Institute, India
cDNA	complementary DNA
CERAAS	Centre d'etude régional pour l'amélioration de l'adaptation à la sécheresse, Senegal
CGIAR	Consultative Group on International Agricultural Research
CGN–WUR	Centre for Genetic Resources–Wageningen University and Research Centre, The Netherlands
CHF	Swiss francs
CIAT	Centro Internacional de Agricultura Tropical (International Center for Tropical Agriculture)
CIHEAM–IAMM	Centre International de Hautes Etudes Agronomiques Méditerranéennes–Institut Agronomique Mediterranéan de Montpellier, France
CIHEAM–IAMZ	Centro Internacional de Altos Estudios Agronómicos Mediterráneos–Instituto Agronómico Mediterráneo de Zaragoza, Spain
CIMMYT	Centro Internacional de Mejoramiento de Maiz y Trigo (the International Maize and Wheat Improvement Center)
CINVESTAV	Centro de Investigación y de Estudios Avanzados, Mexico
CIP	Centro Internacional de la Papa (International Potato Centre)
CIRAD	Centre de coopération internationale en recherche agronomique pour le développement, France
CMD	cassava mosaic disease
CNG	Centre National de Génotypage, France
CNPMF	Centro Nacional de Pesquisa de Mandioca e Fruticultura Tropical (Biotechnology Research Unit of EMBRAPA–Cassava and Tropical Fruits)
CONICET	Consejo Nacional de Investigaciones Científicas y Técnicas, Argentina
CoP	community of practice
CORPOICA	Corporación Colombiana de Investigación Agropecuaria, Colombia
COS	conserved orthologous sequence
CRI	Crops Research Institute, Ghana
CRRI	Central Rice Research Institute, India
CRURRS	Central Rainfed Upland Rice Research Station, India
CSIR	Council for Scientific and Industrial Research, Ghana
CSIRO	Commonwealth Scientific and Industrial Research Organisation, Australia
CSO	civil society organisation
CSU	Colorado State University
DAR	Department of Agricultural Research, Myanmar
DArT	diversity arrays technology
DArT P/L	Diversity Arrays Technology Pty Ltd
DEG	differentially expressed gene
DFID	Department for International Development, UK
DiSTA	Department of Agroenvironmental Science and Technology–Agronomy, Università di Bologna, Italy
DNA	deoxyribonucleic acid
DOA	Indonesian Department of Agriculture
DOA	Philippine Department of Agriculture
DPI	Department of Primary Industries, Australia
DPKit	Delivery Plan Kit
dQTL	disease resistance QTL
DWR	Directorate of Wheat Research, India
EBI	European Bioinformatics Institute, UK
EC	European Commission
ECABREN	Eastern and Central Africa Bean Research Network
Eger–Hungary	Department of Plant Sciences and Plant Physiology, Eszterházy Károly College, Eger, Hungary
EIAR	Ethiopian Institute of Agricultural Research, Ethiopia
EMBRAPA	Empresa Brasileira de Pesquisa Agropecuária (Brazilian Agricultural Research Corporation)
EPMR	External Programme and Management Review
EST	expressed sequence tag
ETH	Eidgenössische Technische Hochschule, (Swiss Federal Institute of Technology), Zürich, Switzerland
EUR	Euros
FRET	fluorescence resonance energy transfer
GBP	British pounds
GCP	Generation Challenge Programme
Genaissance	Genaissance Pharmaceuticals, Inc, France
GFAR	Global Forum on Agricultural Research
GIS	geographic information system(s)
GOST	GreenPhyl Ortholog Search Tool
GSS	Genotyping Support Service
GxE	genotype by environment interaction
HAAS	Hebei Academy of Agricultural Sciences, Institute of Dry Farming, China
HPC	high-performance computing
HTP	high throughput
HZAU	Huazhong Agricultural University, China
IAEA	International Atomic Energy Agency, Austria
IAO	Istituto Agronomico per l'Oltremare, Italy
IARI	Indian Agricultural Research Institute
IAU	Internal Auditing Unit of the CGIAR
IBONE	Instituto de Botánica del Nordeste, Argentina
ICABIOGRAD	Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development
ICAR	Indian Council of Agricultural Research
ICARDA	International Centre for Agricultural Research in the Dry Areas
ICGEB	International Centre for Genetic Engineering and Biotechnology, India
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
ICT	information and communication technology
IEB	Institute of Experimental Botany, Czech Republic
IER	Institut d'Economie Rurale, Mali

IFPRI	International Food Policy Research Institute
IFSSA	Indian Foundation Seed and Services Association
IGAU	Indira Gandhi Agricultural University, India
IGD	Institute for Genomic Diversity, Cornell University, USA
IGKV	Indira Gandhi Krishi Vidyalaya, India
IIAM	Institute of Agricultural Research of Mozambique
IITA	International Institute of Tropical Agriculture
ILRI	International Livestock Research Institute
iMAS	Integrated Marker-Assisted Selection System
INCA	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
INIFAP	Instituto Nacional de Investigaciones Forestales, Agricolas y Pecuarias, Mexico
INRA	Institut National de la Recherche Agronomique, France
INRA	Institut National de la Recherche Agronomique, Morocco
INRAN	Institut National de Recherches Agronomiques du Niger
INTA	Instituto Nacional de Tecnologia Agropecuaria, Argentina
IP	intellectual property
IPB	Institut Pertanian Bogor, Bogor Agriculture University, Indonesia
IPK	Institute for Plant Genetics and Crop Plant Research, Germany
IPR	intellectual property rights
IRAD	Institut de Recherche Agricole pour le Développement
IRC	Interactive Resource Center
IRD	Institut de Recherche Pour le Développment, France
IRRI	International Rice Research Institute
ISAAA	International Service for the Acquisition of Agri-biotech Applications
ISRA	Institut Sénégalais de Recherches Agricoles, Senegal
IT	information technology
JIC	John Innes Centre, UK
JIRCAS	Japan International Research Center for Agricultural Sciences
KARI	Kenya Agricultural Research Institute
LAAS	Luoyang Academy of Agricultural Sciences, China
LD	linkage disequilibrium
LGDP	Laboratoire Génome et Développement des Plantes (Plant Genome and Development Laboratory), University of Perpignan, France
LIMS	Laboratory Information Management System
LZARDI	Lake Zone Agricultural Research and Development Institute, Tanzania
MAB	marker-assisted backcrossing
MAGIC	multiparent advanced generation inter-cross
MARI	Mikocheni Agricultural Research Institute, Tanzania
MAS	marker-assisted selection
MATE	multidrug and toxic compound extrusion
MB	molecular breeding
MBG	micro-assay based genotyping
MDG	United Nations Millennium Development Goal
MoU	Memorandum of Understanding
MPB	micro-plate based
MTP	Medium-Term Plan
NAARI	Namulonge Agricultural and Animal Research Institute, Uganda
NaCRRI	National Crop Resources Research Institute, Uganda
NAFRI	National Agriculture and Forestry Research Institute, Laos
NARS	national agricultural research system(s)
NAU	Nanjing Agricultural University, China
NCGR	National Center for Genome Resources, USA
NCSRC	National Corn and Sorghum Research Center, Thailand
NCSU	North Carolina State University, USA
NDUAT	Narendra Dev University of Agriculture and Technology, Faizabad, India
NEPAD	New Partnership for Africa's Development
NERICA	new rice for Africa
NGO	non-governmental organisation
NH	non-host (disease resistance)
NIAB	National Institute of Agricultural Botany, UK
NIAS	National Institute of Agrobiological Sciences, Japan
NIL	near-isogenic line
NMRI	National Maize Research Institute, Vietnam
NRCPB	National Research Centre on Plant Biotechnology, India
NRCRI	National Root and Tuber Crops Research Institute, Nigeria
NSF	National Science Foundation, USA
NSFCRC	Nakhon Sawan Field Crops Research Center, Thailand
NU	Ningxia University, China
NWSUAF	Northwest Sci-tech University of Agriculture and Forestry, China
OSU	Oregon State University, USA
PAC	Programme Advisory Committee
PAG	Plant and Animal Genome Conference
PASS	Program for African Seed Systems
PAU	Punjab Agricultural University, India
PDG	Project Development Guide
PGRFA	plant genetic resources for food and agriculture
PhilRice	Philippine Rice Research Institute
PI	Principal Investigator
PPD	post-harvest physiological deterioration
PROINPA	Promoción e Investigación de Productos Andinos, Bolivia
PSC	Programme Steering Committee
Pup1	marker diagnostic for phosphorus uptake
QTL	quantitative trait locus
QTLxE	QTL by environment
R&D	research and development
RAP	Review and Advisory Panel
RAU	Rajasthan Agricultural University, India
RCE	regions of correlated expression
RGA—RFLP	resistance gene analogue-restriction fragment length polymorphism
RGDU	Rice Gene Discovery Unit, Thailand
RNA	ribonucleic acid
RNAi	RNA interference
SAAS	Shanxi Academy of Agricultural Sciences, China
SABRN	Southern Africa Bean Research Network
SAG	stress associated gene
Saltol	marker diagnostic for salt tolerance
SARI–Ethiopia	South Agricultural Research Institute, Ethiopia
SARI–Ghana	Savannah Agricultural Research Institute, Ghana
SAU	Sichuan Agricultural University, China
SCAR	sequence-characterised amplified region
SCRI	Scottish Crop Research Institute, UK
SDC	Swiss Agency for Development and Cooperation
SEK	Swedish krona
SHC	Stakeholder Committee
Sida	Swedish International Development Cooperation Agency
SIRDC	Scientific and Industrial Research and Development Centre, Zimbabwe
SMEs	Small- and medium-sized enterprises
SNP	single nucleotide polymorphism
SP	Subprogramme
SP1, SP2 etc	Subprogramme 1, Subprogramme 2 etc
SPCSV	sweet potato chlorotic stunt virus
SPFMV	sweet potato feathery mottle virus
SPL	Subprograme leader
SPVD	sweet potato virus disease
SSR	simple sequence repeat
TBD	to be determined
T–DNA	transfer DNA
TIGR	The Institute for Genomic Research (incorporated into the J Craig Venter Institute), USA
TLI	Tropical Legumes I Project
TLII	Tropical Legumes II Project
TNAU	Tamil Nadu Agricultural University, India
TPE	target population of environments
UAS	University of Agricultural Sciences, India
UBU	Ubon Ratchatani University, Thailand
UCB	Universidade Católica de Brasilia, Brazil
UC–Berkley	University of California, Berkley, USA
UC–Davis	University of California, Davis, USA
UC–Riverside	University of California, Riverside, USA
UGA	University of Georgia, Athens, USA
UKZN	University of KwaZulu–Natal, South Africa
USD	US dollar
USDA–ARS	United States Department of Agriculture–Agricultural Research Service
UVA	University of Virginia, USA
WACCI	West Africa Centre for Crop Improvement, Ghana
WARDA	Africa Rice Center
WUR	Wageningen University and Research Centre, The Netherlands
YAAS	Yunnan Academy of Agricultural Sciences, China

Foreword

Dear friends and colleagues of the Generation Challenge Programme,

Without a doubt, 2007 was yet another exciting year, filled with significant scientific achievements and valuable products, all thanks to the skills and commitment of the GCP community. Through the year, our projects continued to mature, we expanded our network of partners, and we worked more closely with the plant breeding community. Going by the standing of the journals in which most of the refereed papers published in 2007 appeared (see Appendix C), it is clear that GCP conducts high-quality science whose outputs are recognised by peers.

In this fourth year of the Programme, we went beyond impact at the Subprogramme level, increasingly progressing along the GCP pipeline of activities and beginning to make real impacts on crop improvement. These range from characterising germplasm diversity to discover new alleles and identify genomic regions of interest, to developing markers for breeding programmes in developing countries to improve adapted germplasm. Breeding programmes are our bridge to reaching resource-poor farmers. As a result, projects initiated in 2007 clearly build on, and add value to, our previous work. This evolution is reflected in an expanded portfolio of projects in which genes, markers, traits and tools, from and for GCP research, are tested in drought-prone environments.

Most, if not all, of GCP activities aim at generating usable products—in both the short and long term—in the form of knowledge, materials and tools for plant breeders. As a time-bound Programme, GCP must ensure continued and sustainable use of its products after its lifetime. In 2007, we launched a number of support services to promote access to, and use of, GCP products. The Management Team continues to explore concrete ways and means to promote and ensure the sustainability of GCP products for continued breeding support as an international public good. This is with a view to facilitating access, by plant breeders in developing countries, to new alleles and cost-effective modern plant science technologies.

The year also witnessed a fundamental restructuring of GCP's governance. This reform was the culmination of a long and considered process that began in 2005, when GCP's Programme Steering Committee (PSC) recognised the need for a more independent and more functional governance structure, and established a Task Force to formulate recommendations for reform. The PSC resolved at its 2007 meeting to transfer substantive governance to an independent Executive Board. The Board's primary responsibility will be to provide oversight on GCP's strategic direction, as well as to assess our finances and our risk environment. This new Board should be operational by July 2008.

From a financial perspective, 2007 was a year of mixed fortunes, but overall with a happy ending. The uncertainty was not due to funder doubts but related rather to measures to ensure a good match between receipt of contributions through the year and our calendar for disbursing funds, based on our workplan. Fortunately the payment schedule did not greatly hamper our projected 2007 workplan; we reorganised our disbursements to avoid cash-flow problems, and finished the year with a clean bill of health. In fact, 2007 registered our highest income ever since the inception of the Programme due to several factors as explained in the Financial report. In 2008, we should see a return to our standard situation, with a projected income of about USD 16 million. Once again, GCP is grateful to our funders for their generous and continued support.

In summation, the future of the Programme looks bright from a financial, scientific and governance perspective. All signals indicate that our regular funders will continue their support in 2008. The Programme will carry on with 'horizontal' activities across commodities that are mostly 'platform-oriented' (by which we mainly mean focusing on generating and sharing genetic and genomic resources, and related services), as well as with 'vertical' activities that are more crop-specific, targeting genetic gains for drought-prone target environments. The Management Team eagerly anticipates proposals in response to our third competitive call that focuses entirely on drought tolerance. We expect the call to usher in a new generation of complementary projects to enrich our current portfolio, and to accelerate the achievement of our research objectives.

Yet at the same time, the Management Team acknowledges the need to review our priorities and to allocate significant resources to selected vertical activities on key GCP target crops so as to ensure impact by the time that the Programme terminates. The first GCP External Programme and Management Review (EPMR) was conducted in 2007, its report to be published in March 2008. We expect that implementing the review recommendations will see GCP improve its *modus operandi*. This will be critical in helping us to better organise and focus our research portfolio as GCP moves into Phase II. Another important transition point for the Programme in 2008 will be the establishment of the new Executive Board, repositioning of the PSC and revising and revamping the roles and responsibilities of the Stakeholder Committee (SHC) and of the Programme Advisory Committee (PAC), to align them with the new governance structure.

Finally, but most importantly, I would like to reiterate that people at all levels—from stakeholders, to scientists, to GCP staff—are by far the Programme's most valued asset. We are a vibrant community that has cultivated and nurtured extensive and effective partnerships, and leveraged our collective resources to establish an even broader network of R&D participants to support and help realise GCP objectives. I cannot resist ending this message with an excerpt from the conclusion of the EPMR report that captures this 'people' essence of the Programme: "*Perhaps the most important value of GCP thus far, is the opportunities it has provided for people of diverse backgrounds to think collectively about solutions to complex problems, and, in the process, to learn from one another*."

Jean-Marcel Ribaut
Director

Introduction and highlights

The Generation Challenge Programme (GCP) was launched in 2003 as a 10-year activity. Now in the middle of its envisaged lifetime, it continues to build on the foundations laid in its formative years. In 2006, we defined our Strategic Framework[1] complemented by a set of 'reference studies' that provide data on GCP's impact targets (farming systems and crops). This refinement of our research strategy has guided activities and determined priorities in 2007, as well as informing the selection of commissioned projects for 2008, in particular for Subprogrammes 3 and 5. Notwithstanding this sharpening of our focus, GCP remains dedicated to the exploration and characterisation (genotyping and phenotyping) of diversity in staple crops and the development of genomic resources for less-studied crops. We will continue to support this core effort.

Also, as our projects mature and increasingly yield more concrete products, GCP management has been paying particular attention to data quality control, data release, product management and product delivery. Consequently, and looking at the evolution of GCP through time, we have realigned the Management Team and support staff to address more effectively the renewed emphasis on management and delivery of products. In this latter regard, GCP has already taken deliberate steps. The Genotyping Support Service (GSS)[2] initiated in mid-2006 provides national agricultural research systems (NARS) with access to molecular technology, including GCP products, to help analyse their germplasm and learn how to analyse and use the resulting data. To ensure product delivery and relevance, researchers leading projects launched in 2007 formulated Delivery Plans, in consultation with the targeted users of their research products.

Research activities

Alignment to CGIAR and global priorities

GCP has several means of establishing, maintaining and validating its focus, relevance and applicability. The Programme's efforts to develop new knowledge and products contribute to the first of the United Nations Millennium Development Goals (MDG) of halving, by 2015, the number of hungry people and those living on less than a dollar a day. When these efforts result in superior crop varieties, they offer poor farm households the potential to improve their food and nutritional security and their income. They also offer poor consumers the prospect of affordable food. As well as supporting progress towards this first critical Goal, GCP contributes directly and indirectly towards the other MDGs.

At the level of the CGIAR (Consultative Group on International Agricultural Research), all GCP activities address one or more of the System Priorities for 2005–2015[3]. The characterisation of crop diversity is at the heart of GCP's work, fulfilling System Priority 1a: *Promoting conservation and characterisation of staple crops.* This is fundamental to achieving Priority Area 2: *Producing more and better food at lower cost through genetic improvement*, which neatly describes GCP's own overall objective. GCP activities contribute to the overarching goal of Priority Area 2 and make particular contributions to meeting Priorities 2a: *Maintaining and enhancing yields and yield potential of food staples*, and 2b: *Improving tolerance to selected abiotic stresses.*

Research in line with the GCP strategy

In 2007, we completed molecular marker analysis of germplasm diversity for all of our target crops except for faba bean and foxtail millet, expanded the seed multiplication ready-reference samples available for majority of the crops, and extended knowledge frontiers on crop domestication. We also increased access to intra-crop genetic diversity, improved phenotyping approaches and protocols, identified and validated new markers for drought-prone environments, and refined strategies and technologies for marker-assisted selection (MAS) for simple traits and marker-assisted breeding (MAB) for polygenic traits. The searchable GCP Central Registry[4] listing all data sets from GCP projects is now online to facilitate information sharing and data management. Six teams from NARS were the finalists in our inaugural awards for 'Capacity-building *à la carte*', offering support

Box 1. GCP Subprogrammes

Subprogramme 1 (SP1):	Genetic diversity of global genetic resources
Subprogramme 2 (SP2):	Genomics towards gene discovery
Subprogramme 3 (SP3):	Trait capture for crop improvement
Subprogramme 4 (SP4):	Bioinformatics and crop information systems
Subprogramme 5 (SP5):	Capacity-building and enabling delivery

1 http://www.generationcp.org/comm/gcp_framework_final.pdf
2 http://www.generationcp.org/capcorner.php?da=0794844
3 http://www.sciencecouncil.cgiar.org/publications/pdf/SCPriorities_prFinal(l-r).pdf
4 http://gcpcr.grinfo.net/

tailor-made to team needs. The year also saw the launch of a large project to improve tropical legumes, through germplasm characterisation and improvement through molecular markers, for drought-prone environments. The project involves several universities, CGIAR Centres and NARS in sub-Saharan Africa. More details on our accomplishments this year are provided in the Subprogramme sections later in this report and summarised in Box 2.

A strategy is only of value if it is implemented. So, 2007 was a watershed year for GCP with the development of our new project portfolio for 2008 defined by several key elements of the GCP strategy. These defining elements are: better integration of activities across Subprogrammes 1, 2 and 3; more focus on key strategic crops and target regions for SP3 projects; promotion and utilisation of the first GCP products; better integration of breeders in GCP projects; and an increasing leadership role by scientists from national programmes, thus ensuring that crop improvement projects are demand-driven.

Evolution of Subprogramme activities

As we put our strategy into practice, the shape and focus of GCP Subprogrammes is evolving:

- SP1's efforts were initially devoted to characterising a broad germplasm set through molecular markers. The next step is to phenotype the reference sets identified in target environments, and to better define the linkage disequilibrium (LD) in target crops and identify favourable alleles through association studies.
- New SP2 projects will now focus exclusively on identifying genes and gaining a better understanding of regulatory pathways involved in drought tolerance, exploring new approaches through comparative genomics, and taking advantage of the increasing number of genomic sequences available.
- The number of SP3 projects promoting the use of markers is increasing, commensurate with the knowledge generated in SP1 and SP2, as well as from research outside GCP. Thus, SP3 validates and adds value to the products and information generated by the other SPs. All SP3 projects will be geared towards crop improvement in drought-prone environments, focusing on GCP target crops and regions[5].
- For SP4, the basic infrastructure for information exchange within GCP has been developed. Consequently, funding for this line of activities is expected to decrease to maintenance level. The development of software, tools and methodology to sustain GCP's science will continue as before, and support to GCP scientists on biological questions and on data handling and analysis will increase; and

Box 2: Scientific achievements

In 2007, key highlights included:

- Completing molecular marker analysis of germplasm diversity for most GCP target crops, (all except faba bean and foxtail millet);
- Developing reference samples for the majority of GCP mandate crops;
- Generating novel information on gene flow related to crop domestication and implications for crop diversity distribution;
- Producing introgression materials with high genetic resolution for rice, and making them accessible for phenotypic evaluation and trait tagging;
- Developing first mutant populations for common beans and potato, and identifying 'gain-of-function' mutants in rice;
- Developing large-scale single nucleotide polymorphism markers (SNPs) for rice, drought expressed sequence tags (ESTs) for cowpeas and pearl millet, a novel set of simple sequence repeat markers (SSRs) for chickpeas, and bacterial artificial chromosome (BAC) libraries for cowpeas and groundnuts;
- Generating a genetic map for *Musa* species with more than 500 marker loci, plus sequencing of some A- and B-genome BACs for *Musa* species;
- Identifying quantitative trait loci (QTLs) for multiple disease resistances and gene-based markers associated with QTLs for blast resistance in maize;
- Characterising and validating leaf growth QTLs in maize for genetic determinism of growth maintenance under water stress;
- Identifying, and transferring to national programmes, gene-based and linked markers diagnostic for salt tolerance (*Saltol*) and phosphorus uptake (*Pup1*) in rice;
- Identifying gene-based markers for aluminium tolerance in sorghum (Alt_{SB}) and validating SNPs/haplotypes for dissemination in Africa and South America;
- Developing near isogenic lines (NILs) for northern/southern leaf blight in maize, and for aluminium tolerance in sorghum;
- Transferring new sources of resistance to disease and of tolerance to drought from related species into cultivated germplasm of groundnut and cassava;
- Identifying recipient material for groundnuts, cowpeas, beans and chickpeas, including farmer- and consumer-preferred varieties in several African countries, forming the basis for marker-assisted selection (MAS) for simple traits and molecular breeding (MB) for complex traits for better performance in drought-prone environments;
- Developing models to improve MAS and marker-assisted breeding (MAB) strategies and favour their integration into conventional breeding schemes;
- Disseminating low-cost and high-throughput marker technologies developed by GCP to breeding programmes;
- Testing new markers for crop improvement in local environments and in adapted genetic backgrounds (eg, Striga resistance in cowpeas in West Africa);
- Using markers to select for biotic stress resistance and drought tolerance in several breeding programmes (eg, mosaic disease resistance for cassava in Nigeria, drought tolerance for rice in China);
- Establishing the GCP Central Registry for project datasets;
- Releasing iMAS (Integrated Marker-Assisted Selection System), a bioinformatics tool to help breeding programmes conducting MAS;
- Converting the Laboratory Information Management System (LIMS) developed at ICRISAT (International Crops Research Institute for the Semi-Arid Tropics) to open source and installing it at BecA (Biosciences Eastern and Central Africa) and IITA (International Institute of Tropical Agriculture);
- Establishing a pipeline for gene expression analysis;
- Awarding 'Capacity-building *à la carte*' support to six national programmes;
- Implementing a fully-operational Genotyping Support Service (GSS);
- Establishing a large community to improve tropical legumes for Africa and coordination of initial activities; and
- Launching of the Delivery Plan Kit (DPKit) and formulating Delivery Plans for new projects

[5] http://www.generationcp.org/UserFiles/File/gcp-target-systems_brief.pdf

- The role of SP5 is becoming increasingly critical to ensure marketing and delivery of GCP products, while continuing to support capacity-building for target beneficiaries further down GCP's delivery chain. We recently initiated ex ante analysis to evaluate the impact of key GCP products, and to help refine our target traits and regions based on local needs.

Consolidation, targeting and expansion

In keeping with our strategy, we are now using 'reference studies' to confirm and consolidate impact targets, be they farming systems, crops or traits. These reference studies inform GCP's Management Team in priority-setting and resource allocation. As GCP projects increasingly mature and deliver tangible products, there is also increasing integration across the five Subprogrammes as explained above. Our research framework integrates 'horizontal' and 'vertical' activities as shown in the diagram below.

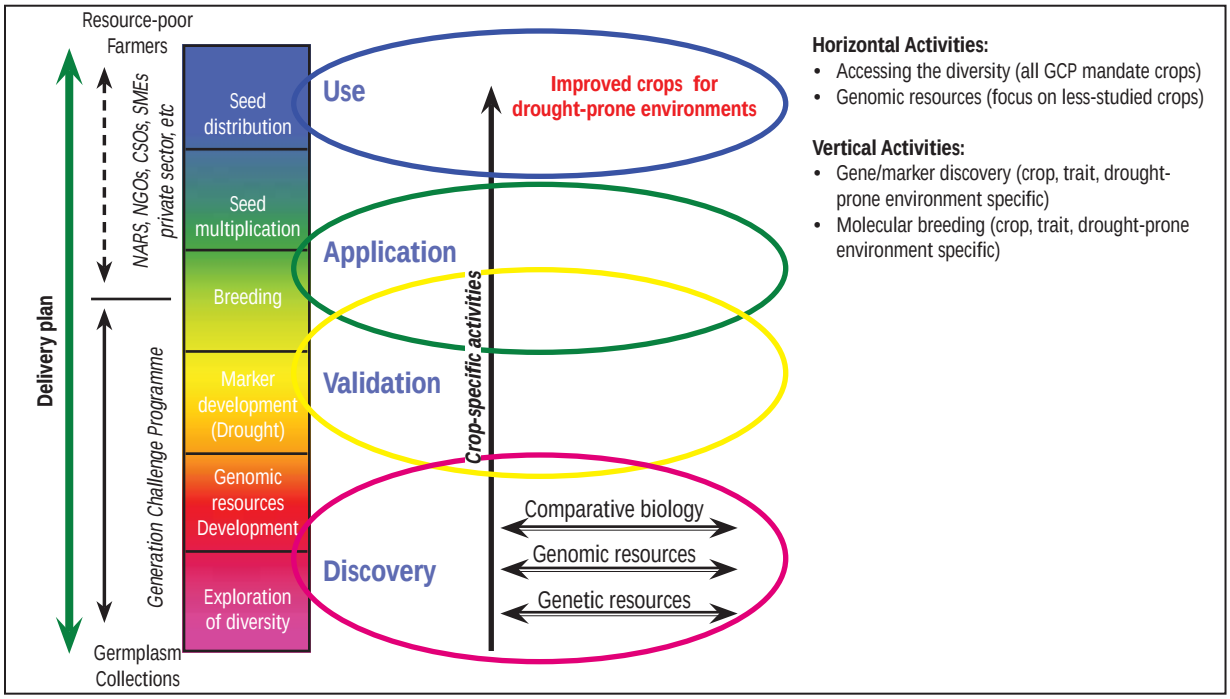
Horizontal research activities expand the knowledge base with respect to cross-cutting biological questions, and across a broad set of crops, to promote the development and refinement of methodologies and of genetic and genomic resources. Examples of horizontal activities include gene discovery through comparative genomics, or the development of new marker systems for less-studied crops. This horizontal axis of knowledge generation, consists of strategic activities to develop appropriate genetic and genomic resources for further genetic studies (in the broad sense from gene cloning to breeding) to be conducted within or outside GCP. Activities could target many farming systems and crops.

Vertical research activities target specific crops and can focus on multiple traits. They are aimed at producing outputs to be used directly in plant breeding in the target farming systems. Vertical activities serve as test cases for integrating and applying new knowledge and biotechnology tools, and for demonstrating the relevance of new approaches to improve the efficiency of plant breeding. Some of the products generated through horizontal activities are critical for bypassing some of the bottlenecks identified along the research pipeline of vertical projects.

A 'classic' example of horizontal activities is the identification of reference sets for GCP mandate crops and development of markers, when necessary, to conduct suitable genotypic characterisation of selected germplasm. We now have reference samples for most GCP mandate crops, and a specific set of SSR markers have been identified for 10 crops for use in large-scale genotyping. Vast genotypic data have been deposited in the GCP registry for, among others, maize, wheat, barley, chickpea, common bean, lentils, potato and coconut. We have almost completed data gathering for pearl millet, finger millet, pigeon peas, cassava and sweet potato. New genotyping methods have been further assessed for whole-genome profiling, with a focus on the use of diversity arrays technology (DArT) for most of the relatively less-studied GCP mandate crops[6] and on Illumina-detected SNPs for rice and cowpeas. Their throughput and cost efficiency will be determined for application of quick genotyping in the thousand-marker range.

[6] http://www.generationcp.org/subprogramme1.php#mandate_crops

Figure 1: GCP research approach



There is a clear orientation towards 'internal' value-adding within GCP. As an example, there are several new projects whose first activity will be to add value to the reference sets mentioned above. Our new major project on 'Improving tropical legume productivity for marginal environments in sub-Saharan Africa' initiated mid–2007 includes the evaluation of reference sets for groundnuts, cowpeas, beans and chickpeas in several countries across the region. In addition, in 2008, a number of commissioned projects will focus on phenotyping reference sets for rice, sorghum and wheat.

Along the vertical axis of research, we are also keen to ensure continuity of our most promising research activities guaranteed to deliver quick payoffs—our 'flagship' projects. For example, EMBRAPA (Empresa Brasileira de Pesquisa Agropecuária; Brazilian Agricultural Research Corporation) has conducted pioneering groundnut research through the creation of amphidiploid synthetics, which effectively broaden the genetic base of the crop and can have direct benefits in breeding programmes. The impact of this work would be heightened if it were conducted where most of the world's groundnut consumers live, i.e. in Africa and Asia, so EMBRAPA has passed its synthetic disease-resistant groundnut lines to Senegal for local testing and application. EMBRAPA is also a key partner in the new project to improve tropical legumes which will use some of the organisation's genomic resources (eg, genetic maps or BAC libraries) generated through a GCP-funded project initiated in 2005.

Our calls for competitive research encourage scientist to build on successful ongoing activities. As a result, some of the competitive proposals selected from our second call are on new activities that stand on the foundations of existing GCP projects. For example, since 2005 GCP has supported a project on the identification and characterisation of a major gene for aluminium tolerance in sorghum. The project is led by Cornell University scientists in collaboration with scientists from EMBRAPA. The gene (Alt_{SB}) has now been cloned. One of the 2007 competitive projects will carry this work a step further by identifying superior Alt_{SB} haplotypes and developing haplotype-specific markers to improve sorghum performance on acid soils in Latin America and West Africa. This second project is led by EMBRAPA, in collaboration with African scientists from national programmes.

We continue to use commissioned projects to consolidate our work, or to fill gaps identified in the GCP competitive research portfolio. As an example, one of the new competitive projects co-led by CIAT (Centro Internacional de Agricultura Tropical; International Center for Tropical Agriculture) and CIRAD (Centre de coopération internationale en recherche agronomique pour le développement, France) will make the entire genetic diversity of *Oryza glaberrima* available to breeders. The diversity will be used in classical breeding schemes or in MAS schemes developing interspecific bridges between selected *O. glaberrima* accessions and reference *O. sativa* recipient cultivars. To add value to this new activity, a project will be commissioned to produce new NERICA rice for West Africa, including large-scale phenotyping of *glaberrima* progenies, training of African scientists at the Africa Rice Center (WARDA), and capacity-building for Mali's national research programme.

We have also expanded the projects under SP3 as we move to product validation as a necessary step to precede product dissemination. Through an IITA-led project initiated in 2005, amplified fragment length polymorphism (AFLP) markers have been developed to discriminate among the different races of *Striga* that reduce cowpea productivity in Africa. These markers have been converted into user-friendly sequence characterised amplified region (SCAR) markers to facilitate rapid identification of pathogen diversity in the field. In addition, new commissioned work led by the national programme in Burkina Faso aims to develop marker-assisted selection for *Striga* resistance in cowpeas in West Africa. Through GCP activities on rice led by scientists from the International Rice Research Institute (IRRI), major QTLs, *Saltol* and *Pup1* have been identified for salinity tolerance and phosphorus deficiency. Markers have been developed and validated for both traits. These markers will be used to introduce salinity tolerance and phosphorus deficiency in adapted rice cultivars in Bangladesh and Indonesia respectively, through commissioned projects led by scientists from national programmes.

GCP does not seek to reinvent the wheel but instead capitalises on discoveries in the plant genomics world. Through our broad network of partners, we are well positioned to tap into the very latest in technological achievements to advance our research and to adjust our research portfolio accordingly. For example, a sorghum genome sequence is now available from an effort coordinated by the Plant Genome Mapping Laboratory of the University of Georgia, USA, which is already involved in GCP activities. This has momentous implications for GCP's work on improving sorghum, opening new doors for both upstream and applied research for geneticists and breeders.

A new initiative on tropical legumes

Considering the critical importance of legumes to enhance income and nutrition for farm-families, especially in drought-prone environments, we are very pleased to report that a new initiative on tropical legumes was launched in mid-2007. This initiative will complement our existing set of projects on legumes such as the introgression of new alleles in groundnuts from wild relatives or the identification of markers for *Striga*

resistance in cowpea. The project, focusing on improving tropical legume productivity for drought-prone environments in sub-Saharan Africa, will promote modern breeding for four legumes: groundnuts, cowpeas, beans and chickpeas. It is dubbed 'Tropical Legumes I' (TLI)[7] because it has a twin project, TLII, the mandate of which is seed multiplication and dissemination. Both TLI and TLII[8] are funded by the Bill & Melinda Gates Foundation, and TLII is led by ICRISAT. TLI will develop key genomic resources that are currently lacking, identify molecular markers for important traits, and improve legume breeding capacity in sub-Saharan Africa. It is a collaborative project with national research activities in sub-Saharan Africa as well as with universities in the USA, the CGIAR Centres and EMBRAPA.

Annual Research Meeting

As always, September was 'ARM month', bringing together the GCP scientific community and stakeholders for the Annual Research Meeting (ARM). This year's meeting was held on African soil for the first time in Benoni, South Africa, with superb ground support from the African Centre for Gene Technologies (ACGT) and excellent coordination by Griselda Marquez, GCP's Executive Assistant. The ARM was structured around themes defined primarily by the products now emerging from GCP's research, but also picking up burning and emerging issues in the arena in which GCP operates.

The ARM gathered together GCP research leaders to share experiences, compare notes and brainstorm on critical issues for the Programme's attaining its objectives. Its title notwithstanding, the ARM was not all about researchers, and the very first session was dedicated to stakeholders. For the first time, their voices were directly heard at ARM, greatly enriching the meeting with perspectives from small-scale farmers, seed entrepreneurs, national researchers, networks and allied projects. The idea was to set the tone, as well as assess needs in, and impediments to, crop improvement. The subsequent research discussions, marked by high enthusiasm, were structured around four overlapping themes: 1) Exploiting allelic diversity; 2) Genomic resources and gene/pathway discovery; 3) Marker development and breeding applications; and 4) Support services and enabling delivery. This year, presentations from the researchers reflected a remarkable growth in tangible products from GCP activities.

Two afternoons were dedicated to brainstorming sessions on the kind of segregating population the GCP user community needs, and on critical bottlenecks in GCP's crop improvement activities. Output from these sessions will be used by the GCP Management Team to identify topics and priorities for the next funding cycle's competitive call and commissioned work. As a result of the discussions, a new project will be initiated in 2008 to develop MAGIC (Multiparent Advanced Generation Inter-Cross) populations for several GCP crops.

Resources and services

In 2007, we made significant and innovative advances in capacity-building. Diversity is what defines the GCP community, given the variety within our research portfolio and the breadth of our mandate, crops and geographical scope. Consequently, our approach to capacity-building is increasingly 'customer-adapted'. Our second call for proposals for the GSS went out in August, extending to crops beyond those addressed in the pilot phase. The call closed in mid-October. Based on user feedback, we will continue to better adapt the service to user needs, and to extend it to cover more crops.

The GCP Intellectual Property (IP) Helpdesk[9] was also launched. The online desk helps the GCP community implement the Consortium Agreement in the context of the broader IP environment. In addition, we launched 'Capacity-building *à la carte*'[10]—a programme for customised high-quality training and sustained technical support to NARS researchers. So far, six national research programmes have benefited from this new programme.

A further important aim of GCP is to provide strategic bioinformatics tools. To this end, iMAS (Integrated Marker-Assisted Selection System) software was released to aid GCP scientists in marker-assisted breeding. It was very positively received and the next step will be to collate user feedback to further improve the software. We also plan to have an online bioinformatics support desk that will guarantee responses to queries from scientists within two working days, with the objective of forging closer links with GCP scientists and improving hands-on support to them.

Product management and delivery

The GCP Delivery Strategy[11] defines the Programme's users and products. A 'user' is defined as anyone who uses a product developed by GCP. A 'product' is defined as any output from any research stage, designed to meet the demands of an identified set of users who will, in turn, process the product for yet another set of users all the way through the value chain to farmers and consumers. Product management and product delivery are intrinsically related; they jointly establish the vital link in connecting upstream research and delivering research-based products that will have tangible impacts on agriculture.

7 http://www.generationcp.org/gcptli/
8 http://www.tropicallegumes.org/
9 http://www.generationcp.org/iphelpdesk.php?da=0629604
10 http://www.generationcp.org/capcorner.php?da=0775534
11 http://www.generationcp.org/capcorner/Final_Delivery_Strategy.pdf

GCP's approach to product management and delivery, in keeping with the new Strategic Framework[12], requires that Principal Investigators (PIs) clearly define research products and users. The Management Team then singles out products that guarantee good returns on value-adding investments. In the GCP management structure, the SP3 Leader compiles an inventory of outputs from the other Subprogrammes, with a view to ensuring the flow of products, identifying products for value-adding in GCP's research projects and validating them. Once products are validated and ready for routine use, the SP5 Leader is responsible for their delivery by marketing and distributing them within and outside the Programme.

The GCP Delivery Strategy requires that all new projects clearly define research products and users right from the start. In this way, GCP scientists working on new projects now have a clearer understanding of two basic concepts for conducting their research: (i) the actual products to be generated by the research, and (ii) the primary and secondary users of the products. In addition, projects with a total budget of USD 250,000 or more must prepare a more formal project Delivery Plan using the Delivery Plan Kit (DPKit)[13] launched in 2007. When there is a suite of projects set to start at the same time, prior to their commencement, GCP organises a joint workshop where, with expert guidance, researchers and users for each project together formulate project Delivery Plans[14]. The DPKit helps researchers identify and propose solutions to potential problems or constraints that could occur along the product delivery chain. For example, to make sure that products reach the intended users, capacity-building can be undertaken to overcome or bypass bottlenecks identified at project planning or implementation. Given its forward-looking focus, the DPKit provides a sound mechanism for researchers to foresee how their products will be applied in the research–development continuum, and a timely opportunity to further improve and refine research products and tools.

Data quality and sharing

A key product from GCP is data generated by the different projects, and the Programme is committed to sharing these data as international public goods for public access at no cost. We do this through the online GCP Central Data Registry[15].

In 2007, with an increasing amount of information generated by GCP's research activities, data quality control was a major item on the agenda of the Management Team. In particular, with the termination of wide-scale systematic genotyping for structure analysis and diversity sampling from the large food crop collections, and the sizeable data this will generate, data quality control and data exploitation will require considerable efforts and human resources. Data quality control is first and foremost the responsibility of the scientist generating the data, overseen by the PI in charge of the project. But it is also the responsibility of GCP to ensure that the quality of the data posted in our Central Registry be of an acceptable standard since this information is deposited there for use by other scientists.

Some 'first level' quality control will be conducted for files already in the Central Registry using control indicators that are developed based on the nature of the data stored (eg, number of alleles per locus in a diploid genome for diversity data). In addition, and mainly for large-scale data production, a limited number of randomly sampled analyses will be conducted again by neutral laboratories to ensure data quality. The tests are not to question the quality of work in GCP projects but rather to conform to conventional policy and practice in quality control as conducted in every service laboratory. Such quality control will also assure GCP scientists that their data are reliable. Should any discrepancy be detected between the results generated by the two independent analyses, we are ready to allocate resources to improving the quality of the data, provided that the underlying issues are understood.

Governance and management

GCP governance

In 2005, the Programme Steering Committee (PSC) set up a task force to review GCP's governance. The Task Force on Governance Structure developed a set of options and recommendations for reform of the Consortium Agreement, which were presented during the 2006 PSC meeting. The PSC did not endorse the proposed recommendations at that time since further clarity was needed on some fundamental issues relating to GCP's identity. The Task Force's Terms of Reference were revised accordingly. The Task Force deliberated for a further year and then suggested delegating most PSC responsibilities to a new governance body. During its 2007 annual meeting in Beijing, China, the PSC approved the resolution to create an Executive Board to ensure that GCP is governed by a panel of independent experts who must be from outside the GCP Consortium.

Consequently, the PSC set up a Selection Committee that will select the seven members of the Executive Board based on suggestions made by the broader GCP stakeholder community, including the Consortium members and the GCP Management Team. In selecting Board members, focus will be on the

[12] http://www.generationcp.org/comm/gcp_framework_final.pdf
[13] http://www.generationcp.org/UserFiles/File/dp-kit.xls
[14] See GCP's rationale for Delivery Plans at: http://www.generationcp.org/gen.php?da=0790433
[15] http://gcpcr.grinfo.net/

independence, capacity and expertise of the candidates. The PSC will transfer substantive governance responsibilities to the Executive Board, including the following functions (quoted from the resolution):

1. *Determining the strategic direction of GCP and setting overall goals for the Challenge Programme;*
2. *Establishing performance criteria to determine the progress of GCP activities, monitoring the implementation of those criteria, and judging whether those criteria have been met;*
3. *Approving audits, annual operating plans, medium-term plans, and budgets. This shall include the receipt of financial audits of the GCP from the Host Agent's finance director and external auditor;*
4. *Ensuring the integrity of the GCP's accounting and financial reporting systems;*
5. *Establishing a policy for managing risks and monitoring the implementation of that policy;*
6. *Monitoring and managing potential conflicts of interests of members of the Executive Board and staff of the GCP Directorate;*
7. *Overseeing the activities of, and providing guidance and advisory support and expertise to, the GCP Director and staff of the GCP directorate;*
8. *Making recommendations to Consortium Members and Supporting Participants regarding the commercialization of Challenge Programme IP under Clause 26 of the GCP Consortium Agreement and any similar provision of any agreement for the conduct of GCP activities by a Supporting Participant; and*
9. *Making recommendations to the PSC members and/or the Consortium members.*

The PSC resolution[16] adopting the Executive Board is posted on the GCP website, and the new Executive Board is expected to be functional before July 2008. In this new context, it will be imperative to clearly define the roles and responsibilities of the Stakeholder Committee (SHC) and the Programme Advisory Committee (PAC) given the ongoing governance reforms. The GCP Management Team is currently working in collaboration with the Global Forum on Agricultural Research (GFAR) on new terms of reference for the SHC, and GCP expects to have a rejuvenated SHC by May 2008. The new Executive Board Members will have discretion on whether to revitalise the PAC or look for alternatives (eg, consultants) to tap into, and bring in, particular scientific expertise as and when required. The PSC will have to redefine its role, internal *modus operandi* and interaction with the GCP Management Team. The PSC will also have to define its mode of interaction vis-à-vis the new Executive Board. The four provisional PSC members will advance to full membership once they sign the Consortium Agreement.

Staff profile

The year witnessed a number of changes in and realignment of GCP's staffing profile. As recommended by the Management Team and approved by the PSC's Task Force on GCP Management, the SP5 Leader position was adjusted to full-time. Carmen de Vicente took up the full-time position in February, relocating to GCP Headquarters at CIMMYT, Mexico in May.

In June, GCP bade farewell to Hei Leung, Subprogramme Leader for SP2 since its launch in January 2004. Hei's hard work and dedication have contributed significantly to GCP's achievements, especially in gene discovery in relation to abiotic stress-tolerance. He leaves GCP in order to dedicate himself fully to research work at IRRI. Hei was replaced by Rajeev Varshney, a senior ICRISAT scientist specialising in applied genomics. Rajeev brings to GCP his enthusiasm and broad expertise in molecular marker development, and in computational, comparative and functional genomics in cereals.

A new arrival to GCP in December was Nosisa Mayaba from South Africa. Among other assignments, Nosisa will work with the SP5 Leader in applying the GCP Strategy on capacity-building to ensure that SP5 links effectively with the expected outputs of each Subprogramme and meets GCP objectives. In addition, Nosisa will play a vital role in implementing Objective 6 (Provide training and capacity-building for sub-Saharan African scientists) of the new project 'Improving tropical legume productivity for marginal environments in sub-Saharan Africa'.

There were changes in the Communications Unit too. Jenny Nelson, Communications Manager, left at the end of 2006, as reported in last year's Annual Report, and was replaced by Antonia Okono, a Kenyan national, in April 2007. Kaitlin Lesnick, the Communications Assistant left in April and was replaced by Kate Durbin from the UK in May.

The Project Office welcomed Paula Maria de León in September to assist Adriana Santiago, GCP Project Officer, in supporting the expanding portfolio of GCP projects. Laura I Ruiz joined in July to provide administrative support to the product management and product delivery functions of SP3 and SP5 respectively. These changes respond in part to the large number of diverse grants and projects in the SP5 portfolio that require dedicated management, as well as to Carmen de Vicente's relocation to Mexico. Carmen's relocation precipitated the departure from GCP of Carlos A Tovar and Sandra Insignares, who were both providing local support to SP5 in Colombia.

[16] http://www.generationcp.org/UserFiles/File/final-resolution_executive-board-15Dec07_final.pdf

Project management

The GCP Manual[17] is an essential handbook for managing GCP projects. Originally designed as an orientation aid for new staff joining the Programme, the publication has turned out to be a valuable resource not only for project managers, but also for funders, partners and anyone interested in GCP. It explains GCP's procedures, culture and the philosophy upon which the Programme was founded, with detailed annexes for each aspect. The Manual is updated on a yearly basis to reflect the state of the Programme.

We reassessed project support this year, and followed up with several project management initiatives. Firstly, we embarked on the Project Development Guide (PDG), an online resource for project design, monitoring, implementation and evaluation, for use by researchers as well as science managers and reviewers. When coupled with our DPKit, the PDG will greatly improve the design of new projects with clear milestones and workplans, which will optimise the planning and improve monitoring of our broad and diverse research portfolio. We also anticipate that when researchers use the PDG, it will enhance the quality of GCP proposals and maximise timely delivery of products. The PDG was mainly funded by the Syngenta Foundation for Sustainable Agriculture in collaboration with GCP. Secondly, we began development of an information and workflow system to streamline our operations.

Thirdly, in a bid to ensure that we deploy the efforts of our scientists on what counts most, ie getting on with the science, we have revised project reporting procedures to give more emphasis to monitoring and evaluation over reporting *per se*. Report templates have been revised to ensure that products and potential users are identified in each new project. Narratives of activities have been reduced and are replaced by statements of project progress in terms of output delivery. Any changes from the original workplan need to be explained, and the logframe adjusted accordingly. The project reporting calendar has also been adjusted, discontinuing the mid-year report; from now on, projects will only submit a single annual report, and a final report at the end of the project. Finally, we resolved to promote more frequent informal interactions between SP Leaders and PIs or Co-PIs, as each project case may require.

Review and evaluation

With GCP almost at mid-point in its 10-year life, 2007 turned out to be a 'review year' and we had no less than three important evaluations in the year, as well as the opportunity for feedback from GCP partners.

[17] http://www.generationcp.org/brochure.php#manuals

Risk assessment

As a follow-up to the GCP audit conducted in October 2006 by the Internal Auditing Unit (IAU) of the CGIAR, GCP underwent a risk assessment exercise in June 2007, also facilitated by IAU. As a starting point, the risk assessment was mostly inward-looking and involved GCP management and staff. The exercise assessed GCP processes and procedures in the context of internal efficiencies and associated internal and external risks. The IAU provided sound recommendations on how to mitigate and minimise the risks identified.

Programme evaluation

In May, the European Commission (EC) which is our largest funder, assessed EC-supported activities across the CGIAR, including GCP projects. Overall, the output of the review was positive. The reviewers identified areas where GCP had made considerable progress, for example, in creating an improved understanding of the structure of the diversity of major world food crops. They also identified areas where progress was slower than had been expected, such as in comparative genomics. A questionnaire developed by the reviewers showed that EC cofinanced research projects implemented by GCP comply with local needs and priorities, and align with national priorities in the countries where the projects are carried out. The reviewers also recognised the pioneer role played by GCP within the CGIAR system in formulating and implementing a delivery strategy.

External Programme and Management Review

September 2007 saw the beginning of GCP's first External Programme and Management Review (EPMR) commissioned by the CGIAR Science Council. The EPMR report was scheduled for March 2008. The three-member EPMR Panel was led by Wallace Beversdorf of the International Service for the Acquisition of Agri-biotech Applications (ISAAA; USA). Panel members were Markus Palenberg (Global Public Policy Institute Consulting, Germany) and Jennifer Thomson (University of Cape Town, South Africa). Wallace attended GCP's Annual Research Meeting and both Wallace and Markus attended the PSC meeting. The Panel spent a week at GCP Headquarters, during which time they consulted closely with the Management Team. In addition, the Panel had telephone interviews with GCP researchers and other stakeholders, and conducted two surveys targeting a total of more than 250 individuals and receiving more than 190 responses. One survey was on GCP stakeholders and the other on governance and management.

ARM and Programme survey

Following the GCP Annual Research Meeting, the Management Team commissioned an internal survey to solicit feedback from the GCP community participating in the meeting, plus a few key partners who did not attend the meeting. It was a two-part survey, the first part focusing exclusively on the ARM, while

the second part was on broader issues at Programme level. The survey was conducted by the Meridian Institute to confer objectivity and encourage frank feedback. Overall, the survey indicated members of the GCP community have positive impressions and feedback about the 2007 ARM and, more broadly, GCP. In particular, community members are pleased with progress to date, clarity of the GCP strategy, and vision for the future. Survey respondents stressed the importance of continued focus on downstream product delivery, which is necessary for meaningful impacts. The results of the survey are available online[18].

Policy and legal matters

In keeping with the spirit of the CGIAR, GCP is committed to generating international public goods, including in the area of intellectual property (IP) and with due regard to intellectual property rights (IPR). To this end, we have taken further steps to ensure that GCP Consortium members comply with the obligation to file annual IPR management reports.

As GCP continues to mature, some current research projects build upon earlier GCP achievements; the IP provisions of the GCP Consortium Agreement[19] encompass such value-adding projects. Respect for IPR must be balanced with furthering the overall humanitarian mission of GCP. Thus, while GCP partners who develop useful research outputs through GCP activities are entitled to claim IPR over those outputs, the rights are qualified and subject to a clear policy to share outputs from GCP-funded research, as spelt out in the GCP Consortium Agreement, including the amended humanitarian licence agreement. Among other provisions, the GCP IP policy ensures that GCP lives up to its commitment to produce international public goods, and that all Consortium members can use research outputs for the public good on a royalty-free basis. However, despite the Consortium Agreement provisions, some parties have not been as forthcoming as had been expected in sharing outputs from GCP-funded work with other GCP researchers. This matter is of concern to GCP Management, and prescriptive and preventive measures will be high on the 2008 agenda.

Communications

The GCP Communications Unit aims to facilitate information flow within GCP, and to communicate to the outside world and wider plant molecular genetics and breeding community. The GCP website[20] is central to our communications. We endeavour to make all of our documents available on the website to serve as a one-stop-shop for information on GCP and ensure fair access to that information. The number of visitors to our website continues to rise steadily, with an average of about 60,000 hits per month.

Besides maintaining and updating the website, the Communications Unit also publishes and distributes *GCP News*[21], an electronic newsletter sent to a growing list of subscribers to update them on upcoming GCP activities, as well as on the latest developments and events in the broader community of crop science. *GCP News* subscribers now number about 2,000.

We also rely on other global fora to further publicise our messages. In 2007, GCP participated in several events, and some of the key ones deserve special mention. Every year, GCP participates in the annual Plant and Animal Genome Conference (PAG). The 2007 PAG was held at San Diego, California (USA) in January, and GCP convened a workshop as a side event. The workshop was to update the community on major results from GCP's research, with eight GCP researchers presenting their work. Later in November, GCP participated in BioAsia 2007 in Bangkok, Thailand and convened a side event for rice researchers in Asia. One of the direct outcomes from the workshop was the establishment of a forum for rice researchers in Asia to facilitate information and resource exchange.

A major task in 2007 was tracking and compiling a list of GCP publications since the Programme's inception, and making them available via the GCP website where possible. This task will continue in 2008. The full list of GCP publications tracked to date is available online[22], while a list of selected 2007 publications is provided in Appendix C.

Other tasks for 2008 include supporting GCP's renewed emphasis on product management and delivery, and marketing drive. One way, in collaboration with SP5, will be through developing a series of factsheets to promote selected GCP products, as well as related documentation. To support project management, the Communications Unit will also compile a comprehensive contact list for GCP researchers as part of the envisaged integrated workflow system.

Collaboration and partnerships

To fulfil its mission, GCP has forged and nurtured R&D partnerships in research, breeding and delivery, and we are interacting increasingly with the private sector. Like other CGIAR Challenge Programmes, GCP was created to yield large impacts in the short term through interdisciplinary approaches. It is therefore imperative that GCP cultivate partnerships and that every activity in GCP be a collaborative

[18] http://www.generationcp.org/UserFiles/File/ARM2007_Survey_Results.pdf
[19] http://www.generationcp.org/UserFiles/File/Consortium_agreement_signed.pdf
[20] http://www.generationcp.org
[21] http://www.generationcp.org/enewsletter.php
[22] http://www.generationcp.org/research.php?da=0642451

exercise with carefully chosen partner institutions offering complementary expertise. The sections that follow provide details on GCP's partnerships, and the full list of GCP partners can be found in Appendix A.

GCP continues to collaborate with the other three CGIAR Challenge Programmes (HarvestPlus, Sub-Saharan Africa Challenge Program, Water and Food) in communication, research planning and impact assessment.

Because GCP research is mostly 'upstream', it is critical for us to collaborate with organisations involved in large-scale plant breeding, seed multiplication and seed distribution. The Tropical Legumes I (TLI) project has a dual focus on research and capacity-building, and relies on TLII for seed multiplication and distribution. For other GCP projects in Africa, we shall consolidate links with the Program for African Seed Systems (PASS), jointly funded by the Bill & Melinda Gates Foundation and The Rockefeller Foundation. GCP will enhance collaboration with small- and medium-sized enterprises, including the private sector and any other organisations to ensure product delivery to, and capacity-building for, Africa and South and Southeast Asia.

In 2006, GCP signed a Memorandum of Understanding (MoU) with the Global Crop Diversity Trust for collaboration on activities of mutual interest, especially conservation, research and development of plant genetic resources for food and agriculture (PGRFA). In September, the Trust opened its first annual call to characterise genebank accessions, mainly at the phenotypic level. GCP also has a similar annual call to characterise genebank accessions, but mainly at the molecular level (through the GSS). The two institutions agreed to align these complementary calls to further each other's work for mutual benefit and synergy. Thus, successful applicants in either call stand a higher chance of qualifying for the other call, resulting in complementary phenotyping and molecular characterisation of the same accessions.

The role of the private sector in GCP, though modest for now, is also evolving, and growing. We recognise private organisations as key partners and we are identifying practical ways to involve them more actively in our research activities. Our goal is to tap the crop science technology and expertise of researchers and managers in large transnational seed companies. In working with the private sector, we take a case-by-case approach to reflect the nature of each partnership, and a few illustrations will suffice.

In designing and developing the PDG, the consultant who took the lead, Viv Anthony, has extensive international private sector experience spanning more than two decades and covering, among other areas, product development, registration and research. We also ensure continuous engagement with the private sector through the independent review panel for our competitive grants, whose composition always includes the private sector. Likewise, the membership of our Review and Advisory Panel (RAP)[23] that works closely with the Management Team reflects private sector representation.

We also engage with the private sector in direct and active scientific collaboration. Over the last few years, scientists at Syngenta have successfully applied marker-assisted recurrent selection to improve maize for polygenic traits like grain moisture content and precocity. A proposal is currently under discussion to apply this expertise to improve sorghum yield under water-stressed condition in Africa. By drawing on Syngenta's expertise and genomic resources, this would be a working example of how technology developed by the private sector can benefit plant breeding in the developing world. In such a scenario, scientists from Syngenta would be active project partners alongside breeders from African countries to improve sorghum.

Another subsector of interest is that of small- and medium-sized enterprises (SMEs). The niche of SMEs is quite different and the idea behind the collaboration is to more widely disseminate GCP tools and value-added germplasm. SMEs are an excellent channel for reaching small-scale farmers. In India, through the Barwale Foundation, contact has already been established with the Indian Foundation Seed and Services Association (IFSSA), itself supported by the Foundation. IFSSA links public–private seed sector partnerships for value-adding and to provide farmers with quality seed. With these new contacts, we expect GCP to have an impact on seed production in India. Africa will, however, be a bigger challenge and we will start by engaging the private sector and non-governmental organisation (NGO) networks in the seed industry. Representatives from several African seed companies and NGOs were invited to the 2007 Annual Research Meeting to present their perspectives at the stakeholder session, thus providing pointers for exploring potential collaboration with GCP.

The Programme reached the end of 2007 with a sense of achievement. The GCP model has been validated, with ever strengthened and diversified partnerships. We have demonstrated a capacity to evolve our structures and *modus operandi* in response to experience and feedback. Our financial basis is secure for the coming year. But most importantly, as the following sections of this report will testify, we are witnessing significant advances in the science that is our core business, enabling us to deliver on our commitment to the community of stakeholders that we serve, for the ultimate benefit of resource-poor farmers in drought-prone environments.

[23] http://www.generationcp.org/rap.php?da=0781418

Subprogramme summaries

Subprogramme 1: Genetic diversity of global genetic resources

SP1 seeks to provide breeders and scientists with representative and thoroughly characterised germplasm, establish standards, and mobilise broad expertise and resources, all contributing to a greater understanding of crop diversity. In 2007, SP1's most significant achievements were: completing molecular marker analysis of germplasm diversity for most GCP crops; generating new knowledge on crop domestication; developing and making available reference samples for most crops; and, for rice, producing high genetic resolution introgression materials. Overall, the background information necessary for taking fuller advantage of the genetic diversity of GCP crops has significantly increased. A number of lessons have also been learnt: Concerned by the uneven quality of project data, SP1 is taking proactive measures to improve data quality and management through workshops organised in collaboration with SP4, repetition of analyses, and GCP-certification of data deposited in the Central Registry. Viable alternatives will be sought and resources allocated to alleviate the time pressure on scientists—a factor that hinders adequate and in-depth data analysis. In addition, options for storage of, and access to, the seed of reference materials will be explored, and SP1 will collaborate with SP5 to connect research and education to sustain the momentum of scientific research-for-development. In 2008, SP1 will particularly focus on developing and delivering its diverse products, conducting fundamental work on the germplasm foundation, finalising and documenting reference samples (phenotyping), and consolidating a global system for seed management and distribution. In collaboration with SP4, SP1 will document biological features to relate phenotype to genotype, and establish and promote a genotyping platform to facilitate information and resource exchange. Genetic material developed in SP1 will be used in SP3's phenotyping activities.

Subprogramme 2: Genomics towards gene discovery

SP2 aims to provide a conducive environment for interdisciplinary and integrated approaches in gene discovery to unravel the underlying genetic mechanisms for effective crop adaptation. In concert with the other Subprogrammes, SP2 establishes and uses cross-cutting research platforms for efficient application of tools and knowledge to decipher genes that control complex traits, pools resources and expertise for efficient identification of genes, supports capacity-building and creates a pipeline to translate results into practice. Major achievements in 2007 included: developing the first mutant populations for common bean and potato and identifying rice mutants with improved drought tolerance; developing genome infrastructure for selected crops including groundnuts, rice, *Musa* and cowpeas; identifying candidate genes, markers and QTLs for stress and disease resistance, and working with SP3 to validate and deploy these resources for breeding; and developing new genetic material for genome analysis and breeding, including advanced backcross lines in rice for salt tolerance, blast resistance and enhanced yield under drought. SP2 places high priority on validating the genes and QTLs already identified for several traits, and incorporating them in popular varieties in GCP target environments, with continued emphasis on drought tolerance and related traits. For sweet potato and pearl millet, 2008 will see research begin on developing genetic and genomic resources for molecular breeding. SP2 will also develop genomic resources (including markers for drought and biotic stress tolerance) for major tropical legumes. Products from several SP2 projects will be transferred to SP3 for validation for molecular breeding.

Subprogramme 3: Trait capture for crop improvement

SP3 aims to maximise the impact of new genes, markers and traits, and promote molecular breeding in tropical staple crops, particularly through linking upstream research with practical product development. SP3's main objectives are to validate genes and markers identified (mainly by SP1 and SP2) in adopted germplasm evaluated in target environments, and to use modern marker approaches to accelerate genetic progress for simple and complex traits. SP3 is consequently in a pivotal position receiving and processing outputs from SP1 and SP2 and, in collaboration with SP5, promoting validation and diffusion of products within GCP and to NARS. As GCP projects mature and deliver outputs resulting in greater inter-project interactions, there is a corresponding increase in synergies upstream and downstream along the research–delivery continuum. In 2007, SP3's main achievements

included: transfer of newly discovered sources of disease resistance and drought tolerance from wild relatives of groundnut and cassava; development of models to improve marker-assisted selection strategies for biotic and abiotic stresses and their integration into breeding programmes via low-cost high-throughput technologies; establishment of phenotyping networks to improve phenotyping capacities within GCP and to address genotype by environment interactions for drought; testing molecular breeding systems under specific environments and in locally adapted backgrounds; and development of tools and products to document GCP outputs and streamline their transfer to users. In 2008, research will focus on drought and related traits, salinity tolerance in rice and tolerance to aluminium toxicity in sorghum. A degree of effort will also be dedicated to disease resistance in root and tuber crops to tackle yield-limiting factors in Africa. Through collaborative activities, particularly with SP5, SP3 will disseminate and scale up drought-tolerant germplasm across crops and regions.

Subprogramme 4: Bioinformatics and crop information systems

Reflecting the central role that biometrics and bioinformatics play in adding value to data, SP4 provides a platform integrating information and analytical tools to maximise the accessibility and utilisation of data from CGP projects. In 2007, efforts have primarily focused on developing an infrastructure to facilitate information flow between researchers, improving information technology and bioinformatics facilities, and providing software tools and data management support. In 2007, particular achievements included: creating a searchable repository for GCP data (with SP1 and SP2); enhancing the ICRISAT Laboratory Information Management System and installing it at two locations in Africa; establishing a pipeline for analysis of expression data (with SP2); and developing improved methodology for QTL x environment analysis (with SP2 and SP3). Based on experience since SP4's early years, problems in software development are now tackled much more hand-in-hand with users from the outset to meet user needs in a better way and to streamline feedback to developers. Another lesson learnt is that a change in organisational culture and more precise contracts with clearer identification of outputs would enhance not only quality, but also timely delivery. A third lesson is to take advantage of all possible means of communication to optimise interactions among globally dispersed partners. In 2008, with the basic infrastructure of the GCP information platform in place, investment in development can be reduced, freeing up more resources to support GCP scientists. A rapid-response helpdesk will be established (in collaboration with SP5) for SP4-related questions, linking queries to the appropriate experts, tools or information sources. And, as the volume of GCP project data increases and some of the older projects come to a close, attention to data quality will continue to be at the forefront.

Subprogramme 5: Capacity-building and enabling delivery

SP5 supports the achievement of CGP objectives and their sustainability by building technical capacity, adding value to products and facilitating their flow to users, and conducting *ex ante* impact analysis. Recognising NARS as crucial partners in contact with farmers, SP5 aims to provide them with training and support for their research. Achievements in 2007 included: completing a set of learning materials on crop diversity (with SP1), on genomics and comparative genetics (with SP2) and on bioinformatics (with SP4); providing training on topical policy issues; launching the Capacity-building *à la carte* programme for teams working on applied research, as well as offering competitive fellowships and travel awards; developing and implementing project Delivery Plans using the GCP Delivery Plan Kit (DPKit); testing the Genotyping Support Service (GSS); and pioneering a community of practice approach for rice with partners in Asia. Two studies were conducted: one was an *ex ante* impact assessment for rice and cassava, and an estimation of benefits of GCP investments. The other was on priority farming systems. A structured approach to project delivery underlines the importance of timely engagement of partners, as well as of their active involvement in needs-assessment and implementation to promote adoption. Analysing team dynamics provided lessons on expectations of the capacity and readiness of partners, underlining the importance of careful assessment of partnerships. Looking to 2008 and beyond, it will be crucial to invest in factors that promote the delivery and dissemination of GCP products. Capacity-building will be on priority topics and tailored to address identified needs. Developing support services, communities of practice and regional crop platforms will also be critical facilitative factors for delivery and impact.

Subprogramme 1: Genetic diversity of global genetic resources

Rationale

Access to genetic diversity is the foundation for breeding. The GCP has devoted an entire Subprogramme to addressing this issue. Thus, SP1 seeks to provide the community of breeders and other scientists with germplasm samples gathered from various sources, selected for diversity and representativeness, and characterised as thoroughly as possible. It aims to establish standards, which will serve as a reference for connecting and integrating future efforts within the global community, thereby mobilising a wide range of expertise and facilities.

SP1 manages a massive campaign of germplasm characterization, with emphasis on the collections held by the CGIAR Centres as part of their mandate. Initial constitution of a composite germplasm sample based on passport information is followed by genotyping with molecular markers which can be applied in, and compared across, laboratories with medium to low technical capacity. The data are then used for selecting reference samples for future genotyping and phenotyping efforts.

In addition, SP1 undertakes activities that contribute data while consolidating capacity within the GCP and providing access to external facilities. This covers exploration of new marker systems and development and optimisation of phenotyping capacities in relation to drought. Altogether, this integration is expected to yield biological understanding of diversity and the genetic and functional architecture of adaptation.

Major achievements

During 2007, SP1's most significant achievements were:

Molecular marker analysis of germplasm diversity

This analysis was completed for all target crops, except for faba bean and foxtail millet, with an achievement rate (percentage of quantitative datapoint target) ranging between 30 and 120 percent depending on the crop, and an average close to 70 percent. Of the 19 crops analysed, 13 were in the 80–120 percent range, four in the 50–80 percent range, and two in the 30–50 percent range.

Novel information on crop domestication

This information included revised relationships among standard ecotypes derived from molecular marker-based clustering (eg, in chickpea, common bean, rice, sorghum); evidence suggesting a somaclonal origin for several germplasm clusters in vegetatively propagated crops (potato and *Musa*); uncovering of the parental origin of the most important triploid varieties in *Musa*; and reconstitution of crop migration histories (eg, in maize, coconut, common bean, sorghum).

Crop background information

Overall, the background information necessary for informed exploitation of genetic diversity has been considerably upgraded for all crops. These results are of immediate and direct utility for all breeders concerned with the diversity and adaptability of their breeding materials.

Distribution of reference samples

Reference samples for most crops were developed and made available or prepared for seed distribution. Depending on the individual user perspectives, they serve to broaden the genetic base of breeding materials, to identify new donors for desired traits and new extremes for phenotypic variation, to direct further germplasm mining efforts and to decipher the genetic basis of adaptive trait variation through association studies. In addition, introgression materials with high genetic resolution were produced in rice and made accessible for phenotypic evaluation and trait tagging.

Activity report

1.1 Creation of an improved understanding of the structure of the diversity of major world food crops

SP1 has undertaken systematic work on crops for which the CGIAR has active breeding programmes. This work started in 2004 for eleven crops, was extended in 2005 to another seven, and again in 2006 for an additional three. Initially, the main undertaking for SP1 has been the identification of representative germplasm samples and their genotyping with simple sequence repeat markers (SSRs). The exercise has now been completed for all crops except for faba bean and foxtail millet, which will be dealt with in 2008. The year 2007 saw

particularly significant progress for *Musa*, yam, lentil and pearl millet. Altogether, the rate of achievement in relation to the datapoint target ranges between 30 and 120 percent, with an overall rate close to 70 percent. The main reason for not reaching a higher rate of achievement was the failure of one partner to deliver expected outputs.

As observed in previous years, the diversity of the sources of the genotyping data requires accurate assessment of quality, coordinated analysis and interpretation of the data, and final depositing in the GCP Central Registry[24]. Plans for a collective publication are progressing in order to complete this extensive genotyping exercise with an important landmark product and asset for future use. However, priority must be given to quality issues, and coordinated data analysis must be organised, despite the severe time pressure on project scientists.

Linkage disequilibrium (LD) along the genome is an important feature of a germplasm sample for relating phenotypic variation to molecular variation. LD is currently being assessed for the main cereals independently of GCP, whereas GCP itself focuses on long generation crops such as cassava, potato, triploid banana and coconut. SSR loci separated by small genetic distances as well as large numbers of anonymous amplified fragment length polymorphism (AFLP) or diversity arrays technology (DArT) markers are being surveyed in order to calibrate LD in these materials. Data analysis is still ongoing, with methodological support from Wageningen University and Research Centre (WUR), The Netherlands.

The extent and type of geographic differentiation, revealing the history of cultivated material, is another component that must be integrated into efforts to interpret diversity. A large-scale effort is ongoing for maize using SSRs to characterise open-pollinated varieties. Informatics tools have been developed to analyse the results of bulked seed samples run on an automatic DNA sequencer, and to make them useable with standard population genetics software. SSR marker data are now complete for all 200 maize landraces and teosinte populations, and are being combined with nearly 700 landraces characterised previously. Global geographic patterns are being analysed. The output has been placed on the GCP Bioinformatics Portal[25], and eighty NARS scientists have been trained in population diversity laboratory and data analysis. Germplasm contributed by various partners has been secured in local and regional genebanks, and in the genebank at CIMMYT.

1.2 Development of a range of flexible high-throughput genotyping techniques accessible in reference laboratories

The collective exercise of SSR genotyping has provided an opportunity to identify laboratories that are well organised and efficient, setting the stage for subsequent initiatives such as the Genotyping Support Service (GSS)[26].

After the first round of positive experiences with diversity arrays technology (DArTs), several studies are being pursued using existing commercially-available services, and a DArT genotyping platform has been established at ICRISAT.

The use of sequences within the 1kb range is being explored through a multi-crop project aimed at initiating a database on allele diversity at orthologous candidate genes. The experience is progressing and is so far demonstrating the complexity of addressing crops with little expressed sequence tag (EST) information and of establishing orthology as well as wide contrasts of polymorphism between crops and between loci.

Single nucleotide polymorphism (SNP)-based technologies are being assessed with the concrete involvement of GCP Consortium members. The International Rice Research Institute (IRRI) and Agropolis in Montpellier, France, in collaboration with the Centre National de Génotypage (CNG) in Evry, France, have developed a set of 1536 SNPs to be used in an Illumina platform. The analyses are progressing at the rate determined by the availability of high-quality DNA. Results for 500 accessions clearly reveal genomic introgression patterns between indica and japonica rice. The same technology is being used on maize with similar success. Another SNP-based protocol developed in barley to study allele mining based on non-coding regulatory SNPs is now routinely available at the Università di Udine, Italy, at the National Institute of Agricultural Botany (NIAB), UK and at the International Centre for Agricultural Research in the Dry Areas (ICARDA).

1.3 Establishment and implementation of a scientific and organisational framework to describe tolerance to drought

This project aims to optimise access to efficient, coordinated multilocal phenotyping platforms, supporting evaluation by environment descriptions and whole-plant modelling, and drawing experience from advanced physiological characterisation in crop-specific projects. Two groups of collaborators involved in a *Drought phenotyping network* at EMBRAPA and in a *Whole plant modelling* activity have taken the initiative for global coordination.

[24] http://gcpcr.grinfo.net/
[25] http://www.generationcp.org/bioinformatics.php
[26] http://www.generationcp.org/capcorner.php?da=0794844

The EMBRAPA platform is being structured across two centres of excellence (Sete Lagoas-MG and Santo Antonio de Goias-GO) and five reference sites (Janauba-MG, Porangatu-GO, Teresina-PI, Parnaiba-PI and Petrolina-PE) in Brazil. For all sites, climatic conditions and soil physical and chemical properties have been carefully characterised. Soil spatial variability at the different sites has been determined, irrigation systems have been installed and evaluated, and water flow rate and water management monitoring devices have been installed. Experiments have been conducted using limited numbers of genotypes of maize, sorghum, rice, wheat, common bean and cowpea. However, Brazil's regulations and quarantine rules have delayed the arrival of new materials from outside the country.

A detailed exercise of target population of environments (TPE) characterisation for rice and maize in the Brazilian Cerrados (a key ecoregion) has been completed. Similar work is being finalised for sorghum in African environments in relation to drought and photoperiod. Data suitable for developing model-assisted phenotyping approaches in studying genotype by environment (GxE) interactions have been acquired in Janauba for maize and in Porangatu for rice.

In order to improve crop models, quantitative trait loci (QTLs) for leaf expansion rate and anthesis-silking interval (ASI) have been integrated in the APSIM (agricultural production systems simulator) crop model platform, making it possible to virtually explore the effect of these QTLs on yield across a wide range of drought patterns (Brazilian maize TPE). The whole-plant growth model ECOMERISTEM has been adapted and successfully tested for its capacity to assist high-throughput phenotyping using a mapping population and using a diverse representative sample of rice.

A global inventory is being made of the phenotyping capacities accessible to GCP worldwide. Two questionnaires (field and non-field) have been developed to capture information for assessing the phenotyping sites and their resources in terms of science, local capacity, methods and human resources. The target crops included maize, rice, wheat, pearl millet, sorghum, groundnut, cowpea, chickpea, cassava and sweet potato. Of 107 questionnaires distributed, 24 field and 13 non-field questionnaires have been returned from 18 locations. A shorter version of the questionnaire has been designed to distribute to additional targeted groups.

1.4 Identification of favourable genes and superior alleles through association studies

Association studies, which relate genes (or chromosome segments) to desirable phenotypic features, and which identify alleles (or haplotypes) that are most favourable, require comparison of molecular and phenotypic data. Such comparisons are incorporated into the plans of various projects using different types of population in maize, rice and barley, under the coordination of CIMMYT, CIAT and ICARDA, respectively. Valuable data have been generated, and final synthesis and actual association analyses have begun.

The most typical study involves maize, using single hybrids with 350 inbreds from a diversity panel. Phenotypic data have been obtained from five field locations, of which four yielded quality data suitable for association analysis. Phenotyping included twelve traits in all sites. In addition, root conductance and chlorophyll content at the beginning and the end of the stress treatment were measured in Mexico and Thailand (in the drought cycle only). Samples of leaves, silk, and ear tip from lines under both well-watered and severely stressed conditions were collected at the time of flowering and sent to Cornell University, USA in June 2007. Metabolite analysis has been completed for sucrose and glucose, and measurements of abscisic acid (ABA) and ABA glucose ester (ABA–GE) were nearly completed in 2007. An SNP chip bearing 991 SNPs in genes of interest and 545 high information content SNPs has been created with the biotechnology company Illumina, and is publicly available.

Implementation of a set of association studies planned for groundnut, chickpea, cowpea and common bean started in mid-2007.

1.5 Development of novel population approaches for relating genotypes to phenotypes

Besides typical association studies which compare phenotypic diversity to molecular variation at target loci, the existence of LD in a species allows the development of LD-based mapping approaches using anonymous markers. A whole-genome survey is being attempted in sorghum with the development of a dense coverage with DArT markers. Current efforts concentrate on integrating mapping information, both recombinational (cM) and genomic (sequence-based, using newly released sorghum macromolecules), on the DArT markers.

Populations obtained from widening the current germplasm base can also serve both breeding and analytical objectives. This is the case for rice, by the production of novel materials through systematic introgression of chromosome segments from related species into cultivated rice, namely *Oryza glaberrima* (already in advanced generations), *O rufipogon*, *O meridionalis*, *O barthi*, and *O glumaepatula*. The populations are now at the BC3 stage and should be ready by mid–2009 for use in genetic analyses to identify key genomic regions involved in target traits. Advancing the generations for

increasing the resolution is being optimised. As an illustration, the progeny with *O meridionalis* involved 43 BC1F1 lines which bear 59 alien chromosome segments covering all twelve chromosomes; the BC2F1 materials are being typed at Cornell University for reference SSR markers covering the genome, whereas the BC3F1 seed has been produced at CIAT and is ready for further propagation after molecular-based screening.

Lessons learnt

The main product of SP1 activities will be the reference samples proposed to the global community as material for integration of research efforts in the future. This raises three particular issues that SP1 is seeking to resolve.

First is the uneven quality of the data produced, detected in some instances using simple coherence indicators, and in other instances by the time taken by the research groups to deliver final data. GCP is now mobilising scientists with the help of SP4 through workshops devoted to data quality; measures are being promoted to establish data quality management in laboratories. Repetition of analyses is practised, either internally on the initiative of the respective data producers, or centrally through a commissioned data quality assessment project. Final data registration will distinguish GCP-certified data packages from unscreened data deposited directly by the source laboratory.

A second issue is the shortage of time for proper in-depth analysis of data destined for scientific publications. Scientists seem under excessive time pressure, yet data analysis and interpretation require time and interactions across disciplines. SP1 is considering promoting data analysis through involvement of students, funded through scholarships and supervised by senior scientists, whose time for this task will also be funded.

The third concern is the management of the seed of reference GCP materials, which requires very close attention and sustained commitment. GCP is considering setting in place a mechanism for attracting long-term involvement of parties who will undertake the mission of verifying, conserving, multiplying and distributing the seed, while applying the highest quality management and developing plans for eventual financial sustainability.

Conclusions and perspectives on 2008

The lessons learnt with the genotyping experience apply more widely, offering broad conclusions on working principles for GCP as a whole. Building a productive research network in a given area has a cost, in that initial intentions and ambitions are circumscribed by institutional and political realities. In addition, determining actual capacities and optimising respective roles require experiment and refinement. It is necessary to connect research and education in order to mobilise complementary communities which will contribute to sustaining the momentum of scientific research for development. This will be done in collaboration with SP5.

Plans for 2008 consist of finalising the development and delivery of SP1's diverse products, and pursuing several research directions in continuity with past efforts. Fundamental work on securing the germplasm foundation must be completed in 2008. Reference samples must all be finalised, associated with characterisation data of validated quality and fully documented and published interpretations of diversity patterns. A global system must be consolidated in order to ensure appropriate seed management and distribution of these samples.

The documentation of biological features which determine the mode of relating phenotype to genotype must be initiated. Linkage disequilibrium patterns and distributions of population genetic parameters for a number of reference genes must be documented for all crops within a period of three years. Support from SP4 will be crucial.

The genotyping platform must be managed to enable progress to be made along several lines. SSR markers must be gradually refined in order to sustain the Genotyping Support Service (GSS) for a community of decentralised users. Appropriate partnerships must be established in order to generalise the use of DArTs as well as to follow developments in model organisms, be they humans, *Arabidopsis* or rice. This responsibility is shared with SP2 and SP3.

Systematic phenotyping must be undertaken, with the dual objective of producing valuable data and consolidating a global platform. SP3 is expected to lead this process.

Subprogramme 2: Genomics towards gene discovery

Rationale

Plant traits for adaptation to environmental stresses are often controlled by complex genetic systems subject to influence by genotype by environment interactions. To combine effectively the right complements of genes and alleles in a breeding programme, we need to have sufficient understanding of the genetic mechanisms underlying the adaptive processes, especially for traits like drought tolerance. Although advances in genomics tools and knowledge from model organisms are important for identifying potentially useful genes controlling complex traits like drought tolerance, translation of the new tools and approaches for agronomic improvement has been limited to a few species.

Therefore, the main objective of this Subprogramme is to provide a scientific and collaborative environment so that interdisciplinary and integrated approaches can be used for gene discovery to dissect the genetic mechanisms underlying the adaptive processes. Specifically, we aim to: a) develop cross-cutting research platforms for efficient application of genomic tools and knowledge to decipher genetic control of complex traits, and b) identify genes to alleviate target problems in the most efficient manner by pooling resources and expertise. Furthermore, to realise the potential of these approaches requires capacity-building in the use of the new tools and creation of a pipeline to translate results into practice.

SP2 will continue to use (and develop, wherever required) genomics and genetic resources tools and technologies, and evaluate interdisciplinary approaches to enhance our understanding of gene function and interaction to improve knowledge of gene systems across crops. We apply comparative approaches to leverage genetic knowledge from multiple plant species to investigate and validate gene functions important to stress tolerance. Interdisciplinary teams are formed to apply the validated genes and/or superior alleles in breeding programmes. While we shall focus more on drought tolerance traits in the coming years, the genes and agronomic characteristics that improve crop resilience in difficult environments will be integrated with drought tolerance.

SP2 activities support the CGIAR System Priorities 2a (*Maintaining and enhancing yields and yield potential of food staples*), and 2b (*Improving tolerance to selected abiotic stresses*). Within the GCP context, SP2 outputs feed into the pre-breeding activities of SP3. The outputs cut across crops and ecosystems, and can be used by researchers and breeders within GCP as well as by the global research community interested in applying genomics to improve agriculture.

Major achievements

While significant progress has been made in different thematic areas, improved germplasm eg, near isogenic lines (NILs) and advance backcross lines have been developed in several cases. Some achievements obtained during 2007 are listed below.

Development and utilisation of mutant populations

First mutant populations were developed for common bean and potato. 'Gain-of-function' mutants for AP2/ERF transcription factor genes (CBF, SHN, HRD) with improved drought tolerance and water-use efficiency phenotype have been identified in rice.

Development of genome infrastructure

Drought responsive ESTs in cowpea and pearl millet, novel sets of SSR markers in chickpea and groundnut and bacterial artificial chromosome (BAC) libraries in cowpea and groundnut have been developed. More than 250,000 non-redundant SNP markers were identified in 20 rice varieties. Genetic maps for *Musa* species with more than 500 marker loci have been developed and 31 A- and B-genome BACs have been sequenced.

Identification of candidate genes, markers and QTLs

QTLs for multiple disease resistances and gene-based markers associated with disease resistance QTLs (dQTLs) for blast resistance in maize have been identified. Gene expression studies in rice revealed regions of correlated expression on some chromosomes that are colocalised within the boundary of known QTLs for drought tolerance, osmotic adjustment and cell membrane stability.

Validation of candidate genes and application of genes/alleles in breeding

Gene-based markers together with candidate SSR markers, diagnostic for salt tolerance (*Saltol*) and phosphorus uptake (*Pup1*) have been identified in rice. Marker-assisted

backcrossing has been initiated to transfer *Saltol* into five popular rice varieties from Bangladesh and the *Pup1* region into two common rice varieties from Indonesia. Gene-based markers for aluminium (Al) tolerance in sorghum (Alt_{SB}) are being transferred to SP3.

Development of improved genetic material for genome analysis and breeding

Advanced backcross lines have been developed in rice for: (i) *Saltol* genomic regions, and (ii) blast resistance and enhanced yield under reproductive drought stress. Similarly, some NILs have been developed for northern/southern leaf blight in maize and for Al tolerance in sorghum.

Activity report

Progress in the Subprogramme is highlighted below, reported by theme.

2.1 Assembly of genetic and genomics resources through consolidating and developing specialised genetic stocks and framework genetic markers

This project focuses on adding value to existing genetic and genomics resources and creating new ones where such investment would open new approaches and leverage collaboration.

First mutant collections have been developed for common beans at CIAT in collaboration with the University of Geneva, Switzerland and for true seed potato at CIP (Centro Internacional de la Papa; International Potato Centre) in collaboration with the Scottish Crop Research Institute (SCRI). In terms of utilisation of mutant collections, reverse genetic screening of 694 stress associated gene (SAG) T-DNA tagged lines for drought sensitivity identified 18 mutant families, out of which 3 mutants (encoding putative lipoxygenase, receptor-like kinase, EDR1 homologue) show cosegregation of insert and phenotype. 'Gain-of-function' overexpression lines for AP2/ERF transcription factor genes (CBF, SHN, HRD) revealed improved drought resistance and water-use efficiency phenotypes at the vegetative stage.

In terms of genomic resources, over 40,000 drought-responsive ESTs were generated in cowpea. These provided 17,000 unique contiguous and single sequences that yielded 3,226 SNPs and 1,806 SSRs. Under the new Tropical Legumes I (TLI) project, 17x coverage BAC library composed of a total of 73,728 clones and 9 cDNA libraries for cowpea, 311 SSRs for chickpea, 160 SSRs and one 6X AA genome BAC library for groundnut have been developed.

In the rice SNP project, a set of 20 diverse rice varieties were resequenced for 100 Mb of the unique, non-repetitive fraction of the genome, and 259,721 non-redundant SNPs were predicted by model-based algorithms. About 71 percent (ca.184,000) of the SNPs were supported by multiple genotypes. The model-based set has been annotated relative to the TIGR release 5 and Rice Annotation Project release 1 gene models, and version 1 of the SNP annotation database[27] has been released to the public.

Another example of developing genomic resource is in *Musa*, where: (i) a genetic map comprising 180 SSR, 380 DArT and 12 resistance gene analogue-restriction fragment length polymorphism (RGA–RFLP) loci was constructed, (ii) BAC DNA pools were produced from Calcutta 4 (A Genome) and Pisang Kluuk Wulung (B genome), and (iii) 31 BACs of A and B genomes have been sequenced and characterised for abiotic and biotic stress-related genes.

2.2 Development of comparative maps within and across species and framework genetic markers for target crops

Generation of common markers and consensus maps across species aims at providing a framework to leverage information across different crop species, some with more advanced molecular information and others with valuable phenotypes.

This project will identify markers that may be functionally conserved across species. Under the TLI project, we plan to develop a significant number of conserved orthologous sequence (COS) markers in cowpea, groundnut, chickpea, common bean and groundnut. In conjunction with a related National Science Foundation (NSF) project, the University of California, Davis (UC–Davis) generated and analysed 2,880 amplicons in the legume species. Cross-species amplification success rates were typically greater than 83 percent and sequencing success rates in the range of 75 percent, with between 800 and 1,000 orthologous amplicons obtained from each species. Currently, parental lines of mapping populations and other diverse lines are being sequenced so that most informative SNPs can be selected for developing the SNP genotyping platform.

2.3 Assignment of genes and pathways to phenotypes through the convergence evidence of genome variation, expression patterns and phenotypic data

This project emphasises comparative analysis to understand the common mechanisms for stress response across species, and to identify candidate genes conditioning stress tolerance

[27] http://irfgc.irri.org

traits. A strategy adopted by these studies is the use of convergent evidence from four main experimental domains: bioinformatics/gene function inference, positional (QTL), expression polymorphism and response to selection (either natural or artificial).

Through comprehensive phenotyping and field testing, QTLs for multiple diseases were found to correlate in maize. For instance, based on QTL mapping in a CML52 × B73 maize population, a locus in maize bin 6.05 was found to condition resistance to two vascular diseases, northern leaf blight and anthracnose stalk rot (ASR). This was confirmed by developing the NIL pair for bin 6.05. However, it needs to be determined whether this is due to pleiotropy or linkage. In the case of rice, gene-based markers were designed for six candidate genes, which, together with several SSR markers, were colocalised with known dQTLs resistant to blast.

Another activity in disease resistance focuses on the unique phenomenon of a lack of rust diseases in rice, and explores the use of non-host (NH) disease resistance in wheat. Based on 811 differentially expressed genes (DEGs), a set of 25 shortlisted wheat NH genes, are currently being mapped in several wheat populations that segregate for NH resistance to rice isolates of the fungus *Magnaporthe*, NH resistance to barley yellow rust, and yellow rust and leaf rust of wheat. This may help to determine the inheritance of non-host resistance.

To identify common mechanisms and candidate genes controlling the maintenance of tissue growth in cereals under water stress, the team led from Agropolis, Montpellier, France, has identified 3 out of 5 QTLs common with those of silk growth maintenance in maize, which colocalise with QTLs for yield. This indicates the possibility of identifying drought-tolerant genotypes at an early stage. In addition, confirmation of the 5 QTLs in insertion lines with different genetic backgrounds present them as strong candidates for genetic determinism of growth maintenance.

The Crop Gene Expression project has accumulated a rich set of genome-wide expression data in rice by undertaking about 100 experiments using a 22K Oligoarray platform. Analysis of the independent datasets revealed two interesting expression patterns: (i) By using NILs for disease resistance, the team detected distinct patterns of pairwise differential gene expression significantly correlated with chromosomal introgressions in NILs. It appears that regions of DEGs can serve as indicators of chromosomal introgressions in plants. (ii) By using sliding window analysis in the Genome Browser database, the team observed patterns of correlated expression among adjacent genes within certain chromosomal regions responsible for water stress tolerance. For example, in the case of expression patterns of anthers under water stress, a total of 23 regions of correlated expression (RCEs) of average size of 443 kb) were detected in N22 (10 RCEs), Moroberekan (7 RCEs), and IR64 (6 RCEs). Three of the RCEs on chromosome 3, 4, and 5 appear to be common among the three rice genotypes. The RCEs and aggregated differentially expressed genes (aDEGs) are being tested for co-segregation with phenotypes in the segregating progeny. This project has strong links with SP4 in terms of developing bioinformatics tools for analysing the gene expression data.

2.4 Validation of genes and pathways through evaluation of under or over-expression constructs or variants (induced or natural) of the target genes

This project comprises studies that have the potential to apply genes and gene combinations for the development of advanced elite lines for on-farm evaluation. It is one component of the interface between SP2 and SP3.

Comparative analysis of wheat and rice transcriptomes and proteomes for water stress at reproductive stages suggested that the peduncle is a major site of fructan accumulation in wheat, but rice fails to accumulate fructans because it lacks the genes for fructan biosynthesis. It was also shown that in the case of rice, drought-induced growth arrest is mediated by abscisic acid (ABA) and contributes to yield loss.

In a second activity, the objective is to identify genes that can enhance tolerance to phosphorus-deficiency and salinity in problem soils in Asia. Progress has been made in fine mapping the *Pup1* (phosphorus uptake) QTL within a 240 kb region that contains 22 candidate genes and the *Saltol* (salt tolerance) QTL within a 1.2 kb region. From both regions, gene-based as well as additional diagnostic SSR markers were developed that are being used in marker-assisted backcrossing. For instance, advanced backcross lines for *Saltol* QTL have been developed in the genetic backgrounds of several popular Bangladeshi rice varieties (BR11, BR23, BR41, BR28 and BR29), while the *Pup1* region is being introgressed in two common rice varieties (IR64 and IR74). In parallel, candidate genes from the *Saltol* and *Pup1* regions are being used for functional validation by transgenic approaches using RNA interference (RNAi) and over-expression.

A third activity aims at identifying genes to alleviate Al toxicity in sorghum and maize in Africa and Latin America. The team completed verification of the cloned major Al tolerance gene

(Alt_{SB}) by analysis of homozygous transgenic T3 *Arabidopsis* lines expressing Alt_{SB}. These lines also showed a large increase in Al-activated root citrate exudation and verified that a member of the Multidrug and Toxic Compound Extrusion (MATE) family is a citric acid efflux transporter that confers Al tolerance in sorghum. The verification also involved Alt_{SB} expression in wheat; transgenic T1 lines of Bobwhite wheat expressing Alt_{SB} were significantly more Al tolerant than wild type Bobwhite wheat lines. Also, in maize, an Alt_{SB} homologue was identified that is a strong candidate for a maize Al tolerance gene that mediates Al-activated root citrate efflux in maize. These analyses indicate the possible utility of this gene for improving cereal Al tolerance in general. Furthermore, a genetic diversity study for Al tolerance in sorghum indicated that there is both significant allelic and non-allelic heterogeneity for Al tolerance in sorghum, which can be used for breeding highly Al-tolerant sorghums. In addition, nine NILs for Alt_{SB}, including those carrying the elite alleles from SC566 and SC283, were developed.

Lessons learnt

A better integration of competitive and commissioned projects was made in 2007, following recommendations from the SP2 Review and Advisory Panel (RAP) member and other experts. To make the GCP investment in stock development, as learnt in 2006, it is important to have institutional commitment for their maintenance and distribution. Therefore, SP2 has emphasised the usage, rather than development of the stocks by the community in a consortium approach.

As a result of consolidated efforts in the area of gene cloning and gene expression studies, gene-based (perfect) markers and candidate gene/QTL region have now been identified for several traits. The validation of these genes/QTLs and their introgression in farmers' preferred varieties in targeted environments is a top priority of the Subprogramme. Indeed, in some cases, significant efforts have already been made, eg, introgression of *Saltol* regions. Identification of superior haplotype/allele combinations for the trait as well as combination of traits (earlier termed 'trait-package') in target environments will be preferred in the future. Although resistance to diseases and soil problems in combination with drought tolerance is desirable, the Subprogramme will focus more on drought tolerance in future years.

Conclusions and perspectives on 2008

Several projects within SP2 already have close collaboration with the projects within other Subprogrammes. In the coming years, we foresee an even stronger integration of activities of SP2 projects with those of other SPs. For instance, collaboration with SP4 will be strengthened in genome analysis and gene expression studies, while validation of identified perfect markers, genes/QTLs and improved germplasm will strengthen ties between SP2 and SP3.

Significant progress has been made in developing basic genomic resources, but more remains to be done, especially for less-studied crops. Therefore, we plan to initiate commissioned research projects on developing both genetic and genomic resources for some of these less-studied crop species (such as sweet potato and pearl millet, whose needs have thus far not been met). These projects are expected to generate resources amenable to molecular breeding. Similarly, a commissioned project on groundnut, in coordination with the TLI project, is expected to generate sequence data and SNP arrays in cultivated groundnut to overcome the low diversity obstacle in molecular breeding. Availability of a 40K array in rice prompted us to enhance our gene expression studies in rice for drought tolerance by using the NILs.

Several SP2 projects are close to completion and are delivering promising practical outputs. Therefore, we anticipate placing more emphasis in 2008 on validating and transferring these products to SP3 for molecular breeding, as well as initiating some other projects to facilitate genome analyses for drought tolerance. While we plan to maximise the use of genomics research (using comparative and omics approaches) in major crop species to identify the QTLs/genes/alleles associated with drought tolerance, we would be interested in developing at least basic genomic resources for less-studied but important crop species in target environments. In 2008, we anticipate delivering a significant amount of genomic resources, eg, markers, genetic and physical maps, ESTs and markers for drought and biotic stress tolerance for four major tropical legumes (cowpea, groundnut, common bean and chickpea) important in sub-Saharan Africa and Asia.

A critical and integrated approach using appropriate genomic tools and strategies with field-proven drought-tolerant genetic material is expected to deliver outputs for molecular breeding for drought tolerance. Focused investment and appropriate combination of competitive and commissioned research projects in 2008 will lead us to achieve our goals as well as build capacity in NARS for using SP2 products.

Subprogramme 3: Trait capture for crop improvement

Rationale

The principal objective of Subprogramme 3 (SP3) is to guarantee widespread impact of new genes, markers and traits in tropical staple crops, and to facilitate rapid and effective uptake of molecular breeding for those crops. Generally speaking, the public sector is characterised by weak research and development links. This is a major impediment to realising the full value of investments in applied research. Accordingly, SP3 aims to link upstream research outputs with practical product development.

SP3 capitalises on the latest advances in genomics, information technology (IT) and biometrics to accelerate genetic progress of simple traits (eg, resistance to biotic stresses), to dissect complex traits (eg, drought tolerance) into component traits, and to develop tools to adopt and adapt the underlying trait genes. In the case of major cereal crops such as rice, maize, sorghum and wheat, advances in research around the world have resulted in gene-based marker systems for components of drought tolerance, with GCP increasingly focusing on value-adding by transforming (or processing) and/or applying pre-existing research outputs for these crops into products for the next set(s) of users. For less-studied crops and crop groups, SP3 carefully prioritises to ensure rapid and compelling proof-of-concept for key crops in each crop group (eg, cowpea and chickpea for legumes, and cassava and sweet potato for clonal crops).

Phenotyping is recognised as essential in drought research, where accurate protocols are a precondition for success. Consequently, establishing, supporting and strengthening phenotyping networks are major priorities for GCP.

SP3 cannot single-handedly attain these ambitious objectives and partnerships are imperative. We therefore establish and cultivate links with plant breeders, involving them in evaluating, validating and refining GCP's molecular breeding technologies.

Finally, SP3's role in product management contributes to the flow, validation and diffusion of products within GCP, and subsequent delivery to breeders in NARS.

Major achievements

Improved access to genetic diversity from related species

For both groundnut and cassava, new sources of disease resistance and drought tolerance have been transferred from wild relatives into cultivated germplasm.

Refinement of marker-assisted selection strategies and technologies

Models have been elaborated to improve marker-assisted selection strategies and promote their integration into conventional breeding. Low-cost and high-throughput technologies developed by GCP are being disseminated to breeding programmes.

Improvement of phenotyping approaches and protocols

Phenotyping networks have been established for different crops, to better address genotype x environment (GxE) interactions for drought, thus promoting quality phenotyping.

Validation of new markers

Molecular breeding systems are being tested under specific environments and in locally adapted backgrounds. Examples include *Striga* resistance for cowpea in West Africa, and salinity tolerance markers for rice in Bangladesh.

Effective marker-assisted selection programmes for biotic and abiotic stresses

Markers for biotic stress resistance and drought tolerance are being used in several breeding programmes, for instance in research on cassava mosaic disease (CMD) resistance in Nigeria, and for drought tolerance in rice and wheat in China.

New tools to improve efficiency of product management

Facilitative templates and a catalogue of products have been developed to better identify, log and describe GCP products, and to streamline transfer to potential users.

Activity report

3.1 Characterisation of segregating populations, identification and/or validation of molecular markers for target traits to increase plant breeding efficiency

By identifying and describing cassava's physiological traits, there is now a better understanding of the biological basis of drought tolerance in the crop. The significance of these traits in enhancing drought tolerance is being tested in different drought-prone environments in Brazil and Africa.

There has been continued progress in several projects to identify and use new genetic variation for useful traits in related species, or from other geographic pools where the crop is grown. For example, twinning genetic and genomic tools has yielded new 'mines' for disease resistance and drought tolerance in groundnut's wild relatives. In addition, a new commissioned project will extend Latin America's potato diversity to Africa by providing African breeders access to a wider range of useful traits. Molecular markers will monitor key resistance genes in elite breeding stocks from several Latin America NARS, and germplasm with proven resistance will be exchanged. For cassava and potato, new and more sustainable varieties will be made available to resource-poor farmers in relatively less developed parts of Africa.

3.2 Development and evaluation of novel breeding or molecular technologies to better serve modern breeding

With the development of new markers across SP2 and SP3, developing and/or testing of the new methodologies is necessary to improve efficiency in molecular breeding. These new methodologies include low-cost and high-throughput markers, refining marker-assisted breeding strategies and modelling these strategies, and developing innovative phenotyping approaches and protocols.

Through a broad-based collaboration between IRRI, CIMMYT and Asian NARS, low-cost technologies and techniques are now being used to screen for bacterial blight resistance in rice, for grain quality in maize, and for and pest and disease resistance in cassava. Methods used include dot-blot assay and micro-plate based (MPB) assay, and high-throughput techniques such as micro-assay based genotyping (MBG) and fluorescence resonance energy transfer (FRET) assay.

To improve screening data (mainly for cereals), new molecular breeding systems, simulation models and decision support tools have been developed. Collaborators in the Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia and the Chinese Academy of Agricultural Sciences (CAAS) are jointly testing such simulation models. The models are being used to pyramid drought tolerance genes via MAS, in collaboration with the wheat breeding programme of CAAS.

SP3 has launched several new projects to improve phenotyping protocols, particularly for tropical legumes such as cowpea. Phenotyping networks have also been established for different crops. The networks will help identify weaknesses, gaps, and training and capacity needs for attention by SP5. They will also facilitate better characterisation and modelling of local environments and drought scenarios worldwide. In addition, the new projects are also testing new innovative phenotyping traits such as the use of thermal imaging and stable isotopes, particularly ^{13}C.

3.3 Marker/allele validation in adapted germplasm under target environments

The general objective of this multi-location theme is to validate, under target environments, alleles and markers identified and developed through GCP projects. Sequence characterised amplified region (SCAR) markers developed by IITA for *Striga* resistance in cowpea are being tested in several breeding programmes in West Africa. Markers for salinity tolerance in rice (from IRRI) are being validated in Bangladesh. The impact of a major sorghum Al toxicity tolerance gene (Alt_{SB}), identified through collaboration between Cornell University (USA) and EMBRAPA is being tested in Niger.

3.4 Application of molecular markers in breeding programmes

There has been significant progress in applying molecular markers to breeding. At the National Root Crop Research Institute of Umudike, Nigeria (the leading cassava producing country in Africa), cassava selection is now done with markers for CMD.

Similar progress is expected for sweet potato. Sweet potato virus disease (SPVD) is a complex of two viral diseases, the sweet potato feathery mottle virus (SPFMV) and the sweet potato chlorotic stunt virus (SPCSV). SPVD is causing serious yield losses, especially in high-virus pressure zones in sub-Saharan Africa. Resistance to the disease has been found in the clone 'Resitan' and the objective is now to introduce resistance into African local germplasm.

CAAS has developed drought-tolerant rice cultivars in China by pyramiding QTLs from diverse origins, and similar steps are being followed for wheat. Activities include establishing a phenotyping network linking the four provinces of Ningxia,

Shanxi, Henan and Hebei, as well as creating a CAAS-facilitated genotyping platform for Northern China. The objectives are to identify drought-tolerant QTLs and elite Chinese wheat backgrounds, then characterise them in different target environments. Candidate accessions with target genes/markers and elite Chinese wheat backgrounds will be identified for molecular breeding.

Integrating genomic tools into conventional screening is expected to accelerate considerably the development and release of NERICA (new rice for Africa) cultivars for West Africa. Drought-tolerant lines have been selected among various *Oryza glaberrima* accessions and interspecific (*O. sativa*/*O. glaberrima*) breeding lines. This germplasm is being genotyped using a genome-wide set of SSR markers in order to characterise quantitative trait loci associated with recovery ability and resistance to rice yellow mottle virus and bacterial leaf blight. Finally, NARS scientists will be supplied with selected interspecific lines (new NERICA lines) having desirable traits, to facilitate further evaluation and dissemination in West Africa.

3.5 Product management implementation

Several tools have been designed and implemented to improve product management and consequently ensure optimal flow of upstream research outputs to more applied research within GCP. As part of product management, new templates now facilitate identification and further processing (if necessary) of outputs and products. A catalogue of products has been developed that provides for each product background information and any other necessary information to elucidate next steps, be they further processing within or outside GCP, transfer to other partners, validation or delivery. This has considerably streamlined and systematised the flow of information and products (eg, new protocols and technical tools, markers, germplasm, etc) across different GCP projects. Consequently, there are now new connections between projects, arising from the regional and thematic 'crop platforms' which have rekindled and rejuvenated interactions between scientists. Pilot product management exercises have been carried out and several commissioned project are now conducted in collaboration with NARS in Asia and Africa to evaluate and use markers, germplasm and protocols from upstream research projects.

On-site visits have continued, further expanding GCP Management's knowledge on project capacities to generate, use and disseminate research products. With this renewed focus on products as GCP projects mature and become increasingly integrated, another result is greater and more frequent communication between the SP3 Leader and project Principal Investigators (PIs).

Lessons learnt

Exciting progress has been made in many areas fundamental to GCP's product development pathway, and in particular in applying MAS to a variety of traits, including drought tolerance. In GCP's research-delivery pathway, SP3 is pivotal, positioned to be primarily responsible for applying technical outputs flowing from SP1 and SP2. The increasingly concerted collaboration and interactions between GCP projects and resulting synergies have spurred progress both upstream and downstream along the research–delivery continuum. More and more national research programmes are laying greater emphasis on validating and refining molecular breeding technologies, and GCP aims to be in step with them.

Conclusions and perspectives on 2008

In 2008, we expect to have more projects and activities aligned to GCP's renewed strategy and refocused research priorities. For this purpose, SP3 has identified several 'flagship' projects for the coming year. One such will use *O glaberrima* to improve disease resistance and drought tolerance in rice. Enhanced tolerance to Al toxicity and salinity will be also developed in sorghum and rice, respectively. Other projects will be on cassava, potato and sweet potato germplasm with enhanced resistance to diseases, thereby tackling the crippling factors limiting yield of these food crops in Africa. In most cases, marker transfer will require capacity-building by SP5 to strengthen partner expertise in MAS. Projects on drought tolerance (for wheat in China and North Africa, for rice in Southeast Asia and for tropical legumes in Africa) will benefit from the projected phenotyping networks and strengthened phenotyping capacity (in collaboration with SP5). These projects are designed to disseminate and scale up germplasm with enhanced tolerance to drought across several crops and regions.

Subprogramme 4: Bioinformatics and crop information systems

Rationale

The value of the data generated in the first three Subprogrammes largely depends on how those data are captured, stored, managed, analysed and made accessible to GCP Consortium members and the rest of the world as international public goods. How these data are analysed depends, in turn, on the analytical tools and other information sources available. SP4 addresses the challenge of linking and integrating information components and analytical tools into a coherent information platform. A bioinformatics, biometrics and advanced data management system is being designed to support an integrated information network for genetic resources, genomics and crop improvement. This platform will provide access to the data generated in GCP and will provide tools to analyse them. Furthermore, it will link GCP data and tools to global biodiversity and bioinformatics networks. Finally, the users of this infrastructure for data handling and analysis are supported through training and assistance in experimental design and in data handling, storage and analysis.

The development of a platform to link and integrate databases and software tools had (and still has) a number of components. Firstly, numerous local systems are already in place. The challenge of combining them into one integrated system was quite daunting, given that we have very limited latitude in dictating the architecture and organisation of existing systems, whether within or outside the GCP Consortium. Secondly, the elements that already exist within the GCP Consortium must meet certain quality standards, and must be accessible. GCP believes that data are managed best when they are managed as closely as possible to where they have been generated. This strategy allows proper data curation in terms of corrections and additions to the data, and avoids ownership problems. However, it also requires an appropriate level of skills and facilities, which is an issue that is also addressed in SP4. Thirdly, to ensure proper data handling in all of the GCP Subprogrammes, support was needed in the selection and integration of tools and data sources, in the creation of new tools and information sources and, last but not least, in support to the scientists using these tools.

Major achievements

SP4 has, in its fourth year, reached a stage of maturity: the basis of the information infrastructure has been created, at both the technical level (programming tools, software architecture, standards) and at an organisational level (training of staff, implementation of initial web services). Use case-specific applications fitting in the GCP information infrastructure can now be developed much more easily. Particularly notable achievements include:

Establishment of the GCP Central Registry

As part of the overall strategy to provide optimal access to data from GCP projects, a searchable repository[28] for data sets has been created where all data sets created in GCP are listed, naming the PI and giving details about availability, and where data sets can be accessed, preferably in a standardised GCP-defined fully interpretable format.

LIMS from ICRISAT converted to open source and installed at BecA and IITA

To create added value to the Laboratory Information Management System (LIMS) developed by ICRISAT, GCP supported converting this LIMS to open source and improving its documentation. The result has been installed at two institutions in Africa, namely IITA and Biosciences Eastern and Central Africa (BecA).

Pipeline for expression analysis established

A complete data storage and analysis pipeline has been set up, making use of the GCP High-Performance Computing (HPC) facilities. The result can be used by all GCP scientists working in expression analysis.

Methodology for QTLxE analysis developed

To improve the analysis of QTL identification experiments, a methodology was developed that allows simultaneous analysis of experiments from different years and locations, thus improving estimates on locations and effects of QTLs.

Activity report

The activities in SP4 closely follow the Subprogramme's themes in the Medium-Term Plan (MTP) published annually by GCP. The three SP4 themes and corresponding activities are described below:

Infrastructure: Facilitation of information flow of ongoing research, both in terms of data and in terms of communication between the researchers.

[28] http://gcpcr.grinfo.net/

Improvement: Creation of facilities to support IT and bioinformatics applications in the GCP Consortium.
Support: Support to other GCP Projects in terms of software tools and data management.

4.1 Infrastructure

The first theme addresses the question: 'How can the information flow between GCP researchers be organised to maintain local curation of data and tools, while also allowing optimal access?' Thus, it aims to create a platform for exchanging information.

The GCP data handling and analysis infrastructure is based on web services technology that allows the 'wrapping' of local databases and analysis tools and making them accessible to the world (ie, machine-readable) via the Internet. Obviously, users then need an interface to access these web services. Finally, a solution is also needed to handle datasets that are not yet available as a web service, or that need to be used outside this infrastructure. These elements were implemented in seven projects with corresponding outputs.

The first project targeted a common language for data exchange protocols. Built on the foundations of the existing 'GCP Domain Models', the project concentrated in 2007 on ontologies. This involved a wide diversity of actors, coordinated by Richard Bruskiewich of IRRI, and resulted in basic ontologies for the passport, genotyping and phenotyping domain.

The second project, coordinated by Milko Škofic (Bioversity International, Rome), is concerned with training staff and installing web services technology for GCP member institutions. In the last two years, web services technology has been installed for most GCP data providers. The focus in 2007 was on consolidating user support. Helpdesk support was organised, reference and training materials were created and disseminated, further mapping was done between local schemas and GCP domain models and, finally, the information offered via the web services was monitored.

The third and fourth projects aimed at providing and sustaining a short-term solution through allowing the storage of GCP data in Excel spreadsheets in a highly standardised and fully interpretable format, thus facilitating uploading to a repository where all GCP data are documented and, in principle, made available. The first component was coordinated by Guy Davenport of CIMMYT, but was delayed due to problems in recruiting appropriate staff. Nevertheless, first steps were taken to develop templates for SNP and expression data, integrity of the available data sets was analysed, and finally, tools for users to populate the templates were developed. The second component, the repository part, coordinated by Tom Hazekamp (Bioversity International, Rome) sought to proactively increase the number of data files by scrutinising proposals and reports, and approaching the PIs of projects that were committed to produce data. As a result, the number of registered datasets increased in the period between September 2006 and 2007 from 78 to 134, and the number of uploaded files increased from 21 to 72. In addition, new features were added to the website, the interface was improved and a helpdesk was created to support users in uploading data to the Central Registry.

The fifth project, coordinated by Martin Senger (European Bioinformatics Institute) ensured that the 'foundation' technology for GCP's web services stayed up to date. Soaplab2, a tool automatically generating and deploying web services on top of existing command-line analysis programs, was released. In parallel, active support for the GCP platform developers was continued. To actually apply the web services in high-end applications, another project, coordinated by Mathieu Rouard (Bioversity International, Montpellier) implemented use cases for each of the first three SPs. The most successful was the SP2 use case where a web-based tool was developed, based on the GreenPhyl database of the Centre de coopération internationale en recherche agronomique pour le développement (CIRAD). Called GOST (GreenPhyl Ortholog Search Tool), it predicts phylogenomic relationships between a particular gene and *Oryza* and *Arabidopsis*, allowing prediction of the function of that gene. This original approach will be developed further in 2008. After integration with Dayhoff (see below), it is expected to be a showcase application for SP4.

The last project in this theme, a relatively small one coordinated by Thomas Metz (IRRI), maintained and supported the use of CropForge and the GCP Wiki. CropForge is a software engineering and collaboration platform for open source software development. It hosts 73 projects, 22 of which are related to GCP, and has 184 registered users. The GCP Wiki is a Wiki platform for collaboration within GCP. It has 188 registered users and includes about 590 content pages.

4.2 Improvement

The second theme concentrated not on only improving data quality and handling, but also on improving access and analysis tools. The quality, management and choice of analysis tools are at the discretion of GCP Consortium members. However GCP tries to create synergy, improve access to mutual resources and create additional resources. The portfolio of activities in this theme included three projects:

The first project, coordinated by Graham McLaren (IRRI), focused on access to the data and tools from Theme 1 above. Three use cases were targeted for development this year. The first was a GCP Platform-compliant web interface for diversity analysis of GCP genotyping data. The second was a GCP-compliant database and platform for access to third party analysis tools for microarray and sequence analysis. The third was a GCP platform-compliant stand-alone tool for analysis and visualisation of data for molecular breeding. Progress has been made on all use cases, with prototypes completed and deployed for the first two and a design developed for the third. All these applications are, or will be, part of the GCP information platform that can be accessed either via web browsers (Koios) or with a stand-alone client (GenoMedium).

The second project in this theme, coordinated by Thomas Metz (IRRI), deals with data quality improvement and assurance. The emphasis of the project was to fund workshops in strategic areas of data quality, covering 'passport data quality assessment and improvement', 'ISO quality certification for genebanks and service laboratories' and 'LIMS adoption and collaborative development'.

The final project, coordinated by Anthony Collins of CIP, has continued to provide access to HPC capacity, and support use by GCP scientists based on the three sites with HPC nodes: IRRI, ICRISAT and CIP. As well as maintaining the HPC operations on geographic information system (GIS)-based site characterisation and adapting the climate interpolator for use on the HPC, activities concentrated on extending the software resources available in the comparative genomics and population genetics toolbox, and embedding HPC analysis directly into the GCP platform using SoapLab2 to allow HPC analysis to seamlessly integrate into biological workflows.

4.3 Support

Now that GCP is going full-steam, and data are becoming available, the need for support in the handling and analysis of these data has become even more apparent. A number of dedicated activities have been developed that create specific tools and methodologies for this support.

Of six projects in all, the first two deal with direct support to scientists in SP1 and SP2 respectively. The first project, coordinated by Marco Bink of WUR, aimed at providing basic statistical support for germplasm data analysis to SP1 scientists and also to scientists involved in the GCP Genotyping Support Service (GSS)[29]. The project organised well-received workshops and gave one-to-one support on issues such as experimental design, phenotypic and genotypic data curation, quality control, diversity analysis, etc. Also, the functionality of the DARwin software package was improved with respect to diversity analysis, and a website was created to provide access to training materials on association mapping and QTL analysis.

The second project, coordinated by Guy Davenport (CIMMYT), concentrated on supporting SP2 scientists working in the area of expression array analysis. A database tool for collating GCP microarray experiments was created, with a central repository at IRRI. Data analysis methods and pipelines were made available as downloadable stand-alone tools or in an HPC web portal analysis service, including appropriate documentation. A workshop on this methodology was organised, and individual support provided to GCP scientists.

The third project under this theme, coordinated by Subhash Chandra (ICRISAT), has further developed iMAS, the Integrated Marker-Assisted Selection System for use by NARS partners. Based on user feedback from a testing workshop, iMAS has been extensively refined and Version 1.0 of the system has been released and distributed to end-users. The system currently comprises six modules: data validation, phenotyping, linkage map building, QTL analysis, genome display and marker-assisted backcrossing (MAB) sample size. A detailed user manual has also been prepared.

The final three projects were all extensions of projects scheduled to end in 2007. They deal with the development of methodology and software for specific analyses: eco-physiological statistical analysis of GxE and QTLxE, coordinated by Fred van Eeuwijk (WUR), the display of ortholog-functions coordinated by Richard Bruskiewich (IRRI), and creating and mining a database for gene expression data, coordinated by Shoshi Kikushi of the National Institute of Agrobiological Sciences (NIAS), Japan. All three projects succeeded in their objectives. The GxE and QTLxE project resulted in novel methodology that was applied in a number of cases where 'old' QTL mapping datasets were re-analysed. A workshop was also organised to deliver these results to the GCP audience. The ortholog project resulted in a comparative plant stress-responsive gene catalogue (called Dayhoff): a compendium of protein families, phylogenetic trees, multiple sequence alignments and associated experimental evidence. The central objective of this resource is to elucidate orthologous and paralogous relationships between plant genes. Finally, the database for gene expression data was

[29] http://www.generationcp.org/capcorner.php?da=0794844

established, storing data from several rice microarray systems, and providing a pipeline system for the cis-element search in the promoter region of the genes.

Lessons learnt

The early years of SP4 have been relatively successful, especially with respect to projects for developing tools and methodology for direct support to users. In software development, however, we have seen that the quality of the products is a direct function of the role of the end-users in the development. Therein lies an inherent problem, since developers are frustrated by persistent unworkable requirements from users, and users are generally too busy to explain their needs to developers. To mitigate all of this, SP4 now tries to include named users in software development projects right from the beginning.

Due to the distribution of GCP actors across the globe, it is very difficult to keep in constant touch with all PIs and other key people involved in GCP projects. This would not be a problem if the agreements on outputs of the projects would meet 'business standards'. However, so far they have not. In GCP organisational culture, contracts are still rather vague, and where GCP managers articulate more concrete requirements, they are not necessarily followed. The only way out is to slowly change the culture and introduce much more binding contracts with quantifiable outputs and verifiable time plans. In addition, all possible means of communication should be explored and exploited. For example, in SP4 we are trying to have more frequent Skype and telephone conversations and video conferences.

Conclusions and perspectives on 2008

It has taken longer than initially planned, but the basic infrastructure for the GCP information platform has been established and is now moving from development into a maintenance phase. This implies that investments can gradually be reduced. Parallel to this reduction, we can see an increase in support to GCP scientists. This has to do with the fact that GCP data have been produced and now need to be stored and analysed. Users need to be supported in selecting and applying the appropriate tools. Anticipating this increase in demand, an initiative was envisaged in 2006 to create an SP4 helpdesk giving access to all expertise and resources in SP4. Due to the GCP financial situation, this initiative was postponed but it is now back on track The helpdesk will give an answer, within two working days, to questions on SP4-related issues, by identifying an expert to approach and/or the tool to be considered, website to be visited, etc.

In analysing recently generated data, we are finding out that not all data are of sufficient quality, pointing to the need for systematic quality assessment. Therefore, as a pre-emptive measure, methods will be developed to improve and assess data quality in the field and laboratory, while continuing to evaluate existing data collections.

Finally, we are entering the last year of the first phase of GCP. The impact of GCP has been large, and SP4 is pleased to have contributed to this effort. SP4 has tried to increase awareness that biometrics and bioinformatics are the disciplines that add value to data, and that investments in these areas are sound and will easily pay off. Scientists are often tempted to generate more and more data but it is only in the analysis that we can create value from those efforts.

Subprogramme 5: Capacity-building and enabling delivery

Rationale

Subprogramme 5 is cross-cutting and mandated to both build capacity and assure delivery of products from the technical Subprogrammes. SP5 fulfils its role not only by building technical capacity for the efficient implementation of research activities in the other Subprogrammes, but also by facilitating the flow of GCP products through the research–delivery continuum. For smooth product flow, SP5 works on international and national policy questions to facilitate delivery. In addition, the Subprogramme conducts *ex ante* impact analysis at the Programme level to inform GCP's research focus in terms of crop, region and trait, for better decision-making and to guide prioritisation and resource allocation.

For GCP, capacity-building is crucial for product delivery. Collaboration between NARS in the developing world and GCP research partners is essential to ensure long-term sustainability of the research platform and toolbox. For GCP to have impact in farmers' fields, such impact is directly proportional to NARS' ability to use GCP's technical outputs in their breeding programmes, and how far these outputs address the needs of the farmers and consumers for whom the NARS work. Indeed, high-calibre researchers in target regions are the best placed to effectively meet the needs of poor farmers, thereby guaranteeing adoption and dissemination of research products. Therefore, building the capacity of national collaborators directly serves GCP's mission. Good links with NARS are also the cornerstone of any proficient research-for-development portfolio.

Effective collaboration with NARS is premised on the twin pillars of adequate, relevant and up-to-date training on the one hand, and support for research and necessary infrastructure on the other. Mindful of this, SP5 is designed to substantively enhance the research capacity of promising plant breeding programmes.

As GCP products increase, SP5 is increasingly processing and/or promoting these products through value-adding, thus assuring delivery and enhancing return on investments. Product delivery is not a given; it requires strategic and sustained effort.

In contrast to the scenario at the time of GCP's founding, SP5 is now in a concerted consolidation phase, evolving to fewer but more sharply focused activities firmly embedded in GCP's other Subprogrammes.

Major achievements

Awarding of the first Capacity-building *à la carte* projects

A competitive call in March attracted proposals from research teams in developing country NARS requesting support for tailored capacity-building. Eighteen applications were received and six grants awarded to teams for their personalised training, equipment and expert technical backstopping. These teams will hopefully grow to be GCP champions and turn into excellent links for product delivery. By supporting teams, we assure greater sustainability from capacity-building investments. Moreover, the focus is on teams that are already engaged in GCP projects.

Implementing delivery plans

August saw the launch meeting for the 2006 competitive projects. The meeting brought together project PIs as well as collaborators and users of the anticipated research outputs. Together, researchers and users of the research outputs drew up a shared Delivery Plan for their project. This involvement of users in GCP Delivery Plans from the outset of each project ensures that their needs inform research implementation.

Conclusion of the first phase of the Genotyping Support Service

The testing phase of the Genotyping Support Service (GSS)[30] was completed. It served the needs of seven developing country teams working on germplasm management and marker-assisted breeding (involving data analysis of 267,791 data points for four crops). All the teams developed implementation plans to advance their research or germplasm management in their home institutions. In all seven cases, each team reports that, as a result, they were able to undertake research that they would not otherwise have undertaken. Based on these positive results, a second call was opened in August and 37 proposals were received.

[30] http://www.generationcp.org/capcorner.php?da=0794844

Establishment of the first community of practice

The community of practice model was pioneered in Southeast Asia led by Thailand and involving Cambodia, Myanmar and Laos. MAS in backcross introgression lines in Thailand was followed by trait validations in target locations in participating countries.

Activity report

5.1 Creating a platform of training resources and a cadre of trained scientists to apply advanced technologies and add value to GCP products

Two sets of training materials were completed on 'Dynamics of diversity of cultivated plants' and 'Basic genomics and comparative genomics'. An online set of materials on basic bioinformatics will be released in the last quarter of 2008. In addition, SP5 is working on two independent sets of learning materials for MAS and phenotyping for drought.

On the policy front, an online course in April on genetic resources international policy issues[31] registered 24 participants. The course was coordinated by Wageningen University. Later in the year, in September, a workshop was convened to bring GCP researchers up to speed on issues related to plant genetic resources in terms of the new rules established by the Multilateral System and the Standard Material Transfer Agreement of the International Treaty on Plant Genetic Resources for Food and Agriculture. Implemented by Bioversity International, the workshop attracted 23 researchers.

5.2 Cultivating research and learning opportunities for GCP collaborators and NARS scientists to further GCP mission and progress

A call for fellowship applications was opened in December 2006 with a deadline of the end of January 2007. Twelve applications were received from Bangladesh, Benin, China, Côte d'Ivoire, Egypt, Ethiopia, Ghana, India, Morocco, Nigeria and Philippines. Five fellowships were awarded as detailed in Box 3.

The 2007 call for the GCP Travel Grants attracted 25 applicants across 17 countries. The call was oriented towards hands-on training and opened at the end of January 2007. In total, 16 grants were awarded: 8 apiece for participation in GCP's Annual Research Meeting (ARM) in Benoni, South Africa and for training. The travel grants to the ARM, mainly targeting researchers working in national programmes in Africa, are listed in Box 4, and the travel grants for training in Box 5.

GCP was invited to the 2nd International Conference on Rice for the Future during BioAsia 2007 held in Bangkok in November, organised by the National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand. This welcome opportunity was used to gather GCP teams working on rice for a workshop, with travel grants awarded to national collaborators from Bangladesh, Cambodia, India, Indonesia, Laos, Myanmar and Vietnam. The workshop was entitled 'GCP rice research products and delivery in Asia'. It directly contributes to GCP's drive to build platforms to encourage and facilitate delivery (see 'Construction of systems for ensuring product delivery' below). The purpose was to stimulate discussions and brainstorming in order to harness interdisciplinary and regional synergies, elicit feedback on users' priorities, and promote the dissemination of GCP products.

A competitive call for Capacity-building *à la carte*[32] was opened in March 2007. The main purpose of the programme was to strengthen NARS teams working on GCP projects to apply knowledge and/or outputs in their home countries. The award provides training, equipment and technical backstopping. A total of 18 proposals were received, of which six from Africa and Asia were selected for their fit with the expectations of the call (see Box 6). The projects are led by researchers from NARS, so contracts were prepared accordingly and funds disbursed directly.

[31] http://www.generationcp.org/distantpolicies/page42.html
[32] http://www.generationcp.org/capcorner.php?da=0775534

Box 3: Fellowships awarded in 2007

Name	Institute	Country	Topic	Host
Asrat Asfaw Amele	Awassa Agricultural Research Center	Ethiopia	Genetic investigation for drought tolerance in common bean (*Phaseolus vulgaris* L)	CIAT, Colombia
Gustave Djedatin	Université d'Abomey–Calavi, Cotonou	Benin	Characterisation and molecular introgression of bacterial leaf blight resistance gene in rice	IRD, France IRRI, The Philippines
Dongcheng Liu	Institute of Genetics and Developmental Biology, CAAS	China	Analysis of leaf and root growth kinetics and related gene expression in rice during progressive soil drying	
Habibul Bari Shozib	University of Dhaka	Bangladesh	Use and application of mapping software to analyse polymorphism data in salt sensitive and tolerant BC2F2 progeny from a cross between salt tolerant rice landrace, Boilam and farmer-popular rice, BR26 and BR27, in an effort to find linkage between tolerance and specific DNA markers	IRRI, The Philippines
Deless Thiemele	Université de Cocody, Abidjan	Côte d'Ivoire	Characterisation and transferring useful genes from *O. glaberrima* to *O. sativa* by molecular markers: A case study of resistance to rice yellow mottle virus	WARDA, Benin

The University of KwaZulu–Natal proceeded with recruitment of a molecular breeder professor at the African Centre for Crop Improvement (ACCI). However, the selected candidate declined the position and therefore recruitment has recommenced.

5.3 Construction of systems for ensuring product delivery

GCP embarked on the 'Project Development Guide', a tool for information and guidance on best practice for GCP-funded projects. It covers project design, management and implementation, and review, and it is organised around eight themes: Project leadership; Product user specifications; Governance and decision-making; Project planning, critical path analysis and risk management; Project monitoring and reports; Project phases and milestones; Interdisciplinary expertise and communication; and Freedom to operate. The tool will be completed in 2008 and will be publicly accessible through the GCP website.

Box 4: Travel grants awarded to attend the 2007 GCP Annual Research Meeting

Name	Institute	Country	Subprogramme
Maxwell Darko Assante	CRI	Ghana	SP5
Gustave Djedatin	Université d'Abomey	Benin	SP5
Heneriko Kulembeka	ARI	Tanzania	SP5
David Mariotte	IIAM	Mozambique	SP3
Nsarellah Nasserlehaq	INRA	Morocco	SP3
Elizabeth Okai	CRI	Ghana	SP5
Emmanuel Okogbenin	NRCRI	Nigeria	SP5
Francisco Vilaró	INIA	Uruguay	SP3

Two project launch meetings took place with major emphasis on product delivery. One brought together the winning teams of GCP's 2006 call for competitive research and was held in Mexico 6–8 August. The second was the first meeting of the Tropical Legumes project teams and was held in Rustenberg Kloof, South Africa, 18–23 September. Delivery Plans and the GCP Delivery Plan Kit (DPKit) were introduced to participants, who then completed their own DPKit in close collaboration with project partners who also attended the meetings. The DPKit collects and collates information on project objectives, expected products, applications and users, constraints and capacity needs for product transfer, timeline and IP considerations for existing and new technologies.

The establishment of a community of practice (CoP) started with the project 'CoP applied to rice production in the Mekong Region: Quick conversion of popular rice varieties with emphasis on drought, salinity and grain quality improvement'. The project is based on workshops to apply MAS in Thailand (with BIOTEC as the lead institution), followed by generation of introgression lines and trait validation in target locations in collaborating countries of Cambodia (at the Cambodian Agricultural Research and Development Institute, CARDI), Laos (at the National Agriculture and Forestry Research Institute, NAFRI) and Myanmar (at the Department of Agricultural Research, DAR). The first MAS workshop was held in Thailand (21–30 May, 2007); others for larger audiences followed in each participating country. A multi-lingual CD and a website were also developed.

Box 5: Travel grants awarded for training

Name	Institute	Country	Topic	Host
Lalith Perera	Coconut Research Institute	Sri Lanka	Association genetics	NIAB, Cambridge, UK
Claudia Guimaraes	EMBRAPA (Maize and Sorghum)	Brazil	Association genetics	Institute for Genomic Diversity, Cornell University, USA
Chiedozie Egesi	NRCRI	Nigeria	Molecular and modern breeding	University of Washington, Seattle, USA
Jude Obidiegwu	NRCRI	Nigeria	Phenotyping for drought	Lancaster Environment Centre, Lancaster University, UK
Geoffrey Mkamilo	ARI	Tanzania	Phenotyping for drought	EMBRAPA (Cassava and Tropical Fruits), Cruz das Almas, Brazil
Joko Prasetiyono	ICABIOGRAD	Indonesia	Molecular and modern breeding	IRRI, The Philippines
Maxwell Asante	CRI	Ghana	Molecular and modern breeding	IRRI, The Philippines
Soraya Bertioli	EMBRAPA (Genetic Resources and Biotechnology)	Brazil	Phenotyping for drought	ICRISAT, India

Box 6: Capacity-building *à la carte* awards 2007

Team Leader	Institute	Country	Project
Masdiar Bustamamm	ICABIOGRAD	Indonesia	Enhancing capacity of ICABIOGRAD in phenotyping and molecular analysis to develop elite rice lines suitable to Indonesian uplands
Chiedozie Egesi	NRCRI	Nigeria	Marker-aided development of nutritionally enhanced cassava for Nigeria
James Gethi	KARI	Kenya	Capacity-building for characterising maize for water stress tolerance
Ousmane Ndoye	ISRA	Senegal	Application of molecular tools for controlled wild introgression into peanut cultivated germplasm in Senegal
Allen Oppong	CSIR	Ghana	Characterisation of maize germplasm found in Ghana, using the bulking technique
Ghasem Hosseini Salekdeh	ABRII	Iran	An integrated proteomics and genomics approach to discover salt tolerance genes

An area of increasing GCP focus is product marketing and dissemination. A joint document on Product Management, Delivery and Marketing[33] was prepared by SP3 and SP5. For SP5, the document presents the concepts of delivery plans, marketing and dissemination of GCP products and principles for implementation. This document is still a work in progress and will be refined in 2008.

5.4 Development and implementation of support services

Three helpdesks are now operational: the Interactive Resource Center (IRC)[34] in collaboration with Cornell University, USA, the Intellectual Property (IP) Helpdesk[35] (both supported by SP5) and the Data Templates Helpdesk[36] (supported by SP4 and linked mainly to SPs 1, 2 and 3). A fourth helpdesk—the Statistical Support Helpdesk—is under development in collaboration with SP4, and will mainly support GSS. The IRC is intended to be both informational (providing protocols, tutorials, literature and news) and interactive. Scientists are encouraged to submit questions on a range of subjects including laboratory protocols, technical problems, data management, and also on funding and training opportunities. The primary aim in developing the IP Helpdesk is to provide online support and feedback and provide a clearing house for GCP members, partners and stakeholders on IP issues. The Data Templates Helpdesk provides support to GCP researchers in the use of the templates created for the different data sets produced by GCP activities.

The testing phase of the GSS was concluded. Out of 22 NARS teams contacted, seven received assistance and contributed to proving the concept. The administrative process was defined, supporting legal documents were designed in compliance with GCP and international policies, two public and two private service providers were tested and solutions were devised for the problems or difficulties encountered. A total of 267,791 data points were generated for four crops and a data analysis workshop was conducted where each team developed an implementation plan for incorporating the results into their research programmes.

5.5 *Ex ante* impact analysis and impact assessment

SP5 *ex ante* impact analysis activities are intended to support decision-making, priority-setting and resource allocation. Two activities were initiated in 2006, were ongoing in 2007 and will continue in 2008. The first is a CIAT-led project targeting broad-scale but high-resolution global impact assessment for GCP. The project comprehensively assesses priority farming systems, including detailed poverty evaluation in priority areas. It reviews the implications of drought for each GCP crop, with in-depth evaluation of constraints and opportunities related to crop production, thus teasing out factors that could impede, or greatly enhance, the end use of GCP technologies.

The second project led by the Virginia Polytechnic Institute and State University (Virginia Tech, USA) uses *ex ante* impact analysis to project early estimates of benefits of GCP investments, and to validate an approach to impact assessment that might be used broadly in GCP to document progress. The study is based on two projects for rice and cassava. Technology impact pathways were mapped and the current status of the various products summarised. Data were collected on production, area, price and trade for both crops, on losses due to salinity and phosphorus deficiency for rice in Asia, and losses due to green mites, white flies, cassava mosaic disease (CMD) and post-harvest physiological deterioration (PPD) for cassava in Africa and Brazil. Per hectare budgets for the crops were devised, with and without the improved varieties. Economic surpluses are now being analysed. The project has three postgraduate students working on the basic analysis for rice, basic analysis for cassava and projected gender impacts of the cassava products.

Lessons learnt

Implementing the Delivery Plans revealed their significance for the success of research-for-development projects and also clearly pointed to the need for a change in mindset in the scientific community, particularly upstream scientists. One of the key criteria when assessing a research project in a value chain is the identification and timely engagement of partners, especially downstream partners, as early as at the proposal stage. These partners include fellow scientists who will be users of the research products generated. The inclusive and active involvement of users in the project broadens ownership, thus increasing chances of later adoption, but most importantly, ensures that user needs drive the generation of products.

This re-emphasises the need for effective teams in downstream research, notwithstanding the difficulties that this could entail in some cases. Generally, there is a tendency

[33] http://www.generationcp.org/UserFiles/File/Product%20Manag%20Delivery%20draft_final%20version_posted
[34] http://irc.igd.cornell.edu/
[35] http://www.generationcp.org/iphelpdesk.php?da=0629604
[36] http://www.generationcp.org/bioinformatics.php?da=0782837

to overestimate the capacity, and to presuppose the readiness of NARS researchers. Factors hindering progress include insufficient institutional support coupled with inadequate funds for breeding, both leading to weak local programmes and curtailed breeding expertise. This situation demands a more careful assessment of partnerships, as well as special consideration to building capacity tailored to the constraints identified in delivery plans.

A telling illustration of the above is the aforementioned difficulty in recruiting a molecular breeder professor at the African Center for Crop Improvement in 2007, a situation that reflects the scarcity of high-quality researchers in this domain working on plant breeding for the developing world.

Conclusions and perspectives on 2008

GCP is now beginning to generate concrete results and products, whose major impact can only be realised when they reach the intended users. Over the next few years, it will be crucial to allocate resources for using, further processing, packaging and disseminating GCP products and results. This has direct consequences for the SP5 agenda and its enabling delivery function, as reflected in the second part of SP5's title.

Capacity-building will build on the developments and advances arising from GCP research, and focus on training excellence, in particular, training on use of markers for germplasm management and molecular breeding, phenotyping and data analyses.

Tailored support will be offered to ensure continuity of downstream research. This will include planning to bypass or overcome constraints identified in the Delivery Plans, building 'champion' teams empowered by the Capacity-building *à la carte* programme, and in general maximising complementarities with vertical and 'flagship' projects.

SP5 will continue to pay close attention to projects that promote delivery *per se*. These include a suite of support services, such as the ongoing GSS, whose concept will be extended to other GCP products in the near future. To spread impact further and assure sustainability, GCP will also help to establish communities of practice and regional crop platforms. These communities and platforms are critical for effective product delivery.

Financial report

The summary financial reports (statement of income and expenditure plus statement of changes in net assets) for 2007 and 2008 are shown respectively in Tables 1 and 2, and in Table 9. Table 2 shows 2007 allocations by research category. Detailed expenditures for 2007 and 2008 are shown in Tables 3 and 10. Financial information presented for 2007 is based on actual financial figures. The 2008 table is a projection based on anticipated income and expenditure. All the financial tables are in US dollars (USD).

GCP is grateful to the funder community that generously finances the Programme. Agencies and foundations that supported GCP in 2007 include the European Commission (EC), the UK Department for International Development (DFID), the Bill & Melinda Gates Foundation, the World Bank, the Swiss Agency for Development and Cooperation (SDC), the Rockefeller Foundation, the Swedish International Development Cooperation Agency (Sida), the Syngenta Foundation for Sustainable Agriculture and Pioneer Hi-Bred International, Inc. We are also grateful to the Institut National de la Recherche Agronomique (INRA), Morocco, and the Government of Hungary who each provided matching funds for specific GCP research activities.

2007 report

The overall picture for the year was positive. The 2007 income (USD 23.6 million) represented by far the largest income ever received by the GCP for a fiscal year, and is almost double the projection presented in our 2006 Annual Report (USD 12.8 million).

The large increase of actual income over expected income for 2007 was due mainly to a confluence of three factors:

- a very large contribution from the EC for 2007 (about USD 13 million, with 10 percent to be paid in 2008) to compensate for non-payment of the 2006 contribution;
- a new three-year project (2007–2009) on tropical legume improvement for sub-Saharan Africa funded by the Bill & Melinda Gates Foundation, for which the Foundation disbursed USD 3.5 million for 2007; and
- very favourable currency exchange rates; about 75 percent of our donor contributions are in European currencies whereas our income and expenses are reported in USD.

Our 2007 projection was, in fact, very conservative due to several financial uncertainties at the close of 2006. By the end of 2006, only part of our projected 2007 funding had been secured. This, along with non-payment of the 2006 EC contribution, created a potential cash-flow problem requiring an adjustment in the schedule of payments for our research activities. Accordingly, we adopted a contingency plan prioritising financial support to ongoing research activities. GCP scaled down its operational budget to a minimum and put new competitive and commissioned projects on hold in order to be able to guarantee funding for all ongoing research projects for a minimum of eight months into 2007.

With the confirmation of DFID support (USD 5.1 million) in June, we were able to revert to the original workplan for 2007. This meant that we were in a position to support all ongoing projects for the entire year and to initiate the new 2007 projects that had been placed on hold. The new 2007 projects were initiated in August–September, after a six-month delay.

Confirmation in September of the EC contribution for 2007 finally brought us back on track. This large contribution (received early January 2008) gave us the flexibility to reallocate our expenses across our different accounts and to generate a substantial carryover to support commitments in 2008.

So, 2007 was a year of mixed fortunes but had a happy ending. It is emphasised that the uncertainty experienced was not because of funder doubts but rather the necessity to synchronise disbursement to projects based on our workplan with the receipt of funds during the year.

Resources allocated to research in 2007 stood at about USD 14.7 million out of a total expenditure of about USD 17 million (ie, USD 19 million, less USD 2 million which went into our reserve). In terms of direct and indirect costs, about 85 percent of our funds went directly to supporting research and capacity-building for GCP and its partners, with indirect costs accounting for about 15 percent of expenditures.

Carryover from 2007 to 2008

The USD 2 million temporarily allocated to our reserve, as approved by the Programme Steering Committee, will be used to support commissioned activities in 2009. A total

surplus for 2007 of USD 4.9 million added to the USD 7.3 million carryover from 2006, plus our reserve of USD 3 million, boosted total net assets at the end of 2007 to around USD 15.3 million. This figure is higher than original projections, reflecting—in part—inclusion of withheld project funds: GCP requires that the final 20 percent of project funds only be paid after the project delivers on all the obligations in the original project proposal. Thus, the carryover into 2008 includes approximately USD 2.4 million committed for research activities conducted before 2008.

It is critical to underline that this high carryover is required to support 2008 activities until such time as we receive the 2008 contributions from our donors. In December 2007, our financial balance was at the level of our reserve, and we consumed the USD 7.3 million carried over from 2006. Considering the USD 2.4 million already committed, as indicated above, the 2007 carryover roughly corresponds to the 2007 EC contribution received in January 2008. Accordingly, GCP is committed to reduce its carryover if funders do indeed shift disbursement to early in the fiscal year, as has been indicated by EC representatives.

2008 report

Predictions for 2008 are positive, although the precise amounts of the 2008 contributions from the EC and DFID are yet to be determined. The support of these funders remains unwavering and we anticipate receiving firm commitment of their 2008 contribution. Importantly, both the EC and DFID are expected to indicate their support, not only for 2008 but also for 2009 and 2010. This will help GCP to budget more effectively and, therefore, plan for activities over a time horizon extending beyond 12 months.

Given this scenario, and to the best of our knowledge, we project the 2008 income at around USD 16.1 million, plus USD 200,000 as interest. This income, plus part of the carryover from 2007, will be used to support a total expenditure for 2008 of USD 22.3 million. Following this plan, our carryover into 2009 should be reduced to USD 6.3 million plus USD 3 million in reserve funds.

Although the projected budget figure for 2008 is as accurate as possible (Table 9), the workplan for 2008 presented in this report (Tables 11 and 12) does not include a significant portion of the 2008 projects. Omitted is a set of new commissioned projects (for about USD 3.4 million) to be finalised by April 2008 and to be initiated by mid-2008. Similarly, also omitted is a new set of competitive projects to be selected by July 2008 for initiation in September 2008 (for about USD 3 million).

The GCP Management Team remains confident about the financial health of the Programme as we continue to enjoy committed support from our current funders, and there are bright prospects for attracting new funders in 2008. The GCP Management Team, especially the Director, will continue to dedicate special efforts in 2008 to diversifying GCP's funding base to bring in additional funds for the purpose of further consolidating the research agenda and assuring product delivery.

List of financial tables

Unless otherwise indicated, currencies in the financial tables are in United States dollars (USD)

Table 1. 2007 summary financial report: Income versus expenditure

	Actual
Income	
Bill & Melinda Gates Foundation (BMGF)	3,540,404
DFID [1/]	5,058,750
EC [2/]	12,121,979
Pioneer Hi-Bred International, Inc	20,000
Rockefeller Foundation	342,840
Sida [3/]	132,651
SDC [4/]	398,300
Syngenta Foundation for Sustainable Agriculture	25,000
World Bank	2,000,000
Subtotal	**23,639,923**
Interest [5/]	**336,984**
Total income [6/]	**23,976,907**
Expenditure	
Salaries and benefits	849,432
Operational travel (GCP management)	78,142
Conferences and PSC expenses	299,254
Office supplies and services	78,792
Vehicle expenses	10,812
Printing and design	35,168
Consulting	251,459
Research (refer to Table 2)	14,664,591
Capital	23,245
Indirect costs (4% / 18%) [7/]	739,524
Contigency reserve (increase)	2,000,000
Total expenditure	**19,030,418**
Surplus for year [8/]	**4,946,489**

[1/] Equivalent to GBP 2.5m
[2/] Contribution expected in 2008 equivalent EUR 9.212m in two instalments: Early in January 2008; 1st instalment (90%) EUR 8.290m; and 2nd instalment retention (10%) EUR 0.922m receivable in June 2008
[3/] Equivalent to SEK 0.850m
[4/] Equivalent to CHF 0.450m
[5/] Includes interest credit for DFID USD 40,000; and BMGF USD 28,000
[6/] Commitment for matching funds in the amount of USD 150,000; USD 100,000 Morocco contribution and USD 50,000 Hungary contribution
[7/] 18% direct costs, and 4% on services and pass-through funds
[8/] See 'Statement of changes in net assets' below

Statement of changes in net assets

	2006	2007	
Designated			
Opening balance	4,853,435	7,341,035	
Net surplus/(deficit) for year	2,487,600	4,946,489	
Closing balance - net assets	7,341,035	12,287,524	[9/]
Undesignated			
Contingency reserve	1,000,000	3,000,000	[10/]
Total net assets	**8,341,035**	**15,287,524**	
Represented by:			
Accounts receivable	1,256,000	12,121,979	
Funds held at CIMMYT	6,085,035	2,165,545	
Cash on deposit	1,000,000	1,000,000	
Total net assets	**8,341,035**	**15,287,524**	

[9/] Carryover breakdown including commitments for 2008 based on contracts:

0.676	m	Prior years Commissioned research
0.078	m	2007 Commissioned research (SP5)
0.213	m	2007 Commissioned research remaining 20%
0.944	m	2007 Competitive grants 1st round remaining 20%
0.193	m	2007 Special projects (BMGF)
0.304	m	2007 Competitive grants 2nd round remaining 10%
9.879	m	2008 Budget—carryover
12.287	**m**	**Total**

[10/]

1.0	m	Funds for Programme management costs in the event of closure of programme activities
2.0	m	Funds for research activities in 2009
3.0	**m**	**Total**

Table 2. 2007 research budget

Particulars			Actual January-December
Research			
Commissioned and competitive research			**11,000,090**
Research commitments prior years		1,068,609	
Commissioned research Year 3 (2006—20%)		544,594	
Commissioned research Year 4 (2007—80/100%)		2,725,723	
Commissioned research Year 4 (2007—20%)		329,808	
Competitive grants—Round 1 Year 3 (2007—80%)		3,590,215	
Competitive grants—Round 2 Years 1–2 (2007–2008—90%)		2,549,475	
Operational support SPLs		191,667	
		11,000,090	
SP1	2,960,725		
SP2	2,336,525		
SP3	3,031,563		
SP4	1,933,411		
SP5	737,866		
	11,000,090		
Special projects			**3,664,501**
TLI Project Year 1 (2007)		3,328,636	
Rockefeller Foundation grants		335,865	
		3,664,501	
Total			**14,664,591**

Table 3. 2007 detailed expenditure schedule

Description	Expenditure	Total
1. Salaries and benefits		**849,432**
1.1 International staff (Headquarters)	519,506	
1.2 National staff	113,864	
1.3 SPL salaries and benefits (half-time SPLs—SPs 1, 2 and 4)	216,061	
2. Travel		**78,142**
Fares and subsistence—GCP staff	78,142	
3. Conferences		**299,254**
GCP Programme Steering Committee	29,957	
GCP Annual Research Meeting	269,177	
CGIAR Annual General Meeting	66	
Others	55	
4. Office supplies and services		**78,792**
Office	14,091	
Shipping and postage	9,286	
Maintenance and repair	43	
Calls and fax	9,851	
ICT service (Information and communication technologies)	34,158	
Subscriptions	7,115	
Recruitment	4,248	
5. Vehicle expenses		**10,812**
Gasoline	4,577	
Insurance	2,985	
Maintenance	3,249	
6. Printing and design		**35,168**
Publications (printing and design)	28,058	
Software/website	7,110	
7. Consultants (salary and benefits, travel)		**251,459**
Science and quality control	13,948	
Web content management	33,302	
Legal consultant	23,677	
Consultants/facilitators	55,532	
EPMR (GCP External Programme and Management Review) [1/]	125,000	
8. Research (refer to Table 2)		**14,664,591**
Commissioned and competitive research	11,000,090	
Special projects	3,664,501	
9. Capital		**23,245**
Vehicle (1)	19,132	
Computer	1,735	
Office equipment	2,378	
Indirect costs [2/]		**739,524**
Indirect costs—18% (Items 1.1, 1.2, 2, 3, 4 and 5)	205,662	
Indirect costs—4% [3/] 15% [4/] (Items 1.3, 6, 7, 8 and 9)	525,601	
Indirect costs—support for TLI project	8,261	
Contingency reserve (increase) [5/]		**2,000,000**
Total expenditure		**19,030,418**

[1/] Not budgeted
[2/] Indirect costs: 18% on direct costs and 4% on services and pass-through funds including a special project
[3/] Research grants for GCP host institution not subject to indirect costs of 4%
[4/] 15% indirect cost on GCP activities in a special project
[5/] Funds for research activities in 2009

Table 4. 2007 budget summary by type (institution and project)

Institution type/ Grant type	Competitive	Commissioned	Special	Total	%
CGIAR Centres	2,143,846	1,395,606	1,258,317	4,797,769	34
ARIs	1,910,776	935,707	797,112	3,643,595	26
NARS	2,341,635	1,365,042	908,975	4,615,652	33
Contracted services	0	293,400	576,000	869,400	6
Total (100%)	**6,396,257**	**3,989,755**	**3,540,404**	**13,926,416**	**100**

Table 5. 2007 budget summary by Consortium members

Institution	2007 Competitive research	2007 Commissioned research	2007 Special projects	Total
ACGT	124,350	0	0	124,350
Agropolis	147,423	264,708	0	412,131
BIOTEC	0	69,689	0	69,689
Bioversity	0	388,090	0	388,090
CAAS	193,260	62,000	0	255,260
CIAT	397,016	18,420	510,384	925,820
CIMMYT	672,505	178,060	0	850,565
CINVESTAV	0	0	0	0
CIP	0	207,841	0	207,841
Cornell University	564,707	49,621	0	614,328
EMBRAPA	489,069	170,686	122,000	781,755
IAO	0	0	0	0
ICAR	2,360	0	0	2,360
ICARDA	227,468	8,410	0	235,878
ICRISAT	100,890	137,560	672,181	910,631
IITA	130,324	0	75,752	206,076
INRA–Morocco	0	85,000	0	85,000
IRRI	654,033	309,732	0	963,765
JIC	15,000	0	0	15,000
NIAS	39,400	50,620	0	90,020
WARDA	62,500	83,780	0	146,280
WUR	73,000	277,005	0	350,005
Total (100%)	**3,893,305**	**2,361,222**	**1,380,317**	**7,634,844**

Table 6. 2007 competitive projects: Budget by Subprogramme and partners

Round 1										Total
Subprogramme 1: Genetic diversity of global genetic resources										
1. G3005.10: Exploring natural genetic variation: developing genomic resources and introgression lines for four AA genome rice relatives										
CIAT	Cornell University	Fedearroz	EMBRAPA	WARDA						
134,600	122,000	23,600	21,400	23,600						**325,200**
2. G3005.13: Development of informative DNA markers through association mapping in maize to improve drought tolerance in cereals										
CIMMYT	Cornell University	Agropolis	KARI	SAU	SIRDC	NSFCRC	Genaissance			
161,660	57,820	14,160	17,228	17,228	17,228	17,228	35,000			**337,552**
3. G3005.14: Characterisation of genetic diversity of maize populations: documenting global maize migration from the centre of origin										
CIMMYT	Agropolis	KARI	IITA	ICAR	NSFCRC	DOA–Indonesia	DOA–Philippines	CAAS	NMRI	
163,725	45,430	2,360	2,360	2,360	2,360	2,360	2,360	2,360	2,360	**228,035**
4. G3005.17: Allele mining based on non-coding regulatory SNPs in barley germplasm										
ICARDA	University of Adelaide	Università di Udine	Tyshreen University							
130,000	83,000	68,000	18,000							**299,000**
Subprogramme 2: Genomics towards gene discovery										
5. G3005.01: Identifying genes responsible for failure of grain formation in rice and wheat under drought										
IRRI	CSIRO	NIAS	TNAU	NAU						
165,370	73,554	35,400	12,272	11,800						**298,396**
6. G3005.02: Revitalising marginal lands: discovery of genes for tolerance of saline and phosphorus-deficient soils to enhance and sustain productivity										
IRRI	CSIRO/Graingene	UC–Davis	Dhaka University	ICABIOGRAD						
101,496	36,580	49,167	29,893	28,320						**245,456**
7. G3005.08: Targeted discovery of superior disease QTL alleles in maize and rice genomes										
Cornell University	IRRI	CSU	NCSU	KARI						
118,137	48,439	55,347	49,938	42,067						**313,928**
8. G3005.11: Functional genomics of cross-species resistance to fungal diseases in rice and wheat (cereal immunity)										
Agropolis	CIMMYT	EMBRAPA	JIC	University of Rennes	NIAS	UC–Davis				
20,000	50,000	27,000	15,000	40,000	4,000	30,000				**186,000**
9. G3005.15: Determination of a common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes										
CIMMYT	ACPFG	Agropolis–INRA	ETH	IRRI	IGAU	SIRDC				
105,020	30,890	64,900	39,600	47,200	9,000	2,000				**298,610**
10. G3005.16: Isolation and characterisation of aluminium tolerance genes in the cereals: an integrated functional genomic, molecular genetic and physiological analysis										
Cornell University	EMBRAPA–maize	EMBRAPA–wheat	EMBRAPA–rice and beans	Moi University						
122,034	102,966	32,500	22,500	20,000						**300,000**
Subprogramme 3: Trait capture for crop improvement										
11. G3005.03: Identifying the physiological and genetic traits that make cassava one of the most drought-tolerant crops										
EMBRAPA	Cornell University	IITA	SARI	ARI	CIAT					
68,230	59,330	29,250	30,225	30,225	56,462					**273,722**
12. G3005.05: Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools										
EMBRAPA	UC–Berkley	CERAAS	ICRISAT–India	ICRISAT–Kenya	Agropolis	IBONE/CONICET	University of Aarhus			
56,998	33,577	16,907	62,540	38,350	2,933	17,430	1,600			**230,335**
13. G3005.06: Marker development and marker-assisted selection for *Striga* resistance in cowpea										
IITA	CERAAS	UVA								
98,714	23,600	177,686								**300,000**
14. G3005.09: Development of low-cost technologies for pyramiding useful genes from wild relatives of cassava into elite progenitors										
CIAT	EMBRAPA/CNPMF	NAARI	CRI	NRCRI	NAARI/CRI/NRCRI					
141,654	46,374	24,300	24,300	24,300	37,620					**298,548**
15. G3005.12: Drought-tolerant rice cultivars for North China and South/Southeast Asia by highly efficient pyramiding of QTLs from diverse origins										
CAAS	IRRI									
190,900	105,600									**296,500**
Subprogramme 4: Bioinformatics and crop information systems										
16. 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										
WUR	CSIRO	CIMMYT	INIA–Uruguay							
73,000	68,700	20,100	750							**162,550**

Table 6. 2007 competitive projects: Budget by Subprogramme and partners (continued)

Round II											Total
Subprogramme 1: Genetic diversity of global genetic resources											
1. G3007.01: Interspecific bridges that give full access to the African allele pool for enhancing drought tolerance of Asian rice											
LGDP	CIAT	Fedearroz	Punjab University	PhilRice	WARDA	IER	INERA	University of Arizona			
78,400	64,300	13,000	28,900	28,900	38,900	14,200	20,100	53,300			**340,000**
2. G3007.02: Genomic dissection of tolerance to drought stress in wild barley											
ICARDA	OSU	INIA–Chile	UC–Riverside	SCRI							
97,468	33,009	51,920	39,994	120,763							**343,154**
Subprogramme 2: Genomics towards gene discovery											
3. G3007.03: Development of genomics resources for molecular breeding of drought tolerance in cassava											
University of Maryland	ACGT	UC–Davis									
109,865	124,350	200,000									**434,215**
4. G3007.06: Genetic dissection of drought adaptive mechanisms in bread and durum wheat through large-scale phenotyping methodologies											
CIMMYT	DWR	ACPFG									
172,000	45,000	84,000									**301,000**
Subprogramme 3: Trait capture for crop improvement											
5. 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 aluminium tolerance gene in sorghum											
EMBRAPA	USDA-ARS	Cornell University									
111,101	103,111	85,386									**299,598**
6. G3007.05: Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-aided breeding											
IRRI	University of Alberta	CRURRS	CRRI	UAS	YAAS	TNAU	Barwale Foundation	Rewa College of Agriculture	IGKV	NDUAT	BAU	
185,928	25,370	9,380	9,000	6,000	12,390	6,390	5,000	6,000	6,000	6,000	7,000	**284,458**
Total (Round I and II, 100%)												**6,396,257**

Table 7. 2007 commissioned projects: Budget by Subprogramme and partner(s)

						Total
Subprogramme 1: Genetic diversity of global genetic resources						
1. 2005-06: Supporting emergence of reference drought tolerance phenotyping centres						
EMBRAPA						
148,430						**148,430**
2. 2006-01: Developing strategies for allele mining within large collections						
IRRI	CIAT	EMBRAPA	ICRISAT	ICARDA		
42,298	12,020	12,256	18,030	6,010		**90,614**
3. 2006-02: A dataset on allele diversity at orthologous candidate genes in GCP crops (ADOC)						
Agropolis	CIP	Agropolis–Services	ICARDA	CIAT		
55,723	54,622	71,855	2,400	2,400		**187,000**
4. 2006-04: Phenotyping in the field: global capacity accessible to the GCP–Inventory of phenotyping resources and capacity for the GCP						
Bioversity						
49,000						**49,000**
5. G4007.01: Composite set genotyping: quality assessment and consolidation						
Agropolis/CIRAD–Services						
50,000						**50,000**
Subprogramme 2: Genomics towards gene discovery						
6. G4007.02: Validation of drought-response/resistance pathway genes by phenotypic analysis of mutants						
Virginia Tech	IRRI	HZAU				
35,400	33,012	31,860				**100,272**
Subprogramme 3: Trait capture for crop improvement						
7. G4007.04: Association mapping of downy mildew resistance in elite maize inbred lines in Thailand						
BIOTEC	NCSRC	NSFCRC				
25,689	4,543	4,543				**34,775**
8. G4007.05: Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco						
INRA–Morocco	DiSTA	CIMMYT				
85,000	12,000	3,000				**100,000**
9. 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						
CAAS	NU	NWSUAF	SAAS	LAAS	HAAS	
57,000	5,400	3,500	2,900	2,900	2,900	**74,600**
10. G4007.07: Marker-assisted selection for sweet potato virus disease (SPVD) resistance in sweet potato germplasm and breeding populations						
CIP						
122,720						**122,720**
11. G4007.08: Integration of genomic tools with conventional screening for developing NERICA rice cultivars for West Africa						
WARDA	IER	Agropolis–IRD				
83,780	57,820	14,750				**156,350**
12. G4007.23: Field evaluation of wheat-barley introgression lines under different water regimes						
ARI–HAS	CIMMYT	CAAS	Eger–Hungary			
28,000	10,000	5,000	5,000			**48,000**
13. G4007.24: Seed smoke treatment to favour germination under water-stressed conditions						
ARI–HAS						
12,000						**12,000**
14. G4007.25: Development of a GCP Drought Phenotyping Network						
Consultants	NARS	ARIs				
10,000	6,250	6,250				**22,500**
Subprogramme 4: Bioinformatics and crop information systems						
15. 2005-22: Development of GCP domain (data) models ontology						
IRRI	CIMMYT	Bioversity				
49,112	86,140	14,750				**150,002**
16. 2005-23: Implementation of web services technology in GCP Consortium						
Bioversity						
120,000						**120,000**
17. 2005-24: Application and development of web services technology						
Bioversity	Agropolis	IRRI				
61,360	10,380	8,260				**80,000**

Table 7. 2007 commissioned projects: Budget by Subprogramme and partner(s) (continued)

					Total
Subprogramme 4: Bioinformatics and crop information systems (continued)					
18. 2005-25: Creation and maintenance of templates for GCP data storage in repositories					
CIMMYT	IRRI	Bioversity			
40,000	28,820	11,180			**80,000**
19. 2005-26: Management of GCP Central Registry					
Bioversity	CIMMYT				
68,200	11,800				**80,000**
20. 2005-27: High-Performance Computing facilities for the GCP					
CIP	ICRISAT	IRRI			
30,499	14,750	14,750			**59,999**
21. 2005-34: GCP software engineering and collaboration platform					
IRRI					
38,940					**38,940**
22. 2006-08: Data analysis support for existing projects in SP2 with emphasis on integrating results across gene expression and QTL mapping experiments					
CIMMYT	IRRI	NIAS	JIC		
21,220	19,760	10,620	10,900		**62,500**
23. 2006-16: Development of an integrated GCP information platform					
IRRI	NIAS	Agropolis–CIRAD	EMBRAPA		
50,000	40,000	50,000	10,000		**150,000**
24. 2006-17: GCP data quality improvement and assurance					
IRRI	ICRISAT	CGN–WUR	Bioversity	SCRI	
15,930	39,530	53,100	29,500	9,440	**147,500**
25. 2006-35: Support for existing projects in SP1 on germplasm data analysis (GDA supp)					
WUR	Agropolis–CIRAD				
63,000	12,000				**75,000**
26. G4007.09: Methodology and software development for marker-trait association analyses					
WUR					
100,000					**100,000**
27. G4007.10: Support to GCP Scientists regarding issues related to bioinformatics and data handling					
WUR					
56,640					**56,640**
28. G4007.11: Refinement and distribution of iMAS for use by NARS and other user communities					
ICRISAT	IRRI	CIMMYT			
65,250	8,850	5,900			**80,000**
29. G4007.12: Development of tools and technology to increase the functionality of the GCP Information Platform					
EBI					
100,000					**100,000**
Subprogramme 5: Capacity-building and enabling delivery					
30. 2005-CB03: The use of molecular markers in efficient crop improvement: marker-assisted breeding (a learning module)					
Cornell University					
20,000					**20,000**
31. 2005-CB13: The Interactive Resource Center and Helpdesk					
Cornell University					
29,621					**29,621**
32. 2005-CB15: Distance-learning course for scientists on plant genetic resource policy					
WUR					
4,265					**4,265**
33. 2006-14: *Ex ante* impact analysis of marker-assisted selection technologies supported by the Generation Challenge Programme (GCP)					
Virginia Tech					
78,430					**78,430**
34. 2006-36: Capacity-building and research activities in sub-Saharan Africa					
UKZN					
100,098					**100,098**

Table 7. 2007 commissioned projects: Budget by Subprogramme and partner(s) (continued)

							Total
Subprogramme 5: Capacity-building and enabling delivery (continued)							
35. G4007.03: The 'Community of Practice' concept applied to rice production in the Mekong region: quick conversion of popular rice varieties with emphasis on drought, salinity and grain quality improvement							
BIOTEC	UBU	NAFRI	CARDI	DAR			
44,000	1,500	6,500	6,500	6,500			**65,000**
36. G4007.13: Capacity-building *à la carte* Programme							
KARI	NRCRI	ISRA	CSIR	ABRII	ICABIOGRAD	NARS (TBD)	
32,863	38,822	39,884	38,350	25,960	39,825	184,296	**400,000**
37. G4007.14: Fellowships and travel grants							
NARS							
160,000							**160,000**
38. G4007.17: Development of a Project Delivery Guide							
Consultant	Consultant						
33,000	7,200						**40,200**
39. G4007.18: Translation and training materials							
Consultant							
1,200							**1,200**
40. G4007.19: Kick-off meeting of the teams involved in the GCP Competitive call 2006–August 2007, Texcoco, Mexico							
CGIAR Centres	ARIs	NARS of respective projects					
53,334	53,333	53,333					**160,000**
41. G4007.20: Managing the Generation Challenge Programme in a post-International Treaty world: a proposal for a technical training workshop and related materials							
Bioversity							
34,100							**34,100**
42. G4007.21: Genotyping Support Service							
Consultant	Workshop–NARS of respective projects		Genotyping Service				
60,000	58,000		182,000				**300,000**
43. G4007.22: GCP Workflow and Repository System							
CIAT	Cropster GmbH						
4,000	16,000						**20,000**
Total							**3,989,756**

Table 8. 2007 special projects: Budget by objectives and partners

						Total
Improving tropical legume productivity for marginal environments in sub-Saharan Africa (Tropical Legumes I—TLI)						
Objective 1: Improving groundnut (*Arachis hypogaea* L) productivity for marginal environments in sub-Saharan Africa						
ICRISAT	UGA	UCB	EMBRAPA	African NARS	Services	
389,833	184,063	149,550	122,000	120,000	110,000	**1,075,446**
Objective 2: Improving cowpea (*Vigna unguiculata* L) productivity for marginal environments in sub-Saharan Africa						
UC–Riverside	UC–Davis	IITA	African NARS	Services		
237,372	146,500	75,752	63,000	406,000		**928,623**
Objective 3: Improving common bean (*Phaseolus vulgaris* L) productivity for marginal environments in sub-Saharan Africa						
CIAT	African NARS	Services				
510,384	100,000	15,000				**625,384**
Objective 4: Improving chickpea (*Cicer arietinum* L) productivity for marginal environments in sub-Saharan Africa						
ICRISAT	African NARS	Services				
282,348	50,000	25,000				**357,349**
Objective 5: Developing cross species resources for comparative biology in tropical crop legumes						
UC–Davis	UCB					
229,177	27,225					**256,402**
Objective 6: Training and capacity-building for sub-Saharan African scientists						
NARS (Africa/Asia)						
297,200						**297,200**
Total for all objectives (100%)						**3,540,404**

Table 9. 2008 summary: Projected income versus expenditure

		Projection January-December
Income		
Expected		
DFID [1/]	4,500,000	
EC [2/]	5,800,000	10,300,000
Confirmed		
Bill & Melinda Gates Foundation (BMGF)		3,143,579
Pioneer Hi-Bred International, Inc		20,000
Rockefeller Foundation		68,500
Sida [3/]		150,000
SDC [4/]		400,000
World Bank		2,000,000
Sub-Total		**16,082,079**
Interest		200,000
Total Income		**16,282,079**
Expenditure		
Salaries and benefits		940,000
Operational travel (GCP Management)		135,000
Conferences and PSC expenses		515,000
Office supplies and services		99,500
Vehicle expenses		23,000
Printing and design		50,000
Consulting		255,000
Research		19,283,331
Research commitments prior years	2,400,000	
Commissioned research Year 4 (2007—20%)	213,067	
Commissioned research Year 5 (2008 80%)—1st wave	5,853,685	
Commissioned research Year 5 (2008 80%)—2nd wave	3,360,000	
Competitive grants—Round 1 Year 3 (2007–20%)	944,500	
Competitive grants—Round 3 Year 1 (2008–100%)	3,000,000	
Operational support SPLs	300,000	
TLI Project Year 2 (2008)	3,143,579	
Rockefeller Foundation projects	68,500	
Capital		20,000
Indirect costs (4%/18%) [5/]		993,383
Total expenditure		**22,314,214**
Surplus/(deficit) for year [7/]		**(6,032,135)**

[1/] Equivalent to GBP 2.5m (Note 6)
[2/] Equivalent to EUR 4.0m in two installments. 1st installment 2008 (90%) EUR 3.6m; and, 2nd installment, retention (10%) EUR 0.400m receivable in 2009. 2008 Contribution includes 2007 retention (10%) EUR 0.922m (Note 6)
[3/] Equivalent to SEK 1.0m (Note 6)
installment SEK 0.500m receivable in 2009 (Note 6)
[4/] Equivalent to CHF 0.450m (Note 6)
[5/] 18% on direct costs and 4% on services and pass-through funds
[6/] All outstanding foreign currency receipts subject to exchange rate fluctuations
[7/] See statement of changes in net assets - below

Statement of changes in net assets

	2007	2008
Designated		
Opening balance	7,341,035	12,287,524
Net surplus/(deficit) for year	4,946,489	(6,032,135)
Closing balance – net assets	**12,287,524**	**6,255,389**
Undesignated		
Contingency reserve	3,000,000	3,000,000 [8/]
Total Net Assets	**15,287,524**	**9,255,389**
Represented by:		
Accounts receivable	12,121,979	-
Funds held at CIMMYT	2,165,545	6,255,389
Cash held at CIMMYT	1,000,000	3,000,000
Total net assets	**15,287,524**	**9,255,389**

[8/] 1.0 m Funds for Programme management costs in the event of closure of programme activities
2.0 m Funds for research activities in 2009
3.0 m Total

Table 10. 2008 projected budget: details

	Projection	
Description	**Expenditure**	**Total**
1. Salaries and benefits		**940,000**
1.1 International staff (Headquarters)	580,000	
1.2 National staff	110,000	
1.3 SPL salaries and benefits (half-time SPLs—SPs 1, 2 and 4)	250,000	
2. Travel		**135,000**
Fares and subsistence—GCP Staff	135,000	
3. Conferences		**515,000**
GCP Programme Steering Committee	100,000	
GCP Annual Research Meeting	300,000	
Stakeholders' Committee (GFAR) (EC)	100,000	
CGIAR Annual General Meeting	10,000	
Others	5,000	
4. Office supplies and services		**99,500**
Office	12,000	
Shipping and postage	14,000	
Maintenance and repair	3,000	
Calls and fax	13,500	
ICT service (information and communication technologies)	45,000	
Subscriptions	7,000	
Recruitment	5,000	
5. Vehicle expenses		**23,000**
Gasoline	8,000	
Insurance	5,000	
Maintenance	10,000	
6. Printing and design		**50,000**
Publications (printing and design)	30,000	
Software/website	20,000	
7. Consultants (salary and benefits, travel)		**255,000**
Science and quality control	120,000	
Web content management	25,000	
Legal consultant	30,000	
Consultants/facilitators	80,000	
8. Research		**19,283,331**
Research commitments prior years	2,400,000	
Commissioned research Year 4 (2007—20%)	213,067	
Commissioned research Year 5 1st Wave (2008 80/100%) [1/]	5,853,685	
Commissioned research Year 5 2nd Wave (2008 80%) [2/]	3,360,000	
Competitive grants—Round 1 Year 3 (2007 20%)	944,500	
Competitive grants—Round 3 Year 1 (2008–100%) [3/]	3,000,000	
Operational support SPLs	300,000	
Rockefeller Foundation grant	68,500	
TLI Project Year 2 (2008)	3,143,579	
9. Capital		**20,000**
	20,000	
Indirect Costs [4/]		**993,383**
Indirect costs—18% (Items 1.1, 1.2, 2, 3, 4, 5)	263,250	
Indirect costs—4% (Items 1.3, 6, 7, 8, 9) [5/]	730,133	
Total expenditure		**22,314,214**

[1/] 2008 budget 1st wave USD 7.018m (80/100%) = USD 5.854m
[2/] 2008 budget 2nd wave USD 4.200m (80%) = USD 3.360m
[3/] 2008 budget round 3 USD 9.0m Year 1 (100%) = USD 3.0m
[4/] Indirect costs: 18% on direct costs and 4% on services and pass-through funds
[5/] Research grants for GCP host institution not subject to indirect costs of 4%

Table 11. 2008 projected budget for competitive projects by Subprogramme and partners

Round 1

												Total
Subprogramme 1: Genetic diversity of global genetic resources												
1. G3005.10: Exploring natural genetic variation: developing genomic resources and introgression lines for four AA genome rice relatives												
CIAT	Fedearroz	EMBRAPA	WARDA									
30,700	16,500	16,500	16,500									**80,200**

Round II

												Total
Subprogramme 1: Genetic diversity of global genetic resources												
2. G3007.01: Interspecific bridges that give full access to the African allele pool for enhancing drought tolerance of Asian Rice												
LGDP	CIAT	Fedearroz	Punjab University	PhilRice	WARDA	IER	INERA	Arizona University				
71,900	64,300	13,000	28,900	28,900	38,100	14,200	14,200	55,500				**329,000**
3. G3007.02: Genomic dissection of tolerance to drought stress in wild barley												
ICARDA	OSU	INIA–Chile	UC–Riverside	SCRI								
78,588	33,929	40,651	20,726	50,556								**224,450**
Subprogramme 2: Genomics towards gene discovery												
4. G3007.03: Development of genomics resources for molecular breeding of drought tolerance in cassava												
University of Maryland	ACGT											
188,536	135,307											**323,843**
5. G3007.06: Genetic dissection of drought adaptive mechanisms in bread and durum wheat through large-scale phenotyping methodologies												
CIMMYT	DWR	ACPFG										
184,000	45,000	72,000										**301,000**
Subprogramme 3: Trait capture for crop improvement												
6. G3007.04: Tailoring superior alleles for abiotic stress genes for deployment into breeding programmes: a case study based on association analysis *Alt*$_{SB1}$ a major aluminium tolerance gene in sorghum												
EMBRAPA	USDA–ARS	Cornell University										
111,101	104,435	87,967										**303,503**
7. G3007.05: Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-aided breeding												
IRRI	University of Alberta	CRURRS	CRRI	UAS	YAAS	TNAU	Barwale Foundation	Rewa College of Agriculture	IGKV	NDUAT	BAU	
232,052	19,470	6,000	6,000	6,000	10,610	6,000	5,000	6,000	6,000	5,000	6,000	**314,132**
Total (100%)												**1,876,128**

Table 12. 2008 projected budget for commissioned projects by Subprogramme and partner(s)

							Total
Subprogramme 1: Genetic diversity of global genetic resources							
1. G4006-02: A dataset on allele diversity at orthologous candidate genes in GCP crops [ADOC]							
Agropolis							
100,000							**100,000**
2. G4007.01: Genotyping data quality and validation							
Agropolis							
100,000							**100,000**
3. G4008.01: Population development to underpin gene discovery and allele validation in rice and sorghum: the multiparent advanced generation inter-crosses (MAGIC)							
NIAB	IRRI	ICRISAT					
41,182	53,559	71,390					**166,131**
4. G4008.02: Phenotyping sorghum reference set for drought tolerance							
ICRISAT							
101,480							**101,480**
5. G4008.03: Precision phenotyping of the GCP spring wheat reference sample for drought							
CIMMYT							
11,800							**11,800**
6. G4008.04: Linkage disequilibrium assessment in legumes							
CIAT							
150,000							**150,000**
7. G4008.05: Connecting performance under drought with genotypes through phenotype associations							
IRRI	HZAU	TNAU	CRRI	IGAU	Agropolis–CIRAD		
63,720	29,500	22,420	17,700	17,700	48,380		**199,420**
Subprogramme 2: Genomics towards gene discovery							
8. G4007.02: Validation of drought-response/resistance pathway genes by phenotypic analysis of mutants							
Virginia Tech	IRRI	HZAU					
34,220	33,012	33,040					**100,272**
9. G4008.06: Single nucleotide polymorphism discovery, validation, and mapping in groundnut							
UGA							
150,000							**150,000**
10. G4008.07: Improving molecular tools for pearl millet							
ICRISAT	AICMIP (and affiliated CAZRI and RAU)		NIAB				
129,800	50,993		11,771				**192,564**
11. G4008.08: Transcriptome analysis of near-isogenic rice lines to identify expression signatures and gene combinations conferring tolerance to drought stress							
NIAS	IRRI						
102,365	71,980						**174,345**
12. G4008.09: Development of genetic and genomic resources for breeding improved sweet potato varieties							
CIP	IIAM	NAARI	INIA–Uruguay	EMBRAPA	DArT P/L		
119,180	7,080	7,080	7,080	2,360	50,000		**192,780**
Subprogramme 3: Trait capture for crop improvement							
13. G4007.04: Association mapping of downy mildew resistance in elite maize inbred lines in Thailand							
BIOTEC							
25,689							**25,689**
14. G4007.05: Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco							
INRA–Morocco	DiSTA	CIMMYT					
85,000	12,000	3,000					**100,000**
15. 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							
CAAS	NU	NWSUAF	SAAS	LAAS	HAAS		
39,000	5,400	3,500	2,900	2,900	2,900		**56,600**
16. G4007.07: Marker assisted selection for sweet potato virus disease (SPVD) resistance in sweet potato germplasm and breeding populations							
CIP							
122,720							**122,720**

Table 12. 2008 projected budget for commissioned projects by Subprogramme and partner(s) (continued)

							Total
Subprogramme 3: Trait capture for crop improvement (continued)							
17. G4007.08: Integration of genomics tools with conventional screening for developing NERICA rice cultivars for West Africa							
WARDA	IER	Agropolis–IRD					
99,120	31,860	17,110					**148,090**
18. G4008.10: Assessment of the breeding value of superior haplotypes for *Alt$_{SB}$* a major aluminium tolerance gene in sorghum: linking upstream genomics to acid soil breeding in Niger and Mali (ALTFIELD)							
EMBRAPA	INRAN	ICRISAT–Niger	ICRISAT–Mali	IGD–Cornell University			
29,700	47,150	11,800	23,600	17,700			**129,950**
19. G4008.11: Dry bean improvement and marker assisted selection for diseases and abiotic stresses in Central America and the Caribbean							
INIFAP	CIAT	INTA	INCA	NGO (TBD)			
42,900	40,120	15,000	15,000	15,000			**128,020**
20. G4008.12: Linking genetic diversity with phenotype for drought tolerance traits through molecular and physiological characterisation of a diverse reference collection of chickpea							
ICRISAT	JIRCAS	UAS					
49,796	30,090	15,400					**95,286**
21. G4008.13: Improving drought tolerance phenotyping in cowpea							
UC–R	IITA	ISRA	INERA	Texas A&M University			
64,062	34,500	29,500	23,600	23,600			**175,262**
22. G4008.14: Breeding for drought tolerance with known gene information							
CIMMYT	CSIRO/University of Queensland		CAAS				
50,000	75,000		25,000				**150,000**
23. G4008.15: Developing potato cultivars adapted to Southern African countries							
INIA–Uruguay	INIA–Chile	INTA–Argentina	EMBRAPA	CIP–Peru	CIP–Malawi		
15,000	15,000	10,000	10,000	7,080	50,000		**107,080**
24. G4008.16: Speeding the development of salt-tolerant rice varieties through marker-assisted selection and their dissemination in salt-affected areas of Bangladesh							
IRRI	BRRI	University of Dhaka	BINA				
93,379	40,150	17,360	12,320				**163,209**
25. G4008.17: Application of marker-assisted selection for *Striga* resistance in cowpea							
INERA	IITA						
51,330	48,616						**99,946**
26. G4008.18: Bringing innovation to African farmers' fields: Development and dissemination of cassava varieties bred for resistance to pests and diseases by molecular marker-assisted selection (MAS)							
NRCRI	CIAT						
127,440	75,520						**202,960**
27. G4008.19: Incorporation of an MSV resistance gene in Mozambican maize varieties, mediated by use of MAS							
UKZN	IIAM						
54,055	25,945						**80,000**
Subprogramme 4: Bioinformatics and crop information systems							
28. G4005.22: Development of GCP domain models and ontologies							
IRRI	Bioversity	CIAT	CIMMYT	CIP	ICRISAT		
30,000	25,000	15,000	10,000	15,000	15,000		**110,000**
29. G4005.23: Implementation of web services technology in the Generation Challenge Programme Consortium							
Bioversity	IRRI						
61,000	5,000						**66,000**
30. G4005.27: High-performance computing facilities for the GCP platform							
CIP	ICRISAT	IRRI					
40,000	15,000	15,000					**70,000**
31. G4006.08: Data analysis support for existing projects in SP2 with emphasis on integrating results from microarray and mapping experiments							
CIMMYT	IRRI	ICRISAT	NIAS	JIC			
61,000	50,000	39,000	25,000	20,000			**195,000**
32. G4006.16: Development of an integrated GCP information platform							
IRRI	CIMMYT	Agropolis–CIRAD	ICRISAT	NCGR			
50,000	25,000	50,000	25,000	10,000			**160,000**

Table 12. 2008 projected budget for commissioned projects by Subprogramme and partner(s) (continued)

							Total
Subprogramme 4: Bioinformatics and Crop Information Systems							
33. G4006.17: GCP quality management and data quality improvement							
IRRI	CIP	ICRISAT	CGN–WUR	Agropolis–CIRAD			
44,840	59,000	30,000	25,000	15,000	173,840		**173,840**
34. G4006.35: Statistical support for the design and data analysis of GCP projects							
WUR	Agropolis–CIRAD	CIMMYT					
60,000	10,000	10,000					**80,000**
35. G4007.09: Design and analysis of marker-trait association studies, with special attention for genetically challenging crops							
WUR	University of Hohenheim	Imperial College	NIAB	SCRI/BIOSS	Leiden University Medical Center		
55,000	10,000	7,500	10,000	10,000	7,500		**100,000**
36. G4007.10: Support to GCP scientists regarding issues related to bioinformatics and data handling							
Institution (TBD)							
50,000							**50,000**
37. G4007.11: Further development and support for use of iMAS by NARS and other user communities							
ICRISAT							
80,000							**80,000**
38. G4007.12: Development of tools and technology to increase the functionality of the GCP Information Platform							
EBI/IRRI	Bioversity						
80,000	5,000						**85,000**
39. G4008.20: Management of the GCP Central Registry and the creation and maintenance of templates for data storage in repositories							
Bioversity	CIMMYT	IRRI					
80,000	40,000	20,000					**140,000**
40. G4008.21: Large-scale phylogenomic analyses to gene function prediction for GCP crops							
Bioversity	Agropolis–CIRAD	IRRI					
25,370	6,678	85,000					**117,048**
41. G4008.22: Methodology development for reconstruction of genealogies based on haplotypes related to geographic patterns (HaploPhyle: graphical haplotype network in the light of external data)							
Institution (TBD)							
150,000							**150,000**
Subprogramme 5: Capacity-building and enabling delivery							
42. G4005.63: The Interactive Resource Center and Helpdesk							
IGD–Cornell University							
29,966							**29,966**
43. G4006-14: *Ex ante* impact analysis of marker-assisted selection technologies supported by the Generation Challenge Programme							
Virginia Tech							
70,188							**70,188**
44. G4006.36: Capacity-building and research activities in sub-Saharan Africa							
UKZN							
99,987							**99,987**
45. 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							
BIOTEC	UBU	NAFRI	CARDI	DAR			
34,000	1,500	6,500	6,500	6,500			**55,000**
46. G4007.13: Capacity-building *à la carte* Programme							
NARS (TBD)							
600,000							**600,000**
47. G4007.14: Fellowships and Travel Grants							
NARS (TBD)							
280,000							**280,000**
48. G4007.21: Genotyping Support Service							
NARS–Africa, Asia, Latin America		NARS (GCP travel/workshop)		Contracted Services			
125,000		25,000		250,000			**400,000**
49. G4008.23: Statistical rules for defining characteristic genotype and marker sets							
WUR							
35,000							**35,000**

Table 12. 2008 projected budget for commissioned projects by Subprogramme and partner(s) (continued)

						Total
Subprogramme 5: Capacity-building and enabling delivery (continued)						
50. G4008.24: From attractiveness to feasibility: A strategic assessment of the capacity to develop and adopt technologies						
IFPRI	CIAT	CIAT/CIMMYT				
65,695	17,749	44,890				**128,334**
51. G4008.25: Advanced course on 'Applied statistical methods in plant genomics'						
WUR						
25,000						**25,000**
52. G4008.26: A cassava breeding Community of Practice in Africa for accelerated production and dissemination of farmer-preferred cassava varieties resistant to pests and diseases						
CIAT	NRCRI	CRI	NaCCRI	ARI-Naliendele		
84,960	23,100	23,100	23,100	23,100		**177,360**
53. G4008.27: Phenotyping course for drought-related traits across tropical legumes–Concepts and practices						
ICRISAT	INRA	UAS				
98,506	5,900	12,390				**116,796**
Total (100%)						**7,018,123**

Table 13. 2008 special projects: Projected budget by objectives and partners

Improving tropical legume productivity for marginal environments in sub-Saharan Africa (Tropical Legumes I—TLI)						
						TOTAL
Objective 1: Improving groundnut (*Arachis hypogaea* L) productivity for marginal environments in sub-Saharan Africa						
ICRISAT	UGA	UCB	EMBRAPA	African NARS	Services	
401,393	249,858	89,255	93,526	120,000	60,000	**1,014,031**
Objective 2: Improving cowpea (*Vigna unguiculata* L) productivity for marginal environments in sub-Saharan Africa						
UC–Riverside	UC–Davis	IITA	African NARS	Services		
217,123	126,500	95,751	80,000	25,000		**544,373**
Objective 3: Improving Common bean (*Phaseolus vulgaris* L) productivity for marginal environments in sub-Saharan Africa						
CIAT	African NARS	Services				
514,009	100,000	15,000				**629,009**
Objective 4: Improving chickpea (*Cicer arietinum* L) productivity for marginal environments in sub-Saharan Africa						
ICRISAT	African NARS	Services				
289, 008	50,000	25,000				**364,800**
Objective 5: Developing cross-species resources for comparative biology in tropical crop legumes						
UC–Davis	UGA	UCB				
128,645	102,871	63,650				**295,166**
Objective 6: Training and capacity-building for sub-Saharan African scientists						
NARS (Africa/Asia)						
297,200						**297,200**
Total for all objectives						**3,143,582**

Table 14. Competitive projects Round I: Budget by year

No	Project No	Project title	Year 1: 2005	Year 2: 2006	Year 3: 2007	Year4: 2008	Total
1	G3005.01	Identifying genes responsible for failure of grain formation in rice and wheat under drought	305,836	295,768	298,396		900,000
2	G3005.02	Revitalising marginal lands: discovery of genes for tolerance of saline and phosphorus deficient soils to enhance and sustain productivity	312,300	342,244	245,456		900,000
3	G3005.03	Identifying the physiological and genetic traits that make cassava one of the most drought-tolerant crops	298,540	294,883	273,722		867,145
4	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	169,550	175,050	162,550		507,150
5	G3005.05	Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools	390,311	277,589	230,335		898,235
6	G3005.06	Marker development and marker-assisted selection for *Striga* resistance in cowpea	300,000	300,000	300,000		900,000
7	G3005.07	Measuring linkage disequilibrium across three genomic regions in rice	100,000				100,000
8	G3005.08	Targeted discovery of superior disease QTL alleles in the maize and rice genomes	294,297	291,386	313,928		899,611
9	G3005.09	Development of low-cost technologies for pyramiding useful genes from wild relatives of cassava into elite progenitors	298,194	298,164	298,548		894,906
10	G3005.10	Exploring natural genetic variation: Developing genomic resources and introgression lines for four AA genome rice relatives	331,700	337,800	325,200	80,200	1,074,900
11	G3005.11	Functional genomics of cross-species resistance to fungal diseases in rice and wheat (CERALIMMUNITY)	387,000	327,000	186,000		900,000
12	G3005.12	Drought-tolerant rice cultivars for North China and South/Southeast Asia by highly efficient pyramiding of QTLs from diverse origins	296,500	296,500	296,500		889,500
13	G3005.13	Development of informative DNA markers through association mapping in maize to improve drought tolerance in cereals	268,080	293,420	337,552		899,052
14	G3005.14	Characterisation of genetic diversity of maize populations: documenting global maize migration from the centre of origin	305,620	183,490	228,035		717,145
15	G3005.15	Determination of a common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes	297,678	302,398	298,610		898,686
16	G3005.16	Isolation and characterisation of aluminium tolerance genes in the cereals: an integrated functional genomic, molecular genetic and physiological analysis	300,000	300,000	300,000		900,000
17	G3005.17	Allele mining based on non-coding regulatory SNPs in barley germplasm	300,000	300,000	299,000		899,000
		Total (100%)	**4,955,606**	**4,615,692**	**4,393,832**	**80,200**	**14,045,330**

Table 15. Competitive projects Round II: Budget by year

No	Title	SP	Year 1: 2007	Year 2: 2008	Total
G3007.01	iBridges: Interspecific bridges that give full access to the African rice allele pool for enhancing drought tolerance of Asian rice	1	340,000	329,000	669,000
G3007.02	Genomic dissection of tolerance to drought stress in wild barley	1	343,154	224,450	567,604
G3007.03	Development of genomics resources for molecular breeding of drought tolerance in cassava	2	434,215	323,843	758,058
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 aluminium tolerance gene in sorghum	3	299,598	303,503	603,101
G3007.05	Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-aided breeding	3	284,458	314,132	598,590
G3007.06	Genetic dissection of drought adaptive mechanisms in bread and durum wheat through large scale phenotyping methodologies	2	301,000	301,000	602,000
Total (100%)			**2,002,425**	**1,795,928**	**3,798,353**

A note on commissioned projects

Commissioned projects have not been presented in this budget-by-year section which reflects the full project budgets for competitive and special projects only. This is because unlike the other two types of project which are either a set of competitive projects (within the same timeframe and budget), or special projects on particular themes or tasks with funds earmarked for that specific purpose, commissioned projects are, by design, not homogeneous and are also more flexible: their timeframe is anywhere between one and five years, depending on the task. Commissioned projects are designed to add value to the array of genetic and genomics resources publicly available through GCP, by addressing a specific need, or by collating outputs from one or more research projects.

Table 16. Special projects: Budget by year

Improving tropical legume productivity for marginal environments in sub-Saharan Africa						
Axapta No	**Objective No**	**Objective title**	**Year 1: 2007**	**Year 2: 2008**	**Year 3: 2009**	**Total**
G6007.01	1	Improving groundnut (*Arachis hypogaea* L) productivity for marginal environments in sub-Saharan Africa	1,075,446	1,014,030	948,036	3,037,512
G6007.02	2	Improving cowpea (*Vigna unguiculata* L) productivity for marginal environments in sub-Saharan Africa	928,623	544,374	479,011	1,952,008
G6007.03	3	Improving common bean (*Phaseolus vulgaris* L) productivity for marginal environments in sub-Saharan	625,384	628,009	613,934	1,867,327
G6007.04	4	Improving chickpea (*Cicer arietinum* L) productivity for marginal environments in sub-Saharan Africa	357,348	364,800	351,978	1,074,126
G6007.05	5	Developing cross-species resources for comparative biology in tropical crop legumes	256,402	295,166	316,120	867,688
G6007.06	6	Training and capacity-building for sub-Saharan African scientists	297,200	297,200	257,200	851,600
Total for all objetives			**3,540,404**	**3,143,579**	**2,966,279**	**9,650,262**

Appendix A: Generation Challenge Programme Consortium members and partners

Consortium members

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 Agropecuària (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

NARS partners

1. African Centre for Crop Improvement (ACCI) at the University of KwaZulu–Natal, South Africa
2. Agricultural Biotechnology Institute of the University of Pretoria, South Africa
3. Agricultural Biotechnology Research Institute of Iran (ABRII)
4. Agricultural Research Institute (ARI)–Naliendele Research Station, Tanzania
5. Awassa Agricultural Research Centre, Ethiopia
6. Bangladesh Rice Research Institute (BRRI)
7. Beijing Genomics Institute, China
8. Cambodia Agricultural Research and Development Institute (CARDI)
9. Central Arid Zone Research Institute (CAZRI), India
10. Central Rainfed Upland Rice Research Station (CRURRS), India
11. Central Rice Research Institute (CRRI), India
12. Centre africain de recherche sur bananiers et plantains (CARBAP), Cameroon
13. Centre d'Etude Régional pour l'Amélioration de l'Adaptation à la Sécheresse, (CERAAS), Senegal
14. Chitedze Research Station, Malawi
15. Coconut Research Institute, Sri Lanka
16. Corporación Colombiana de Investigación Agropecuaria (CORPOICA), Colombia
17. Crop Breeding Institute, Department of Research for Development, Zimbabwe
18. Crop Research Institute (CRI), Ghana
19. Department of Agricultural Research (DAR), Myanmar
20. Directorate of Wheat Research (DWR), India
21. Ethiopian Institute of Agricultural Research (EIAR), Ethiopia
22. Fedearroz, Colombia
23. Huazhong Agricultural University (HZAU), China
24. Indian Agricultural Research Institute (IARI)
25. Indira Gandhi Agricultural University (IGAU), India
26. Indira Gandhi Krishi Vidyalaya (IGKV), India
27. Indonesian Centre for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD), Indonesia

28. Indonesian Cereal Research Institute (ICERI)
29. Indonesian Department of Agriculture
30. Institut de l'Environnement et de Recherches Agricoles (INERA), Burkina Faso
31. Institut d'Economie Rurale (IER), Mali
32. Institut de Recherche Agricole pour le Développement (IRAD), Cameroon
33. Institut National de Recherches Agronomiques du Niger (INRAN)
34. Institut Pertanian Bogor (IPB), Bogor Agriculture University, Indonesia
35. Institut Sénégalais de Recherches Agricoles (ISRA), Senegal
36. Institute of Biotechnology and Genetic Engineering, Pakistan
37. Institute of Dry Farming, Hebei Academy of Agricultural Sciences, China
38. Instituto de Botánica del Nordeste (IBONE), Argentina
39. Instituto de Investigaciones Agropecuarias (INIA), Chile
40. Instituto Nacional de Ciencias Agricolas (INCA), Cuba
41. Instituto Nacional de Investigacao Agronómica (IIAM), Mozambique
42. Instituto Nacional de Investigación Agropecuaria (INIA), Uruguay
43. Instituto Nacional de Tecnologia Agropecuaria (INTA), Argentina
44. International Centre for Genetic Engineering and Biotechnology (ICGEB), India
45. Kasetsart University, Thailand
46. Kenya Agriculture Research Institute (KARI)
47. Lake Zone Agricultural Research and Development Institute (LZARDI), Tanzania
48. Liaonin Academy of Agricultural Sciences, China
49. Mikocheni Agricultural Research Institute (MARI), Tanzania
50. Moi University, Kenya
51. Nakhon Sawan Field Crops Research Center (NSFCRC), Thailand
52. Namulonge Agricultural and Animal Research Institute (NAARI), Uganda
53. Nanjing Agricultural University (NAU), China
54. National Agriculture and Forestry Research Institute (NAFRI), Laos
55. National Corn and Sorghum Research Center (NCSRC), Thailand
56. National Crop Resources Research Institute (NaCRRI), Uganda
57. National Maize Research Institute (NMRI), Vietnam
58. National Research Centre on Plant Biotechnology (NRCPB), India
59. National Root and Tuber Crop Research Institute (NRCRI), Nigeria
60. Ningxia University, China
61. Philippine Department of Agriculture
62. Philippine Rice Research Institute (PhilRice)
63. Pohang University of Science and Technology, South Korea
64. Pontificia Universidad Católica de Valparaíso, Chile
65. Promoción e Investigación de Productos Andinos (PROINPA), Bolivia
66. Punjab Agricultural University (PAU), India
67. Rajasthan Agricultural University (RAU), India
68. Rayong Field Research Station, Thailand
69. Rewa College of Agriculture, India
70. Rice Gene Discovery Unit (RGDU), Thailand
71. Rice Research and Training Centre, Egypt
72. Savannah Agricultural Research Institute (SARI), Ghana
73. Scientific and Industrial Research and Development Centre (SIRDC), Zimbabwe
74. Shandong Academy of Agricultural Sciences, China
75. Shanxi Academy of Agricultural Sciences (SAAS), China
76. Shenyang Agricultural University, China
77. Sichuan Agricultural University (SAU), China
78. South Agricultural Research Institute (SARI), Ethiopia
79. Tamil Nadu Agricultural University (TNAU), India
80. Tyshreen University, Syria
81. Ubon Ratchatani University (UBU), Thailand
82. Universidad Autónoma Chapingo, Mexico
83. Universidad de la República, Urguguay
84. Universidad Peruana Cayetano Heredia, Peru
85. Universidade Católica de Brasilia (UCB), Brazil
86. Université d'Abomey–Calavi, Benin
87. Université de Cocody, Côte-d'Ivoire
88. University of Agricultural Sciences (UAS), India
89. University of Agricultural Sciences, Dharwad, India
90. University of Agriculture and Forestry, China
91. University of Chile
92. University of Dhaka, Bangladesh
93. University of Hyderabad, India
94. University of Indonesia
95. University of KwaZulu–Natal (UKZN), South Africa
96. University of Southern Mindanao, The Philippines
97. University of the Witwatersrand, South Africa
98. West Africa Centre for Crop Improvement (WACCI), Ghana
99. Yunnan Academy of Agricultural Sciences (YAAS), China

ARI partners

1. Agricultural Biotechnology Center (ABC), Gödöll , Hungary
2. Agricultural Research Institute of the Hungarian Academy of Sciences (ARI-HAS), Hungary
3. Australian Centre for Plant Functional Genomics Pty Ltd (ACPFG)
4. Australian National University
5. Biogemma, France
6. Biomathematics and Statistics Scotland Research Institution (BIOSS), UK
7. Botanic Garden and Botanical Museum Berlin–Dahlem (BGBM), Germany
8. Centre International de Hautes Etudes Agronomiques Méditerranéennes–Institut Agronomique Mediterranéan de Montpellier (CIHEAM-IAMM), France
9. Centre National de Génotypage (CNG), France
10. Centre National de la Recherche Scientifique, France
11. Centro Internacional de Altos Estudios Agronómicos Mediterráneos–Instituto Agronómico Mediterráneo de Zaragoza (CIHEAM–IAMZ), Spain
12. Colorado State University (CSU), USA
13. Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia
14. Cornell University, USA
15. Department of Plant Sciences and Plant Physiology, Eszterházy Károly College (Eger), Hungary
16. Department of Primary Industries (DPI), Australia
17. Eidgenössische Technische Hochschule, (Swiss Federal Institute of Technology) Zurich, Switzerland
18. European Bioinformatics Institute (EBI), UK
19. GrainGenes (CSIRO), Australia
20. Imperial College London, UK
21. Institut für Pflanzenbau und Pflanzenzüchtung, Germany
22. Institute for Genomic Diversity (IGD), Cornell University, USA
23. Institute for Plant Genetics and Crop Plant Research (IPK), Germany
24. Institute of Experimental Botany (IEB), Czech Republic
25. Institute of Genetics and Cytology, Russia
26. Instituto de Agricultura Sostenible, Spain
27. J Craig Venter Institute (incorporating TIGR, The Institute for Genomic Research), USA
28. Japan International Research Center for Agricultural Sciences (JIRCAS), Japan
29. Kansas State University, USA
30. Leiden University Medical Center, The Netherlands
31. Max Planck Institut for Developmental Biology, Germany
32. McMaster University, Canada
33. National Center for Genome Resources (NCGR), USA
34. National Institute of Agricultural Biology (NIAB), UK
35. North Carolina State University (NCSU), USA
36. Oregon State University (OSU), USA
37. Plant Genome and Development Laboratory (LGDP), University of Perpignan, France
38. Queen Mary Intellectual Property Research Institute, University of London, UK
39. RIKEN laboratories, Japan
40. Scottish Crop Research Institute (SCRI), UK
41. Temasek Lifesciences Laboratory, Singapore
42. Texas A&M University, USA
43. Texas Agricultural Experiment Station, USA
44. The Hebrew University of Jerusalem, Israel
45. The Institute for Genomic Research (TIGR), USA (see J Craig Venter Institute)
46. United States Department of Agriculture–Agricultural Research Service (USDA–ARS)
47. Università di Bologna, Italy
48. Università di Udine, Italy
49. University of Aarhus, Denmark
50. University of Adelaide, Australia
51. University of Alberta, Canada
52. University of Arizona, USA
53. University of California, Berkley (UC–Berkley), USA
54. University of California, Davis (UC–Davis), USA
55. University of California, Riverside (UC–Riverside), USA
56. University of Geneva, Switzerland
57. University of Georgia, Athens (UGA), USA
58. University of Hohenheim, Germany
59. University of Leicester, UK
60. University of Madrid, Spain
61. University of Missouri, USA
62. University of Queensland, Australia
63. University of Rennes, France
64. University of Tsukuba, Japan
65. University of Virginia (UVA), USA
66. Virginia Tech (Virginia Polytechnic Institute and State University), USA

Funders

1. Bill & Melinda Gates Foundation
2. Department for International Development (DFID), UK
3. European Commission (EC)
4. Pioneer Hi-Bred International, Inc
5. Swedish International Development Cooperation Agency (Sida)
6. Swiss Agency for Development and Cooperation (SDC)
7. Syngenta Foundation for Sustainable Agriculture
8. The Rockefeller Foundation
9. The World Bank

CGIAR Centres and Challenge Programmes

1. International Food Policy Research Institute (IFPRI)
2. International Livestock Research Institute (ILRI)
3. Challenge Program on Water and Food
4. HarvestPlus Challenge Program
5. Sub-Saharan Africa Challenge Programme

Private sector

1. Diversity Arrays Technology Pty Ltd (DArT P/L), Australia
2. Genaissance Pharmaceuticals, Inc, France
3. Perlegen Sciences, Inc, USA
4. Syngenta

Other partners

1. African Molecular Marker Applications Network (AMMANET)
2. Barwale Foundation, India
3. Biosciences Eastern and Central Africa (BecA), Kenya
4. Eastern and Central Africa Bean Research Network (ECABREN)
5. Global Crop Diversity Trust, Italy
6. Horticulture Research International
7. International Atomic Energy Agency (IAEA), Austria
8. International Rice Functional Genomics Consortium, coordinated by IRRI, The Philippines
9. New Partnership for Africa's Development (NEPAD)
10. Southern Africa Bean Research Network (SABRN)

Appendix B: GCP staff—2007

Name	Function	Location	Joined
Jean-Marcel Ribaut	Director	GCP Headquarters, Mexico	2005
Jean-Christophe Glaszmann	Subprogramme 1 Leader	CIRAD, France	2004
Hei Leung	Subprogramme 2 Leader	IRRI, Philippines	2004 (left 2007)
Rajeev Varshney	Subprogramme 2 Leader	ICRISAT, India	2007
Philippe Monneveux	Subprogramme 3 Leader	GCP Headquarters, Mexico	2006
Theo van Hintum	Subprogramme 4 Leader	Wageningen University, The Netherlands	2004
Carmen de Vicente	Subprogramme 5 Leader	GCP Headquarters, Mexico	2004
Nosisa Mayaba	Associate Scientist, SP5	GCP Headquarters, Mexico	2007
Antonia Okono	Communications Manager	GCP Headquarters, Mexico	2007
Kaitlin Lesnick	Communications Assistant	GCP Headquarters, Mexico	2005 (left 2007)
Kate Durbin	Communications Assistant	GCP Headquarters, Mexico	2007
Griselda Marquez	Executive Assistant	GCP Headquarters, Mexico	2004
Adriana Santiago	Project Officer	GCP Headquarters, Mexico	2004
Laura I Ruiz	Programme Assistant	GCP Headquarters, Mexico	2007
Paula Maria de León	Administrative Coordinator	GCP Headquarters, Mexico	2007
Imelda Rosas	Accounting/Administrative Assistant	GCP Headquarters, Mexico	2006
Sandra Insignares	Financial Administrator	CIAT, Cali, Colombia	2005 (left 2007)
Carlos A Tovar	Administrative Assistant	CIAT, Cali, Colombia	2005 (left 2007)
Aida Martinez	Intern	GCP Headquarters, Mexico	2007

Appendix C: Selected publications—2007

In the interests of space, the list below is limited to books, book chapters and journal articles only. For a full list of all GCP publications in 2007, as well as through the years, please visit http://www.generationcp.org/research.php?da=0642451

a) Programme publications

Generation Challenge Programme (2007). *2006 Annual report and year four (2007) workplan*. Generation Challenge Programme, Mexico DF, Mexico, 40 pp. http://www.generationcp.org/comm/AR_CP_06_internet.pdf

Generation Challenge Programme (2007). *2007 Project mid-year and final reports: competitive and commissioned projects*. Proceedings of Generation Challenge Programme Annual Research Meeting, Benoni, South Africa, 12–16 September 2007. Generation Challenge Programme, Mexico DF, Mexico, 190 pp. http://www.generationcp.org/UserFiles/File/ARM%20PROCEEDINGS%202007_Finalversion_front+back%20cover.pdf

Generation Challenge Programme (2007). *2007 Poster abstracts* (Annual Research Meeting, 12–16 September 2007). Generation Challenge Programme, Mexico DF, Mexico, 90 pp. http://www.generationcp.org/UserFiles/File/Abstracts.pdf

Generation Challenge Programme (2007). *Medium-term plan 2008–2010*. Generation Challenge Programme, Mexico DF, Mexico, 67 pp. http://www.generationcp.org/UserFiles/File/MTP%202008-2010_FINAL%20COPY.pdf

Generation Challenge Programme (2007). *Partner and product highlights*. Generation Challenge Programme, Mexico DF, Mexico, 44 pp. http://www.generationcp.org/UserFiles/File/Highlights07.pdf

Generation Challenge Programme (2007). *The Generation Challenge Programme–Cultivating plant diversity for the resource-poor*. Brochure, Generation Challenge Programme, Mexico DF, Mexico, 4 pp. http://www.generationcp.org/UserFiles/File/gcp-brocure_short%20version_revised.pdf

b) Books

Varshney R and Tuberosa R, eds (2007). *Genomics-assisted crop improvement, Volume I: Genomics approaches and platforms*. Springer, Dordrecht, The Netherlands. http://www.generationcp.org/UserFiles/File/gaci_flyer_250108.pdf

Varshney R and Tuberosa R, eds (2007). *Genomics-assisted crop improvement, Volume II: Genomics applications in crops*. Springer, Dordrecht, The Netherlands. http://www.generationcp.org/UserFiles/File/gaci_flyer_250108.pdf

c) Book chapters

Baum M, Von Korff M, Guo P, Lakew B, Hamwieh A, Lababidi S, Udupa SM, Sayed H, Choumane W, Grando S and Ceccarelli S (2007). Molecular approaches and breeding strategies for drought tolerance in barley. In: *Genomics-assisted crop improvement, Volume II: Genomics applications in crops* (Varshney RK and Tuberosa R, eds). Springer, Dordrecht, The Netherlands, pp 51–79. (DOI: 10.1007/978-1-4020-6297-1_3).

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Blair M, Fregene M, Beebe S and Ceballos H (2007). Marker-assisted selection in common beans and cassava. In: *Marker-assisted selection: current status and future perspectives in crops, livestock, and foresty, and fish* (Guimaraes E, Ruane J, Scherf B. Sonnino A and Dargie J, eds). Food and Agricultural Organization (FAO) of the United Nations, Rome, Italy, pp 1–116.

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d) Journal articles

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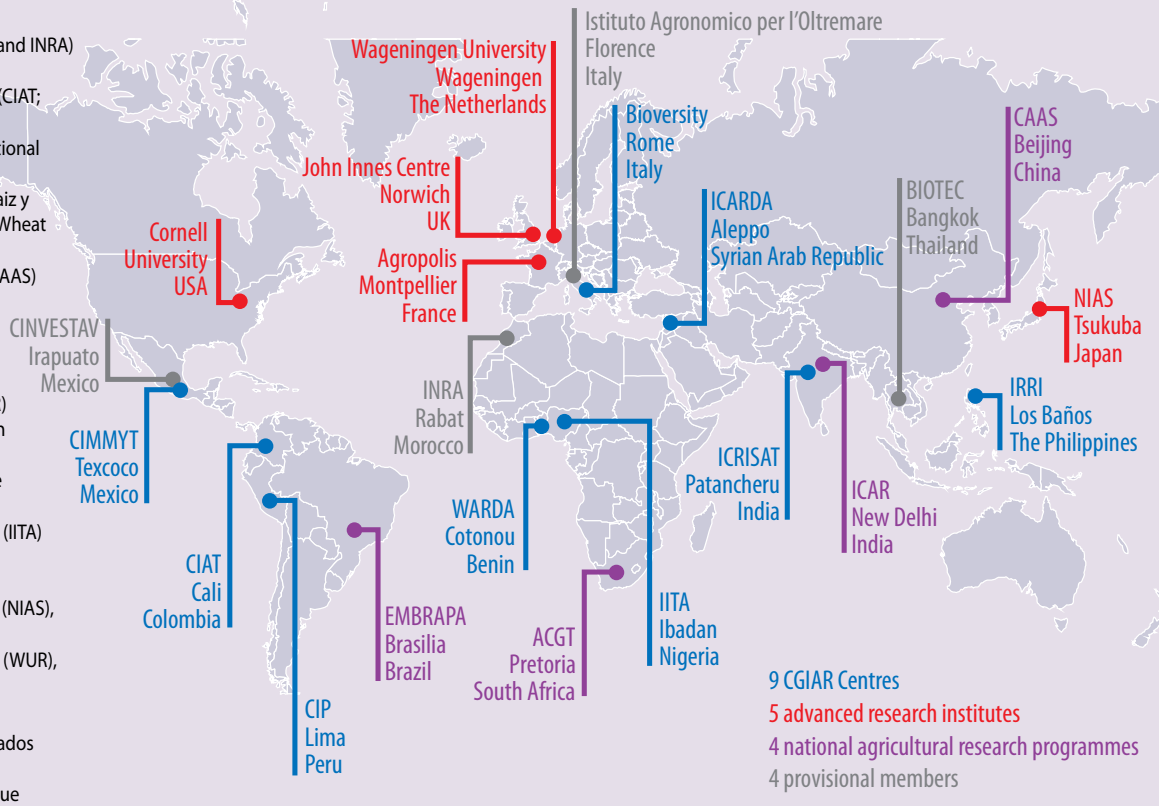
The GCP Consortium

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

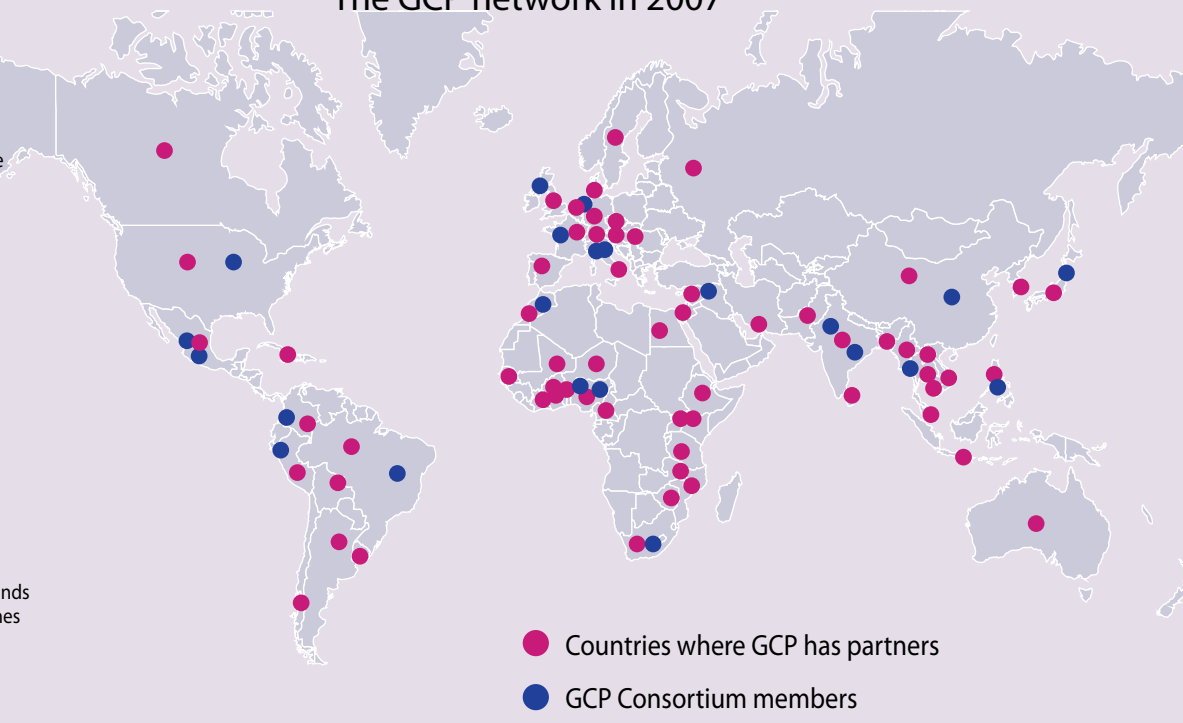


Where in the world is GCP?

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

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

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