Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE-POOR

Medium-Term Plan 2008-2010

June 2007

Generation
Cultivating Plant Diversity for the Resource-Poor

Generation Challenge Programme
Medium-Term Plan: 2008–2010

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Acronyms and abbreviations

ABA	abcissic acid
ABS	access and benefit-sharing
ACCI	African Centre for Crop Improvement (South Africa)
ACGT	African Centre for Gene Technologies (South Africa)
ADOC	allelic diversity for orthologous candidate genes
AFLP	amplified fragment length polymorphism
Al	aluminium
ARI	advanced research institute
ARM	Annual Research Meeting
ASR	ABA-stress-ripening
BAC	bacteria artificial chromosome
BC1F1	backcross 1 hybrid of first generation
BecA	Biosciences Eastern and Central Africa
BIOTEC	National Center for Genetic Engineering and Biotechnology (Thailand)
BLB	bacterial leaf blight
bp	base pair
BRRI	Bangladesh Rice Research Institute
BSA	bulk segregant analysis
CAAS	Chinese Academy of Agricultural Sciences
CARBAP	African Centre for Research on Banana and Plantain (Cameroon)
CAS	Chinese Academy of Sciences
CBB	cassava bacterial blight
cDNA	complementary DNA
CGIAR	Consultative Group on International Agricultural Research
CGM	cassava green mites
CIAT	International Center for Tropical Agriculture
CIMMYT	International Maize and Wheat Improvement Center
CIP	International Potato Center
CIRAD	Centre de Cooperation Internationale en Recherche Agronomique pour le Développement
CMD	cassava mosaic disease
CNRS	Centre National de la Recherche Scientifique (France)
COS	conserved orthologous sequences
CRI	Crop Research Institute (Ghana)
CRURRS	Central Rainfed Upland Rice Research Station (India)
CSIRO	Commonwealth Scientific and Industrial Research Organisation (Australia)
CSS	chromosome segment substitution
CSSLs	chromosome segment substitution lines
CWANA	Central and West Asia and North Africa
DArT	diversity array technology
DFID	Department for International Development (UK)
DNA	Deoxyribonucleic acid
DREB	DREB Dehydration responsive element binding
EBI	European Bioinformatics Institute
EC	European Commission
EMBRAPA	Empresa Brasileira de Pesquisa Agropecuária (Brazilian Agricultural Research Corporation)
EST	expressed sequence tag
FAO	Food and Agriculture Organisation of the United Nations

FSTs	flanking sequence tags
GCP	Generation Challenge Programme
GIS	Geographic Information System
GPL	General Public License
GSS	Genotyping Support Service
GxE	Genotype times environment interaction
HPC	high-performance computing
HTP	high-throughput
HW	Hardy Weinberg
IAEA	International Atomic Energy Agency
IARCs	International agricultural research centres
IBN	Insituto de Botánica del Nordeste (Argentina)
ICABIOGRAD	Indonesian Centre for Agricultural Biotechnology and Genetic Resources and Research Development
ICARDA	International Center for Agricultural Research in the Dry Areas
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
IER	Institut d’Economie Rurale (Mali)
IFSSA	Indian Foundation Seed and Services Association
IITA	International Institute of Tropical Agriculture
ILRI	International Livestock Research Institute
ILs	inbred lines
INERA	Institut National de l'Environnement et de Recherches Agricoles (Burkina Faso)
INIA	Instituto Nacional de Investigación Agropecuaria (Uruguay)
INRA	Institut national de la recherche agronomique (France)
INRAN	Institut National de Recherches Agronomiques du Niger
IP	intellectual property
IPRs	intellectual property rights
IRD	Institut de Recherche pour le Développement
IRRI	International Rice Research Institute
IT	information technology
JIRCAS	Japan International Research Center for Agricultural Sciences
KARI	Kenya Agricultural Research Institute
kb	kilobase
LD	linkage disequilibrium
LGPL	Lesser General Public License
LIMS	Laboratory Information Management System
MAB	marker-assisted backcrossing
MARI	Mikocheni Agricultural Research Institute, Tanzania
MAS	marker-assisted selection
MDGs	Millennium Development Goals
MoU	Memorandum of Understanding
MTP	Medium-Term Plan
NAARI	Namulonge Agricultural and Animal Research Institute (Uganda)
NARS	national agricultural research system
NCBI	National Center for Biotechnology Information
NCGR	National Center for Genome Resources, USA
NERICA	new rice for Africa
NIAB	National Institute of Agricultural Biology (UK)
NIAS	National Institute of Agrobiological Sciences (Japan)
NILs	near-isogenic lines
NRCRI	National Root Crops Research Institute (Nigeria)
NSFCRC	Nakhon Sawan Field Crops Research Center (Thailand)

OFSP	orange-fleshed sweet potatoes
OPV	open pollinated variety
OSI	open source initiative
P	phosphorous
PASS	Program for African Seed Systems
PDG	Project Development Guide
PGRFA	International Treaty on Plant Genetic Resources for Food and Agriculture
PPD	post-harvest physiological deterioration
PROINPA	Promoción e Investigación de Productos Andinos, Bolivia
PSS	phenotyping support service
Pup1	phosphorus-uptake 1
QTL	quantitative trait loci
QTLxE	Quantitative trait loci times environment interaction
QxE	QTL times environment interaction
R&D	research and development
RFLP	restriction fragment length polymorphism
RT–PCR	real-time polymerase chain reaction
RYMV	rice yellow mottle virus
SCAR	sequence-characterised amplified regions
SGRP	Systemwide Genetic Resources Programme of the CGIAR
SIRDC	Scientific and Industrial Research and Development Centre
SNP	single nucleotide polymorphism
SP	Subprogramme
SPCSV	sweet potato chlorotic stunt virus
SPFMV	sweet potato feathery mottle virus
SPVD	sweet potato virus disease
SSR	simple sequence repeat
STS	sequence tag site
TIGR	The Institute for Genomic Research (USA)
TNAU	Tamil Nadu Agricultural University (India)
UAS	University of Agricultural Sciences, Bangalore (India)
VARTC	Vanuatu Agriculture Research and Technical Centre
WUR	Wageningen University and Research Centre (The Netherlands)
YAAS	Yunnan Academy of Agricultural Sciences (China)

Overview

Introduction

Launched in 2003 as a 10-year initiative, the Generation Challenge Programme (GCP, or simply Generation) is now entering its fourth year and consequently submitting its fourth Medium-Term Plan (MTP). In the past three years, GCP has made remarkable progress in intensive research and strategic planning. A key highlight in 2006 was the development of a strategy framework, a set of guiding principles for GCP's strategic decisions. This strategy framework is complemented by 'reference studies' that provide data on GCP's impact targets (farming systems and crops). This refinement of our research strategy sharpened our focus and informed the selection of commissioned projects to be initiated in 2008, in particular for Subprogrammes (SPs) 3 and 5. However, Generation remains dedicated to the exploration and characterisation (genotyping and phenotyping) of diversity in staple crops, and will continue to support this core effort.

Despite a delayed start date due to unexpected financial issues, the second round of GCP competitive projects and the new 2007 commissioned projects should start in July 2007. A major three-year project targeting the improvement of tropical legume productivity for marginal environments was also approved in May 2007. GCP management has been paying special attention to data quality control, data release, product management and delivery. Consequently, and looking at the evolution of GCP through time, we realigned the Management Team to better address our renewed emphasis on product management and delivery.

GCP's niche and network

GCP was created to undertake what is often referred to as 'upstream' research—characterising crop genetic diversity using molecular markers, creating diversity by making wild crosses or creating mutant collections, identifying favourable alleles for crop performance using comparative genomics, quantitative trait loci (QTL) analysis and 'omics' approaches, developing bioinformatic infrastructure and tools to conduct those studies in a suitable way and ensuring data availability to the research community. To this end, GCP cultivates partnerships for innovative science and conducts research to better understand the genetic basis of GCP target traits. However, GCP also has, as a major objective, linking basic research with applied science, by generating useful knowledge and developing practical tools such as molecular markers for target traits to complement phenotypic selection and impact crop breeding for adapted germplasm in target environments. In this way, GCP bridges the gap between high-tech bench scientists and the plant breeders and resource-poor farmers the research is supposed to help. It is this duality that makes Generation unique within the CGIAR and the broader agricultural research-for-development community.

GCP was also assigned a trait of focus: drought tolerance, which affects almost all crops and all regions worldwide, thereby providing opportunities to apply useful discoveries across crops. As no single institution can command the breadth of expertise and resources necessary to achieve these objectives, GCP operates as a network that leverages significant resources—funds, skills, equipment, knowledge and social capital—through partnerships with a broad base of public and private institutions and initiatives. GCP partners are diverse and complementary in their skills. This ensures seamless continuity of activities all along the pipeline of GCP activities, starting from characterising and creating diversity, up to the delivery of value-added crops for marginal environments. A critical benefit of the network is that it provides access to vast stores of plant genetic resources, as well as to cutting-edge technologies and scientific expertise, bringing all the three together for crop improvement.

Evolution of the GCP strategy

GCP's first two years were devoted to establishing and implementing our operational structure and research portfolio. In the third year (2006), we started to identify where we were doing well and where we could be doing better. GCP's founding document[1] had a clear pathway to get the programme up and running. However, by GCP's third year, critical questions began to arise such as: How should resources be balanced to ensure that GCP contributes to scientific knowledge while also delivering products to benefit resource-poor farmers? How should GCP prioritise regions and crops?

To tackle these questions, the GCP Management Team, comprising the Director and the five Subprogramme Leaders, was of the view that a strategic framework[2] outlining GCP's internal reflections on its mission, structure, research approach and resource allocation would be useful at this point in GCP's development, in keeping with our ultimate goal of ensuring our products impact crop breeding for the benefit of resource-poor farmers. To this end, the GCP Strategic Framework was refined, building upon the existing strategy and clarifying fundamental issues such as how GCP articulates its research approach and allocates resources. The strategic framework is a set of guiding principles for strategic decision-making and helps identify, and further clarify,

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[1] *A Proposal to Establish a Challenge Programme for Unlocking the Genetic Diversity of Crops for the Resource-Poor* http://www.generationcp.org/brochure.php under 'Strategy Documents'

[2] *Generation Challenge Programme Strategic Framework*. February 2007 http://www.generationcp.org/comm/gcp_framework_final.pdf

important issues in the large and complex task assigned to GCP. The strategy is complemented by 'reference studies' (such as the one by Glenn Hyman et al[3]) that provide data on GCP's impact targets (in terms of crops and regions). Those data are key for informed decisions and strategy implementation.

GCP's reworked strategy was approved by the Programme Steering Committee (PSC) in November 2006. This framework shall guide GCP's activities in the final years of Phase I and the beginning of Phase II (2009–2013). Now that Generation is fully operational, we are currently refining the notion of 'products' in the context of GCP and how best to manage them. A major objective is to ensure optimal flow of upstream research outputs to more applied research within GCP. The Management Team strongly believes that Generation's long-term success will depend mainly on the ability to learn from our experiences, and to make the appropriate adjustments in both strategy and structure.

Products and delivery plan at the heart of GCP
In 2007, GCP will launch its Delivery Plan Kit designed by a panel of experts in technology transfer, research management, impact assessment and marketing. For each new major project, a delivery plan is now required.

Project development and reporting will be further streamlined by a new Web-based tool for project design and management, the Project Development Guide (PDG). Improving the design of our new projects with clear milestones and workplans will optimise the planning of research activities and improve project monitoring for our broad and diverse research portfolio.

Product management and product delivery are intertwined: product management ensures the flow of products along the research–delivery chain. It is not all products that are ideal candidates for value-adding. Product management helps to identify the best options for returns on value-adding investments. It comprises identifying, gathering, storing and packaging the various products. To facilitate those critical steps, specific Web-based templates for project proposal and reports have been developed and implemented for the new 2007 projects (both commissioned and competitive). The spectrum of GCP products is really broad and at almost every step along the GCP research pipeline, products generated can directly impact breeding efficiency or can be used in the next step of the pipeline. As an example, the high upstream germplasm characterisation conducted by SP1 can not only lead to the identification of a new pool of diversity to be use in pre-breeding activities by local national programmes, but will also help identify contrasting lines for genetic studies under SP2, or lines with favourable alleles for desirable traits to be used as donor lines in marker-assisted selection experiments in SP3.

GCP products can be classified into five broad categories (genetic resources, genomic resources, validated markers for breeding, new tools and methodologies, and training material). Validation is central to product management and must precede delivery: it confirms the suitability and potential benefit of a given product in a given environment. Once validated, products can be widely disseminated. Product management is a crucial link in connecting upstream research and the deployment of research-based products that will have tangible impacts on agriculture.

GCP Management Team realignment
Consistent with our view on the importance of product management and delivery, SP3 and SP5 leader positions were adjusted from half-time to full-time positions. The SP3 Leader position now also includes product management to ensure the flow of products along the research–delivery chain, while the SP5 Leader, in addition to managing capacity-building, will continue to be responsible for product marketing and delivery outside GCP.

Applying the GCP strategy
A strategy is only of value if it is implemented and in this regard, 2007 is a watershed year for Generation. Our new project portfolio for 2008 is defined by several key elements of our strategy: 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 (e.g. Genotyping Support Service), better integration of breeders in GCP projects and an increasing leadership role by scientists from national programmes, thus ensuring 'downstream' projects are demand-driven.

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 under target environments, and to better define the linkage disequilibrium (LD) in target crops, so as to go to the alleles through association studies.
- New SP2 projects will now exclusively focus on identifying genes and to better understand regulatory pathways involved in drought tolerance, exploring new approaches through comparative genomics, and taking advantage of the increasing genomic sequences available.
- The number of SP3 projects promoting the use of markers is increasing commensurate with the knowledge generated in SPs 1 and 2. SP3 validates and adds value to the products and information generated

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[3] Poster summarising this study available at: http://www.generationcp.org/comm/drought_poverty_poster.jpg

by the other subprogrammes. All SP3 projects will target crop improvement in drought-prone environments, focusing on GCP target crops and environments.

- 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, while support to GCP scientists on biological questions and data handling and analysis will increase.
- 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. The time has also come to initiate *ex ante* analysis to evaluate the impact of key GCP products and to help refine our target traits and regions based on local needs.

In addition, there is a clear orientation towards 'internal' value-adding within GCP. As an example, there are several new projects whose first activity will be evaluating the reference sets identified through SP1 commissioned work. For example, our new major project on 'Improving tropical legume productivity for marginal environments in sub-Saharan Africa' includes the evaluation of reference sets of groundnuts, cowpeas, beans and chickpeas in several countries across sub-Saharan Africa.

We are also keen on ensuring continuity of our most promising research activities guaranteed to deliver quick payoffs. Our new set of competitive projects is clearly oriented towards short- to mid-term products that can impact breeding for marginal environments. Therefore, some of the competitive proposals are on new activities standing on the shoulders of existing GCP projects.

To illustrate the progression, over the last three years, GCP has supported a project on the identification and characterisation of a major gene for aluminum tolerance in sorghum. The project is led by Cornell University scientists in collaboration with scientists from the Brazilian Agricultural Research Corporation (EMBRAPA). The gene has now been cloned (Alt_{SB}). Starting in July 2007, a new competitive project will carry this work a step further by identifying superior Alt_{SB} haplotypes by association mapping (Output 3.4), and developing and using haplotype-specific markers for introgression into pre-breeding near-isogenic lines (Output 3.14). A major output of this project is the development of markers to improve sorghum performance under acid soil in Latin America and West Africa. This second project is led by EMBRAPA, in collaboration with African scientists from national research programmes.

Because the second call for proposals had the benefit of being informed by preceding and ongoing research, the call was designed to dovetail with our research priorities. In this way, we complement competitive projects with strategic commissioned activities. One of the selected competitive projects will make available to breeders the entire genetic diversity of *O. glaberrima*. The diversity will be used in classical breeding schemes or marker-aided selection schemes developing interspecific bridges between selected *O. glaberrima* accessions and reference *O. sativa* recipient cultivars. To add value to this new activity, a commissioned project is to be initiated to produce new NERICA rice for West Africa, including large-scale phenotyping of glaberrima progenies, training African scientists at the Africa Rice Center (WARDA) and capacity-building for Mali's national research programme.

Finally, we have initiated targeted actions to ensure good communication, consolidate the research and guarantee the flow of products considering the portfolio of activities for a given crop and/or region. For instance, through the 6th Asian Crop Science Association Conference, and the 2nd International Conference on Rice for the Future in Thailand in late 2007, GCP will organise a two-day pre-conference workshop for all Generation partners and selected stakeholders working on rice in Asia. The fora are a good platform to showcase GCP's work, get the GCP rice community up to speed and explore new opportunities.

In conclusion, we can confidently say that Generation is a healthy and fully functional challenge programme with a fine-tuned strategy. The Management Team is fully committed to implementing our 2006 strategy, as reflected by the new set of projects identified in 2007 for implementation in 2008. The research portfolio presented in this MTP shows greater inter-subprogramme cohesion. And while the entire set of our mandate crops will continue to be the focus of some of our activities especially in SP1, specific research themes have been identified and will be pursued for important crops identified in GCP target farming systems. To ensure GCP is premised on a solid base, the Management Team committed to the following fundamentals: 1) data release and quality control (obligatory check points and external reviews); 2) maintaining some of our existing infrastructure (e.g. bioinformatics); and, 3) ensuring access to, and delivery of, GCP products (e.g. helpdesks, Genotyping Support Service).

Context

Crop improvement for poverty alleviation

For the foreseeable future, public sector research on staple food crops, especially crops for marginal environments, will be indispensable for poor households in such environments. Economic alternatives to agriculture are often extremely limited in these areas. Yet to promote more rapid economic growth and improve the welfare of poor and marginalised populations, investments in agriculture are among the most promising a nation can make. GCP contributes to the goals of national and regional development strategies in our partner countries by adding value to their efforts to improve agriculture.

The agricultural sectors of many developing countries are changing rapidly in response to a host of local and global factors. Farmers in more productive environments can now diversify beyond staple food crops and have increasing access to new global and domestic agricultural markets. Farmers in marginal areas—areas typically characterised by high-risk crop production, poor agricultural yields and rampant poverty—are still isolated from markets, agricultural inputs and support services.

Accessing technology

Advances in plant breeding could literally transform landscapes in developing countries by addressing threats to agriculture such as drought. Yet most developing countries—with the exception of a few large and advanced national plant breeding programmes—have little access to the new technologies and skills that have improved plant breeding in wealthy nations.

More than ever before, threats to agriculture underscore the increasing need for what has been termed 'translational biology'—creating strong links between basic and applied research to support agriculture worldwide, ensuring, in the case of GCP, that the huge financial resources invested globally in biotechnologies will impact crop breeding for marginal environments.

It is farmers in these environments who are the primary focus of GCP's research. We now have reference samples for most GCP mandate crops and we have characterised genes of high importance for plant performance under stress. Through our network, we tap into the very latest in technological achievements to advance our research, and to adjust our research portfolio accordingly. For example, sorghum genome sequence is now available. This has momentous implications for GCP's work on improving sorghum, opening new doors for both upstream and applied research for geneticists and breeders.

The global agenda: agriculture, drought and climate change

It is clear from events in Europe in 2004 and other regions of the world that drought can have a devastating impact on the productivity of many crop species. There is an increasing consensus of opinion among scientists, policymakers and politicians that human activities are leading to changes in global climate, and one likely consequence will be changes in the magnitude of the impact of water stress in different and hitherto unaffected and unexpected parts of the world. For instance, a dry and cold winter followed by a heat wave in August were key factors contributing to an estimated fall of 25 million tons (or 12%) in cereal production in the European Union for 2003/04. In particular, maize suffered from the drought and heat wave that hit southern Europe in 2003, with an estimated 20% decrease in productivity corresponding to a drop in yield to 7.4 t/ha. This type of unpredictable and extreme weather will likely be more commonplace in future years and impacts will be dramatic for crops in marginal environments.

The outlook is bleak and exacerbated by adverse climate change: global climate models are predicting more extended, and more extreme, weather events. Among the effects of climate change, the spectre of more prolonged and intense droughts is particularly disturbing. Today, even favourable and irrigated environments are at greater risk from drought.

The onset of global warming is leading to an increasingly erratic climate, with a higher localised incidence of drought and severe storms. The prediction is that sub-Saharan Africa is likely to suffer most from the combined effects of higher temperature and reduced rainfall, which imply a higher frequency of drought conditions during the crop growing season. Crop improvement on its own cannot mitigate the full economic loss caused by drought, but it can play a key role in at least maintaining production levels in drought-prone areas. For this reason, drought continues to be GCP's number one priority in the quest for greater drought tolerance for food crops in GCP's target regions.

Drought is one of the biggest threats facing agriculture today, with devastating and far-reaching effects on entire landscapes and regions. It drastically reduces crop yields, more often than not resulting in total crop failure. The Food and Agriculture Organization of the United Nations (FAO) ranks drought as the single most common cause of severe food shortages in developing countries. In a comparison of food emergencies between 2002 and 2004, drought was involved in 50 to 70% of the cases, significantly surpassing other causes such as conflict, flooding and economic problems. More than three-quarters of the world's maize-growing regions suffer up to 50% yield losses each year due to drought.

Programme discussion

Generation's research, capacity-building and delivery activities are organised under five subprogrammes (SPs) and executed through three funding schemes: competitive grants, commissioned research projects and special projects. The five subprogrammes are the operational structure for allocating and managing research projects. Building on CIMMYT's accounting software, Axapta, we will develop a customised GCP workflow system. This Web-based system will ensure easy and seamless access by our geographically distributed Management Team to project progress reports and financial information. The system will further enhance GCP project monitoring and also promote transparency on GCP's achievements since some of the information will be publicly available through our Web site, and accessible to the entire GCP scientific community worldwide.

Subprogramme 1: Genetic diversity of global 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: Comparative genomics for 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: Comparative trait capture for crop improvement
Validates gene function and refines molecular breeding systems and the resulting enhanced germplasm, so as to increase the efficiency, speed and scope of plant breeding.

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

Subprogramme 5: Capacity-building and enabling delivery
Empowers scientists in developing country 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.

Research framework
GCP's research framework is unique, composed of three complementary funding mechanisms—competitive grants, commissioned research projects and special projects. These three mechanisms are well-suited to our agile funding system and also guarantee that GCP's research portfolio is fine-tuned to the latest developments in the dynamic research-for-development world in which GCP operates. In the logframe, we identify the funding mechanism for each output. This includes discretionary funds granted annually to GCP's half-time SP leaders (SPLs) to conduct research directly applicable to SP objectives. Results from this research count as specific GCP outputs.

1) Competitive grants
    a. The 1st round of competitive grants comprised 17 projects, each with an annual budget of about US$300,000. They were launched in January 2005 and are scheduled to end in January 2008. However, as is common with new programmes, a number of first-round projects started late, or had a slow start. Realistically, we expect most of these 1st round projects to continue beyond January 2008 on a no-cost extension, which is why they feature in the current logframe.
    b. The 2nd round of competitive grants has 6 two-year (2007–2008) projects of between $300–400,000 per year. The call went out in February 2006 and the six projects were selected in October 2006. However, due to delays in disbursement of EC funds, the projects are on hold and will commence in mid–2007.

2) Commissioned research projects: These are typically one- to two-year complementary projects with an annual budget ranging between US$ 20,000–300,000. They are designed to add value to the array of genetic and genomic resources publicly available through GCP by addressing a specific need, or by collating outputs from research projects. New commissioned projects have been delayed in 2007 due to delayed funding.

3) Special projects: For these projects, budget and activities are developed in close collaboration with donors based on specific requirements. An example is the three-year project, funded by the Bill & Melinda Gates Foundation, on 'Improving tropical legume productivity for marginal environments in Africa'. This special project starts in 2007 and its outputs are reported in this MTP.

The management realises that a good balance between the three kinds of project is important to optimise programme efficiency. We want to continue to capture new ideas, approaches and bring in partners that fit our research priorities, keeping the flexibility of consolidating our project portfolio around the most important and most promising axes. In this sense, GCP would like to have a competitive call about every 18 months. Given our financial prospects, we are confident that a third call will be made by the end of 2007, or in early 2008. Like the second one, the third call will also be thematic, drawing from GCP's Strategy Framework and outputs of the reference studies.

Centre Financial Indicators

GCP has maintained a healthy financial position, thanks in large part to support from committed funders. Our major funders are the European Commission (EC), the UK's Department for International Development (DFID) and the World Bank—they jointly contribute about 90% of our total income in 2006. The Rockefeller Foundation, the Swiss Agency for Development and Cooperation and the Swedish International Development Cooperation Agency also support GCP.

The EC contribution alone accounts for about 40% of our annual budget. Because the EC and the World Bank were unable to arrive at a working arrangement for disbursement in 2006, the EC contribution was formally cancelled in November 2006, significantly crippling GCP operations in 2007. However, most of the 2006 funds should be recovered in 2007, on top of the 2007 contribution, and the EC's support to GCP remains unwavering.

Because the non-delivery of the EC's 2006 CGIAR contribution resulted in significant negative impact on the CGIAR's 2006 operations, the CG secretariat allocated $6 million from the World Bank's CGIAR account as partial compensation for the loss of EC funds. This compensation, accounted for as 2006 revenue, was calculated on a pro rata basis for the resources allocated by the EC to different Centres and Challenge Programmes, and GCP received $1.3 million.

The $10m-Bill & Melinda Gates Foundation project on 'Improving tropical legume productivity for marginal environments in Africa' will commence in mid- to late 2007. The project will promote modern breeding to improve the productivity in sub-Saharan Africa of four legumes (groundnuts, cowpeas, beans and chickpeas). The three-year project will develop key genomic resources that are currently lacking, identify molecular markers for important traits and improve breeding capacity in sub-Saharan Africa. It will be a collaborative project between US universities, CGIAR centres, EMBRAPA and NARS in sub-Saharan Africa.

So despite a temporary setback, funding prospects for GCP are positive for 2007 and the years that follow. Although funds are not secured yet, we have indications that DFID will maintain their contribution to GCP at the same level as previous years. We have also been informed that because of the problem that occurred in 2006, the 2007 EC contribution will include a (partial) compensation of the 2006 non-funding. Switzerland also began supporting GCP at the end of 2006. The new Bill & Melinda Gates Foundation-funded legume project represents an increase of about 20% above our 2006 income.

Alignment with CGIAR Systemwide Priorities

Generation's fundamental efforts to develop new knowledge and products support the United Nations Millennium Development Goal (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 potential for poor farm households to improve their food and nutritional security and income. They also offer the prospect of affordable food for poor consumers.

Aside from supporting progress towards this first critical Millennium Development Goal, GCP contributes directly and indirectly towards the other MDGs.

GCP has several means of establishing and maintaining its focus, relevance and applicability. All GCP activities fulfil one—or more—of the CGIAR System Priorities for 2005–2015. The characterisation of crop diversity is at the heart of GCP's work, fulfilling Priority 1a: *Promoting conservation and characterisation of staple crops.* However, the most important for GCP is Priority Area 2: *Producing more and better food at lower cost through genetic improvement*. This Priority Area easily describes GCP's own overall objective. GCP activities that fulfil other System Priorities nevertheless contribute to the overarching goal of Priority Area 2. These activities fulfil the following CG priorities:

1a: Promoting conservation and characterisation of staple crops
2a. Maintaining and enhancing yields and yield potential of food staples
2b. Improving tolerance to selected abiotic stresses

We would like to highlight a change in resource allocation from what was reported last year for Priority 5D—*Improving research and development options to reduce rural poverty and vulnerability.* Last year, we allocated all our resources for training and capacity-building in 5D because we did not realise that 5D aggregates stand-alone activity in development and capacity-building. In the case of GCP, training and capacity-building are not an independent effort: they are both firmly embedded in our research projects. We therefore decided to shift the resources previously allocated under 5D to the other research priorities identified and listed above.

The project narrative section that follows provides a detailed analysis of GCP Subprogrammes, and how their outputs to fulfil these CG System Priorities.

Collaboration and Partnerships

The GCP Stakeholder Committee was convened by the Global Forum for Agricultural Research (GFAR) in response to an EC recommendation to incorporate GFAR in the development and implementation of EC-supported Challenge Programmes. The rationale is to ensure better representation in GCP decision-making of regional and sub-regional agricultural fora and other stakeholders such as farmer groups, NGOs, CSOs and the private sector. The Stakeholder Committee should serve as a neutral platform for inter-stakeholder dialogue, and as a link between GCP and the various stakeholders. The Committee provides input and feedback to the PSC and recommendations to improve multi-stakeholder involvement, especially from the Global South and civil society. The GCP Director and the SP5 Leader are the liaison with the Committee. However, the Committee has not functioned as envisioned. In this period when the entire GCP governance structure is under review, there are plans by the EC, GFAR and GCP's Management Team to revamp and revitalise this vital Committee, and dialogue has already been initiated.

To fulfil its mission, GCP has forged and nurtured R&D partnerships in research, breeding and delivery, but more needs to be done to improve interactions with the private sector. Like other CGIAR Challenge Programmes, Generation was created to yield large impacts in the short term through multidisciplinary approaches. It is therefore imperative that GCP cultivates partnerships and every activity in GCP is a collaborative exercise with carefully chosen partner institutions that have complementary expertise. The project narratives in the sections that follow provide details on GCP's partnerships, and the full list of GCP partners is in Appendix A.

GCP continues to collaborate with the other three CGIAR Challenge Programmes in communication, research planning and impact assessment. We are also exploring partnership with the HarvestPlus Challenge Programme in developing the Project Development Guide below.

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 Program for African Seed Systems (PASS), jointly funded by the Bill & Melinda Gates Foundation and The Rockefeller Foundation, is of great interest to GCP. And the interest is mutual: The Rockefeller Foundation perceives GCP as an important player and conduit in developing and bringing new molecular markers for plant breeding to Africa, while GCP sees PASS as an efficient pathway for GCP products to be used by breeders and reach farmers' fields. In this way, GCP will train African breeders, involve them in GCP activities and get a better handle on African breeding programmes, with the added potential of identifying fruitful new partnerships. As a first step, GCP has committed to supporting training at the African Centre for Crop Improvement at the KwaZulu-Natal University in South Africa, a centre supported by The Rockefeller Foundation. GCP will cultivate further collaboration with PASS as a crucial pathway for product delivery to Africa.

An additional partner for our new project on improving tropical legumes is the Kirkhouse Trust. The Trust supports the development of genomic resources for cowpeas in Africa and is considering branching further out to beans and/or chickpeas. The Trust has also invested in enhancing laboratory capacity for molecular markers in Africa. This is of great interest to GCP as we begin to consider new approaches for marker work in Africa.

In 2006, GCP signed a Memorandum of Understanding (MoU) with the Global Diversity Trust for collaboration on activities of mutual interest, especially conservation, research and development of plant genetic resources for food and agriculture (PGRFA).

The role of the private sector for GCP is also evolving, and growing. We recognise the private sector 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 this regard, a couple of initiatives started in early 2007.

First, a project to develop a web-based Project Development Guide (PDG) was initiated in April 2007. This initiative, supported mainly by the Syngenta Foundation for Sustainable Agriculture in collaboration with GCP, will generate a project management knowledge-based tool to increase the quality of GCP proposals and maximise timely delivery of products. The consultant leading the project has over 20 years of broad international experience in agribusiness, specialising in product development, registration and research. In developing the tool, we are drawing on Syngenta's private sector experience.

The other initiative relates to 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 tap into this expertise to improve sorghum yield under water-stressed condition in Africa. By tapping into 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 South. 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 the small- and medium-size 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), supported by the Barwale Foundation. IFSSA links public–private seed sector partnerships for value-adding and to provide farmers with quality seed. With these new contacts, we expect Generation 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 NGO networks in the seed business. Representatives from several African seed companies and NGOs will be invited to GCP's 2007 Annual Research Meeting (ARM) in South Africa to discuss potential collaboration with Generation.

Governance and Consortium

In 2005, the PSC set up a Task Force on Governance Structure to review GCP's governance. The task force developed a set of options and recommendations for reform, which were presented during the 2006 PSC meeting. However, the PSC did not endorse the proposed recommendation since further clarity was needed on some fundamental issues on Generation's identity. Therefore, the Task Force's Terms of Reference were revised: new recommendations for reforming GCP's governance will be tabled in 2007, and a final decision made when the PSC meets in early December. Any changes in governance will affect the Consortium Agreement,[4] and could also have implications for Consortium composition.

Meantime, in 2006, the Australian Centre for Plant Functional Genomics applied for Consortium membership. The PSC ruled that the application be shelved pending the approval of recommendations from the Task Force. Likewise, for provisional members approved last year (see Appendix A); their ratification as full consortium members shall be postponed until the Task Force completes its work.

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[4] GCP Consortium Agreement accessible at: http://www.generationcp.org/whoweare.php

Achievements in 2006

2006 Impact Highlights

- New representative samples finalised for six crops and new SSR markers identified for 10 crops for use in large-scale genotyping
- Targeted genotyping for candidate genes: 79 drought-related maize genes studied for screening 350 inbred lines
- Universal Core Genetic Map for rice developed and advances made in chromosome segment substitution and backcrossing with wild relatives for several populations (10 in total)
- Drought phenotyping network strengthened and a community of practice established for less-studied and slow-to-breed crops such as potato, cassava, *Musa* and coconut
- New expressed sequence tag (EST) for pearl millet and cowpea, more genomic resources generated for *Musa,* and contribution to the production of SNP data across the genomes of 20 rice lines
- Transcriptome analysis to bridge the gene–phenotype gap for efficient identification of candidate genes responsible for target traits
- Gene for Al tolerance sorghum identified; 288 maize lines phenotyped for Al tolerance and six genes found associated with maize Al tolerance
- Gene for P-deficiency tolerance (*Pup1)* fine-mapped to within 300 kb (kilobase). Twelve gene-specific markers diagnositic of *Pup1*and 25 candidate genes identified
- Phenotyping approaches and protocols improved and a publication under development
- Support-systems for marker-assisted selection developed to convert gene-based knowledge into robust molecular breeding approaches
- Molecular breeding systems pilot-tested with simply inherited traits
- Markers for virus resistance in cassava and *Striga* resistance in cowpea available for generating more resistant germplasm
- Low-cost, high-throughput markers developed for maize grain quality, and for bacterial blight resistance in rice, providing essential methodological insights for routine, large-scale marker conversion
- Experience and technologies transferred to less-studied crops: wide crosses and molecular marker analysis leading to a new paradigm in groundnut breeding based on successful use of synthetics in breeding of other complex polyploid crops (e.g., wheat and canola)
- GCP Central Registry and GCP data templates established and data uploaded for public download
- ICRISAT's Laboratory Information Management System (LIMS) installed at BecA and IITA–Ibadan
- iMAS software to aid marker-assisted breeding released for testing in 2007
- Course on genetic resource policies and freedom to operate assessed
- Global Genotyping Support Service for NARS launched, bridging laboratory and field research
- Delivery Plan Kit developed for implementation in 2007 to streamline research product management and delivery
- *Ex ante* impact targeting conducted for regions, crops and traits to guide decision-making and resource allocation
- Concept for *à la carte* (tailor-made) capacity-building for applied research NARS teams developed
- IP Helpdesk for the GCP community launched to help implement the GCP Consortium Agreement in the context of the broader IP context

Subprogramme 1: Genetic diversity of global genetic resources

1. *Progress in genotyping, marker development and application for analysing the structure of the diversity in major food crops*

The analysis of germplasm structure has progressed markedly for most of the 21 GCP crops. New representative samples were finalised for six crops and new SSR markers were identified for ten crops for use in large-scale genotyping. The SSR genotyping effort *per se* has been completed for several new crops, providing a definite basis for identification of reference samples; massive data have been deposited in the GCP registry for maize, wheat, barley, chickpea, common bean, lentil, potato and coconut. Data for pearl millet, finger millet, pigeon pea, cassava and sweet potato leads are near completion. New genotyping methods were further assessed for whole-genome profiling, with focus on DArTs for sorghum and on Illumina-detected SNPs for rice; their throughput and cost efficiency will be determined, for application of quick genotyping in the thousand-marker range. More specific methods have been set up in barley for the revelation of non-coding SNPs that may cause allelic imbalance.

2. *Targeted genotyping for candidate genes*

Complementary to structure analysis, the survey of specific candidate genes aims at accessing functional diversity. This is pursued in several projects. A study on maize encompassed 79 drought-related genes, whereby 1–3 amplicons per gene, and 2–3 SNPs per amplicon have been found, and will be included into a chip that will be used to screen the 350 inbred lines in this study. In a coordinated study across several species, there have been successful efforts to develop comparative diversity studies for ABA-Stress–Ripening (ASR) protein genes (most advanced in rice, sorghum and barley), for ERECTA and

ERECTA-like protein genes (rice, sorghum, barley, common bean, chickpea, potato and cassava) and for DREB2A.

3. *Genetic base in rice increased*

A pilot project on rice refined interspecific introgression population panels between Asian and African cultivated rices and further developed interspecific backcrosses with various wild species. At the end of 2006, the project had numerous achievements. Five interspecific genetic maps were developed, two populations (*O. sativa* x *O. glaberrima)* were advanced towards fixation of chromosome segment substitution (CSS), four cultivated x wild BC1F1 populations were genotyped, four cultivated x wild BC2F1 populations were derived, a Universal Core Genetic Map for rice was established with distributed clusters of SSR loci, and a set of bioinformatics tools were developed to facilitate development and exploitation of CSS lines. This has fostered vibrant international collaboration, thus opening up avenues for further research.

4. *And also…*

A drought phenotyping network was strengthened by integrating modelling approaches with the EMBRAPA capacities in a multidisciplinary effort. A more general inventory of capacities has been started. The understanding of linkage disequilibrium has progressed for rice and sorghum. A community of practice has emerged for less advanced and slow-to-breed crops such as potato, cassava, *Musa* and coconut. Altogether, this will facilitate association studies in various types of populations.

Subprogramme 2: Comparative genomics for gene discovery

1. *Enhanced public genomic and genetic resources*

Through GCP investments in different consortium activities, we see increasingly more genomic and genetic resources in the public domain. Two GCP-sponsored EST projects have generated new pearl millet EST from differential cDNA libraries, and they were annotated and submitted to GenBank. This represents a significant addition to the pearl millet EST resource. Similarly, additional EST data from cowpea were added to the public database. Under the project 'Targeted *Musa* genome sequencing and frame map construction', *Musa* EST are anchored to the rice genome, and additional genomic resources (BAC and EST sequences, SSR markers) are generated for *Musa*[5]. GCP also contributed to the production of SNP data across the genomes of 20 rice lines. A full dataset has been generated from Perlegen Sciences. Preliminary statistics show a total of about 260,000 SNP calls, yielding an average of 2.6 SNP per 1,000 base pair (bp) between a pair of rice lines.

As of mid-2007, the OryGenes database[6] developed at CIRAD has over 140,000 insertion sequences tagged by flanking sequence tags (FSTs) on the rice genome. This database can be used to search for knockout inserts in candidate stress-associated genes and has a 50% success rate, providing a valuable resource for extracting mutants of many plant genes.

2. *Bridging the gene–phenotype gap with transcriptome analysis*

Work led by National Institute for Agrobiological Resources (NIAS) has demonstrated the potential of applying transcriptome analysis to shortlist candidate genes. The team found that genome-wide expression patterns in a pair of isogenic lines can inform chromosomal introgression, and hence can lead to efficient identification of candidate genes responsible for target traits. Because advanced backcross or near-isogenic lines are common products in plant genetics research and crop breeding, the experimental approach developed by the group should have broad appeal to the plant science community, forming a foundation for further research.

3. *Candidate genes and genetic regions for stress tolerance identified*

The Cornell-led project on tolerance to aluminium (Al) toxicity in cereals has made significant progress on both sorghum and maize Al tolerance. In sorghum, the team verified that the gene identified via map-based cloning was responsible for the major sorghum Al tolerance locus, Alt_{SB}. Function of the gene was supported by over-expression in Arabidopsis, where the gene confers Al tolerance via its function as an Al-activated root citrate efflux transporter. For the maize Al tolerance work, the team phenotyped 288 maize lines for Al tolerance. From this analysis, six genes were found associated with maize Al tolerance. Four of these genes are putatively involved in root organic acid exudation, while the other two may be involved in cell wall composition. Research on these genes is ongoing.

The IRRI-led project on identifying genes underlying tolerance to salinity and P-deficiency in rice has identified narrow chromosomal regions containing candidate genes. Markers were identified in the 1.2 kb *Saltol* region, which together with genome-wide markers, can be used in marker-assisted backcrossing (MAB) to transfer *Saltol* into popular varieties. The gene for P-deficiency tolerance (*Pup1)* was fine-mapped to within 300 kb (kilobase). Twelve gene-specific markers diagnositic of *Pup1* were developed. Based on *in silico* and RT-PCR expression analyses, 25 candidate genes were shortlisted. Further

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[5] See http://www.musagenomics.org

[6] See http://orygenesdb.cirad.fr

analyses are being conducted to identify a few candidates for transformation experiments.

Subprogramme 3: Trait capture for crop improvement

Subprogramme 3 (SP3) aims to create product-driven teams that span the innovation-to-impact continuum and bridge the gap between the development of research outputs and their actual use in breeding programmes. The ongoing commissioned projects use various approaches to develop a better understanding of, and better methods for, incorporating complex traits, including improved phenotyping approaches and protocols, MAS simulation and the development of decision-support tools and markers development for more efficient breeding. Because SP3 projects build on what has been achieved in SPs 1 and 2, the resources allocated to SP3 have been modest in Generation's first years. It is however clear that the situation will change given increasing outputs from SPs 1 and 2. SP3's progress in 2006 is described below.

1. *Phenotyping approaches and protocols improved*

Several projects have contributed to the improvement of phenotyping approaches and protocols, but this information still needs to be disseminated and applied in the evaluation of GCP material (sets of reference, segregating populations, etc.). Phenotyping issues were intensively discussed during GCP's ARM in 2006. A recommendation from the ARM is a phenotyping document currently being compiled by SP3 that includes contributions from many partners in the GCP community, describing new approaches or providing guidelines for a series of crops. This document should be published at the end of 2007. The SP3 Leader visited EMPRAPA to acquaint himself with EMBRAPA's phenotyping platform and analyse its potentialities for evaluating GCP genetic materials. This platform can be considered as the first strand in a GCP network for accurate phenotyping of GCP's reference collections and segregating populations for different crops.

2. *Support-systems for marker-assisted selection developed*

The overall objective of SP3 is to apply the new gene-based knowledge generated by SP1 and SP2, or outside the GCP, across a wide range of crops (cereals, legumes and clonal crops) focusing on the target regions identified recently by GCP. This knowledge must be rapidly converted by SP3 into robust molecular breeding approaches and tools for abiotic stress tolerance and related traits. The traits/approaches and tools are then evaluated in different germplasm. A range of facilitating technologies, such as simulation, modelling and decision-support tools, are essential for rapid and widespread adoption of these molecular breeding approaches and tools among conventional breeding programmes. For example, simulation work based on wheat breeding at CSIRO aims to identify optimal strategy (nature and size of segregating populations) to combine known genes (using perfect or near-perfect markers) into single genotypes for use as parents for further field screening.

3. *Molecular breeding systems pilot-tested with simply inherited traits*

Good progress has been made in the development of technologies for gene-based MAS of disease resistance. It is clear that the main focus for SP3 is still crop breeding for marginal environments with drought tolerance as the focus trait. However, the number of validated markers for drought tolerance is quite limited today and there is an urgent need to promote the use of markers in some of the GCP target environments. As a compromise, the use of markers for simple inherited traits available today will be considered in terms of their extent to impact crop performance in GCP marginal target environments. For example, markers for virus resistance in cassava and *Striga* resistance in cowpea are already available to generate germplasm with enhanced pest and disease resistance. Low-cost and high-throughput markers have also been developed for grain quality in maize, and for bacterial blight resistance in rice. These proof-of-concept activities provide essential methodological insights for routine, large-scale marker conversion activities once GCP develops gene-based technologies for drought tolerance.

4. *Experience and technologies transferred to lesser studied crops*

GCP investments are already catalysing exciting new approaches to breeding less-studied crops. For these crops, it is important that we move ahead with the technologies available. For example, the project 'Unlocking the Genetic Diversity in Peanut's Wild Relatives with Genomic and Genetic Tools' uses wide crosses and molecular marker analysis to drive a new paradigm in groundnut breeding based on the successful use of synthetics in breeding of other complex polyploid crops, such as wheat and canola. Given the narrow genetic base of groundnut varieties, this approach is likely to have large impacts on groundnut breeding.

Subprogramme 4: Bioinformatics and crop information systems

Subprogramme 4 (SP4, Project 4 in the MTP) is the most inward- and support-oriented GCP subprogramme, facilitating the biometric and bioinformatic components of GCP research including public access to tools and data. As a result of this inward orientation, the achievements of SP4, though considerable, are not always very visible (we don't build Eiffel towers: we build roads and sewage systems). Some of the more visible achievements include:

1. *GCP Central Registry and GCP data templates firmly established*

To create access to the data produced in GCP projects, GCP is implementing a system of web services in all institutes involved. But since this system is only gradually taking shape, a parallel short-term low-tech solution has been implemented. Based on the GCP Domain Models, which are also used in software development and web services, templates have been designed that allow the storage of a wide array of data in a fully interpretable form, usually in spreadsheets. In this way, GCP scientists can easily copy their data from their local computers into a common portable format. These datasets are uploaded to a GCP Central Registry where they are made available for download to the world via a website with search facilities. Also, the datasets that are not yet available for download, or available in public databases, are documented there with the contact details of the scientists who created them (Ref gcpcr.grinfo.net). With the templates now in place, we will continue to populate the Central Registry with data formatted consistent with the long-term goal of a system web service.

2. *ICRISAT's LIMS installed at BecA and IITA–Ibadan*

Partly funded by GCP, ICRISAT has created and installed a Laboratory Information Management System (LIMS). This modular system allows proper tracking of samples and capture and handling of data from laboratory equipment. Based on a request from the Biosciences Eastern and Central Africa (BecA) facility and IITA–Ibadan, GCP supported ICRISAT in adapting and installing their LIMS in these two institutes. The result is much more reliable data handling and thus higher quality data production in these two institutes. It illustrates that relatively small investments in data handling can increase the value of the output considerably (Ref cropforge.org/projects/icrisatlims). LIMS will be disseminated to more Consortium member institutes and staff trained to increase efficiency in bioinformatics for crop improvement programmes, and to facilitate better data exchange and analysis.

3. *iMAS released*

On marker-assisted selection, many software packages are available to support experimental design, map creation, QTL location, visualisation and the choice of parents for breeding. Some packages are commercial but most are free; most software is good, some is not. As a result, the choice of software is very difficult for a MAS breeder-to-be. To support this choice, GCP analysed the workflow of MAS and selected alternative packages that could be used for each required functionality. The quality of these packages was tested, and the best were selected, together covering the entire workflow. Permission to use the packages was also obtained from the owners. An interface was created that allows access to each package handling the complicated format conversions, documentation was written, and the entire package, iMAS, was released as a stand-alone application. In 2007, the package is being extensively tested by potential users from NARS, for further improvement and to help determine additional tools to be added to iMAS.

Subprogramme 5: Capacity-building and enabling delivery

Subprogramme 5 (SP5, Project 5 in the logframe) is GCP's product delivery arm. At GCP, capacity-building is not an independent stand-alone activity. Rather, it is firmly anchored in the direct activities of all the other SPs (1 to 4). As Generation matures and generates more and more products, capacity-building and product delivery are also evolving and increasingly coming to the foreground. For instance, Generation's new strategy requires that all new project designs have a clear product delivery plan. The role of SP5 is therefore not an end-of-pipeline activity but right from conceptual stage. This is clearly illustrated in all the new projects set to start in 2007. Project kick-off meeting will identify partner training needs and formulate product delivery plans, in line with GCP's new strategy which emphasises product delivery.

In GCP's early years, SP5 undertook numerous capacity-building projects alongside ongoing research in the other SPs. As we approach the end of Phase I and refine our approach to capacity-building, SP5 is in a better position to more accurately identify needs and target users in support of the other Subprogrammes. In 2006, SP5 began implementing the product delivery strategy developed in 2005. Main achievements in 2006 included launching the Genotyping Support Service (GSS) and developing the Delivery Plan Kit, to be launched in 2007. GSS adds value to, and ensures continuity of the work of, SP1 to promote genetic diversity analysis of germplasm; SP2 and SP3 to support modern plant breeding for NARS; and SP4 in ensuring data analysis and interpretation. In 2007 and beyond, SP5 will also strengthen links with SP3 in pre-breeding product management, ensuring the smooth flow of GCP research products along the research–delivery continuum.

Over and above direct GCP activities, SP5 also supports capacity building in the global arena to ensure partners are attuned to scientific and policy advances that affect their work. An example is the 2007 workshop on the International Treaty on Plant Genetic Resources for Food and Agriculture. By 2008, course materials will be available online and on CD/DVD. Another forward-looking activity in SP5 is *ex ante* analysis to evaluate the impact of key GCP products and to help refine Generation target traits and regions based on local needs. The first results on impact assessment are already available to guide GCP's decision-making and resource allocation.

SP5's key achievements in 2006 are briefly outlined below.

1. *Genotyping Support Service*

The Genotyping Support Service was launched in 2006. It is a landmark achievement that facilitates access by national agricultural research systems (NARS) to genotyping technologies, providing a much-needed bridge between laboratory and field research worldwide. GSS is an all-inclusive package that offers cost-efficient genotyping services, providing access to data and support (which builds local capacity), and including training for proper interpretation of genotype and phenotype data to assist modern plant breeding in the global South. In its first year, GSS was used by breeding programmes across three continents, specifically on *Musa* (Brazil and the Philippines), groundnut (Bangladesh and Bolivia), potato (Bolivia and Chile) and cassava (Nigeria, Uganda and Tanzania). GSS adds value to SP1's work on genotyping by promoting the use of molecular markers to assess the potential value of germplasm and breeding materials for relevant agronomic traits. This extends the scope and reach of SP1's work, bridges the gap between molecular laboratories and field practitioners, and also generates useful tools. Also, GSS encourages the application of validated markers for molecular breeding to advance activities in SP2 and SP3. Based on user feedback, we will continue to improve GSS the coming years, and extend it to cover more crops.

2. *Delivery Plan Kit developed*

SP5's role in product delivery is crucial in the implementation of GCP's Delivery Strategy. By developing the Delivery Plan Kit, SP5 spearheaded the implementation of the strategy. This kit is a tool for streamlining product management and delivery. It comprises a set of linked MS-Excel worksheets, which will be converted to a user-friendly and interactive template with a glossary and guidance notes. To ensure proper project design and implementation, the sheets have prompts on expected products and users of GCP projects, anticipated constraints to product transfer and user capacity-building needs, plus intellectual property issues relevant to the project. The kit will be implemented in 2007 starting with the suite of six competitive projects awarded in 2006 and the special project on improving tropical legumes for Africa. The kit was designed with the help of a panel of experts in technology transfer, research management, impact assessment and marketing. For each new major GCP project, a delivery plan is now a pre-requisite.

3. *Early results on* **ex ante** *impact targeting*

To ensure product delivery and informed decision-making, GCP commissioned a study as a foundation for a credible, realistic, needs-driven resource allocation strategy that will result in measurable impacts to solve the problems of resource-poor farmers. The study identified geographical areas with a high incidence of poverty and high drought risk, and the crops grown and consumed there. Because the findings are significant and of global relevance, a paper summarising this study has been submitted to a refereed journal for publication. Additionally, a pilot study was conducted to examine the relative importance of secondary breeding objectives, relative to drought, for selected crops. Both these studies will inform and guide research in SPs 1 and 2, and help to better select pre-breeding materials in SP3.

5. **A la carte** *capacity-building*

SP5 focuses on both the global picture and local needs by harnessing the benefits of the broader scope to address local realities. With these two aspects in mind, and in close collaboration with the other SPs, SP5 developed a new customised capacity-building concept, which we dubbed 'Capacity-building *à la carte*'. This concept guided a proposal call to identify and provide tailored capacity-building to applied research NARS teams engaged in GCP-related research. The call required a customised plan comprising training needs, mini-grants for basic equipment, hands-on research in advanced research institutions and *in situ* expert technical assistance. We expect that this team approach to capacity-building will be more effective than the individual training Fellowship Programme, which will be phased out in 2009.

6. IP Helpdesk

GCP's success in its mission largely depends on having contracts or agreements that conform to the CGP Consortium Agreement.[7] These subsidiary agreements and the provision of necessary materials (including germplasm) should facilitate research to deliver expected outputs as global public goods. The online intellectual property (IP) Helpdesk[8] is tailored to provide an understanding of the GCP Consortium Agreement, thereby facilitating its implementation. The Helpdesk answers questions on IP issues, and provides the GCP community with general information on IP and access and benefit-sharing (ABS). The goal is to help GCP member institutions, scientists and staff fulfil GCP consortium-related IP management requirements. Launched in September 2006, the Helpdesk has three main sections: GCP Consortium Agreement Information, IP information and an FAQ section. It also features a 'Services' section which includes a facility for posing questions to a panel of experts, and a 'Resources' section with links to IP information in the broader global context beyond GCP. The IP helpdesk is the first in a series of several self-sustaining self-help services being developed by GCP.

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[7] GCP Consortium Agreement available at: http://www.generationcp.org/UserFiles/File/Consortium_agreement_signed.pdf

[8] IP Helpdesk accessible at: http://www.generationcp.org/iphelpdesk.php?da=0629604

Deviations from 2006–2008 MTP

Due to our current uncertain financial situation, most new activities for 2007 have been put on hold (both competitive and commissioned projects), but as soon as financial support is assured, GCP will adjust its research portfolio to what was originally planned for 2007. We are fairly optimistic that all pending projects will be initiated in July 2007. This unexpected obstacle has delayed our workplan for new 2007 projects by 6 months. The project for tropical legume improvement is one year behind schedule since project approval was delayed on account of management staff turnover at the Bill & Melinda Gates Foundation. The project was to have been approved in the last trimester of 2006 but the approval only came in May 2007. Consequently, 2007 outputs for all of Generation's five Subprogrammes have been carried forward to 2008.

Subprogramme 1
Uneven efficiencies have been observed between laboratories involved in massive SSR genotyping. A few laboratories have accumulated delays or will be able to deliver only part of the expected data. A comparative data quality assessment will be performed before final delivery as a public good. The necessity to invest in further characterisation in other more efficient laboratories will be determined on the basis of the analysis of available data. The delayed availability of SSR data has had consequences on other projects, which depend on them for data comparison or for the extraction and distribution of reference samples. SNPs in candidate genes benefited from increased technical efficiency, but cross-species comparisons suffered from the complexity of determining orthology relationships, due to the more and more clearly documented reality of ancient polyploidy; this will be a permanent difficulty in GCP, which relies on comparative genomics, and it points to the need to further develop basic genomic resources such as ESTs. The integration of modelling approaches in phenotyping suffered some misunderstanding between agronomists, geneticists and physiologists, which resulted in failure of some trials to deliver proper data. Communication efforts are key to multidisciplinary approaches meant to reconcile disciplinary views and produce novel knowledge.

Subprogramme 2
The increasing accessibility of genome-wide gene arrays has rendered unnecessary the initial plan of developing 'stress genes' array. Also, there is still no consensus on what constitutes a comprehensive set of stress-related genes. Thus, we will not pursue the development of stress gene arrays any further. Rather, we will facilitate the use of whole-genome arrays that have been developed for an increasing number of species. Results generated from different array platforms can be integrated into a common dataset to enable data mining.

GCP recognises that well-designed genetic stocks are a prerequisite for gene identification; however, development of mutant stocks faces delay due to the time required to advance the seed stocks to achieve homozygosity. Stock development is a time-intensive activity that requires institutional commitment, often beyond the normal lifespan of a GCP project. For GCP investment to be effective, we will selectively support institutions and teams committed to the development, maintenance and distribution of stocks. Furthermore, to realise the benefits of such genetic stocks, there must be a concrete plan to promote usage, probably through existing research consortia.

Subprogramme 3
GCP's theme-based second call for competitive grants, opened in February 2006, has two thematic areas that fall directly under SP3's objectives. The first is the identification of superior alleles for aluminium tolerance genes for deployment into sorghum breeding programmes (output 4 in the SP3 logframe). The second is the detection and fine-mapping of QTLs with major effects on rice yield under drought stress (output 18 in the SP3 logframe). Both projects have been delayed due to the delay in disbursing EC and DFID funds. Most of the new commissioned projects for 2007 have been also delayed for the same reasons. Output 19, which contributes to the project on improving tropical legumes in sub-Saharan Africa was also delayed due to late approval of funding. The evolution from methodological activities to molecular applications in breeding was slightly slowed by the transitional phase in SP3 management: a new SP3 leader came on board on 1 July 2006.

Subprogramme 4
This year's MTP is clearly a continuation of last year's; some activities have been added (see next paragraph), and some completed so they do not appear in the logframe anymore. The new activities all concern support to GCP scientists in designing experiments and analysing their data. Some activities (Outputs 4.2 and 4.13 in the current MTP) were to have been completed, but will continue—the first, as a result of the developments in technology; the second, anticipating the success of the product, and therefore making it suitable for adoption by a wider audience. The output targets listed in last year's MTP have largely been met, except in a number of cases (Outputs 4.13, 4.15 and 4.19 in the current MTP) where delay was inevitable due to problems in hiring staff, or due to the fact that a number of projects were postponed as a result of GCP's financial situation. However, there were no fundamental methodological problems.

Subprogramme 5
Output targets on developing and translating training materials were not fully met but are in progress. A total of six projects were planned. In all but two cases, the reason for not meeting the time target was that principal

investigators took a conscientious approach and hence the work took more time than had been anticipated. In addition, GCP has requested two independent reviews of the drafted materials to ensure a high-quality product. In the other two cases, staff turnover saw the departure of those in charge. However, both cases have now been solved and the work is in progress.

Output target 5.14 on a product distribution strategy is in progress but the strategy document has not yet been developed because it requires closer links with SP3. For the strategy document to be comprehensive (and hence the strategy effective) it must be preceded by a revised set of templates for commissioned proposals and progress reports. The templates are being developed in SP3 as part of the product management function, and will inform SP5 in developing the comprehensive strategy document.

Finally, Outputs 5.6 (implementing mini-grants programme) and 5.19 (technical backstopping for NARS) were merged into a new Output (5.6 in the present MTP, Capacity-building *à la carte* Programme). This resulted from the development of the new *à la carte* concept, which provides better metrics for impact assessment and is a safeguard against spreading too thinly. The Capacity-building *à la carte* Programme provides an adequate framework for comprehensive assistance, including training and mini-grants for basic equipment and technical backstopping.

Highlights of 2008 Portfolio

2007–2008 Targets

- In-house capacity established for fully documented scientific management of germplasm collections
- Linkage disequilibrium assessment extended to legumes
- More information on genotypic and phenotypic functional diversity: large-scale characterisation of reference germplasm in drought-stressed environments
- Identify or develop high resolution germplasm for genetic analysis
- Whole-genome profiling on sweet potato
- Generate new genomic resources for under-resourced crops, starting with sweet potato and pearl millet
- Generate new genetic and physical mapping resources produced for drought breeding in cassava
- Discover genes conferring stress tolerance using well-characterised near-isogenic lines (NILs)
- Implement new phenotyping techniques, especially for drought response
- Produce new ESTs and marker resources for four tropical legumes species: groundnut, cowpea, bean and chickpea
- Identify orthologous genes across the key legume species
- Improve phenotyping network and establish a phenotyping support service (PSS)
- Validation and integration of new markers for crop breeding in GCP target farming systems
- Molecular breeding strategies transferred to NARS and regional molecular breeding communities established
- Application of modern breeding approaches to tropical legumes (beans, chickpea, cowpea and groundnut) by integrating markers, phenotyping tools and protocols, and enhanced germplasm
- Web services tools and technology further developed and Web services technology applied in reference GCP applications
- Bioinformatics and data handling support to GCP scientists
- Methodology for reconstruction of genealogies based on haplotypes related to geographic patterns
- Genotyping Support Service (GSS) extended to more crops
- Capacity-building à la Carte Programme launched for customised high-quality training and sustained technical support to NARS researchers
- Project Development Guide (PDG) designed and implemented to systematise and streamline GCP project planning and management and to ensure product delivery
- *Ex ante* socio-economic impact studies continued on GCP crops, traits and target regions for better-informed decision-making and resource allocation
- Policy course on the International Treaty for PGRFA conducted for the GCP community

Subprogramme Highlights

Subprogramme 1: Genetic diversity of global genetic resources

Year 2008 will see the termination of the large wave of systematic genotyping for structure analysis and diversity sampling from the large food crop collections. Data quality control and data exploitation will require significant efforts of a large community, as well as publication in a visible, accessible and detailed fashion. Data and methodologies will be turned to germplasm bank curators in order to establish in-house capacity for fully documented scientific management of germplasm collections. This will be ensured by significant communication, exchanges and training efforts from SP1 in close collaboration with SP5 and SP4. Linkage disequilibrium assessment will be extended to more crops, in particular legumes, in order to refine the ground for association analyses.

At the same time, there will be more attention on generating information on functional diversity. This will be both on the genotypic side, with the characterisation of candidate gene SNPs, and on the phenotypic side, with large-scale characterisations of reference germplasm in drought-stressed environments. A reference of materials with contrasting behaviours in relation to drought will be constituted on the basis of such experiments, as well as a more general collection of field-proven highly drought-tolerant (or susceptible) genotypes detected by the whole community, be it formally in controlled experiments, or incidentally in opportune circumstances. All this will contribute to the era of drought-focused specialised initiatives in SP1.

The identification or development of germplasm with high resolution power in terms of genetic analysis will be reinforced. Production of introgression panels, such as rice chromosome segment substitution lines (CSSLs), as well as/or other interspecific materials in both rice and barley, will be emphasised. Production of recombinants from multiple diverse parents will be initiated for several crops. In an effort to explore existing materials from germplasm banks, mining collections will be undertaken for extracting panels with spontaneous introgression pattern or spontaneous clinal differentiation which will lend themselves to genetic analysis of adaptation to drought. Whole-genome profiling will be undertaken with DArTs on sweet potato, in order to investigate heterosis, a major ground for improvement of vegetatively propagated crops.

Subprogramme 2: Comparative genomics for gene discovery

Genetic resources and genomic toolkits are needed for individual species in order to capitalise on new knowledge and tools. Given the steady decline in sequencing cost (and many sequencing centres now in fact have over-capacity in sequencing), it is possible for GCP to sponsor (or co-sponsor) cost-effective targeted sequencing projects for crops that are currently under-resourced. We plan to support the GCP community to generate new genomic resources for two under-resourced crops—sweet potato and pearl millet—both of which have potential to aid the exploration of germplasm.

An exciting addition to the SP2 portfolio are new activities on four tropical legumes species: groundnut, cowpea, bean and chickpea. Under this set of activities, we will generate molecular markers and create a reference map for groundnut. A large collection of ESTs and SNP markers will be produced for cowpea. For common bean, the research team will produce drought-induced gene libraries to aid the identification of candidate genes controlling water use efficiency, osmotic adjustment or root development. Similarly, new markers will be produced for chickpea to construct a reference map with at least 1000 loci. The genomic resources produced in each of these species will enable the identification of orthologous genes across the key legume species. Together, the legume research network aims at integrating over 1,000 orthologous markers into the genetic maps for the four target species. We expect these efforts will enrich the basic genetic and sequence resources for legumes. Because these legumes have common as well as unique drought tolerance mechanisms, cross-species maps will significantly improve the community's ability to apply comparative biology in legume improvement.

New developments in genome-wide expression analyses and production of genotypes with reliable drought-tolerant phenotypes give us optimism in identifying genes and pathways with significant effects on drought tolerance. Results from a series of experiments using independent derived NILs support the hypothesis that expression signatures from one genome are highly correlated with introgressed chromosomal segments. This presents an opportunity to pinpoint genes responsible for drought tolerance using well characterised NILs. We will support such approaches to discover genes conferring stress tolerance.

We expect increasing integration of projects in SP1, SP2 and SP3. This will involve the production of recombinant genetic stocks that are suitable for phenotyping at molecular and whole-plant level. Several projects are planned to implement new phenotyping techniques particularly for drought response (e.g., carbon isotope discrimination). A new project will be initiated to explore the use of large-scale phenotyping methodologies to identify drought-adaptive mechanisms in bread and durum wheat.

With the available cloned genes or gene markers tightly linked to the trait, we are in a position to transfer the markers for implementatin in NARS breeding programmes. New projects are formulated in conjunction with SP3 to deliver these results and tools to breeding programmes. We will emphasise the validation of genes or genomic regions for their effects on local germplasm. This will enable national breeding programmes to package the necesasry traits into target varieties.

Subprogramme 3: Trait capture for crop improvement

From now, GCP will increasingly evaluate germplasm for resistance/tolerance to diverse biotic/abiotic stresses, validate genes/markers in different target water-stressed environments, and organise the exchange of potentially useful germplasm developed by different projects. To reach these objectives, a phenotyping support service (PSS) will be established. Its activities will include: the identification, for GCP target crops, of potential phenotyping locations with adequate facilities and accurate levels of expertise; the evaluation of their needs and, in collaboration with SP5, strengthening them through training and capacity-building activities; and monitoring germplasm exchange. Geographic Information System (GIS) tools may play an important role in the deployment of PSS to select testing locations that are representative of target environments, to determine to what extent phenotyping data collected in a given testing site can be used in other locations/areas worldwide, and finally, to better understand GxE and QxE interactions and better manage germplasm exchange.

In GCP's early years, most commissioned and competitive projects employed various approaches for a better understanding of, and better methods for, incorporating complex traits, including MAS simulation, decision-support tools and marker development for more efficient breeding. This effort has been fruitful and productive (e.g., low-cost, high-throughput markers). Many of the products from these early years are still used by ongoing and new projects. Subprogramme 3 is now entering a new phase, emphasising the validation of these products (Theme 3) and their integration in breeding programmes (Theme 4). It can be estimated that in 2008 for example, almost 70% of SP3 commissioned projects and resources will be devoted to validation and integration of new markers for crop breeding in target farming systems. Some of the validation activities will be conducted jointly with SP1 and SP2 and it is clear that a strong collaboration with SP5 will be imperative to ensure NARS breeders will have the capacity and expertise to conduct the work. In the frame of these 'joint projects', reference collections developed by SP1 (wheat, cowpea, chickpea and sorghum) will be evaluated in target environments, while some genes/markers identified by SP2 will be validated by NARS in Africa (e.g., aluminium toxicity genes from SP2 projects, etc.).

Other significant developments in SP3 are the increasing importance of drought and the active participation of NARS breeders in projects and activities. Previously, most SP3 projects focused on simply inherited traits pending the availability of resources for drought tolerance. More projects are now dealing with drought and other abiotic stresses. The enhanced involvement of breeders and NARS in the new projects will ensure quick dissemination of markers in conventional breeding.

GCP investments are already catalysing exciting new approaches to breeding less-studied crops. For these crops, it is important to move ahead with the technologies available. For this reason, several SP3 projects still focus on simply inherited traits (e.g., multiple disease resistance in groundnut, pest resistance in cowpea and virus resistance in cassava and sweet potato). But for all these crops, there are efforts to generate the necessary resources for phenotyping, mapping and developing MAS for drought tolerance. Through the new project on tropical legumes, a new set of activities will be initiated in SP3, targeting the application of modern breeding to those crops (Output 19). This project will integrate the products (markers, phenotyping tools and protocols, enhanced germplasm) generated by other activities on tropical legumes (Outputs 2, 8, 10 and 20).

Subprogramme 4: Bioinformatics and crop information systems

The SP4 outputs planned in the current 2008–2010 MTP could largely be copied from the previous MTP, with the changes listed in the previous SP4 section on 'Deviations from 2006–2008 MTP'. A few new outputs have been added:

- Last year's Output 4.4. (Web services technology further developed and applied in reference GCP applications) has been split in two outputs—Output 4.5 (Web services tools and technology further developed) and Output 4.6. (Web services technology applied in reference GCP applications). This was opportune given the possibility to strengthen the link with the European Bioinformatics Institute (EBI), and thus tapping their expertise more effectively.
- In the framework of forging closer links with GCP scientists and improving their hands-on support, Output 4.11 (Bioinformatics and data handling support to GCP scientists) was added. This output aims to provide a clear overview of all SP4 products by creating a website and will give quick help (response time 48 hours) to GCP scientists by mediating between the user requesting support and the expert.
- In response to a request from SP1 and in anticipation of new scientific developments, we have added Output 4.17 (methodology development for reconstruction of genealogies based on haplotypes related to geographic patterns). This output will explore new possibilities on analysing genotypic data for structuring genetic diversity.

In terms of the focus on outputs and the expected impact, a gradual shift can be observed from infrastructure building to user support. Apart from outputs directly supporting specific users, where feasible, all activities are now expected to have users of the products listed in the workplans which will ensure they are relevant and user-friendly. These users have to be specifically identified, thus allowing GCP management to monitor these activities from a user perspective. This approach is expected to continue in the coming years.

Subprogramme 5: Capacity-building and enabling delivery

A number of SP5 activities will continue from the previous MTP in support of the other subprogammes. These include the Fellowship Programme, the Travel Grant Programme, developing and translating training materials and selected training courses. Two workshops are planned for 2007. One will focus on the significance—to the Generation Challenge Programme—of the International Treaty on Plant Genetic Resources for Food and Agriculture. The intention is to raise awareness among GCP collaborators on their options when acquiring and distributing PGRFA, a fundamental function in GCP. The second workshop will be a distance-learning course on genetic resource policies and freedom to operate. It will also serve as a forerunner for designing regional courses on the same topics. The workshop passed a test-run by GCP collaborators (ARM 2006). Results from the test run were used to design a regional course on the same topic, tested in CWANA region in November 2006. The course will be offered online in 2007.

Also in 2007, SP5 will have several new activities reflecting the increasing emphasis on product delivery, greater cohesion with research in SPs 1 to 3, and *ex ante* impact analysis to guide GCP's investment decisions.

The Capacity-building *à la Carte* Programme will be implemented for high-quality training and sustained technical support to NARS researchers. The programme will nurture and strengthen a core community of scientists ('champions' at national research institutions). Such champions will ensure rapid uptake of GCP results and products, furthering GCP's mission and goals. We also hope that the benefits from this customised and intensive capacity-building effort will spill over within the institutions and regions involved.

The Web-based Project Development Guide (PDG) will be designed and implemented to systematise and streamline GCP project planning and management and to ensure product delivery. In collaboration with SP1 and SP3, the Genotyping Support Service (GSS) will be extended to cover germplasm characterisation and routine application of known markers in marker-assisted selection schemes of breeding programmes for sorghum, millet, groundnut, chickpea, cowpea, bean, cassava, sweet potato, potato, coconut and *Musa*. To further enhance GSS, SP5 will work with SP4 on a helpdesk for statistical support. On the *ex ante* impact assessment front, socio-economic studies will be undertaken for refined assessment of potential impact on GCP crops, traits and target regions for better-informed decision-making and resource allocation. So far, two studies have been commissioned. The first one focused on crop-specific drought severity. The second centred on *ex ante* impact analysis of selected marker-assisted selection technologies supported by GCP (rice for saline and phosphorus deficient soils, and pyramiding useful genes from wild relatives of cassava). A third study will focus on the relative importance of secondary breeding objectives for sorghum, cassava and cowpea. These studies will inform research priorities for SPs 1, 2 and 3.

Given the renewed emphasis on product delivery in line with GCP's new strategy, SP5 will also undertake product packaging and strategic marketing to broaden the reach of GCP research products. As the delivery arm of GCP, and starting with projects beginning in 2007, SP5 is putting into practice GCP's new delivery-centred strategy. More specifically, SP5 is developing a strategy for product marketing and distribution. The strategy is in the preliminary stages. Besides ensuring clear product delivery plans for the six competitive projects, SP5 will also conduct complementary customised capacity-building, in collaboration with all the other subprogrammes, for the special project on tropical legumes. As with all new projects from now on, a product delivery plan will be developed before the project begins. In addition, there will be a consultative needs assessment for NARS partners in bioinformatics, and laboratory and field research. The needs assessment will be the basis for tailor-made capacity-building for partners in the legume project to guarantee sustainability and ensure product delivery.

Project Narratives

Subprogramme 1: Genetic diversity of global genetic resources

Rationale

Providing access to sources of genetic diversity that may supply genes and alleles involved in key agricultural traits, especially stress tolerance, is the foundation of GCP. Through our network of consortium members and partners, vast germplasm collections are available to GCP. But to unlock the genetic diversity present in those collections, the structure of the collections must be understood through coordinated surveys of molecular and phenotypic variation. With hundreds of thousands of accessions across more than 20 crops in gene banks around the world, high-throughput molecular screening techniques must be applied to suitable genotype representatives of the collections. Appropriate methods to characterise germplasm subsamples for traits such as drought tolerance also need to be developed, and applied, in order to obtain reliable and analysable phenotype descriptions accompanied by relevant descriptions of the environment and weather conditions. Once the genotypes and phenotypes have been established, sound association studies must be conducted to understand their interactions.

This basic rationale has several components. The first consists of evaluating germplasm collections for enhancing the description of global diversity. Molecular markers are the tool of choice and particular attention is paid to developing and applying user-friendly markers that can be easily applied by national programmes for integrating and comparing their own materials. The second component is the operational portion and consists of developing and consolidating a global facility for the molecular description of germplasm with specific attention to efficiency, throughput, flexibility and accessibility. The third component addresses how to assess drought tolerance, a particularly complex and challenging feature. The fourth component is the actual implementation of germplasm evaluation within an analytical framework that will yield information on the underlying genetic factors (genes, alleles and haplotypes).This combines the comparative description of molecular polymorphisms and phenotypic variation and the study of associations. This fourth component thus rests on complementary modules, which must be coordinated for the best global efficiency, and must be managed in the most open fashion, so that it can attract enthusiasm of national programmes. The fifth component looks at new approaches for relating genotype to phenotype by connecting genetic analyses directly to breeder activities and farmer practices.

Subprogramme 1, along with the other GCP Subprogrammes, contributes to the CGIAR System Priority 2: *Producing more and better food at lower cost through genetic improvement*, and specifically targets Priority 2b: *Improving tolerance to abiotic stresses*. As Subprogramme 1 is also specifically concerned with the characterisation of plant genetic diversity, this project also contributes to several CGIAR System Priorities, and most specifically to Priorities 1a and 1b: *Promoting conservation and characterisation of stable crops* and *Promoting conservation and characterisation of underutilised plant genetic resources*.

Impact Pathways

Theme 1. Creation of an improved understanding of the structure of the diversity in major world food crops

The activities within this theme aim to provide better access to genetic diversity for more efficient plant breeding. A basic prerequisite for any breeding effort is a good description of the diversity available in germplasm collections. Every breeder and germplasm specialist guides his or her strategy—hybridisation or investigation—with knowledge on global diversity structure, and uses reference samples for integrated in-depth characterisation. Molecular markers help tremendously in acquisition of this knowledge. The markers chosen for systematic characterisation are essentially Simple Sequence Repeats (SSRs, or microsatellites), and the task for a given crop is usually shared between several laboratories of GCP Consortium members, under the coordination of the CGIAR centre that has the conservation mandate for the crop. For operational reasons, these activities are split into two batches, Outputs 1.1 and 1.2, respectively corresponding to the most advanced crops in terms of molecular tools (‘tier 1’ crops: rice, maize, sorghum, wheat, barley, cowpea, chickpea, common bean, cassava, potato and *Musa*), and to the less advanced crops (‘tier 2 and tier 3’ crops: finger millet, pearl millet, foxtail millet, pigeon pea, lentil, groundnut, sweet potato, faba bean, yam and coconut).

Particular attention is given to the description of the technique, the results and the allelic series; in addition, seeds or DNA samples bearing the allelic series as well as detailed data and results of analyses are made available, so that each subsequent study has autonomy in this comparison. All this is essential for connecting local, national and regional diversity to the reference GCP global diversity. These activities will enable national systems to localise their own germplasm diversity in relation to global diversity, and thus to be able to request and use the complement on a rational basis. By itself, Output 1.3 has high potential to improve the efficiency of breeding activities worldwide. Due to its allogamous breeding system and the associated capacity of rapid evolution, maize receives specific emphasis in order to refine the description of races outside its continent of origin and to trace the population dynamics along migrations in Africa and Asia. This is the focus of a competitive grant led by CIMMYT (Output 1.6).

Consolidation of the reference germplasm samples as genetic stocks in the respective CGIAR centres receives specific support in order to facilitate quick and steady distribution to breeders and germplasm specialists. This will help integration of information in the long term and extraction of trait correlations and phenotype–gene associations.

Linkage disequilibrium (LD) is one of the factors that determine if and how association studies can be performed and is the focus of Outputs 1.4 ,1.5 and to a certain extent 1.22. LD can exist in traditional materials if the germplasm has gone through significant bottlenecks in its history. Domestication itself may have induced sufficient bottlenecks to induce LD. This prospect is being monitored in rice by Cornell University for Indonesian germplasm. LD can also be established in cases of admixture between various forms that are clearly differentiated from one another. This prospect is being explored by a group led by IRRI on rice, focusing on the Indica-Japonica differentiation, and by Agropolis on sorghum, with emphasis on populations that show clear introgression patterns *in situ* in Africa. Through these activities, expertise will be gained among cereal geneticists and breeders for implementing association studies in autogamous crops. LD assessment will be extended to more species, in particular legumes, in order to refine the ground for association analyses.

As a complement to this integration effort, a methodology is under development for resampling diversity in large collections in order to enable the best use of existing information for further tapping of the collections (Output 1.7). Rice and chickpea are used for this activity, led by SGRP. An additional molecular description of a thousand accessions of each of these data-rich crops will allow the assessment of the efficiency of algorithms for iterative selection within data-sparse collections. More generally, data and methodologies will be turned to germplasm bank curators in order to establish in-house capacity for fully documented scientific management of germplasm collections. This will be ensured by significant communication, as well as exchanges and training efforts from SP1 in liaison with SP5 and SP4.

Theme 2. Development of a range of flexible HTP genotyping techniques accessible in reference laboratories

GCP needs access to laboratories capable of diverse and preferably high-throughput genotyping. The first round of massive characterisation involves mostly SSRs. This is being handled in a decentralised manner and will have extensions that can be absorbed by laboratories in some international Centres. Future needs essentially correspond to two types of approaches: 1) genome-wide surveys with anonymous markers, and 2) gene-targeted surveys for monitoring allelic variation for candidate genes.

Genome-wide surveys with anonymous markers aim at locating useful genes on the basis of linkage disequilibrium analysis, be it in segregating progenies of simple hybrids or more complex populations.

The Diversity Array Technology (DArT) is one of the potential technologies. DArTs are being validated with various species, such as rice, sorghum and wheat where arrays already exist, as well as cassava, *Musa* and coconut, for which new arrays are being developed within a commissioned project implemented by Agropolis, with DArT Pty Ltd (Canberra, Australia) as the main actor (Output 1.8). The technology has proven to be highly efficient in terms of throughput and cost. The diversity revealed through this activity is completely coherent with that revealed by SSRs in other GCP activities.

Gene-targeted surveys for monitoring allelic variation at candidate genes aim to validate the involvement of specific genes and identify superior alleles. Led by IRRI, EcoTILLing is being tested as a technology for SNP discovery and forms the substance of Output 1.9. Results in rice are very convincing and provide access to a cheap technique to investigate potential functional polymorphisms. ICARDA leads Output 1.10 on barley, focusing on a methodology to reveal SNPs that affect allele expression. Up to 50 candidate genes will be used as substrate for revealing allelic imbalance, and these variations will tentatively be associated with stress tolerance. The new information on expression polymorphisms may yield an improved understanding of adaptive value of molecular variation.

Allele resequencing is the current preferred approach when high-throughput sequencing is possible, providing full length sequence variation for the target candidate genes. In conjunction with Subprogramme 2, an activity is being initiated through a partnership with the Centre National de Génotypage (France) and Agropolis involving three laboratories for identification of orthologous genes, and five laboratories for providing crop-specific information and materials. Output 1.11 will generate a database with detailed information on allelic variation for seven crops. This database will be useful for planning pertinent phenotypic evaluation with a view to future association studies. The seven crops are barley, rice, sorghum, chickpea, common bean, cassava and potato.

For those crops where large resequencing information is available, gene-targeted as well as whole-genome profiling techniques can be accessible through various SNP genotyping platforms. The current prominent standards are provided by Illumina and Affymetrix companies. Rice is used as the indicator crop to assess efficiency and cost of these techniques in conjunction with other important initiatives.

In addition to the activities above, a support service has been established (in conjunction with Subprogramme 5, Output 5.18) for genotyping populations that have high-quality phenotypic information, in order to enhance the access of GCP and NARS scientists to quick and efficient screening of relevant germplasm.

Theme 3. Establishment and implementation of a scientific and organisational framework to describe drought tolerance

Proper phenotyping requires high-quality facilities and contributions from physiologists, modellers and breeders, with a specific modelling support for: 1) a quantification of traits and integration of their impact on yield, 2) genetic analysis of adaptive traits, and 3) characterisation of target environments. Before initiating a genetic study, it is imperative to have a clear view on available contrasting germplasm for drought (output 1.12)

In Ouput 1.13, EMBRAPA is upgrading existing facilities within its network of research stations to provide GCP scientists access to a high-quality, high-capacity phenotyping service. The network will first serve as a hub for evaluating cereal reference samples, but will gradually extend to other crops. The network of environments covered by EMBRAPA will be further expanded to other sites in Latin America and Africa.

Concurrently, under the coordination of Agropolis, a modelling framework that characterises environments for several target regions for the major crops using long-term daily weather data is being developed in Output 1.14. This characterisation includes the major breeding locations, and a balanced sample of other locations, to represent the production area of the region. Relevant soil types and management options will be simulated, and the results will be summarised by cluster of environment types. The other main component is an assessment of trait impacts on yield in several situations. The relevance of traits currently used in breeding programmes for drought tolerance will be evaluated by simulating the relationship between these traits and yield and/or yield components (when possible) for the main climatic scenarios. In consultation with breeders in each crop, sensitivity analyses will be conducted for a series of traits using an appropriate level of genetic variation for traits that can be simulated. Where possible these data will be verified using breeder experiments, and heritability of target traits and their genetic correlation with yield will be assessed. Several case studies of trait integration from plant to crop level will be undertaken for maize and rice.

In parallel, a phenotyping capacity inventory accessible to GCP scientists is being produced by Bioversity/SGRP in Output 1.15, in order to further specify options of phenotyping protocols and facilities by crops and regions, including operation costs. This will foster the use of the best drought-tolerance screening facilities within GCP. In addition, a support service will be put in place to support the characterisation of specific populations/samples that have a high potential for delivering novel information through genetic analysis.

Simultaneously, a reference of materials with contrasting behaviours in relation to drought will be constituted in Output 1.16 on the basis of phenotyping experiments as well as more general collection of field-proven highly drought-tolerant (or susceptible) genotypes detected by the whole community, be it formally through controlled experiments, or incidentally in opportune circumstances.

Theme 4. Identification of potential genes (or genome segments) and superior alleles (or haplotypes) through association studies (in conjunction with Subprogramme 2)

Association studies are undertaken through the comparison of molecular diversity and phenotypic diversity for target traits in Outputs 1.17, 1.18 and 1.19. The main expected outcome is the identification of genetic factors or genome segments that favourably contribute to trait elaboration and can be incorporated into breeding progenies through marker-assisted selection. This will serve all breeders in the crops under consideration.

Theme 4 builds on the broad set of actions planned under themes 1, 2, and 3 that yield genotyping and phenotyping data on the same materials. This theme intersects with Subprogramme 2, which highlights the best candidate genes, and together, Subprogrammes 1 and 2 deliver tools for more efficient breeding products to Subprogramme 3. The activities under this theme represent the core of the whole GCP, and will increase in importance during the period of this Medium-Term Plan.

Early results have been generated in a CIMMYT-led project in maize, looking at specific environments and specific target traits through the analysis of unrelated genotypes (Output 1.17). The project focuses on various candidate genes involved in plant response to water-limited conditions: carbohydrates, ABA and polyamines. The project’s phenotyping activities involve field evaluations and quantification of specific metabolites in leaves and silks.

Phenotyping experiments will also be implemented on, among others, rice, sorghum and pearl millet in order to enable association studies using the GCP reference samples. The new project on four tropical legumes funded by the Bill & Melinda Gates Foundation provides opportunity for applying the Theme 4 rationale (Output 1.19). Reference samples of groundnut, cowpea, chickpea and common bean will be distributed and planted in diverse environments in sub-Saharan Africa and evaluated for their reaction to major stresses. This will serve as the basis for identifying markers and developing new recombinant populations for better adapted breeding varieties for Africa.

Theme 5. Development of novel populational approaches for relating genotypes to phenotypes

This theme deals with the co-occurrence, in a panel of materials, of i) molecular tags; and, ii) desired values for traits which point to those genes or chromosome segments that are involved in traits of agricultural interest. This is commonly undertaken through segregation analysis in controlled progenies, or, more recently, with association analyses within unrelated germplasm. The results generally suffer from several drawbacks: 1) the materials often represent types that are far from the cultivation standards, exhibiting potential interactions between traits that may confound variation for the target features; 2) phenotyping is often done with a limited number of plants, i.e., few repetitions over space, and even fewer over time; and 3) the use of the materials thus monitored is not easy, and they are seldom incorporated in the breeding process. Theme 5 is about creating alternatives to this option.

One alternative is to make use of materials and evaluation data that are regularly produced in mainstream breeding activities. From the collections of potential parents, to the advanced breeding materials going to multilocation trials, and to the elite materials close to varietal release, there is a wealth of information produced that is not efficiently used for deriving genetic information that could in turn be used to enhance global understanding. The condition for using these materials is that there be significant linkage disequilibrium (LD) that correlates variation in genetically linked genes/markers (Outputs 1.22 and 1.23). The general diversity structure and the level of LD are being assessed in breeding materials of potato, cassava, yam, *Musa*, sweet potato and coconut, in order to assess feasibility and propose potential case studies.

Applying this rationale even further, the creation of materials by introgression from distantly related forms generates opportunities for fine analysis of trait genetic control and widens the range of alleles amenable to recombination by plant breeders. CIAT is leading such an activity on rice, producing a range of chromosome segment substitution lines from four wild species (Output 1.24). Production of introgression panels, such as the rice CSSLs, as well as or other interspecific materials will be further emphasised in rice and in barley (Outputs 1.25 and 1.26). Production of recombinants from multiple diverse parents will be initiated for several crops.

Finally, as part of the effort to explore existing materials from germplasm banks, current collections will be mined in Output 1.20 to extract panels with peculiar introgression pattern or clinal differentiation which will lend themselves to genetic analysis of adaptation to drought.

Contribution to international public goods

The activities under this Subprogramme result in numerous international public goods, including: 1) a very large database with molecular marker diversity data on core germplasm samples of the 20 main food crops worldwide; 2) kits of molecular markers (protocols, DNA for allelic series, etc.) for comparative diversity studies; 3) accurate diversity analysis, including geographic pattern highlighting complementarity and mutual dependence between political entities; 4) germplasm reference samples with increasing body of information attached; 5) a database of multi-species allelic diversity for candidate genes with potential for drought tolerance; and 6) improved methodologies for managing, mining and exploiting diversity in germplasm.

Partnership

Genotyping activities typically involve several GCP partners for each crop, with tasks split between markers or between accessions. With the exception of coconut, the coordinator is the CGIAR centre which has the mandate on the crop. EMBRAPA and CAAS genotype accessions from Brazil and China, respectively. However, sending germplasm out of these two countries remains a major difficulty, jeopardisng access by other partners to this material.

Competitive grants open the doors for an impressive range of partners in advanced research. One such is the project entitled ‘Allele mining based on non-coding regulatory SNPs in barley germplasm’, which brings together the Australian Centre for Plant Functional Genomics Pty Ltd, the University of Adelaide (Australia), National Institute of Agricultural Biology (Cambridge, UK) and the University of Udine (Italy), along with ICARDA and Tyshreen University (Syria). These organisations bring innovative approaches inspired by recent developments in human genetics. Other proposals allow the creation of broad networks of NARS, such as in the proposals on genetic diversity and association studies in maize, with Kenya Agricultural Research Institute, the Scientific and Industrial Research and Development Centre in Zimbabwe, the Department of Agriculture of Indonesia, the National Maize Research Institute of Vietnam, the Sichuan Agriculture University in China and Nakhon Sawan Field Crops Research Center in Thailand. Activities on rice involve Fedearroz in Colombia and the Indonesian Centre for Agricultural Biotechnology and Genetic Resources and Research Development.

The project for validating new markers links both the best actors in the technology and NARS representatives, who receive training in the technology. As an example, in the project on validation of DArTs as a genome-wide molecular characterisation technology, scientists from the Rayong Field Research Station in Thailand and the Coconut Research Institute in Sri Lanka went to DArT Pty Ltd in Australia for training, together with Agropolis trainees. Activities aimed at integrating markers in the process of breeding involve NARS breeding components, such as the African Centre for Research on Banana and Plantain (CARBAP) in Cameroon and the Vanuatu Agriculture Research and Technical Centre (VARTC). The theme on improving phenotyping approaches attracted the best groups on crop and whole plant modelling, such as the University of Queensland and CSIRO, both in Australia.

The ADOC initiative (Allelic Diversity for Orthologous Candidate genes) deserves special mention Supported by Subprogrammes 1 and 2, the initiative aims at organising GCP to rapidly transpose the most recent results in a plant species to all GCP crops. 'Gene champions' such as the Australian National University in Canberra, Australia, and Centre National de la Recherche Scientifique in Gif-sur-Yvette, France, (as well as IRRI) contribute specific expertise on the most relevant candidate genes and the corresponding biological analysis; three laboratories of GCP partners act as 'ortholabs' to quickly identify proper orthologs; five 'crop laboratories' of GCP partners contribute crop-specific know-how and resources; and the Centre National de Génotypage in Evry, France, conducts high sequencing. Working together, the group develops a GCP database on allelic diversity on key genes across GCP crops, thereby providing inputs for designing association analyses.

Subprogramme 2: Comparative genomics for gene discovery

Rationale

Plant traits for adaptation to environmental stresses are often controlled by complex genetic systems subject to influence by genotype x environment interactions. To effectively combine the right complements of genes and alleles in a breeding programme, we need to have an adequate understanding of the genetic mechanisms underlying the adaptive processes. Such an understanding is particularly important in cases such as drought tolerance, where the genetic effects are often small and the phenotypes are difficult to measure. Advances in genomic tools and knowledge from model organisms provide exciting opportunities to dissect the genetic control of complex traits and identify potentially useful genes. Yet, practical applications of the new tools for agronomic improvement require a level of integration that is often difficult for individual disciplines to implement.

A main objective of this Subprogramme is to provide a scientific and collaborative environment to enable gene discovery and concomitant flow of benefits. Specifically, we aim at a) developing cross-cutting research platforms for efficient application of genomic tools and knowledge to decipher genetic control of complex traits, and b) identifying genes to alleviate target problems in the most efficient manner by pooling resources and expertise. Furthermore, to realise the potential requires capacity-building on using the new tools and to create the pipeline to translate results into practice. Importantly, successful demonstration in solving problems in a few targeted cases defines the roadmap for broad applications of the new science.

To meet these objectives, SP2 is designed to maximise the use of genomic and genetic resources available in the research community. We support the production of specialised stocks that will elevate the level of genetic research in different crops. We apply comparative approaches to leverage genetic knowledge from multiple plant species to investigate and validate gene functions important for stress tolerance. Multi-disciplinary teams are formed to incorporate the validated genes into breeding programmes.

Since GCP's inception, there has been continued growth in sequence information across all plant species. Improved efficiency in sequencing technologies also makes whole-genome sequencing feasible for an increasing number of species. Rich sorghum genome information is now available, and that of maize is expected in the new future. The expanding gene content (sequence) and order (chromosomal position) information will help define orthologous genes across species. Parallel to these advances, gene expression platforms are also increasingly accessible for many plants. Expression level polymorphisms and patterns of expression along a chromosome can become the intermediate phenotype to bridge the gap between DNA variation and whole-plant performance. Advances in human and medical genetics continue to illustrate the power of SNP haplotypes and association genetics to identify functional genes. SP2 strives to absorb the new knowledge gained and adopt new approaches where appropriate.

SP2 activities support the CGIAR System Priorities 2a and 2b. The genetic resource and tools developed (genetic stocks, markers) enhance breeding efficiency and lay the foundation for efficient gene identification. Within the GCP context, SP2 outputs feed into the pre-breeding activities of SP3. The outputs cut across crops and ecosystems and can contribute to any breeding programme in the world. In particular, most of the outputs involve improving the understanding of abiotic stresses (e.g., drought, salinity, problem soils) that fully align with System Priority 2b on abiotic stresses. When these outputs together are jointly applied to crop improvement programmes, they contribute to yield stability of staple food crops (Priority 2a).

Impact Pathways

Theme 1: Assembly of genomics and germplasm resources through consolidating and developing specialised genetic stocks

One of the bottlenecks in the development of stress tolerance in crops is an inadequate understanding of the genetic basis of stress tolerance. The complexity of stress response requires a multi-prong approach to reveal the underlying mechanisms. The four themes of this Subprogramme—genomic resources, comparative mapping, genetic pathway analysis and gene validation—represent a progression of gene discovery through use of comparative biology. In the first theme (assembly and production of specialised genetic resources), we recognise the importance of mutants, isogenic lines, cytogenetic stocks and chromosome substitution lines as tools for identification of gene functions. However, with a few exceptions, most crops have little specialised germplasm to support gene identification and confirmation.

In its first three years, GCP played a catalytic role by supporting the assembly of wheat stocks and the production of mutant collections in bean and true-seed potato. These start-up activities have stimulated interest from diverse institutions and research laboratories, thus increasing the likelihood that more specialised stocks in other crops will be shared or produced by other initiatives. The production of new genetic resources and development of tools will expand the research community's means for understanding gene function relevant to stress tolerance.

Just within the past year, new comprehensive genomic resources for several crops (sorghum, maize, cowpea, cassava) have been produced, or are in the pipeline. As genome sequencing becomes less costly, we expect whole-genome genotyping, ultimately at the sequence level, to be increasingly feasible. In this context, GCP will engage the community to produce genomic and genetic resources, particularly in crop species that are under-resourced. Under this theme, we will continue to take advantage of the large collection of rice mutant collections around the world by supporting phenotyping of these mutants for stress tolerance. There will be greater focus on the mutant phenotyping work by linking with the ADOC project. The new resource-building activities will focus on four legume species (common bean, chickpea, cowpea and groundnut). For bean, gene libraries under drought-stress response will be produced to enable selection of candidate genes associated with drought tolerance traits. Similarly, EST and BAC clone sequences will be produced for chickpea, cowpea and groundnut. The activities on these four legumes will create a permanent genomic resource base for each species, enabling the construction of genetic maps and marker-aided selection applications at various stages of genetic analyses and breeding.

Theme 2: Develop comparative maps within and across species and framework genetic markers for target crops

The second theme of this Subprogramme aims at generating common markers and consensus maps across species, and at providing a framework for leveraging information across different crop species. GCP's investments in mapping orthologous genetic markers and the genomic investigation of *Musa* are a modest attempt towards this aim. This was followed by a set of projects: the 'ADOC' project on allelic diversity of orthologous candidate genes and cross-species marker project on legumes. The development of cross-species markers for legumes will be integrated with the genomic resource development for the four legume species in Theme 1. Emphasis will be on identifying orthologous markers that are related to biotic and abiotic stress tolerance.

For cassava, a physical map with SNP markers will be produced by a team led by The Institute for Genomic Research (TIGR). For sweet potato and pearl millet, we aim for an expansion of genome sequence data which will be aligned with genetic maps using mapping populations in breeding programmes. A main emphasis in these activities is that the genomic resources should be anchored in well-used mapping or breeding populations. Our approach is to maximise the return on our investment in a sequencing project by coupling it with SP1's development of genetic recombinant populations, so as to make use of the sequence data. By developing parallel genomic and genetic resources, we can reap benefits in a relatively short time.

The new activities will generate improved genetic maps for several species, including cassava, sweet potato and pearl millet. The new efforts are expected to increase the genetic knowledge base of important crops that have thus far suffered under-investment. Outputs from these projects will promote the mapping and genetic dissection of a suite of traits, particularly drought tolerance.

Theme 3: Assign genes and pathways to phenotypes through the convergence evidence of genome variation, expression patterns and phenotypic data

In the third theme—analysis of genetic pathways—emphasis is on the application of genome-wide tools such as gene chip technology to reveal the causal relationship between gene expression patterns and phenotypes. A unique feature of GCP's research is the use of agronomically relevant experimental conditions and genetic materials such that the genetic knowledge generated from these experiments is relevant to researchers and breeders. The adoption of genome-wide approaches has proven to be fruitful in suggesting new genes or regulatory mechanisms for validation. Gene expression studies in first round projects have shown that variation in gene expression (or expression-level polymorphisms) offers a new dimension of genetic diversity that can bridge the gap between genotypes and phenotypes. A whole-genome view of plant response to stress in relevant genotypes under realistic agronomic conditions will be important for identifying QTL of large to moderate effects.

Two on-going research projects aim at discovering genes and genomic regions controlling broad-spectrum disease resistance in maize, rice and wheat. The results from these projects are important as disease resistance is often a requisite trait in drought-prone environments. New activities will maximise the use of advanced genetic materials such as near-isogenic lines to determine if expression patterns are casually related to target phenotypes. We foresee the production of a multi-stage 'expression atlas' of genotypes with contrasting phenotypes in near-isogenic lines, followed by co-segregation analysis between expression patterns and relevant phenotypes. Parallel projects involving several crop species would be desirable as they will enable comparison between genes/pathways, hence providing support for orthologous candidate genes for validation. This approach, if demonstrated successful, will provide an efficient way of assigning gene functions and identifying relevant pathways.

In order to have the right genetic materials for gene identification, we must have methods to generate high-quality phenotypes with respect to drought tolerance. It has been shown in several situations that drought-tolerant/response phenotypes can be reliably measured provided that water stress is properly administered in the field or under equivalent agronomic conditions. In conjunction with SP3, we are interested in accelerating the progress in these proven systems. We will also sponsor activities to improve current phenotyping methods. The aim is to fast-track the identification of genotypes with relevant phenotypes.

Theme 4: Validate genes and pathways through evaluation of under- or over-expression constructs or variants (induced or natural) of the target genes

The gene validation activities under SP2's fourth theme aim to identify genes with useful functions, for delivery to breeding programmes. There are four outputs in this theme concerning the identification of stress tolerance genes in wheat, rice, sorghum and maize. The cloning of the gene that confers tolerance to aluminum toxicity in sorghum has laid the foundation for cloning other tolerance genes in cereals. Considerable progress is also being made towards cloning rice genes that control tolerance to salinity and phosphorus-deficient soils. These projects will produce a suite of genes useful for coping with drought-prone and marginal environments. For example, knowledge of the tolerance genes against soil problems in sorghum and rice can be immediately exploited to find similar genes in other cereals or legumes.

Two outputs are related to wheat. One concerns the identification of candidate genes responsible for failure of grain formation in rice and wheat under drought stress. If validated, such genes would provide new markers for germplasm selection for tolerance against stress at reproductive stage. A new addition to the wheat research is determining drought-adaptive mechanisms in bread and durum wheat aided by large-scale phenotyping methodologies. With improved phenotyping techniques, this project is expected to produce new wheat mapping resources for gene identification.

In the original formulation of this thematic research, our main concern was to determine the functions of the target genes. Such functional validation is a necessary, but insufficient, criterion to establish the usefulness of the identified genes. A key issue relating to gene function validation is whether the alleles identified can add value to existing varieties. It is important to test this sufficiently early to ensure that the right alleles are used in breeding programmes. For example, can the aluminium toxicity tolerant genes found in sorghum and maize provide tolerance above that seen in currently used varieties? A second issue is that the discovered genes must be delivered in genotypic backgrounds suitable for a target environment. For example, in order to deploy the phosphorus-uptake (*Pup1*) gene in upland rice, it must be combined with disease resistance in the environment where disease is a constant threat. Thus, to ensure impact, secondary traits need be considered such that a 'trait package' is in place for delivery in advanced breeding lines. New projects have been formulated in conjunction with SP3 to evaluate the genes/markers generated from several SP2 projects.

The outputs from these themes are geographically neutral. The primary users of outputs from Subprogramme 2 will be researchers, plant biologists and breeders worldwide. Uptake of these outputs by researchers and breeders is expected to expand the capability and increase the efficiency of NARS breeding programmes, an outcome beyond the immediate users. At the global level, the resources and knowledge of gene function generated by SP 2 activities are expected to be taken up by the plant biology community. The knowledge when applied to a range of crop systems can increase the potential of finding new genes from diverse plant species.

A potential factor that may impede the dissemination of knowledge and new tools is intellectual property (IP) protection in information and genetic resources where there is a strong commercial interest. Although GCP requires complete open access to the results and resources generated by GCP-funded projects, there are still issues of prior IPs that may deter total access and sharing. This issue should be addressed by the appropriate government authorities to enable faster and freer movement of materials. A second factor relates to institutional commitment to produce and use specialised genetic stocks. GCP has stimulated interest in the production of selective genetic resources, but further propagation and dissemination of such genetic stocks will depend on institutional investment. However, unlike conserved germplasm, sufficient provisions are rarely available to maintain specialised genetic stocks for long-term use, a common problem that deserves close attention by research institutions.

Project contribution to international public goods

The overall research portfolio of this Subprogramme focuses on drought-tolerance traits as well as genes and agronomic characters that improve crop resilience in difficult environments. The outputs are primarily resources, knowledge and technologies that are international public goods consistent with the goals of the System Priorities 2a and 2b. The key resources and tools produced are specialised genetic stocks (e.g., mutants and advanced backcross lines), gene expression data, cloned genes for specific trait improvement (tolerance to diseases, water stress conditions, and soil problems) and desirable gene combinations in elite genetic backgrounds (pre-breeding materials). These materials will be used primarily by researchers and breeders within GCP, but many outputs will be useful to the global research community interested in applying genomics to improve agriculture. While most of the activities aim at improving understanding of complex traits, several projects will produce advanced breeding materials as key outputs to alleviate problems in resource-poor areas in Asia (e.g., rice tolerant to P-deficiency in Indonesia) and Africa (e.g., maize tolerant to aluminum toxicity in Kenya). These outputs are global in nature but achieve specific impacts at regional scale.

Partnership

Under the theme developing genomic and specialised genetic resources, we continue to develop partnerships with institutes and laboratories that have rich specialised genetic stocks and ability to generate new resources or knowledge from these stocks. The partnership includes major wheat genetic research centres to assemble wheat stocks, laboratories working on rice mutants from the International Rice Functional Genomics Consortium; University of Geneva and CIAT on making legume mutants; the Scottish Crop Research Institute, the Hebrew University of Jerusalem and CIP on producing true-seed mutants of potato. Under the *Musa* frame map construction project, the National Institute of Agrobiological Sciences (NIAS) in Japan, with its sequencing and informatic capacity, coordinates a collaboration between laboratories active in *Musa* research. The new tropical legumes project will involve a large number of universities, IARCs, and NARS partners. For example, University of California–Davis will lead a network of legume researchers and breeders to develop cross-species marker resources for four legume species. In the new projects on generation of genomic and genetic resources for pearl millet and sweet potato, we will involve IARCs and NARS producing and propagating mapping populations. For improved efficiency, we may consider outsourcing the sequencing tasks to the private sector.

Under the themes of gene identification and validation for specific traits, the projects involve contributions from institutions and laboratories with strong expertise in biological analysis of target traits, comparative biology and breeding. For example, the comparative analysis of tolerance to aluminum toxicity in sorghum, maize and other cereals span multiple disciplines in comparative genomics, soil nutrition, physiology and breeding. These activities involve Cornell University, EMBRAPA and Moi University in Kenya. Another illustration of bringing resources and technical expertise together is in the project on developing tolerance to salinity and P-deficiency in rice. In this project, IRRI coordinates collaboration with the University of California–Davis; the University of California–Riverside; Japan International Research Center for Agricultural Sciences; University of Dhaka (Bangladesh); the Indonesian Centre for Agriculture Biotechnology and Genetic Resources Research and Development; Agricultural Biotechnology Research Institute of Iran and the National Institute of Agrobiological Sciences in Japan. These institutions have combined expertise in trait and agronomic analysis, gene expression, transgenics and breeding. Other trait-based projects have similar types of collaboration covering the range of expertise needed.

In the upcoming competitive grant projects, new partners will be brought in to provide the complementary expertise in the development of genomics resources, marker validation, mapping, trait analysis and breeding. The cassava project will involve The Institute for Genomic Research (USA), the African Centre for Gene Technologies, the Agricultural Biotechnology Institute of the University of Pretoria, University of the Witwatersrand and the University of California–Davis. For analysing drought-adaptive mechanisms in wheat, the team consists of CIMMYT, the Australian Centre for Plant Functional Genomics and the Directorate of Wheat Research (Karnal, India). Appendix A has the full list of partners.

In summary, the composition of partners in SP2's individual projects demonstrates successful leveraging of institutions and researchers who are not traditionally oriented to agricultural research, thus substantially enhancing GCP's research capacity. With this large pool of researchers and intellectual capital in place, there are still more gains to be made by promoting collaboration between projects.

Subprogramme 3: Trait capture for crop improvement

Rationale

Subprogramme 3 (Project 3 in the MTP) aspires to link conventional upstream research outputs with practical product development. These links are greatly neglected in public sector research, but their absence constitutes a major obstacle to the uptake of research results and the ultimate impact of investments in applied research. Subprogramme 3 plays a vital role in building links across the community of plant breeders involved in the evaluation, validation and refinement of molecular breeding technologies generated by GCP. The Subprogramme is equally important in building links among CGIAR Centres, NARS, small and medium breeding programmes and SMEs. SP3 plays also a critical role in adding value to the products and the knowledge generated by the other subprogrammes to ensure the investment made by the GCP in upstream research will impact crop breeding in marginal environments.

The priorities of SP3 are in complete conformity with CGIAR System Priority 2, *producing more and better food at lower cost through genetic improvements.* About 80% of SP3 activities align with CGIAR Priority 2B, *improving tolerance to selected abiotic stresses,* and the remaining 20% align with Priority 5D, *improving research and development options to reduce rural poverty and vulnerability*.

Significant direct spillovers from sequence, gene function and plant phenotype in model species are expected to substantially impact progress in those closely related crops that lack genomic resources and expertise. All crops are likely to benefit from generic advances in genomic platform technologies, low-cost marker screening technologies and molecular breeding simulation and decision-support systems. Global research progress in cereals such as rice, maize, sorghum, wheat, or barley is sufficient to begin the development and application of gene-linked or gene-based marker systems for components of tolerance to drought and other abiotic stresses. Emphasis in these crops in SP3 is more on the translation and/or application of pre-existing research outputs to ensure short-term impact on cereal breeding. Conversely, in legumes and clonal crops, the global genomics resources are still below critical mass, and current GCP priorities are defined to ensure rapid and compelling proof of concept in key representative legumes (groundnut, cowpea) or clonal crops (cassava).

Beyond providing technologies that help breeders effectively manipulate beneficial genetic variation for drought tolerance, SP3 must consequently validate gene function and interaction identified in SP2 and/or alleles identified through association tests by quantifying the genetic gains achieved from using target molecular markers in adapted genetic backgrounds under local target conditions.

Keeping a level of activities dealing with the refinement of phenotyping and molecular breeding methodologies is still important in SP3, and these activities and allocated resources are expected to be maintained at the same level in the future.

The projects/activities in this Subprogramme are presented as outputs in the MTP logframe and are organised under the following themes:
Theme 1: *Characterisation of segregating populations and identification of genomic regions for plant breeding*
Theme 2: *Development and evaluation of novel breeding or molecular technologies to better serve modern plant breeding*
Theme 3: *Markers/alleles validation in adapted germplasm under target environments*
Theme 4: *Application of molecular markers in breeding programmes*

Although diverse, SP3 themes and activities are complementary and clearly oriented towards the discovery, validation and application of molecular markers for plant breeding. Titles for Themes 1 and 2 have been simplified since the 2007–2009 Medium-Term Plan, while Themes 3 and 4 have been slightly modified to better highlight the two activities of increasing importance in SP3, ie, i) to validate, under target environments, alleles identified or markers developed within GCP; and, ii) to apply these markers in breeding programmes.

Impact pathways

Theme 1: Characterisation of segregating populations and identification of genomic regions for plant breeding

This theme represents the ‘discovery’ research activities of SP3: the evaluation of segregating populations towards the characterisation and validation of genomic regions involved in the expression of target traits. The first output under this theme aims at developing a better understanding of drought tolerance in cassava by investigating physiological pathways and their effects on plant phenotype, and identifying drought-tolerant cassava genotypes for further use as progenitors by breeding programmes in Africa.

A second output target is to use genomic and genetic tools to unlock genetic diversity of groundnut's wild relatives. Microsatellite-based genetic maps have been produced for the AA and BB genomes of *Arachis*. A bank of 3500 assembled ESTs from *A. stenosperma* and a BAC library for the AA genome of *Arachis* (*A. duranensis*) have been generated. A range of synthetic amphidiploids have been created and are currently being evaluated for disease resistance and drought tolerance.

Output 3 deals with the identification, through association mapping, of a set of indicative DNA markers available for allele discrimination and MAS for downy mildew resistance in maize. This project is led by maize breeding programmes in Thailand.

Tailoring superior alleles for the aluminium toxicity gene, *AltSB*, for further deployment into sorghum breeding programmes constitutes Output 4. A diverse sorghum collection has already been phenotyped for aluminium tolerance and genotyped at *AltSB*. Superior *AltSB* haplotypes have been identified. The molecular markers identified as outputs of these different activities will be applied in African countries facing aluminium toxicity problem due to soil acidity (Theme 3).

The last output of theme 1 (Output 5) is to extend Latin America's potato diversity to Africa. Molecular markers will be used to monitor the presence of key resistance genes in elite breeding stocks of several Latin American NARS, the short-days adapted germplasm will be converted into long-days adapted to be more available for African NARS, and databases, protocols, gene primers and germplasm resistant for known resistance genes will be exchanged. The expected impact is a set of new and more sustainable varieties deployed to resource-poor farmers in less developed areas and countries in Latin America and Africa.

Theme 2: Development and evaluation of novel breeding or molecular technologies to better serve modern plant breeding

In addition to the discovery of novel markers, there is also a need to develop and/or test new methodologies to improve the efficiency of molecular breeding. This is the objective of activities under Theme 2. The new methodologies essentially cover three areas: the development of low-cost, high-throughput markers, the refinement of marker-assisted breeding strategies and their modelling, and the development of innovative phenotyping protocols.

The first output in this theme is the development of low-cost, gene-based marker technologies for virus and pest resistance in cassava (Output 6). Crosses between virus-resistant and farmer varieties have been done and lines have been selected through MAS for virus resistance. The lines will be disseminated in Brazil, Uganda, Ghana and Nigeria.

As an output of the theoretical research conducted in SP3 and SP4 to improve the development of molecular breeding systems, simulation models are now being developed in Output 7 to pyramid multiple genes via MAS. This exercise of molecular breeding simulation and monitoring is conducted in collaboration with on-going SP3 projects (particularly Outputs 4 and 11). MAS monitoring software, for the entire molecular breeding community, will be developed in collaboration with Project 4 (Bioinformatics).

The development of innovative phenotyping protocols is conducted through Output 8. The objective is to use stables isotopes (particularly ^{13}C) in drought tolerance phenotyping. The corresponding activities will be developed jointly with SP2, in collaboration with FAO/IAEA. Output 8 aims to develop phenotyping protocols using stables isotopes for cowpea and chickpea, two tropical legumes included in outputs 19 (theme 4).

Theme 3. Markers/alleles validation in adapted germplasm under target environments

The general objective of this theme is to validate, under target environments, alleles that were identified or markers that were developed in the same output, in Theme 1 outputs, or in other SPs (mainly SP2).

Drought-tolerant rice cultivars have been developed, through Output 9, for North China and South/Southeast Asia by highly efficient pyramiding of QTL from diverse origins. Through Output 10, AFLP markers have been developed to discriminate among the different races of *Striga* that parasitise cowpea in West Africa, and converted into SCAR markers to facilitate rapid identification of pathogen diversity in the field. Resistance markers have also been developed for several races. Output 11 aims at integrating marker-assisted selection into conventional breeding to improve wheat in the drought-prone areas of Northern China. Activities include the development of a phenotyping network involving Ningxia, Shanxi, Henan and Hebei Provinces, and a genotyping platform developed at CAAS for Northern China. Objectives are to have drought-tolerant QTLs identified and elite Chinese wheat backgrounds characterised in diverse target environments, and candidate accessions carrying target genes/markers and elite Chinese wheat backgrounds identified for molecular breeding.

Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco constitutes Output 12. It includes the development of MAS approaches for drought tolerance improvement, and an enhanced utilisation of wheat and barley diversity using exotic/core collections and the reference sets developed by GCP.

Ouputs 13 and 14 aim to validate genes previously identified in other GCP outputs or themes. Validation of *AltSB*, a major aluminium tolerance gene in sorghum, is being validated by IRAN, the national research programme in Niger, while *Saltol*, a major salinity tolerance gene in rice generated in theme 2, is being validated by a consortium of rice-breeding institutions in Bangladesh.

The global objective for the coming years is an evolution towards a global and rationalised selection/management of validation projects, using project management techniques to integrate scientific quality (evaluated from reports, on-site visits and opinion of experts) and risk factors, alignment on the strategic plan, competitive advantage for users (breeder, farmer), synergy with other projects and products, feasibility and expected adoption.

Theme 4. Application of molecular markers in breeding programmes

This theme targets the current application of markers developed by GCP (or by others) in breeding programmes via the most efficient approaches. Output 15 aims to integrate genomic tools with conventional screening for developing NERICA (new rice for Africa) cultivars for West Africa. Drought tolerance lines have been selected among various *glaberrima* accessions and interspecific (*O. sativa*/*O. glaberrima*) breeding lines. This germplasm is being genotyped using a genome-wide set of 400 SSR markers in order to characterise quantitative trait loci associated with recovery ability and phenotyped for two major diseases (rice yellow mottle virus and bacterial leaf blight). Markers associated with rice yellow mottle virus (RYMV) and bacterial leaf blight (BLB) resistance will be identified. Finally, selected interspecific lines (new NERICA lines) with desirable traits will be supplied to NARS scientists for further evaluation and dissemination in the region.

This project will also train a Malian NARS scientist on genomic technology. This output is closely linked to an SP2 competitive project titled ‘Interspecific bridges that give full access to the African rice allele pool for enhancing drought tolerance of Asian rice’, through the ‘NERICA platform’. This competitive project aims to deliver a large set of fertile interspecific lines derived from crosses between *O. sativa* and *O. glaberrima* that will be extensively used by Output 15.

Output 16 deals with the improvement of virus resistance in sweet potato. Sweet potato is an important food crop and due to extreme high pro-vitamin A content orange-fleshed sweet potatoes (OFSP) can alleviate vitamin A deficiency in many regions of the world. However, sweet potato virus disease (SPVD), which is a complex of two virus diseases—the sweet potato feathery mottle virus (SPFMV) and the sweet potato chlorotic stunt virus (SPCSV), is causing serious yield losses, especially in high-virus pressure zones in Sub-Saharan Africa, where OFSPs are often not sufficiently SPVD virus-tolerant. SPVD resistance was found in the clone ‘Resitan’. Markers for SPVD will be developed using backcross populations, AFLP and SSR or SNP markers. In a third step, OFSP breeding populations and CIP germplasm will be screened with the marker system to increase the use of parental material segregating for the phenotype ‘SPVD Resistance’.

Output 17 focuses on rice in the Mekong region and involves Thailand, Laos, Cambodia and Myanmar national programmes. Drought, salinity, diseases and insect pests (such as blast, bacterial leaf blight, brown plant hopper, white back plant hopper and gal midge) are the main constraints of rice production in this region. Genes/QTL associated with pest and disease resistance and with cooking quality traits (amylose content, gel consistency, gelatinisation temperature and aroma) were identified by BIOTEC’s Rice Gene Discovery Unit. Marker-assisted selection for the traits mentioned is now being implemented in well-accepted cultivars in the Mekong countries. Quality traits are transferred to rice with drought resistance in Thailand and Cambodia, salt tolerance traits are transferred to cultivars with good quality in Myanmar, and rice quality traits are transferred to cultivars with wide adaptation in Laos.

Output 18 aims at detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-aided breeding. Output 19 relates to the new special project on tropical legumes. New molecular markers identified for disease resistance and drought tolerance will be deployed to breeding programmes in Africa for groundnut, bean, cowpea and chickpea. Similarly, Outputs 20 and 21 respectively aim to develop marker-assisted selection for resistance to *Striga gesnerioides* in cowpea in West Africa (based on the products delivered by Output 10) and for resistance to streak virus in maize in Mozambique.

Output 22 aims at accelerating adoption in Africa of varieties produced by MAS that are resistant to the cassava mosaic disease (CMD), cassava bacterial blight (CBB) and cassava green mites (CGM). For this purpose, molecular breeding capacities of the National Root Crop Research Institute at Umudike, Nigeria (the leading cassava producing country in Africa) will be strengthened and new CMD-, CBB-, and CGM-resistant cassava varieties will be disseminated by integrating formal (scientist-led) and farmer-driven cassava seed systems. *Ex ante* impact assessment studies will evaluate the adoption of the new cassava varieties in target sites.

Output 23 initiates a public–private sector collaboration. The experience in marker-assisted recurrent selection gained by Syngenta in maize will be transferred to sorghum in Africa, through a collaboration between Syngenta, and two national programmes in West Africa—Institut National de Recherches Agronomiques du Niger (INRAN) in Niger and Institut d’Economie Rurale (IER) in Mali.

Project contribution to international public goods

This Subprogramme is delivering marker technologies that are available as international public goods to generate germplasm with resistance to pests and diseases and with enhanced tolerance to drought, salinity or acid soils. The new approaches pioneered in SP3 for molecular breeding (development of low-cost, high-throughput markers, modelling for better monitoring of marker-assisted breeding strategies, development of innovative phenotyping protocols), especially in the understudied crops, are also international public goods, as well as the products generated from these approaches, technologies and protocols (e.g., virus-resistant cassava and sweet potato, cowpea resistant to *Striga*, or rice resistant to bacterial blight). For example, in groundnut, the combination of wide crosses and molecular marker analysis has allowed us to repeat the huge success of synthetics in breeding programmes for other complex polyploid crops such as wheat or canola. Groundnut's narrow genetic base makes it very likely that this approach will deliver dramatic breeding gains for this orphan crop.

Partnership

Projects in Subprogramme 3 involve myriad players from the CGIAR, ARIs, and NARS. SP3 fosters innovative partnerships that allow us to capitalise on national experience for the benefit of other countries in the region, and on regional experience for the benefit of other regions.

Projects targeting new methodologies (Theme 2) involve scientists from the private sector as well as experts in public institutes with strong expertise in quantitative genetics. The projects oriented towards the application of molecular markers in breeding programmes are led by national breeding programmes with the technical support of ARIs or CGIAR Centres. But because SP3 focuses on the application of modern breeding tools, the role of national breeding programmes is of primary importance, and they are major partners in most SP3 projects, particularly in Themes 3 and 4. For instance, EMBRAPA 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—in Africa and Asia—so EMBRAPA has passed its synthetic disease-resistant groundnut lines to Senegal for local testing and application.

The cassava improvement activities under SP3 are multi-institutional, involving Cornell University, CIAT and EMBRAPA, with important implications for African partners, including the National Root Crops Research Institute (Nigeria), Namulonge Agricultural and Animal Research Institute (Uganda) and Crop Research Institute (Ghana).

In the current SP3 portfolio, two-thirds of the commissioned projects are now led by NARS breeding programmes. To speed this evolution, commissioned research from 2007 aims to establish regional molecular breeding communities that share common facilities (e.g., Mekong countries for rice, North China provinces for wheat), and begin using GCP research outputs in their breeding programmes to improve drought tolerance. Such projects offer excellent opportunities for assembling a diverse group of breeders who work on a set of target crops and will begin using GCP research outputs in their breeding programmes.

Another strategy used by SP3 for capturing interdisciplinary synergies and end-user feedback on priorities and outputs, is the development of 'strategic platforms' in which the flow or exchange of products between partners sharing a common objective is strongly encouraged. As for commissioned projects, the target cropping systems and regions are defined following the priorities defined by the GCP *Strategic Framework*. A first case concerned the development of NERICA, which is based on the joint efforts and collaboration between one competitive and one commissioned project. Similar strategic platforms are being developed for rice in Southeast Asia and for cowpea and cassava.

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 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. Subprogramme 4 (Project 4 in the MTP) addresses the challenge of linking and integrating these information components and analytical tools into a coherent information gateway. A bioinformatics, biometrics and advanced data management system is being designed to support an integrated genetic resources, genomics and crop improvement information network. 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 need to be 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 has a number of components. First, numerous local systems are already in place. The challenge of integrating them into one system is quite daunting, given that the ability to dictate the architecture and organisation of existing systems, inside and outside the GCP Consortium, is very limited. Second, 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 are generated. This strategy allows proper data curation (in terms of corrections and additions to the data) and avoids ownership problems. However, making data management a local responsibility requires an appropriate level of skills and facilities—an issue that is also addressed in SP4. Third, for all of the GCP Subprogrammes to function properly with respect to bioinformatics tools and access to databases, they need support in the selection of tools, identification of data sources, the integration of existing tools and databases and the creation of new tools and information sources.

This analysis shows that the objective of SP4 to create an integrated platform for access to, and analysis of, GCP data boils down to three specific problems:

1. Infrastructure: How can the information flow between researchers in GCP be organised to maintain local curation of data and tools but also to allow optimal access?
2. Improvement: How can GCP facilitate proper curation of data and tools to ensure that the quality improves to an acceptable standard?
3. Support: How can GCP accommodate its bioinformatics needs for tools and data sources?

To address these three problems, SP4 pursues activities corresponding to three themes. Each theme is oriented towards ‘internal users’—in other words, towards benefiting GCP. This orientation does not mean that GCP is the only beneficiary from SP4 activities. The efforts of SP4 will greatly benefit the global biodiversity and bioinformatics community, because GCP is increasingly becoming a major player, providing access to valuable data and tools and developing tools, software and standards for efficient data exchange and integration.

SP4 activities feature extensive collaboration with institutions outside the Consortium to ensure quality products, no matter where the expertise may reside. A good example is the ontology development (standards for exchanging data and accessing data and tools to address the first problem listed earlier). SP4 works with the global community to ensure that existing standards and protocols are adopted or incorporated into the ones GCP develops, but also to create ownership among users, so that the new standards become widely adopted ‘world standards’, not necessarily ‘GCP standards’.

Impact Pathways

Activities in SP4 are presented by theme, corresponding to the MTP logframe:

- Theme 1. Infrastructure: Facilitation of information flow of ongoing research, both in terms of data and in terms of communication between the researchers
- Theme 2. Improvement: Creation of facilities to support IT and bioinformatics applications in the GCP Consortium
- Theme 3. Support: Support to other GCP Projects in terms of software tools and data management

Impact pathways for each theme are detailed below.

Theme 1. Infrastructure: Facilitation of information flow of ongoing research, both in terms of data and in terms of communication between the researchers

As described earlier, Theme 1 addresses the question: ‘How can the information flow between researchers in GCP be organised to maintain local curation of data and tools but also to allow optimal access?’ Still the largest theme in SP4 in terms of investment, it aims to create a platform for exchanging information. This has taken shape, and it can be observed that funding is decreasing to maintenance level.

The GCP data handling and analysis infrastructure is based on web services technology: the technology that allows the ‘wrapping’ of local databases and analysis tools and making them visible to the world via the Internet. Obviously, the user needs an interface to access these web services. And, finally, a solution is needed to handle datasets that are not yet available as a web service, or that need to be used outside of this infrastructure.

This implies that a number of elements are needed, implemented in seven activities with corresponding outputs:

- The first is the development of a common language for data exchange protocols. This is being created by first developing ‘GCP Domain Models’, which were completed last year, and then to develop ontologies that can be used in these models. This ontology development involves a wide diversity of actors and requires clear prioritisation over the years. In 2008, the ontologies for the passport domain, genotyping domain and phenotyping domain will become available (see Output 4.1, coordinated by Richard Bruskiewich, IRRI). This activity is expected to decrease over the next three years to maintenance level.
- The second output is concerned with training staff and implementing web services technology in GCP member institutions. This started two years ago, and was to have been completed in 2007. However, given the developments in web services technology, it will be continue for one more year, with possibly very limited

activities in 2009 (see Output 4.2, coordinated by Milko Skofic, Bioversity).

- The third output delivers a short-term solution: templates for GCP data capture, storage and use. These templates (usually MS-Excel spreadsheets) guarantee full interpretability of information and try to be as compliant as possible with the GCP Data Domain. The data in these templates can be made centrally available, via a GCP Central Registry (see next output), but can also be maintained locally. Basic versions for all data types have been made available over the last few years. However, thus far, only the passport and genotype template have been tested and used sufficiently. In 2008, the use of these and the other templates will be further supported, and the templates will be further improved based on user feedback (see Output 4.3, coordinated by Guy Davenport, CIMMYT).
- The fourth output organises the GCP Central Registry, a Web portal where all GCP datasets are listed and made available as far as possible (in the templates listed in the previous output). Based on GCP project descriptions, a list is curated with all available and expected datasets, with descriptions and PIs responsible. As soon as the datasets are made available, they can be downloaded from the portal. The basic infrastructure has been established and is functioning. In 2008, the set of available datasets will be extended via a pro-active approach (see Output 4.4, coordinated by Tom Hazekamp, Bioversity).
- The fifth output ensures that the technology underlying the GCP application of web services is up to date. It elaborates the GCP platform architecture for data transformation and data visualisation, and applies this architecture in the reference implementation of a search engine. Furthermore, it allows for integration of bioinformatics workflow management into the GCP infrastructure. Finally it covers the technical backstopping of all developers involved in web services related software development (see Output 4.5, coordinated by Martin Senger, European Bioinformatics Institute).
- The sixth output aims at applying the web services technologies in high-end applications. In 2007, the goal is one web service each for Subprogrammes 1, 2 and 3. This serves a triple aim: (1) demonstrating that the investments in the technology (from the perspective of both GCP and Consortium members) has paid off, (2) creating functionality for GCP scientists, and, (3) raising GCP’s profile in the bioinformatics community (see Output 4.6, coordinated by Mathieu Rouard, Bioversity Montepllier).
- The seventh and final output deals with creating and maintaining a GCP software engineering and collaboration platform: CropForge for open source software development and GCP Wiki for collaboration. These platforms have successfully been established and are functioning. This activity will be scaled down to maintenance level (See Output 4.7, coordinated by Thomas Metz, IRRI).

Theme 2. Improvement: Creation of facilities to support IT and bioinformatics applications in the GCP Consortium

The second theme concentrates on improving data quality and handling, but also the quality of data access and the tools to analyse them. Obviously, it cannot be the GCP that implements quality management for GCP consortium members. This is an institutional responsibility. But the need to improve the quality of the data is clear. By creating the web services, we hope to increase the quality of data access.

The portfolio of activities in this theme will have three outputs:

- The first output focuses on the access to the data tools made available in the first theme. It has developed two interfaces with the GCP infrastructure: Koios, a web-based infrastructure, and Genomedia, a software package that needs to be installed locally. Both packages allow access to the web services created by GCP, offering tools for analysis. These tools will be further developed in the coming years. In 2008, three new functionalities are foreseen: (1) in-depth analysis of biological diversity to answer a broad range of questions about domestication and genetic organisation of species and a comparison between different crop models, (2) analysis of microarray data: with integration to other structural and functional genomic data, and, (3) marker-assisted backcrossing (MAB) protocols, for routine management of genotyping and evaluation data for molecular breeding (see Output 4.7, coordinated by Graham McLaren, IRRI).
- The second output in this theme deals with data quality and handling. It develops, in close collaboration with a range of actors, definitions of best practices and how to implement them (cf LIMS), increases the knowledge of quality management and develops protocols and methods to assess the quality of pre-existing data collections (see Output 4.8, coordinated by Thomas Metz, IRRI).
- The third and final output in this theme provides access to high-performance computing (HPC) capacity to GCP scientists. An HPC facility has been created within the GCP consortium and a range of software has been installed. In the coming years, the challenge will be integrating HPC functionality into the GCP platform. Also, the question of whether to upgrade the current hardware, or to outsource the function, will need to be addressed (see Output 4.9, coordinated by Anthony Collins, CIP).

Theme 3. Support: Support to other GCP Projects in terms of software tools and data management

Now that GCP is going full-steam, and data are becoming available, the need for support in the handling and analysis of these data is even more apparent. SP4 aims at accommodating this need as fully as possible by providing a central helpdesk that will match the question of the scientist with the solution (or expertise) from SP4. In addition to this, a number of dedicated activities have been developed that create specific tools and methodologies.

This theme has a large number of activities:

- First of all, there is the SP4 helpdesk that will respond to email requests from GCP scientists within 48 hours, indicating the most appropriate contact for the support needed. This is a new activity (see Output 4.11, probably coordinated by WUR).
- Specific questions concerning SP1 and SP2 respectively are covered by the second and third outputs in this theme. They deal with data analysis support for SP1 activities, with emphasis on sampling germplasm, and data analysis support available for SP2 with emphasis on microarray and mapping experiments. The first of the two also supports the NARS users of the Genotyping Support Services in the design and analysis of their experiments. These are ongoing activities, that both develop targeted methodology, but mainly support the GCP (and NARS) scientists bilaterally (see Output 4.12 coordinated by Marco Bink, WUR, and Output 4.13, coordinated by Guy Davenport, CIMMYT).
- The fourth output also concerns service to the NARS: in the last few years, a software package has been developed by integrating existing software into one platform (using web services technology) that allows users to use markers more efficiently in breeding programmes. The product, called iMAS, was launched in 2007, but can still be developed further to also handle cross-pollinators and other breeding systems. The training of users will be high on the agenda (see Output 4.14, coordinated by Subhash Chandra, ICRISAT).
- The next three outputs deal with new activities aimed at the development of methodology and software for specific analysis: LD-based phenotype analysis, association analysis in non-HW populations and reconstruction of genealogies based on haplotypes related to geographic patterns. All three issues are either very important or potentially very important to GCP, and require additional research to get access to, and further develop, the appropriate knowledge (see Output 4.15, coordinated by Fred van Eeuwijk, WUR; Output 4.16, probably coordinated by Cornell University; and Output 4.17, probably coordinated by CIRAD).
- The final three outputs are all extensions of projects scheduled to end in 2007, and also all deal with the development of methodology and software for specific analysis: eco-physiological–statistical analysis of GxE and QTLxE, the display of ortholog-functions, and creating and mining a database for gene expression data (see Output 4.18, coordinated by Fred van Eeuwijk, WUR; Output 4.19, coordinated by Richard Bruskiewich, IRRI; and Output 4.20, coordinated by Shoshi Kikushi, NIAS).

Project Contribution to International Public Goods

SP4 is primarily concerned with producing international public goods or making them available to the world:

- All software developed in SP4 is, in principle, made available under licenses approved by the Open Source Initiative (OSI), preferably the GNU General Public License (GPL) or GNU Lesser General Public License (LGPL).
- All web services created in SP4, both for databases and analytical facilities, are freely available to any interested user.

Partnership

Subprogramme 4 works with a wide array of partners, including software developers, biometricians and end-users of the technology. Some of SP4's partners include, in alphabetical order: (within the Consortium), ACGT, Agropolis, Bioversity, CIAT, CIMMYT, CIP, Cornell University, EMBRAPA, ICRISAT, ICARDA, IITA, IRRI, National Institute of Agrobiological Sciences (Japan) and Wageningen University and Research Centre. Outside the Consortium, SP4's partners include CSIRO, European Bioinformatics Institute, Hitachi Software Engineering Co Ltd, ILRI, INIA (Uruguay), Keygene, National Center for Genome Resources (USA), Universidad Autónoma Chapingo (Mexico) and the University of California (USA).

IRRI plays a major role in technical aspects of software development, domain modelling and ontology development. It has supplied the principal investigators for a number of important activities and uses its international network to draw in important players from outside the Consortium, either as partners in activities or as advisors in meetings.

The role of Bioversity is to make information available and train GCP staff on new technologies, involving other partners where appropriate. The other GCP member institutes contribute specific expertise as appropriate. For example, NIAS provides important input for activities related to gene expression; CIP gives useful guidance for GIS applications; ICRISAT contributes biometrical and programming skills plus LIMS experience; and WUR brings its extensive experience in biometrics and teaching.

Subprogramme 5: Capacity-building and enabling delivery

Rationale

Given its focus on building capacity and enabling delivery, Subprogramme 5 (‘Project 5’ in the MTP), contributes directly and indirectly to several CGIAR System Priorities, especially Priority 2, *producing more and better food at lower cost through genetic improvements*. Because SP5 activities cut across, and are in direct support of, all of the other GCP Subprogrammes, SP5 contributes to the same System Priorities as the other Subprogrammes (usually to Priorities 1b, 2a, and 2b). SP5 fulfils its role by not only 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. SP5 conducts research in international and national policy questions to facilitate delivery and, more recently, consolidated *ex ante* impact studies to identify GCP research priorities in terms of crop, region and trait for better decision-making and to guide resource allocation.

SP5 therefore adds value to the activities of the other subprogrammes. As the quantity of GCP products increases, it is equally increasingly important to efficiently manage and promote these products to not only add value but also guarantee a return on investments. Product delivery is not a given: it requires strategic and sustained effort.

GCP’s focus on product delivery cannot be realised without capacity-building. Our emphasis on capacity-building stems from the belief that education and knowledge are key ingredients for development. We believe 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. In this belief, GCP actively seeks collaboration with NARS, in the realisation that fruitful and meaningful partnerships, in addition to adequate up-to-date training, also depend on infrastructure and research support. For these reasons, SP5 activities are designed to increase NARS’ research capacity for meaningful collaboration, and to ensure product delivery to resource-poor farmers through efficient plant breeding programmes geared to meet those needs.

In the early years, GCP of necessity had numerous capacity-building activities. Capacity-building has now entered a consolidation phase as GCP generates more and more research products. This consolidation is evident in the evolution to fewer but more sharply focused activities, firmly embedded in GCP’s other Subprogrammes. Consequently, in the SP5 logframe, outputs are organised by theme, reflecting this consolidation and lessons learned from the foundation years of GCP, and SP5 adapting to needs and opportunities. The logframe illustrates the interaction of SP5 activities, and how these activities then complement the research in the other Subprogrammes towards a common goal and in line with GCP’s new strategy—product delivery for real impacts on institutions and individual scientists within and outside the GCP community.

Subprogramme 5 outputs all fall under the following five interactive themes:

- Theme 1—Creation of a platform of training resources and a cadre of trained scientists to apply advanced technologies and add value to GCP products: This theme includes training courses as well as designing learning materials in selected languages. Training covers phenotyping, marker-assisted breeding, genomics, bioinformatics and policies relevant to GCP’s work.
- Theme 2—Cultivation of research and learning opportunities for GCP collaborators and NARS scientists to further GCP mission and progress: Although this theme, like Theme 1 above, funds training and skill-building for scientists, it is more flexible than Theme 1. Grants are not tied to pre-determined courses or GCP activities, leaving room for input and ideas from NARS scientists. In other words, this theme is an open scheme that recognises outstanding individual scientists by building their capacity to champion the delivery and uptake of GCP products. In the future, SP5 will promote and support the best ideas generated from this collaboration for wider benefits targeting research teams. This re-orientation to teams will fall under Theme 3.
- Theme 3—Construction of systems for ensuring delivery of GCP products: This theme includes outputs to facilitate the flow of products along the delivery chain, from the scientists in laboratories to breeders in the field in GCP target regions.
- Theme 4—Development and implementation of support services: GCP aims to benefit the scientific community within and outside the Consortium. This theme has several technical outputs to support researchers such as information resources, advice from experts and data production and tools for smooth transition from theory to practice.
- Theme 5—*Ex ante* impact analysis and impact assessment: This theme includes research to help prioritise resource allocation as well as to identify impact indicators of GCP projects based on target regions, crops and traits.

Impact pathways

Theme 1: Creation of a platform of training resources and a cadre of trained scientists to apply advanced technologies and add value to GCP products

GCP has selected a few high-priority regions as the principal focus. Consequently, SP5 will complement this focus. SP5 activities will primarily benefit researchers and institutions in the target regions, or whose work impacts farmers in those regions. Training course participants will also be selected on the same rationale, but in some instances, scientists beyond GCP's immediate scope may be invited. The goal is to expand the pool of scientists able to conduct GCP-related research, thus providing GCP with strong and highly skilled collaborators, and more capable intermediaries for regional product delivery.

Programme selection for training courses and learning materials will be in close consultation with the other Subprogrammes to ensure selection and training are relevant and in tandem with researchers' demand for additional knowledge and skills in areas of GCP expertise. A set of training and reference materials is nearly complete for LD and association studies, marker-assisted selection, phenotyping and bioinformatics. Once completed, the material will be on the GCP website and on CD for researchers with poor access to the Internet. The material will also be used in GCP training courses and will be translated to several selected languages to ensure widespread reach to a broader research community interested in improving crop varieties. Reference materials for genetic diversity and basic genomics are already available.

SP5 also scans the external environment beyond GCP and carefully selects workshops on topical and relevant issues of interest to GCP. For instance, a workshop will be conducted in 2007 on the International Treaty for Plant Genetic Resources for Food and Agriculture (PGRFA). The focus will be on the treaty's implications for GCP research and partnerships in terms of germplasm and research products. On one hand, the GCP community needs to be aware of the Treaty and the complex issues its implementation implies. On the other hand, it is equally important that GCP collaborators understand the opportunities and make full use of them to advance their mission, while conforming to international legal standards and obligations. As in all cases, materials from this workshop will be available online for maximum access and reach. This open access to course materials is with a view to promoting a better understanding of procedures and conditions for exchanging germplasm and for enhancing collaboration worldwide.

Theme 2: Cultivation of research and learning opportunities for GCP collaborators and NARS scientists to further GCP mission and progress

Among other things, this theme supports NARS research and collaboration in priority GCP regions. We have a three-pronged approach covering teams, individuals and institutions. Specific activities include the Capacity-building à la Carte Programme, fellowships, travel grants and the professorship at the African Centre for Crop Improvement. NARS in GCP target regions engaged in GCP projects are the frontline users of this theme's outputs since their role and active participation are critical ingredients for product delivery. The overall goal is to increase the use of GCP-generated products, by engaging target users directly involved in GCP research.

Another activity is the customised Capacity-building à la Carte Programme that provides tailor-made capacity-building to selected teams of applied researchers in developing country research programmes. Teams are selected from a competitive call or in consultation with the other Subprogrammes whose activities the training supports. Teams submit a customised plan for training (through GCP or non-GCP events), mini-grants for basic equipment, hands-on research with advanced research institutions and *in situ* technical expert assistance. The Programme will result in a core community of highly skilled researchers to advance GCP research. These champions will guarantee rapid uptake of GCP results and products, thus furthering GCP's mission and goals, and hopefully spilling over within their institutions and regions. This would help realise the product delivery goals of GCP's new strategy framework and ensure that pre-breeding materials, generated by SP3 from the outputs of SPs 1 and 2, flow through the research–delivery pipeline.

SP5 does not fail to see the trees for the forest: individual training is just as important as team training. The Fellowship Programme provides opportunities for outstanding NARS scientists in ongoing GCP projects to increase their technical knowledge in any GCP target area. The Travel Grant Programme facilitates hands-on research opportunities and participation in GCP's Annual Research Meeting. It is open to all NARS scientists working at, or collaborating with, a GCP Consortium member institution. The Travel Grant Programme provides opportunities to forge or strengthen collaborations and to trigger and broaden interest in GCP's work in NARS and the wider scientific community.

In order to increase the number of plant breeders with skills in molecular breeding in Sub-Saharan Africa, GCP is supporting a professorship in molecular breeding at the African Centre for Crop Improvement of the University of KwaZulu–Natal (South Africa), complementing support to the University by The Rockefeller Foundation. The incumbent will participate in the selection of PhD candidates and research topics. Students will mostly conduct research in their home countries. Intended users and beneficiaries will be PhD professionals in selected African countries and breeding programmes who will be able to participate in GCP research and delivery activities. The objective is to increase skilled plant breeders in Africa, which will improve breeding programmes, resulting in better crop varieties for target farmers.

Theme 3: Construction of systems for ensuring product delivery

Theme 3 is anchored in the GCP Delivery Strategy[9] and focuses on capacity-building to meet project goals and ensure product uptake by targeted user groups. GCP allocates funds for competitive projects to develop delivery plans, ensuring the flow of products from source to intermediate users and ultimately to end-users. GCP also funds interactions—around a common theme—among collaborators in ongoing projects. The theme could be a region, crop, or technology, with the objective of sharing results, and identifying common interests and new users for research products.

Outputs 5.10 and 5.11 are on product delivery plans and capacity-building needs for the project on tropical legume improvement for Africa and GCP's second round of competitive projects. The resulting delivery plans will provide a two-way flow of communication at different stages of the delivery chain. The anticipated impact is that all GCP products will be delivered to users, and each intermediate user will develop additional products to improve farmer livelihoods.

Output 5.12 refers to the first of a series of joint workshops with SP3 on product management and delivery in ongoing GCP projects. This first meeting will bring together partners working on rice in Asia. Expected projects results will be reviewed and the delivery capacity of partner institutions assessed. This information will help GCP to identify appropriate partners and to refine capacity-building to better address the needs of the beneficiaries. The direct beneficiaries of the activity will be NARS researchers.

The Project Development Guide (PDG) will be designed in 2007 in close collaboration with all the other Subprogrammes. The PDG is a web-based project design and management tool for streamlining the preparation, approval, implementation and reporting of GCP research projects to enhance product delivery. An early prototype was piloted with a sample of GCP Principal Investigators and all were enthusiastic about its utility.

For effective and far-reaching product delivery, SP5 also looks beyond GCP. The last output of this theme is to develop a strategy for product marketing and distribution and the concept is in the preliminary stages. Intended users are not only GCP collaborators but also the wider community of beneficiaries who, once they access GCP products, continue improving them for end-users. With this expansive and inclusive marketing and distribution plan, we hope to reach an ever-widening community of beneficiaries accessing GCP products.

Theme 4: Development and implementation of support services

GCP remains committed to building public access platforms for useful tools and technologies, enhancing human capacity and strengthening institutions. However, impacts may be limited in the real world, where developing-country research institutions have limited resources to apply new tools and technologies. Online helpdesks (for example, on intellectual property and policy matters, laboratory protocols and other issues) provide remote support and advice to GCP and the wider scientific community, assisting researchers in their own working environments. They are still a work in progress and their utility will be evaluated next year. These resources will ultimately contribute to the self-reliance of NARS researchers.

Along this line, SP5 and SP1 jointly launched a genotyping support service (GSS) to promote the use of molecular markers to assess the potential value of germplasm and breeding materials for relevant agronomic traits. This will help GCP reach more national research programmes and should help bridge the gap between molecular laboratories and field practitioners. The service was successfully tested and is now available for crop and breeding programmes based on priority areas and emerging opportunities.

We have developed a tool to register assets produced in the GCP framework. The inventory system will evolve into a full-scale database of products, expertise and third-party materials associated with specific GCP products. The inventory will be an important tool for developing and implementing delivery plans. In addition, it could also be an indicator of progress and serve to measure impact.

Theme 5: Ex ante *analysis and impact assessment*

Gauging the impact of GCP research has now come to the foreground, given the complex and challenging context in which Generation operates. GCP's ultimate goal is to benefit resource-poor farmers, but most of the direct users of GCP products will be intermediaries in the research–delivery chain. Once the products are further developed by intermediate users and diffused, the ultimate benefits of GCP research will need to be measured in terms of increased productivity or income, or other indicators related to the use of new technologies or practices.

For now, this theme's objective is to refine GCP's priorities in terms of regions, crops, traits and technologies. The second objective is to define indicators for future impact assessments. The primary user of this information will be GCP's Management Team. However, in keeping with GCP's tradition of transparency and in the spirit of capacity-building, the information will be publicly available and for the benefit of other researchers and

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[9] See http://www.generationcp.org/capcorner/Final_Delivery_Strategy.pdf.

research managers in science and technology programmes for development.

Project contribution to international public goods

All products generated in SP5—such as training materials, delivery plans, support services and impact studies—are intended to benefit not only Consortium members but the wider scientific community. They are always made available, without restrictions, to the widest audience possible. SP5 also offers capacity-building opportunities, which strengthens institutions and individuals in target regions. While at first glance the activities may appear to only benefit a selected group of collaborators, they can be considered public goods in the sense that they aim to solve the needs of resource-poor farmers, and a spillover effect is expected to influence a wider community of researchers in the countries and regions from which the collaborators come.

Partnership

Projects and activities in SP5 are collaborative, involving Consortium institutions as well as institutions within and outside the Consortium. This partnership philosophy is at the heart of the GCP in general but is even more ingrained in this Subprogramme, which, by definition, begins by first building internal partnerships with the other GCP Subprogrammes. Outside the GCP management structure, SP5 deals with building capacity, creating links, building public knowledge platforms, providing services, supporting collaborators, disseminating knowledge, and much more. None of the outputs would be possible without the complementary participation of a variety of external collaborators, who are carefully selected depending on the activity.

Partnerships within the Consortium are sought, for example, for the development of training materials relying mainly on advanced research institutions – Cornell University will develop reference materials for a course in marker-assisted selection, CIRAD-Agropolis will translate materials on genetic diversity analysis that were already developed, INRA-Agropolis will finalise a set of teaching materials on phenotyping for drought and WUR will do the same for materials on association genetics. Policy courses will be organised and conducted by WUR (online) and Bioversity International (GCP issues regarding the International Treaty on PGRFA).

Training activities, such as the Fellowship Programme, the Travel Grant Programme and the Capacity-building Support Programme rely on partnerships with ARIs, the Future Harvest Centres and NARS at large, including academic institutions in the South. For the Fellowship and Travel Grant Programmes, the immediate beneficiary is a NARS researcher joining a research team at an advanced institution for time-bound hands-on training. A few examples of these partnerships supported in 2007 are: two researchers—one from Bangladesh University and another from CAS in China, to be trained at IRRI; a researcher from the Awassa Agricultural Research Center in Ethiopia to be trained at CIAT and a student from the University of Abomey-Calavi in Benin to be trained at IRD–Agropolis. Awards for the Capacity-building *à la carte* Programme will go to research teams in institutions in the South outside the Consortium, but engaged in an ongoing GCP project. Examples include the maize breeding team at KARI in Kenya, which collaborates with INRA–Agropolis, and NRCRI in Nigeria which collaborates with CIAT.

SP5 has established a special partnership with the African Center for Crop Improvement at the University of Kwazulu-Natal in South Africa for training PhD students enrolled at ACCI; the benefits should in turn spill over to numerous research institutions in Eastern and Southern Africa. Another special partnership is for preparing the Project Development Guide, in collaboration with the Syngenta Foundation for Sustainable Agriculture.

The launching of the Genotyping Support Service represents a different type of partnership. On one hand, it subsidises genotyping services for breeding programmes in the South (for example at MARI in Tanzania, PROINPA in Bolivia and University of Southern Mindanao in the Philippines) by linking them with providers in advanced institutions such as DArT P/L in Australia, ICRISAT in India, CIAT in Colombia and Genome Quebec in Canada.

One partnership that deserves special mention is the collaboration of partners in the new project ‘Improving tropical legume productivity for marginal environments in sub-Saharan Africa’. In this project, SP5 will collaborate with all the partners in both upstream as well as downstream research, in particular overseeing the implementation of capacity-building in the different research components as they relate to ensuring product delivery in the medium term.

New approaches bring in new partners and new ways of doing business: SP5’s *ex ante* impact assessment studies are already informing decision-making and resource allocation. Impact targeting and assessment projects have also opened doors for collaboration with experts in a different area such as Virginia Tech (USA) for *ex ante* impact analysis of two GCP first-round competitive projects, CIAT for drought and poverty mapping and CIMMYT for the study of secondary breeding objectives of selected GCP crops.

Appendices

Appendix A: 2007 GCP Consortium members and partners

Consortium Members

Full members

1. Africa Rice Center (WARDA)
2. African Centre for Gene Technologies (ACGT)
3. Agropolis, France
4. Bioversity International
5. Chinese Academy of Agricultural Sciences (CAAS)
6. Cornell University
7. Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA; Brazilian Agricultural Research Corporation)
8. Indian Council of Agricultural Research (ICAR)
9. International Center for Agricultural Research in the Dry Areas (ICARDA)
10. International Center for Tropical Agriculture (CIAT)
11. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
12. International Institute of Tropical Agriculture (IITA)
13. International Maize and Wheat Improvement Center (CIMMYT)
14. International Potato Center (CIP)
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)

Provisional members

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

NARS Partners

1. African Centre for Crop Improvement (ACCI) at KwaZulu–Natal University, South Africa
2. Agricultural Biotechnology Institute of the University of Pretoria, South Africa
3. Agricultural Biotechnology Research Institute of Iran (ABRII), Iran
4. Agricultural Research Institute–Naliendele Research Station, Tanzania
5. Awassa Agricultural Research Centre, Ethiopia
6. Cambodia Agricultural Research and Development Institute (CARDI)
7. Central Rainfed Upland Rice Research Station (CRURRS), India
8. Central Rice Research Institute (CRRI), India
9. Centre Africain de recherche sur bananas et plantains (CARBAP), Cameroon
10. Centre d'Etude Régional pour l'Amélioration de l'Adaptation à la Sécheresse (CERAAS), Senegal
11. Centre Research for Biotechnology, Bogor Agriculture University (IPB), Indonesia
12. Chinese Academy of Sciences
13. Chitedze Research Station, Malawi
14. Cocody University, Côte-d'Ivoire
15. Coconut Research Institute, Sri Lanka
16. College of Agriculture, Rewa, India
17. Crop Research Institute (CRI), Ghana
18. Department of Agricultural Research (DAR), Myanmar
19. Directorate of Wheat Research (India)
20. Ethiopian Institute of Agricultural Research (EIAR)
21. Fedearroz, Colombia
22. Huazhong Agricultural University, China
23. Indian Agriculture Research Institute (IARI)
24. Indira Gandhi Agricultural University IGAU, India
25. Indonesian Centre for Agricultural Biotechnology and Genetic Resources and Research Development (ICABIOGRAD)
26. Indonesian Department of Agriculture
27. Institut de l'Environnement et de Recherches Agricoles (INERA), Burkina Faso
28. Institut d'Economie Rurale (IER), Mali
29. Institut National de l'Environnement et de Recherches Agricoles (INERA), Burkina Faso
30. Institut National de Recherches Agronomiques du Niger (INRAN)
31. Institut Sénégalais de Recherches Agricoles (ISRA)
32. Institute of Dry Farming, Hebei Academy of Agricultural Sciences (HAAS), China
33. Instituto de Botánica del Nordeste (IBONE), Argentina
34. Instituto de Investigaciones Agropecuarias (INIA-Remehue), Chile
35. Instituto Nacional de Investigación Agropecuaria (INIA), Uruguay
36. International Centre for Genetic Engineering and Biotechnology (ICGEB), India
37. Kasetsart University, Thailand
38. Kenya Agriculture Research Institute (KARI)
39. Lake Zone Agricultural Research and Development Institute (LZARDI), Tanzania
40. Luoyang Academy of Agricultural Sciences (LAAS), China
41. Mikocheni Agricultural Research Institute (MARI), Tanzania
42. Moi University, Kenya
43. Nakhon Sawan Field Crops Research Center, Thailand
44. Namulonge Agricultural and Animal Production Research Institute (NAARI), Uganda
45. Nanjing Agricultural University (NAU), China
46. National Agricultural and Forestry Research Institute (NAFRI), Laos
47. National Agriculture Research Centre (INIA), Chile
48. National Crop Resources Research Institute, Namulonge, Uganda
49. National Maize Research Institute, Vietnam
50. National Root Crops Research Institute (NRCRI), Nigeria

51. Ningxia University, China
52. Philippine Department of Agriculture
53. Philippine Rice Research Institute (PhilRice), Philippines
54. Promoción e Investigación de Productos Andinos (PROINPA), Bolivia
55. Punjab Agricultural University, India
56. Rayong Field Research Station, Thailand
57. Rice Gene Discovery Unit (RGDU), Thailand
58. Rice Research and Training Centre, Egypt
59. Scientific and Industrial Research and Development Centre (SIRDC), Zimbabwe
60. Shanxi Academy of Agricultural Sciences (SAAS)
61. Sichuan Agriculture University, China
62. Tamil Nadu Agricultural University (TNAU), India
63. Tyshreen University, Syria
64. Ubon Ratchatani University (UBU), Thailand
65. Universidad Autónoma Chapingo, México
66. Universidade Católica de Brasilia (UCB), Brazil
67. Université d'Abomey–Calavi, Benin
68. University of Agricultural Sciences, Dharwad (DWR), India
69. University of Agriculture and Forestry (NWSUAF), China
70. University of Dhaka, Bangladesh
71. University of Hyderabad, India
72. University of KwaZulu–Natal, South Africa
73. University of Southern Mindanao, Philippines
74. University of the Witwatersrand, South Africa
75. Unversidade Católica de Brasilia (UCB), Brazil
76. Vanuatu Agricultural Research and Training Centre (VARTC)
77. Yunnan Academy of Agricultural Sciences (YAAS), China

ARI Partners

1. Australian Centre for Plant Functional Genomics Pty Ltd (ACPFG)
2. Australian National University
3. Botanic Garden and Botanical Museum Berlin–Dahlem (BGBM), Germany
4. Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), France
5. Centre National de Génotypage (CNG), France
6. Centre National de la Recherche Scientifique (France)
7. Colorado State University, USA
8. Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia
9. DArT P/L, Australia
10. ETH-Zurich, Switzerland
11. European Bioinformatics Institute (EBI), United Kingdom
12. Genaissance, France
13. Graingenes (CSIRO), Australia
14. Hebrew University of Jerusalem, Israel
15. Institut Agronomique Mediterranéan de Montpellier (CIHEAM-IAMM), France
16. Institut de Recherche pour le Dévelopment (IRD), France
17. Institut für Pflanzenbau und Pflanzenzüchtung, Germany
18. Institut National de la Recherche Agronomique (INRA–Agropolis), France
19. Institute for Plant Genetics and Crop Plant Research (IPK), Germany
20. International Rice Functional Genomics Consortium
21. Japan International Research Center for Agricultural Sciences (JIRCAS)
22. Kansas State University, USA
23. MOBY-S, Canada
24. National Center for Genome Resources, USA
25. National Institute of Agricultural Biology (NIAB), UK
26. Oregon State University, USA
27. Scottish Crop Research Institute (SCRI)
28. The Institute for Genomic Research (TIGR), USA
29. United States Department of Agriculture–Agricultural Research Service (USDA–ARS)
30. United States Department of Agriculture, North Carolina State University
31. Università di Udine, Italy
32. University of Aarhus, Denmark
33. University of Adelaide, Australia
34. University of Agricultural Sciences, India
35. University of Alberta, Canada
36. University of Arizona, USA
37. University of Bologna, Italy
38. University of California–Berkley, USA
39. University of California–Davis, USA
40. University of California–Riverside, USA
41. University of Geneva, Switzerland
42. University of Georgia–Athens, USA
43. University of Madrid, Spain
44. University of Missouri, USA
45. University of Queensland, Australia
46. University of Tsukuba, Japan
47. University of Virginia, USA
48. Virginia Tech, USA

Private Sector

1. DArT Pty Ltd (Australia)
2. Hitachi Software Engineering Co Ltd
3. Pioneeer Hi-Bred International, Inc, Canada
4. Syngenta

Other partners and funders

1. Barwale Foundation, India
2. Bill & Melinda Gates Foundation, USA
3. Biosciences Eastern and Central Africa, Kenya
4. Department for International Development (DFID), UK
5. Eastern and Central Africa Bean Research Network (ECABREN)
6. European Commission (EC)
7. Global Crop Diversity Trust, Italy
8. International Atomic Energy Agency (IAEA)
9. Kirkhouse Trust, UK
10. New Partnership for Africa's Development (NEPAD), South Africa
11. Southern Africa Bean Research Network (SABRN)
12. Swedish International Development and Cooperation Agency (SIDA)
13. Swiss Agency for Development and Cooperation (SDC)
14. Syngenta Foundation for Sustainable Agriculture
15. The Rockefeller Foundation,USA
16. The World Bank

Appendix B: Centre financial indicators

Generation-Cost Allocation: Allocation of Projects Cost to CGIAR System Priorities, 2006-2010

(in $ million)

Project	System Priorities	2006 (actual)	2007 (estimated)	2008 (proposal)	2009 (plan 1)	2010 (plan 2)
Subprogramme 1: Genetic diversity of						
global genetic resources	2A	0.000	0.435	0.291	0.232	0.092
	1A	2.282	3.042	2.039	1.621	0.641
	2B	0.978	0.869	0.583	0.463	0.183
	TOTAL BY PROJECT	3.260	4.346	2.913	2.316	0.916
Subprogramme 2: Comparative						
genomics and gene discovery	2A	0.692	1.084	0.844	0.656	0.233
	2B	2.770	4.334	3.378	2.622	0.930
	TOTAL BY PROJECT	3.462	5.418	4.222	3.278	1.163
Subprogramme 3: Trait capture for crop						
Improvement	2B	1.691	2.945	2.126	1.587	0.570
	2A	0.000	0.736	0.531	0.397	0.143
	5D	0.423	0.000	0.000	0.000	0.000
	TOTAL BY PROJECT	2.114	3.681	2.657	1.983	0.713
Subprogramme 4: Bionformatics and						
crop information systems	2A	0.000	0.364	0.326	0.328	0.134
	2B	1.566	1.456	1.305	1.310	0.534
	1A	0.447	0.607	0.544	0.546	0.223
	5D	0.224	0.000	0.000	0.000	0.000
	TOTAL BY PROJECT	2.237	2.427	2.175	2.184	0.891
Subprogramme 5: Capacity-building and						
enabling delivery	2B	0.392	1.211	0.962	0.926	0.318
	5D	1.566	0.000	0.000	0.000	0.000
	2A	0.000	0.606	0.481	0.463	0.159
	1A	0.000	1.211	0.961	0.926	0.318
	TOTAL BY PROJECT	1.958	3.028	2.404	2.316	0.795
	TOTAL BY CENTRE	13.031	18.900	14.372	12.077	4.478

Generation-Undertaking, Activities and Sectors, 2006-2010

(in $ million)

Undertaking, Activities and Sectors	2006 (actual)	2007 (estimated)	2008 (proposal)	2009 (plan 1)	2010 (plan 2)
Increasing Productivity	8.731	12.663	9.630	8.092	3.000
Germplasm Enhancement & Breeding	8.731	12.663	9.630	8.092	3.000
Production Systems Development & Management	0.000	0.000	0.000	0.000	0.000
Cropping systems	0.000	0.000	0.000	0.000	0.000
Livestock systems	0.000	0.000	0.000	0.000	0.000
Tree systems	0.000	0.000	0.000	0.000	0.000
Fish systems	0.000	0.000	0.000	0.000	0.000
Protecting the Environment	0.000	0.000	0.000	0.000	0.000
Saving Biodiversity	1.955	2.835	2.156	1.812	0.672
Improving Policies	0.261	0.378	0.287	0.242	0.090
Strengthening NARS	2.085	3.025	2.299	1.932	0.716
Training and Professional Development	0.834	1.210	0.920	0.773	0.287
Documentation, Publications, Info. Dissemination	0.313	0.454	0.345	0.290	0.107
Organisation & Management Couselling	0.417	0.605	0.460	0.386	0.143
Networks	0.521	0.757	0.574	0.483	0.179
TOTAL BY CENTRE	13.031	18.900	14.372	12.077	4.478

Generation-Cost Allocation: Allocation of Projects Cost to CGIAR Regions, 2006-2010

(in $ million)

Project	Regions	2006 (actual)	2007 (estimated)	2008 (proposal)	2009 (plan 1)	2010 (plan 2)
Subprogramme 1: Genetic diversity of global genetic resources						
	SSA	1.054	1.405	0.941	0.749	0.296
	Asia	1.469	1.958	1.312	1.043	0.413
	LAC	0.527	0.702	0.471	0.374	0.148
	CWANA	0.210	0.281	0.188	0.150	0.059
	TOTAL BY PROJECT	3.260	4.346	2.913	2.316	0.916
Subprogramme 2: Comparative genomics and gene discovery						
	SSA	1.363	2.133	1.662	1.291	0.458
	Asia	1.636	2.560	1.995	1.549	0.549
	LAC	0.273	0.427	0.332	0.258	0.092
	CWANA	0.190	0.299	0.233	0.181	0.064
	TOTAL BY PROJECT	3.462	5.418	4.222	3.278	1.163
Subprogramme 3: Trait capture for crop improvement						
	SSA	0.888	1.546	1.116	0.833	0.299
	Asia	0.803	1.399	1.010	0.754	0.271
	LAC	0.254	0.442	0.319	0.238	0.086
	CWANA	0.169	0.294	0.213	0.159	0.057
	TOTAL BY PROJECT	2.114	3.681	2.657	1.983	0.713
Subprogramme 4: Bioninformatics and crop information systems						
	SSA	0.722	0.784	0.703	0.706	0.288
	Asia	1.008	1.093	0.980	0.984	0.401
	LAC	0.362	0.392	0.351	0.353	0.144
	CWANA	0.145	0.157	0.141	0.141	0.058
	TOTAL BY PROJECT	2.237	2.426	2.175	2.184	0.891
Subprogramme 5: Capacity Building						
	SSA	0.643	0.995	0.790	0.761	0.261
	Asia	0.929	1.436	1.141	1.098	0.377
	LAC	0.214	0.332	0.263	0.254	0.087
	CWANA	0.172	0.266	0.210	0.202	0.070
	TOTAL BY PROJECT	1.958	3.029	2.404	2.315	0.795
	TOTAL BY CENTRE	13.031	18.900	14.372	12.077	4.478

Generation-Expenditures, 2006-2010

Object of Expenditure, (in $million)

Object of Expenditures	2006 (actual)	2007 (estimated)	2008 (proposal)	2009 (plan 1)	2010 (plan 2)
Personnel	0.324	0.614	0.664	0.700	0.730
Supplies and services	1.468	1.767	1.462	1.425	1.313
Collaboration/ Partnerships	11.185	16.384	12.113	9.818	2.300
Operational Travel	0.055	0.136	0.134	0.134	0.135
Depreciation	0.000	0.000	0.000	0.000	0.000
TOTAL BY CENTRE	13.031	18.900	14.372	12.077	4.478

Generation-Centre Incomes, 2006-2010

(in $million)

Centre Incomes	2006 (actual)	2007 (estimated)	2008 (proposal)	2009 (plan 1)	2010 (plan 2)
	0.327	0.150	0.070	0.050	0.050

Generation-Financing: Members/Non Members Unrestricted Grants, 2006-2008

(in $million)

Members/Non Members	2006 (actual)	2007 (estimated)	2008 (proposal)
MEMBERS			
European Commission	5.674	5.500	5.500
Sweden	0.098	0.050	0.000
Switzerland	0.370	0.300	0.000
United Kingdom	4.731	4.400	4.500
World Bank	3.256	2.000	2.000
TOTAL MEMBERS	14.128	12.250	12.000
NON MEMBERS			
Pioneer	0.020	0.020	0.000
TOTAL NON MEMBERS	0.020	0.020	0.000
TOTAL BY CENTRE	14.148	12.270	12.000

Generation-Financing: Allocation of Members/Non Members Grants to Projects, 2006-2008

(in $million)

Project	Members/Non Memebers	2006 (actual)	2007 (estimated)	2008 (proposal)
Subprogramme 1: Genetic diversity of	MEMBERS			
global genetic resources	Rockefeller Foundation	0.142	0.204	0.000
	TOTAL MEMBERS	0.142	0.204	0.000
	NON MEMBERS			
	Bill & Melinda Gates Foundation	0.000	0.597	0.510
	TOTAL NON MEMBERS	0.000	0.597	0.510
	TOTAL MEMBERS + NON MEMBERS	0.142	0.801	0.510
	Unrestricted + Centre Income	3.118	3.545	2.403
	TOTAL BY PROJECT	3.260	4.346	2.913
Subprogramme 2: Comparative genomics	MEMBERS			
and gene discovery	Rockefeller Foundation	0.301	0.101	0.000
	TOTAL MEMBERS	0.301	0.101	0.000
	NON MEMBERS			
	Bill & Melinda Gates Foundation	0.000	2.048	1.826
	TOTAL NON MEMBERS	0.000	2.048	1.826
	TOTAL MEMBERS + NON MEMBERS	0.301	2.150	1.826
	Unrestricted + Centre Income	3.161	3.268	2.396
	TOTAL BY PROJECT	3.462	5.418	4.222
Subprogramme 3: Trait capture for	MEMBERS			
crop improvement	Rockefeller Foundation	0.284	0.000	0.000
	TOTAL MEMBERS	0.284	0.000	0.000
	NON MEMBERS			
	Bill & Melinda Gates Foundation	0.000	0.597	0.510
	TOTAL NON MEMBERS	0.000	0.597	0.510
	TOTAL MEMBERS + NON MEMBERS	0.284	0.597	0.510
	Unrestricted + Centre Income	1.830	3.083	2.147
	TOTAL BY PROJECT	2.114	3.681	2.657
Subprogramme 4: Bioninformatics and	MEMBERS			
crop information systems				
	NON MEMBERS			
	Bill & Melinda Gates Foundation	0.000	0.000	0.000
	TOTAL NON MEMBERS	0.000	0.000	0.000
	TOTAL MEMBERS + NON MEMBERS	0.000	0.000	0.000
	Unrestricted + Centre Income	2.237	2.427	2.175
	TOTAL BY PROJECT	2.237	2.427	2.175
Subprogramme 5: Capacity-building and	MEMBERS			
enabling delivery	Rockefeller Foundation	0.317	0.106	0.000
	TOTAL MEMBERS	0.317	0.106	0.000
	NON MEMBERS			
	Bill & Melinda Gates Foundation	0.000	0.297	0.297
	TOTAL NON MEMBERS	0.000	0.297	0.297
	TOTAL MEMBERS + NON MEMBERS	0.317	0.404	0.297
	Unrestricted + Centre Income	1.641	2.624	2.107
	TOTAL BY PROJECT	1.958	3.028	2.404
	TOTAL BY CENTRE	13.031	18.900	14.372

Generation Staff Composition: Internationally and Nationally Recruited Staff, 2006 – 2010

Staff Type	2006 (actual)	2007 (estimated)	2008 (proposal)	2009 (plan 1)	2010 (plan 2)
Internationally-Recruited Staff (IRS)	3	5	5	5	5
National-Recruited Staff (NRS)	2	4	4	4	4
TOTAL BY CENTRE	5	9	9	9	9

Generation-Financial Position: Currency Structure of Expenditures, 2006-2008

(in $million)

	2006 (actual)			2007 (estimated)			2008 (proposal)		
Currency	Amount	US$Value	%Share	Amount	US$Value	%Share	Amount	US$Value	%Share
US Dollar (USD)	0.000	13.031	100.000%	0.000	18.900	100.000%	0.000	14.372	100.000%
TOTAL BY CENTRE		13.031	100.000%		18.900	100.000%		14.372	100.000%

Generation Statements of Activities

For the Year Ended December 31, 2006 (in $million)

	Unrestricted	Restricted		Total	Total	Total
		Temporary	Challenge Programmes	2006	2007	2008
Revenue and Gains						
Grant Revenue	15.192	0.000	0.000	15.192	16.222	15.144
Other revenue and gains	0.327	0.000	0.000	0.327	0.150	0.070
Total revenue and gains	15.519	0.000	0.000	15.519	16.372	15.214
Expenses and Losses						
Programme-related expenses	11.185	0.000	0.000	11.185	16.384	12.112
Management and general expenses	1.846	0.000	0.000	1.846	2.516	2.260
Other losses expenses	0.000	0.000	0.000	0.000	0.000	0.000
Sub Total expenses and losses	13.031	0.000	0.000	13.031	18.900	14.372
Indirect cost recovery	0.000	0.000	0.000	0.000	0.000	0.000
Total expenses and losses	13.031	0.000	0.000	13.031	18.900	14.372
Net Surplus / (Deficit) from ordinary activities	2.488	0.000	0.000	2.488	-2.528	0.842
Extraordinary Items	0.000	0.000	0.000	0.000	0.000	0.000
NET SURPLUS / (DEFICIT)	2.488	0.000	0.000	2.488	-2.528	0.842
Object of Expenditure						
Personnel	0.324	0.000	0.000	0.324	0.614	0.664
Supplies and services	1.468	0.000	0.000	1.468	1.767	1.462
Collaboration/ Partnerships	11.185	0.000	0.000	11.185	16.384	12.111
Operational Travel	0.055	0.000	0.000	0.055	0.136	0.136
Depreciation	0.000	0.000	0.000	0.000	0.000	0.000
TOTAL BY CENTRE	13.031	0.000	0.000	13.031	18.900	14.372

Generation Statements of Financial Position

December 31, 2006 (in $million)

	2006	2007	2008
A S S E T S			
Current Assets			
Cash and cash equivalents	0.000	0.000	0.000
Investments	1.000	1.000	1.000
Accounts receivable			
Donor	0.000	0.000	0.000
Employees	0.000	0.000	0.000
Other CGIAR Centres	7.341	4.813	5.655
Others	0.000	0.000	0.000
Inventories	0.000	0.000	0.000
Prepaid expenses	0.000	0.000	0.000
Total current assets	8.341	5.813	6.655
Non-Current Assets			
Property, Plant and Equipment	0.000	0.000	0.000
Investments	0.000	0.000	0.000
Other Assets	0.000	0.000	0.000
Total Non-Current Assets	0.000	0.000	0.000
TOTAL ASSETS	8.341	5.813	6.655
LIABILITIES AND NET ASSETS			
Current Liabilites			
Overdraft/Short term Borrowings	0.000	0.000	0.000
Accounts payable			
Donor	0.000	0.000	0.000
Employees	0.000	0.000	0.000
Other CGIAR Centres	0.000	0.000	0.000
Others	0.000	0.000	0.000
Accruals	0.000	0.000	0.000
Total current liabilities	0.000	0.000	0.000
Non-Current Liabilities			
Accounts payable			
Employees	0.000	0.000	0.000
Deferred Grant Revenue	0.000	0.000	0.000
Others	0.000	0.000	0.000
Total non-current liabilities	0.000	0.000	0.000
Total liabilities	0.000	0.000	0.000
Net Assets			
Unrestricted			
Designated	7.341	4.813	5.655
Undesignated	1.000	1.000	1.000
Total Unrestricted Net Assets	8.341	5.813	6.655
Restricted	0.000	0.000	0.000
Total net assets	8.341	5.813	6.655
TOTAL LIABILITIES AND NET ASSETS	8.341	5.813	6.655

Appendix C: Generation Challenge Programme 2008-2010 MTP Logframe

NB: In departure from the 2007-2009 MTP, the funding mechanism is indicated for each output in the logframe. The reference numbers correspond to our internal monitoring system and they link to the online project reports which will be operational in late 2007

Outputs	Output Targets	Intended user	Outcome	Impact
Project 1. Genetic diversity of global genetic resources				
Theme 1. Creation of an improved understanding of the structure of the diversity for the major world food crops				
Output 1.1. Structure of genetic resources for the most advanced (tier-1) crops accurately described (including tools) and summarised in a reference sample (*competitive 2005-01a to 2005-01n, 2005-02a to 2005-02k*)		Plant breeders and germplasm specialists	Enhanced possibilities to explore genetic diversity in breeding and in further characterisation for phenotypic and molecular traits	Better access to genetic diversity for breeding, resulting in more efficient crop improvement programmes
output target 2008	Description of molecular variation and germplasm classification for tier-1 crops published/reference samples identified			
output target 2009	*completed*			
Output 1.2. Structure of genetic resources for the less advanced (tiers 2 and 3) crops accurately described (including tools) and summarised in a reference sample (*competitive 2005-03a to 2005-03h, 2006-05, 2006-30, 2006-31*)		Plant breeders and germplasm specialists	Possibility to explore genetic diversity in breeding and in further characterisation for phenotypic and molecular traits	Better access to genetic diversity for breeding, resulting in more efficient crop improvement programmes
output target 2008	A compilation of description of molecular variation and germplasm classification for all GCP crops published			
output target 2009	*completed*			
Output 1.3. Seed of reference germplasm readily available for all crops (*competitive 2005-02; commissioned 2006-29*)		Plant breeders and germplasm specialists	For each crop, reference materials which will serve for representing wider collections and integrating information in the long term	Better access to genetic diversity for breeding, resulting in more efficient crop improvement programmes
output target 2008	Implementation for all priority crops, including *in vitro* propagated cassava			
output target 2009	*sustained distribution*			
output target 2010	*sustained distribution*			
Output 1.4. Global assessment of linkage disequilibrium in the genome of rice conducted (*commissioned 2006-03*)		Rice and other cereal geneticists and breeders	Prospects for association studies in rice and other diploid selfing crops refined	Increased efficiency in crop research and improvement
output target 2008	Global LD pattern in rice documented with focus on intersubspecific recombination/LD-based mapping strategies for diploid selfing crops refined			
output target 2009	*completed*			
Output 1.5. Linkage disequilibrium assessed across several legumes along conserved gene stretches (*commissioned 2008*)				
output target 2008	Targeted resequencing for LD assessment along conserved gene stretches in legumes			
output target 2009	LD assessed in legumes through extended resequencing along conserved gene stretches			
output target 2010	*completed*			
Output 1.6. Detailed analysis conducted of maize diversity after migration out of America (*competitive 2005-14*)		Maize breeders and crop geneticists	Improved understanding of crop evolution during major migrations across continents	Better access to genetic diversity for breeding, resulting in more efficient crop improvement programmes
output target 2008	A comprehensive analysis of maize diversity in landraces around the world available			
output target 2009	*completed*			
Output 1.7 Methodology developed for resampling genetic diversity in large germplasm collections (*commissioned 2006-01*)		Germplasm specialists and plant breeders	Ability to best use information available in order to further tap useful diversity in large collections	Better access to genetic diversity for breeding, resulting in more efficient crop improvement programmes
output target 2008	An additional description of SSR diversity for 1,000 accessions of rice and chickpea			

Outputs	Output Targets	Intended user	Outcome	Impact
output target 2009	An algorithm for iteratively selecting accessions from a large, data-sparse collection given a data-rich subset of accessions			
output target 2010	*Completed/Implementation for various collections, to be decided*			
Theme 2. Development of a range of flexible HTP genotyping techniques accessible in reference laboratories				
Output 1.8. DArTs validated as a genome-wide molecular characterisation technology (*competitive 2005-04*)		All germplasm specialists using molecular markers	A cheap and quick technique for mapping useful genes in progenies and more complex populations	Increased efficiency in genome mapping, thereby contributing to increased efficiency in plant breeding programmes
output target 2008	*Completed/Integration in the Genotyping Support Service*			
Output 1.9. EcoTILLing assessed as a gene-targeted molecular characterisation technique (*commissioned 2005-05*)		All germplasm specialists using molecular markers	Cheap technique available to explore allelic variation at candidate genes	Increased efficiency in functional diversity characterization, thereby contributing to increased efficiency in plant breeding programmes
output target 2008	*Completed/Integration in the Genotyping Support Service (SP5)*			
Output 1.10. Methodology developed to assess SNPs with effect on allele expression (Non Coding SNPs) (*competitive 2005-17*)		All germplasm specialists using molecular markers	Enhanced access to expression polymorphisms	Improved understanding of adaptive value of molecular variation, thereby contributing to increased efficiency in plant breeding programmes
output target 2008	Associations between allelic imbalance-related SNPs and drought-related phenotype in barley			
output target 2009	*Completed/implemented in SP2-SP3*			
Output 1.11. Database on allele diversity at candidate genes across species developed (*commissioned 2006-02*)		All germplasm specialists using molecular markers	Efficient comparative functional molecular diversity analysis available for transposing results across crops	Improved understanding of adaptive value of molecular variation, thereby contributing to increased efficiency in plant breeding programmes
output target 2008	A database with detailed information on allelic variation at several candidate genes across 7 crops (rice, sorghum, barley, bean, chickpea, potato, and cassava)			
output target 2009	An extended database, genes and crops to be decided			
output target 2010	An extended database, genes and crops to be decided			
Theme 3. Establishment and implementation of a scientific and organisational framework to describe tolerance to drought				
Output 1.12. A database on field-proven drought-tolerant and drought-susceptible genotypes established (*commissioned 2008*)		Crop scientists around the world	Reference materials for assessment and dissection of drought tolerance in germplasm	Enhanced knowledge about drought tolerance available to the scientific community
output target 2008	Information on various drought-related extreme behaviors in diverse materials and conditions			
output target 2009	A framework for collecting information on field-proven drought tolerance or susceptibility/Transfer of new genotypes to other projects			
output target 2010	A sustained process for collecting information on field-proven drought tolerance and supplying breeding and genetic studies			
Output 1.13. Set of phenotyping facilities in Brazil made accessible for GCP germplasm evaluation (*commissioned 2005-06*)		GCP scientists	High-quality and high-capacity GCP phenotyping network available for use	Increased efficiency in crop research and improvement
output target 2008	Embrapa network used for evaluation of GCP reference samples			
output target 2009	*Completed/Integration in a Phenotyping Support Service*			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 1.14. A crop and whole-plant modelling framework developed to support assessment of tolerance to drought (*commissioned 2005-07*)		Crop scientists around the world	Improved assessment of drought tolerance in germplasm and breeding materials available	Enhanced knowledge about drought tolerance available to the scientific community
output target 2008	Improvement of whole-plant model to support drought tolerance phenotyping in cereals/ transposition of rationale to legumes			
output target 2009	*Completed/Integration in a Phenotyping Support Service*			
Output 1.15. Phenotyping capacity accessible to the GCP is inventoried (*commissioned 2006-04*)		GCP scientists	Improved knowledge and use of the best drought tolerance screening facilities within the GCP	Increased efficiency in evaluating and screening for tolerance to drought
output target 2008	Options of phenotyping protocols and facilities by crops and regions documented, including operational costs			
output target 2009	*Completed/Integration in a Phenotyping Support Service*			
Output 1.16. Drought-related phenotyping of specific populations with high quality molecular information implemented/Support service consolidated (*commissioned 2008*)		GCP scientists/Pearl millet, sorghum and other cereal geneticists and breeders	Access to the best drought tolerance screening facilities within the GCP/More targets available for MAS for improving drought tolerance in cereals	Increased efficiency in analysing the genetic control of tolerance to drought
output target 2008	Phenotyping reference samples for pearl millet, sorghum and a couple of other crops (year 1)			
output target 2009	Phenotyping reference samples for pearl millet, sorghum and a couple of other crops (year 2)			
output target 2010	Further phenotyping after collective prioritisation/Consolidation of a Phenotyping Support Service for the GCP			
Theme 4. Identification of favourable genetic factors (i.e., potential genes or genome segments) and superior alleles (or haplotypes) through association studies				
Output 1.17. Favourable genetic factors for drought tolerance in maize identified (*competitive 2005-13*)		Maize and other cereal geneticists and breeders	More targets available for MAS for improving drought tolerance in cereals	Increased efficiency in crop research and improvement
output target 2008	Integrated association analysis using functional molecular markers, metabolomic characterisation and field evaluations among 350 maize genotypes/allelic diversity at 100 genes			
output target 2009	*completed/implemented in SP2-SP3*			
Output 1.18. Favourable genetic factors for drought tolerance in rice identified (*commissioned 2008*)		Rice and other cereal geneticists and breeders	More targets available for MAS for improving drought tolerance in cereals	Increased efficiency in crop research and improvement
output target 2008	Phenotyping and association analysis using whole-genome SNPs among 300 rice accessions			
output target 2009	Integrated phenotyping and association analysis using whole-genome SNPs among 500 rice accessions			
output target 2010	Repeated integrated phenotyping and identification of favourable alleles/haplotypes in rice			
Output 1.19. Favourable genetic factors for stress tolerance in four legume species identified (*special G6007.05*)		Legume scientists around the world	More targets available for MAS for improving stress tolerance in legumes	Increased efficiency in crop research and improvement
output target 2008	Reference samples identified, distributed, and planted in diverse environments for groundnut, cowpea, chickpea, and common bean			
output target 2009	First association studies performed/new recombinant populations created			
output target 2010	Identification of favourable donors of drought tolerance and localisation of favourable alleles/haplotypes in legumes, application in SP2-SP3			

Outputs	Output Targets	Intended user	Outcome	Impact
Theme 5. Development of novel populational approaches for relating genotypes to phenotypes				
Output 1.20. Ecogeographic/genetic clines related to drought identified for selection pattern analysis (*commissioned 2008*)		Germplasm specialists and crop geneticists	Prospects for application of linkage disequilibrium mapping in contrastingly adapted traditional populations	Increased efficiency in germplasm management and crop research and improvement
output target 2008	Inventory of germplasm sets with accurate passport geo-referencing			
output target 2009	Identification of germplasm distributed in narrowly distributed diverse environments			
output target 2010	Comparative ecological and genetic pattern analyses, to be determined			
Output 1.21. Populations for multiple allelic segregation developed through intercrossing (*commissioned 2008*)		Crop geneticists and breeders	Prospects for application of linkage disequilibrium mapping in crops opened and refined	Increased efficiency in crop research and improvement
output target 2008	Initiation of multiparent intercrossing for various representative crops			
output target 2009	Advancment of intercrossing generations			
output target 2010	Further advancment of intercrossing generations			
Output 1.22. Linkage disequilibrium and patterns of selection in the genome of sorghum used for mapping useful genes (*discretionary, SP1 Leader*)		Sorghum (and other cereals) geneticists and breeders	Prospects for association studies in sorghum and other diploid selfing crops refined	Increased efficiency in crop research and improvement
output target 2008	Introgression patterns monitored between various sorghum cultivated and wild forms using DArT markers			
output target 2009	Patterns of selection monitored along the genome of sorghum/Association analysis using phenotyping data			
output target 2010	Association analysis and identification of favourable haplotypes in sorghum			
Output 1.23. Diversity patterns in the genome of sweet potato used for mapping useful genes in relation to heterosis (*commissioned 2008*)		Sweet potato geneticists and breeders	Prospects for association studies in sweet potato and other vegetatively propagated crops refined	Increased efficiency in crop research and improvement
output target 2008	Development of DArT markers and dense diversity survey in diverse germplasm of sweet potato			
output target 2009	Comparison of patterns of molecular diversity and of heterosis			
output target 2010	*to be decided*			
Output 1.24. Base broadened of current crop diversity in rice using related species *(competitive 2005-10*)		Germplasm specialists and plant breeders	Novel rice germplasm tailored for genetic analysis of trait variation and innovative breeding	Increased efficiency in crop research and improvement
output target 2008	Genetic dissection of phenotypic contribution of wild germplasm in rice/materials bearing favourable alien chromosome segments			
output target 2009	*completed/implemented in SP2-SP3*			
Output 1.25. Base broadened of current crop diversity in rice using interspecific bridges with African rice (*competitive G3007.01*)		Germplasm specialists and plant breeders	Novel rice germplasm tailored for genetic analysis of trait variation and innovative breeding	Increased efficiency in crop research and improvement
output target 2008	Genetic dissection of phenotypic contribution of African cultivated rice			
output target 2009	Identification of favorable alien chromosome segments/Establishment of a bridge between Asian and African rices			
output target 2010	*completed/implemented in SP2-SP3*			
Output 1.26. New alleles introgressed from wide crosses using crop wild relatives in barley (*competitive G3007-02*)		Germplasm specialists and plant breeders	Novel barley germplasm tailored for genetic analysis of trait variation and innovative breeding	Increased efficiency in crop research and improvement

Outputs	Output Targets	Intended user	Outcome	Impact
output target 2008	A range of recombinant genotypes that segmentally display introgression of the whole genome of wild barley			
output target 2009	Genetic dissection of phenotypic contribution of wild germplasm in barley through introgressed materials useable in breeding			
output target 2010	*completed/implemented in SP2-SP3*			
Project 2. Comparative genomics for gene discovery				
Theme 1. Assembly of genomics and germplasm resources through consolidating and developing specialised genetic stocks				
Output 2.1. Systematic evaluation of rice mutant collections conducted for conditional phenotypes with emphasis on stress tolerance (*competitive 2005-09*)		Crop researchers and genetic resource curators	Laboratories producing the largest collection of rice mutants in the world linked, providing unique resource pools and expertise to identify gene function in a model crop species	Enhanced access to genomic tools and resources for scientific community for increased efficiency in crop research and improvement
output target 2008	Rice mutants with insertions/activations identified for >40 conserved orthologous drought-response genes used in ADOC project; constitutive and conditional phenotypes of these mutants determined.			
output target 2009	*none*			
Output 2.2. Bean genetic and genomic resources developed (*special G6007.03*)		Crop researchers and plant breeders	New markers for drought tolerance deployed in the bean research and breeding communities	Improved efficiency in developing adaptive bean varieties for the resource-poor
output target 2008	Two subtractive root and shoot tissue libraries (drought vs control) developed to provide a pool of stress-tolerance candidate genes for evaluation			
output target 2009	Six candidate genes controlling transpiration/water use efficiency identified; osmotic adjustment and root development screened for association with drought tolerance traits			
output target 2010	20,000 EST sequences obtained for root and full-length libraries; 200 new SSR, COS or SNP markers developed or mapped from EST, BAC and cross-legume sequences.			
Output 2.3. Chickpea genetic and genomic resources developed (*special G6007.04*)		Crop researchers and plant breeders	New markers being used in the chickpea research and breeding communities	Improved efficiency in developing adaptive chickpea varieties for the resource-poor
output target 2008	500 new markers tested (linked with "Cross-species marker" Output 2.19)			
output target 2009	Reference map with 1,000 loci			
output target 2010	to be determined			
Output 2.4. Cowpea genetic and genomic resources developed (*special G6007.02*)		Crop researchers and plant breeders	Permanent genome resources (including ESTs) and physical map available; source of SNPs, gene knowledge; foundation of high-density SNP map, and high-throughput marker system	Improved efficiency in developing adaptive cowpea varieties; stress resistant cowpea cultivars for African countries
output target 2008	cDNA libraries of 6 diverse cowpea genotypes produced			
output target 2009	14x genome coverage of cowpea BAC libraries produced; 200,000 ESTs generated			
output target 2010	~10,000 BAC end sequences and BAC contigs placed onto genetic map; 1000 SNP markers on map,1440 genotypes scored			
Output 2.5. Groundnut genetic and genomic resources developed (*special G6007.01*)		Crop researchers and plant breeders	New markers being used in the groundnut research and breeding communities	Improved efficiency in developing adaptive groundnut varieties for the resource-poor
output target 2008	1,000 molecular markers established in groundnut (linked with 'cross-species marker, Output 2.7)			

Outputs	Output Targets	Intended user	Outcome	Impact
output target 2009	Unified existing RFLP and SSR maps of *Arachis*; 20,000 ESTs from drought-stressed lines			
output target 2010	One reference map for AA diploid genome; one linked physical and genetic map for AA genome			
Output 2.6. Validation of drought-response/resistance pathways genes by phenotypic analysis of mutants (*commissioned G4007.02*)			Leveraging existing mutant resources to generate supporting evidence for selecting high-confidence candidate genes for cross-species comparative studies.	
output target 2008	50-100 mutant lines segregating for variant drought response phenotypes identified			
output target 2009	50-100 sib-lines characterised by physiological measurements on transpiration rate, stomatal conductance, root and water-use efficiency traits using field screen and high-throughput phenotyping technique (e.g., infrared imaging); drought resistance/sensitive phenotypes for 100 candidate gene mutants in Arabidopsis/rice at vegetative and reproductive stage drought stress			
output target 2010	Dataset on comparative rice-Arabidopsis candidate drought related gene index with physiological mutant phenotypes			
Theme 2. Development of comparative maps within and across species and framework genetic markers for target crops				
Output 2.7. Cross-species resources for comparative biology in tropical crop legumes developed (*special G6007.05*)		Crop researchers and plant breeders	Leveraged knowledge of genomic information and agronomic traits across legume species, leading to increased use of molecular-genetic markers for legume improvement	General principles established for genomics-enabled breeding in tropical legumes; development of improved legume varieties based on MAS
output target 2008	>1500 simple sequence repeats (SSRs) to the NCBI STS database for diploid groundnut; informatics pipeline to generate cross-legume anchor markers implemented			
output target 2009	Integration of >300 orthologous markers into genetic maps for bean, cowpea, chickpea and groundnut; linkage of ~50 gene-based markers to biotic and abiotic stress tolerance determined			
output target 2010	Relationship of the ancestral genome segments in target legumes determined; public repository of genetic marker data for crop legumes; portal for communication between researchers using common genetic marker resources; marker platforms to use the anchor markers in breeding programmes of four legume crops; online navigation between legume genomes			
Output 2.8. Genetic and physical mapping resources produced for drought breeding in cassava (*competitive G3007.03*)			Expanded cassava genomic resources offering opportunities for improvement of multiple traits in cassava	
output target 2008	A BAC-based physical map of the cassava genome anchored to the genetic map			
output target 2009	1000 SNP markers on a genome-wide scale with emphasis on regions with known QTL for drought tolerance			
output target 2010	Public database for accessing mapping and SNP data of cassava through web interfaces			
Output 2.9. Genomic and mapping populations for sweet potato developed to enable trait/gene identification (*commissioned 2008*)			Increased knowledge-base in under-resourced crops, opening up opportunities for genetic manipulation of various traits.	

Outputs	Output Targets	Intended user	Outcome	Impact
output target 2008	Genome-wide sequence data produced for a selected sweet potato strains (coverage depending upon available resources)			
output target 2009	Genomic sequence aligned with genetic maps; segregating/mapping populations developed and propagated for phenotyping and mapping of priority traits identified in SP3			
output target 2010	Public database for accessing mapping and sequence data of sweet potato through web interfaces			
Output 2.10 Genomic resources and mapping populations developed and assembled for pearl millet to enable trait/gene identification (*commissioned 2008*)			Increased knowledge-base in under-resourced crops, opening up opportunities for genetic manipulation of various traits.	
output target 2008	Genome-wide sequence data produced for a selected pearl millet line (coverage depending upon available resources)			
output target 2009	Genomic sequence aligned with genetic maps; permanent mapping populations assembled and propagated for phenotyping and mapping drought tolerance traits			
output target 2010	Public database for accessing mapping and sequence data of pearl millet through web interfaces			
Theme 3. Assignment of genes and pathways to phenotypes through the convergence evidence of genome variation, expression patterns and phenotypic data				
Output 2.11. Targeted discovery of superior disease QTL, alleles in the maize and rice genomes conducted (*competitive 2005-08*)		Crop researchers and plant breeders	Superior disease resistance QTL identified, characterised, and used in maize and rice breeding programmes	Model available for integrating gene discovery and breeding activities for increased efficiency in crop research and improvement programmes
output target 2008	Maize loci showing changes in allele frequency under recurrent selection and production of introgression lines carrying multiple favourable alleles by recurrent selection; genomic locations of deletions identified in selected disease response mutants; chromosomal segments associated with desirable resistance combined and incorporated into elite maize (for Kenya) and rice lines (for India and Indonesia)			
output target 2009	*completed*			
Output 2.12. Functional genomics of cross-species resistance to fungal diseases in rice and wheat conducted (*competitive 2005-11*)		Crop researchers and plant breeders	Detailed information available on the molecular mechanisms governing non-host resistance (cross-species) resistance to fungal diseases in cereals	Novel strategies developed to generate durable disease resistance
output target 2008	Functions of candidate genes in rice in relation to host vs non-host resistance to blast and rust validated; host and non-host resistance to blast and rust in rice and wheat revealed via comparative QTL analysis			
output target 2009	*completed*			
Output 2.13. Common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes investigated and determined (*competitive 2005-15*)		Crop researchers and plant breeders	Common genetic mechanisms (candidate genes) underlying the maintenance of tissue growth in plants under water deficit determined in maize, rice and wheat	Increased knowledge about genomics for aiding crop improvement
output target 2008	Models predicting impact of different allelic combinations on organ growth under different drought scenario developed; a set of DNA markers developed from candidate genes; new phenotypic and genetic selection criteria for efficient breeding for drought tolerance identified		Enabling development of drought-tolerance maize in breeding programmes	
output target 2009	*completed*			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 2.14. Causal relationship between whole-genome expression patterns and stress tolerance determined via analysis of near-isogenic lines (*commissioned 2008*)			Gene expression polymorphisms serve to bridge the genotype-phenotype gap; providing a generalised method to assign gene functions to phenotypes in crop studies.	
output target 2008	Genome-wide expression maps of rice aligned with at least 5 narrow regions of stress response QTL in independently derived NILs; demonstration of robust methods to shortlist expression candiate genes for stress tolerance.			
output target 2009	Cosegregation of gene expression patterns with drought tolerance phentoypes established in selected pairs of rice isogenic lines			
output target 2010	Generalisation of transcritptome analysis with NILs for multiple crops			
Theme 4. Validation of genes and pathways via evaluation of under- or over-expression constructs or variants (induced or natural) of target genes				
Output 2.15. Genes responsible for failure of grain formation in rice and wheat under drought identified (*competitive 2005-01*)		Crop researchers	Improved understanding of the physiological, genetic and biochemical bases of two yield determinants	Improvement of performance of rice and wheat in drought-prone areas
output target 2008	A shortlist of candidate genes validated by combined evidence of segregation analysis, expression and mutational analyses; allelic polymorphisms suitable for MAB identified; novel alleles of validated genes in germplasm pools assessed for impact on relevant physiological traits under drought stress		Use of functional polymorphisms found in rice and wheat genes for other species	
output target 2009	*completed*			
Output 2.16. Genes for tolerance of saline and phosphorus-deficient soils to enhance and sustain productivity in rice identified (*competitive 2005-02*)		Crop researchers and plant breeders	Genes associated with salinity and P-deficiency tolerance identified in rice and a marker system to incorporate these genes into popular varieties developed	Improved farmer livelihoods through increased productivity of marginal land
output target 2008	Set of contrasting NILs for the Pup1 and Saltol loci tested at multiple sites with NARS partners; impact of Pup1 and Saltol loci in multiple-stress environments (saline/drought/P-deficient) assessed; transformed rice characterised for gene expression and assessed for P-efficiency and salinity tolerance; stress tolerance of transformed plants in the greenhouse and the field assessed		Enhanced root growth and health via P-uptake efficiency provide a mechanism to resist drought stress; potential to identify orthologs of salinity and P-deficiency tolerance genes in other cereals	
output target 2009	*completed*			
Output 2.17. Aluminium tolerance genes in the cereals identified and characterised (*competitive 2005-16*)		Crop researchers and plant breeders	Improved understanding of the diversity and functioning of molecular and physiological mechanisms for Al-tolerance in crops	Improved farmer livelihoods through increased productivity of marginal land
output target 2008	Candidate Al-tolerance genes in maize molecularly characterised; Al-tolerance genes from sorghum, maize, and rice identified; physiological characterisation and mapping of Al tolerance in Kenyan maize genotypes completed; field testing of elite sorghum hybrids from EMBRAPA and transgenic maize		Gene markers available to combine desirable combinations of Al-tolerance genes in elite lines and commercial varieties	Sorghum and maize genotypes with improved Al- tolerance available to farmers in acid soil regions in Africa
output target 2009	*completed*			
Output 2.18 Drought-adaptive mechanisms in bread and durum wheat determined through large-scale phenotyping methodologies (*competitive G3007.06*)			New wheat mapping resources coupled with phenotyping techniques offer new opportunities for drought tolerance improvement	

Outputs	Output Targets	Intended user	Outcome	Impact
output target 2008	High-throughput precision phenotyping protocols developed, characterised by good correlation to drought tolerance field screening and international trial performance			
output target 2009	The contribution of the D genome in drought tolerance in wheat determined			
output target 2010	Biometrical approaches developed and optimised for mapping drought tolerance QTL in wheat.			
Project 3. Trait capture for crop improvement				
Theme 1. Characterisation of segregating populations and identification of genomic regions for plant breeding				
Output 3.1. Physiological and genetic traits that make cassava one of the most drought-tolerant crops identified *(competitive 2005-03)*		CGIAR (CIAT), ARI (Cornell) and NARS (Brazil, Ghana and Tanzania)	Improved understanding of drought-tolerance traits and their biological basis	More efficient cassava plant breeding strategies generating new drought-tolerant cassava germplasm
output target 2008	Drought-tolerant contrasting cassava varieties identified and micropropagated, identification of drought tolerance related traits, crossing blocks of drought constrasting cassava varieties established			
output target 2009	*Completed*		Drought-tolerant cassava genotypes ready for introduction into breeding programmes	
Output 3.2. Genetic diversity of groundnut's wild relatives unlocked with genomic and genetic tools *(competitive 2005-05*)		CGIAR (ICRISAT), ARIs (Brazilian Universities, CIRAD, IBN Argentina) and NARS (Brazil, India, Senegal)	New peanut varieties resistant to disease and drought; creation of a single genetic system for legumes linking groundnut to model plants	New genes made available through crosses with wild relatives
output target 2008	Microsatellite-based genetic maps for the AA and BB genomes of *Arachis*, a bank of 3500 assembled ESTs from *A.stenosperma*, a BAC library for the AA genome of Arachis (*A.duranensis*), lines derived from amphidiploid x cultivated cross selected for disease resistance and drought tolerance			
output target 2009	*Completed*		Backcrossed populations and new improved selected lines for groundnut beeding programmes worldwide	
Output 3.3. Association mapping of downy mildew resistance in elite maize inbred lines in Thailand (*commissioned G4007.04*)		Maize breeding community in Thailand (Kasetsart University and Nakhon Sawan Field Crop Research Centre)	Association mapping applied in maize breeding in Thailand, and new maize varieties resistant to powdery mildew developed	Maize varieties with improved resistance to downy mildew available to farmers in the region
output target 2008	Maize inbred lines with resistance to powdery mildew identified, resistant maize inbred lines genotyped			
output target 2009	Haplotypes for selected candidate genes identified and a set of indicative DNA markers available for allele discrimination and MAS			
output target 2010	*Completed*		Backcrossed populations and new improved selected lines for breeding	
Output 3.4. Tailoring superior alleles for abiotic stress genes for deployment into breeding programmes: association analysis of AltSB, a major aluminum tolerance gene in sorghum *(competitive G3007.04)*		Plant breeders and breeding programmes facing soil acidity problems	Superior AltSB haplotypes identified by association mapping and incorporated into pre-breeding lines by using haplotype-specific markers	Improvement of breeding efficiency under acid soil conditions conditions
output target 2008	A diverse sorghum collection phenotyped for aluminum tolerance and genotyped at *AltSB*, superior *AltSB* haplotypes identified			
output target 2009	A set of *AltSB* haplotype-specific markers identified and easy to use SNP genotyping assays developed.			
output target 2010	*Completed*			

Outputs	Output Targets	Intended user	Outcome	Impact
Ouput 3.5. Making Latin America potato diversity available for Africa (*commissioned 2008)*		Potato breeders and breeding programmes in Latin America and Africa	New breeding tools as DNA-based markers used in NARS in Latin America and Africa, improving selection speed and efficiency	New and more sustainable varieties deployed to resource-poor farmers in less developed areas and countries (Latin America and Africa)
output target 2008	Molecular markers used to monitor the presence of key resistance genes in programme's Elite breeding stocks, conversion of short-days adapted germplasm into long days adapted, and germplasm resistant for known resistance genes exchanged			
output target 2009	elite germplasm phenotyped for drought tolerance and markers developed for priority resistance traits (e.g., Late Blight, Potato Tuber Moth, *Diabrotica*, Bacterial wilt, Potato Leaf Roll Virus).			
output target 2010	*Completed*	Capacity-building and expertise of key personnel of breeding programmes improved, advanced germplasm disseminated to less developed countries		
Theme 2. Development and evaluation of novel breeding or molecular technologies to better serve modern plant breeding				
Output 3.6. Low-cost technologies developed for pyramiding useful genes from wild relatives of cassava into elite progenitors (*competitive 2005-9*)		CGIAR (CIAT), NARS (Brazil, Ghana, Nigeria and Uganda) and other breeding programmes	Low-cost MAS technologies for pyramiding pest and disease resistance and delayed post-harvest physiological deterioration (PPD) genes development, new collections of wild *Manihot* established	Improved breeding strategy available integrating MAS approach and accessing new alleles in improved and wild relative germplasm
output target 2008	Crosses between virus resistant and farmers' varieties, lines with virus resistance selected through MAS			
output target 2009	*Completed*		Low-cost markers and new capacity building for MAS in cassava	
Output 3.7. Application of simulation models to pyramid multiple genes via MAS (*commissioned 2008*)		MAS programmes	MAS modeled and monitored in several breeding programmes in Asia and Africa	More efficient MAS strategies and protocols available for breeding programmes in Asia and Africa
output target 2008	Simulation models developed and applied to several MAS projects in Asia and Africa			
output target 2009	Simulation softwares developed			
output target 2010	*Completed*			
Output 3.8. Phenotyping tropical legumes for drought tolerance using carbon isotope discrimination (linked to SP2) (*commissioned 2008*)		Tropical legumes (cowpea, chickpea) breeding programmes in Asia and Africa	Innovative phenotyping tool and protocols developed, phenotyping capacity and expertise for tropical legumes strengthened	Large-scale phenotyping facilitated for tropical legumes in Africa and Asia
output target 2008	Relationship between grain yield and carbon isotope discrimination described under different drought scenarios, breeding germplasm and mapping populations evaluated for carbon isotope discrimination in different locations			
output target 2009	QTLs for carbon isotope discrimination identified			
output target 2010	*Completed*			
Theme 3. Markers/alleles validation in adapted germplasm under target environments				
Output 3.9. Drought-tolerant rice cultivars developed for North China and South/Southeast Asia by highly efficient pyramiding of QTL from diverse origins (*competitive 2005-12*)		CGIAR (IRRI), NARS (North China and S/SE Asia), and other breeding programmes, and ultimately small-scale farmers in resource-poor cropping systems	New elite allele identified at drought-tolerant QTL in broad elite rice background; improved strategy for genetic improvement of complex traits.	New drought-tolerant germplasm for farmers in Asian rainfed areas

Outputs	Output Targets	Intended user	Outcome	Impact
output target 2008	Drought tolerance QTL confirmed, pyramiding of drought tolerant QTL in japonica genetic background, MAB lines with improved drought tolerance, farmer testing (North China) and release of drought tolerant lines			
output target 2009	*Completed*		New pre-breeding rice material for North China and S/SE Asia	
Output 3.10. Markers developed for *Striga* resistance in cowpea (*competitve 2005-6*)		Plant breeders and breeding programmes	Superior-performing, well-adapted cowpea varieties for sustainable resistance to disease and pests, especially *Striga*	Better source of germplasm for African cowpea farmers (productivity, disease- and pest-resistance traits)
output target 2008	A reference genotype set for race specific *Striga* resistance, SCAR markers for resistance to *Striga* races 1 and 3, MAS protocol for *Striga* resistance		New breeding tools for cowpea	
output target 2009	*Completed*		New breeding tools for *Striga* resistance in cowpea	
Output 3.11. Integrating marker-assisted selection into the conventional breeding procedure for improvement of wheat (*Triticum aestivum* L.) in the drought-prone areas of Northern China (*commissioned G4007.06*)		Breeders from Ningxia, Shanxi, Henan and Hebei Provinces	Drought-tolerant QTLs identified and transferred into elite Chinese wheat backgrounds	Breeding efficiency improved in several Province of Northern China
output target 2008	Target QTLs confirmed and characterised in elite Chinese wheat backgrounds and target environments		Phenotyping network established in Northern China, genotyping platform developed at CAAS for Northern China	
	candidate accessions carrying target genes/markers and the elite Chinese wheat backgrounds from the ILs for molecular breeding identified			
output target 2010	*Completed*		Wheat molecular breeding capacities enhanced in Ningxia, Shanxi, Henan and Hebei Provinces	
Output 3.12. Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco (*commissioned G4007.05*)		Plant breeders and breeding programmes, and ultimately small-scale farmers in resource-poor cropping systems	Development of MAS approaches for drought-tolerance improvement, enhanced utilisation of wheat and barley diversity using exotic/core collections and the reference sets developed by GCP	More efficient MAS strategies available for wheat/barley improvement programmes under drought-prone environments
output target 2008	Segregating populations developed of for tagging loci involved in stress tolerance and new markers generated, including candidate gene/allele-based molecular markers			
output target 2009	Novel genes and alleles conferring tolerance to stresses and improving end use quality mined from the germplasm collection of Morocco, the wheat reference set developed by GCP			
output target 2010	*Completed*			
Ouput 3.13. Validation of *AltSB*, a major aluminium tolerance gene in sorghum (*commissioned 2008*)		Sorghum breeding programmes facing soil acidity constraints	*Validation of AltSB* in acid soils by an African NARS (INRAN, Niger)	Aluminium toxicity genes/markers available for MAS in sorghum, and improved sorghum germplasm for acid soil conditions
output target 2008	Development of allele-specific markers for *AltSB*			
output target 2009	Comparision of performance, under acid soil conditions, of a set of prebreeding near-isogenic lines (NILs) carrying different *AltSB* haplotypes			
output target 2010	*Completed*			

Outputs	Output Targets	Intended user	Outcome	Impact
Ouput 3.14. Validation of *Saltol*, a major salinity tolerance gene in rice (*commissioned 2008*)		Rice breeding programmes facing salinity constraints	*Saltol*, a major salinity tolerance gene in rice validated in salinity conditions by an Asian NARS (BBRI and Dhaka University, Bangladesh)	
output target 2008	*Saltol* gene from Pokkali, FL378 and FL478 introgressed into wet and dry season rice varieties			
output target 2009	Comparision of performance, under salinity conditions, of prebreeding near-isogenic lines (NILs)			
output target 2010	*Completed*			
Theme 4. Application of molecular markers in breeding programmes				
Output 3.15. Integration of genomic tools with conventional screening for developing NERICA rice cultivars for West Africa (*commissioned G4007.08*)		Plant breeders and breeding programmes, and ultimately small-scale farmers in resource-poor cropping systems	New improved germplasm combining African (*Oryza glaberima*) and Asian (*O. sativa*) sources	Improved rice germplasm for Africa
output target 2008	New segregating germplasm evaluated under abiotic stress conducted, segregating material evaluated under abiotic stress			
output target 2009	MAS for target traits conducted, germplasm developed and links established with farmer communities			
output target 2010	*Completed*			
Output 3.16. Virus resistance enhanced in sweet potato through exploration of heterosis (*commissioned G4007.07*)		Plant breeders and breeding programmes, and ultimately small-scale farmers in resource-poor cropping systems	Improved drought-tolerant and virus-resistant sweet potato lines	Improved sweet potato germplasm for Africa
output target 2008	Germplasm evaluated for virus (SPVD) resistance under greenhouse and field conditions, new SSR loci identified.			
output target 2009	Backcross populations developed, shared with NARI Uganda and screened for virus resistance.			
output target 2010	Markers closely linked to SPVD resistance genes identified and MAS developed in two breeding populations.			
Output 3.17. Quick conversion of popular rice varieties in the Mekong region, with emphasis on drought, salinity and grain quality improvement (*commissioned G4007.03*)		Plant breeders and breeding programmes, and ultimately small-scale farmers in resource-poor cropping systems	Demonstrated adoption of new molecular breeding tools and germplasm products thereof in pilot delivery pathways in representative locations in key production areas	Capacity of Mekong NARS to conduct MAS in rice improved and more efficient MAS strategies available for crop improvement programmes
output target 2008	Line converted through marker-assisted selection			
output target 2009	Introgression lines validated for target trait performance, yield and agronomic characteristics			
output target 2010	*Completed*			
Output 3.18. Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-aided breeding (*competitive G3007.05*)		IRRI, TNAU-Coimbatore, CRURRS-Hazaribag, and UAS-Bangalore (India), YAAS-Kunming (China)	Large-effect QTLs for yield under drought stress identified and validated, a QTL finemapped, and a low-cost system developed for detecting alleles with effects on drought tolerance	Rice germnplasm with improved drought tolerance disseminated in Asia, improved capacity to map and deploy drought yield QTLs developed in Asian NARS
output target 2008	QTLs with consistent effects on drought yield across genetic backgrounds verified or disproved and effects of drought tolerance QTLs in other backgrounds evaluated			
output target 2009	Low-cost system for detecting alleles with effects on drought tolerance across a range of backgrounds developed based on bulk segregant analysis (BSA) and dissemination of advanced breeding lines			
output target 2010	*Completed*			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 3.19. Local germplasm enhanced via molecular breeding for target traits in tropical legumes (groundnut, bean, cowpea, and chickpea) (*special G6007.05*)		Breeding programmes and ultimately small-scale farmers in resource-poor cropping systems	Increased yields in farmers' field and increased incomes due to improved local varieties	New germplasm and improved breeding programmes for tropical legumes in Africa
output target 2008	Farmer/market preferred varieties and germplasm lines identified for introgression of resistances through MAB			
output target 2009	New backcross populations incorporating farmer/market preferences and disease resistance developed			
output target 2010	Diversified breeding populations developed for marginal drought prone areas			
Output 3.20. Marker-assited selection for resistance to *Striga gesnerioides* in cowpea (*commissioned 2008*)		Cowpea breeding programmes and ultimately small-scale farmers in resource-poor cropping systems in West Africa	Markers available for resistance to *Striga gesnerioides* in cowpea	New cowpea germplasm (with improved *Striga* resistance) for West Africa
output target 2008	*Striga* resistance markers used by INERA-Burkina Faso to select *Striga* resistant cowpea germplasm			
output target 2009	*Striga* resistance markers deployed in West African cowpea breeding programmes			
output target 2010	*Completed*			
Output 3.21. Marker-assisted selection for resistance to streak virus in maize (*commissioned 2008*)		Maize breeding programmes and ultimately small-scale farmers in resource-poor cropping systems in Southeast Africa	MAS for maize streak virus developed in Southeast Africa	New maize germplasm (with improved resistance to streak virus) for Southeast Africa
output target 2008	Streak virus resistance markers deployed by ACCI and resistant lines identified in the maize breeding programme of IIAM (Mozambique)			
output target 2009	OPVs and hybrids with resistance to streak virus resistance developed			
output target 2010	*Completed*			
Output 3.22. MAS and dissemination of cassava varieties with resistance to pests and diseases (*commissioned 2008*)		Cassava breeding programmes and small-scale farmers in resource-poor cropping systems in Central Africa	Cassava varieties with resistance to pests and diseases developed by NRCI (Nigeria) and distributed to farmers	Capacity of Central Africa NARS to conduct MAS in cassava improved and new cassava germplasm (with improved virus resistance) available for Central Africa farmers
output target 2008	MAS capacities improved at NRCI (Nigeria) and cassava varieties with resistance to cassava mosaic disease (CMD), cassava bacterial blight (CBB) and cassava green mites (CGM) developed			
output target 2009	New cassava varities with resistance to CMD, CBB, and CGM disseminated and adopted			
output target 2010	*Completed*			
Output 3.23. Marker-assisted recurrent selection for drought tolerance in sorghum (*commissioned 2008*)		Sorghum breeding programmes in resource-poor cropping systems in West Africa	Sorghum varieties with improved drought tolerance developed by West African NARS	Capacity of West Africa NARS to conduct MAS in sorghum improved and sorghum germplasm with improved drought tolerance available for West Africa farmers
output target 2008	Development of populations from well-adapted varieties			
output target 2009	Generation of advanced families			
output target 2010	Genotyping at Syngenta and phenotyping in Niger (INRAN) and Mali (IER)			

Outputs	Output Targets	Intended user	Outcome	Impact
Project 4. Bioinformatics and crop information systems				
Theme 1. INFRASTRUCTURE: Facilitation of information flow of ongoing research, both in terms of data and in terms of communication between the researchers				
Output 4.1. GCP domain models developed *(commissioned 2005-22)*		GCP software developers	Better integration of software and web services for use in germplasm conservation and crop improvement	Increased efficiency in bioinformatics for crop improvement programmes
output target 2008	Ontologies for GCP the datadomains passport, genotyping and phenotyping published			
output target 2009	Available ontologies are further developed; new ones published			
output target 2010	Further development and maintenance *(prioritisation to be done later)*			
Output 4.2: Web services technology implemented in GCP Consortium (*commissioned 2005-23*)	Consortium IT staff		Data from consortium members available as web services	Increased efficiency in data analysis
output target 2008	Web services further deployed in GCP Consortium member institutes; staff trained			
output target 2009	Small additional implementations and trainings			
output target 2010	*none*			
Output 4.3. Templates for GCP data capture, storage and use created, made available to the research community and maintained (*commissioned 2005-25*)		GCP scientists	Scientists better able to maintain, use and upload their GCP data	Better access to research data for crop researchers and improvement programmes
output target 2008	All templates further developed or maintained, users actively supported			
output target 2009	All templates further developed or maintained, users actively supported			
output target 2010	*to be determined*			
Output 4.4. GCP Registry created and maintained (*commissioned 2005-26*)		Bioinformatics and biodiversity scientists all over the world	Central access to all GCP-generated data	Increased efficiency in application of data for crop research and improvement
output target 2008	Registry is updated with all produced GCP data sets			
output target 2009	Maintenance and further expansion			
output target 2010	Maintenance and further expansion			
Output 4.5. Web services tools and technology further developed (*commissioned G4007.12)*		Bioinformatics scientists all over the world	Improved technology enhances GCP's contribution to the global bioinformatics community	Increased efficiency in data exchange and analysis
output target 2008	Application software framework code documented and posted to CropForge, "Taverna" workflow integrated with elaborated search engine			
output target 2009	*to be determined*			
output target 2010	*to be determined*			
Output 4.6. Web services technology applied in reference GCP applications (*commissioned 2005-24*)		Bioinformatics and biodiversity scientists all over the world	GCP applications prove utility of web services approach and provide instruments for more efficient research	Increased efficiency in application of data for crop research and improvement
output target 2008	Three model GCP applications are ready, one for each of the first three SPs			
output target 2009	*to be determined*			
output target 2010	*to be determined*			
Output 4.7. GCP software engineering and collaboration platform established and maintained (*commissioned 2005-34*)		GCP software developers	Simultaneous software and document development facilitated	More efficient scientific collaboration among bioinformaticians and crop researchers
output target 2008	CropForge and GCP Wiki maintained and promoted, users supported			
output target 2009	CropForge and GCP Wiki maintained and promoted, users supported			

Outputs	Output Targets	Intended user	Outcome	Impact
output target 2010	CropForge and GCP Wiki maintained and promoted, users supported			
Theme 2. IMPROVEMENT: Creation of facilities to support IT and bioinformatics applications in the GCP Consortium				
Output 4.8. Integrated GCP Information Platform created (*commissioned 2006-16*)		GCP informatics staff	Improved access by GCP scientists to integrated tools and databases	More efficient bioinformatics research for crop improvement programmes
output target 2008	GCP bioinformatics client further developed; three new functionalities released			
output target 2009	GCP bioinformatics client further developed; new functionalities released			
output target 2010	*to be determined*			
Output 4.9. Data quality within the GCP further improved and assured (commissioned *2006-17*)		GCP informatics staff	Data quality of existing data bases improved	Increased efficiency in application of data for crop research and improvement
output target 2008	Best practices for two domains defined, data quality assesment protocols defined, staff trained			
output target 2009	Further best practices defined and staff trained			
output target 2010	*to be determined*			
Output 4.10. High-Performance Computing (HPC) facilities integrated in the GCP toolbox (*commissioned 2005-27*)		GCP scientists	HPC facility fully functional and used by GCP bioinformatics and genetics researchers	Higher efficiency in application of data for crop research and improvement
output target 2008	Three use cases developed, documented and promoted			
output target 2009	HPC facilities are a widely used tool in GCP research			
output target 2010	*to be determined*			
Theme 3. SUPPORT: Support to other GCP Projects in terms of software tools and data management				
Output 4.11. Bioinformatics and data handling support to GCP scientists (*commissioned G4007.10*)		GCP scientists	Better access to GCP SP4 products and expertise	Increased efficiency in GCP crop research and improvement
output target 2008	48-hour response helpdesk for GCP scientists; website giving overview of products and expertise in the field of data handling and analysis developed			
output target 2009	helpdesk and website maintained			
output target 2010	*to be determined*			
Output 4.12. Data analysis support for Project 1 activities with emphasis on sampling germplasm (*commissioned 2006-35*)		Germplasm specialists and plant breeders (Project 1 and NARS)	More efficiency in data handling and analysis in Project 1 and in NARS activities	Increased efficiency in crop research and improvement
output target 2008	Pro-active support to Project 1 scientists and NARS in data handling and analysis provided, website created			
output target 2009	Pro-active support to Project 1 scientists and NARS in data handling and analysis provided, website maintained and expanded			
output target 2010	*to be determined*			
Output 4.13. Data analysis support available for Project 2 with emphasis on microarray and mapping experiments (*commissioned 2006-08*)		Crop geneticists and genomics specialists	Microarray and mapping experiments can be better analysed	Increased efficiency in crop research and improvement
output target 2008	Analysis pipeline for integrating results from microarray and mapping experiments established			
output target 2009	*none*			
output target 2010	*none*			
Output 4.14. Decision support tools for MAS and MAB further developed (*commissioned G4007.11*)		Plant breeders	More efficient use of markers by plant breeders	Increased efficiency in NARS molecular breeding programmes
output target 2008	Extension of iMAS published, users supported			

Outputs	Output Targets	Intended user	Outcome	Impact
output target 2009	*to be determined*			
output target 2010	*to be determined*			
Output 4.15. Methodology and software developed for LD-based phenotype analysis (in support of Projects 1 and 2) (*commissioned G4007.09*)		Germplasm specialists and crop geneticists	LD-based phenotype analysis more efficient and accessible to GCP scientists	Increased efficiency in crop research and improvement
output target 2008	*(intermediate project goals)*			
output target 2009	Methodology and software for LD-based phenotype analysis developed			
output target 2010	*to be determined*			
Output 4.16 Methodology development for association analysis in non-HW populations (*commissioned 2008*)		Germplasm specialists and crop geneticists	Possibility to better analyse associations in populations that are not in HW equilibrium	Increased efficiency in crop research and improvement
output target 2008	*(intermediate project goals)*			
output target 2009	Methodology and software for association analysis in non-HW populations.			
output target 2010	*none*			
Output 4.17. Methodology development for reconstruction of genealogies based on haplotypes related to geographic patterns (*commissioned 2008*)		Germplasm specialists and crop geneticists	Better insight in structure of genepools	Increased efficiency in crop research and improvement
output target 2008	*(intermediate project goals)*			
output target 2009	Methodology and software for reconstruction of genealogies based on haplotypes related to geographic patterns			
output target 2010	*none*			
Output 4.18. An eco-physiological–statistical framework for GxE and QTLxE analysis developed (in support of Project 3) (*competitive 2005-04*)		Crop researchers and plant breeders	Understanding in GxE and QTLxE improved and QTL detection more efficient	Increased efficiency in crop research and improvement
output target 2008	An eco-physiological–statistical framework for the analysis of GxE and QTLxE, with applications to the CIMMYT drought stress programmes developed and available (extension of 2007)			
output target 2009	*none*			
output target 2010	*none*			
Output 4.19. Ortholog-function display tools developed (in support of Project 2) (*commissioned 2005-31*)		Bioinformatics scientists all over the world	Gene orthology relationships across species and related paralogy relationships within a gene families readily accessible to scientists	Increased efficiency in crop research and improvement
output target 2008	Public comparative gene catalogue, user interfaces and data integration protocols developed (extension of 2007)			
output target 2009	*none*			
output target 2010	*none*			
Output 4.20. Crop gene expression database and data mining tools developed (in support of Project 2) (*commissioned 2005-32*)		Bioinformatics scientists all over the world	Expression data easily searchable	More efficient bioinformatics research for crop improvement programmes
output target 2008	User-friendly gene expression database in which the data are connected by the linkage of orthologous genes developed and made available through web service (extension of 2007)			
output target 2009	*none*			
output target 2010	*none*			
Output 4.21. Core collection methodology further developed and consolidated (*discretionary, SP4 leader*)		GCP scientists and genebank curators all over the world	Clarity on the quality of different core collection methodologies	More efficient usage of germplasm collections
output target 2008	Inventory of core collection methodologies made, and evaluated.			

Outputs	Output Targets	Intended user	Outcome	Impact
output target 2009	*none*			
output target 2010	*none*			
Project 5. Capacity-building and enabling delivery				
Theme 1. Creation of a platform of training resources and a cadre of trained scientists to apply advanced technologies and add value to GCP products				
Output 5.1. Selected training courses in molecular analysis of germplasm, genomics/molecular breeding, bioinformatics and phenotyping conducted		Researchers collaborating directly or indirectly with the GCP	Regional courses in subject matters of critical importance to furthering GCP goals conducted for researchers in Africa, Asia and Latin America	Increased capacity of researchers in target countries to collaborate with GCP and conduct their own research towards improved crop varieties for farmers
output target 2008	At least 15 researchers trained per course			
output target 2009	At least 15 researchers trained per course			
output target 2010	At least 15 researchers trained per course			
Output 5.2. Course and training materials on intellectual property, freedom-to-operate, and genetic resources policies, including the International Treaty for Plant Genetic Resources for Food and Agriculture (PGRFA), developed		GCP Consortium and collaborating institutions, researchers, and staff, as well as stakeholders	Training materials on policy issues of major importance to the GCP developed and disseminated	Increased understanding in the GCP and wider scientific community of genetic resources policies and their implications for research
output target 2008	Materials for online course available online and distributed to GCP Institutions in electronic format (CD-ROM/DVD)			
output target 2008	At least 20 researchers trained on the significance of the International Treaty on PGRFA to GCP			
output target 2009	*continued*			
output target 2010	*continued*			
Output 5.3. Training materials for association studies/linkage disequilibrium mapping developed *(commissioned 2006-11)*		GCP researchers and collaborators, especially germplasm specialists and crop geneticists	Guide to alternatives to conventional linkage mapping made available	Increased capacity of scientists in target countries to collaborate with GCP and conduct their own research on improved crop varieties for farmers
output target 2008	Course materials online and on CD-ROM			
output target 2009	*completed*			
Output 5.4. Training materials for phenotyping developed *(commissioned 2006-9)*		GCP researchers and collaborators, particularly crop geneticists and breeders	Learning materials on phenotyping, with emphasis on drought, made available	Increased capacity of scientists in target countries to collaborate with GCP and conduct their own research toward improved crop varieties for farmers
output target 2008	Course materials made available online and as CD-ROM			
output target 2009	*completed*			
Output 5.5. GCP training materials translated into selected languages (Spanish, French, Chinese, Portuguese and Arabic) (*commissioned 2006-26)*		Crop researchers relying on languages other than English	Training materials publicly available in several languages	More scientists gaining capacity in GCP-related research fields, thus able benefitting from GCP's research
output target 2008	Training materials for molecular breeding and bioinformatics translated and made available via the web and CD-ROM			
output target 2009	Training materials for association analysis/LD mapping and phenotyping translated and made available via the web and CD-ROM			
output target 2010	Selected materials translated into missing languages			
Theme 2. Cultivation of research and learning opportunities for GCP collaborators and NARS scientists to further GCP mission and progress				
Output 5.6. Capacity-building *à la carte* Programme (*commissioned G4007.13*)		NARS in GCP target regions and their collaborators	Support for targeted individual and team training opportunities, including facilities/supplies upgrade and technical backstopping provided to GCP target NARS to optimise collaboration	GCP products more readily used by developing country researchers for crop improvement

Outputs	Output Targets	Intended user	Outcome	Impact
output target 2008	At least 8 grants provided to collaborating GCP researchers and their institutions for comprehensive capacity- building			
output target 2009	At least 10 grants provided to collaborating GCP researchers and their institutions for comprehensive capacity- building			
output target 2010	At least 10 grants provided to collaborating GCP researchers and their institutions for comprehensive capacity- building			
Output 5.7. GCP Fellowship Programme continued (initiated in 2005) (*G4007-14.1*)		GCP collaborators, particularly those engaged in ongoing projects	Research and capacity-building support provided to collaborators to boost capacity to participate in GCP research in their home institutions	Increased capacity of scientists in target countries to collaborate with GCP and conduct their own research toward improved crop varieties for farmers
output target 2008	8 fellowships awarded			
output target 2009	Discontinued			
output target 2010	Discontinued			
Output 5.8. GCP Travel Grant programme continued (initiated in 2005) (*G4007-14.2)*		GCP collaborators, particularly those from developing countries engaged in ongoing projects	Research and capacity-building support provided to collaborators to boost capacity to participate in GCP research in their home institutions	Increased capacity of scientists in target countries to collaborate with GCP and conduct their own research toward improved crop varieties for farmers
output target 2008	16 travel grants awarded for hands-on training opportunities and participation in GCP's Annual Research Meeting			
output target 2009	10 travel grants awarded for participation in GCP's Annual Research Meeting			
output target 2010	10 travel grants awarded for participation in GCP's Annual Research Meeting			
Output 5.9. Academic position in molecular breeding established and supported (*commissioned 2006-36*)		PhD candidates in selected African countries and breeding programmes	Programme established to train African plant breeders	Increased human capacity in national breeding programmes in Africa
output target 2008	10 PhD candidates acquainted with topics on advanced technologies, genomics and molecular markers for breeding			
output target 2009	An inventory of molecular tools available for important crops and traits, especially in Africa. 10 PhD candidates acquainted with topics on advanced technologies, genomics and molecular markers for breeding			
output target 2010	10 PhD candidates acquainted with topics on advanced technologies, genomics and molecular markers for breeding			
Theme 3. Construction of systems for ensuring product delivery				
Output 5.10. Capacity-building mechanisms and product pipelines established for tropical legume improvement in Africa (*special G6007.06*)		African legume researchers and plant breeders	African researchers trained in modern breeding techniques and applications	Improved groundnut, bean, cowpea, and chickpea varieties delivered to resource-poor farmers
output target 2008	A workshop completed and delivery plans developed for projects focused on cowpea, common bean, chickpea and groundnut			
output target 2008	Training and equipment (field, laboratory and computer infrastructure) needs among the sub-Saharan African partners identified and plans to fulfill them in place			
output target 2009	At least 10 NARS scientists trained in plant phenotyping			
output target 2009	Improved computer and bioinformatic infrastructure in at least 5 African countries			
output target 2010	At least 10 NARS scientists trained in marker assisted selection			
output target 2010	Improved field and laboratory infrastructure in at least 5 African countries			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 5.11. Comprehensive support provided to competitive projects to define and implement delivery and capacity-building plans (*internally commissioned, 2006-12*)		Project investigators of competitive grants, their collaborators, and NARS researchers	Two-way flow of communication activated from users to producers, and capacity needs identified and fulfilled	Increased capacity in NARS to adopt GCP products, and GCP products used by researchers in developing improved crops
output target 2008	Linkages established or strengthened between research and delivery partners for each of the new competitive grants, and plans developed to fulfil needs of NARS to benefit from the project			
output target 2009	Support to new projects continued following the GCP workplan			
output target 2010	Support to new projects continued following the GCP workplan			
Output 5.12. Partnership and delivery options for the GCP surveyed and assessed (*commissioned G4007.15*)		GCP community and potential partner scientists and institutions	GCP understanding of partner needs enhanced and capacity-building activities refined to better address partner needs, enhancing probability of success of delivering GCP products	Increased capacity of scientists and institutions in target countries to collaborate with GCP, adopt GCP products and conduct their own research on improved crop varieties for farmers
output target 2008	Research, infrastructure and human resource capacity of collaborating NARS of at least 3 GCP research projects in GCP target regions assessed; information used to inform development of new partnerships			
output target 2009	Assessment continued			
output target 2010	Assessment continued			
Output 5.13. A project development guide (PDG) designed and implemented		GCP Management Team, Principal Investigators and Project team members, and the review teams for competitive grants, the internal Review and Advisory Team, and the External review teams reporting to donors	Systematic, unified, transparent approach to project management and planning within GCP	GCP's product-driven approach reinforced by better quality project plans, more products from research programmes being fully used, smooth and rapid hand-overs of products, and improved communication between project members and potential users
output target 2008	A project management knowledge-based tool to maximise the delivery of GCP products on time and on budget			
output target 2009	A project development and management knowledge-based tool			
output target 2010	The PDG completed and implemented			
Output 5.14. Strategy developed for product distribution		GCP community and stakeholders in target regions	GCP products reach intended users	Increased access to, and use of, GCP products
output target 2008	An implementation plan developed			
output target 2009	Plan for product distribution implemented			
output target 2010	*Continued*			
Theme 4. Development and implementation of support services				
Output 5.15. Helpdesk for intellectual property and access and benefit-sharing issues established and maintained (*commissioned 2005-CB16*)		GCP community, wider scientific community and stakeholders	Resource established for continued education of researchers and their institutions on relevant IP and ABS issues related to products being used and/or generated by GCP research	Increased understanding in the GCP and wider scientific community of IP and ABS issues and their implications for research and delivery
output target 2008	Materials and advice available via the web, and distributed in electronic format upon demand. Helpdesk function continued			
output target 2009	Helpdesk function continued			
output target 2010	Helpdesk function continued			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 5.16. Asset inventory system for the GCP developed *(commissioned 2005-CB17)*		GCP community, wider scientific community and stakeholders	A database created of products, expertise and third-party materials associated with specific products for GCP	Increased access to asset information, critical to delivering research outputs
output target 2008	An inventory of GCP products available			
output target 2009	Completed			
Output 5.17. Interactive Resource Centre established and maintained *(commissioned 2005-CB13)*		Researchers worldwide working on plant genetic diversity and genomics	One-stop shop for information, references and advice established	Increased access to information, resources and expertise, thereby enhancing capacity, particularly in developing countries
output target 2008	New educational/training resources for scientific research and helpdesk available online			
output target 2009	Completed. Helpdesk function continued			
output target 2010	Helpdesk function continued			
Output 5.18. Genotyping support service established (*commissioned 2005-CB23*)		NARS researchers	Enhanced access to quick and efficient genotyping of relevant germplasm	Increased capacity of molecular breeding programmes in developing countries to develop improved crop varieties
	Services (genotyping and data interpretation) provided for germplasm or routine MAS in breeding programmes for sorghum, millet, groundnut, chickpea, cowpea, bean, cassava, sweetpotato, potato, coconut and Musa			
output target 2009	Services (genotyping and data interpretation) provided for germplasm or routine MAS in breeding programmes of selected crops			
output target 2010	Services (genotyping and data interpretation) provided for germplasm or routine MAS in breeding programmes of selected crops			
Theme 5. *Ex ante* impact analysis and impact assessment				
Output 5.19. Potential impact of GCP research assessed (*commissioned 2006-13; 2006-14*)		GCP Management Team, wider scientific and development community and other decision makers	Detailed information available about potential impact of GCP research in target regions, crops and traits	Impact of GCP increased, contributing to reduced poverty and hunger
output target 2008	Impact targeting of crop-specific drought severity and type as well as analysis of GCP priority farming systems and their patterns of technology adoption at disaggregated levels			
output target 2009	Relative importance of secondary traits for selected crops (sorghum, cassava, cowpea) studied			
output target 2009	*Ex ante* impact analysis of selected marker-assisted selection technologies supported byGCP			
output target 2010	*to be determined*			

Generation

Cultivating Plant Diversity for the Resource-Poor

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