Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE POOR

Medium-Term Plan 2007-2009

June 2006

Generation Challenge Programme

2007-2009 Medium Term Plan

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Acronyms and Abbreviations

ACGT	African Centre for Gene Technologies
AGROPOLIS	International Complex for Research and Higher Education in Agriculture (France)
ARI	Advanced research institute
BAC	Bacteria artificial chromosome
BioMOBY	Open source biological web services project, "Model Organisation Bring Your Own Database"
CAAS	Chinese Academy of Agricultural Sciences
CBR	C-repeat binding factor
cDNA	Complementary DNA
CENARGEN	National Center for Genetic Resources and Biotechnology Research (Brazil)
CGIAR	Consultative Group on International Agricultural Research
CIAT	International Center for Tropical Agriculture
CIMMYT	International Maize and Wheat Improvement Center
CIP	International Potato Center
CNG	Centre National de Génotypage (France)
COS	Conserved orthologous sequences
DFID	Department for International Development (UK)
DNA	Deoxyribonucleic acid
DREB	Dehydration responsive element binding
EMBRAPA	Brazilian Agricultural Research Corporation
eQTL	Expressed quantitative trait loci
EC	European Commission
EST	Expressed sequence tag
Fst	Proportion of the total genetic variance contained in a subpopulation relative to the total genetic variance. Values can range from 0 to 1. High F_{ST} implies a considerable degree of differentiation among populations.
FAO	Food and Agriculture Organisation of the United Nations
GCP	Generation Challenge Programme
Gramene	A comparative mapping resource for grains
GxE	Genotype by environment interaction
HTP	High Through Put
IAO	Instituto Agronomico d'Oltremare (Italy)
ICAR	Indian Council for Agricultural Research
ICARDA	International Center for Agricultural Research in the Dry Areas
ICIS	International Crop Information System
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
IITA	International Institute of Tropical Agriculture
ILAC	Institutional Learning and Change
INIBAP	International Network for Improvement of Banana and Plantain
IPGRI	International Plant Genetics Resources Institute
IRIS	International Rice Information System
IRRI	International Rice Research Institute
IWIS	International Wheat Information System
JIC	John Innes Centre, UK
LD	Linkage disequilibrium
LIMS	Laboratory information management systems
MAS	Marker-assisted selection

MTA	Material transfer agreement
MTP	Medium Term Plan
NARS	National agricultural research system
NCGR	National Center for Genome Resources (USA)
NGO	Non-governmental organisation
NIAS	National Institute of Agrobiological Sciences (Japan)
PAC	Programme Advisory Committee
PCR	Polymerase chain reaction
PSC	Programme Steering Committee
QTL	Quantitative trait loci
RFLP	Restriction fragment length polymorphism
RIL	Recombinant inbred line
SGRP	System-wide Genetic Resources Programme
SINGER	System-wide Information Network for Genetic Resources
SME	Small- and medium-sized enterprises
SNP	Single nucleotide polymorphism
SP	Subprogramme
SSR	Simple sequence repeat
TRIPS	Trade-Related Aspects of Intellectual Property Rights
USAID	United States Agency for International Development
USDA	United States Department of Agriculture
WARDA	Africa Rice Centre
WTO	World Trade Organisation

Introduction, Context, and Programme Discussion

Introduction

The Generation Challenge Programme (GCP) has made rapid progress since its inception in 2003. The 2007-2009 Medium Term Plan (MTP) is the third such plan the Programme has submitted. This new MTP reflects the increasing depth of the GCP in terms of research conducted, collaborations formed, new directions forged, and lessons learned.

The GCP is a 10-year programme with a dual mandate to (1) cultivate innovative partnerships for ground-breaking science and (2) conduct research that delivers products to develop improved crop varieties for resource-poor farmers. This mandate compels the GCP to take advantage of new scientific opportunities, pursue research that is highly focused on solving major problems faced by farmers, and build systems that ensure the sustained relevance and impact of GCP research and products. In developing this MTP, we have sought to capture the vision, complex inter-institutional dynamics, and progress required to translate this mandate into tangible and useful results.

The GCP's operational and technical foundation is now in place. Currently the Programme supports 17 competitive projects and about 60 commissioned projects, representing US$12.7 million in research investment for this year alone. The second call for competitive GCP grants, which will total US$2 million per year over two years, opened in early 2006; projects will begin in 2007. The technical infrastructure and knowledge systems for supporting GCP research are in place, and a capacity-building programme that provides both hands-on learning within research projects and regional training courses is running at full speed. In late 2005, a strategy for ensuring that GCP products are delivered to and implemented by users[1] was also approved and launched.[2] Delivery plans that trace the research process from producer to user are now required for all major GCP projects; they will serve as a means of monitoring and assessing the impact of GCP research and of incorporating feedback into project design. These systems and strategies enable the GCP to fulfil its mandate and maintain its accountability to Programme partners, supporters, and beneficiaries.

The first GCP products are now available. For example, 21 of the 22 mandate crops[3] of the GCP have been genotyped and analysed,[4] and reference collections have been derived for each of them. The GCP also established a genotyping support service in 2005 to aid national agricultural research systems (NARS) in characterising their germplasm and comparing it with the GCP reference collections. The reference collections and genotyping support service have direct and important applications for plant breeders, who are critical users of GCP products. Other GCP products include: *an improved understanding of gene function*, which enables researchers to discover genes that control stress tolerance; *genetic maps and QTL characterisation*, which researchers use to develop QTL or gene-based molecular markers to heighten the efficiency of plant breeding programmes; and *support services and training,* which enable national programme researchers to benefit from GCP products.

The GCP is sharpening its strategy and priorities. While the GCP's first two years focused primarily on building the operational and technical foundation for its research, priority setting was not neglected. Much thought has been given to the future of the GCP. The Programme's mission is expansive: to serve as a research and capacity building network that uses plant genetic diversity, advanced genomic science, and comparative biology to develop tools and technologies that enable plant breeders to produce better crop varieties for resource-poor farmers. Given this mission and 22 mandate crops, the GCP can work in many important areas—but which are vital? Because GCP research does not yield products for farmers' immediate use (improved varieties, farming practices, and such), a Programme-wide strategy is needed to navigate the vast range of research opportunities and ensure that the GCP's activities ultimately have an impact in farmers' fields.

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[1] A 'user' *is anyone who uses a product developed by the* GCP, such as molecular geneticists, gene bank curators, and plant breeders. The value chain of research for product development and delivery extends from gene bank curators to molecular geneticists to plant breeders, and then on to extension agents, seed distributors, and farmers themselves. The GCP does not develop products directly for every single one of the numerous user groups along that value chain. Instead, GCP products contribute to the development of products at downstream stages of the value chain through which they ultimately reach farmers.

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

[3] Andean roots and tubers, barley, cassava, chickpea, coconut, cowpea, finger millet, forages, groundnut, lentil, maize, *Musa*, pearl millet, *Phaseoulus*, pigeon pea, potato, rice, sorghum, soybean, sweet potato, wheat, and yam.

[4] Up to 3,000 accessions with 50 SSR markers.

The GCP must focus on areas where, in the shortest time, its research can lead to improved livelihoods for the greatest number of the poorest people living in marginal environments.[5] The short term vision must also be part of a strategy for long term impacts. In 2006, the GCP is finalizing its strategy and identifying research priorities for the coming years. The strategy is not a departure from the establishment documents of the GCP but rather a refinement of them. Research priorities are based on types of farming systems (classified through socioeconomic as well as agronomic criteria); global crop production statistics; and the genetic, genomic, phenotyping, and breeding resources available for each of the staple food crops. The GCP expects to publish its strategy by the end of 2006, following approval by the Programme Steering Committee. This MTP includes new projects that the GCP will implement in 2007, in line with the updated strategy and priorities. While the GCP will consolidate its research agenda around some newly articulated priorities, it remains dedicated to the exploration of diversity in staple crops and will continue to support this core effort.

An integral part of the GCP mission is its network. The GCP was created to bring scientists, institutions, research disciplines, and other stakeholders together to apply the advances of genomics to unlock genetic diversity and develop tools, techniques, and technologies that will revolutionise plant breeding. Through this network, the GCP aims to harness the power and potential of billions of dollars of research investment in the developed world to serve the poor in the developing world. This approach, which bridges the traditional gap between basic and applied research, has attracted both donors and research partners alike. The Programme's founding donors—the World Bank and the European Commission—were joined by the UK Department for International Development in 2004. The Swedish International Development Cooperation Agency, the Rockefeller Foundation, and Pioneer Dupont are among other donors that support the GCP. The GCP Consortium grew in 2005 to 22 members, by welcoming four new members:[6] INRA (Morocco), CINVESTAV (Guanajuato Campus, Mexico), BIOTEC (Thailand), and IAO (Italy). More than 30 NARS in developing countries and over 25 advanced research institutes (ARIs) are involved in GCP research projects. The capacity-building activities of the GCP—which include research fellowships, travel grants, and training courses—have involved over 100 institutes, the vast majority in the South.

Context

Food insecurity and severe poverty continue to plague the developing world, even in places characterised by recent, dramatic economic growth, and despite tremendous gains in crop yields in some countries only a few decades ago. The vulnerability of the poor is heightened by growing threats to global agriculture, including disease epidemics, the effects of climate change, and especially drought. The UN Food and Agriculture Organization (FAO) ranks drought as the single most common cause of severe food shortages in developing countries. In a comparison of food emergencies from 2002 to 2004, for example, drought was involved in 50-70% of the cases, significantly outweighing other causes such as conflict, flooding, and economic problems. By 2025, 1.8 billion people will live in areas that FAO classifies as experiencing an 'absolute water shortage', and fully two-thirds of the world's population will live in areas experiencing 'water stress'.

Advanced genomics and comparative biology offer capabilities and opportunities in the biological sciences that were undreamt of when the Consultative Group on International Agricultural Research (CGIAR) took up its scientific and humanitarian mission over 30 years ago. The genetic diversity of farmer varieties of staple crops, their wild relatives, landraces, and other germplasm held in national and CGIAR Centre collections represents a wealth of untapped potential for crop improvement that could mitigate the disastrous effects of drought, diseases, and pests on poor farmers. Comparative biology and association genetics provide powerful tools for illustrating relationships between gene function, metabolic pathways, and plant performance, contributing to our understanding of control mechanisms for complex traits like drought. The spectacular advances in pharmacology and human genetics made possible by the Human Genome Project and model mammalian systems projects demonstrate what is possible—on an even greater scale—in plants, when we combine the potential of genetic diversity with the power of advanced genomics and comparative biology. These major advances also illustrate the importance of creating a strong coalition—and leveraging the strategic resources—of a wide range of institutions with common interests. Because the GCP is based on a similar, highly networked institutional model, in which an array of partners contribute diverse capacities and perspectives to the Programme at different times and places, the GCP can remain agile and responsive in achieving its goals and making an impact.

[5] 'Marginal environments' are characterised by high risk factors for crop production, low agricultural yields, and concentrated poverty.

[6] These new members are provisional while the Program Steering Committee reviews the GCP Consortium Agreement. When any changes have been finalized in the agreement, these provisional members will be asked to sign the Consortium Agreement and thereby become full members.

An important component of the GCP network and comparative biology approach is the development and adoption of common procedures for experimental protocols and data collection, analysis, and storage. Access to the immense amounts of data being produced by project partners is integral to analysis and application—and ultimately the success of the GCP. Since the GCP's inception, emphasis has been placed on creating an interoperable information platform and a central data registry, and the GCP recently inaugurated several policies for ensuring release of data.

Programme Discussion

The GCP's five subprogrammes (SPs) are the operational structure for allocating funds and managing research projects:

- **Subprogramme 1: Genetic Diversity of Global Genetic Resources**
  Characterises the diversity of crop germplasm collections held by the CGIAR and national programmes, and assesses both the genetic structure of the collections and the phenotypic variation associated with that structure.
- **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: Trait Capture for Crop Improvement**
  Validates gene function and refines molecular breeding systems and the resulting enhanced germplasm, with the purpose of increasing the efficiency, speed, and scope of plant breeding.
- **Subprogramme 4: Genetic Resource, Genomic, and Crop Information Systems**
  Integrates GCP information components and analysis tools into a coherent information gateway, and provides support for the data analysis needs of other Subprogrammes.
- **Subprogramme 5: Capacity Building and Enabling Delivery**
  Empowers scientists in developing country national programmes to use modern breeding approaches via workshops, fellowships, grant opportunities, and thesis projects, and coordinates the development and implementation of project delivery plans.

A notable change implemented in 2005 in the GCP's operating structure was the shift of all policy and intellectual property research activities from SP1 to SP5, and the addition of the 'Enabling Delivery' component to Subprogramme 5. SP5 is also responsible for monitoring the training activities embedded in the research projects of Subprogrammes 1 through 4.

A unique aspect of the GCP is its research framework, composed of three complementary funding mechanisms:

1) *Competitive grants:*
   a. First-round competitive grants: These 17 projects are three-year projects of about US$300,000 each per year. Initiated in January 2005, they will end in January 2008. Their output targets are reported in 2007 and 2008.
   b. Second-round competitive grants: These projects (number to be determined) are two-year projects of about US$300,000 each per year. They will begin in January 2007 and end in December 2008. Their output targets should be reported in 2007 and 2008, but because the projects will not be selected until October 2006, no output targets are reported in the logframe of this MTP.
2) *Commissioned research projects*. These projects typically run from one to two years at a cost of US$20,000-300,000 per year They are designed to contribute to the array of genetic and genomic resources publicly available through the GCP or to help combine outputs of several research projects.
3) *Special projects*. These are usually three-year projects for which budget and research activities are developed in close collaboration with specific donors.

The GCP operates with a 50-50 split between competitive and commissioned grants. The competitive grants scheme of the GCP, the only one like it in the CGIAR, requires every proposed project to feature the participation of a GCP Consortium member, an advanced research institute, and a NARS from the South. A transparent and merit-based process, the competitive grants scheme stimulates competition in the research community and has resulted in high-quality proposals and projects. To ensure that the grants target priority areas in the GCP, the second call for proposals (opened in February 2006) identifies target 'thematic areas', of which every proposal must address one or more.

As in years past, the development of the 2007-2009 MTP was complicated owing to the nature and timing of funding. Many of the research outputs from GCP projects initiated in 2005 and 2006 will be delivered during 2007-2009, as specified in the MTP logframe. Some new projects will pick up where old projects left off; other new ones are specifically designed to address new research priorities;[7] and others will be closed. Because we do not yet know if and how the current set of

7 Upon approval of the GCP strategy and research priorities document, all activities in the GCP will be aimed directly or indirectly at addressing priority crops and farming systems.

competitive grants (initiated in 2005) will be supported again by the GCP after their official completion date (2008), for the purposes of this MTP no output targets are reported for 2009, and those projects are considered completed. Likewise, it is difficult to anticipate the specific research topics for the new set of competitive grant projects that remain to be identified. As a result, the output descriptions, intended users, outcomes, and impacts for these projects are presented in generic language, based on the thematic areas identified in the call for proposals: http://www.generationcp.org/latestnews/2006_comp_grants_call.pdf.

There are several exciting prospects on the horizon in relation to a project (for which a proposal is currently under development) targeting the genetic improvement of tropical legumes for Africa. Because the probability of success is high and the new grant would represent close to 30% of the GCP's research portfolio in 2007, it is included in this MTP, even though the funds are pending.

In addition, the 2007-2009 period coincides with the transition from Phase 1 to Phase 2 of the GCP, which represents a planned shift in activities away from platform building[8] and towards the application of the platform in plant breeding. This MTP addresses these preliminary plans, anticipated changes, and areas of uncertainty with as much clarity as possible.

8 'Platform building' refers to germplasm characterization, marker development, the exploration and refinement of gene discovery techniques, and the creation of information systems and infrastructure.

Achievements in 2005

2005 Impact Highlights

- Reference sets of germplasm produced for 21 crops and significant progress made in marker development and application
- GCP phenotyping capacity enhanced and refined
- Genetic base of rice increased through systematic introgression of chromosome segments from related species into cultivated rice
- Conserved orthologous markers linked on different species maps, providing the dual benefits of integrating functionality and genomic positions (at least within a crop group) and serves as an important long-term tool for using comparative genomics to identify common genome regions controlling target traits.
- New candidate genes and gene-based markers for abiotic stress tolerance (low-P, aluminium) revealed through genome-wide expression analysis and isolation of QTL
- Inclusive teams established to develop molecular breeding systems, and new molecular breeding systems pilot-tested and refined
- Low-cost assay technologies developed for NARS and small- and medium-size breeding enterprises
- GCP 'knowledge base' under construction, including data templates and repositories, tools for data analysis, and access points for databases
- Web services implemented at several GCP institutions, allowing scientists to access and share data with the global research community
- Software development standards created and GCPWiki launched, now serving as a platform for development of software and sharing of bioinformatics tools and resources
- Capacity building accelerated to full speed: six GCP training courses and numerous other project workshops organised to train NARS scientists in analysis and application of plant genetic diversity, association genetics, DNA extraction methods and data mining tools, project proposal development, and others. Fellowships (8) and travel grants (30) awarded to support NARS scientists research in the themes of the GCP
- Microsatellite marker kits developed for 7 crops, allowing researchers at any lab anywhere in the world to compare the genetic diversity of their germplasm collection to a GCP reference sample.
- "Genetic Resource Policies and the Generation Challenge Programme" published, outlining the international and national policy context within which the GCP functions
- GCP Delivery Strategy developed, defining "users" and "products" in the GCP context and establishing how the GCP will ensure impacts

Subprogramme 1: Genetic Diversity of Global Genetic Resources

1. Progress in genotyping, selection of core samples, marker development and application, and evaluation of whole-genome survey methods

Subprogram 1 is charged with the characterization of genetic resources for the purpose of describing the global genetic diversity in staple crops, knowledge which is critical to crop improvement programmes. Significant process has been made in this activity, which involves first the collation of information on the various germplasm collections (the "composite set") and then extraction of a representative sample ("core sample") of 200-3,000 accessions that best represent the diversity available in each crop. In 2005, core samples were finalized for 21 crops. Major progress was also recorded in systematic efforts to use molecular markers to structure the diversity in germplasm collections that support active crop breeding programs in the CGIAR Centres. The array of molecular markers that have been mastered and implemented is widening. The throughput of genotyping with SSR markers is increasing; several partner laboratories have improved local organisation since the beginning of the activity in 2004. Complementary methods with proven efficiency are now available: DArT as a whole-genome genotyping method is remarkable for its high throughput and low cost, and EcoTILLing is impressive for its simplicity with the use of agarose gels.

2. Molecular characterisation of genetic diversity

This activity has been conducted within several competitive grant projects. For example, a project led by CIMMYT seeks to develop informative DNA markers through association mapping in maize to improve drought tolerance in cereals. The project focuses on candidate genes involved in

carbohydrate and ABA pathways, and plant phenotyping will be conducted in 5 environments across 3 continents. Another project, led by CIAT, explores natural genetic variation; it is developing genomic resources and introgression lines for four AA genome rice relatives and uses SSRs and SNPs to monitor interspecific introgression. The CIAT project is an example of how additional gene sources are mobilised by broadening the genetic base of the pools accessible for recombination and breeding.

3. Phenotyping capacity of GCP enhanced and refined

The phenotyping network under development at Embrapa (Brazil) has considerably optimised access to efficient, coordinated multilocational phenotyping platforms, supporting the evaluation by environment descriptions and drawing experience from advanced physiological characterisation performed in crop-specific projects. This network now works in coordination with the whole plant modelling project led by CIRAD, enhancing capacity in both projects.

4. Genetic base in rice increased

Complementary to the typical crop reference samples under development, the current germplasm base in rice is being widened by the production of novel materials through systematic introgression of chromosome segments from related species into cultivated rice.

Subprogramme 2: Comparative Genomics for Gene Discovery

1. Successful resource leveraging

The assembly and development of specialised genetic and genomic resources have encouraged many players to contribute to this effort, which has mobilised resources from leading institutions and stimulated partners to create and utilise specialised genetic stocks for gene discovery. For example, the rice mutant network has linked multiple laboratories to apply the mutant resources in systematic phenotyping. Currently, the OryGenes DB (http://orygenesdb.cirad.fr) developed at CIRAD (France) has about 56,000 publicly available insertion sequences tagged by FST sequence on the rice genome sequence as annotated by TIGR. As of mid-2005, the OryGenes DB was used to search for knockout inserts in candidate stress-associated genes and had a 22% success rate, providing a treasure trove for extracting mutants of many plant genes.

2. Conserved markers to link different maps

The use of orthologous markers to link different species maps has the dual benefits of integrating functionality and genomic positions (at least within a crop group) and will be an important long-term tool for using comparative genomics to identify common genome regions controlling target traits. Despite initial difficulties, positive progress is seen in the development of conserved markers to link different species (within the dicots and the monocots). We expect progress from the marker projects through use of information being generated by the research community at large and through more extensive international linkages.

3. Genome-wide expression analysis reveals new candidate genes

Positive results are seen from experiments using genome-wide expression as a means to identify candidate genes to contribute to target phenotypes. A large gene expression dataset has been generated using available rice oligo chips from NIAS (Japan) (22K) and the Beijing Genomics Institute (60K) to correlate gene expression with genetic regions expressing QTL or mutant phenotypes. Integration of QTL and expression analyses can be used to narrow the choice of candidate genes and determine the causal relationships between expression and phenotypes.

4. Isolation of large QTL to derive gene-based markers

Progress in the fine mapping and near-isolation of tolerance genes to aluminium toxicity, phosphorus deficiency, and salinity are encouraging. The cloning of the aluminium toxicity tolerance gene in sorghum will hasten the development of elite breeding lines. Markers tightly linked to phosphorus uptake efficiency are being used in a selection programme to combine traits suitable for the drought-prone environments in Indonesia. We can fast-track the delivery of useful genes to breeding programmes to address specific problems arising from stresses that are often associated with drought-prone environments. The availability of such markers will also help build capacity in breeding programmes to apply marker-aided selection.

Subprogramme 3: Trait Capture for Crop Improvement

Subprogramme 3 (SP3) strives to create product-driven teams that span the innovation-to-impact continuum. The particular goal is to bridge the divide between the development of research outputs and their actual use in breeding programmes. Notable progress was made in 2005.

1. Inclusive teams established to develop molecular breeding systems

Subprogramme 3 projects have established strong collaboration across disciplines, crops, and types of institution. For example, the project 'Development of Low-Cost Technologies for Pyramiding Useful Genes from Wild

Relatives of Cassava into Elite Progenitors' brings together scientists in a number of African and Latin American NARS, while the project 'Development of Low-tech, Gene-based Trait Assay Technologies in Rice and Wheat' brings together scientists in a number of African and Asian NARS.

2. New plant breeding paradigms fostered

GCP investments are already driving exciting new approaches to breeding lesser studied crops. 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. Based on the narrow genetic base of groundnut varieties, this approach is likely to have large impacts on groundnut breeding gains.

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

It is important for less-studied crops that we move ahead with whatever technologies are available. For this reason, several SP3 projects focus on simply inherited traits pending the availability of resources for drought tolerance. Thus the proof-of-concept for using synthetic germplasm in groundnut breeding is being carried out via multiple disease resistance, whereas pest resistance is the focus for deploying MAS in cowpea. In both projects, efforts are simultaneously being made to generate the necessary resources for mapping and MAS of drought tolerance.

4. Low-cost assay technologies developed for NARS and small- and medium-size breeding programmes

Good progress is being made in the development of low-cost assay technologies for gene-based MAS of disease resistance in rice and of grain quality in maize, and for linked markers for pest and disease resistance in cassava. These proof-of-concept activities provide essential methodological insights for routine, large-scale marker conversion activities, once GCP gene-based technologies for drought tolerance emerge.

Subprogramme 4: Bioinformatics

The achievements of Subprogramme 4 (SP4) were considerable although not always very visible. Because SP4 is truly a work in progress, there are not many Eiffel Towers to show, but the achievements in domain model development, software development, and the creation of a collaborative environment can all be considered highlights.

1. Development of GCP Knowledge Base started

The GCPWiki serves as an example of the type of infrastructure that is being developed through SP4. GCPWiki provides an environment in which users contribute to the content of the web pages. As such, it allows the joint development of documents and, in the process, the creation of a common knowledge base. Since the system also stores older documents, allows users to compare versions, and easily see which documents have been changed recently, users can have full control over the evolving content. This model has been followed in several SP4 activities and is being promoted in the other Subprogrammes.

2. Software development standards developed

To support all software development, a recommended platform has been selected with respect to language, software development tools, and type of environment (open source). On this basis, a large number of projects have developed applications that will be integrated into a common client next year.

3. Web services implemented

A package for installation within the CGIAR Centres participating in the GCP was developed, training has been provided to technical staff, and many of the Centres have now installed their first GCP web services. These Centres are now ready to make the GCP data available to the GCP and the wider bioinformatics community—a fundamental part of the GCP mission.

Subprogramme 5: Capacity Building and Enabling Delivery

Subprogramme 5 (SP5) registered significant achievements in its three main areas in 2005: capacity building, policy, and the development of a strategy for delivering GCP products.

1. Capacity building and capacity needs assessment

More than 150 NARS scientists participated in GCP training courses or hands-on training within GCP-funded projects. Emphasis was given to building linkages with a selected community of NARS scientists (for example, to provide training to accommodate a specific role in GCP research and delivery) and to strengthening links among partners. Training events were used to find out about the capacities of participants and their organisations to contribute to the aims of the GCP, especially to identify possible roles for them in the delivery chain of GCP products. These opportunities were also used to identify additional training and capacity building needs that the GCP could support under its mandate. As well as fulfilling expectations for training per se, courses and workshops played a significant role in raising general awareness of the GCP, the value of broad research partnerships, and the need to promote tighter linkages between laboratory and field scientists.

Eight fellowships were awarded for short periods of research at GCP organisations, and one PhD fellowship was granted. Approximately 30 travel grants facilitated attendance at GCP-related conferences or helped to build linkages among Consortium scientists. Other activities were conducted in collaboration with other Subprogrammes to promote sharing of technical knowledge generated in the GCP with national programme researchers outside the Consortium, so that the benefits could extend to their institutions.

2. Policy achievements

Protocols were analysed and developed to facilitate germplasm exchange and proper access and benefit-sharing of the derivatives of the Programme, in line with the published policies of the Convention on Biological Diversity and the FAO International Treaty on Plant Genetic Resources. Reports were produced for generic questions of immediate importance to the GCP, and a seminar was conducted to call attention to policy issues influencing the operation of the GCP, especially those related to access to genetic resources and intellectual property rights.

3. A new Delivery Strategy

The newly completed Delivery Strategy,[9] a major milestone for the GCP, describes mechanisms that the Programme will employ to ensure its products reach their intended users (most often 'intermediate' users in the larger value chain of product development). The document defines the users of the outputs of GCP projects (who they are and how they will use these outputs) and establishes that every GCP project will have a product delivery plan in place, developed in coordination with the appropriate set of users of the project outputs. The aim of the Delivery Strategy is to ensure—from conception through implementation to completion of research projects—that GCP products reach the next level of users, who will in turn be able to produce another product in the value chain, linking laboratories to breeding programmes to farmers' fields.

Deviations from 2006-2008 MTP

Subprogramme 1

Despite global improvement in SSR genotyping activities, the multiple partnerships that sustain these activities have slowed their completion, which in turn delayed publication of the first molecular descriptions for tier-1 crops. This situation will be remedied by identifying the reference laboratories best able to perform this type of task.

Use of SSCP as a SNP discovery and survey technique was not assessed. The John Innes Centre has made progress in this area, and the GCP will shortly compare the efficiency of their method with that of EcoTILLing.

The feasibility assessment of mapping genes in the course of breeding has been delayed for some crops owing to a diversity of viewpoints among the partners. Theoretical background work will have to be undertaken to predict the evolution of LD along generations in different situations and to serve as a common reference. The option of mapping the genome using populations managed in situ has not been explored owing to the lack of opportunity.

Subprogramme 2

Exploration of rice oligo arrays as a heterologous gene expression assay for wheat and maize was discontinued. Because maize and wheat arrays are available for experimentation, expression analysis will be done on 'homologous platforms'. Research will concentrate on integrative analysis of expression data from different platforms to infer function of orthologous genes. The assembly and production of special wheat stocks was delayed by the slow clearance of material transferred from collaborators. Production of true-seed tuber mutants was also delayed owing to the need to produce adequate pure seed for mutagenesis. The cowpea EST project was delayed due to infrastructural problems at the principal investigator's laboratory.

Subprogramme 3

A major deviation from the previous logframe is the delay in creating integrated communities of practice. We are still convinced that this project offers excellent opportunities for capturing interdisciplinary synergies and end-user feedback on priorities and outputs. But as this project is relatively large in the SP3 portfolio, the GCP Management Team decided to postpone approval of the proposal until the new SP3 Leader is on board (1 July 2006). The project will still be initiated in 2006.

The first round of competitively funded projects started in January 2006. These projects focus on applying proven technologies, with particular emphasis in orphan crops. All of those projects achieved major progress in 2006, but some started later than anticipated owing to issues in negotiating subcontractor arrangements and transferring funds.

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

Subprogramme 4

This SP produced all foreseen outputs on time. In some cases the impact of the output was smaller than anticipated, however. Output 4.1.3, 'GCP repository is created and populated with available GCP datasets' was realised, for example, but the number of available GCP datasets proved very low because of unclear communication in earlier GCP projects concerning data availability requirements. All new GCP contracts for projects that generate data explicitly state the requirements for data availability. Output 4.1.6, 'Use cases are developed and documented in accessible databases', anticipated the emerging requirements of users and changed its scope accordingly. It was reformulated as 'GCP use case collaboration and software engineering management are organised', and it was achieved with great success. It now provides, among other things, the open-source environment and concurrent versioning system used by several GCP software development projects.

Subprogramme 5

Subprogramme 5 has evolved rapidly since the beginning of the GCP and continues to accommodate emerging elements needed for the GCP to succeed. For this reason, small modifications will be made each year to the SP5 logframe and workplan to guarantee completion of expectations, respond to lessons learned, and implement new ideas. All of the well-defined output targets in the previous MTP were achieved as planned, although several outputs and output targets were still undefined. In this MTP, the SP5 logframe has been reorganised for the sake of clarity, coherence, and precision. It now closely reflects the SP5 vision and clearly indicates the mechanisms by which it will provide benefits within and outside the Consortium. The definition of new outputs and the description of new output targets will facilitate the organisation of activities and attainment of objectives.

Highlights of 2007 Portfolio

2006-2007 Targets

- Reference germplasm sets and sampling methodologies refined and phenotyping capacity within the GCP inventoried and enhanced, facilitating identification of favourable genes and alleles through association studies
- Potential of admixture mapping explored through pilot studies in whole-genome typing in rice and sorghum, two genomic information-rich crops, ensuring value capture of sequence information
- New alleles introgressed through wide crosses using wild relatives (in crops to be determined)
- QTL data from multiple sources consolidated with gene expression data
- A set of 10-12 genes corresponding to regulatory components of drought tolerance/water use efficiency investigated for their orthologous relationships among crops, and their sequence polymorphism assessed in a sample of 300 reference accessions for each crop
- Universal markers developed for four legume crops to provide a platform for comparative genomics in the legumes
- Marker-assisted breeding schemes for drought tolerance further tested and refined
- Communities of practice for MAS formed and applying GCP outputs in their breeding programs
- Software developed and deployed among GCP researchers for sampling germplasm and processing micro-array and mapping experiments
- 'Plug-ins' available for download by GCP scientists to access databases that are part of GCP information network/platform
- NARS 'centres of excellence' established and offering training courses (1 course per centre) for scientists in the region in genetic diversity of genetic resources, advanced genomics for gene discovery, phenotyping, marker-assisted breeding, and/or bioinformatics
- Marketing Strategy for GCP product distribution developed
- Ex-ante impact analyses conducted and used by GCP Management in strategic decision-making

Subprogramme Highlights

Subprogramme 1: Genetic Diversity of Global Genetic Resources

Most activities that will begin in 2007 will refine the information and methods generated so far. A methodology will be developed for efficient resampling of the genetic diversity in large collections after a first round of characterisation, making the best use of all existing information. A detailed survey of allelic variation at candidate genes will be undertaken across several crops to: (1) build expertise in the GCP for efficient transposition of information between crops; (2) initiate a specific GCP database on functional diversity; and (3) link the GCP with new partners—some with capacities for in-depth analysis of biological pathways and others with high data production capability. In this way, GCP members and partners will gain better access to proper genotyping capacities. The phenotyping component will be augmented by an inventory of the capacity accessible to the GCP, which will identify options in relation to specific crops, protocols, regions, and costs. Use of this capacity for phenotyping reference materials will be facilitated by an ad hoc support service.

Together these activities will facilitate identification of favourable genetic factors through association studies. New projects that compare molecular and phenotypic traits among cultivars are expected from the ongoing competitive grant cycles or from a potential project on four tropical legume species. Pilot studies that involve whole-genome typing will be implemented in rice and sorghum to explore the potential of admixture mapping. Choosing two of the most advanced species in terms of genome sequence availability ensures capturing the value of the sequence information, or future connection with it. In rice, 1,500 SNPs covering the genome will be monitored among 900 accessions with emphasis on Indica-Japonica derivatives. In sorghum, over 1,000 DArT markers will be evaluated, with emphasis on populations that feature introgression between cultivated and wild forms. The most useful markers will then be sequenced for anchoring the information onto the genome sequence, expected soon. A new activity selected through the ongoing competitive call will address another case of introgression of new alleles: from wide crosses using wild relatives.

Subprogramme 2: Comparative Genomics for Gene Discovery

Most SP2 projects have reached the mid-point. Project investigators agree that more attention should be given to the systematic consolidation of QTL data from multiple sources with expression data (if available). In response, SP4 has commissioned research over 2006-07 to provide analytical support for data analysis and integration, to bring out the benefits of combining datasets across projects.

Under the sponsorship of SP1 and SP2, a new project called 'A Dataset on Allele Diversity at Orthologous Candidate Genes in GCP Crops (ADOC)' has been initiated. The GCP plays a unique role in this project by supporting a global approach with parallel

components in a wide range of crops. The project, coordinated by Agropolis, involves 8 institutions/labs and 11 scientists. The project investigates the allele diversity in a common set of genes with putative roles in drought stress response in seven crop species. A set of 10-12 genes corresponding to enzymes involved in sugar metabolism, or regulatory components of drought tolerance/water use efficiency, will be investigated for their orthologous relationships among crops, and their sequence polymorphism will be assessed in a sample of 300 reference accessions for each crop. This reference germplasm, derived from selection after SSR genotyping in SP1 and intended for drought-related phenotyping in complementary projects, will allow the association between observed polymorphism and trait variability to be tested. The project and the resources derived from it will allow the GCP to quickly capture the value of results obtained in the most advanced genetic studies with regards to drought tolerance. It will enable the production of scientifically coherent sets of (ortho)allelic diversity data with high information content and wide scope for application and impact. The project will also facilitate collaboration with partners with high-throughput (HTP) genomics facilities (such as CNG, France) and attract partnership with advanced research groups interested in particular biological processes, metabolic pathways, and gene families.

As indicated in the introduction, a new set of projects targeting tropical legume improvement might be initiated soon. Although the initiative is in the planning stage, active consultation with key players in the legume genetics and breeding community has resulted in a framework that focuses on improving the productivity of groundnut, common bean, cowpea, and chickpea for drought-prone environments in Africa and South Asia. For each of these commodity-based projects, the GCP will explore and identify useful genetic diversity in the rich germplasm collections maintained at CGIAR Centre genebanks, generate genomic resources and the needed genetic knowledge on target traits (with an emphasis on stress tolerance), and apply the knowledge and tools to modernise legume breeding. To link the projects, a cross-cutting project on universal legume markers for the four crops will provide a comparative genetic platform that will benefit legume breeding programmes in the near and long term.

Subprogramme 3: Trait Capture for Crop Improvement

As in SP2, in SP3 most projects have reached their mid-point. The ongoing commissioned projects employ various approaches to develop a better understanding of and better methods for incorporating complex traits, including evaluation of high epistasis and genotype-by-environment (GxE) interactions, MAS simulation and the development of decision-support tools, and marker development for more efficient breeding.

This Subprogramme will initiate several new activities in 2007. As agreed at the GCP start-up meeting in Wageningen in 2003, the budget allocation to SP3 is proportionally increasing over time in relation to the other Subprogrammes. The GCP's second call for competitive grants, opened in February 2006, contains two 'research thematic areas' that fall directly under SP3's objectives. One research thematic area is the identification of new, or refined, traits associated with crop drought tolerance (Output 6 in the SP3 logframe). The other research thematic area will apply MAS to improve drought tolerance in a target crop (Output 14). Both will start on January 2007.

SP3 will play a key role in the implementation of the GCP strategy (discussed above), and two large commissioned projects to begin in 2007 are the 'flagships' of the strategy. Those projects, one in rice and the other in sweet potato, will employ a multidisciplinary research approach to take advantage of existing resources (germplasm, screening methodologies, markers, and others) that are available for specific crops, to demonstrate that significant genetic gains can be obtained in a few years in well-defined farming systems in target environments. Another newly commissioned research activity starting in 2007 is the establishment of molecular breeding communities of practice. These communities of practice will play a critical role in the GCP by 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.

If the special project on tropical legumes is approved, it will imply a new set of activities in SP3, targeting the genetic dissection of selected traits for biotic stress resistance (Output 4) and drought adaptation and related traits (Output 5) for groundnut, bean, cowpea, and chickpea. Though not a major activity in the first year of the project, the application of modern breeding to those legumes (Output 17) will increase in importance and investment over the life of the project.

Subprogramme 4: Bioinformatics and Crop Information Systems

The focus of SP4 will change from building basic infrastructure to creating products. Current activities will not change too much in terms of organisation and subject matter, but results will become more visible to GCP scientists. An example is Output 4.7, in which an Integrated GCP Information Platform is created. So far this activity has concentrated on selecting appropriate technology and creating beta versions of applications. Soon it will result in the production of a client system that can be downloaded by GCP scientists. They can install it on their computers, 'plug in' the software already developed in the GCP, and access all databases that are either available as web services or maintained locally (provided they follow GCP standards for structure and access). This change in focus is also shown in Outputs 5 and 6 of Theme 3, where active support will be given to scientists in the other Subprogrammes for activities identified as paramount and/or problematic (for example, sampling germplasm and processing micro-array and mapping experiments).

A slight sideline that is implemented this year is Output 4.10 'ICRISAT LIMS installed and implemented at the Biosciences Eastern and Central Africa (BecA) facility and IITA-Ibadan'. This relatively small activity adds value to investments made in the LIMS of ICRISAT and strengthens the capabilities of BecA/IITA to participate in GCP activities.

Subprogramme 5: Capacity Building and Enabling Delivery

A number of SP5 activities will continue as implemented. These include the Fellowship Programme, the Travel Grant Programme, the contribution to special conferences, training courses based on the content of the technical Subprogrammes, and the construction of important resources related to policy (intellectual property rights, information and germplasm exchange, access and benefit-sharing, and so forth).

New activities in SP5 are: (1) establishment of a professorship in molecular breeding at the University of Kwazulu-Natal in South Africa, to supervise a substantial number of PhD candidates in plant breeding, selected in collaboration with the GCP to work in regions and projects of interest to the GCP; (2) support to competitive projects in developing and implementing delivery plans, through the identification of expected products and corresponding users and their capacity needs; (3) a Mini-Grants Programme to fill gaps in small equipment or consumables at collaborating NARS, which are often urgently needed for success in their engagement with the GCP; (4) the development of a Strategy for Product Marketing and Distribution, as a complement to the Delivery Strategy, to guarantee that the GCP reaches users; (5) specialised training courses at selected centres of excellence identified in the different regions; (6) translation of training and reference materials, in the interest of reaching out as far as possible to ensure the GCP's impact; (7) the Genotyping Support Service, a means to provide support to NARS in the production of suitable marker data and subsequent data interpretation; (8) technical backstopping missions by expert researchers to supply on-site support to NARS involved in ongoing GCP research; and (9) socioeconomic studies to establish a baseline for impact assessment and guide strategic decisions in the GCP.

Alignment with CGIAR System Priorities

The GCP has several means of establishing and maintaining its focus, relevance, and applicability. Chief among those are the CGIAR System Priorities for 2005-2015. All activities in the GCP fulfil one or more System Priorities. The most important for the GCP, however, is Priority Area 2: *Producing more and better food at lower cost through genetic improvement*. This Priority Area could easily substitute as the overall objective of the GCP. GCP activities that fulfill other System Priorities nevertheless contribute to the overarching goal of Priority Area 2:

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
5d. Improving research and development options to reduce rural poverty and vulnerability

In the project narrative section that follows, the Subprogrammes of the GCP provide a detailed analysis of how their outputs full these System Priorities.

Collaboration: New and Existing Partnerships

The GCP, like the other CGIAR Challenge Programmes, was created to yield large impacts in the short term through thematic, multidisciplinary research approaches involving a wide range of research, breeding, and delivery organisations. Every activity in the GCP, therefore, is a collaborative exercise conducted by carefully chosen partner institutions with complementary expertise.
In the project narratives that follow, partnerships within each Subprogramme are described in detail. A complete list of partners can be found in Appendix A. Special mention must to be given to collaborations with the other Challenge Programmes: HarvestPlus, Water and Food, and Sub-Saharan Africa. Though not currently engaged in research together, the GCP has active collaborations in communications, research planning, and impact assessment approaches with all three of the other Challenge Programmes. Discussions are underway about specific collaborative projects that could be undertaken in the Sub-Saharan African region, as all four CPs have activities there. The GCP expects these and other interactions with the CPs to increase in the next few years.

Another notable new partnership is that between the Global Crop Diversity Trust and the GCP. Our programmes go hand-in-hand; the Global Crop Diversity Trust was created to ensure the conservation and availability of crop diversity for food security worldwide, and the GCP is the global platform for accessing and applying crop genetic diversity in plant breeding programmes. Together, we link genebanks to farmers' fields. A memorandum of understanding was recently developed to establish the relationship between these two programmes, and collaboration will begin in 2007.

To avoid spreading resources too thinly and diluting its impact, the GCP forms smart partnerships that achieve the most value for funds with the highest likelihood for rapid, high-quality results. *The GCP funds outputs, not inputs,* and so seeks partners who can do the best work for the best price. Another reason for the GCP's creation, however, is the power of this model to increase the capacity of research institutions, especially in developing countries, to conduct and apply innovative research. Therefore, all GCP competitive projects require the participation of a NARS institution, and significant resources have been set aside in SP5 to ensure that NARS scientists involved in GCP projects receive specific, hands-on training. Other projects are aimed at evaluating NARS' capacity to participate in and apply GCP research.

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 the GCP and at the core of Subprogramme 1 ('Project 1' in the MTP). Through our network of Consortium members and partners, vast germplasm collections are available to the 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 of more than 20 crops in genebanks around the world, highly efficient HTP molecular screening techniques must be applied to genotype suitable representatives of the collections. Appropriate methods to characterise germplasm subsamples for traits such as drought tolerance also need to be developed and applied 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—the operational portion—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/haplotypes). This component, which combines the comparative description of molecular polymorphisms and phenotypic variation and the study of associations, thus rests on complementary modules. These modules must be coordinated for the best global efficiency and must be managed in the most open fashion to capture the interest and enthusiasm of national research programmes. The fifth component looks at new approaches for relating genotype to phenotype by connecting genetic analyses directly to breeders' activities and farmers' practices. Accordingly, activities in SP1 are organised under the following themes:

- Theme 1: Creation of an improved understanding of the structure of the diversity for the major world food crops.
- Theme 2: Development of a range of flexible HTP genotyping techniques accessible in reference laboratories.
- Theme 3: Establishment and implementation of a scientific and organisational framework to describe tolerance to drought.
- Theme 4: Identification of favourable genetic factors—specifically, potential genes (or genome segments) and superior alleles (or haplotypes) through association studies.
- Theme 5: Development of novel populational approaches for relating genotypes to phenotypes.

Subprogramme 1, along with the other Subprogrammes of the GCP, contributes to CGIAR System Priority 2, *Producing more and better food at lower cost through genetic improvements*, and specifically targets Priority 2b, *Improving tolerance to selected abiotic stresses*. As Subprogramme 1 is also specifically concerned with characterising plant genetic diversity, it also contributes to System Priorities 1a and 1b, *Promoting conservation and characterisation of staple 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 for the 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/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 acquiring this knowledge. The markers chosen for systematic characterisation are essentially SSRs (or micro-satellites), 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 that crop. For operational reasons, these activities are split into two sets,

corresponding to crops with the greatest advances in molecular tools ('tier-1 crops': rice, maize, sorghum, wheat, barley, cowpea, chickpea, common bean, cassava, potato, and *Musa*) and to those with fewer advances ('tier-2 and -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, seed 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 of these activities are 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. This output alone has high potential to improve the efficiency of breeding activities worldwide.

Maize, because of its allogamous breeding system and associated capacity of rapid evolution, receives specific emphasis in order to refine the description of races outside their continent of origin and to trace maize population dynamics along migrations in Africa and Asia. This research is the focus of a competitive grant led by CIMMYT.

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

As a complement to this integration effort, a methodology for resampling diversity in large collections is under development to enable the best use of current information in further tapping diversity in the collections. Rice and chickpea are used for this activity. An additional molecular description of 1,000 accessions of each of these data-rich crops will make it possible to assess the efficiency of algorithms for iterative selection within data-sparse collections.

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

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

Genome-wide surveys with anonymous markers aim at locating useful genes on the basis of LD analysis, be it in segregating progenies of simple hybrids or more complex populations. One potential technology is DArT, which is being validated with various species, such as rice, sorghum, and wheat (for which arrays exist), as well as cassava, *Musa*, and coconut (for which new arrays are being developed within a commissioned project handled by Agropolis with DArT Pty Ltd of Canberra, Australia, as the main actor). The technology has proven highly efficient in throughput and cost. The diversity revealed through this activity is being compared 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. EcoTILLing is being tested as a technology for SNP discovery under the leadership of IRRI. Results are very promising in rice, and validation is in process on sorghum and in *Musa* (as a low polyploid crop). This activity will provide access to a cheap technique to investigate potential functional polymorphisms. ICARDA leads an activity on barley that focuses 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 the adaptive value of molecular variation.

Allele resequencing is the current preferred approach when HTP sequencing is possible, providing full-length sequence variation for the target candidate genes. In conjunction with SP2, an activity is being initiated through a partnership with CNG and Agropolis that involves three laboratories for identification of orthologous genes and five laboratories for providing crop-specific information and materials. A database with detailed information on allelic variation among seven crops is being generated and will serve for planning pertinent phenotypic evaluation with a view to future association studies.

In addition to the activities just mentioned, a support service has been established (in conjunction with SP5) 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. (This output appears in the SP5 logframe.)

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

Proper phenotyping requires high-quality facilities and contributions from physiologists, modellers, and breeders, with specific modelling support for: (1) quantification of traits and integration of their impact on yield, (2) genetic analysis of adaptive traits, and (3) characterisation of target environments.

Embrapa is upgrading 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 reference samples of cereal crops but will gradually extend to more crops. The network of environments covered by Embrapa will be expanded to other sites in Latin America and Africa. Concurrently, a modelling framework that characterises environments for several target regions for the major crops using long-term daily weather data is being developed, under the coordination of Agropolis. These characterisations include 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 results will be summarised by clusters 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 in maize and rice.

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

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. The main expected outcome is the identification of genetic factors or genome segments that contribute favourably to trait elaboration and can be incorporated into breeding progenies through MAS. This resource will serve all breeders working on the crops under consideration. Theme 4 builds on the many activities planned under Themes 1, 2, and 3 that yield genotyping and phenotyping data on the same materials. This theme also intersects with SP2, which highlights the best candidate genes; together, SP1 and SP2 deliver products to SP3 for use in breeding. As mentioned, activities under this theme represent the core of the whole GCP, and they will increase in importance during the period of this MTP.

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. 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.

The current call for competitive grant projects includes a specific call for projects that will improve methodologies for validating the genetic basis of marker-phenotype associations. The project (to be selected) should help identify a good case study.

There are also prospects for applying the Theme 4 rationale to four legume species in a special project for which funding is pending. Under this project, reference samples of groundnut, common bean, cowpea, and chickpea would be distributed and planted in diverse environments and their reaction to major stresses evaluated. The resulting information would serve as the basis for identifying markers and developing new recombinant populations for breeding varieties better adapted for Africa.

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

The identification of useful genes or chromosome segments involved in traits of agricultural interest rests on the search for co-occurrance of molecular tags with desired values for target traits. Their identification is commonly undertaken by 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 (few repetitions over space and still fewer over time); and (3) it is not easy to use the materials monitored in this way, and they are seldom incorporated in the breeding process. Theme 5 creates alternatives to current options.

One alternative is to use materials and evaluation data that are regularly produced in mainstream breeding activities. For example, a wealth of information is produced on collections of potential parents, on advanced breeding materials going

to multilocational trials, and on elite materials close to release—yet little of this information is used efficiently for deriving genetic information that could enhance the global understanding of genotype-phenotype relationships. To use these materials, there must be significant LD that correlates variation in genetically linked genes/markers. Under the leadership of IPGRI, the general diversity structure and the level of LD are being assessed in breeding materials of potato, cassava, yam, *Musa,* and coconut, to assess feasibility and propose potential case studies.

LD can exist among landraces if they have gone through significant bottlenecks in their history. Domestication itself may have induced sufficient bottlenecks to induce LD in some species. This prospect is being monitored in rice by Cornell University with emphasis on genome regions bearing resistance to bacterial leaf blight in 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 in rice by a group led by IRRI, with emphasis on the Indica-Japonica differentiation, and in sorghum by Agropolis, 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.

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. Another activity aimed at introgressing new alleles from wide crosses using crop relatives will be identified in the ongoing call for competitive grant projects.

Project 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, and so forth) for comparative diversity studies; (3) accurate diversity analysis, including analysis of geographic patterns of diversity, to highlight complementarity and mutual dependance between political entities; (4) germplasm reference samples, with an increasing body of information attached; (5) a database of multispecies allelic diversity at candidate genes potentially involved in 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 with the mandate for the crop. Embrapa and CAAS (China) could genotype accessions from Brazil and China, respectively, without obtaining authorisation for sending out the materials; this capacity is convenient, but moving germplasm outside their borders remains a major difficulty.

The competitive grant process fostered new collaborations between GCP members and impressive new partners. For example, the project on 'Allele Mining Based on Non-Coding Regulatory SNPs in Barley Germplasm' assembles the Australian Centre for Plant Functional Genomics Pty Ltd; University of Adelaide (Australia); NIAB (UK); the University of Udine (Italy); ICARDA; and Tyshreen University (Syria). Several of these organisations bring innovative approaches inspired by recent developments in human genetics. Other competitive grant projects facilitated the creation of wide networks of NARS, as in the proposals on genetic diversity and association studies in maize, with KARI (Kenya), SIRDC (Zimbabwe), the Department of Agriculture (Indonesia), the NMRI (Vietnam), the Sichuan Agriculture University (China), and NSFCRC (Thailand). Activities on rice involve Fedearroz (Colombia) and ICABGRRD (Indonesia).

The project for validating new markers links the best players in marker technology with NARS, whose researchers receive training in the technology. For instance, in the project to validate DArTs as a genome-wide molecular characterisation technology, scientists from the Rayong Field Research Station (Thailand) and the Coconut Research Institute (Sri Lanka) came to DArT Pty Ltd in Australia for training, together with Agropolis trainees. Activities aimed at integrating markers into the conventional breeding process 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 research groups on crop and whole-plant modelling, such as the University of Queensland and CSIRO in Australia.

A special mention goes to the ADOC initiative, supported under SP1 and SP2, which aims at organising the GCP for quickly transposing the most recent results in a plant species to all GCP crops. 'Gene champions' such as the Australian National University, CNRS (France), and 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 knowledge and resources; and the CNG contributes high sequencing power. ADOC participants are developing a GCP database on allelic diversity on key genes across GCP crops, which will serve to design association analyses to inform breeding strategies .

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 by 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 the development of practical applications of these new tools for agronomic improvement requires a level of integration that is often difficult to implement in a single discipline. A main objective of Subprogramme 2 ('Project 2' in the MTP) is to provide the scientific and collaborative environment to enable gene discovery as well as applications.

Specifically, SP2 aims to (1) develop cross-cutting research platforms for efficient applications of genomic tools and knowledge for deciphering genetic control of complex traits and (2) identify genes to alleviate targeted problems in the most efficient manner, by pooling resources and expertise. To realize the potential of these new tools, it is also essential to build the capacity to apply them and create the delivery chain that will move results into practice. Successful demonstration of how these tools are used to solve problems in a few targeted cases helps to develop the roadmap for broad applications.

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

Since the inception of the GCP, there has been continued growth in sequence information across all plant species. A high-quality rice genome sequence is now complete, and maize and sorghum sequences are expected in the near future. Multiple genome-wide gene expression platforms in plants are available. It is increasingly feasible to use gene *content* (that is, sequence information) rather than gene *order* as the entry point to identify orthologous genes and determine their functional relationships between species. Furthermore, the power of SNP haplotypes and association genetics to identify functional genes has been well demonstrated in studies of human and medical genetics. This Subprogramme strives to absorb this new knowledge and adopt new approaches where appropriate.

Subprogramme activities are organised under the following four themes in the MTP Logframe:

- Theme 1: Assembly of genomics and germplasm resources through consolidating and developing specialised genetic stocks.
- Theme 2: Develop comparative maps within and across species and develop framework genetic markers for target crops.
- Theme 3: Assign genes and pathways to phenotypes through the convergence evidence of genome variation, expression patterns, and phenotypic data.
- Theme 4: Validate genes and pathways through evaluation of under- or over-expression constructs or variants (induced or natural) of the target genes.

The activities of this Subprogramme support CGIAR System Priorities 2a and 2b. The results from Subprogramme 2 outputs include genetic resource and tools development (genetic stocks, markers) that will enhance breeding efficiency and lay the foundation for efficient gene identification. Within the context of GCP, Subprogramme 2 outputs will feed into the pre-breeding activities of Subprogramme 3. The outputs cut across crops and ecosystems and can contribute to any breeding programme around the world. In particular, a majority of the outputs involve improving the understanding of abiotic stresses (e.g., drought, salinity, problem soils) that exactly align with System Priority 2b on biotic stresses. Together, these outputs, when applied to crop improvement programmes, will 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

A bottleneck in the development of stress tolerance in crop species is an inadequate understanding of the genetic basis of stress tolerance. The complexity of the stress response means that a multipronged approach is needed 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 the use of comparative

biology. This first theme (assembly and production of specialised genetic resources), recognises the importance of mutants, isogenic lines, cytogenetic stocks, and chromosome substitution lines as tools for identifying gene function, but with few exceptions, little of this specialised germplasm is available to support gene identification and confirmation in most crops.

The GCP has played a catalytic role in responding to this problem 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, increasing the likelihood that more specialised stocks of other crops will be shared or produced. Taking advantage of existing rice mutant collections around the world, the GCP supports the systematic phenotyping of rice mutants with relevance to stress tolerance, thereby channelling many existing resources to serve GCP objectives. 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.

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

The generation of common markers and consensus maps across species will provide a framework for leveraging information across crop species, some with advanced molecular information available and others with valuable phenotypes. The GCP's investments in mapping orthologous genetic markers and the genomic investigation of *Musa* represent a modest attempt to achieve this goal. Building upon these initial investments, more focused activities are planned through a new set of projects: the ADOC project on allelic diversity of orthologous candidate genes and the proposed cross-species marker project for legumes. 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

The third theme—analysis of genetic pathways—emphasizes the application of genome-wide tools such as gene chip technology to reveal the causal relationship between gene expression patterns and phenotypes. The results generated by GCP-sponsored projects may be small compared to global research efforts, but a unique feature of the GCP research is the use of agronomically relevant experimental conditions and genetic materials. For this reason, genetic knowledge generated from these experiments can be used by researchers and breeders in pre-breeding activities in SP3.

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 the fourth theme of this Subprogramme aim to identify genes with useful functions, which can be delivered to breeding programmes. The cloning of the gene that confers tolerance to aluminium toxicity in sorghum has laid the foundation for cloning other tolerance genes in cereals. Considerable progress is also being made towards cloning 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.

Observations

Outputs from these themes are geographically neutral. The primary users of outputs from Subprogramme 2 will be researchers, plant biologists, and breeders. Uptake of outputs by researchers and breeders is expected to expand the capability and increase the efficiency of national breeding programmes, an outcome that extends beyond the immediate users.

At the global level, the resources and knowledge of gene function generated by SP2 are expected to be taken up by the plant biology community. This knowledge, when applied to a range of crop systems, can increase the prospects for finding new genes from diverse plant species.

Intellectual property protection in information and genetic resources with strong commercial interest may impede the dissemination of knowledge and new tools. Although the GCP requires completely open access to results and resources generated by the projects it funds, issues of prior intellectual property rights may deter total access and sharing. This issue should be addressed by the appropriate government authorities to enable faster and freer movement of materials.

Institutional commitment to produce and use specialised genetic stocks may also influence progress. The GCP has stimulated interest in the production of selective genetic resources, but further propagation and dissemination of such genetic stocks must rely on institutional investment. However, 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 CGIAR System Priorities. The key resources and tools produced are specialised genetic stocks (e.g., mutants and advanced backcross lines), gene expression assays, cloned genes to improve specific traits (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 the GCP, but many outputs will be useful across the global research community, wherever there is interest in applying genomics to agricultural improvement. While a majority of SP2 activities aim at improving the understanding of complex traits, several projects will produce advanced breeding materials as key outputs to alleviate problems in resource-poor areas in Asia (for example, rice tolerant to phosphorus deficiency in Indonesia) and Africa (for example, maize tolerant to aluminium toxicity in Kenya). These outputs are global in nature but achieve specific impacts on a regional scale.

Partnership

As with other Subprogrammes, partnerships in SP2 often involve three generic sets of players: NARS, ARIs, and CGIAR Centres. In addition to the Consortium members, a large number of universities and public research institutions are involved SP2 activities. Under the theme *Developing genomic and specialised genetic resources*, partnerships include institutes and laboratories that have rich specialised genetic stocks and the ability to generate new resources or knowledge from these stocks. These include major wheat genetic research centres working with CIMMYT to assemble wheat stocks; laboratories working on rice mutants from the International Rice Functional Genomics Consortium; the University of Geneva and CIAT for legume mutants; and the Scottish Crop Research Institute, the Hebrew University of Jerusalem, and CIP for producing true-seed mutants of potato. TIGR, Hyderabad University, IITA, and ICRISAT combine the genetic resources and sequencing capacity to produce stress-response ESTs for cowpea and pearl millet. In developing cross-species marker resources, a network of laboratories led by CIP and CAAS are involved in designing and testing conserved orthologous markers across different crops. Under the *Musa* frame map construction project, NIAS with its strong sequencing and informatics capacity coordinates a collaboration among laboratories active in *Musa* research, including IPGRI-INIBAP, CIRAD, Embrapa, University of Leicester, and IEB.

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 analyses of tolerance to aluminium toxicity in sorghum and maize and other cereals span multiple disciplines in comparative genomics, soil nutrition, physiology, and breeding. These activities involve Cornell University, Embrapa, and Moi University. Another example of bringing resources and technical expertise together is shown by the project on developing tolerance to salinity and phosphorus deficiency in rice. In this project, IRRI coordinates the collaboration with: the University of California-Davis; the University of California-Riverside; JIRCAS (Japan); Dhaka University; ICABGRRD, the Agricultural Biotechnology Research Institute (Iran); and NIAS. These institutions have combined expertise in trait and agronomic analysis, gene expression, transgenics, and breeding. Other trait-based projects feature similar collaboration covering the range of expertise needed. In the new initiative on legumes, we also aim for complementary expertise in the development of genomics resources, marker validation, mapping, trait analysis, and breeding. A detailed list of partners is provided in Appendix A.

In summary, the composition of partners in individual projects of this Subprogramme demonstrates successful leveraging of institutions and researchers who are traditionally not oriented to agricultural research, thus representing a substantive gain in the research capacity of the GCP (and by extension CGIAR Centres and partners). With this large pool of intellectual capital in place, further gains can 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 linkages 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 linkages across the community of plant breeders who help orient and set priorities within the GCP, and who are also heavily involved in the evaluation, validation, and refinement of molecular breeding technologies generated by the GCP. The Subprogramme is equally important in building linkages among CGIAR Centres, NARS, and small and medium breeding programmes.

The priorities of SP3 are in total 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 cereals 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 validate gene function and interaction identified in SP2 by testing the genetic gains achieved from using target molecular markers in new genetic backgrounds. Finally, a range of facilitating technologies, such as simulation, modelling, and decision-support tools, are essential for rapid and widespread adoption of molecular breeding technologies among conventional breeding programmes. From the GCP's perspective, these are critically important supporting activities. They will substantially influence how fast and how well the outputs of SP1 and SP2 are taken up and make an impact.

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, identification, and/or validation of molecular markers for target traits to increase plant breeding efficiency.
- Theme 2: Development and evaluation of novel breeding or molecular technologies to better serve modern plant breeding.
- Theme 3: Application of molecular markers in breeding programmes.
- Theme 4: Multidisciplinary approaches towards specific crop improvement under target environments.

Many activities in this Subprogramme are highly interdependent and cover a wide range of research topics: for example, dealing with the challenges of complex traits with high epistasis and GxE interaction; building holistic simulation and decision-support tools; evaluating transgenes in multiple genetic backgrounds, crop species, and mega-environments; developing user-friendly markers for breeding programmes; and validating new technologies for routine application in NARS and community support labs. Although diverse and complementary, SP3 activities are clearly oriented towards the discovery, validation, and application of molecular markers for plant breeding.

Finally, the creation of effective, systemically integrated communities of practice offers excellent opportunities for capturing interdisciplinary synergies and user feedback on priorities and outputs. Such communities foster strong technology uptake and product delivery pathways.

Impact pathways

The overall objective of SP3 is to apply the new-gene based knowledge generated by SP1 and SP2 across a wide range of crops (cereal, legume, and clonal crops). This knowledge must be rapidly converted by SP3 into robust molecular breeding tools and approaches for abiotic stress tolerance and related traits, and their evaluation in diverse germplasm.

Theme 1: Characterisation of segregating populations and identification and/or validation of molecular markers for target traits to increase plant breeding efficiency

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. One 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, such as the effect of the cytokinin synthesis gene on leaf water retention and related traits during drought. Another output targets the evaluation of cowpea material for *Striga* resistance (Output 3). This project has already identified a series of AFLP markers to discriminate among the different races of *Striga* that parasitize cowpea. These AFLP markers are now being converted into SCAR markers to facilitate rapid identification of pathogen diversity in the field. For both projects, the major outputs should be the identification of molecular markers linked to genomic regions of interest to improve breeding efficiency. The same objective, via a different approach, has been pursued under the leadership of scientists at Embrapa, who are undertaking marker-assisted introgression breeding in groundnut using synthetic amphidiploids (Output 2). A range of synthetic amphidiploids have already been created with putative resistance to diseases, which will be used for proof of concept while new drought-tolerant synthetics are

being generated and/or identified. Another output (pending funding) is the genetic dissection of segregating germplasm in groundnut, bean, cowpea, and chickpea to help identify new molecular markers (Outputs 4 and 5). The molecular markers identified as outputs of those different activities will be applied in breeding programmes (Themes 3 and 4).

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 first output is the development of low-cost, gene-based marker technologies for virus and pest resistance in cassava (Output 7). During the first year of the project, a RAPD marker for mosaic disease (CMD) was converted into a SCAR marker for HTP, low-cost MAS applications. Emphasis has now shifted to the development of markers for resistance to pests and diseases with the phenotyping evaluation of mapping populations at NARS in Brazil, Uganda, Ghana, and Nigeria. Low-tech, gene-based trait assay technologies are also being developed in rice and maize. The development of improved rice markers for bacterial blight resistance is conducted in collaboration with China, the Philippines, Indonesia, India, and African countries (Output 8). In maize, large-scale MAS to convert well-adapted tropical highland, tropical lowland, and subtropical varieties into varieties of quality protein maize (QPM) has been conducted, and NARS in Africa and Asia are now following this approach. An allele-specific dot-blot (gel-free) assay is being developed, using the rice bacterial blight system as a pilot test.

This research theme also includes a project that is evaluating the genetic gains obtained via a transgenic approach (DREB1A gene introgressed in various genetic backgrounds, Output 9). Multilocational evaluation of transgenic putative drought-tolerant lines of rice, wheat, groundnut and potato constitutes the first output of this topic. Because preliminary results show that impact on grain yield remains limited, and because our knowledge of multiple transgene insertion technologies and tissue-specific stress promoters needs to improve, the evaluation of the transgenic material to improve yield performance under water-limited conditions will be put on hold at the end of 2007.

Theoretical research to improve the development of molecular breeding systems, simulation models, and decision support tools is also conducted under this research theme (Output 10). The aim of this project is to develop some simulation examples that can be extended to other crops and different genetic models. The initial work is based on an existing case study (wheat breeding at CSIRO) to combine known genes (using perfect or near-perfect markers) into single genotypes for use as parents for further field screening. A population genetics model has been developed, focused on the efficient use of marker-based selection in plant breeding, and a case study in wheat has been completed. The QUCim breeding module is now being modified to link with physiological models. The major output of these activities will be novel and more efficient MAS schemes.

Theme 3: Application of molecular markers in breeding programmes

This theme targets the application of markers developed by the GCP (or by others) in breeding programmes via the most efficient approaches. Projects under this theme are currently limited in number, but several activities in this area will be initiated in 2007, and over time these application activities (Themes 3 and 4) should balance the ones in marker discovery (Theme 1) and technology implementation (Theme 2). One current project involves marker-assisted pyramiding of QTL for drought tolerance in rice. Drought-tolerant lines already identified are now being employed in a large-scale backcross programme in China with a high-yielding restorer line. The final objective is to produce rice cultivars with enhanced drought tolerance and water use efficiency.

Another output looks at mapping product development and delivery pathways for new GCP technologies (genomic, transgenic, and computational outputs). A final output, the development of molecular breeding communities of practice, was conceived to strengthen conventional breeding programmes (especially national breeding programmes) in the application of modern plant breeding best practices. This effort will create a smooth flow from knowledge discovery to application, avoid redundancies, and more efficiently meet farmers' demands.

Theme 4: Multidisciplinary approaches towards specific crop improvement under target environments

The projects under this theme serve as the implementing mechanism for the GCP's forthcoming strategy and research priorities. These 'flagship projects' employ the expertise of many research disciplines to develop improved crop varieties for specific target environments. One output aims to apply the wealth of information and recent advances in tolerance to phosphorus-deficient soils in Asian rice varieties to NERICA rice for Africa. This work must be conducted in close collaboration with national programmes in Africa that can use the pre-breeding materials that the GCP will develop. The second flagship project is aimed at improving drought and virus tolerance in sweet potato for Africa by investigating the relationship between heterosis and tolerance to drought. Both projects are in the very early stages of development but will be conducted over the 2007-2009 period covered in this MTP.

Project contribution to international public goods

This Subprogramme uses low-cost, gene-based marker technologies that are already available as international public goods to generate germplasm with enhanced resistance to pests and diseases (for example, cassava that resists mosaic disease, cowpea that is more resistant to *Striga*, or rice resistant to bacterial blight). The Subprogramme also applies these technologies to more complex traits, such as drought and other abiotic stresses, in cereals. The new approaches pioneered in SP3 for molecular breeding, especially in the understudied crops, are international public goods. 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 in 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 regional experience for the benefit of other regions. 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. 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 fungus-resistant groundnut lines to Senegal for local testing and application. The cassava activities under SP3 are a typical tripartite GCP project, involving Cornell University, CIAT, and Embrapa, whose many advanced resources for cassava improvement have important implications for the African partners, including NRCRI (Nigeria), NAARI (Uganda), and CRI (Ghana).

Projects targeting the development and testing of 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.

The new projects to be initiated in 2007 will bring even more highly skilled and well-connected partners to the Consortium and will follow the same partner composition pattern, to ensure that the GCP meets its objectives.

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 stored, managed, analysed, and made accessible to the GCP and the rest of the world as international public goods. How these data can be analysed depends, in turn, on how analytical tools and other information sources are made 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, biometric, 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 the GCP and will provide tools to analyse them. Furthermore, it will link GCP data and tools to global biodiversity and bioinformatics networks.

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 large, given that the ability to dictate the architecture and organisation of existing systems, inside and outside the GCP Consortium, is quite limited. Second, the elements that already exist within the GCP Consortium must meet certain quality standards. The 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. Making data management a local responsibility requires an appropriate level of skills and facilities, however—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. How can the information flow between researchers in the GCP be organised to maintain local curation of data and tools?
2. How can the GCP support local curation of data and tools to ensure that their quality improves to an acceptable standard?
3. How can the 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 the GCP. This orientation does not mean that the GCP is the only beneficiary from SP4 activities, however. The efforts of SP4 will greatly benefit the global biodiversity and bioinformatics community, because the GCP is developing into a major player, providing access to valuable data and tools and developing tools, software, and standards for efficient data exchange and integration.

Subprogramme activities feature extensive collaboration with institutions outside the Consortium to ensure the quality of SP4 products. A good example is the development of standards for exchanging data and accessing data and tools (to address the first problem listed earlier). The Subprogramme works with the global community that will use these standards to ensure that existing standards and protocols are incorporated and to create ownership among users, so that the new standards become widely adopted 'world standards' instead of 'GCP standards'.

Impact pathways

Activities in SP4 are organised by theme, as presented in the MTP logframe:

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

Impact pathways for each theme are detailed below.

Theme 1: 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 the GCP be organised to maintain local curation of data and tools?' The largest theme in SP4 in terms of investment, it aims to create a platform for exchanging information. This platform will have three elements: solutions for data storage, with appropriate levels of access to data; tools to analyse these and other datasets; and an environment allowing users to access data and use tools.

The issue of data storage is addressed by two approaches. The first—a short-term solution—is to store data in GCP templates (usually MS-Excel spreadsheets) that guarantee full interpretability of information. The data in these templates can be made centrally available, via a GCP repository, but can also be maintained locally. Tools to export data in desired formats are made available, and the CGP is sure that the data can be imported easily when the second approach—a long-term solution—is implemented and databases are made available as web services. Web services make it possible to 'wrap up' local databases so that they appear to be part of one system. They can be approached via a common language through the internet. This language is translated by the wrapper into the language understood by the local database, which answers the query. The wrapper translates the output back into the common language. A number of components are involved in implementing this approach: the technology has to be made available and the common language developed; the technology should be implemented by the Consortium members (requiring training); and the technology should be used.

A number of activities and corresponding outputs are related to this theme. The first is the development of the common language, to be achieved by developing 'GCP Domain Models'. This activity involves a wide diversity of actors and requires clear prioritisation over the years. The second output is concerned with training staff and implementing web services technology in GCP member institutions. The third output is a repository for links to the datasets ('yellow pages') or for datasets that are not yet available as web services. The fourth output aims at improving the web services technology and applying it in a number of demonstration cases, to establish the GCP as a relevant player in the international arena. The fifth output is to provide solutions to short-term issues that arise before the web services technology is implemented (for example, to develop small applications for uploading and centrally storing datasets). The sixth and final output is to provide software developers with appropriate methodologies (for example, a platform for simultaneous software development).

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

To ensure the quality of local data curation, several issues must be considered: the bioinformatics capacity of GCP member institutions to support their scientists' work, the quality of the data supplied, and finally the HTP computing capacity needed by GCP scientists, which cannot be supplied by one single institution. With respect to institutional capacity, GCP policy is that Consortium members are now responsible for creating their own appropriate capacity; GCP investment to support development of that capacity was phased out over the past three years. Where the GCP can create synergies for further capacity development, however, these opportunities will be used. The GCP will continue to support the development of specific software needed by all Programme scientists to access bioinformatics tools and data available within and outside the

GCP. With respect to data quality, clearly there is a need for continued emphasis in this Subprogramme on monitoring and improving data quality to ensure that data produced can be applied to crop improvement efforts. Finally, with respect to the computing capacity required to run complex data analysis operations, the creation, implementation, and integration into the GCP toolbox of a high-performance computing facility is a step in that direction.

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

The first three Subprogrammes have needs for data collection, curation, and analysis that SP4 must address for optimal deployment of GCP outputs. Seven activities will yield the outputs to address those needs. The first activity will provide access to gene orthology relationships across species and related paralogy relationships within gene families. The second will create a crop gene expression database that allows scientists to easily find and compare expression data across species. The third output will allow breeders to use markers more efficiently in breeding programmes by integrating existing software into one platform (using web services technology). The fourth output will create an eco-physiological–statistical framework for analysing GxE and QTLxE in abiotic stress trials, which will improve the understanding of the results of phenotyping experiments. The fifth and sixth outputs will support data analysis in SP1 and SP2 by developing methodologies, providing access to information about solutions, and giving bilateral support in the most appropriate way. The seventh output will develop tools for LD-based phenotype analysis.

Project contribution to international public goods

Subprogramme 4 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 involves a wide array of partners, including software developers, biometricians, and end-users of the technology. Examples of partners include: IRRI, CIMMYT, CIP, IPGRI, ICRISAT, ICARDA, CIAT, IITA, Agropolis, ACTG, WUR, NIAS, Embrapa, and Cornell University (within the Consortium); and University of California, Hitachi Software Engineering Co. Ltd., CSIRO, Keygene, ILRI, NCGR, Universidad Autónoma Chapingo (Mexico), and INIA (Uruguay) (outside the Consortium).

IRRI is viewed as playing a major role in technical aspects of software development and domain modeling. 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 to meetings. The role of IPGRI is to make information available and train GCP staff to use new technologies, also involving other partners where appropriate. The other GCP member institutes contribute specific expertise as appropriate; for example, NIAS gives important input for activities related to gene expression; CIP provides useful guidance for GIS applications; ICRISAT contributes biometrical and programming skills; and Cornell University contributors draw on their Genomic Diversity and Phenotype Connection (GDPC) experience.

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 all of the other GCP Subprogrammes, whenever SP5 supports research in a given Subprogramme (for example, through support services, the Fellowship Programme, or other kinds of training and teaching), it contributes to the System Priorities related to that Subprogramme (most often Priorities 1b, 2a, and 2b). In addition, SP5 activities related to facilitating delivery of GCP products, researching international and national policy questions, and conducting impact studies relate to System Priority 5d, *improving research and development options to reduce rural poverty and vulnerability.*

In the GCP, the focus on capacity building stems from the belief that education and knowledge form the basis for development. The GCP actively seeks collaboration with NARS, but in many cases basic infrastructure, research support, and/or training are needed for those partnerships to fulfil their potential. The GCP's capacity to have impact in farmers' fields is directly associated with the capacity of national research institutions to use GCP research products in their breeding programmes. For this reason, SP5 activities aim both (1) to increase NARS' capacity for research collaboration and (2) to

develop mechanisms to ensure that GCP research addresses resource-poor farmers' needs and that research products are applied efficiently in plant breeding programmes to meet those needs.

In this MTP, the SP5 logframe has been reorganised by theme, with the corresponding outputs and output targets. This new organisation reflects what has been learned in this Subprogramme following two years of building the foundation for SP5 efforts, defining parameters, and adapting to GCP needs and opportunities. The logframe illustrates how SP5 activities interact with each other and the research activities of the other Subprogrammes to make real impacts on institutions and individual scientists within and outside the Consortium. This new organisation should facilitate the management of activities, attainment of objectives, and assessment of achievements.

Subprogramme 5 now comprises the following themes:

- Theme 1: Creation of a platform of relevant training resources and a cadre of trained scientists to apply advanced technologies and products. This theme includes training courses and the development of training materials in phenotyping, marker-assisted breeding, genomics, bioinformatics, and policies relevant to the work of the GCP.
- Theme 2: Cultivation of research and learning opportunities for GCP collaborators and NARS scientists to further GCP mission and progress. Although this theme funds training and facilitates the development of skilled scientists, it differs from Theme 1 in that grants are not targeted to particular courses or GCP activities, providing the flexibility to encourage input and ideas from NARS scientists. In other words, this theme is viewed as an open scheme that helps to identify the best people and capacity-building mechanisms to champion and ensure the delivery and uptake of GCP products. In the future, SP5 will promote and support the best ideas generated through this collaboration on a larger scale, as part of Theme 3 (below).
- 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 fields of GCP target regions.
- Theme 4: Development and implementation of support services. The GCP aims to benefit the scientific community within and outside the Consortium. This theme contains a number of outputs to support researchers in their technical endeavours: information resources, advice from experts, and tools to smooth the path from theory to practice.
- Theme 5: Ex ante impact analysis and impact assessment. This theme includes the definition and design of indicators of the effects of GCP research on its 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 products

The GCP is currently carrying out a priority-setting exercise to guide the activities that will be conducted from now until the end of the GCP, to achieve the greatest impact with the limited resources available. A few high-priority regions will be selected as the focus for many GCP activities; consequently, many capacity-building activities will be directed to researchers at national institutions in these regions. Training courses included in this theme will be conducted by centres of excellence and by national research institutions with expertise in the subject area, which will organise, design, and run the course annually for scientists in the region. Programme training courses will meet researchers' demand for additional knowledge and skills in areas of GCP expertise, such as genetic diversity of genetic resources, advanced genomics for gene discovery, marker-assisted breeding, bioinformatics, and policies relevant to the work of the GCP. One course will exclusively cover phenotyping, expertise which is much in demand among scientists and is absolutely critical to advances in genomics. Another course will cover genomics and molecular breeding, and another is designed to teach basic bioinformatics skills. A one-time course on policy issues relevant to germplasm exchange will also be offered to test the suitability and completeness of the course materials that have already been developed by the GCP. Thereafter, the course will be available online; open access to course materials by researchers worldwide should promote a better understanding of procedures and conditions for exchanging germplasm and enhance collaboration worldwide. Training events will benefit researchers directly or indirectly involved with the GCP, and they may include a number of scientists beyond the GCP scope. As a result, the number of researchers able to conduct GCP-related research will increase, providing the GCP with a stronger group of collaborators for hands-on activities and more capable intermediaries for regional product delivery.

The development of training materials in other topics relevant to the GCP (but for which courses will not be organised) also falls under this theme. An online learning module on intellectual property, freedom-to-operate, and genetic resources policies will provide basic and practical information to help GCP scientists understand the importance of limitations to the rights to use plant genetic resources and tools, methods, and products protected by intellectual property rights. A set of training and reference materials for LD and association studies will also be developed, providing a

guide to alternatives to conventional linkage mapping, a very relevant topic for some of the long-generation crops in the GCP. These materials will be accessible through a repository in the Capacity Building Corner of the GCP website; they may be provided on CD to researchers with poor access to the internet; and they will also be used as reference materials for training courses organised by the GCP. All training materials will be translated into Spanish, French, Chinese, and Arabic to ensure widespread use.

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

This theme is intended to create research and collaboration opportunities for NARS (in this case, encompassing national research institutions, academic institutions, and other research institutions) in priority regions. A mini-grant programme will address the lack of equipment or supplies that hinder critical research collaboration, adoption of technologies, and product delivery. For example, a mini-grant may purchase small equipment to facilitate phenotyping in the field or marker work in the laboratory. The main users of this output are NARS in GCP target regions, in particular those currently engaged in GCP projects (whose participation is critical to delivering the research products of those projects).

The Fellowship Programme provides opportunities for scientists—particularly those working in NARS—engaged in ongoing GCP projects to increase their technical knowledge in any of the GCP content areas. The Travel Grant Programme is a similar mechanism, open to all NARS scientists working at or in collaboration with a GCP Consortium institution, to enable their contributions to conferences and thus widen their participation in the research community. The GCP also specifically supports NARS scientists' participation in certain special conferences each year. Both the Travel Grants and conference support provide new opportunities to form collaborations and trigger interest in NARS and the wider scientific community in the work of the GCP.

In this theme, the GCP will also support an academic position in molecular breeding in Africa. The objective is to increase the number of plant breeders with skills in molecular breeding in Sub-Saharan Africa. In the past, the GCP helped degree candidates study either in the United States or Europe, but for various reasons (including cost and potential failure to return), it is preferable to help PhD candidates obtain degrees in their own region. This output builds on an activity at the University of Kwazulu-Natal, promoted and funded by the Rockefeller Foundation. The GCP will fund a professorship in molecular breeding and will participate in the selection of PhD candidates and research topics. Students will mostly conduct this research in their home countries. The 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 impact of a higher number of skilled plant breeders in Africa will include an increase in good breeding programmes and better varieties developed for farmers.

Theme 3: Construction of systems for ensuring product delivery

Theme 3 is grounded in the GCP Delivery Strategy. Starting in 2006, the GCP allocated funds to assist with the development of delivery plans within competitive projects, ensuring the flow of products from producers to intermediate users to end users. This output includes the organisation of preliminary meetings at the onset of competitive projects to bring all partners together to evaluate and coordinate their participation in research and delivery for maximum impact. During this meeting, partners develop a delivery plan to address capacity-building needs for the NARS involved. The output targets for Theme 3 focus on capacity-building activities to meet project goals and ensure that user groups take up the resulting products. The resulting delivery plan 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 work toward the development of further products that improve farmers' livelihoods.

Another output under this theme involves a survey of research and delivery capacity in a wide range of potential GCP partner institutions. The information gathered from this survey will be used by the GCP community to ensure that the appropriate partners are selected for every research project and that relevant capacity-building opportunities are designed for the new partners. The direct beneficiaries of the activity will be the NARS and their scientific staff.

This theme also includes the development of a strategy for product marketing and distribution. This concept was not included in the original plan for the GCP, and its development is still in the preliminary stages. The intended users of this output will be close GCP collaborators as well as a wider community of beneficiaries that will receive access to GCP products to continue improving them for end-users. With this marketing and distribution plan, the widest possible community of beneficiaries will have access to GCP products.

The last output, part of a large proposal under development, addresses specific training activities and delivery mechanisms to ensure the flow of products to users under a proposed project on tropical legume improvement for Africa.

Theme 4: Development and implementation of support services

The GCP is committed to building public platforms of useful tools and technologies, enhancing human capacity, and strengthening institutions. However, the impacts of this work 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 the GCP and the wider scientific community, assisting researchers in their own working environments. This resource helps to strengthen linkages between advanced and developing institutions, and ultimately will contribute to the self-reliance of NARS researchers.

The GCP has launched a genotyping support service to help assess the potential value of particular breeding materials for identifying good markers for relevant agronomic traits. This effort will allow the GCP to reach more national research programmes and help create or strengthen linkages between molecular laboratories and field practitioners. The plan will be tested in the first year, but the intention is to offer it on a rolling basis, with crops and breeding programmes to be determined based on priority areas and emerging opportunities.

This theme also comprises the development of a tool to register assets produced in the GCP framework. The inventory system will become a database of products, expertise, and third-party materials associated with specific products for the GCP. The inventory will help the GCP community at large and will be an important tool for the development and implementation of delivery plans. Later, it may be considered an indicator of progress and serve to measure impact.

Theme 5: Ex ante analysis and impact assessment

Gauging the impact of GCP research is a key issue. The ultimate goal of the GCP 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, economic profits, or other indicators related to the use of new technologies or practices. Measurement of impact can be achieved at two levels: ex ante (predictive studies to facilitate decision making) and ex post (studies at the end of an activity to quantify impact).

For now, this theme's purpose is to gather detailed information about *potential impact* in priority regions selected by the GCP. Potential impact is assessed in terms of the prospective application of technologies for crop improvement and development of varieties. The first objective is to refine the GCP's ongoing priority-setting exercise to guide strategic decision making. The second objective is to define impact indicators to be used in future impact assessments. The first user of this information will be the Management Team of the GCP; however, information will be publicly available and will certainly benefit other research managers involved 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 will always be made available, without restrictions, to the widest audience possible.

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 deals with building capacity, creating linkages, building public knowledge platforms, providing services, supporting collaborators, disseminating knowledge, and more. None of the outputs would be possible without the complementary participation of a variety of collaborators, who are carefully selected depending on the activity.

Appendix A. 2006 Generation Challenge Programme Consortium Members and Partners

Consortium Members

Africa Rice Centre (WARDA)
African Centre for Gene Technologies (ACGT)
Agropolis
Brazilian Agricultural Research Corporation (Embrapa)
Chinese Academy of Agricultural Sciences (CAAS)
Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional (Cinvestav-Guanajuato Campus, Mexico)*
Cornell University
Indian Council on Agricultural Research (ICAR)
Institut National de la Recherche Agronomique (INRA-Morocco)*
Istituto Agronomico d'Oltremare (IAO)*
International Centre for Tropical Agriculture (CIAT)
International Maize and Wheat Improvement Centre (CIMMYT)
International Potato Centre (CIP)
International Centre for Agricultural Research in the Dry Areas (ICARDA)
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
International Institute for Tropical Agriculture (IITA)
International Plant Genetic Resources Institute (IPGRI)
International Rice Research Institute (IRRI)
John Innes Centre (JIC)
National Center for Genetic Engineering and Biotechnology (BIOTEC-Thailand)*
National Institute of Agrobiological Sciences (NIAS-Japan)
Wageningen University (WUR)

NARS Partners

Agricultural Biotechnology Research Institute of Iran (ABRII), Iran
Centre Africain de recherché sur bananas et plantains (CARBAP), Cameroon
Centre Research for Biotechnology, Bogor Agriculture University (IPB), Indonesia
Centre d'Etude Régional pour l'Amélioration de l'Adaptation à la Sécheresse (CERAAS), Senegal
Coconut Research Institute, Sri Lanka
Crop Research Institute (CRI), Kumasi, Ghana
Dhaka University, Bangladesh
DOA, Indonesia
Fedearroz, Colombia
Huazhong Agricultural University, China
Instituto de Botánica del Nordeste (IBONE), Argentina
IGAU, India
Indian Agriculture Research Institute (IARI)
Indonesian Centre for Agricultural Biotechnology and Genetic Resources and Research Development (ICABGRRD), Indonesia
Indonesian Department of Agriculture
Instituto Nacional de Investigación Agropecuaria (INIA), Uruguay
International Centre for Genetic Engineering and Biotechnology (ICGEB), India
Kenya Agriculture Research Institute (KARI), Nairobi, Kenya
Moi University, Kenya
Nakhon Sawon Field Crops Research Centre, Thailand
Namulonge Agricultural and Animal Production Research Institute (NAARI), Uganda
Nanjing Agricultural University (NAU), China
National Maize Research Institute, Vietnam
National Root Crop Research Institute (NRCRI), Umudike, Nigeria
New Partnership for African Development (NEPAD), Union of South Africa
NSFCRC, Thailand
Philippine Department of Agriculture
Rayong Field Research Station, Thailand
Scientific and Industrial Research and Development Centre (SIRDC), Zimbabwe
Sichuan Agriculture University, China
Tamil Nadu Agricultural University (TNAU), India
Tyshreen University, Syria
Universidade Católica de Brasília (UCB), Brazil
University or Hyderabad, India
Universidad Autónoma Chapingo, Mexico
Vanuatu Agricultural Research and Training Centre (VARTC), Vanuatu

ARI Partners

AfricaBio
Australian Centre for Plant Functional Genomics Pty Ltd, Australia
Australian National University, Australia
Centre National de Genotypage, France
CNRS, France
Colorado State University (CSU), USA
Commonwealth Scientific & Industrial Research Organisation (CSIRO), Australia
DArT P/L, Australia
ETH-Zurich, Switzerland
Genaissance, France
Graingenes (CSIRO), Australia
Hebrew Univ. of Jerusalem, Israel
Institut für Pflanzenbau und Pflanzenzüchtung, Germany
Institute Agronomique Mediterranean de Montpelier (CIHEAM-IAMM), France
Institute for Sustainable Agriculture, Spain
JIRCAS, Japan
Kansas State University, USA
MOBY-S, Canada
National Center for Genome Resources, USA
National Institute of Agricultural Botany, UK
Scottish Crop Research Institute (SCRI)
The Institute for Genomic Research (TIGR), USA
United States Department of Agriculture, North Carolina State University (NCSU)
Universita' di Udine, Italy
University of Aarhus, Denmark
University of Adelaide, Australia
University of California-Berkley, USA
University of California-Davis, USA
University of California-Riverside, USA
University of Capetown, South Africa
University of Queensland, Australia
University of Tsukuba, Japan
University of Virginia, USA

* Provisional member.

Appendix B. Centre Financial Indicators

Generation-Cost Allocation: Allocation of Projects Cost to CGIAR System Priorities, 2005-2009 (in $ million)

Project	System Priorities	2006 (estimated)	2007 (proposal)	2008 (plan 1)	2009 (plan 2)
Subprogramme 1: Genetic Diversity of Global Genetic Resources					
	Priority 1A	2.608	2.735	1.920	0.727
	Priority 2B	1.118	1.172	0.823	0.312
	TOTAL BY PROJECT	3.725	3.907	2.743	1.039
Subprogramme 2: Comparative Genomics and Gene Discovery					
	Priority 2A	0.742	0.818	0.637	0.350
	Priority 2B	2.967	3.272	2.546	1.398
	TOTAL BY PROJECT	3.709	4.090	3.183	1.748
Subprogramme 3: Trait Capture for Crop Improvement					
	Priority 5D	0.593	0.791	0.717	0.432
	Priority 2B	2.374	3.164	2.870	1.729
	TOTAL BY PROJECT	2.967	3.955	3.587	2.161
Subprogramme 4: Genetic Resources, Genomic, and Crop Information Systems and Bioinformatics					
	Priority 1A	0.529	0.497	0.314	0.147
	Priority 5D	0.264	0.248	0.157	0.074
	Priority 2B	1.851	1.738	1.100	0.515
	TOTAL BY PROJECT	2.645	2.483	1.571	0.736
Subprogramme 5: Capacity Building					
	Priority 5D	1.828	2.543	1.766	1.120
	Priority 2B	0.457	0.636	0.442	0.280
	TOTAL BY PROJECT	2.285	3.179	2.208	1.400
	TOTAL BY CENTER	15.331	17.613	13.291	7.083

Undertaking, Activities and Sectors	2006 (estimated)	2007 (proposal)	2008 (plan 1)	2009 (plan 2)
Increasing Productivity	10.037	11.296	8.731	4.730
Germplasm Enhancement & Breeding	10.037	11.296	8.731	4.730
Production Systems Development & Management	0.000	0.000	0.000	0.000
Cropping systems	0.000	0.000	0.000	0.000
Livestock systems	0.000	0.000	0.000	0.000
Tree systems	0.000	0.000	0.000	0.000
Fish systems	0.000	0.000	0.000	0.000
Protecting the Environment	0.000	0.000	0.000	0.000
Saving Biodiversity	2.608	2.735	1.920	0.727
Improving Policies	0.914	1.271	0.883	0.560
Strengthening NARS	1.772	2.311	1.758	1.066
Training and Professional Development	0.709	0.924	0.703	0.426
Documentation, Publications, Info. Dissemination	0.266	0.347	0.264	0.160
Organization & Management Couselling	0.354	0.462	0.352	0.213
Networks	0.443	0.578	0.439	0.266
TOTAL BY CENTER	15.331	17.613	13.291	7.083

Generation-Cost Allocation: Allocation of Projects Cost to CGIAR Regions, 2005-2009 (in $ million)

Project	Regions	2005 (actual)	2006 (estimated)	2007 (proposal)	2008 (plan 1)	2009 (plan 2)
Subprogramme 1: Genetic Diversity of Global Genetic Resources						
	SSA	0.967	0.931	0.977	0.686	0.260
	Asia	0.967	0.931	0.977	0.686	0.260
	LAC	0.967	0.931	0.977	0.686	0.260
	CWANA	0.967	0.931	0.977	0.686	0.260
	TOTAL BY PROJECT	3.869	3.725	3.907	2.743	1.039
Subprogramme 2: Comparative Genomics and Gene Discovery						
	SSA	0.976	0.927	1.022	0.796	0.437
	Asia	0.976	0.927	1.022	0.796	0.437
	LAC	0.976	0.927	1.022	0.796	0.437
	CWANA	0.976	0.927	1.022	0.796	0.437
	TOTAL BY PROJECT	3.902	3.709	4.090	3.183	1.748
Subprogramme 3: Trait Capture for Crop Improvement						
	SSA	0.708	0.742	0.989	0.897	0.540
	Asia	0.708	0.742	0.989	0.897	0.540
	LAC	0.708	0.742	0.989	0.897	0.540
	CWANA	0.708	0.742	0.989	0.897	0.540
°	TOTAL BY PROJECT	2.832	2.967	3.955	3.587	2.161
Subprogramme 4: Genetic Resources, Genomic, and Crop Information Systems and Bioinformatics						
	SSA	0.637	0.661	0.621	0.393	0.184
	Asia	0.637	0.661	0.621	0.393	0.184
	LAC	0.637	0.661	0.621	0.393	0.184
	CWANA	0.637	0.661	0.621	0.393	0.184
	TOTAL BY PROJECT	2.546	2.645	2.483	1.571	0.736
Subprogramme 5: Capacity Building						
	SSA	0.603	0.571	0.795	0.552	0.350
	Asia	0.603	0.571	0.795	0.552	0.350
	LAC	0.603	0.571	0.795	0.552	0.350
	CWANA	0.603	0.571	0.795	0.552	0.350
	TOTAL BY PROJECT	2.410	2.285	3.179	2.208	1.400
	TOTAL BY CENTER	15.560	15.331	17.613	13.291	7.083

Generation-Expenditures, 2005-2009 Object of Expenditure, (in $million)

Object of Expenditures	2005 (actual)	2006 (estimated)	2007 (proposal)	2008 (plan 1)	2009 (plan 2)
Personnel	0.262	0.368	0.430	0.450	0.450
Supplies and services	1.310	1.670	1.750	1.712	1.473
Collaboration/ Partnerships	13.979	13.213	15.353	11.049	5.080
Operational Travel	0.009	0.080	0.080	0.080	0.080
Depreciation	0.000	0.000	0.000	0.000	0.000
TOTAL BY CENTER	15.560	15.331	17.613	13.291	7.083

Generation-Financing: Members/Non Members Unrestricted Grants, 2005-2007 (in $ million)

Members/Non Members	2005(actual)	2006(estimated)	2007(proposal)
MEMBERS			
European Commission	6.027	5.674	5.000
Sweden	0.189	0.000	0.100
United Kingdom	4.417	4.109	4.000
World Bank	2.500	2.000	2.000
TOTAL MEMBERS	13.134	11.783	11.100
NON MEMBERS			
Kirkhouse Trust	0.015	0.000	0.000
Pioneer	0.020	0.020	0.020
TOTAL NON MEMBERS	0.035	0.020	0.020
TOTAL BY CENTER	13.169	11.803	11.120

Generation-Financing: Allocation of Members/Non Members Grants to Projects, 2005-2007 (in $ million)

Project	Members/Non Members	2006(estimated)	2007(proposal)
Subprogramme 1: Genetic Diversity of Global Genetic Resources	**MEMBERS**		
	Rockefeller Foundation	0.142	0.204
	TOTAL MEMBERS	0.142	0.204
	NON MEMBERS		
	Others	0.000	0.394
	TOTAL NON MEMBERS	0.000	0.394
	TOTAL MEMBERS + NON MEMBERS	0.142	0.597
	Unrestricted + center inc	3.583	3.309
	TOTAL BY PROJECT	3.725	3.907
Subprogramme 2: Comparative Genomics and Gene Discovery	**MEMBERS**		
	Rockefeller Foundation	0.200	0.203
	TOTAL MEMBERS	0.200	0.203
	NON MEMBERS		
	Others	0.000	0.958
	TOTAL NON MEMBERS	0.000	0.958
	TOTAL MEMBERS + NON MEMBERS	0.200	1.160
	Unrestricted + center inc	3.509	2.929
	TOTAL BY PROJECT	3.709	4.090
Subprogramme 3: Trait Capture for Crop Improvement	**MEMBERS**		
	Rockefeller Foundation	0.284	0.000
	TOTAL MEMBERS	0.284	0.000
	NON MEMBERS		
	Others	0.000	0.875
	TOTAL NON MEMBERS	0.000	0.875
	TOTAL MEMBERS + NON MEMBERS	0.284	0.875
	Unrestricted + center inc	2.683	3.080
	TOTAL BY PROJECT	2.967	3.955
Subprogramme 4: Genetic Resources, Genomic, and Crop Information Systems and Bioinformatics	**MEMBERS**		
	NON MEMBERS		
	Others	0.000	0.160
	TOTAL NON MEMBERS	0.000	0.160
	TOTAL MEMBERS + NON MEMBERS	0.000	0.160
	Unrestricted + center inc	2.645	2.323
	TOTAL BY PROJECT	2.645	2.483
Subprogramme 5: Capacity Building	**MEMBERS**		
	Rockefeller Foundation	0.210	0.213
	TOTAL MEMBERS	0.210	0.213
	NON MEMBERS		
	Others	0.000	0.494
	TOTAL NON MEMBERS	0.000	0.494
	TOTAL MEMBERS + NON MEMBERS	0.210	0.706
	Unrestricted + center inc	2.075	2.472
	TOTAL BY PROJECT	2.285	3.179
	TOTAL BY CENTER	15.331	17.613

Generation Staff Composition: Internationally and Nationally Recruited Staff, 2005 - 2009

Staff Type	2005 (actual)	2006 (estimated)	2007 (proposal)	2008 (plan 1)	2009 (plan 2)
Internationally-Recruited Staff (IRS)	2	3	3	3	3
Other Staff	1	2	2	3	3
TOTAL BY CENTER	3	5	5	6	6

Generation-Financial Position: Currency Structure of Expenditures, 2005-2007
(in $ million)

	2005(actual)			2006(estimated)			2007(proposal)		
Currency	Amount	US$Value	%Share	Amount	US$Value	%Share	Amount	US$Value	%Share
US Dollar (USD)	15.560	15.560	100.000%	15.331	15.331	100.000%	17.613	17.613	100.000%
TOTAL BY CENTER		15.560	100.000%		15.331	100.000%		17.613	100.000%

Generation
STATEMENTS OF ACTIVITIES
For the Year Ended December 31, 2005
(in $million)

	Unrestricted	Restricted Temporary	Challenge Programs	Total 2005	Total 2004
Revenue and Gains					
Grant Revenue	14.007	0.000	0.000	14.007	10.965
Other revenue and gains	0.186	0.000	0.000	0.186	0.000
Total revenue and gains	14.193	0.000	0.000	14.193	10.965
Expenses and Losses					
Program related expenses	13.647	0.000	0.000	13.647	6.764
Management and general expenses	1.913	0.000	0.000	1.913	0.642
Other losses expenses	0.000	0.000	0.000	0.000	0.000
Sub Total expenses and losses	15.560	0.000	0.000	15.560	7.406
Indirect cost recovery	0.000	0.000	0.000	0.000	0.000
Total expenses and losses	15.560	0.000	0.000	15.560	7.406
Net Surplus / (Deficit) from ordinary activities	-1.367	0.000	0.000	-1.367	3.559
Extraordinary Items	0.000	0.000	0.000	0.000	0.000
NET SURPLUS / (DEFICIT)	-1.367	0.000	0.000	-1.367	3.559
Object of Expenditures					
Personnel	0.262	0.000	0.000	0.262	0.253
Supplies and services	1.310	0.000	0.000	1.310	0.890
Collaboration/ Partnerships	13.979	0.000	0.000	13.979	6.193
Operational Travel	0.009	0.000	0.000	0.009	0.070
Depreciation	0.000	0.000	0.000	0.000	0.000

TOTAL BY CENTER	15.560	0.000	0.000	15.560	7.406

Generation
STATEMENTS OF FINANCIAL POSITION
December 31, 2005
(in $million)

	2005	2004
A S S E T S		
Current Assets		
Cash and cash equivalents	0.000	0.000
Investments	0.000	0.000
Accounts receivable		
Donor	0.000	0.000
Employees	0.000	0.000
Other CGIAR Centers	5.853	6.720
Others	0.000	0.000
Inventories	0.000	0.000
Prepaid expenses	0.000	0.000
Total current assets	5.853	6.720
Non-Current Assets		
Property, Plant and Equipment	0.000	0.000
Investments	0.000	0.000
Other Assets	0.000	0.000
Total Non-Current Assets	0.000	0.000
TOTAL ASSETS	5.853	6.720
LIABILITIES AND NET ASSETS		
Current Liabilites		
Overdraft/Short term Borrowings	0.000	0.000
Accounts payable		
Donor	0.000	0.000
Employees	0.000	0.000
Other CGIAR Centers	0.000	0.000
Others	0.000	0.000
Accruals	0.000	0.000
Total current liabilities	0.000	0.000
Non-Current Liabilities		
Accounts payable		
Employees	0.000	0.000
Deferred Grant Revenue	0.000	0.000
Others	0.000	0.000
Total non-current liabilities	0.000	0.000
Total liabilities	0.000	0.000
Net Assets		
Unrestricted		
Designated	4.853	6.220
Undesignated	1.000	0.500
Total Unrestricted Net Assets	5.853	6.720
Restricted	0.000	0.000
Total net assets	5.853	6.720
TOTAL LIABILITIES AND NET ASSETS	5.853	6.720

Appendix C. Logframe

Generation Challenge Programme 2007-2009 MTP Logframe

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 summarized in a reference sample		Plant breeders and germplasm specialists	Enhanced possibilities to explore genetic diversity in breeding and in further characterization for phenotypic and molecular traits	Better access to genetic diversity for breeding, resulting in more efficient crop improvement programs
output target 2007	Description of molecular variation and germplasm classification for tier-1 crops published/reference samples identified			
output target 2008	*completed*			
Output 1.2.Structure of genetic resources for the less advanced (tiers 2 and 3) crops accurately described (including tools) and summarized in a reference sample		Plant breeders and germplasm specialists	Possibility to explore genetic diversity in breeding and in further characterization for phenotypic and molecular traits	Better access to genetic diversity for breeding, resulting in more efficient crop improvement programs
output target 2007	Description of molecular variation and germplasm classification for tier-2 crops completed/reference samples identified			
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 tier-1 crops		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 programs
output target 2007	Implementation for all priority crops, including in vitro propagated cassava			
output target 2008	*completed*			
Output 1.4. Detailed analysis conducted of maize diversity after migration out of America		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 programs
output target 2007	A detailed description of 300 maize populations from Africa and Asia			
output target 2008	A comprehensive analysis of maize diversity in landraces around the world available			
output target 2009	*completed*			
Output 1.5. Methodology developed for resampling genetic diversity in large germplasm collections		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 programs
output target 2007	An additional description of SSR diversity for 1,000 accessions of rice and chickpea			
output target 2008	An algorithm for iteratively selecting accessions from a large, data-sparse collection given a data-rich subset of accessions			
output target 2009	*completed*			

Outputs	Output Targets	Intended user	Outcome	Impact
Theme 2. Development of a range of flexible HTP genotyping techniques accessible in reference laboratories				
Output 1.6. DArTs validated as a genome-wide molecular characterization technology		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 programs
output target 2007	Comparison of DArTs with other markers in rice, sorghum, wheat, banana, cassava, and coconut			
output target 2008	*completed*			
Output 1.7. EcoTILLing gene-targeted assessed as a molecular characterization technique		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 programs
output target 2007	Comparative assessment of EcoTILLing resolution power in rice, sorghum, and Musa (3n) using 10 candidate genes			
output target 2008	*completed*			
Output 1.8. Methodology developed to assess SNPs with effect on allele expression (Non Coding SNPs)		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 programs
output target 2007	Allelic imbalance assays performed for 50 candidate genes for abiotic stress tolerance in barley			
output target 2008	Associations between NC SNPs and drought-related phenotype in barley			
Output 1.9. Database on allele diversity at candidate genes across species developed	Phylogenetic analyses for six important gene families across seven species: rice, sorghum, barley, bean, chickpea, potato, and cassava	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 programs
output target 2007	Phylogenetic analyses for 12 most promising genes across 7 species: rice, sorghum, barley, bean, chickpea, potato, and cassava			
output target 2008	A database with detailed information on allelic variation at 15 genes across 7 crops/guidelines for implementing phenotypic evaluations in corresponding reference samples			
output target 2009	*continued*			
Theme 3. Establishment and implementation of a scientific and organizational framework to describe tolerance to drought				
Output 1.10. Set of phenotyping facilities in Brazil made accessible for GCP germplasm evaluation		GCP scientists	High-quality and high-capacity GCP phenotyping network available for use	Increased efficiency in crop research and improvement
output target 2007	Open GCP access to Embrapa network for evaluation of cereal reference samples			
output target 2008	Embrapa network used for evaluation of legume reference samples			
output target 2009	*continued*			
Output 1.11. A crop and whole-plant modelling framework developed to support assessment of tolerance to drought		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 2007	Characterization of environments within phenotyping network; improvement of whole-plant model to support drought tolerance phenotyping in cereals			
output target 2008	Improvement of whole-plant model to support drought tolerance phenotyping in cereals/ transposition of rationale to legumes			
output target 2009	*completed*			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 1.12. Phenotyping capacity accessible to the GCP is inventoried		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 2007	A detailed central repository of phenotyping protocols, facilities, and capacities available			
output target 2008	Options of phenotyping protocols and facilities by crops and regions documented, including operational costs			
output target 2009	*completed*			
Output 1.13. Support service for drought-related phenotyping of specific populations with high quality molecular information implemented		GCP scientists	Access to the best drought tolerance screening facilities within the GCP	Increased efficiency in analysing the genetic control of tolerance to drought
output target 2007	A mechanism for prioritising phenotyping experiments			
output target 2008	Phenotyping reference samples for several crops, to be decided			
output target 2009	*to be decided*			
Theme 4. Identification of favourable genetic factors (i.e., potential genes or genome segments) and superior alleles (or haplotypes) through association studies				
Output 1.14 (pending). Favourable genetic factors for drought tolerance in maize identified		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 2007	Molecular characterization and accurate phenotypic characterization of 460 maize genotypes/allelic diversity at 50 candidate genes monitored			
output target 2008	Integrated association analysis using functional molecular markers, metabolomic characterization and field evaluations			
output target 2009	*completed*			
Output 1.15. Improved methodology developed for validating the genetic basis of marker-phenotype associations		Crop scientists around the world	*ongoing competitive call*	Increased efficiency in crop research and improvement
output target 2007	ongoing competitive call			
output target 2008	ongoing competitive call			
output target 2009	ongoing competitive call			
Output 1.16 (pending). Favourable genetic factors for stress tolerance in four legume species identified		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 2007	(Coordination between all types of germplasm characterization refined)			
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			
Theme 5. Development of novel populational approaches for relating genotypes to phenotypes				
Output 1.17. Favourable genes mapped in the course of breeding		Plant breeders	Production of genetic information from ongoing field experiments	Increased efficiency in crop research and improvement
output target 2007	Assessment of LD in various populations in potato, cassava, yam, banana, and coconut/identification of potential case studies			
output target 2008	*to be decided*			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 1.18. Local assessment of linkage disequilibrium in the genome of rice conducted		Rice geneticists and breeders	Prospects for association studies in rice refined	Increased efficiency in crop research and improvement
output target 2007	Measurement of LD in three regions of the rice genome/refining the localization of bacterial blight resistance genes			
output target 2008	*completed*			
Output 1.19. Global assessment of linkage disequilibrium in the genome of rice conducted		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 2007	Description of SNP diversity (1,500 SNPs) along the genome among 900 rice accessions/costs per datapoint (Illumina platform) assessed			
output target 2008	Global LD pattern in rice documented/LD-based mapping strategies for diploid selfing crops refined			
output target 2009	*completed*			
Output 1.20. Linkage disequilibrium in the genome of sorghum used for mapping useful genes		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 2007	Description of DArT diversity (1,000 markers) along the genome among 200 sorghum accessions			
output target 2008	Monitoring introgression patterns between various sorghum cultivated and wild forms			
output target 2009	Monitoring patterns of selection along the genome of sorghum			
Output 1.21. Base broadened of current crop diversity in rice using related species		Germplasm specialists and plant breeders	Novel rice germplasm tailored for genetic analysis of trait variation	Increased efficiency in crop research and improvement
output target 2007	A range of recombinant genotypes that segmentally display introgression of the whole genome of four wild rices			
output target 2008	Genetic dissection of phenotypic contribution of wild germplasm in rice			
output target 2009	*completed*			
Output 1.22. New alleles introgressed from wide crosses using crop wild relatives		Germplasm specialists and plant breeders		Increased efficiency in crop research and improvement
output target 2007	ongoing competitive call			
output target 2008	ongoing competitive call			
output target 2009	ongoing competitive call			
Project 2. Comparative Genomics for Gene Discovery				
Theme 1. Assembly of genomics and germplasm resources through consolidating and developing specialized genetic stocks				
Output 2.1. Wheat genetic stock assembled and utilized		Crop researchers and database curators		Enhanced access to genomic tools and resources for scientific community for increased efficiency in crop research and improvement
output target 2007	Consolidation, multiplication, and distribution of specialized wheat stocks for use by the GCP	Crop researchers, plant breeders, and genebank curators	Broadened access to specialized genetic stocks of wheat; creating a common platform for sharing stocks and derived phenotypic and genotypic data	
output target 2008	*completed*			
output target 2009	*none*			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 2.2. Systematic evaluation of rice mutant collections conducted for conditional phenotypes with emphasis on stress tolerance		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 2007	Mutant phenotypes (drought- and disease-sensitive/tolerant) of about 300 stress-associated genes determined; stress-associated gene/phenotype-expression database available for studies on QTLs and breeding of cereal crops		Known genes controlling drought/ disease stress available to plant science community; unique database on conditional mutant (stress) traits evaluated in a realistic agronomic setting in a crop species	
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 2.3. Legume mutant resources developed		Crop researchers and genetic resource curators	Unique bean genetic stock available for public use	Enhanced access to genomic tools and resources for scientific community for increased efficiency in crop research and improvement
output target 2007	Demonstration of EcoTILLING technique in common bean using TILLING technologies; a mutant collection of common bean amenable for forward and reverse genetics; systems in place to maintain and distribute mutant seeds			
output target 2008	*completed*			
output target 2009	*none*			
Output 2.4. Tuber genetic stocks and gene function validation tools developed		Crop researchers and genetic resource curators	The only known true-seed potato mutant stock that can be easily distributed (unlike tubers)	Enhanced access to genomic tools and resources for scientific community for increased effiency in crop research and inprovement
output target 2007	M3 seeds available for distribution and information integrated into the SGN database; mutant stock for forward and reverse genetic screens in true-seed potato established; activities integrated in to new legume initiative			
output target 2008	*completed*			
output target 2009	*none*			
Output 2.5. Stress-response-enriched EST resources for cowpea created		Crop researchers	Enhanced collection of cowpea ESTs available in public database; potential use for gene-based markers	Enhanced access to genomic tools and resources for scientific community
output target 2007	Using subtractive and normalised libraries from drought-sensitive and drought-tolerant cowpea lines, ESTs from drought-stressed and non-stressed cowpea lines (susceptible and tolerant) produced, annotated and maintained at BECA			
output target 2008	*completed*			
output target 2009	*none*			
Output 2.6. Stress-response-enriched EST resources for pearl millet created		Crop researchers	Expanded collection of millet ESTs, bridging the gap in millet genomic resources, available to the public; potential use for gene-based markers	Enhanced access to genomic tools and resources for scientific community for increased efficiency in crop research and improvement
output target 2007	Using pearl millet ESTs from drought- and salinity-stressed plants of pearl millet produced (using parental lines 841B-P3 and 863B-P2 of mapping population), EST-derived PCR markers for drought tolerance pearl millet developed			
output target 2008	*completed*			
output target 2009	*none*			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 2.7. Multiple rice genotypes sequenced		Crop researchers	First extensive genome-wide SNP data for a crop species, leading to applications of SNP and association genetics by NARS scientists	Public platform to extract alleles and useful germplasm from rice collections, model for association genetics application in other self-pollinating crop species, toward enhanced crop improvement programs
output target 2007	Genome-wide SNP dataset available for 20 rice lines as foundation for developing haplotype tags in multiple rice lines			
output target 2008	*completed*			
output target 2009	*none*			
Output 2.8 (pending). Bean genetic and genomic resources developed		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 2007	Two subtractive root and shoot tissue libraries (drought vs control) developed to provide a pool of stress-tolerance candidate genes for evaluation			
output target 2008	Eight candidate genes controlling transpiration/water use efficiency, osmotic adjustment, and root development screened for association drought tolerance traits identified			
output target 2009	Allelic series in 8 candidate genes for drought tolerance characterized in 25 elite genotypes; 4 traits (yield potential; shoot and seed ash; non-struct. carbohydrates) evaluated over multiple sites and analyzed for QTL			
Output 2.9 (pending). Chickpea genetic and genomic resources developed		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 2007	500 new markers tested (linked with "Cross-species marker" Output 2.19)			
output target 2008	Gene chip(s) with 20,000 genes			
Output 2.10 (pending). Cowpea genetic and genomic resources developed		Crop researchers and plant breeders	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 2007	>1 million cDNAs from cDNA libraries of 6 diverse genotypes			
output target 2008	14x genome coverage of 2 cowpea BAC libraries produced; 240,000 ESTs generated			
output target 2009	At least 1536 SNPs identified			
Output 2.11 (pending). Groundnut genetic and genomic resources developed		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 2007	1000 molecular markers established in groundnut (linked with "Cross-species marker" Output 2.18)			
output target 2008	Unified existing RFLP and SSR maps of Arachis; 20,000 ESTs from drought-stressed lines			
output target 2009	One reference map for AA and BB diploid and AABB tetraploid genomes; one linked physical and genetic map for AA genome			

Outputs	Output Targets	Intended user	Outcome	Impact
Theme 2. Development of comparative maps within and across species and framework genetic markers for target crops				
Output 2.12. Validation of conserved orthologous markers conducted		Crop researchers	Efficiency of COS markers assessed for several selected crops; rationale for next steps in linking different maps	Increased knowledge about genomics for aiding crop improvement
output target 2007	25 new universal PCR-based markers related to drought or disease resistance identified and validated across monocots and dicots. Activities integrated into ADOC project and legume activities			
output target 2008	*completed*			
output target 2009	*none*			
Output 2.13. Comparative QTL mapping for drought tolerance in bean conducted		Crop researchers	Enriched QTL and molecular characterization of two key bean mapping populations; ready for candidate gene identification by broader users	Increased knowledge about genomics for aiding crop improvement
output target 2007	QTL isolines with high photosynthate mobilization trait created; activities integrated into new legume initiative			
output target 2008	*completed*			
output target 2009	*none*			
Output 2.14. Comparative QTL mapping for drought tolerance in rice conducted		Crop researchers	Genetic resources and a framework for converging root traits, drought -related QTL, and candidate genes produced	Increased knowledge about genomics for aiding crop improvement
output target 2007	Based on a synthetic map with QTL for root development and drought-response characters from rice and sorghum, BC4F3 lines with narrow chromosomal segments carrying QTL produced; candidate genes in the subsegments identified in silico			
output target 2008	*completed*			
output target 2009	*none*			
Output 2.15. Targeted *Musa* genome sequencing conducted and frame map constructed		Crop researchers and database curators	Consolidated genetic and genomic resources leading to enhancement of *Musa* genetic research	Increased knowledge about genomics for aiding crop improvement
output target 2007	Major repeat classes in relation to genomic diversity in *Musa* characterized; using integrated genetic maps of rice and Musa, the rice-Musa genome relationship evaluated, providing guidelines for future use of the rice genome sequence in *Musa* and other CGIAR mandate crops; data management and database constructed similar to the public data and genomic resource established in rice		Rice-Musa relationship assessed at the genomic level, and the basis of applying rice sequencer information to *Musa* evaluated	
output target 2008	*completed*			
output target 2009	*none*			
Output 2.16 (pending). Cross-species resources for comparative biology in tropical crop legumes developed		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 2007	Common bean BAC ends (~50,000) sequenced, and ~1,000 SSR markers identified for bean; informatics pipeline to generate cross-legume anchor markers implemented			
output target 2008	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 2009	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 programs of four legume crops; online navigation between legume genomes			

Outputs	Output Targets	Intended user	Outcome	Impact
Theme 3. Assignment of genes and pathways to phenotypes through the convergence evidence of genome variation, expression patterns, and phenotypic data				
Output 2.17. Targeted discovery of superior disease QTL, alleles in the maize and rice genomes conducted		Crop researchers and plant breeders	Superior disease resistance QTL identified, characterized, and used in maize and rice breeding programs	Model available for integrating gene discovery and breeding activities for increased efficiency in crop research and improvement programs
output target 2007	Introgression maize lines carrying an array of alleles at selected QTL regions from maize germplasm developed and characterized; disease QTL NIL tested for correlation between resistance phenotypes and gene expression patterns; disease resistance QTL tested for spectrum of resistance to multiple pathogens		Efficient methodologies developed for detecting introgression segments through simultaneous genotyping and expression profiling analysis; demonstrated efficiency in using heterogeneous inbred families for breeding and QTL fine mapping in diverse genetic backgrounds	
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 2.18. Functional genomics of cross-species resistance to fungal diseases in rice and wheat conducted		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 2007	Upon establishing phenotypes and cytology of non-host resistance in wheat and rice to rust and blast, map positions of non-host resistance identified in wheat mapping populations; phenotypes and genotypes of rice and wheat germplasm for non-host interaction to blast and rust characterized			
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 2.19. Common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes investigated and determined		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 2007	Based on improved screening methodologies under controlled and field conditions; sets of QTL involved in tissue growth regulation in cereals identified; correlation between tissue growth regulation and overall plant performance determined; a set of tissue/species-specific candidate genes and QTL regions for tissue growth regulation identified		Gene markers adopted by breeding program to select for drought tolerance traits	
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 programs	
output target 2009	*completed*			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 2.20. Crop gene expression profiles and stress-gene arrays created			Contribution to GCP crop stress gene database and gene networks involved in drought conditions	Increased knowledge about genomics for aiding crop improvement
output target 2006	Based on candidate genes (approximately 100) identified from expression analyses, subarrays of orthologous stress response/tolerance genes tested for usage (especially molecular phenotyping for drought) in selected cereals	Crop researchers		
output target 2007	*completed*			
output target 2009	*none*			
Theme 4. Validation of genes and pathways via evaluation of under- or over-expression constructs or variants (induced or natural) of target genes				
Output 2.21. Genes responsible for failure of grain formation in rice and wheat under drought identified		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 2007	Based on established stress protocols to manipulate peduncle elongation and floret sterility, expression profiles in peduncle and florets under stress effects in contrasting genotypes obtained; roles of GA/ABA antagonisms in controlling the behaviour of peduncle and floret response under stress determined		General methodologies for assessing reproductive drought stress available for use in other cereals	
output target 2008	A short list 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 2.22. Genes for tolerance of saline and phosphorus-deficient soils to enhance and sustain productivity in rice identified		Crop researchers and plant breeders	Genes associated with salinity and P-deficiency tolerance in 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 2007	After completion of fine mapping of Saltol and Pup1 loci using NIL populations, candidate genes for Pup1 and Saltol identified based on combined evidence of expression analysis (transcript and proteomics) and sequence information (SNP haplotypes); allele-specific markers identified for salinity and P-deficiency tolerance in selected germplasm and the range of applicability in breeding determined			
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 characterized 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 2.23. Aluminium tolerance genes in the cereals identified and characterized		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 2007	Based on successful cloning of aluminium-tolerance gene (Alt) in sorghum, ALMT1 homologs cloned from Triticeae and rice; expression profiling of sorghum and maize NIL completed; homologs of sorghum alt gene in Triticeae and rice cloned; generation of transgenic maize and wheat lines with Al tolerance genes for marked-assisted backcross breeding			
output target 2008	Candidate Al-tolerance genes in maize molecularly characterized; Al-tolerance genes from sorghum, maize, and rice identified; physiological characterization 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*			

Outputs	Output Targets	Intended user	Outcome	Impact
Project 3. Trait Capture for Crop Improvement				
Theme 1. Characterization of segregating populations, identification and/or validation of molecular markers for target traits to increase plant breeding efficiency				
Output 3.1. Physiological and genetic traits that make cassava one of the most drought-tolerant crops identified		CGIAR (CIAT), NARS (Brazil, Ghana, and Tanzania), university (Cornell), and other breeding programs	Improved understanding of drought-tolerance traits and their biological basis for cassava	New drought-tolerant cassava germplasm and more efficient cassava plant breeding strategies available
output target 2007	Progeny for drought segregating crosses (20 tolerant with 12 susceptible); transformed clones with cytokinin synthesis gene; trained cassava physiologists (NARS, including Embrapa)		Cassava transgenic event for drought tolerance	
output target 2008	Characterized effect of cytokinin synthesis gene on leaf water retention and related traits during drought; cassava drought QTL and candidate genes characterized including protein expression		Molecular markers for key drought traits and cassava genotypes ready to be introduced into breeding programs	
output target 2009	*completed*			
Output 3.2. Genetic diversity of peanut's wild relatives unlocked with genomic and genetic tools		CGIAR (ICRISAT), NARS (Brazil, India, Senegal), university (Brazilian universities, CIRAD, IBN Argentina), and other breeding programs	New peanut varieties resistant to disease and drought; creation of a single genetic system for legumes linking groundnut to model plants	A new approach available--introduction of new genes through artificial crosses with wild relative--to overcome bottleneck in groundnut breeding
output target 2007	Gene-rich diploid maps (100-200 genic markers); BAC libraries for diploid genomes and candidate genes for target drought tolerance traits			
output target 2008	Tetraploid reference map; 50 genic markers between groundnut and Lotus japonicus; new drought amphidiploids and cytogenetic probes selected		Backcrossed populations and new improved selected lines for breeding	
output target 2009	*completed*			
Output 3.3. Markers developed and marker-assisted selection conducted for Striga resistance in cowpea		Plant breeders and breeding programs	Superior-performing, well-adapted cowpea varieties for sustainable resistance to disease and pests, especially Striga	Better source of germplasm for African cowpea farmers (agronomic productivity, disease and pest resistance traits)
output target 2007	Field-characterized RILs for Striga and related traits, new SCAR/IDP markers			
output target 2008	New germplasm resistant to Striga; tool box for MAS in cowpea, and training of NARS scientists in the use of tool box		New breeding tools for cowpea	
output target 2009	*completed*			
Output 3.4. Evaluation and characterization of segregating populations of tropical legumes for biotic stresses (groundnut, bean, cowpea, and chickpea) conducted		Plant breeders and breeding programs	QTL, candidate genes, and QTL/gene-based markers for biotic stresses	New genes and markers being used to improve tropical legume varieties for pest and/or disease resistance
output target 2007	Development and/or evaluation of segregating material, implementation of phenotypic characterization; complementation of genetic maps and testing of candidate genes			
output target 2008	Evaluation of segregating material; implementation of phenotypic characterization; testing of candidate genes			
output target 2009	MAS with QTL/gene-based markers for abiotic stress resistance; improved germplasm			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 3.5. Evaluation and characterization of segregating populations of tropical legumes for abiotic stresses (groundnut, bean, cowpea, and chickpea) conducted		Plant breeders and breeding programs	QTL, candidate genes, and QTL/gene-based markers for drought adaptation	New genes and markers being used to improve tropical legumes varieties for drought adaptation
output target 2007	Development and/or evaluation of segregating material, implementation of phenotypic characterization; complementation of genetic maps			
output target 2008	Evaluation of segregating material; implementation of phenotypic characterization; testing of QTL and candidate genes and development of material for MAS			
output target 2009	Validation of QTL and candidate genes involved in drought tolerance and development of material for MAS			
Output 3.6. Traits for drought tolerance improvement (crops) identified and/or refined		Plant breeders and breeding programs	New, or refined, traits associated with crop drought tolerance; better methodology for plant phenotypic characterization under drought.	Improved plant breeding under drought environments
output target 2007	ongoing competitive call			
output target 2008	ongoing competitive call			
output target 2009	ongoing competitive call			
Theme 2. Development and evaluation of novel of novel breeding or molecular technologies to better serve modern plant breeding				
Output 3.7. Low-cost technologies developed for pyramiding useful genes from wild relatives of cassava into elite progenitors		CGIAR (CIAT), NARS (Brazil, Ghana, Nigeria, and Uganda), and other breeding programs	Low-cost MAS technologies for pyramiding pest and disease resistance and delayed post-harvest physiological deterioration (PPD) genes development; new collections of wild Manihot	Improved breeding strategy available integrating MAS approach (CMD, CGM, and PPD) and accessing new alleles in improved and wild relative germplasm
output target 2007	Genetic crosses between CMD/CGM and farmers' varieties, characterization of wild Manihot species for pest and disease			
output target 2008	Selected lines through MAS for CMD/CGM; MAS functioning labs in NARS; evaluation by new Manihot species by NARS		Low-cost markers and new capacity building for MAS in cassava (human and infrastructure)	
output target 2009	*completed*			
Output 3.8. Low-cost, gene-based trait assay technologies developed for cereals		Plant breeders and breeding programs	Better and cheaper markers for rice for bacterial blight (BB) resistance and maize quality grain	Improved rice and maize germplasm through more efficient MAS approach
output target 2007	Routine and large-scale screening of rice for BB resistance and maize for QPM			
output target 2008	*completed*			
output target 2009	*none*			
Output 3.9. Transgenic drought-tolerant varieties evaluated and deployed		Plant breeders and breeding programs	Impact of DREB1A transgene on drought tolerance in several crops	Improved molecular breeding for drought tolerance using transgenic material
output target 2007	Quantification of DREB1A on drought tolerance (yield components and related secondary traits) for rice, wheat, groundnut, potato, and sweet potato transgenic plants evaluated under screenhouse/field conditions			
output target 2008	*completed*			
output target 2009	*none*			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 3.10. Marker-assisted breeding systems for drought tolerance in cereals optimized through linkage of physiological and genetic models		Plant breeders and breeding programs	Improved breeding schemes to increase the selection response for improved performance under drought conditions	More efficient MAS strategies available for crop improvement programs
output target 2007	Collect information for the wheat and sorghum study cases; incorporate leaf growth model for maize into APSIM; refined modern breeding strategies through simulations			
output target 2008	Quantified gene-trait interaction for wheat and sorghum; Improved linkages between APSIM and QU-GENE; electronic forum to discuss the use of GCP web tools for modern breeding			
output target 2009	Development and evaluation of new breeding strategies to optimise the utilisation of the increasing amount of gene marker information; friendly interface for QU-GENE			
Theme 3. Application of molecular markers in breeding programs				
Output 3.11. Drought-tolerant rice cultivars developed for North China and South/Southeast Asia by highly efficient pyramiding of QTL from diverse origins		CGIAR (IRRI), NARS (NE/NW China and S/SE Asia), and other breeding programs, and ultimately small-scale farmers in resource-poor cropping systems	New elite allele identified at drought-tolerant (DT) QTL in broad elite rice background; improved strategy for genetic improvement of complex traits.	New drought-tolerant germplasm for farmers in Asian rainfed areas
output target 2007	DT QTL confirmed, selection of F2 genotypes in new segregating populations; pyramiding of DT QTL in japonica genetic background			
output target 2008	BC1F2-derived MAB lines with improved DT; farmer testing (N/NE China) and release of DT Lioa-Jing454 and C418 lines		New pre-breeding material for S/SE Asia	
output target 2009	*completed*			
Output 3.12. Plans for effective product development, delivery, and use developed		Plant breeders and breeding programs	Improved priority setting and product design	More GCP products reach end-users
output target 2007	Mapping product development pathways for key representatives of genomics, transgenic, and computational outputs			
output target 2008	Mapping product development and delivery pathways for new GCP technologies			
output target 2009	In collaboration with SP5, evaluation of efficiency GCP of delivery plans			
Output 3.13. Communities of practice for molecular breeding of target crops formed and supported by the GCP to access new tools, technologies, and markers		Plant breeders and breeding programs, 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	More efficient MAS strategies available for crop improvement programs
output target 2007	Identification of communities of practices and their needs			
output target 2008	Use of markers for breeding activities			
output target 2009	Use of markers for breeding activities and impact assessment of the MAS activities			
Output 3.14. Molecular breeding for abiotic stress conducted		Plant breeders and breeding programs, and ultimately small-scale farmers in resource-poor cropping systems	Application of existing, or development of new, MAS approaches for drought tolerance improvement.	More efficient MAS strategies available for crop improvement programs
output target 2007	ongoing competitive call			
output target 2008	ongoing competitive call			
output target 2009	ongoing competitive call			

Outputs	Output Targets	Intended user	Outcome	Impact
Theme 4. Multidisciplinary approaches towards specific crop improvement under target environments				
Output 3.15. NERICA rice improved for abiotic stress tolerance		Plant breeders and breeding programs, and ultimately small-scale farmers in resource-poor cropping systems	New improved germplasm combining African (Oryza glaberima) (O. sativa) sources	Improved rice germplasm for Africa
output target 2007	Field evaluation of new segregating germplasm under abiotic stress conducted; marker needs identified			
output target 2008	Field evaluation of segregating material under abiotic stress continued; MAS for target traits conducted			
output target 2009	Germplasm developed and links established with farmer communities			
Output 3.16. Drought tolerance and virus resistance enhanced in sweet potato through exploration of heterosis		Plant breeders and breeding programs, 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 2007	Identification of segregating material for drought and development of MAS for virus resistance			
output target 2008	*to be decided*			
output target 2009	*to be decided*			
Output 3.17 (pending). Germplasm enhanced via molecular breeding for target traits for tropical legumes (groundnut, bean, cowpea, and chickpea)		Breeding programs and ultimately small-scale farmers in resource-poor cropping systems	Improved groundnut, bean, cowpea, and chickpea germplasm	New germplasm and improved breeding programmes for tropical legumes in Africa
output target 2007	*to be decided*			
output target 2008	*to be decided*			
output target 2009	*to be decided*			
Project 4. Bioinformatics and Crop Information Systems				
Theme 1. 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		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 programs
output target 2007	Models for main GCP data types are published with involvement of all relevant actors inside and outside GCP Consortium			
output target 2008	Models are further developed; models are integrated			
output target 2009	Models are further developed; models are integrated (prioritisation will be done later)			
Output 4.2. Web services		Bioinformatics and biodiversity scientists all over the world	Web services used in the GCP	Increased efficiency in bioinformatics for crop improvement programs
output target 2007	Web services further deployed in the GPC Consortium member institutes; staff trained			
output target 2008	*completed*			
output target 2009	*none*			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 4.3. GCP Repository created and maintained		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 2007	Repository is updated with (references to) all produced GCP data sets			
output target 2008	Repository is updated with (references to) all produced GCP data sets			
output target 2009	Repository is updated with (references to) all produced GCP data sets			
Output 4.4. Web services technology further developed and applied in reference GCP applications		Bioinformatics and biodiversity scientists all over the world	Improved technology enhances GCP's contribution to the global bioinformatics community	Increased efficiency in application of data for crop research and improvement
output target 2007	Development of Bio-MOBY is further supported, reference GCP implementations have been made			
output target 2008	to be determined			
output target 2009	to be determined			
Output 4.5. Templates for GCP data capture, storage, and use created, made available to the research community, and maintained		GCP scientists	Scientists better able to maintain, use, and upload their GCP data	Better access to research data for crop researchers and improvement programs
output target 2007	Templates for micro-array data created and implemented; other templates maintained			
output target 2008	Templates for other data (to be decided) created and implemented; other templates maintained			
output target 2009	*to be determined*			
Output 4.6. GCP software engineering and collaboration platform established and maintained		GCP software developers	Simultaneous software and document development facilitated	More efficient scientific collaboration among bioinformaticians and crop researchers
output target 2007	Infrastructure for collaborative software development created; GCP Wiki maintained and promoted			
output target 2008	Infrastructure for collaborative software development maintained; GCP Wiki maintained and promoted			
output target 2009	Infrastructure for collaborative software development maintained; GCP Wiki maintained and promoted			
Theme 2. Creation of facilities to support IT and bioinformatics applications in the GCP Consortium				
Output 4.7. Integrated GCP Information Platform created		GCP informatics staff	Improved access by GCP scientists to integrated tools and databases	More efficient bioinformatics research for crop improvement programs
output target 2007	GCP bioinformatics client released; web services made available			
output target 2008	GCP bioinformatics client further developed; website with bioinformatics functionalities released			
output target 2009	*to be determined*			
Output 4.8. Data quality within the GCP further improved and assured		GCP informatics staff	Data quality of existing data bases improved	Increased efficiency in application of data for crop research and improvement
output target 2007	Wide array of quality improvement activities have been performed			
output target 2008	Quality standards and procedures have been created			
output target 2009	*to be determined*			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 4.9. High Performance Computing (HPC) facilities integrated in the GCP toolbox		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 2007	HPC facilities are used by (selected) GCP scientists			
output target 2008	HPC facilities are a widely used tool in GCP research			
output target 2009	*to be determined*			
Output 4.10. ICRISAT LIMS installed and implemented at the Biosciences Eastern and Central Africa (BecA) facility and IITA-Ibadan		Bioinformatics staff at BecA and IITA	LIMS capabilities at BecA and IITA greatly improved	More effective use of laboratory capacity for crop improvement programs for Africa
output target 2007	ICRISAT LIMS installed and implemented at BecA and IITA			
output target 2008	*none*			
output target 2009	*none*			
Theme 3. Support to other GCP Projects in terms of software tools and data management				
Output 4.11. Ortholog-function display tools developed (in support of Project 2)		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 2007	Public comparative gene catalog, user interfaces, and data integration protocols developed			
output target 2008	*none*			
output target 2009	*none*			
Output 4.12. Crop gene expression database and data mining tools developed (in support of Project 2)		Bioinformatics scientists all over the world	Expression data easily searchable	More efficient bioinformatics research for crop improvement programs
output target 2007	User-friendly gene expression database in which the data are connected by the linkage of orthologous genes developed and made available through web service			
output target 2008	*none*			
output target 2009	*none*			
Output 4.13. Decision support tools for MAS and MAB developed (in support of Project 3)		Plant breeders	More efficient use of markers by plant breeders	Increased efficiency in NARS molecular breeding programs
output target 2007	Integrated decision support system for marker-assisted plant breeding developed by integrating (largely existing) software			
output target 2008	*none*			
output target 2009	*none*			
Output 4.14. An eco-physiological – statistical framework for GxE and QTLxE analysis developed (in support of Project 3)		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 2007	An eco-physiological – statistical framework for the analysis of GxE and QTLxE, with applications to the CIMMYT drought stress programs developed and available			
output target 2008	*none*			
output target 2009	*none*			
Output 4.15. Data analysis support available for Project 1 activities with emphasis on sampling germplasm		Germplasm specialists and plant breeders	Selection of germplasm for Project 1 activities is done more efficiently	Increased efficiency in crop research and improvement
output target 2007	DSS DarWIN for diversity analysis and sampling germplasm implemented; support to Project 1 scientists in using the software provided			
output target 2008	*none*			
output target 2009	*none*			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 4.16. Data analysis support available for Project 2 with emphasis on microarray and mapping experiments		Crop geneticists and genomics specialists	Microarray and mapping experiments can be better analysed	Increased efficiency in crop research and improvement
output target 2007	Analysis pipeline for integrating results from microarray and mapping experiments established			
output target 2008	*none*			
output target 2009	*none*			
Output 4.17. Methodology and software developed for LD-based phenotype analysis (in support of Projects 1 and 2)		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 2007	(*intermediate project goals*)			
output target 2008	Methodology and software for LD-based phenotype analysis developed			
output target 2009	*to be determined*			
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 products				
Output 5.1. Annual training courses in genomics/molecular breeding, bioinformatics, and phenotyping conducted		Researchers collaborating directly or indirectly with the GCP	Regional courses in the subject matter of critical importance to furthering the goals of the GCP conducted in Africa, Asia, and Latin America	Increased capacity of scientists in target countries to collaborate with GCP and conduct their own research toward improved crop varieties for farmers
output target 2007	At least 15 researchers trained per course			
output target 2008	At least 15 researchers trained per course			
output target 2009	At least 15 researchers trained per course			
Output 5.2. Course and training materials on intellectual property, freedom-to-operate, and genetic resources policies 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 made available	Increased understanding in the GCP and wider scientific community of genetic resources policies and their implications for research
output target 2007	Materials developed and a test-run of the course provided to GCP researchers and collaborators			
output target 2008	Course materials made available online, distributed to GCP Institutions in electronic format (CD-ROM/DVD)			
output target 2009	*completed*			
Output 5.3. Training materials for association studies/linkage disequilibrium mapping developed		GCP researchers and collaborators, particularly 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 toward improved crop varieties for farmers
output target 2007	Training materials and a curriculum for a course in association analysis/LD mapping for collections of diverse crop germplasm generated			
output target 2008	Course materials made available online and as CD-ROM			
output target 2009	*completed*			
Output 5.4. GCP training materials translated into Spanish, French, Chinese, and Arabic		Crop researchers relying on Spanish, French, Chinese, or Arabic	Training materials in five languages made publicly available	More scientists able to gain capacity in these research fields, and thus able to benefit from the GCP's research
output target 2007	Training materials for genetic diversity analysis, genomics, and comparative genomics translated and made available via the web and CD-ROM			
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			

Outputs	Output Targets	Intended user	Outcome	Impact
Theme 2. Cultivation of research and learning opportunities for GCP collaborators and NARS scientists to further GCP mission and progress				
Output 5.6. Mini-grants program implemented		NARS in GCP target regions and their collaborators	Support for facilities/supplies upgrade provided to GCP target NARS to boost ability to collaborate	GCP products more readily employed by researchers in developing countries in the development of improved crops
output target 2007	At least 10 mini-grants provided to collaborating GCP researchers and their institutions for upgrading facilities			
output target 2008	At least 10 mini-grants provided to collaborating GCP researchers and their institutions for upgrading facilities			
output target 2009	At least 10 mini-grants provided to collaborating GCP researchers and their institutions for upgrading facilities			
Output 5.7. GCP Fellowship Program continued (initiated in 2005)		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 2007	Eight fellowships awarded			
output target 2008	Eight fellowships awarded			
output target 2009	Eight fellowships awarded			
Output 5.8. GCP Travel Grant program continued (initiated in 2005)		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 2007	Sixteen travel grants awarded			
output target 2008	Sixteen travel grants awarded			
output target 2009	Sixteen travel grants awarded			
Output 5.9. Contributions to special conferences		Scientists in developing countries with an interest in GCP-related research	Enhanced awareness in the wider scientific community of the GCP's mission and goals	Increased capacity of scientists in target countries to collaborate with GCP and conduct their own research toward improved crop varieties for farmers
output target 2007	At least 10 NARS participants selected to attend a conference of relevance to the content of the GCP			
output target 2008	At least 10 NARS participants selected to attend a conference of relevance to the content of the GCP			
output target 2009	At least 10 NARS participants selected to attend a conference of relevance to the content of the GCP			
Output 5.10. Academic position in molecular breeding established and supported		PhD candidates in selected African countries and breeding programs	Program established to train African plant breeders	Increased human capacity in national breeding programs in Africa
output target 2007	A molecular breeding professor posted at the African Center for Crop Improvement, who advises at least 10 PhD candidates			
output target 2008	10 new PhD candidates advised			
output target 2009	10 new PhD candidates advised			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 5.11. Capacity-building mechanisms and product pipelines established for tropical legume improvement in Africa		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 2007	Training courses, hands-on training, and degree opportunities offered to groundnut, bean, cowpea, and chickpea researchers			
output target 2008	*continued*			
output target 2009	*continued*			
Theme 3. Construction of systems for ensuring product delivery				
Output 5.12. Partnership and delivery options for the GCP surveyed and assessed		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 and conduct their own research toward improved crop varieties for farmers
output target 2007	Research, infrastructure, and human resource capacity of NARS in GCP target regions assessed; information used to inform development of new partnerships			
output target 2008	Assessment refined			
output target 2009	Assessment refined			
Output 5.13. Comprehensive support provided to competitive projects to define and implement delivery and capacity building plans		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 being employed by researchers in the development of improved crops
output target 2007	Linkages established between research and delivery partners for each of the competitive grants, and plans developed to fulfil needs of NARS to benefit from the project			
output target 2008	Plan for capacity building of NARS implemented			
output target 2009	Plan for capacity building of NARS 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 2007	A strategy document developed			
output target 2008	An implementation plan developed			
output target 2009	Plan for product distribution implemented			
Theme 4. Development and implementation of support services				
Output 5.15. Helpdesk for intellectual property and access and benefit-sharing issues established		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 2007	E-versions of all GCP documents and related websites relevant to IP and ABS management posted to the web			
output target 2008	Materials and advice available via the web			
output target 2009	Materials distributed to GCP institutions in electronic format (CD-ROM/DVD)			
Output 5.16. Asset inventory system for the GCP developed		GCP community, wider scientific community, and stakeholders	A database of products, expertise, and third-party materials associated with specific products for the GCP created	Increased access to asset information, critical to delivering research outputs
output target 2007	E-versions of asset/product identification forms provided via the web			
output target 2008	An inventory of GCP products available			
output target 2009	An update of the inventory with new products identified and reported			

Outputs	Output Targets	Intended user	Outcome	Impact
Output 5.17. Interactive Resource Center established and maintained		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 2007	Educational/training resources for scientific research available online			
output target 2008	*completed*			
output target 2009	*none*			
Output 5.18. Genotyping support service established (Phase 1. genotyping, Phase 2. identification of markers) -- phases rolling every year		NARS researchers	Enhanced access to quick and efficient genotyping of relevant germplasm	Increased capacity of molecular breeding programs in developing countries to develop improved crop varieties
output target 2007	Genetic diversity of selected germplasm (potato, cassava, coconut, Musa, groundnut) in selected breeding programs compared with GCP reference samples			
output target 2008	Measures of linkage disequilibrium in selected germplasm (cassava) available, and appropriate markers to advance to a molecular breeding scheme of selected germplasm identified			
output target 2009	Measures of linkage disequilibrium in selected germplasm (crops to be determined) available, and appropriate markers to advance to a molecular breeding scheme of selected germplasm identified			
Output 5.19. Technical backstopping provided		NARS in GCP target regions and their collaborators	Critical support provided to GCP collaborating NARS	Increased capacity in NARS to partner effectively with the GCP and adopt GCP products in the development of improved crops
output target 2007	At least 10 GCP researchers provide on-site support to NARS involved in GCP ongoing research			
output target 2008	At least 10 GCP researchers provide on-site support to NARS involved in GCP ongoing research			
output target 2009	At least 10 GCP researchers provide on-site support to NARS involved in GCP ongoing research			
Theme 5. Ex ante impact analysis and impact assessment				
Output 5.20. Potential impact of GCP research assessed		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 2007	An impact study based on selected crops, technologies, and target regions commissioned			
output target 2008	Results of impact study available and used to guide GCP strategic decisions			
output target 2009	*to be determined*			