Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE POOR

Medium-Term Plan

2006-2008

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Generation Challenge Programme

2006-2008 Medium Term Plan

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Contents

Acronyms and Abbreviations

ACGT	African Center for Gene Technologies
AGROPOLIS	International Complex for Research and Higher Education in Agriculture
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
COS	Conserved orthologous sequences
DNA	Deoxyribonucleic acid
DREB	Dehydration responsive element binding
EMBRAPA	Brazilian Agricultural Research Corporation
eQTL	Expressed quantitative trait loci
EST	Expressed sequence tag
FAO	Food and Agriculture Organisation of the United Nations
GCP	Generation Challenge Programme
Gramene	A comparative mapping resource for grains
GxE	Genotype times environment interaction
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 Center, 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
NGO	Non-governmental organisation
NIAS	National Institute of Agrobiological Sciences, Japan
PAC	Programme Advisory Committee
PCR	Polymerase chain reaction

PRMT	Programme Research Management Team
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 Center
WTO	World Trade Organisation

Introduction

Since the inception of the Generation Challenge Programme in September 2003, rapid progress has been made in the implementation of the GCP research and capacity building portfolio. At the same time, the vision and strategies have matured substantially, now aimed more solidly toward consolidating and refining the research mandate and implementing a strategy to ensure product delivery to intermediate users and farmers. A strong base has been created – in terms of organisation, technical infrastructure, knowledge systems, and novel research activities – that makes steady progress toward the GCP goal of creating a public platform of genetic, genomic, and bioinformatics tools for use in plant breeding programs. It is recognized, however, that the research agenda needs additional focus, within and across the subprogrammes, to demonstrate: 1) the value of the multidisciplinary approach, including comparative genomics, considered in the GCP; and 2) the ability to quickly deliver targeted products to plant breeding programs for short-term impact in farmers' fields.

The GCP approach of applying the newest advances in genomics to unlock crop genetic diversity and develop improved, stress tolerant varieties for farmers in the developing world has appealed to scientists and donors alike. The founding sponsors of the GCP – the World Bank and the European Commission – have been joined by the UK Department for International Development, who committed to fund the GCP for five years at 2.5 million each year. The Rockefeller Foundation and several other non-traditional CGIAR donors have also made significant contributions. Partnerships with GCP member institutions have been enhanced and enriched as a result of the new consortium research model championed by the GCP. In the 2005 research portfolio, there are 26 non-GCP NARS partners and 27 non-GCP ARI partners. The GCP itself has also increased its membership to complement the capacity of the current consortium: during 2004, the Africa Rice Center (WARDA), the African Center for Gene Technologies in South Africa, and the Indian Council for Agricultural Research were added to the consortium.

Since the submission of the 2005-2007 Medium Term Plan in August 2004, the Generation Challenge Programme (GCP) has awarded 17 competitive grants spanning projects in cutting-edge research themes across 9 crops. The commissioned research process – designed to tie the competitive projects together into a cohesive package and contribute to the broader technology platform the GCP has created – was also initiated, and 34 research projects and 15 capacity building/enabling delivery activities are underway in 2005, with investment in 20 of the CGIAR mandate crops[1]. Hundreds of scientists around the world are now engaged or affiliated with GCP research. Though this scientific network has huge potential for research synergies and spillovers across disciplines and areas of expertise, the challenge remains to chart a cohesive vision to uphold the commitment to deliver meaningful products to poor farmers during the life of the GCP.

The development of the 2006-2008 MTP was an important but difficult exercise for the Generation Challenge Programme. The 2004 outputs were integral to establishing the set of basic tools, technologies, and products the GCP has to work with to achieve the medium term goals of gathering and applying essential genomic information of the target CGIAR crop species; establishing the technical and scientific foundation for the future activities of the GCP; and creating the institutional structure that will support such a complex international undertaking. Now that the foundation has been laid, however, greater emphasis is being given to the development of tools and products that can rapidly improve plant breeding, and therefore impact the livelihoods of resource-poor farmers.

The GCP realizes the importance of making the tools and the products it generates available to potential users in a quick and efficient manner, and this evolving emphasis on product development and delivery is reflected in the new MTP. Interaction with potential beneficiaries, for example, is one integral activity of Subprogram 5, which provides the GCP with an iterative mechanism to solicit feedback on the products that we should deliver and the best way of doing so. Although this orientation towards product delivery is only just beginning, by the end of 2008 the GCP should be strongly positioned with an effective delivery pathway for its emerging pipeline of improved seed-based products. For the upstream research activities, this product-driven focus is also starting to bloom. The change of the directorship during the middle of

[1] 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. Currently, there are no projects in finger millet or forages.

2005 provides a timely opportunity for refocusing the research portfolio based on the achievements we have made so far, our areas of comparative advantage, and the needs of the potential users of GCP products. The 2006-2008 Medium Term Plan reflects the evolution and shift in leadership of the GCP, and presents an overview of our current research activities designed to reach our medium and long term goals.

Achievements of Year 1

In its first year the GCP has seen tremendous activity. For a detailed description of achievements, please consult our 2004 Annual Report (http://www.generationcp.org/workplan.php). Here we provide a sampling of Year 1 achievements:

- After selection of core samples from the global diversity available in international and national collections, a massive genotyping activity using microsatellites has been started, that will result in more than a million SSR datapoints by the end of 2005, corresponding to detailed characterization of eleven crops and gross characterization of seven other crops. This large-scale genotyping effort should allow for the identification of a set of composite genotypes that would serve as main genetic pool for gene discovery and germplasm improvement.
- Phenotyping protocols have been developed, and phenotyping activities on germplasm and advanced breeding lines were undertaken in a range of crops under investigation in the GCP (e.g., potato, bean, chickpea, cowpea, maize, wheat, rice, barley, and banana). Two workshops were conducted at Agropolis and IRRI to discuss the criteria for choosing measured traits in the different species of the GCP, and methods and criteria to impose and characterise stresses.
- A set of methods for studying molecular variation are being tested and applied. Some reveal anonymous markers used for genome-wide surveys (DArTs), while others reveal variation within candidate genes (EcoTILLing) or in their regulating factors (non-coding SNPs in barley).
- The Affymetrix barley array chips (22,840 ESTs/each chip) were applied to study the response to drought in barley and rice. The 60K BGI chips were also successfully tested. Further gene expression data were produced for maize, potato, and *Arabidopsis*.
- Activities were conducted in marker-assisted selection of drought tolerance in maize, pearl millet and common bean, and the stay-green component of drought tolerance in sorghum. Genetic populations for mapping root trait components of drought avoidance in chickpea were also generated.
- A high performance computing capacity was created, involving installation of Paracel hardware at three locations (CIP, IRRI and ICRISAT), installing appropriate software such as Structure and R, and linking the facilities to each other with LSF Multicluster software and to the Internet by creating a gateway website. All consortium members can get access now to this 'super computer' to perform analysis that require large amounts of CPU and memory, such as whole genome blasts, specific simulations, etc.
- A wide range of capacity building activities were developed and undertaken, including a needs assessment workshop, the GCP fellowship programme, the travel grant programme, the Pioneer-GCP fellowship, and the launching of a Virtual Resource Center and on-line helpdesk.

Context

Three simultaneous technological revolutions over the past decade have had dramatic impact on the development-oriented research programme of the CGIAR. The revolutions in the fields of molecular biology and genetics, data storage and management, and communications introduce capabilities and opportunities that were undreamt of as the CGIAR was taking shape over thirty years ago. The Generation Challenge Programme, more than any other, represents how the CGIAR is demonstrating the flexibility to respond positively to dramatic changes in its operating environment.

The spectacular advances in pharmacology and human genetics made possible by the Human Genome Project and model mammalian systems projects (e.g., the mouse) are harbingers of what is to come for plant systems. The application of cross species comparative genomics and association genetics has revealed surprisingly simple genetic relationships for physiologically complex syndromes in humans. It is reasonable to expect that complex traits, such as tolerance to drought and other abiotic stresses, may be deciphered in important food crops using approaches similar to those undertaken during the completion of the decoding of the rice genome and the dicot model species *Arabidopsis thaliana* and *Medicago truncatula*. Indeed, there is a steady flow of reports in the scientific literature describing advances in our understanding of the relationship between gene sequence, function, plant physiology, and performance. That the private sector is now investing heavily in the development of drought tolerant cultivars through the application of plant genomics is a clear signal that practical results are possible for even the most difficult traits.

Nonetheless, the extraordinary discoveries of plant molecular biology, largely led by advanced research institutions in the "North" have yet to be used in ways that will benefit the world's poor; likewise, the rich pools of genetic resources collections held by national agricultural research systems (NARS) and the CGIAR have yet to be tapped in a systematic way. The GCP creates a strong coalition of institutions dedicated to alleviating poverty by applying the recent advances of the biological sciences. This alliance aims to harness the powerful tools of the genomics revolution to unlock the genetic potential within crop germplasm to address the needs of the resource-poor. One of the principal products of the GCP will be a unique *public platform* for accessing and developing new genetic resources using new molecular technologies and traditional means. The GCP will make available as public goods an unprecedented array of genomic and genetic resources, ready for direct use in plant improvement. These products will be in the form of enabling technologies and intermediate products for crop improvement programmes in NARS and elsewhere. To make sure that the products meet the needs of the users, feedback mechanisms are being created that allow the breeders from NARS and other crop improvement programmes to directly influence decision making concerning the research agenda and delivery. Finally, to enable crop improvement programmes—particularly NARS breeders, who are our primary target users—to effectively use the products, an extensive capacity building programme has been initiated to train scientists in the tools and methodologies of the GCP.

Why a Challenge Programme?

There is a clear and convincing case that the revolutions in biology, data management, and communications provide tremendous opportunities for solving some of the world's most serious agricultural and food security issues. But, what advantage comes with creating a new programme, rather than simply providing additional funding to the individual commodity programmes? From a strictly scientific perspective, it is clear that new major advances in crop improvement will be derived via comparative biology and comparative genomics. The profound insights afforded by the discovery of broad synteny in genome organisation among related species argue that it is far more informative and efficient to study genetic variation in sets of related species than to focus on one alone. Fundamental questions related to the genetics and physiology of adaptation to drought, root architecture, and/or low phosphorus in legumes must be addressed by teams that involve scientists from several centers. By creating a framework in which cross species research can be conducted, the GCP captures the expertise and knowledge specific to individual crops in different centers and incorporates this into a common research programme.

The GCP framework for multi-institutional research is further enhanced by the competitive grants programme established in 2004. The competitive grants scheme is a transparent, merit-based process to attract new and powerful partners to address its research agenda. The strong response from the research community (over 130 non-consortium member institutions participated in the proposal process) indicates that this will be a successful model.

An important component of the GCP comparative genomics approach is that common procedures for data collection and measurement must be developed. As an independent programme, the GCP provides the global forum appropriate to create these common operating procedures. In addition to standard and agreed upon means of data collection, a comparative biology approach demands that data from many experiments be accessible to the broader community. This means that there must be assured interoperability among databases and the analytical tools used to query them. The GCP offers the means to develop effective interoperability and to create a global public platform for data access, analysis, and interpretation, linking the GCIAR institutes to the resources in the rest of the world.

Programme Strategic Focus

The GCP's development goal is to increase food security and improve livelihoods in developing countries by unlocking the genetic potential and enhancing the use of public genetic resources in plant breeding programmes through the concerted generation, management, dissemination, and application of comparative biological knowledge. In pursuit of this goal, the GCP will create an integrated platform for dissecting genetic diversity in crop plant genetic resources, identifying important genes to reduce the impacts of environmental and biotic stresses on crop productivity, enhancing yield, and improving nutritional quality of crop products. Beyond this, the GCP will identify, manipulate, and validate gene expression resulting in plants with potential value far beyond present-day crops. These plants, through seeds or vegetative propagules, will be transferred to breeding programmes. An important GCP contribution will be to enhance the capacity of NARS scientists to participate in this programme, and help steer the programme so that it will create the proper products and use the proper approaches to deliver them.

The key feature of the GCP platform will be its applicability to any crop and any trait, thereby ensuring that all 22 CGIAR mandate crops will be supported by the platform. Despite the broad applicability of the GCP platform, there is still a need for focusing GCP activities. The research agenda of the GCP has to be adjusted to take into account: 1) the different levels of knowledge (sequence, gene, phenotype) available in the various crops and the sheer amount of information being generated today; 2) the activities already underway in the public and private sectors to tackle the genetic basis of drought tolerance in cereals; and 3) the current resources allocated to the GCP. Given the considerations above, the GCP must demonstrate the efficiency of the comparative genomics approach to address important biological questions in a few target crops in the medium term. Traits and crops must be selected so as to benefit the greatest numbers of the resource poor as soon as possible; consequently, regional considerations are important in setting research priorities.

The GCP has several means of establishing and maintaining its focus, relevance, and applicability. First, with the support of GFAR we have created a diverse global Stakeholders' Committee comprised of representatives of NARS from the regional fora, NGOs, farmer associations, and the private sector. An informal mechanism of maintaining the proper focus is the interaction of GCP staff with NARS' and other breeders in the target areas during the many courses that are organized in the framework of the capacity building projects. In addition to these mechanisms, the CGIAR Research Priorities 2005-2015 as formulated by the Science Council act as our guiding principles. Far and away the most important of these is System Priority 2: "Producing more and better food at lower cost through genetic improvement", in which priorities 2a, 2b, and 2d are directly addressed by the GCP:

2a. Maintaining and enhancing yields and yield potential of food staples
2b. Tolerance to selected abiotic stresses
2d. Genetic enhancement of selected species to increase income generation by the poor

The GCP also contributes to priority 1a.: Conservation and characterization of staple crops.

Internal Organisation of Research

The GCP is organised in five subprogrammes to collectively address the following comprehensive objective:

> To develop a platform for and conduct analysis of genetic diversity of international crop genetic resources and apply this to improve major crops for drought tolerance and other related traits of importance to resource-poor farmers, and to strengthen the capacity of NARS and GCP scientists to apply the tools of genomics, molecular biology, and bioinformatics to the analysis of genetic diversity and use this knowledge to improve crop breeding programmes and develop new stress-tolerant varieties.

All five subprogrammes aim at the GCP purpose of creating a freely available public platform to access and utilise the vast genetic diversity held in germplasm collections of crops and their wild relatives. In addition to gene/trait discovery and application, the GCP subprogrammes also establish the mechanisms at a CGIAR level for capturing, storing, analysing, accessing and interpreting the vast amount of biological data that the GCP and its partners will generate. Integrated into all the subprogrammes is a strong capacity-building component that assures that scientists from developing countries will be active partners in the Programme and help ensure that the products of GCP research will ultimately reach the intended beneficiaries. Considering the global priority given to water use and managing its scarcity, and its relevance to all production systems, the GCP has selected drought tolerance as the over-arching trait around which to organise and focus its activities.

Each of the subprogrammes has a set of clearly defined and measurable outputs that relate directly to its rationale and objectives. These subprogrammes are tightly linked to each other in terms of exchange of knowledge and material. Integrated into all the subprogrammes is a strong capacity-building component that assures that scientists from developing countries will be active partners in the Programme and help ensure that the products of GCP research will ultimately reach the intended beneficiaries.

The GCP subprogrammes and their operational objectives are:

Subprogramme 1: Genetic Diversity of Global Genetic Resources

This subprogramme aims to characterise the diversity of the crop germplasm collections held by the CGIAR and its partners. This characterisation includes an assessment of the genetic structure of the collections as well as the phenotypic variation associated with that structure.

Subprogramme 2: Comparative Genomics for Gene Discovery

This subprogramme focuses on genomic tools, technologies, and approaches to achieve an understanding of gene systems across many species of importance to developing country agriculture. Comparative biology and genomics will be used to discover and validate the function of key genes central to the practical objectives of the Generation CP.

Subprogramme 3: Trait Capture for Crop Improvement

This subprogramme focuses on the validation and refinement of molecular breeding systems and the resultant enhanced germplasm with the primary purpose of increasing the efficiency, speed, and scope of plant breeding gains. This includes the creation of appropriate technologies for the application of marker-assisted selection in national breeding programmes, and the development of communities of practice.

Subprogramme 4: Genetic Resource, Genomic, and Crop Information Systems

This subprogramme addresses the challenge of linking and integrating the GCP information components and analysis tools into a coherent information gateway. A bioinformatics, biometric, and advanced data management system is under development to support an integrated genetic resources, genomics, and crop improvement information network.

Subprogramme 5: Capacity Building and Enabling Delivery

This subprogramme has two dimensions: one is to better enable GCP members to carry out this cutting edge research agenda, and the second is to empower national programme scientists to participate in GCP activities. In combination, these two activities create mechanisms by which GCP products can reach crop improvement programmes and farmers. Because of its cross-cutting character, much of the GCP's policy-related activities are also incorporated in this subprogramme.

Highlights of 2006 Project Portfolio

In this section we describe changes in the project portfolio since the submission of the last MTP. At the time of submitting the MTP last year, the GCP had not completed the process of awarding all competitive and commissioned grants; as a result, the output statements were estimates of potentially funded projects. The format and terminology of the current MTP is also different: the Activities of last year correspond to Projects in the new logframe, and the output statements are specific to the objectives and deliverables of each funded project.

Subprogramme 1: Genetic Diversity of Global Genetic Resources

One significant shift in SP1 concerns the genotyping activities, which have met with some difficulties that have affected most laboratories: difficulties in equipment maintenance, reagent supply, instability of the quality of the results, and comparability between laboratories. As a result of these factors some delay occured in data production and extra costs were generated. The possible financial solution to decrease the price per datapoint, proposed in 2004 by the subprogramme to the genotyping groups in 2005, appears to be difficult to implement, despite initial approval of several laboratory heads, and should probably be revised. Moreover, as exemplified by the community of researchers on the human genome, there may be a need to refine the genotyping tools by continuously replacing existing markers by those rare markers that appear technically easy and repeatable among labs, in order to tend towards a truly universal kit for each crop. Thus, there will have to be some remnant genotyping activity in the coming years.

The strategy for phenotyping for drought tolerance was discussed in length in May 2005 at Embrapa, at the workshop for the "Phenotyping network" and the "Whole plant modeling" projects and will likely shift. At the workshop, it was clear that phentyping strategy needs to be harmonized with the genotyping work in terms of calendar, capacity of accommodation, and number of accessions. We may start with 5-10 diverse accessions that will be used by modelers to calibrate their models. The "reference samples" that SP1 is developing may also be thought of in a more flexible way than before and their integration into the phenotyping process may happen in a more gradual manner that previously planned.

Subprogramme 2: Comparative Genomics for Gene Discovery

Overall, the research portfolio from 2005 onwards reflects an improvement over Year 1 due to the implementation of a competitive grants programme which imposes greater discipline on the workplan and outputs. In Year 2, we see a "filtering" of research activities that reflect better coordination among collaborators and more focused research targets. The competitive grants together with commissioned projects also provide the Subprogramme Leader a better framework to promote linkages. This results in an agenda that demonstrates a logical progression from resource development to development of longer-term common research platforms to achieving near-term targets. Building upon Year 1 collaboration, it also becomes more feasible to package traits (combining traits tolerant to biotic and abiotic stresses) through coordination within SP2 and between Subprogrammes. Furthermore, results generated in Year 1 also modify the approaches taken in Year 2. Specifically, we see a shift in emphasis towards:

- Creating new, unique genetic materials not available in the international research community
- Enabling more exploitation of model species and accessible genomic tools (e.g., rice genome sequence and associated resources)
- Adopting multiple technology platforms (rice, barley, and maize oligo chips) whenever accessible, and benefiting from comparative analysis via bioinformatics
- More focused phenotyping and characterization of advanced genetic materials.
- Sequence-based analysis of orthologous genes and functionality

In contrast to last year's MTP, where we were not able to specify the near-term results, the current MTP highlights activities with promising outcomes from projects involving fine-scale QTL mapping and candidate gene analyses (e.g. phosphorus uptake, aluminum toxicity tolerance, and salinity tolerance).

In the current MTP, there are no major changes at the higher levels of subprogramme organisation. To better match outputs to Project objectives, we have re-positioned some of the competitive and commissioned projects: "EST development" is now placed in Project 2.1 (Genomic resources), "*Musa* sequencing" is now in Project 2.2 (Comparative mapping), "Target discovery of superior disease QTL..." and "Association mapping in maize.."º are now in Project 2.3 (Assign genes and pathways.), and "Isolation of Aluminum tolerance genes .." and "Revitalizing marginal land.." are now in Project 2.4 (Validate gene function...)."

Subprogramme 3: Trait Capture for Crop Improvement

The current portfolio of activities differs considerably from the founding vision and first year workplan of subprogramme 3. The evolution of the subprogramme represents the heavier investment needed to define a more effective product development strategy and pilot testing of finished products in farmers' fields. The following table lists which activities have been removed from SP3 and why:

2005-2007 MTP Activity	New Location	Explanation
Whole plant physiology modeling	SP1	To establish better continuity and linkage with the year one phenotyping community
QTL mapping	SP2	To establish better continuity and priority setting between upstream activities and a defining focus on development of gene-based marker technologies
Technical assistance for the rapid and effective uptake of molecular breeding in tropical staple crops	SP5	Generic capacity building activities now consolidated in SP5 to enable SP3 to focus on specific product development and pilot testing
Development of communities of practice supported by regional centers of excellence and state-of-the-art technologies and approaches	SP5	Generic capacity building activities now consolidated in SP5 to enable SP3 to focus on specific product development and pilot testing

The strategic changes in the structure of SP3 reflect a commitment to gene-based marker technologies as a fundamental operational pillar for the defining comparative genomics mandate of the GCP. However, in the short-term, several competitive projects were granted that are based on the use of linked markers. These provide an opportunity to establish the product delivery pathway using traits that are somewhat less complex and/or marker systems that have been well validated.

Subprogramme 4: Information Systems and Bioinformatics

The activities listed in last year's MTP have largely been done as planned, and the planned activities for 2006 are still in the MTP. The only significant changes occurred in Activity 1.4.4: "New data processing and analysis tools developed that serve the needs of Subprogrammes 1, 2 and 3" that corresponds to the current Project 4.3: "Specific activities in the GCP supported in terms of software tools". These changes were based on an inventory of needs of the SPLs of the first three subprogrammes.

Since the format and set up of this year's MTP is rather different from last year's and since the last workplan of SP4 reformulated and regrouped activities the correspondence between last year's and this year's MTP is not obvious in all cases. It can be expected however that the current organisation of the MTP will remain stable over the coming years.

Subprogramme 5: Capacity Building and Enabling Delivery

This year's MTP for SP5 reflects the following major changes: 1) the relocation of the policy area from SP1; 2) the steps for putting in place a coherent delivery strategy; 3) the requirement of a targeted selection of NARS based on their own intention of involvement with the GCP and their capacity needs; 4) the use of monitoring mechanisms for updating activities and refocusing the capacity building programme; and 5) the identification of different regional approaches for delivery of sustainable GCP-related capacity. In all, the changes are the result of the first year of experience and represent the determination for a more focused programme.

The reasons for including policy and the development of a delivery strategy have already been presented in the first parts of this MTP. The following two changes (3 and 4) are based on the acceptance of intrinsic limitations to the willingness to spread the GCP work and impact as broadly as possible. It is the view of the GCP that all NARS should have a place in our programme to collaborate and benefit from the outputs and products; however, in practice it is impossible to reach an unlimited number of NARS with the expectation of having immediate and high impact. This insight has led to the design of a targeted plan, which will be used for better selecting participants for capacity building activities as well as for adding the necessary focus to the activities themselves. The GCP's capacity building activities will be delivered in accordance with NARS country policies, institutional priorities and rationalization, and present technical and infrastructural

capacity. The last change incorporated in this MTP reflects the discussion with NARS representatives during the workshop to assess capacity needs: it was concluded among the NARS representatives that different regions need different approaches for sustainable delivery of capacity in the long term. Thus, while the proposal of regional research hubs was welcomed as a plausible strategy for Africa, Asia and Latin America representatives seemed to prefer the adoption of other mechanisms. Options will be explored to ensure that GCP investments in infrastructure and human resources in national programmes are the most cost-effective and appropriate for the various regions.

Collaboration

The GCP was designed to be an innovative, collaborative research programme, and in the first year we saw an explosion of emerging partnerships that were unthinkable only a few months before and would not have happened without the incentive and facilitation of the GCP. The competitive grants programme in particular stimulated a whole range of impressive new collaborations across CG centers, ARIs, and NARS.

Some examples of new collaborations in the competitive and commissioned research projects:

- The CIMMYT-led wheat genetic resource project brings together major wheat genetic stock centers around the world to agree upon sharing, distribution, and phenotyping of special genetic materials.
- The Wageningen-led project on rice mutant phenotyping involves 9 PIs and 3 collaborators of leading laboratories around the world that together have produced over 100,000 sequence-indexed rice mutants. Under the GCP, these laboratories agree to a coherent plan to generate genetic and phenotypic data on sequence-tagged mutant lines related to stress-response.
- CIP is collaborating with the University of Jerusalem and the Scottish Crop Research Institute to produce true-seed potato mutant stock, a unique genetic resource suitable for wide distribution.
- The *Musa* project involving NIAS and the *Musa* genomics community represents a new partnership capitalizing on the rich experience of genome sequencing and bioinformatics of NIAS.
- The CAAS-led project on gene expression analysis involves Beijing Genomics Institute, NIAS, and CIAT, representing a novel combination of partners that apply the expertise in genomics and gene chip analysis to well-characterized genetic resources.
- The IRRI-led project on cloning and deployment of salinity tolerant and P-uptake efficiency genes in rice has mobilized contribution from CSIRO, University of California-Davis, NIAS, and NARES from Indonesia, Bangladesh and Iran.
- The Cornell-led project on aluminum toxicity tolerance in cereals brings together collaboration with Embrapa and NARS in Kenya.
- The WUR lead project dealing with QTL and GxE interaction analysis involves new partners Instituto de Investigaciones Agropecuarias (INIA) in Chile and Universidad Autónoma Chapingo in Mexico.
- The 'Domain Modeling' activity in SP4 involves a large number of new partners in the discussions about the models under development. For example, all members of a task force based on the Internet Advisory Group of the European Cooperative Programme on Crop Genetic Resources (ECP/GR) that were involved in the preparation of a project proposal for the EU were invited to join the discussion in the newly created GCP Wiki environment. Some of them play active roles.
- The exploration and validation of new genotyping techniques (SP1) brought up collaborations with new institutions: University of Adelaide (Australia) and NIAB (UK) on NC-SNPs; University of Washington and Fred Hutchinson Cancer Research Center (USA) on EcoTILLing; and DArT Pty Ltd, Canberra (Australia) on DArTs.

The list of institutes and organisations with which some sort of collaboration exists is obviously much larger. Just to name an additional few:

NARS – Bangladesh (DU), Colombia (CORPOICA), Ghana (CRI), India (CPRI, IGAU, IIPR, NDUAT, TNAU, UASB), Indonesia (ICABGRRD), Kenya (KARI), Malawi (CC), Nigeria (NRCRI), Philippines, Senegal (CERAAS), Tanzania (UCABREN), Thailand (NSFCFC), Uganda (NARO, PRAPACE), Zimbabwe (SIRDC)

International centers/programmes – CAS-IPGRI, FAO, Harvest Plus CP, Water and Food CP

Regional networks – NEPAD's Biosciences East and Central Africa, Rockefeller Foundation East and Southern Africa Marker-assisted Selection Network, Kirkhouse Trust, West Africa Legume Molecular Breeding Network

Advanced Research Institutions – Australia (CSIRO), Belgium (UNU-TECH), Japan (JIRCAS), South Africa (ARC), UK (US, DU), USA (CU, UCF, UVA, KSU, PGEC, UF, UCDC, USDA)

We are aware of the risk of spreading GCP resources too thin and diluting our effect and impacts. It is important to facilitate the formation of smart partnerships to get the most value for project funds with the highest likelihood for rapid results and on-the-ground impact. The GCP operates on the principle that we fund outputs, not inputs, so we seek partners who can produce high quality outputs at the best price. But the GCP recognizes the need to include more NARS partners, not just in capacity building activities but also in the research programme, so over the next several years, our calls for proposals and commissioned activities will be increasingly designed to encourage more and more targeted partnerships with NARS scientists.

Centre Financial Indicators

For the GCP to maintain the flexibility and innovation needed to continue achieving its research objectives, a stable and sufficient funding base is essential. Projected income for the period 2006-2008 is expected to be US$13 million for 2006 and $12 million per year for 2007 and 2008. The projected decline is due to the completion of the Rockefeller Foundation projects, which are managed by the GCP.

Expenditures in 2006 will exceed 2006 income by about $3.6 million, which will be covered by carryover from years 2003 through 2005. This large carryover is explained by the remaining funds (20%) of commissioned grants that will be disbursed in 2006 and the shift of the first instalment of the second round of competitive grants from 2005 to 2006 to accommodate the GCP's call for proposals in late 2005. As there will be a very small carryover from 2006 to 2007 and the projected income for 2007 is $12 million, the commissioned research budget in 2007 was provisionally decreased for the purposes of this MTP. Because the GCP aims to maintain the momentum of the complementary competitive and commissioned research schemes at the level of funding they currently enjoy or higher, a short-term fundraising scheme will be developed in late 2005 to help plan for additional funding.

See Annex 2 for the GCP 2006-2008 Finance Plan.

Project Narratives

Subprogramme 1: Genetic Diversity of Global Genetic Resources

Rationale

Access to sources of genetic diversity that may supply genes and alleles involved in key agricultural traits is essential to the mission and objectives of the GCP. 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 across 22 crops collected in gene banks around the world, high-throughput molecular screening techniques must be developed to genotype the collections for fast results. Appropriate screening techniques to phenotype the collections for traits such as drought tolerance also need to be developed and applied to obtain reliable and analyzable phenotype descriptions accompanied by the associated descriptions of environmental and weather conditions. Once the genotypes and phenotypes have been established, association studies and/or population genetics approaches must be conducted to illustrate their interactions.

This basic rationale has several components. The first consists of monitoring global and easily accessible germplasm 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 used by national programmes for integrating and comparing their own materials. The second component is the operational portion and consists of developing and consolidating a global facility for the molecular description of germplasm with specific attention to efficiency, throughput, flexibility, and accessibility. The third component specifically addresses drought tolerance, the GCP's priority trait: how to assess this 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 combines the comparative description of molecular polymorphisms and phenotypic variation and the study of associations. This fourth component thus rests on complementary modules, which must be coordinated for the best global efficiency, and be managed in the most open fashion to attract enthusiasm of national programmes. The fifth component looks at new approaches for relating genotype to phenotype by connecting genetic analyses directly to breeder activities and farmer practices.

Project descriptions

The activities in this Subprogramme are organized under the following themes presented as Projects in the MTP logframe:

- 1.1. Creation of an improved understanding of the structure of the diversity for the major world food crops
- 1.2. Development of HTP (high-throughput) genotyping techniques accessible in reference laboratories
- 1.3. Establishment and implementation of a scientific and organisational framework to describe tolerance to drought
- 1.4. Identification of potential genes or genome segments, and superior alleles or haplotypes through association studies
- 1.5. Development of novel populational approaches for relating genotypes to phenotypes

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

The first project is the foundation activity of SP1 and the GCP: the molecular characterization of global diversity, as represented in core germplasm samples chosen from the global diversity accessible in international and national collections. (The markers chosen are essentially Simple Sequence Repeats [SSRs, or microsatellites].) Such characterization highlights the structure of the diversity and provides a key to accessing diverse traits and a broad base for breeding. A good understanding of the genetic structure will help crop specialists to select germplasm samples they will use to explore the diversity available for particular traits. It will also help plant breeders to rationalize their strategy for reshuffling complementary genotypes in order to create new combinations or, alternately, to preserve balanced combinations by limiting the genetic distance between parents. The project will provide firm bases for establishing a reference to which any subsequent study can be compared. Particular attention will be given to the description of the technique, the results, and the allelic series; in addition, seeds or DNA samples bearing the allelic series as well as detailed data and results of analyses will be made available, so that each subsequent study has autonomy in this comparison. All this is essential for connecting local, national, regional diversity to the reference GCP global diversity. These activities will enable national systems to localize their own germplasm diversity in

relation to global diversity, and thus to be able to request and use the complement on a rational basis. By itself, this output has potential impact in improving the efficiency of breeding activities worldwide.

This project also aims at providing reference germplasm samples for analyzing associations between molecular markers and phenotypic traits. SP1 uses genome-wide data (generally 50 SSR loci) to select samples with continuous variation, which will be promoted across scientists in order to try and integrate all sorts of phenotypic and molecular characterization on the same materials. In cases where phenotypic data already exist, the genome-wide data can be used to correct the components of associations due to structure (e.g., STRUCTURE software). Information such as passport data, phenology, agropedoclimatic adaptation, etc., will be gathered and made available together with the seeds. As far as possible, the data will include an assessment of the level of linkage disequilibrium for those crops/populations which will be used for conducting association studies, so that the respective advantages of genome-wide surveys vs gene-targeted surveys can be weighed and their resolution power can be assessed. This will empower germplasm specialists to establish associations and identify genes/chromosome segments and alleles/haplotypes for use in marker assisted selection.

The development of this project has been determined by the choice of certain species for a first tier (rice, maize, sorghum, wheat, barley, cowpea, chickpea, common bean, cassava, potato, and *Musa*), and leaving other species for a second (finger millet, pigeon pea, lentil, groundnut, sweet potato, yam, and coconut) or a third tier. The former are generally analysed for a larger number of accessions and loci. The concrete outputs are expected in 2006 for tier 1 crops, in 2007 for the tier 2 crops, and in 2008 for the others.

The project can be considered closed in 2008. Its legacy will be a free dataset with growing amounts of information, with tools (e.g., marker kits, DNA for allelic series, etc.) and available seed. The quality and ease of use of the tools will be constantly evaluated and improved.

1.2. Development of HTP genotyping techniques accessible in reference laboratories

The GCP needs access to laboratories where high throughput genotyping can be conducted on its materials. The first round of massive characterization involves mostly SSRs. This is being handled in a decentralized manner and will have extensions that can be absorbed by the laboratories in the international centers. Future needs will essentially correspond to two types of 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 linkage disequilibrium analysis. Linkage disequilibrium is often significant in inbreeders; it may extend to the cM scale among traditional cultivars, and be higher in modern breeding materials, with high influence of the populations under consideration. It can also be high in some sections of germplasm in outbreeding species, e.g., due to admixture between divergent types. In some species like rice, where the amount of sequence information is high, SNPs can be the marker of choice. In others, it may be worth developing alternative non-sequence-dependant methodologies. Throughput, cost, easiness of access, and transferability are criteria for assessing such methodologies. Output 1 includes evaluation of the DArT technology on diverse representative crops; a first assessment will be completed in 2006.

Gene-targeted surveys for monitoring allelic variation at candidate genes aim at validating the involvement of specific genes and identifying superior alleles. Allele resequencing is so far the approach used in exploratory studies, but the cost is high. When a panel or representative germplasm has been monitored, the various haplotypes detected can be differentiated by specific SNPs, which in turn can be used to survey large numbers of accessions. Techniques to identify SNPs in large collections are very valuable in such a process. Output 2 includes the evaluation of the EcoTILLing technology and a study on barley to address SNPs in non-coding regulatory regions.

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

The third project aims to establish and implement a scientific and organisational framework to describe tolerance to drought. This framework began to take root at the GCP phenotyping workshop organised in July 2004 in Montpellier, where more than 40 breeders and physiologists from inside and outside the consortium met for a one-week workshop. Conclusions of the workshop stressed the importance of modelling in supporting the phenotyping process for drought tolerance by: 1) quantification of traits and integration of their impact on yield, 2) genetic analyses of adaptive traits, and 3) characterization of target population of environments. Through these efforts, SP1 seeks to promote better interactions between physiologists, modellers, and breeders to develop a comprehensive approach and improve phenotyping methods and outputs. Output 1 is the development of a set of phenotyping facilities that GCP and other crop specialists may access to screen germplasm. In coordination with some of the most advanced research groups in the world, this activity will provide: 1) access to a coordinated network of stations, scientists and facilities, and 2) a crop- and plant-modeling-based improved mode of phenotyping for tolerance to

drought stresses. The network of environments covered by Embrapa, further opened to other sites in Latin America and Africa, has very high potential for impact.

Output 2 consists of a modelling framework that will characterize environments for several target regions for the major crops using long-term daily weather data. These characterizations will include the major breeding locations, and a balanced sample of other locations to represent the production area of the region. Relevant soil types and management options will be simulated, and the results summarized by clustering 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 done 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 from experiments done by breeders, 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.

The competitive project "An ecophysiological-statistical framework for the analysis of G X E and QTL X E", which focuses on developing advanced statistical concepts, also complements the activities under this project. Another important effort is focused on cassava and uses progeny segregation analysis as well as a transgenic genotype over expressing a cytokinin synthesis gene for determining the peculiar mode of reaching high tolerance to drought in this crop.

1.4. Identification of potential genes (or genome segments) and superior alleles (or haplotypes) through association studies

Association studies compare molecular diversity with phenotypic diversity to identify genetic factors or genome segments that favorably contribute to the elaboration of target traits. The outcome is better identification of genetic factors to be combined in breeding progenies, as well as the molecular tools for doing so. Within the GCP, the main intended users are SP2 for cross validations and SP3 for implementation in marker assisted breeding. More generally, this will serve all breeders in the crops under consideration. Early activities began in 2005 for maize, rice, and wheat in specific environments and with specific target traits through analysis of unrelated cultivars. As an example, the work on maize focuses on various candidate genes involved in plant response to water-limited conditions: carbohydrates, ABA, and polyamines. This activity involves field evaluations in several locations under two water regimes over two years. The use of the phenotyping facilities will gradually increase over the life of the project. In 2006, a first set of a few contrasting genotypes, chosen to represent the various types of adaptation, will be characterized for rice, maize and sorghum in the GCP phenotyping platform. Wider samples will be accommodated in 2007 and 2008, enabling the assessment of the efficiency of the platform and allowing association analyses to be performed.

1.5. Development of novel populational approaches for relating genotypes to phenotypes

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. This 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 limited number of plants, i.e. few repetitions over space and still fewer over time; and 3) the use of the materials thus monitored is not easy and they are seldom incorporated in the breeding process. This project looks for alternative options.

One option will be to try to make use of materials and evaluation data that are regularly produced in mainstream breeding activities. From the collections of potential parents to the advanced breeding materials going to multilocation trials and to the elite materials close to varietal release, there is a wealth of information produced that is not efficiently used for deriving genetic information that could in turn be used to enhance global understanding. The condition for using these materials is that there be significant linkage disequilibrium (LD) that correlates variation in genetically (recombinationally) linked genes/markers. LD can exist among traditional (modern-pedigree wise unrelated) materials if the germplasm has had known significant bottlenecks in the past. For example, LD is actually generated in the breeding materials by the crosses made; in well-documented breeding programmes, the multi-generation pedigrees can be used to derive linkage information more efficiently. Such an approach is especially useful for those crops where refined materials for genetic analysis, such as inbred lines, NILs, or sets of substitution lines, cannot be produced and for those crops where the generation time is long. Within the CGIAR mandate, these crops include most of the vegetatively propagated crops, which are highly heterozygous, such as cassava, potato (and possibly other Andean roots and tubers), yam, banana and plantain, and the perennial coconut tree. These happen to be

mostly "orphan" crops where sequence information (which would allow other strategies to be applied) is scarce and unlikely to be generated quickly. The first output will be a first identification of areas that lend themselves to association mapping via knowledge of linkage disequilibrium.

Another option is to integrate genetic analysis among materials directly documented by *in situ* management practices. The objective is to relate the observations and choices of farmers to the genetic constitution of the selected materials. There are three main conditions necessary: 1) a clear and documented diversity and hierarchy of the local materials in terms of the target trait, 2) a genetic connection between these materials by gene flow (e.g., pollination) that ensures regular recombination, and 3) a good understanding of the local practices of the farmers. This would provide the possibility to map genome regions associated with the trait or to validate potential candidate genes. Situations with necessary feasibility in place will be researched and documented in 2006, in order to develop proof-of-concept pilot studies in 2007 and 2008. The outcome will be additional selection criteria for marker assisted selection in breeding programs, and a novel generic approach for taking advantage of *in situ* activities in direct collaboration with farmers and crop researchers.

Subprogramme 2: Comparative Genomics for Gene Discovery

Rationale

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

To achieve an understanding of the genetic mechanisms underlying the adaptive processes, a scientific and collaborative environment to enable gene discovery as well as applications is needed. To achieve this, a cross-cutting research platform for efficient applications of genomic tools and knowledge to decipher genetic control of complex traits must be established. Using these platforms, the genes to alleviate the targeted problems can be identified efficiently by pooling resources and expertise. To realize the potential of these approaches, however, capacity to apply new tools must be enhanced and a pipeline to move results into practice must be developed. Demonstrating the success of these approaches in a few targeted cases in the short to medium term is important to help lay the road map for broad applications of these new areas of science.

To meet these objectives, Subprogramme 2 is designed to maximize the use of genomic and genetic resources available in the research community. We support the production of specialized stocks that will elevate the level of genetic research in different crops. We apply comparative approaches to leverage genetic knowledge from multiple plant species to investigate and validate gene functions important for stress tolerance. Multi-disciplinary teams are formed to 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. High-quality rice genome sequence is now complete, and maize genome sequence is expected in the near future. Multiple genome-wide gene expression platforms in plants are available. It is increasingly feasible to use gene content (sequence information) rather than gene order as the entry point to identify orthologous genes and determine their functional relationships between species. Furthermore, from human and medical genetics, the power of SNP haplotypes and association genetics to identify functional genes is now well demonstrated. Subprogramme 2 strives to absorb the new knowledge gained and adopt new approaches where appropriate.

The overall research portfolio focuses on drought-tolerance traits as well as genes and agronomic characters that improve crop resilience in difficult environments. The key resources and tools produced are specialized genetic stocks (e.g., mutants and advanced backcross lines), gene expression assays, cloned genes for specific trait improvement (tolerance to diseases, water stress conditions, and soil problems), and desirable gene combinations in elite genetic backgrounds (pre-breeding materials). These materials will be used primarily by researchers and breeders within the GCP, but some outputs will be useful across the global research community interested in applying genomics to agricultural improvement. While a majority of the activities aims at improving understanding of complex traits, several projects will produce advanced breeding materials to alleviate problems in resource-poor areas in Asia (e.g., rice tolerant to P-deficiency in Indonesia) and Africa (e.g., maize tolerant to aluminium toxicity in Kenya).

At the level of research collaboration, the Subprogramme has brought together "unconventional" partnerships between research laboratories and institutions. For example, University of Jerusalem and Scottish Crop Research Institute are working with CIP to produce true-seed potato mutants. Beijing Genomics Institute is participating in gene expression analysis with CAAS, CIAT and NIAS (see list of partnerships below). These partnerships would not have occurred if the GCP had not actively sought out the expertise and provided an attractive research agenda.

Project Descriptions

The activities in this Subprogramme are organized under the following themes presented as Projects in the MTP logframe:

- 2.1. Assembly of genomics and germplasm resources through consolidating and developing specialized genetic stocks and framework genetic markers
- 2.2. Development of comparative maps within and across species and framework genetic markers for target crops
- 2.3. Assignment of genes and pathways to phenotypes through the convergence evidence of genome variation, expression patterns, and phenotypic data
- 2.4. Validatation of genes and pathways through evaluation of under or over-expression constructs or variants (induced or natural) of the target genes

2.1. Assembly of genomics and germplasm resources through consolidating and developing specialized genetic stocks and framework genetic markers

The first project focuses on adding value to existing genetic and genomic resources and creating new ones where such investment would open new approaches and leverage collaboration. Output 1 concerns the assembly of special wheat genetic stocks relevant for gene discovery, and makes them available for systematic phenotyping. Output 2 involves over 7 laboratories working on phenotyping of stress-response (drought and disease) rice mutants, taking advantage of the large mutant collections produced by different institutions over the past several years. It is envisioned that the rice mutant population (many of them with flanking sequence tags) will provide a platform for evaluating genes in an agronomically relevant context.

In addition to adding value to existing genetic resources, we are creating new resources that are unlikely to be available without investment from this Subprogramme. Outputs 3 and 4 involve the creation of mutants (bean and true-seed potato). Currently, there is a paucity of mutant resources in major agricultural crops. The investment into bean and true-seed potato will stimulate the use of mutational analysis into target problems. The lead centers are well suited for providing long-term maintenance and distribution of the genetic materials.

Outputs 5 and 6 involve the production of drought-response EST libraries for cowpea and pearl millet. The expansion of the EST libraries will enable the researchers to consider applying gene-based markers to associate drought-tolerance phenotypes.

The creation and enhancement of specialized genetic resources is expected to open new research opportunities. The primary users are researchers and genetic resource curators. The consolidation of genetic stocks will allow systematic evaluation to produce data amenable for comparative analysis. The immediate outputs of this Project will be high-quality, focused phenotypic data on genetically well-characterized materials. This Project leverages the wealth of resources (e.g., rice mutants) produced by different institutions and countries and at the same time strengthens linkages among these institutions. The impact of this Project will be long-term leading to broadly accessible research platforms for discovery gene functions in multiple crops.

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

Well-characterized genetic maps provide an anchoring framework for all genetic and phenotypic data. Comparative mapping across species is built upon the premise of common gene order (synteny) among related species. The syntenic relationship provides a means to identify genes with similar functions across species based on map position. Because of the rapid accumulation of sequence data across all species, the initial objective and technical approaches set forth three years ago will be modified accordingly. As more sequence information becomes available, the identification of orthologous genes will shift from parallel mapping to direct sequence comparison. New techniques to cross-reference conserved markers have also been developed. We will view syntenic relationships as supportive evidence for finding functionally related genes across species rather than as the core strategy to identify genes by comparative mapping.

This project emphasizes the alignment of biological/phenotypic traits onto well characterized molecular maps. This project will make use of the expanding sequence information and new tools available to assess the efficiency of using conserved orthologous markers across monocot and dicot species. Drought-related traits in bean and rice will be fine mapped using both recombinant inbred populations and advanced backcross lines. The fine-scale QTL analysis is expected to facilitate identification of candidate genes. An investment is made in assisting the *Musa* research community to consolidate the available genetic and genomic resources and to assess the relationship between rice and *Musa* at the genomic level.

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

This project emphasizes comparative analysis to understand the common mechanisms for stress response across species and to identify candidate genes conditioning stress-tolerance traits. A common strategy adopted by these studies is the use of convergent evidence from four main experimental domains: bioinformatics/gene function inference, positional (QTL), expression polymorphism, and response to selection (either natural or artificial). Integration of these data is expected to reveal the causal relationship between genetic/genomic variation and phenotypes. The studies involve linking molecular variation at candidate gene loci with phenotypes at the biochemical and whole plant levels that will eventually lead to identification of functional nucleotide polymorphisms to be used effectively in breeding programmes.

Output 1 will identify disease resistance alleles in maize and rice through a combination of fine-scale QTL analyses using introgression lines and expression analysis. Output 2 examines the unique phenomenon of a lack of rust diseases in rice and explores the use of non-host disease resistance in wheat. Output 3 will identify common mechanisms and candidate genes controlling the maintenance of tissue growth in cereals under water stress conditions. Output 4 explores the use of association genetics to identify genetic polymorphisms important for drought tolerance in maize. In the fifth output, gene expression analysis using genome-wide gene chips is explored to provide common methodologies and tools for assessing stress tolerance across species. Functional validation of candidate genes in these studies will be supported by the resource platform provided in Project 2.1. For example, the large collection of sequence-indexed rice mutants will provide a reverse genetic system to assess phenotypes of candidate genes identified from various studies.

Another common feature of these studies is to maximize the use of advanced breeding materials for both breeding and gene discovery. Several experiments are using heterogeneous inbred families for simultaneous breeding and fine-scale analysis of QTL in diverse genetic backgrounds. This approach has the advantages of actively engaging breeding programmes of NARS and shortening the time line to move favourable gene combinations into genetic backgrounds of popular local varieties.

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

This project comprises studies that have potential to apply genes and gene combinations for the development of advanced elite lines for on-farm evaluation. Output 1 will identify genes important for tolerance during water stress at reproductive stages through comparative analysis of wheat and rice. Output 2 will identify genes that can enhance tolerance to phosphorus-deficiency and salinity in problem soils affecting large tracks of land in Asia. Output 3 will identify genes to alleviate aluminum toxicity in maize in Africa and Latin America.

An interesting outcome expected from these studies is an understanding of the interrelatedness among response and tolerance mechanisms against different stresses.
Outputs 2 and 3 have high likelihood for impact in the near term and are of particular relevance to the GCP because of the advanced stage of the research in identifying candidate genes for addressing problem soils in target environments that are highly drought-prone. This is consistent with the view of the Subprogramme that while not all the studies are directly addressing drought tolerance, the phenotypic consequences of enhancing crop resilience (to problem soils and biotic stresses) in drought-prone environments are equally important and beneficial in achieving GCP objectives. For example, improving P-uptake and aluminum toxicity tolerance in crops leads to better root health to cope with water stress. Better resistance to diseases is a prerequisite for productivity in these environments.

It is important to note that all three outputs build upon the progress made in previous work by different laboratories and institutions around the world. The activities in this Project provide examples of how the GCP has created the venue for international collaboration by which research results are targeted at practical regional problems.

Subprogramme 3: Trait Capture for Crop Improvement

Rationale

The development of effective systems for breeding complex traits such as drought tolerance has eluded most practitioners despite a great deal of R&D investment which for some crops has spanned more than 50 years. However, the recent developments in genomics, computation systems, and biometrics offer a real opportunity for simultaneously manipulating the component traits of drought tolerance. Yet the greater challenge remains to use this knowledge and skill to develop products that will have significant impact on the livelihoods of farmers in resource-poor cropping systems. This will require a substantial change in how public sector scientists operate. First, holistic, product-driven teams that span all R&D levels in the innovation to impact continuum are needed. Second, the gap between research outputs and product delivery must be closed. Alliances with the private sector

(both multi-national corporations and small- and medium-size enterprises) will be especially critical to achieve these goals. Subprogramme 3 is tasked with these challenges in its effort to move genes and alleles for traits of interest in public sector crop improvement programmes.

The comparative genomics and biology theme of the GCP provides an operational structure for priority setting and focusing research activities across three crop groups: cereals, legumes, and clonal crops. Inevitably, global research progress in many of the cereals is sufficient to begin the development and application of gene-based marker systems for components of tolerance to drought and other abiotic stresses (rice, maize, sorghum, wheat, barley). Thus, emphasis in these crops is more on the translation and/or application of pre-existing research outputs. However, additional targeted investments are required for example in pearl millet (the most drought tolerant but least studied of the major cereal crops). Conversely, the critical mass of genomics researchers and resources in the legume and clonal crops does not yet exist. However, the resources currently available to the GCP are insufficient to support a comprehensive programme in all crops. For this reason, careful prioritization of crop focuses will be applied to ensure rapid and compelling proof-of-concept in key representatives of these crop groups: for example cowpea (legumes), groundnut (oilseeds), and cassava (clonal crops). In this way, the GCP will pilot test solutions along the entire product development and delivery pathway for these selected crops in target breeding programmes in diverse regional locations.

In addition, significant direct spillovers from sequence, gene, and trait analyses in model species are expected to significantly impact progress in those closely related crops with a minimum of genomics resources and critical mass expertise. Examples for this are *Medicago* for cowpea, chickpea, lentil, and pigeonpea; and *Lotus* for groundnut. Molecular breeding research outputs in soybean also offer a substantial spillover opportunity for all the legumes. Establishing a related model system for many clonal crops remains a major constraint to extending the GCP philosophy to this crop group, although Arabidopsis may be a suitable model for European potato. 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.

The selection of appropriate background genotypes is a critically important process for molecular breeding programmes to ensure widespread impact of newly introgressed alleles, genes, and traits. Thus, we will ensure that all necessary information is collated, collected, and/or generated to enable the most appropriate varieties and breeding lines to be selected based on agronomic performance in diverse environments. Farmer, processor, and consumer preferences and trading potential of varieties are also integral to the selection of the appropriate background genotypes. In addition, we are documenting baseline information for those varieties (including production and constraint mapping) that will be used in subsequent impact assessment studies. Similarly, the intellectual property rights and biosafety aspects of different transgene constructs must also be comprehensively evaluated at the very outset of research projects. For these reasons we have a substantial commitment to mapping the product development and delivery pathways for all activities in this subprogramme. Implicit in this is a movement away from linear technology hand-over to a systemic integration between those who need the knowledge and those who supply, validate, and refine it. In turn, this requires the capacity building activities of SP5 to move beyond just providing expertise and knowledge to also building skills and systems.

Many activities in this subprogramme are highly dependent on an effective consortium approach: for example, dealing with the challenges of complex traits with high epistasis and genotype-by-environment interaction; building holistic simulation and decision-support tools; and evaluating transgenes in multiple genetic backgrounds, crop species and mega-environments which require by their very nature coordinated input from many scientists. At the same time, many allied activities in this subprogramme can capture substantial economies in time, cost, and efficiency through following a community-based approach: for example, SP3 can facilitate centralized validation and refinement of new technologies for routine application in NARS and community support labs by developing low cost high-throughput genotyping services based on technologies beyond the reach of most national breeding programmes. Finally, the creation of effective systemically integrated communities of practice offers excellent opportunities for capturing interdisciplinary synergies and end-user feedback on priorities and outputs. Such communities foster strong technology uptake and product delivery pathways.

Project Descriptions

The activities in this Subprogramme are organized under the following themes presented as Projects in the MTP logframe:

- 3.1. Development, evaluation, and refinement of marker-assisted breeding systems with end-users (CGIAR, NARS, university, and SME breeding programmes)
- 3.2. Development and/or comprehensive assessment of gene introgression products under field conditions
- 3.3. Mapping of, development of pilot tests for, and assessment of molecular enhanced breeding product development pathways with end-users

3.1. Development, evaluation, and refinement of marker-assisted breeding systems with end-users (CGIAR, NARS, university and SME breeding programmes)

In the medium-term, the pipeline of new gene-based knowledge and resources for manipulating abiotic stress tolerance will be flowing out of SP1 and SP2 for application across a wide range of crops in SP3. These must be rapidly converted into robust tools for effective molecular breeding, with a particular focus on drought tolerance. However, due to the current state of the art, in the short-term the first output will focus on pre-existing research outputs, mainly from the better studied crops. Output 2 focuses on the development and evaluation of molecular breeding systems for pyramiding QTL in lesser-studied crops using linked markers (particularly SSR markers) for a range of complex traits that mimic components of drought tolerance. The third output is the development of a range of options for the low cost application of molecular breeding in a range of end-user environments. The GCP is committed to a continuous and iterative process that generates, adopts, and/or adapts new technological advances and seeks maximum synergy from optimum combinations of conventional and molecular enhanced breeding strategies. In some cases, recent bioscience research outputs offer new opportunities for making dramatic gains in genetic progress but only if breeding systems can be radically redesigned. In this context, it will be critically important to have simulation and decision support tools that help plant breeders determine the optimum combination of the available technologies in ways that best serve their needs and capacities. This will be delivered in output 4.

3.2. Development and/or comprehensive assessment of gene introgression products under field conditions

There is a range of pre-existing GMO products both within and outside the GCP consortium that are of interest as potential solutions for components of certain types of drought tolerance. The first output is the comprehensive evaluation of the physiological and agronomic performance of these products under large-scale replicated field trials in a range of drought stresses (timing, duration, intensity) and comparison with performance under optimum conditions. Since it is unlikely that any single gene insertion will provide a comprehensive solution, it is critical to test a range of approaches for pyramiding different drought tolerance genes in single elite breeding lines. Output 2 will achieve this through multiple transgene insertion technologies and/or marker-assisted backcross breeding. Finally, it is highly probable that transgenic products that adjust entire metabolic pathways will have deleterious effects on economic productivity, particularly under optimum conditions. For this reason, for the third output, target transgenes will be introgressed into a range of elite agronomic backgrounds in order to identify those with positive combining ability for reducing such negative effects.

3.3. Mapping, development of pilot tests for, and assessment of molecular enhanced breeding product development pathways with end-users

The development of abiotic stress tolerant transgenic products is likely to present a very different profile of considerations as compared to the two main events widely deployed to date (pest and herbicide resistance). The first output of this project will investigate in depth if we are to design realistic delivery pathways for products based on such technologies. Since this type of activity is not the comparative strength of the GCP, progress will be achieved through strategic alliances with regional and international biosafety programmes such as the USAID-BSP. Output 2 – mapping the product development and delivery pathways for genomics, transgenic, and computational outputs – is a critical prior step to effective programme priority setting, project planning, and product design. Finally, it will be important to take key technology products and demonstrate their delivery to representative end-users in key regional production areas. During these pilot processes, the products must be comprehensively evaluated, the cost-benefit analyzed, and the impact assessed in conjunction with diverse third party end-users (CGIAR, NARS, university, and SME breeding programmes).

Subprogramme 4: Information Systems and Bioinformatics

Rationale

The value of the data generated in the first three subprogrammes will largely depend on the way they are stored, managed, analyzed, and made accessible to the GCP, but also to the rest of the world. The way they can be analyzed will, in turn, depend on the way analysis tools and other information sources are made available. Subprogramme 4 addresses the challenge of linking and integrating these information components and analysis 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 give access to the data generated in the GCP, and will provide analytic tools to analyze these data. Furthermore, it will link GCP data and tools to the global biodiversity and bioinformatics networks.

There are a number of components to the development of such a platform. First of all there are numerous local systems in place at this moment; the challenge of integrating those into one system is large since the ability to dictate architecture and organisation of existing systems, both inside and outside the GCP consortium, is limited. Secondly, the elements that do

exist within the GCP consortium need to be of sufficient quality. The GCP believes that data management can best be done as close as possible to the place where the data are generated. This allows proper curation in terms of corrections and additions to the data and avoids problems of ownership. However, making data management a local responsibility requires an appropriate level of skills and facilities to do so. This is also addressed in SP4. Thirdly and finally, to allow the other subprogrammes to function properly in terms of 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 organized in such a way that local curation of the data and tools can be maintained?
2. How can the local curation of data and tools be supported by the GCP such that the quality improves up to a standard that is acceptable by the GCP?
3. How can the GCP accommodate its bioinformatics needs in terms of tools and data sources?

All three of these problems are in the first place oriented towards 'internal users;' in other words, they will benefit the GCP itself. As an important spin off, the solution of all three problems will greatly benefit the global biodiversity and bioinformatics community since the GCP is a major new player providing access to valuable data and tools and developing tools, software, and standards for efficient data exchange and integration. To assure proper quality of the products the projects will collaborate extensively with institutions outside the consortium. For example, in the case of the development of standards to allow exchange of data and access to data and tools (to solve problem 1,) we will need to involve the global user community of these standards to assure incorporation of existing standards and protocols, and to create ownership in these groups since we would want the standards to become 'world standards' instead of 'GCP standards'.

Project descriptions

The activities in this Subprogramme are organized under the following themes presented as Projects in the MTP logframe:

- 4.1. Establishment of the GCP Information Platform.
- 4.2. Improvement of the GCP Information Platform Components
- 4.3. Creation of software in support of GCP activities

4.1 Establishment of the GCP Information Platform

This is the largest project in SP4 and aims at actually creating the platform needed for information exchange. This will be done by implementing web services. Web services allow a wrapping up of local databases and software tools in such a way that they appear to be part of one system: they can be approached via a common language via the internet.
This language is translated in the language understood by the local database or software tool, which answers the query or does the analysis. The output is then translated back to the common language. Implementation of this approach has a number of components: the technology should be available and the common language developed; the technology should be implemented by the consortium members requiring training; and the technology should be used. And since this can not be accomplished immediately, some short term solutions should be created that are compatible with the final solutions.

This requires a number of activities, each with their own outputs. The first output is the development of the common language by the development of 'GCP Domain Models' involving a wide diversity of actors and clear prioritization over the years. The second output is concerned with the training of staff and implementation of web services technology in the institutions. The third output concerns the creation of a repository for links to the datasets (yellow pages) or datasets themselves that are not available as web services yet. The fourth output aims at improving the web services technology and applying it in a number of show cases, to establish the GCP as a relevant player in the international arena. The fifth output concerns a solution to the short term issues that are not resolved yet by applying the web services technology, by creating small applications for uploading and centrally storing data sets. And the sixth and final output aims at properly capturing and analyzing the wishes of the users in a use-case database, and providing a platform for simultaneous software development, both facilitating effective software development.

4.2. Improvement of the GCP Information Platform components

To ensure quality local curation of data, a number of issues have to be considered. There is the issue of institutional capacity needed to act as data supplier to the GCP, the issue of the quality of the data that are supplied, and finally the capacity needed by GCP scientists that can not be supplied by one single center. Concerning institutional capacity, the CGP has the policy that consortium members are responsible themselves for creating appropriate capacity. However, where the GCP can create synergies, these opportunities will be used. In addition, the GCP aims to kick-start the development of institutional bioinformatics capacity by supporting the building of that capacity. Concerning the data quality issue,

there clearly is a need for monitoring activities and activities aimed at improving the quality. Output 1 addresses this need through a significant investment in the improvement of quality of existing databases. Finally, regarding joint institutional capacity, the creation, implementation, and integration into GCP toolbox the of a high performance computing facility is a first step in that direction.

4.3. Creation of software in support of GCP activities
The first three Subprogrammes have data collection, curation, and analysis needs that SP4 must address for optimal deployment of GCP outputs. Based on the needs formulated by the other SPs, five activities were articulated whose outputs would address the needs. The first aims at facilitating germplasm sampling based on all available passport, phenotype, and genotype data, depending on the nature of the sample required. The second aims at creating access to gene orthology relationships across species and related paralogy relationships within gene families. The third will create a crop gene expression database that will allow scientists to easily find and compare expression data across species. The fourth output will allow breeders to more efficiently use markers in breeding programmes by integrating existing software in an integrated platform (using web services technology). The fifth output in this project will create an eco-physiological – statistical framework for the analysis of GxE and QTLxE as occurring in abiotic stress trials, facilitating a better understanding of results of phenotyping experiments.

Subprogramme 5: Capacity Building and Enabling Delivery

Rationale

The technological divide between developed and developing countries in contemporary, cutting edge knowledge is a distressing reality. In the context of the GCP, major knowledge gaps exist in the effective use of genetic resources, awareness of developments in genomics, access to the tools and funds needed for comparative genetics and genomics studies, and the prospects of merging new knowledge and methods with traditional crop improvement practices. Access to the wealth of information already available about research in the developed world is also a major constraint for developing countries. Institutional and national policies on biosafety, intellectual property, and access and benefit sharing that govern the scientific research themes and products covered by the GCP are also woefully lacking, both in the developing and developed world.

In the GCP, the focus on capacity building stems from the belief that education and knowledge form the basis for development. The GCP needs mechanisms to build capacity in NARS to enable collaboration with partners in the developing world and to ensure long-term sustainability of the research platform and toolbox of the GCP itself. The GCP's ability to have impact in farmers' fields is directly associated with the ability of NARS to use the technical outputs of the GCP in their breeding programmes to address the needs of the farmers and consumers they work with. As such, linking with NARS is also essential to the development of an effective delivery plan for GCP products. Subprogramme 5 is a cross-cutting theme of the GCP, meaning that it is mandated to build capacity in and deliver the products of all four technical Subprogrammes.

Project Descriptions

The activities in this Subprogramme are organized under the following themes presented as Projects in the MTP logframe:

- 5.1. Increase in NARS scientists' capacity to participate in the GCP
- 5.2. Establishment of broad regional mechanisms for sustainable capacity to participate in the GCP
- 5.3. Development and adoption of policies and protocols to allow proper access and benefit sharing from the derivatives of the programme
- 5.4. Articulation and implementation of the GCP product delivery strategy

5.1. Increase in NARS scientists' capacity to participate in the GCP
This project addresses the basic activities for a programme on capacity building. It contains an output to ensure that needs assessment of the participating NARS is the basis of the capacity that the GCP delivers, and that activity evaluation and impact monitoring are used as essential feedback to adapt and reshape the content and format of the GCP research portfolio and capacity building programme. Output 2 is the hands-on involvement of NARS scientists in the commissioned and competitive research projects of the GCP. Output 2 takes advantage of the opportunity of Subprogramme and project workshops and technical meetings to extend participation to NARS scientists who may not be directly involved in the target activities but could learn and apply the methodologies and tools at home in their own research. Output 4 is the GCP Training Programme and basically includes the development of training materials and the delivery of training through courses. The last output consists of the different fellowships and grants schemes.

This project addresses what has been defined as one of the major goals of the GCP, i.e. providing capacity to partners and NARS in the developing world in the different research aspects that form the basis of the Programme. In doing so, the GCP aims to expand its portfolio of collaborators in the regions

where, in principle, lay the main target of the Programme, the resource-poor farmers. These collaborators are, in principle, the logical bridge in the programme by being placed between the end-users and those scientists working in upstream research. In one sense they may convey the needs to drive the research agenda to one end and in the opposite sense they may be the right instruments to transfer the products and associated technologies to the farmers.

5.2. Establishment of broad regional mechanisms for sustainable capacity to participate in the GCP

This project contains one output. The basis of the project is to ensure self-reliance of national programme institutions, at the regional level, during the life of the GCP but most importantly after the GCP. The project focuses first on the identification and establishment of mechanisms in the different regions, the capacity needs for these organisations to carry out the work as expected and the development of joint programmes to help sustain activities related to the GCP.

The Generation CP has limitations both in the amount of NARS institutions and scientists it can reach and in its life span. That does not diminish the efforts to focus on the increase of capacity to the extent possible, mainly limited by availability of funds. However, it is essential to simultaneously establish parallel mechanisms to secure long-term capacity building in the regions where most is needed.

5.3. Develop and adopt policies and protocols to allow proper access and benefit sharing from the derivatives of the programme

An increased awareness of the linkages that policy issues have with products and situations arising in different subprogrammes led to place policy activities in SP5, moving from its previous location in SP1. This was because of its cross-cutting character, but also because of the appreciation that there would be a need for capacity in GCP-concerned policies at large. Project 5.3 is now the policy project within SP5. It includes two outputs that address respectively capacity building and the development of tools to guarantee the products arising from the Programme can indeed be transferred to those more in need as global public goods.

The GCP is collaboration among researchers, breeders, and social scientists from a wide variety of institutions, serving an equally broad group of potential users. Much of the success of the programme depends upon having access to materials (including germplasm) and technologies under clear agreements; a clear freedom to operate on the materials, tools and methods; plans in place that encourage communication among the scientists, participation of end-users in project design and implementation, as well as effective product development, distribution and uptake; having GCP assets and products used and taken up by as broad a user-base as possible. Outputs in this Project aim to fulfilling all different needs for a successful Programme, both with national programme institutions partners of the GCP and their scientists (output 1), and within the Consortium scientists and institutions (output 2).

5.4. Articulation and implementation of the GCP product delivery strategy

This project addresses the development and implementation of a strategy for product delivery in the GCP. It encompasses four outputs. One will concentrate on the analysis of existing mechanisms of delivery in different organisations, but also taking into consideration crops and regions and the linkages between the different components of the delivery chain. The second output will inventoriate products, users, limitations and impact, as expected from the GCP technical subprogrammes. Output three will deal with the partnerships that can make our endeavour more effective, by identifying initiatives and organisations involved in ongoing delivery activities and with which an association is possible in the circumstances of the CPs. Output four is meant to house case studies, in which the GCP can prove whether or not the delivery principles set are appropriate and identified drawbacks used as feedback to adapt the strategy accordingly.

At the beginning of this GCP, there was an understanding that the generation of products through the research programme would be done in association with the CGIAR Centers and NARS in the Consortium, with NARS outside the Consortium, so that they would be in charge of devolving them to the farmers in general and the resource-poor farmers in particular. With some more time, some argued that the expectations from the GCP were higher than those just stated, and that the Programme should envisage some type of delivery strategy to ensure that indeed the GCP products reach the intended end-users.

Discussions were held with the Stakeholders Committee and with the Programme Steering Committee (PSC) at the appropriate time, hoping to gather ideas in which building the GCP delivery strategy. In April 2005, an electronic forum started after attracting the interest of an important number of experts in relevant fields (social sciences, marketing, plant breeding, legal sciences, etc...) for this subject. Experts were drawn from within and outside the GCP Consortium, and included the public and the private sectors. The forum was driven by selected questions about a justification for the involvement of the GCP in product delivery, the definition of intended users, the mechanisms possible in the areas where the resource-poor live, indicators of impact, among others. At

the moment of this writing, a face to face small workshop is planned to take place with the participation of a selected group of experts. The outcome of the workshop should be a draft document outlining a strategy for product delivery in the GCP and a work plan to start fulfilling the expectations. The draft will be circulated among a higher number of resource people within and outside the GCP Consortium. The PSC will lastly receive the draft and with its contribution it is expected that actions can take place soon after.

In consequence, it is difficult at this point to describe the plans for the following three years. Important changes can be expected to affect this project at the end of this year. A number of outputs have nonetheless been identified, that seem necessary based on the discussions held up to date.

Annex 1: LOGFRAME

Generation Challenge Programme 2006-2008 MTP

Project	Outputs	Intended user	Outcome	Impact
GCP Project 1.1	**creation of an improved understanding of the structure of the diversity for the major world food crops**			
1.1 Output 1	structure of genetic resources for each crop acurately described (including tools)	all breeders and germplasm specialists	possibility to explore genetic diversity in breeding and in further characterization	better access to germplasm collections
output target 2006	published description of molecular variation and germplasm classification for tier 1 crops			
output target 2007	published description of molecular variation and germplasm classification for tier 2 crops			
output target 2008	published description of molecular variation and germplasm classification for tier 3 crops			
1.1 Output 2	a set of reference germplasm, data and methods available for designing comparative studies with the view to identifying associations for each crop (including LD assessment for priority crops)	all germplasm specialists involved in association studies	entry point to explore diversity for fany trait; reference germplasm recommended for integrated characterization and identification of genes and superior alleles	better access to germplasm collections
output target 2006	implementation for tier 1 crops			
output target 2007	implementation for some of tier 2 crops			
output target 2008	*none*			
GCP Project 1.2	**development of a range of HTP genotyping techniques accessible in reference laboratories**			
1.2 Output 1	assessment of various genome-wide molecular characterization techniques for representative crops	all germplasm specialists using molecular markers	guidelines for appropriate use of molecular techniques for genome-wide surveys	higher efficiency in crop research and improvement
output target 2006	preliminary assessment of DArTs			
output target 2007	to be decided: validation of existing techniques or assessment of emerging techniques			
output target 2008	to be decided: validation of existing techniques or assessment of emerging techniques			
1.2 Output 2	assessment of gene-targetted molecular characterization techniques (SNPs, Ecotilling, SSCP, NC-SNPs)	all germplasm specialists using molecular markers	guidelines for appropriate use of molecular techniques for SNP surveys	higher efficiency in crop research and improvement
output target 2006	assessment of EcoTILLing; assessment of SSCPs			
output target 2007	assessment of Non Coding SNP detection approach; assessment of various SNP detection techniques			
output target 2008	*continued*			
1.2 Output 3	identification of reference laboratories for high throughput molecular characterization	GCP scientists	optimization of the access to high efficiency facilities	higher efficiency in crop research and improvement
output target 2006	analysis of efficiency of techniques and localisations within the CGIAR and out of it			
output target 2007	reinforcement of facilities in selected laboratories			
output target 2008	*to be decided*			
GCP Project 1.3	**establishment and implementation of a scientific and organizational framework to describe tolerance to drought**			
1.3 Output 1	a set of phenotyping facilities accessible for GCP germplasm samples	GCP scientists	high quality- and capacity- GCP phenotyping network	higher efficiency in crop research and improvement
output target 2006	consolidation of phenotyping network in Embrapa			
output target 2007	open GCP access to Embrapa network; extension of network to other continents			
output target 2008	*continued*			
1.3 Output 2	a crop and whole plant modeling framework to support assessment of tolerance to drought	crop scientists around the world	improved assessment of drought tolerance in germplasm and breeding materials	knowledge about drought tolerance available to the scientific community
output target 2006	coordination with phenotyping network			
output target 2007	characterization of environments within phenotyping network; improvement of whole plant model to support drought tolerance phenotyping in cereals; first insights into drought tolerance components in cassava			
output target 2008	improvement of whole plant model to support drought tolerance phenotyping in cereals, cassava, and legumes			

Project	Outputs	Intended user	Outcome	Impact
GCP Project 1.4	**identification of potential genes (or genome segments) and superior alleles (or haplotypes) through association studies**			
1.4 Output 1	potential genes (or genome segments) and superior alleles (or haplotypes) in cereals	crop scientists around the world	targets for marker assisted selection for improving drougt tolerance in cereals	higher efficiency in crop research and improvement
output target 2006	intermediate project outputs			
output target 2007	validation of some candidate genes in maize, wheat and rice			
output target 2008	*to be decided*			
1.4 Output 2	potential genes (or genome segments) and superior alleles (or haplotypes) in legumes	crop scientists around the world	targets for marker assisted selection for improving drougt tolerance in legumes	higher efficiency in crop research and improvement
output target 2006	*to be decided*			
output target 2007	*to be decided*			
output target 2008	*to be decided*			
GCP Project 1.5	**development of novel populational approaches for relating genotypes to phenotypes**			
1.5 Output 1	mapping favorable genes in the course of breeding	plant breeders	production of genetic information from ongoing field experiments	higher efficiency in crop research and improvement
output target 2006	feasability assessment for five cases in potato, cassava, yam, banana and coconut			
output target 2007	*to be decided*			
output target 2008	*to be decided*			
1.5 Output 2	mapping favorable genes using in situ-managed populations	crop scientists and plant breeders	production of genetic information from existing traditional populations	higher efficiency in crop research and improvement
output target 2006	feasability assessment in several cases, to be decided			
output target 2007	*to be decided*			
output target 2008	*to be decided*			
GCP Project 2.1	**assembly of genomics and germplasm resources through consolidating and developing specialized genetic stocks and framework genetic markers**			
2.1 Output 1	wheat genetic stock assembled and utilized	researchers, database curators		access to genomic tools and resources for scientific community
output target 2006	recommendations of consultation workshop implemented and database established on important genetic stocks relevant for genetic discovery	researchers, breeders, genebank curators	broaden access to specialized genetic stocks of wheat; creating a common platform for sharing stocks and derived phenotypic and genotypic data	
output target 2007	consolidation, multiplication and distribution of stocks for use by the GCP			
output target 2008	*none*			
2.1 Output 2	systematic evaluation of rice mutant collections for conditional phenotypes with emphasis on stress tolerance	researchers, genetic resource curators	linkage of laboratories producing the largest collection of rice mutants in the world; providing a unique resource pools and expertise to identify gene function in a model crop species	access to genomic tools and resources for scientific community
output target 2006	about 500 rice stress associated genes linked to insertion and activation mutants identified			
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	*none*			
2.1 Output 3	legume mutant resource development	researchers, genetic resource curators	unique bean genetic stock for public use	access to genomic tools and resources for scientific community
output target 2006	demonstration of a reverse genetics system using bean mutant population			
output target 2007	a mutant collection of common bean amenable for forward and reverse genetics; systems in place to maintain and distribute mutant seeds			
output target 2008	*none*			

Project	Outputs	Intended user	Outcome	Impact
2.1 Output 4	tuber genetic stocks and gene function validation tools	researchers, genetic resource curators	represent the only known true-seed potato mutant stock that can be easily distributed (unlike tubers)	access to genomic tools and resources for scientific community
output target 2006	mutation frequency and phenotypic variability in M2 plants assessed			
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			
output target 2008	*none*			
2.1 Output 5	stress response-enriched EST resources for cowpea	researchers	added value to collection of cowpea EST in public database; potential use for gene-based markers	access to genomic tools and resources for scientific community
output target 2006	subtractive and normalised libraries from drought-sensitive and drought tolerant cowpea lines produced.			
output target 2007	ESTs from drought stressed and non-stressed cowpea lines (susceptible and tolerant) annotated and maintained at BECA			
output target 2008	*none*			
2.1 Output 6	stress response-enriched EST resources for pearl millet	researchers	expanded collection of millet ESTs, bridging the gap in millet genomic resources available to the public, potential use for gene-based markers	access to genomic tools and resources for scientific community
output target 2006	5000 pearl millet ESTs from drought and salinity-stressed plants of pearl millet produced (using parental lines 841B-P3 and 863B-P2 of mapping population)			
output target 2007	EST-derived PCR markers for drought tolerance pearl millet developed			
output target 2008	*none*			
GCP Project 2.2	**development of comparative maps within and across species and framework genetic markers for target crops**		**enhanced value of comparative maps with phenotypes anchored**	**contribution of public research platform**
2.2 Output 1	validation of conserved orthologous markers	researchers	assessment of the efficiency of COS markers for several selected crops; rationale for next steps in linking different maps	increased knowledge about genomics for aiding crop plant improvement
output target 2006	50 universal EST markers related to drought tolerance, disease resistance and other agronomically important traits validated for use across monocots and dicots, respectively.			
output target 2007	25 new universal PCR-based markers related to drought or disease resistance; identified and validated across monocots and dicots respectively.			
output target 2008	*none*			
2.2 Output 2	comparative QTL mapping for drought tolerance (bean)	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 plant improvement
output target 2006	candidate genes identified based on integration with QTL data and available as genetic markers for the manipulation of drought tolerance in common bean and other legumes			
output target 2007	QTL isolines with high photosynthate mobilization trait created			
output target 2008	*none*			
2.2 Output 3	comparative QTL mapping for drought tolerance (rice)	researchers	genetic resources and a framework for converging root traits, drought-related QTL, and candidate genes	increased knowledge about genomics for aiding crop plant improvement
output target 2006	synthetic map produced with positions of QTLs and candidate genes for root development and for other drought related characters from rice and sorghum			
output target 2007	BC4F3 lines produced with narrow chromosomal segments carrying QTL identified and candidate genes in the sub-segments identified *in silico*			
output target 2008	*none*			

Project	Outputs	Intended user	Outcome	Impact
2.2 Output 4	targeted *Musa* genome sequencing and frame map construction	researchers, database curators	consolidated genetic and genomic resources leading to enhancement of *Musa* genetic research	increased knowledge about genomics for aiding crop plant improvement
output target 2006	current markers developed in *Musa* for diversity analysis and EST-derived SSR integrated onto rice and *Musa* genetic maps; sequence information produced on targeted genomic regions harbouring potential stress tolerance genes (drought and/or biotic stress tolerance)			
output target 2007	major repeat classes in relation to genomic diversity in *Musa* characterized; the rice-*Musa* genome relationship evaluated and guidelines for future use of the rice genome sequence in *Musa* and other CGIAR mandated crops; data management and database constructed similar to the public data and genomic resource established in rice		assessment of the rice-*Musa* relationship at the genomic level and the basis of applying rice sequencer information to *Musa*	
output target 2008	*none*			
GCP Project 2.3	**ssignment of genes and pathways to phenotypes through the convergence evidence of genome variation, expression patterns and phenotypic data**		**detailed understanding of genetic control of stress response in advanced crop systems; demonstration of strategies and applications**	
2.3 Output 1	targeted discovery of superior disease QTL, alleles in the maize and rice genomes	researchers, breeders	superior disease resistance QTL identified, characterized, and used in maize and rice breeding programs	model for integrating gene discovery and breeding activities
output target 2006	diverse sources of quantitative resistance and adaptive traits identified in maize and rice; NIL (heterogenoeous inbred families) derived from rice genotypes with superior resistance to blast and sheath blight; non-conventional disease assays (based on quantification of pathogen biomass) developed for maize; deletion rice mutants (at least five) with altered disease response identified		efficienct methodologies developed for detecting introgression segments through simultaneous genotyping and expression profiling analysis; demonstrated efficiency in using heterogeneous inbred families for breeding and QTL fining mapping in diverse genetic backgrounds	
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			
output target 2008	maize loci showing changes in allele frequency under recurrent selection and production of introgression lines carrying multiple favorable 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)			
2.3 Output 2	functional genomics of cross-species resistance to fungal diseases in rice and wheat	researchers, breeders	detailed information on the molecular mechanisms governing non-host resistance (cross-species) resistance to fungal diseases in cereals	novel strategies to generate durable disease resistance
output target 2006	phenotypes and cytology of non-host resistance in wheat and rice to blast and rust characterized; a set of differentially expressed genes during non-host interaction in rice and wheat identified			
output target 2007	map position 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 non-host resistance 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			

Project	Outputs	Intended user	Outcome	Impact
2.3 Output 3	determination of a common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes	researchers	common genetic mechanisms (candidate genes) underlying the maintanence of tissue growth in plants under water deficit determined in maize, rice and wheat	increased knowledge about genomics for aiding crop plant improvement
output target 2006	screening methodologies for tissue growth regulation under controlled and field conditions improved		gene markers adopted by breeding program to select for drought tolerance traits	
output target 2007	set 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			
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 sequences of candidate genes; new phenotypic and genetic selection criteria for efficient breeding for drought tolerance identified	breeders	enabling development of drought-tolerance maize in breeding programs	
2.3 Output 4	development of informative DNA markers through association mapping in maize to improve drought tolerance in cereals	researchers and breeders	genes invovled in the regulation of drought tolerance mechanisms in tropical maize, and DNA markers developed for used in MAS for improving drought tolerance in cereals	increased knowledge about genomics for aiding crop plant improvement
output target 2006	Set of maize inbred lines (about 400 lines) in different precosity groups classified and seed-increased for association studies; suitable candidate genes involved in drought response pathways (about 12/year) for association studies determined			
output target 2007	large-scale screening protocols for target biochemicals/ metabolites improved; phenotypic data for three target tissues (leaf, ear, silks) collected for association studies			
output target 2008	haplotypes of selected candidate genes determined; polymorphisms in candidate genes associated with target traits determined; set of indicative DNA markers for allele discrimination and MAS identified	researchers and breeders	understanding of gene networks for selected drought-related pathways (carbohydrate and ABA regulation) in tropical maize	
2.3 Output 5	crop gene expression profiles and stress-gene arrays		contribution to GCP crop stress gene database and gene networks involved in drought conditions	increased knowledge about genomics for aiding crop plant improvement
output target 2006	candidate genes (100 genes) for specific trait of interest for drought tolerance identified	researchers		
output target 2007	subarrays of orthologous stress response/tolerance genes tested for usage (especially molecular phenotyping for drought) in multiple crops	researchers	common metholodogies and tools for assessing stress tolerance across species	
output target 2008	*none*			
GCP Project 2.4	**validatation of genes and pathways through evaluation of under or over-expression constructs or variants (induced or natural) of the target genes**	**researchers and breeders**	**utility of agronomically important genes validated**	**productivity in drought-prone envirnoment enhanced**
2.4 Output 1	identifying Genes Responsible for Failure of Grain Formation in Rice and Wheat under Drought	researchers	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 2006	standard stress protocols to predictably alter peduncle elongation and floret sterility established under greenhouse and field conditions for rice and wheat; peduncle and floret behavior in contrasting genotypes under standard stress protocols (well-watered, drought-stressed, re-watered) characterized thorugh microscopy and biochemistry		general methodologies for assessing reproductive drought stress available for use in other cereals	
output target 2007	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			
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	

Project	Outputs	Intended user	Outcome	Impact
2.4 Output 2	revitalizing Marginal Lands: Discovery of Genes for Tolerance of Saline and Phosphorus Deficient Soils to Enhance and Sustain Productivity	researchers and breeders	genes associated with salinity and P-deficiency tolerance in identified in rice and a marker system to incorporate these genes ionto popular varieties developed	enable production of rice varieties in marginal area plagued by high salt or P-deficiency that would otherwise be unproductive
output target 2006	further fine-mapping of *Saltol* locus using a NIL population of about 10,000 individuals completed; further fine-mapping of the Pup1 locus using a NIL population of about 2,000 individuals completed; expression analysis of genes affected by the Pup1 and Saltol loci completed			
output target 2007	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		enhanced root growth and health via P-uptake efficiency provide a mechanism to resistant drought stress; potential to identify orthologs or salinity and P-deficiency tolerance genes in other cereals	
output target 2008	set of contrasting NILs for the *Pup1* and *Saltol* loci tested at multiple sites with NARES 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			
2.4 Output 3	isolation and characterization of aluminum tolerance genes in the cereals	researchers and breeders	improved understanding of the diversity and functioning of molecular and physiological mechanisms for Al-tolerance in crops	improve livelihood of farmers through increased productivity of marginal land
output target 2006	positional cloning of aluminum-tolerant gene (Alt) in sorghum completed; ALMT1 homologs cloned from Triticeae and rice			
output target 2007	expression profiling of sorghum and maize NIL completed; homologs of sorghum alt gene in Triticeae and rice cloned			
output target 2008	candidate Al tolerance genes in maize molecularly characterized; Al-tolerance genes from sorghum, maize, and rice identified; physiological chacterization and mapping of Al tolerance in Kenyan maize genotypes completed		gene markers available to combine desirable combinations Al-tolerance genes in elite lines and commercial varieties	improved genotypes available to farmers in acid soil regions in Africa
GCP Project 3.1	**development, evaluation, and refinement of marker-assisted breeding systems with end-users (CGIAR, NARS, university and SME breeding programs)**			
3.1 Output 1	gene-based markers for abiotic stress tolerance developed and evaluated in diverse germplasm			more effective marker-assisted selection systems
output target 2006	physical mapping of salinity and low phosphorus tolerance in rice	project scientists	physical location of genes for salinity and low phosphorus tolerance determined	
output target 2007	gene-based markers for salinity and low phosphorus tolerance in rice	CGIAR, NARS, university and SME breeding programs	perfect markers for use in the development of robust molecular breeding systems for salinity and low phosphorus tolerance in rice	
output target 2008	candidate gene-based markers for drought tolerance in at least one cereal, legume and clonal crop	CGIAR, NARS, university and SME breeding programs	perfect markers for use in validation tests for the development of robust molecular breeding systems for drought tolerance	
3.1 Output 2	marker-assisted selection systems for complex traits developed and evaluated in diverse breeding programs	CGIAR, NARS, university and SME breeding programs		
output target 2006	develop closely linked allele-specific markers for striga resistance in cowpea and for diverse sources of drought tolerance in rice		validated markers for indirect selection of striga resistance in cowpea and drought tolerance in rice	more effective marker-assisted selection for striga resistance in cowpea and drought tolerance in rice
output target 2007	marker-assisted pyramiding of QTL for drought tolerance in rice and striga resistance in cowpea		improved molecular breeding systems for striga resistance in cowpea and drought tolerance in rice	enhanced germplasm with improved biotic stress tolerance available
output target 2008	marker-assisted pyramiding of abiotic stress tolerance QTL in key representatives from cereal, legume and clonal crops		improved molecular breeding systems for abiotic stress tolerance in at least one representative of cereal, legume and clonal crops	enhanced germplasm with improved abiotic stress tolerance available

Project	Outputs	Intended user	Outcome	Impact
3.1 Output 3	low cost high throughput marker screening technologies developed and evaluated with end-users	CGIAR, NARS, university and SME breeding programs		robust low cost assays adopted in key end-user breeding programs
output target 2006	development of low cost gene-based trait assay technologies in rice and maize		low cost gene-based marker technologies available for blast resistance in rice and quality protein maize	
output target 2007	low cost MAS for virus and pest resistance in cassava		low cost marker technologies available for virus and pest resistance in cassava	
output target 2008	low cost gene-based marker technologies for abiotic stress traits		low cost gene-based marker technologies available for abiotic stress traits in key representatives of cereal, legume and clonal crops	
3.1 Output 4	molecular breeding systems, simulation models and decision support tools developed and evaluated with end-users	CGIAR, NARS, university and SME breeding programs		
output target 2006	integration of synthetics in molecular breeding of groundnut		access to a substantial range of new sources of pest and disease resistance, and tolerance to drought stress	significant increase in genetic gains for priority target traits in groundnut
output target 2007	simulation of marker-assisted selection strategies for optimizing molecular breeding systems for drought tolerance in cereals		decision support tools to help redesign cereal breeding programs to best capture the value of molecular screening data	dramatic increase in selection power and cost efficiency of cereal breeding programs across the world
output target 2008	simulation of marker-assisted selection strategies for optimizing molecular breeding systems for drought tolerance in legumes and clonal crops		decision support tools to help redesign legume and clonal crop breeding programs to best capture the value of molecular screening data	dramatic increase in selection power and cost efficiency of legume and clonal crop breeding programs across the world
GCP Project 3.2:	**development and/or comprehensive assessment of gene introgression products under field conditions**			
3.2 Output 1	pre-existing transgenic products with putative drought tolerance comprehensively evaluated in large-scale multi-environment field trials	CGIAR, NARS, university and SME breeding programs		
output target 2006	physiological evaluation of transgenic putative drought tolerant lines of rice, wheat, groundnut and potato		demonstration of the physiological value of DREB transgenics in rice, wheat, groundnut and potato	basic knowledge of the physiological effects of DREB transgenics on which to basis future priority setting
output target 2007	agronomic evaluation of transgenic putative drought tolerant lines of rice, wheat, groundnut and potato		demonstration of the agronomic value of DREB transgenics in rice, wheat, groundnut and potato	promising material for introduction in drought tolerance breeding programs identified
output target 2008	multilocational evaluation of transgenic putative drought tolerant lines of rice, wheat, groundnut and potato		knowledge of the stability and GxE effects of DREB expression	identification of robust promising material for introduction into drought tolerance breeding programs
3.2 Output 2	pyramiding of promising new drought tolerance genes in elite breeding lines	CGIAR, NARS, university and SME breeding programs		
output target 2006	development and evaluation of diverse drought tolerance transgenes in selected cereal crops		understanding of the epistatic relationships between different sources of transgenic drought tolerance in cereals	more effective transgene-based cereal molecular breeding programs
output target 2007	development and evaluation of diverse drought tolerance transgenes in selected legume and clonal crops		understanding of the epistatic relationships between different sources of transgenic drought tolerance in legumes and clonal crops	more effective transgene-based legume and clonal crop molecular breeding programs
output target 2008	refinement of multiple transgene insertion technologies		targeted insertion of multiple target transgenes in the same end-user preferred variety	more effective development of transgenic products with different profiles of transgenes
3.2 Output 3	promising transgenic drought tolerant material integrated into large-scale breeding and evaluation programs	CGIAR, NARS, university and SME breeding programs		improved molecular breeding of drought tolerance using transgenic material
output target 2006	development and evaluation of various drought tolerance transgenes in diverse genetic backgrounds of selected cereal crops		knowledge of the epistatic effects between transgenes and the genetic background in cereal crops	
output target 2007	development and evaluation of various drought tolerance transgenes in diverse genetic backgrounds of selected legume crops		knowledge of the epistatic effects between transgenes and the genetic background in legume crops	
output target 2008	development and evaluation of various drought tolerance transgenes in diverse genetic backgrounds of selected clonal crops		knowledge of the epistatic effects between transgenes and the genetic background in clonal crops	

Project	Outputs	Intended user	Outcome	Impact
GCP Project 3.3	**mapping of, development of pilot tests for, and assessment of molecular enhanced breeding product development pathways with end-users**			
3.3 Output 1	implications of key product delivery issues assessed and best practice guidelines developed	CGIAR, NARS, university and SME breeding programs		
output target 2006	biosafety issues of abiotic stress tolerance transgenic products investigated		improved understanding of the unique biosafety issues related to abiotic stress transgenics	more effective product development and delivery pathways for transgenic products
output target 2007	best practices for deploying abiotic stress tolerance transgenic products defined		improved deployment of abiotic stress tolerant transgenics lines	more transgenic-based drought tolerant lines released for farmer adoption
output target 2008	*none*			
3.3 Output 2	product development pathways mapped for all Subprogramme 3 technologies	CGIAR, NARS, university and SME breeding programs		
output target 2006	mapping product development pathways for key representatives of genomics, transgenic and computational outputs		improved priority setting and product design	more GCP products reach end-users
output target 2007	mapping product development and delivery pathways for new GCP technologies		improved priority setting and product design	more GCP products adopted by end-users
output target 2008	*none*			
3.3 Output 3	molecular breeding products piloted and evaluated with diverse end-users	CGIAR, NARS, university and SME 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	new and better varieties available
output target 2006	cost-benefit analysis of low cost MAS systems applied by diverse end-users	CGIAR, NARS, university and SME breeding programs	low cost high throughput marker screening technologies adopted by end-users in key production areas across the world	improved efficiency of molecular breeding
output target 2007	impact of new molecular breeding systems	CGIAR, NARS, university and SME breeding programs	new breeding systems adopted by end-users in key production areas across the world	improved efficiency of breeding
output target 2008	evaluation of products in farmers' fields based on GCP technologies	farmers in key production areas across the developing world	new varieties based on GCP products adopted by farmers in pilot sites in key production areas across the world	increase in economic value of agricultural production
GCP Project 4.1	**establishment of the GCP Information Platform**		**information flow of ongoing research facilitated, both in terms of data and in terms of communication between the researchers**	
4.1 Output 1	GCP domain models are developed		GCP SP4 software developers possibility to better integrate software and webservices for use in germplasm conservation and crop improvement	better access to and higher quality of GCP data
output target 2006	models for the passport and genotype are developed with involvement of all relevent actors in and outside the GCP consortium			
output target 2007	models for (probably) the geneology and site description are developed			
output target 2008	other models are developed (prioritisation will be done later)			
4.1 Output 2	web services technology is implemented in the GCP Consortium			better access to and higher quality of GCP data
output target 2006	staff is trained in webservices in the GPC consortion member institutes	informatics staff in GCP consortium	GCP consortium staff is able to use webservices in their organisation	
output target 2007	webservices are deployed in the GPC consortion member institutes	bioinformatics and biodiversity	webservices are used in the GCP scientists all over the world	higher efficiency in crop research and improvement
output target 2008	*none*			
4.1 Output 3	GCP Repository is created and being maintained	bioinformatics and biodiversity scientists all over the world	central accesss to all GCP generated data	better access to and higher quality of GCP data
output target 2006	GCP repository is created and populated with available GCP data sets			
output target 2007	GCP repository is updated with (references to) all produced GCP data sets			
output target 2008	GCP repository is updated with (references to) all produced data sets			

Project	Outputs	Intended user	Outcome	Impact
4.1 Output 4	MOBY is further developed and applied in the GCP Consortium	bioinformatics and biodiversity scientists all over the world	based on improved technology the GCP will contribute to the global bioinformatics community	better access to and higher quality of GCP data
output target 2006	development of MOBY is supported, reference GCP implemetations have been made			
output target 2007	development of MOBY is further supported, reference GCP implemetations have been made			
output target 2008	*to be decided*			
4.1 Output 5	templates for GCP data capture and strorage are available and being maintained	GCP scientists producing data	scientists will better be able to standardise and upload their GCP data	better access to and higher quality of GCP data
output target 2006	templates for passport and genotype data have been created and implemented			
output target 2007	templates for (probably) geneology and site descriptions have been created and implemented			
output target 2008	templates for other data types (to be decided) have been created and implemented			
4.1 Output 6	use cases are developed and documented in accessible databases	GCP-SP4 software developers		better access to and higher quality of GCP data
output target 2006	infrastructure for documentation and implementation of GCP platform and network use cases, and related facilities, have been developed		simultaneous software development sis facilitated	
output target 2007	infrastructure has been populated and is maintained		software developers have access to all use cases and software that has been or is being developed	
output target 2008	infrastructure has been further populated and is maintained			
GCP Project 4.2	**improvement of the GCP Information Platform Components**		**capacity and facilities to support IT applications in the GCP consortium created**	
4.2 Output 1	improvement of quality of existing databases	informatics staff in GCP consortium	quality of existing data bases will be improved both in terms of management of data as of data quality	better access to and higher quality of GCP data
output target 2006	wide array of quality improvement and reference system building activities has been performed			
output target 2007	wide array of quality improvement and reference system building activities has been performed			
output target 2008	*to be decided*			
4.2 Output 2	creation of institutional bioinformatics capacity	informatics staff in GCP consortium plus the scientists that use this capacity	the bioinformatics capacity in the GCP consortium is improved	better access to and higher quality of GCP data
output target 2006	investments in training and hiring bioinformatics staff have been made			
output target 2007	investments in training and hiring bioinformatics staff have been made			
output target 2008	*none*			
4.2 Output 3	integration of the High Performance Computing (HPC)-facilities in the GenerationCP toolbox	informatics staff in GCP consortium	the HPC facility is fully used in GCP bioinformatics and genetics research	efficient analysis of genomic data
output target 2006	HPC facilities on 3 sites have been consolidated with inputs of all consortium members			
output target 2007	HPC facilities have been expaned and software has been added			
output target 2008	*to be decided*			
GCP Project 4.3	**creation of software in support of GCP activities**		**specific activities in the GCP supported in terms of software tools**	
4.3 Output 1	development of decision support systems for sampling germplasm (supports SP1)	GCP-SP1 scientists		higher efficiency in crop research and improvement
output target 2006	DDS, in the form of validated algorithms for sampling germplasm have been developed		the selection of material for specific purposes is greatly facilitated	
output target 2007	*none*			
output target 2008	*none*			
4.3 Output 2	development of ortholog-function display tools (supports SP2) bioinformatics scientists all over the world	gene orthology relationships across species and related paralogy relationships within a gene families are readily accessible to scientists	efficient analysis of genomic data	
output target 2006	*intermediate project targets*			
output target 2007	public comparative gene catalog, user interfaces and data integration protocols have been developed			
output target 2008	*none*			

Project	Outputs	Intended user	Outcome	Impact
4.3 Output 3	development of crop gene expression database and data mining tools (supports SP2)	bioinformatics scientists all over the world	scientists can easily search and compare expression data	efficient analysis of genomic data
output target 2006	*intermediate project targets*			
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*			
4.3 Output 4	development of decision support tools for MAS and MAB (supports SP3)	plant breeders in the CGP-SP3 and in the rest of the world	plant breeders all over the world can more efficiently use markers in their breeding programmes	higher efficiency in crop improvement
output target 2006	*intermediate project targets*			
output target 2007	integrated decision support system for marker-assisted plant breeding has been developed by integrating largeley already existing software			
output target 2008	*none*			
4.3 Output 5	an eco-physiological – statistical framework for the analysis of GxE and QTLxE as occurring in abiotic stress trials (supports SP3)	scientists and plan breeders in GCP-SP3 and the rest of the world	understanding in GxE and QTLxE improves and QTL detection is more efficient	efficient analysis of phenotipic data - higher efficiency in crop research and improvement
output target 2006	*intermediate project targets*			
output target 2007	*intermediate project targets*			
output target 2008	an eco-physiological – statistical framework for the analysis of GxE and QTLxE as occurring in abiotic stress trials, with applications to the CIMMYT drought stress programs in tropical maize and bread wheat has been developed and made available			
GCP Project 5.1	**increase NARS scientists' capacity to participate in the GCP**			
5.1 Output 1	capacity needs of NARS are assessed	national research institutions at large	efficiency in the delivery of capacity due to an appropriate targeting of recipients	extended coverage and benefits of the GCP generated knowledge and products
output target 2006	NARS' own target level and criteria for their capacity building development and involvement in the GCP defined; questionnaires, evaluation forms and follow-up surveys circulated among partners/beneficiaries in GCP activities			
output target 2007	NARS' own target level and criteria for their capacity building development and involvement in the GCP defined; questionnaires, evaluation forms and follow-up surveys circulated among partners/beneficiaries in GCP activities			
output target 2008	questionnaires, evaluation forms and follow-up surveys circulated among partners/beneficiaries in GCP activities		updated materials and activities to refocus mechanisms and criteria on which capacity building activities were originally based	
5.1 Output 2	hands-on capacity components built into commissioned and competitive research programs	national research institutions at large and their individual scientists in the different fields of the GCP	partners in national institutions of developing countries with higher capacity in GCP related matters	national programs strengthened in the areas of knowledge of the GCP
output target 2006	NARS institutions and scientists engaged in hands-on GCP research in each of the approved commissioned and competitive projects throughout SP1, SP2, SP3 and SP4			
output target 2007	NARS institutions and scientists engaged in hands-on GCP research in each of the approved commissioned and competitive projects throughout SP1, SP2, SP3 and SP4			
output target 2008	NARS institutions and scientists engaged in hands-on GCP research in each of the approved commissioned and competitive projects throughout SP1, SP2, SP3 and SP4		more and stronger links established between NARS, Consortium Institutions and additional ARIs; communities of practice of regional and GCP consortium scientists	increased number of institutions self-reliable on GCP related work
5.1 Output 3	NARS scientists participate in targeted SP group activities	national research institutions at large and their individual scientists in the different fields of the GCP	partners in national institutions of developing countries more acquainted with GCP work	national programs strengthened in the areas of knowledge of the GCP
output target 2006	SP-targeted group training with NARS involvement conducted			
output target 2007	SP-targeted group training with NARS involvement conducted			
output target 2008	SP-targeted group training with NARS involvement conducted		partners in national institutions of developing countries with higher capacity in GCP related matters; more and stronger links established between NARS, Consortium Institutions and additional ARIs	increased number of institutions self-reliable on GCP related work

Project	Outputs	Intended user	Outcome	Impact
5.1 Output 4	GCP Training Program	national research institutions and their scientists, GCP Consortium scientists and the wide scientific community more and stronger links established between NARS, the GCP Consortium, additional ARIs and educational institutions	partners in national institutions of developing countries with higher capacity in GCP related matters increased number of institutions self-reliable on GCP related work	national programs strengthened in the areas of knowledge of the GCP
output target 2006	training materials available and translated to Spanish and French; training courses on different SP matters conducted in developing country regions; consultation with worldwide capacity building initiatives conducted; analysis of capacity delivery modes and identification of the best cost-effective options for different subjects		communities of practice of regional and GCP consortium scientists	
output target 2007	training courses on different SP matters conducted in developing country regions		communities of practice of regional and GCP consortium scientists	
output target 2008	training courses on different SP matters conducted in developing country regions		communities of practice of regional and GCP consortium scientists	
5.1 Output 5	GCP Fellowships and Grants Program	national research institutions and their scientists	partners in national institutions of developing countries with higher capacity in GCP related matters	national programs strengthened in the areas of knowledge of the GCP
output target 2006	Pioneer-GCP fellowship (1), GCP fellowships (8) and travel awards (16) granted; IFS-GCP research grants (6) awarded			
output target 2007	Pioneer-GCP fellowship, GCP fellowships and travel awards granted; IFS-GCP research grants awarded			
output target 2008	Pioneer-GCP fellowship, GCP fellowships and travel awards granted; IFS-GCP research grants awarded		more and stronger links established between NARS, the GCP Consortium, additional ARIs and educational institutions	increased number of institutions self-reliable on GCP related work
GCP Project 5.2	**establishment of broad regional mechanisms for sustainable capacity to participate in the GCP**			
5.2 Output 1	regional approaches for sustainable GCP-related capacity identified and partnerships established	GCP Consortium institutions, national program scientists and the wide scientific community	adequate regional capacity to apply knowledge in crop breeding programs	self-reliance built in regional institutions and scientists in national programs
output target 2006	work program for SSA jointly developed with BECA; other RRH identified in SSA; a consultation conducted among regional partners and the Stakeholders Committee to develop an alternative to the Regional Research Hub scheme for Asia and LatinAmerica; a telecommunications- and web-supported help desk available and running		sustainable crop research programs in the regions; adequate and sustainable support to capacity recipients in all its forms	
output target 2007	capacity needs of RRH and similar mechanisms identified and a joint plan to address them developed; work program jointly developed with alternative RRH options in Asia and Latin America; some functions of the helpdesk are devolved to the Regional Research Hubs or similar figure			
output target 2008	regional initiatives sustained			
GCP Project 5.3	**development and adoption of policies and protocols to allow proper access and benefit sharing from the derivatives of the program**			
5.3 Output 1	capacity in GCP policy-related aspects developed	scientists and science managers from GCP partners and not immediately GCP-involved NARS in Asia, Africa and Latin America	a curriculum for regional courses on institutional genetic resource policies	institutional policies and tools for handling Freedom to Operate on IPR and ABS in partner institutions of the CP developed and strengthened
output target 2006	training courses conducted in developing country regions			
output target 2007	training courses conducted in developing country regions			
output target 2008	training courses conducted in developing country regions		adequate support in GCP policy-related matters awareness, knowledge and experiences shared among scientists and science managers	

Project	Outputs	Intended user	Outcome	Impact
5.3 Output 2	tools to support GCP scientists in policy and IPR matters			
output target 2006	a distance learning module for scientists on Genetic Resource Policies and their implications for Freedom-to-Operate; an Intellectual Property and Access&Benefit Sharing-helpdesk and On-line-Resource for the GCP Community, Partners and Stakeholders; an asset inventory system for the GCP	the GCP community, as a whole, i.e. Consortium and collaborating institutions, scientists, researchers, and staff, as well as stakeholders and users of GCP products	a basic on-line course; a helpdesk service on matters related to IP, ABS, and product delivery; a database of products, expertise, and 3rd party materials associated with specific products for the GCP	understanding of GCP scientists of intellectual property rights
output target 2007	operating distance-learning modules and regional courses; facilitating unrestricted use of GCP-products by target groups	GCP Consortium institutions, national program scientists and the wide scientific community		
output target 2008	operating distance-learning modules and regional courses; synthesis and publication of the CP experience on international cooperation in genomics-based germplasm enhancement			
GCP Project 5.4	**articulation and implementation of the GCP product delivery strategy**			
5.4 Output 1	review of existing linkages and approaches to reaching end-users	regional and local organizations workers and scientists in a diversity of disciplines, local seed industries, producers and farmers	analysis documents that will guide the development and refinement of a GCP strategy for product delivery	delivery of GCP products to end-users
output target 2006	consultation among all relevant actors on linkages between laboratory research, plant breeding and end-user; strengths and weaknesses of linkages collated and used as contribution to design regional mechanisms; priorization of crops, traits and regions on which to build the delivery strategy and develop the case studies			
output target 2007	regional consultations with farmers, the people who reach farmers, and the people who developproducts for farmers for iterative planning of research and delivery		feedback documents to inform the scientists upstream the delivery chain	
output target 2008	regional consultations with farmers, the people who reach farmers, and the people who developproducts for farmers for iterative planning of research and delivery		feedback documents to inform the scientists upstream the delivery chain	
5.4 Output 2	mapping of GCP outputs, its intended users and anticipated impact	GCP scientists and their partners involved in a given project, and the rest of the community in the delivery chain	for each project proposal, a sketched plan of products, steps to reach the following component of the chain, and indicators of anticipated impact	access of end-users to GCP products
output target 2006	delivery plans and pathways embedded into competitive research projects			
output target 2007	delivery plans and pathways embedded into competitive research projects			
output target 2008	delivery plans and pathways embedded into competitive research projects			
5.4 Output 3	establishment of appropriate partnerships in the delivery chain	GCP scientists and their partners involved in a given project, and the rest of the community in the delivery chain	alliances, memoranda of understanding, agreements, clear share of responsibilities	access of end-users to the products arising of the GCP
output target 1 2006	consultation with significant private sector actors, at the multinational, regional and local levels; consultation and analysis of options with other Challenge Programs			
output target 2007	*to be decided*			
output target 2008	*to be decided*			
5.4 Output 4	case studies	GCP scientists and their partners, the community involved in the delivery chain, farmers	an assembly of good practices, successes and lessons learned	access of end-users to the products arising of the GCP
output target 2006	*to be decided*			
output target 2007	*to be decided*			
output target 2008	*to be decided*			

Annex 2: GCP 2006-2008 Financial Plan

Generation-Cost Allocation:

Allocation of Projects Cost to CGIAR Outputs, 2004-2008 **(in $million)**

Project	Outputs	2004 (actual)	2005 (estimated)	2006 (proposal)	2007 (plan 1)	2008 (plan 2)
Subprogram 1: Genetic Diversity of Global Genetic Resources						
	Germplasm Improvement	0.275	0.402	0.387	0.294	0.278
	Germplasm Collection	2.479	3.613	3.479	2.641	2.503
	TOTAL BY PROJECT	2.754	4.015	3.866	2.935	2.781
Subprogram 2: Comparative Genomics and Gene Discovery						
	Germplasm Improvement	0.419	1.037	1.095	0.909	0.582
	Germplasm Collection	0.838	2.074	2.191	1.818	1.165
	Sustainable Production	0.140	0.346	0.365	0.303	0.194
	TOTAL BY PROJECT	1.397	3.457	3.651	3.030	1.941
Subprogram 3: Trait Capture for Crop Improvement						
	Germplasm Improvement	0.630	2.447	2.458	2.009	0.982
	Sustainable Production	0.180	0.699	0.702	0.574	0.281
	Policy	0.090	0.349	0.352	0.287	0.140
	TOTAL BY PROJECT	0.900	3.495	3.512	2.870	1.403
Subprogram 4: Genetic Resources, Genomic, and Crop Information Systems and Bioinformatics						
	Germplasm Improvement	0.863	1.193	1.267	0.880	1.167
	Germplasm Collection	1.079	1.491	1.584	1.100	1.459
	Policy	0.216	0.298	0.317	0.220	0.292
	TOTAL BY PROJECT	2.158	2.982	3.168	2.200	2.918
Subprogram 5: Capacity Building						
	Policy	0.040	0.511	0.553	0.373	0.611
	Enhancing NARS	0.157	2.043	2.212	1.492	2.446
	TOTAL BY PROJECT	0.197	2.554	2.765	1.865	3.057
	TOTAL BY CENTER	7.406	16.503	16.962	12.900	12.100

Generation-Investment, 2004-2008

Investments by Sectors and Commodities (in $million)

Sectors & Commodities	2004 (actual)	2005 (estimated)	2006 (proposal)	2007 (plan 1)	2008 (plan 2)
Crops					
Banana/ Plantain	0.473	0.523	0.537	0.303	0.421
Barley	0.299	0.768	0.789	0.528	0.589
Bean	0.778	0.466	0.479	0.250	0.383
Cassava	0.807	0.097	0.099	0.052	0.079
Chickpea	0.292	0.619	0.636	0.332	0.509
Coconut	0.000	0.289	0.297	0.178	0.229
Cowpea	0.757	0.741	0.762	0.745	0.484
Groundnut	0.000	0.865	0.889	0.810	0.585
Legumes (soybean)	0.000	0.097	0.099	0.052	0.079
Lentils	0.000	0.097	0.099	0.052	0.079
Maize	0.880	1.652	1.698	1.332	1.197
Millet	0.104	0.174	0.178	0.093	0.143
Pigeonpea	0.000	0.097	0.099	0.052	0.079
Potato	0.658	0.463	0.475	0.271	0.372
Rice	1.031	6.328	6.504	5.556	4.419
Roots and Tubers	0.000	0.048	0.050	0.026	0.040
Sorghum	0.478	0.946	0.972	0.546	0.763
Sweetpotato	0.000	0.097	0.099	0.052	0.079
Wheat	0.849	1.995	2.050	1.570	1.458
Yam	0.000	0.141	0.151	0.100	0.113
TOTAL BY CENTER	**7.406**	**16.503**	**16.962**	**12.900**	**12.100**

Generation-Cost Allocation:

Allocation of Projects Cost to CGIAR Regions, 2004-2008 **(in $million)**

Project	Regions	2004 (actual)	2005 (estimated)	2006 (proposal)	2007 (plan 1)	2008 (plan 2)
Subprogram 1: Genetic Diversity of Global Genetic Resources						
	SSA	0.689	1.004	0.967	0.734	0.695
	Asia	0.689	1.004	0.967	0.734	0.695
	LAC	0.689	1.004	0.967	0.734	0.695
	CWANA	0.689	1.004	0.965	0.733	0.696
	TOTAL BY PROJECT	2.754	4.015	3.866	2.935	2.781
Subprogram 2: Comparative Genomics and Gene Discovery						
	SSA	0.349	0.864	0.913	0.758	0.485
	Asia	0.349	0.864	0.913	0.758	0.485
	LAC	0.349	0.864	0.913	0.758	0.485
	CWANA	0.349	0.865	0.912	0.756	0.486
	TOTAL BY PROJECT	1.397	3.457	3.651	3.030	1.941
Subprogram 3: Trait Capture for Crop Improvement						
	SSA	0.225	0.874	0.878	0.718	0.351
	Asia	0.225	0.874	0.878	0.718	0.351
	LAC	0.225	0.874	0.878	0.718	0.351
	CWANA	0.225	0.873	0.878	0.716	0.350
	TOTAL BY PROJECT	0.900	3.495	3.512	2.870	1.403
Subprogram 4: Genetic Resources, Genomic, and Crop Information Systems and Bioinformatics						
	SSA	0.539	0.746	0.792	0.550	0.730
	Asia	0.539	0.746	0.792	0.550	0.730
	LAC	0.539	0.746	0.792	0.550	0.730
	CWANA	0.540	0.744	0.792	0.550	0.728
	TOTAL BY PROJECT	2.158	2.982	3.168	2.200	2.918
Subprogram 5: Capacity Building						
	SSA	0.050	0.639	0.691	0.466	0.764
	Asia	0.050	0.639	0.691	0.466	0.764
	LAC	0.050	0.639	0.691	0.466	0.764
	CWANA	0.049	0.637	0.692	0.467	0.765
	TOTAL BY PROJECT	0.198	2.554	2.765	1.865	3.057
	TOTAL BY CENTER	7.406	16.503	16.962	12.900	12.100

Generation-Expenditures, 2004-2008

Object of Expenditure, **(in $million)**

Object of Expenditures	2004 (actual)	2005 (estimated)	2006 (proposal)	2007 (plan 1)	2008 (plan 2)
Personnel	0.253	0.314	0.350	0.350	0.350
Supplies and Services	0.890	1.326	0.748	0.980	0.688
Collaborators/Partnership	6.193	14.783	15.784	11.490	10.982
Operational Travel	0.070	0.080	0.080	0.080	0.080
Depreciation	0.000	0.000	0.000	0.000	0.000
TOTAL BY CENTER	**7.406**	**16.503**	**16.962**	**12.900**	**12.100**

Generation-Financing:

Members/Non Members Unrestricted Grants, 2004-2006 **(in $million)**

Members/Non Members	2004 (actual)	2005 (estimated)	2006 (proposal)
MEMBERS			
European Commission	5.225	6.027	5.875
Rockefeller Foundation	0.000	0.855	0.845
Sweden	0.000	0.104	0.100
Syngenta Foundation	0.015	0.050	0.000
United Kingdom	4.676	4.250	4.500
World Bank	1.000	2.500	2.000
TOTAL MEMBERS	**10.915**	**13.786**	**13.320**
NON MEMBERS			
Kirkhouse Trust	0.000	0.015	0.000
Pioneer	0.050	0.050	0.025
TOTAL NON MEMBERS	**0.050**	**0.065**	**0.025**
TOTAL BY CENTER	**10.965**	**13.851**	**13.345**

Generation-Financing:

Allocation of Members/Non Members Grants to Projects, 2004-2006 (in $ million)

Project	Members/Non Memebers	2004 (actual)	2005 (estimated)	2006 (proposal)
Subprogram 1: Genetic Diversity of Global Genetic Resources	**MEMBERS**			
	European Commission	0.000	0.000	0.000
	Rockefeller Foundation	0.000	0.000	0.000
	Sweden	0.000	0.000	0.000
	United Kingdom	0.000	0.000	0.000
	World Bank	0.000	0.000	0.000
	TOTAL MEMBERS	0.000	0.000	0.000
	NON MEMBERS			
	TOTAL MEMBERS + NON MEMBERS	0.000	0.000	0.000
	Unrestricted + center inc	2.754	4.015	3.866
	TOTAL BY PROJECT	2.754	4.015	3.866
Subprogram 2: Comparative Genomics and Gene Discovery	**MEMBERS**			
	European Commission	0.000	0.000	0.000
	Rockefeller Foundation	0.000	0.000	0.000
	Sweden	0.000	0.000	0.000
	United Kingdom	0.000	0.000	0.000
	World Bank	0.000	0.000	0.000
	TOTAL MEMBERS	0.000	0.000	0.000
	NON MEMBERS			
	TOTAL MEMBERS + NON MEMBERS	0.000	0.000	0.000
	Unrestricted + center inc	1.397	3.457	3.651
	TOTAL BY PROJECT	1.397	3.457	3.651
Subprogram 3: Trait Capture for Crop Improvement	**MEMBERS**			
	European Commission	0.000	0.000	0.000
	Rockefeller Foundation	0.000	0.000	0.000
	Sweden	0.000	0.000	0.000
	United Kingdom	0.000	0.000	0.000
	World Bank	0.000	0.000	0.000
	TOTAL MEMBERS	0.000	0.000	0.000
	NON MEMBERS			
	TOTAL MEMBERS + NON MEMBERS	0.000	0.000	0.000
	Unrestricted + center inc	0.900	3.495	3.512
	TOTAL BY PROJECT	0.900	3.495	3.512
Subprogram 4: Genetic Resources, Genomic, and Crop Information Systems and Bioinformatics	**MEMBERS**			
	European Commission	0.000	0.000	0.000
	Rockefeller Foundation	0.000	0.000	0.000
	Sweden	0.000	0.000	0.000
	United Kingdom	0.000	0.000	0.000
	World Bank	0.000	0.000	0.000
	TOTAL MEMBERS	0.000	0.000	0.000
	NON MEMBERS			
	TOTAL MEMBERS + NON MEMBERS	0.000	0.000	0.000
	Unrestricted + center inc	2.158	2.982	3.168
	TOTAL BY PROJECT	2.158	2.982	3.168
Subprogram 5: Capacity Building	**MEMBERS**			
	European Commission	0.000	0.000	0.000
	Rockefeller Foundation	0.000	0.000	0.000
	Sweden	0.000	0.000	0.000
	Syngenta Foundation	0.000	0.000	0.000
	United Kingdom	0.000	0.000	0.000
	World Bank	0.000	0.000	0.000
	TOTAL MEMBERS	0.000	0.000	0.000
	NON MEMBERS			
	Kirkhouse Trust	0.000	0.000	0.000
	Pioneer	0.000	0.000	0.000
	TOTAL NON MEMBERS	0.000	0.000	0.000
	TOTAL MEMBERS + NON MEMBERS	0.000	0.000	0.000
	Unrestricted + center inc	0.197	2.554	2.765
	TOTAL BY PROJECT	0.197	2.554	2.765
	TOTAL BY CENTER	7.406	16.503	16.962

Generation Staff Composition:

Internationally and Nationally Recruited Staff, 2004 - 2008

Staff Type	2004 (actual)	2005 (estimated)	2006 (proposal)	2007 (plan 1)	2008 (plan 2)
Internationally-Recruited Staff (IRS)	1	2	2	2	2
National-Recruited Staff (NRS)	1	1	1	1	1
TOTAL BY CENTER	2	3	3	3	3

Generation-Financial Position:

Currency Structure of Expenditures, 2004-2006 (in $ million)

	2004(actual)			2005(estimated)			2006(proposal)		
Currency	**Amount**	**US$Value**	**%Share**	**Amount**	**US$Value**	**%Share**	**Amount**	**US$Value**	**%Share**
Euro (EUR)	3.984	5.016	67.729%	4.600	6.027	36.523%	4.500	5.875	34.636%
Pound Sterling (GBP)	0.100	0.187	2.525%	3.536	6.614	40.077%	2.339	4.375	25.793%
Swedish Krona (SEK)	0.000	0.000	0.000%	0.683	0.104	0.629%	0.683	0.100	0.590%
US Dollar (USD)	2.203	2.203	29.746%	3.758	3.758	22.772%	6.612	6.612	38.981%
TOTAL BY CENTER		7.406	100.000%		16.503	100.000%		16.962	100.000%

Generation Statements of Activities

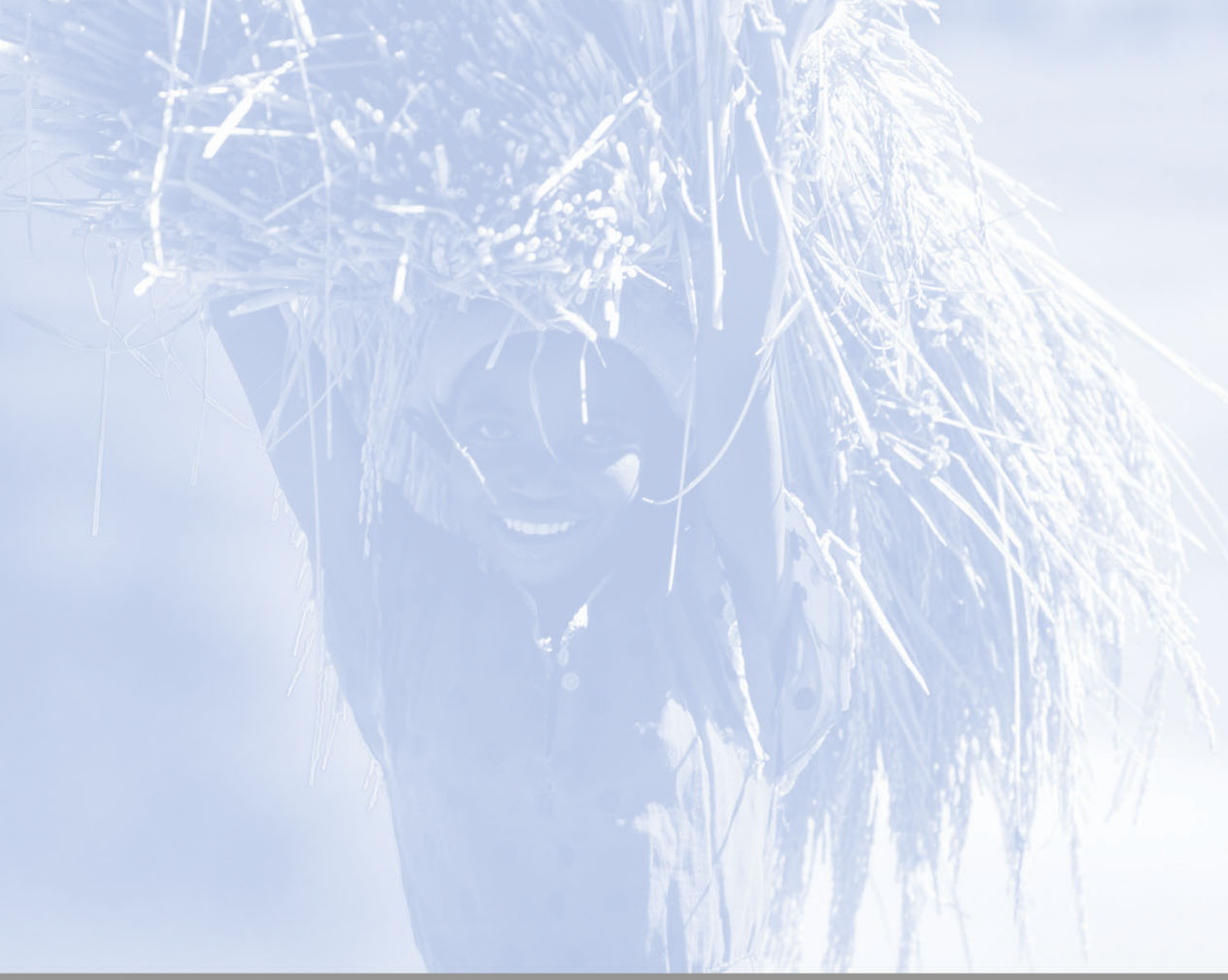
For the Year Ended December 31, 2004 (in $million)

	Unrestricted	Restricted		Total 2004	Total 2003
		Temporary	Challenge Programs		
Revenue and Gains					
Grant Revenue	10.965	0.000	0.000	10.965	3.161
Other revenue and gains	0.000	0.000	0.000	0.000	0.000
Total revenue and gains	10.965	0.000	0.000	10.965	3.161
Expenses and Losses					
Program related expenses	6.264	0.000	0.000	6.264	0.117
Management and general expenses	0.642	0.000	0.000	0.642	0.384
Other losses expenses	0.000	0.000	0.000	0.000	0.000
Sub Total expenses and losses	6.906	0.000	0.000	6.906	0.501
Indirect cost recovery	0.000	0.000	0.000	0.000	0.000
Total expenses and losses	6.906	0.000	0.000	6.906	0.501
Net Surplus / (Deficit) from ordinary activities	4.059	0.000	0.000	4.059	2.660
Extraordinary Items	0.500	0.000	0.000	0.500	0.000
NET SURPLUS / (DEFICIT)	3.559	0.000	0.000	3.559	2.660
Object of Expenditures					
Personnel	0.253	0.000	0.000	0.253	0.016
Supplies and Services	0.890	0.000	0.000	0.890	0.368
Collaborators/Partnership	6.193	0.000	0.000	6.193	0.036
Operational Travel	0.070	0.000	0.000	0.070	0.081
Depreciation	0.000	0.000	0.000	0.000	0.000
TOTAL BY CENTER	7.406	0.000	0.000	7.406	0.501

Generation Statements of Financial Position

December 31, 2004 (in $million)

	2004	2003
ASSETS		
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	6.219	2.660
Others	0.000	0.000
Inventories	0.000	0.000
Prepaid expenses	0.000	0.000
Total current assets	6.219	2.660
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	**6.219**	**2.660**
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	0.000	0.000
Undesignated	6.219	2.660
Total Unrestricted Net Assets	6.219	2.660
Restricted	0.000	0.000
Total net assets	6.219	2.660
TOTAL LIABILITIES AND NET ASSETS	**6.219**	**2.660**



Generation

Cultivating Plant Diversity for the Resource Poor

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