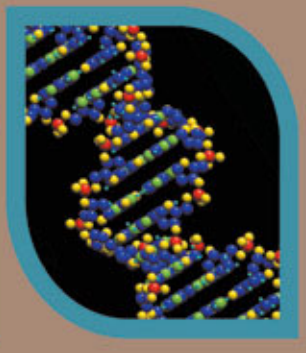
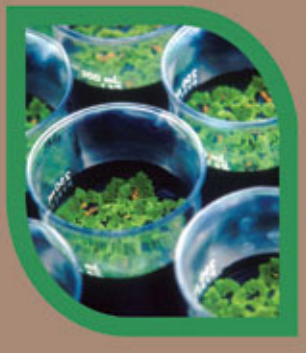
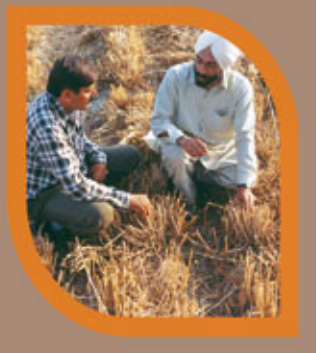
2004 Annual Report and Year Two Workplan

Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE POOR



Generation Challenge Program

Annual Report and Year Two Workplan

Submitted by Robert Zeigler, Director, and Jenny Nelson, Communications Coordinator

February 25, 2005

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Dear Friends of the Generation Challenge Programme,

It is my pleasure to submit the research and financial report for our first full year of operations. It has been an exciting, eventful, productive, and fulfilling year, indeed.

As you will see in the following report, we have launched a dynamic and comprehensive research programme. Through this initial work we have begun translating the vision incorporated in our original concepts into reality at a rapid rate. Beyond simply supporting research, we are constructing an information management and analysis platform that will allow all participants in the GCP to have access to our data, analytical tools, and reports. This bioinformatics resource, a first of its kind in the CGIAR, will serve as a resource for all CGIAR scientists and their partners who are involved in genomics- and crop improvement-related research. Perhaps most importantly, this platform will fully integrate the GCP, and by extension the entire CGIAR, into the broader global plant genomics research community. Such integration is essential if the CGIAR is to continue to play a leading role applying cutting-edge science to critical agricultural problems in developing countries.

Our research programme builds upon our first workplan that was derived from an initial planning session held in Wageningen in August 2003. This first plan was critical for initiating our research activities, but involved relatively few participants from almost exclusively within the Consortium. From this rather closed process of commissioning initial work, we have moved to a more open competitive and commissioned grants process involving over one hundred partners over the next three years. These rigorous and externally peer-reviewed processes also represent major new steps for the CGIAR in partnerships and accountability.

Another major dimension of our work for the first year has been the formulation of a capacity-building strategy and corresponding workplan. This Subprogramme includes a number of innovative activities, including the initiation of GCP Fellowships, the creation of regional hubs of research excellence, and the establishment of help desks (including on-line access) in the areas of genomics, policy, and intellectual property.

From a rather strategic launch document, we have developed a more refined and specific three-year rolling Medium Term Plan (based on a logical framework) that shows clearly where we are headed and provides milestones by which we can measure our progress. This MTP was reviewed and approved by the Science Council of the CGIAR in September of 2004.

As we developed our research programme we also developed a management and governance framework that will support and sustain the research programme. A Consortium Agreement has been developed and signed by all members. This agreement sets forth specific operating procedures and, perhaps most importantly, stipulates how we handle intellectual property. Clarity on this issue is essential to effective partnerships in the field of crop genomics and genetic resources.

Our first year has also been encouraging from the perspective of donor support. From our initial base from the European Commission and the World Bank in our first year, we have added the United Kingdom, Sweden, Austria, the Rockefeller Foundation, Syngenta Foundation, Pioneer Hybred Foundation, and the Kirkhouse Trust. Thus we are optimistic that we will continue to obtain the financial support needed to carry our research and capacity-building programme forward.

On behalf of all of our stakeholders, I would like to thank the donor community for their confidence in our programme. Most importantly, I would like to thank the scientists in the national and international institutions that make up the Generation Challenge Programme and who have committed so much into seeing that this innovative approach to international agricultural research is successful.

I look forward to another year of exciting developments and progress.

Robert S. Zeigler
Director

INTRODUCTION

The inception year of the Generation Challenge Programme (GCP) has been one of impressive scientific productivity, exceptional institutional growth, expansion of exciting scientific and institutional partnerships, and increasing international recognition beyond the CGIAR. The productive and promising arrival of this new model for the application of cutting-edge science to addressing problems of the world's poorest people is proving to be attractive to leading scientists from around the world. This appeal extends to traditional donors to the CGIAR and offers an attractive portal for non-traditional donors and the private sector to participate in the CGIAR. Our success in translating the vision of the GCP into operational research and capacity-building activities was recognised by the CGIAR as it approved the GCP for full implementation at the 2004 AGM in Mexico.

Mapping the broad approaches of the original proposal document for the Generation Challenge Programme onto a well-anchored and concrete Medium Term Plan for 2005-2007 began with the initial work planning meeting held at the end of August 2003, in Wageningen, Netherlands. There, representatives from the institutions that form the core consortium of the GCP (see Appendix A) initiated the development of the Year 1 Workplan. This plan, subjected to external peer review, was approved by the two largest donors at that time, the World Bank and the European Commission, and became operational in early 2004 (see http://www.generationcp.org for both the original Challenge Programme proposal and the Year 1 Workplan).

The Year 1 Workplan laid out three main domains of activity. The first domain was to initiate the gathering and application of essential genomic information of the target CGIAR crop species. The second domain was to begin the establishment of the technical and scientific foundation for the future activities of the GCP. Both of these domains involved a range of specific research and capacity-building undertakings whose progress will be summarised under each Subprogramme section. The third activity domain was to establish the institutional structure that would support such a complex international undertaking.

Programme Structure

The GCP activities for 2005 – 2007 are organised within five subprogrammes that fall into two broad objectives:

Objective 1: Develop a platform for and conduct analysis of genetic diversity in international crop genetic resources and apply this to improve major crops for drought tolerance and other related traits of importance to resource-poor farmers

Objective 2: Strengthen the capacity of NARS and Generation CP scientists to apply the tools of genomics, molecular biology, and bioinformatics to the analysis of genetic diversity held in germplasm collections, and to use this knowledge to improve crop breeding programmes and to develop new stress-tolerant varieties.

Each contributes directly to 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.

The application of new and existing tools of modern plant genomics and comparative biology to this germplasm will identify new genes for traits of importance that will be incorporated into crop improvement programmes targeting the poorest of people in developing countries. Each of the subprogrammes has a set of clearly defined and measurable outputs that relate directly to its rationale and objectives. These outputs are presented in a time frame that will allow unambiguous assessment of progress and productivity. The ultimate beneficiaries will be resource-poor farmers and consumers as varieties with improved tolerance to difficult environments contribute to improved productivity and use of natural and applied resources. 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.

The GCP operational objectives and Subprogrammes are:

Objective 1

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. As many of the policy questions that confront the GCP are associated with access to and application of genetic resources, much of the GCP's policy-related activities are incorporated in this subprogramme.

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 a substantial commitment to create appropriate technologies for the application of marker-assisted selection in national breeding programmes, to provide technical assistance for the rapid and effective uptake of molecular breeding in tropical staple crops, and to foster the development of communities of practice supported by regional centres of excellence and state of the art technologies and approaches.

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

The value of the data generated in the first three Subprogrammes will largely depend on the way they are stored, managed, analysed, and made accessible. The way they can be analysed will, in turn, be dependent on the way analysis tools and other information sources are made available. This Subprogramme 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 will be designed to support an integrated genetic resources, genomics, and crop improvement information network.

Objective 2

Subprogramme 5: Capacity Building and Enabling Delivery

Like Subprogramme 4, this Subprogramme addresses a major cross-sectional theme of the GCP. It has two dimensions: one is to better enable GCP members to carry out this cutting edge research agenda. 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.

Strategic Overview

The world has experienced three simultaneous technological revolutions over the past decade, which have had dramatic impact on the CGIAR development-oriented research programme. These revolutions are in the fields of molecular biology and genetics, data storage and management, and communications. Each of these areas brings capabilities and opportunities that were undreamt of as the GCIAR 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 from 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 (e.g., the recent identification of gene[s] controlling "asthma"). With the completion of the decoding of the rice genome and the dicot model species *Arabidopsis thaliana* and *Medicago truncatula*, 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 similar approaches. 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 deemed 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. This Challenge Programme will make available as public goods an unprecedented array of genomic and genetic resources, ready for direct use in plant improvement, first to the national agricultural research systems (NARS) of developing countries that have plant improvement programmes, and later to any other entities that have crop improvement goals, especially those dedicated to resource-poor farmers. These products will be in the form of enabling technologies and intermediate products for crop improvement programmes in NARS and elsewhere.

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 Challenge Programme 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 Challenge Programme 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 of research.

This Challenge Programme will serve as a platform to assemble and use the intricacies of applied genomic sciences for the benefit of crop improvement efforts by NARS and others targeting the world's poorest regions. A major challenge, however, is how to satisfy the needs of a very large set of stakeholders within and outside the CGIAR. 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 may be supported by the platform. The platform will also be applicable to the Water for Food, Harvest Plus, and Sub-Saharan Africa Challenge Programmes.

Despite the broad applicability of the GCP platform, there is still a need for focusing GCP activities. Even considering the power of comparative genomics and biology, resources must be allocated to only a limited set of crops for primary analysis. Likewise, the traits and crops that are selected must benefit the greatest numbers of the resource poor as soon as possible, implying regional considerations in setting research priorities.

As we refine our priorities over the next 12 months, we will work within the following guidelines that have established our programme to date:

- **Poverty alleviation:** The world's greatest absolute numbers of the very poor are in South Asia (SA), the greatest proportion of the population that is poor is in Sub-Saharan Africa (SSA), and significant zones of stagnant agricultural productivity associated with recalcitrant rural poverty are in Central and West Asia and North Africa (CWANA), Northeast Brazil, the Andean zone and Central America. Thus, our crop x trait focus must first and foremost address these areas of greatest need.
- **Crop targets:** Our comparative biology approach will in the first instance have greatest impact within three crop groups: cereals, legumes, and clonal crops. Within the cereals both the availability of scientific tools and poverty alleviation indicate that our initial concentration should be on rice (SA), maize (SSA), and wheat (CWANA). Research on these species will be complementary in that they will generate knowledge of broader applicability. For example, rice will focus on functional genomics, maize on the development of association genetics capacity, and wheat on gene identification, taking advantage of global genetic stocks. Sorghum and the millets should benefit rapidly from the progress made in these key cereals. The legumes are behind the cereals, yet investment in *Phaseolus* and cowpea genomics will have important impact for breeding programmes targeting SSA and the Andean zone. Modest and targeted investment in potato should yield insights into carbohydrate metabolism and starch accumulation that is relevant to cassava and *Musa*, as well. Since we expect the "orphan crops" to benefit substantially from our investments in the major crops, we will complete the initial characterization of their germplasm collections that began during the GCP inception phase and modestly assist in the development of genetic stocks. This will permit these crops to more effectively use genomics tools and insights derived from other crops in the coming years. If we are successful in securing additional funding this will be expanded in SSA.

- **Trait targets:** Drought was chosen as the long-term case study because drought affects all of the CGIAR mandate crops, it is the main constraint in the three largest poverty-stricken areas of the world, and it has resisted resolution using conventional approaches. This effort will be reinforced by the long history of drought research and by current global interest in water conservation. Furthermore, drought and associated water use efficiency emerged as the top priorities in the CGIAR System Priorities. The interaction of plants with water deficit ("drought") is a complex phenomenon, as are the genetic and physiological strategies by which plants manage water deficit. Thus, we will examine a range of traits associated with this broader target. Non-drought related traits – especially those with a shorter time horizon for impact such as disease and pest resistance, food quality, and plant architecture – will be addressed if they contribute substantially to tool and technique development. There is a need for parallel analysis of stress-response. An important aspect of the comparative biology underpinnings of the GCP is to make use of well-characterised systems, not only for bringing near-term results, but for enabling identification and manipulation of "drought tolerance genes." Understanding and predicting the interaction of stress–response traits, either synergistic or antagonistic, is critical to assembling useful gene combinations for pre-breeding products.

We do not underestimate the challenge of going from "gene" to "trait" to "breeding programme" to "crop" for a trait such as drought. Therefore, we will incorporate a significant modelling component to critically evaluate our assumptions and predict the consequences of various approaches *in silico*. This will present opportunities to understand the interactions of multiple pathways with bearings on whole-plant stress response.

PROGRESS REPORT

Administration and Governance

It is essential that there be an effective management and governance system in place to assure that the GCP funds are managed efficiently and effectively, that they are allocated in a transparent and orderly fashion, and that the research and capacity-building agendas are executed in a high-quality way. This is a particular challenge for virtual programmes like the GCP, since they do not have legal status, nor do they have physical infrastructure in which to execute their research agendas. Thus, in this first Annual Report it is appropriate to summarise briefly our progress in establishing the mechanisms that will assure a smoothly functioning Challenge Programme. The major accomplishments are summarised below.

Governance

- Established a Program Steering Committee
  - Process in place for the orderly change in Chairman
- Programme Advisory Committee recruited following consultation with Programme Steering Committee
  - Terms of Reference (TOR) for the PAC developed
- Selected a Stakeholders' Committee with GFAR after detailed and transparent selection process led by GFAR
  - TOR for Stakeholders' Committee developed with GFAR
- First year workplan agreements
  - Include reporting requirements
- Developed Consortium Agreement after exhaustive consultation with Consortium members to reconcile needs and requirements of CGIAR and no-CGIAR members (and after detailed inputs from the private sector) which includes major sections on:
  - Responsibilities of Consortium membership
  - TOR for PSC
  - IP policy
- Quantified in-kind contributions of CGIAR centres to GCP
- Fund and resource mobilisation yielded major investment by DFID, with strong expectations that the Rockefeller Foundation and Pioneer Hybred/DuPont Company will contribute over the next year

Research Management

- A Director was internationally recruited and appointed, followed by appointment of a communications coordinator, and 50% time secretary; an intern assistant was added in August
- The Director's office oversaw execution of first year workplan
- Funds for first year were disbursed following the development of terms and letters of agreement between GCP institutions and CIMMYT/GCP Director's office
- Recruited and appointed research management team following a competitive, transparent search from within GCP consortium members (3 Subprogramme Leaders from CGIAR centres and 2 ARIs)
- Designed and conducted a transparent competitive grants programme
- Developed capacity-building strategy
  - Needs assessment consultation with NARS
- Established strategic linkages with other Challenge Programmes and NEPAD Biosciences (BECA, Nairobi)
- Undertook a wide range of intensive consultations with GCP participating scientists to establish norms and standards for research approaches, protocols, and data management
- CIMMYT provided excellent accounting and other managerial support

Research Grants

The Year 1 (2004) grants were assigned based on consultations initiated during the Wageningen meeting and continued over the following six weeks. Some of these projects, but by no means all, were continued into Year 2 as commissioned research. Non-continuity was determined by a number of factors, such as the activity being originally planned as only a one-year project, relatively low priority considering the available funds for Year 3, or, in rare cases, unsatisfactory progress.

In the second year, rigorous procedures were designed and executed for identifying projects to fund using both competitive and commissioned grants. The details of the process can be found at http://www.generationcp.org/workplan.php. In 2005, the GCP will be funding over 45 projects. In competitive grants alone there are over 40 non-CGIAR partners from both developed and developing countries contributing over $2 million in in-kind matching resources for the projects in 2005. This is hard evidence that one of our main challenges – to open the research process to better take advantage of new sources of expertise – is being met. A list of competitively awarded grants is shown in Appendix B and commissioned grants shown in Appendix C. A summary of our projects matched against our MTP activities is in Appendix F.

Resource Mobilisation and Utilisation

From a rather narrow funding base dependent on two visionary donors, the World Bank and the European Commission, the GCP has significantly expanded its funding base. We now receive major support from DFID. We also expect to receive important project funding from the Rockefeller Foundation. A particularly exciting development is the addition of cash contributions from the private sector. We are in discussions with several other donor organisations that have expressed interest in supporting parts of the GCP agenda. Summaries of our 2003 and 2004 income and expenses and our 2005 projected income and expenses are shown in Tables 1, 2, and 3 and Appendices D and E.

Private Sector and Other Partnerships

The private sector is making enormous investments in crop biotechnology – quite possibly approaching $1 billion per year. A significant portion of this investment is targeting drought, according to our discussions with major company executives. Senior scientists in Syngenta, Pioneer, and Monsanto have confirmed that they believe they have made major headway in identifying genetic factors controlling resistance or tolerance to drought in major crop and model species. What is particularly exciting is that these companies have each expressed a strong desire for their discoveries to contribute to solving drought-related production constraints, but in a way that does not compromise their legitimate business interests in developed countries. The GCP is in a position to help the CGIAR leverage the hundreds of millions of dollars invested in private sector research to benefit the resource poor in developing countries. The salient points around our discussions to date are:

- *Syngenta*: Through its philanthropic arm, the Syngenta Foundation, Syngenta has expressed a desire for its research findings in rice, maize and *Arabidopsis* to be made available for crop improvement in Sub-Saharan Africa. They are particularly interested in supporting sorghum and millet improvement. The GCP Director participated in a first planning meeting to explore how this could be done (November 2004). The meeting included representatives from African NARS as well as leading international scientists in the fields of genomics and crop improvement. A follow up meeting to plan in more detail was held in January 2005, in Nairobi at the Biosciences East and Central Africa (BECA) headquarters on the ILRI campus. The Syngenta Foundation has also made a cash contribution to the marker-assisted selection course that was held in BECA in 2004.
- *Pioneer – DuPont*: Senior scientists and administrators visited GCP headquarters in May 2004 to initiate discussion on how Pioneer could contribute to GCP research activities. These discussions have continued and resulted in Pioneer supporting several research projects through technology donations, including a large number of maize SNPs (single nucleotide polymorphisms) that are expensive to develop but essential to a number of the projects that the GCP wishes to execute in maize. Other projects and collaborative activities are in rather advanced stages of planning. Pioneer, through its foundation, is also providing cash support for the 2004 MAS course in BECA and it is also providing funding for a Pioneer – GCP Fellowship that will support one graduate student for four years. We are planning for an expansion of this programme as we gain more experience working together.
- *Monsanto*: Scientists from this company have discovered "dozens" of genes that confer drought tolerance via a number of different mechanisms in maize, rice, soybean, and *Arabidopsis*. Monsanto has expressed its desire to see that these tools are placed in the hands of resource-poor farmers in developing countries in such a way that serious production constraints can be addressed, while not threatening the company's commercial interests in developing countries. The GCP Director attended a meeting in November 2004 in Washington, DC with Monsanto executives and scientists along with representatives from the Monsanto Biotechnology Advisory Committee, an NGO, the Rockefeller Foundation, and USAID. There was general agreement that we should proceed with exploring how to translate these good intentions in workable programme and a follow-up planning meeting is being scheduled for early 2005.

Although there are promising signs, the challenges of working with the private sector should not be underestimated. Means will have to be found to allow the GCP to utilise the findings offered by the private companies in a way that does not encumber its freedom to operate, threaten its ability to create global public goods, or limit access of farmers using GCP technology to global markets. We will explore the possibility of bringing the companies together to develop multilateral agreements for GCP access to their technology that also protect their interests.

Other important partnerships that we have been cultivating over the past year are with the Harvest Plus Challenge Programme and BECA. Harvest Plus has an aggressive programme to reach end-users that the GCP can certainly benefit from. At the same time our programme to work closely with breeders in developing countries can support the Harvest Plus programme. Since we will be working with the same NARS scientists on the same crops in the same countries it only makes sense to develop coordinated efforts. Indeed, Harvest Plus recognises that it cannot expect for its products to reach farmers' fields unless they are adapted to their conditions. In most cases this translates to nutritionally

enhanced varieties having drought tolerance or tolerance to other major production constraints. We are planning to jointly support a scientist working at BECA and to develop a work programme for the end-user specialist in Uganda to meet the needs of both of our programmes. The East India Rainfed Rice Breeding Network (RF – GCP) should serve as an important partnership node, as well.

With BECA we have agreed to jointly seek support for programmes of common interest. Programmatically, the GCP is an excellent complement to the priorities and strategies outlined by the BECA Steering Committee. We are already jointly sponsoring the MAS course in BECA and have submitted a project to the Rockefeller Foundation to support genotyping of germplasm being used in East and Central Africa breeding programmes for cassava, sorghum, and, eventually, *Phaseolus*.

Communications

This first year of GCP operations has been exciting and challenging in terms of communications. The communications coordinator and the GCP director developed a communications strategy in early 2004 (http://www.generationcp.org/sccv10/sccv10_upload/Comm_strategy.pdf) that details the communications philosophy, objectives, methods, and outputs for 2004. Both external and internal communications fall under the mantle of the GCP communications office. The 2004 communications objectives and achievements are detailed below.

Facilitate the flow of information within the GCP

- **E-newsletter:** All GCP member scientists receive the monthly newsletter, with information about workshops, funding opportunities, changes within the GCP, and partner contacts. In response to scientists' requests not to swamp them with lengthy emails, the e-newsletter is short – less than one page – with links to relevant documents, which are posted to the GCP website.
- **Maintain extensive contacts database:** The GCP is a virtual research programme; as such, it is imperative that our contacts database is extensive and current. At last count, there are over 300 GCP member scientists on the contact list.
- **Virtual Workspace:** The GCP virtual workspace (www.generationcp.org/vw) is a password-protected document repository and virtual community that helps link scientists across continents. Currently under revision, the workspace is intended to serve as a virtual home for GCP members. The communications team is committed to designing, revising, and maintaining the workspace with the input of GCP members, so that it is maximally useful.

Create a clear and recognised public image for the GCP

- **Developed a name, tagline, and logo for the programme:** After extensive consultation with communications specialists, GCP members, and external stakeholders, the Challenge Programme on Unlocking Genetic Diversity in Crops for the Resource Poor chose a new name: Generation: Cultivating Plant Diversity for the Resource Poor. Marcelo Ortiz, at CIMMYT, designed the winning logo.
- **Produced a brochure, folder, and poster:** In developing these materials, the goal was to present the Generation Challenge Programme in such a way that our mission is understandable and interesting to the general public and scientifically compelling to the research community. We also aimed to cast the GCP as a people-focused programme, and not one solely dedicated to upstream technology development.
- **Built an attractive and informative public website:** www.generationcp.org. The GCP contracted a design group in Rome to develop all of our publicity materials, including the website. They also designed the Global Crop Diversity Trust website, www.startwithaseed.org.

Inform target audiences about the GCP's mission and progress

- **E-newsletter distributed to over 250 non-GCP people – and counting:** The e-newsletter served as the GCP's primary public awareness tool in 2004.
- **GCP in the news:** The Generation Challenge Programme attracted significant media attention in 2004:
  - "Crop Plan: Genomics Resources For Developing Countries," Genome Technology, March 2004
  - "Crop Improvement Meeting in Kenya," Crop Biotech Update, 7 April 2004
  - "Genética para paliar pobreza," La Nación (Costa Rica), 4 August 2004
  - "Update on Generation Challenge Programme," CGIAR News, June 2004
  - "Robert Zeigler Returns to CGIAR," Phytopathlogy News, June 2004
  - "A New 'Generation' Arrives at CIMMYT," CIMMYT Annual Report, 2003-2004
  - "Generation Challenge Programme: Linking the Green Revolution to the Gene Revolution," Proceedings of the Double Helix Congress, fall 2004
  - "A New Global Initiative to Unlock Genetic Diversity in Crops for the Resource-Poor," Geneflow, fall 2004
  - "Generation Challenge Programme for Developing Countries," Crop Biotech Update, 1 October 2004
  - "Biologists Launch 'Open-Source Movement'," *Nature*, 30 September 2004

Disseminate research findings – Year 1 of the GCP was heavily devoted to setting up the programme and determining a research strategy; we anticipate that communications activities to disseminate research outputs will be ramped up in Year 2.

- Subprogramme Updates pages on website
- Targeting scientific media to garner publicity

Position the GCP as a leader in research and development

- **GCP presence at major international scientific meetings:** Plant and Animal Genome Conference (San Diego, January 2004), Rockefeller Drought Conference (Cuernavaca, Mexico, May 2004), USDA – USAID SLO/Linkage Programme Conference (Davis, California, June 2004), Legumes for the Benefit of Agriculture, Nutrition and the Environment (Dijon, France, June 2004), Annual Meeting of the American Phytopathology Society (Anaheim, California, August, 2004), Eucarpia: European Association for Research on Plant Breeding (Budapest, Hungary, September 2004), among others.
- Publicity of GCP grant and partnership opportunities to help recruit top scientists.

Aid in fundraising

- **Keep close contact with donors:** To cultivate good relationships with donors, current and potential, the GCP aims to keep lines of communication open and to incorporate as much as possible their input into activities.

Additional communications activities include: providing support to the Subprogramme Leaders, planning and executing meetings/workshops, and assisting capacity-building efforts.

SUBPROGRAMME UPDATES
Subprogramme 1: Genetic Diversity of Global Genetic Resources

The first year (2004) of the GCP in SP1 focused on starting molecular analysis of genetic diversity (or "genotyping") of the global genetic resources that will serve as the base of many GCP activities. This work was designed in several research methodology workshops (in early January and in late June/ early July, as well as at the first Annual Meeting), and resulted in the elaboration of an SP-specific Medium Term Plan, the selection of projects within a competitive granting action, and the invitation of commissioned research projects, whose selection was finalised in December 2004.

Analysing Molecular Diversity of Composite Germplasm Samples

The principal Year 1 activities focused on selecting representative samples within germplasm banks for the purpose of estimating and analysing molecular diversity in global germplasm collections. The analysis of global collections typically involved several laboratories for a given crop. This required coordination and planning, which was accomplished by several workshops over the period. For some participants, partitioning their collections into representative subsets and genotyping them was a new, GCP-inspired, activity.

Twenty seven participants representing the eleven crops selected for genotyping in the first year met in January at the Plant and Animal Genome meeting to decide on marker selection and sampling strategies, laboratory protocols, data collection, and deadlines. A composite germplasm set was identified for genotyping for each crop, generally following the criteria set forth in the first workplan. The list of accessions to be genotyped with structural markers was determined by consultations among the various partners to assure that their priority germplasm was included. The global organisation of the work was reviewed at a "data analysis workshop" that had been planned at the PAG workshop and took place in Zaragoza, Spain, in late June. In several instances the identification of the composite set was performed in two steps: analysis of a first set of accessions agreed upon early in the year provided for preliminary organisation of the collections; these data guided the choice of the remaining accessions that make up the complete composite sets. The projected completion dates of the genotyping decided for the first year were revised in some instances at the June meeting; these calendars were further refined at the Annual Meeting in Brisbane and are presented in the table below. In general the work is on track. The extended completion dates were caused by delays in equipment arrival and the care in negotiations to be sure that the proper germplasm was being analysed.

At the data analysis workshop in June the participants agreed to use a common file format for data exchange. The fields are: Laboratory/Institute, Species, Sample ID, Germplasm ID, Locus, Name of internal standard (=name of the molecular

Crop	Partners	Objective 2004 (acc x marker loci)	Expected Completion date
Barley	CAAS, ICARDA	500 x 50	February 2005
Wheat	CIMMYT, Agropolis, ICARDA, CAAS	3000 x 50	May 2005
Maize	CIMMYT, Agropolis, CAAS	1700 x 50	May 2005
Sorghum	ICRISAT, Agropolis, CAAS	700 x 30	February 2005
Rice	IRRI, CIAT, Agropolis, Embrapa, WARDA	3000 x 50	May 2005
Potato	CIP	1079 x 50	October 2004
Cassava	CIAT, Embrapa, IITA, IPGRI	3000 x 36, 500 x DArTs	March 2005
Cowpea	IITA, CAAS	(100*+2000) x 50	May 2005 (40 gSSR)
Chickpea	ICRISAT, ICARDA	288 x 50	October 2004
Common bean	CIAT, Embrapa	3000 x 50	March 2005
Musa	IPGRI, Agropolis, IITA	960 x 50	March 2005

* 100 accessions analyzed for 10 plants individually

weight standard for peak size estimation), Dye, Allele (size in bp), Peak size, Quality (scale from 1 to 100), Peak height, Volume (area under the curve), Allele amount (2n, 3n, 4n,..., bulk). The content of the file can be pasted in a web site and converted to various input file formats adapted to various software packages using a Web tool box. The suggested software includes global packages such as SAS, Genstat, PowerMarker, and specific software such as DarWin, Structure, Partition, Mstrat. The input formats will include SAS files, Individual x allele matrices with various column types (1 column per ploidy level, alleles separated by a "/" or concatenated alleles); disjunctive tables (1 column per allele); fully disjunctive tables (2 columns per allele). The list is not restrictive. SP4 will provide the Web interfaces for these conversions as well as clear any IP issues that could arise from using copyrighted software.

An important issue confronting any programme undertaking global germplasm diversity analyses is comparability of results among laboratories. In many cases, the markers were chosen based on prior information from different laboratories. Robustness is essential as the GCP is establishing reference information that will be accessible and repeatable for subsequent studies conducted anywhere in the world regardless of the technique (provided it is well defined and rigorously applied).

It was clear early on, however, that direct comparisons of existing data across laboratories were not assured. SP1 scientists used two approaches to assess this issue. The two groups analysing sorghum and banana chose to formally validate the comparability of the results between laboratories by conducting parallel analyses of their first batch of accessions. This served to identify the highest quality markers among the larger set of those used across labs as well as highlight inconsistencies that occur due to slight differences in technique. In other species the tasks were split across labs by assigning specific marker sets to each lab for survey across all accessions. These two approaches identified out several difficulties that are currently being sorted out (see lessons learned).

The composition of the initial composite set includes wild materials (W), landraces (L) and improved (I) materials. Although there is no single rule for the diverse crops, a distribution of 5%W:75%L:20%I was agreed to be an acceptable target by the participants. The issue of heterogeneous accessions was considered: when possible and efficient (suitable multiplication rate), it was agreed to extract DNA from a single plant per accession and to self it (for inbreeding species) and use the seeds as foundation stock for all analyses. For out-crossing species not clonally propagated, such as maize, a range of methods is possible; CIMMYT and INRA have acquired considerable experience in the handling of bulks to evaluate allele frequencies. However, the statistical power of accessions with within accession diversity to reveal functional associations still remains to be demonstrated.

The application of phenotyping with the view to conducting association studies requires an extrapolation from the original genotyped collections for field/growth chamber/greenhouse experiments. The extrapolation from the composite set to yield reference sample that will be preferentially used for association studies must include:

- representatives of the main components of the diversity to cover the range of allelic diversity
- continuous coverage of the global range of genotypic diversity, ideal for species-wide association studies
- those sectors of the diversity that seem derived from recombination between two distinct components, ideal for linkage disequilibrium (LD) mapping
- some components with large continuous variation, ideal for subspecific association studies.

GCP participants appreciate the value of using as many common accessions as possible across experiments for subsequent integration of information (and cross-comparisons). Reference samples will be standard, but it was agreed that more specific materials such as preferred checks for each institution/environment will be included and that those materials that are not adapted to the experimental environment could be excluded at the investigator's discretion. The combination of all these criteria requires development of simple, easy-to-use software for elaborating the set of materials for any new experiment.

Phenotyping Framework for the GCP

It is widely recognised that for the volumes of genotype data to ultimately relate to plant and crop performance and be useful in crop improvement programmes, there must be highly reliable, consistent and interpretable phenotype data associated with the germplasm that has been genotyped. Therefore, the GCP is devoting considerable resources towards establishing GCP-wide norms and standards. The first round of intensive consultation was organised during a workshop held early July in Montpellier, involving a well-balanced proportion of scientists from the CG centres, ARIs and NARS (40, 30 and 30%) and yielded the following positions:

- A draft minimum set of environmental data which should characterise the environment of all experiments of the GCP, in field, greenhouse or growth chamber experiments has been drawn up. The next step will be to determine how these will be incorporated into individual projects, and in the construction of the GCP database.

- Methods have been proposed to combine detailed measurements on a very small number of test genotypes and a very small number of affordable and quick measurements on all genotypes These will address an important set of environmental data concerns: (i) the "perception" of the environment by each studied individual genotype; and, (ii) the synchrony of the phenology of individual genotypes with environmental stressing events.
- It is not desirable that the GCP selects a set of relevant traits which would be common to all projects. In contrast, elements for evaluating the "quality" of traits have been proposed. A database of trait characterisation is under construction.
- Some decisions, such as the choice of traits, the control and manipulation of environmental variables or the respective roles of genetic, modelling, physiology and transcript/protein analyses are of the responsibility of individual projects. Indeed, they are major determinants of the scientific quality of the projects. It this respect, the GCP scientists and external advisers aimed to help and propose, but not to fix, general rules.
- Genetic variation within the samples, e.g. in cases of (partial) outbreeders (not clonally propagated), is considered incompatible with association studies. Simplification of the genetic constitution of the samples, with or without selection pressure, is considered a prerequisite for treating this kind of material.
- The importance of specific characters to be homogenised among the materials that are to be compared in a phenotypic evaluation, such as phenology and gross morphology, clearly emerged. It is likely that the phenotypic characterisation of the reference sample will require a season of gross field observation in the environment of future characterisation in order to select those accessions that are most comparable and that will yield the most meaningful comparisons; this can also serve to increase seed for subsequent phenotyping experiments.

One of the working hypotheses at the outset of the workshop was that phenotyping is not a series of repetitive trait measurements aimed to a standard characterisation of the genetic material, but a creative activity based on scientific hypotheses. It requires a combination of skills including physical and physiological concepts and methods, modelling approaches, and genetic strategies. This working hypothesis emerged as a consensus hypothesis from the workshop participants.

A consequence is that there is considerable room for progress in the different consortia of the GCP to integrate modelling approaches and physical or physiological concepts in the phenotyping process. Means to achieve this progress include exchange of scientists, PhD theses elaborated in common, addition of a course, and other possibilities.

Elaborating a Medium Term Plan and Implementing It through a Combination of Competitive Grants and Commissioned Projects

An MTP was developed, as described in the corresponding document. The main expected outputs have been used as a framework for calling proposals in the competitive granting and the commissioning schemes. Output 5 (issues surrounding intellectual property) was moved to SP5 during this year. The other four outputs extend, organise, and focus the lines initiated in Year 1 activities.

The competitive projects (in italics) or commissioned projects that were granted are organised as follows:

1. An improved understanding of the structure of the diversity for the major world food crops, diagnostic molecular markers for subsequent germplasm analysis and a set of reference samples designed for integrated characterisation
   - *Characterisation of genetic diversity of maize populations: Documenting global maize migration from the centre of origin*
   - *Measuring linkage disequilibrium across three genomic regions in rice*
   - Measuring linkage disequilibrium in sorghum and coconut (SPL budget)
   - Completing genotyping of composite germplasm set of barley, wheat sorghum, and chickpea
   - Molecular characterisation of tier 2 (orphan) crops — pearl millet, finger millet, pigeon pea, sweet potato, yam, lentil, grass forage, legume forage, groundnut, coconut, and soybean

2. A range of techniques accessible in key laboratories applied for high-throughput molecular characterisation of germplasm
   - *Allele Mining Based on Non-Coding Regulatory SNPs in barley germplasm*
   - Assessing DArTs as a genome-wide scanning technology
   - Assessing Ecotilling as a methodology for targeted genotyping and SNP discovery

3. Establishment and implementation of a scientific and organisational framework to describe tolerance to drought
   - Supporting emergence of reference drought tolerance phenotyping centres
   - Whole-plant physiology modelling

4. Molecular polymorphisms associated with higher tolerance to drought; integration of methodological improvements
   - *Development of informative DNA markers through association mapping in maize to improve drought tolerance in cereals (SP1&2)*

- *Identifying the physiological and genetic traits that make cassava one of the most drought tolerant crops*
- *Exploring Natural Genetic Variation: Developing Genomic Resources and Introgression Lines for Four AA Genome Rice Relatives*
- Association analysis in the course of varietal improvement (long generation crops)
- Supporting distribution of reference germplasm (11 Year 1 crops)

Lessons Learned

The SP1 Year 1 workplan was largely determined by a distribution of genotyping commitments between partners that was organised during the last few months of 2003. Eleven crops were selected at the Wageningen meeting in August 2003, on the basis of the declared availability of markers. The ideal number of accessions to be genotyped would depend on the genetic resources available, and the biology and genetics of the species that were put forward. The genotyping activities thus had a constrained framework: identifying a composite set of a given (optimum) size irrespective of the diversity of collections and institutional dynamics for the various crops.

The workshop in January allowed timely identification of markers and planning of marker development. The workshop in Zaragoza came late, on the one hand, because it was the first opportunity for a collective discussion on the global rationale and on particular issues shared among crops. On the other hand, it came early because few data were yet available, the first efforts having been concentrated on preparing DNA samples. So the final goal of identifying balanced reference samples in view of association studies was still far from concrete. Nonetheless, it was very useful for starting a community within SP1. A number of groups (per crop) revised their calendar and now plan completion of the work from 0 to 5 months later than expected.

Several cases of delay were due to a slow start in communication of information and in exchanges of materials. Within this type of partnership, the slowest partner determines the rate of progress for the whole group. In some cases the speed may probably be improved by more institutional commitment: some partners are very large and it takes time to have the GCP recognised as a high priority. And, some issues related to material exchange rules may be out of the institutional control. The most immediate priority is to assure timely exchange of information. Some of these constraints to progress can be addressed at the scientists' level while some institutional support may become necessary for others.

A particular difficulty appeared regarding comparability of results between laboratories. This is an issue: irreproducible data are of little value in general, especially in the context of an international undertaking. A first source of difficulty was the difference of intensity of allele appearance, especially in heterozygous polyploids (e.g. *Musa*). This apparently results from different dosage patterns across labs. If the global intensity of the pattern is variable, this may result in missing the allele(s) corresponding to the fainter bands or smaller peaks, leading to erroneously diverging data. Another seems to be insufficient mastering of the techniques, exacerbated by unstable staff. Both yield inappropriately interpreted results. This is a matter of concern to be addressed, in part, by our capacity-building activities.

There was also notice of diverging estimations of allele sizes in the different systems used. Although intellectually unsatisfactory, this is not a surprise and it can be avoided by relating all allele sizes to a reference accession/DNA (e.g. ref + 3 bases, ref + 6 bases, etc.) and providing access to a group of representative accessions that have a diverse array of alleles to serve as global references in subsequent studies. This obviously requires identifying these accessions, securing them, and making them available in some form to all relevant GCP participants.

The phenotyping workshop was prepared and held with much enthusiasm from the organisers and the participants. The particular complexity of the trait chosen led to long and fruitful discussions. However the discussion was very constructive and identified clear future steps to be followed. The establishment of a trait ontology group and the recommendation for a minimal set of environmental descriptors are crucial developments. The importance of specific characters to be homogenised among the materials that are to be compared in a phenotypic evaluation, such as phenology and gross morphology is also an essential piece of information that clearly emerged. Most probably the typical extension of the first step in SP1, that is the identification of a reference sample, will be a year of gross field observation in the environment of future characterisation in order to select those accessions that are most comparable and that will give the most meaningful phenotypic comparisons. This can also serve as seed increase to provide some flexibility and independence to the scientists in charge of phenotyping.

Finally, as observed in other subprogrammes, the involvement of non-consortium experts has proven very useful and promising for the future of the Generation CP.

Subprogramme 2: Comparative Genomics for Gene Discovery

The Year 1 Workplan of Subprogramme 2 is organised into four work clusters designed to gather germplasm and genomic resources for identifying and validating stress tolerance genes with an emphasis on drought. Overall, we have developed a coordinated strategy among researchers in using diverse genetic materials that exhibit certain attributes of drought tolerance. In coordination with SP1, a common phenotyping framework of techniques (though not necessarily the same methodologies), plant developmental stages, and parameters has been developed to enable cross-species comparison. Each participating team has planted selected stocks for detailed drought phenotyping in the field studies (results expected toward the end of 2004). Each research team on drought has also expanded characterisation of QTL in selected species. For consensus markers across species, we have initiated marker design using orthologous sequences across species. Genetic materials (RNA) from different genotypes and species have been prepared and shared among laboratories for testing with different gene array platforms (actual hybridisation data expected in July and August). We have expanded and improved the characterisation of EST libraries of *Musa* and cassava.

Below, we highlight specific achievements to illustrate the tangible results and collaborative nature of the work cluster activities:

- **A set of germplasm with drought-tolerant attributes or representative of donor gene pools has been selected from individual crops (e.g., sorghum, barley, wheat, rice, maize, chickpea, common beans, cassava, and potato) for detailed phenotypic analysis under water stress conditions.** In coordination with Subprogramme 3, recurrent parents for backcrossing have been identified in different crops. At ICRISAT, for example, a sorghum variety susceptible to end-of-season terminal drought stress but well-adapted to the drought-prone environments in India was selected as the key recurrent parent for backcrossing of the stay-green component of terminal drought tolerance. Thirty-five additional recurrent parents were selected on the basis of their adaptation to other important drought-prone sorghum production environments.

- **Phenotyping protocols for assessing drought tolerance are being implemented in selected crops and field methodologies for drought tolerance are under testing using advanced breeding lines.** For example, common protocols for the accurate characterisation of silk and leaf elongation across temperate and tropical maize and have been developed and a set of CIMMYT lines are currently being screened. A first set of field methodologies for drought tolerance for use in the GCP have been tested using advanced breeding lines. In sorghum, replicated field experiments were designed to assess effects of putative drought tolerance QTLs at ICRISAT. Twenty-one QTL introgression lines and their common recurrent parent were evaluated, but none of the early-generation (BC_3F_3) stay-green QTL introgression lines were more productive than the recurrent parent in a mild terminal drought stress environment. In potato, methodologies for field and greenhouse experiments were evaluated to identify key parameters for monitoring drought response. The method involves the establishment of drought conditions at tuber onset in the stressed group and continued watering in the control group. Experiments are being planned with 20 native Andean potato genotypes (selected from highlands field trials) under controlled greenhouse conditions.

- **Conserved orthologous markers (COS) are under design and evaluation in monocots and dicots.** CAAS has defined more than 1,700 markers from conserved cereal ESTs with potential for producing cross-species markers for wheat, rice, maize, and barley. A subset of these primers (aliquots) will be sent to IRRI to test across monocots (rice, maize, sorghum, wheat, and banana) to define conserved orthologous genes useful across a broad range of species. IRRI has selected genes with supporting evidence from rice and other species for their involvement in drought. Sequences across the monocots were retrieved from GenBank. Multiple sequence alignments were accomplished and 119 primers with or without degeneracy were designed for conserved domains. Conditions for product amplification across selected monocots are currently being optimised. Preliminary results indicate amplification is possible among the monocots with genomes the size of maize or smaller (including *Musa*). ICARDA, in collaboration with Montana State University, developed COS markers by targeting exonic sequences flanking introns based on the rice whole-genome sequence database. A total of 136 primers (targeting 50 contigs) have been tested on durum, dicoccoides, and barley genotypes. The majority of the primers showed high specificity (one to two developed fragments). Sequencing has been conducted on some fragments from different genotypes to validate the targeted exonic region.

Through the coordination of CIP and Cornell, a list of potato tentative consensus sequences exhibiting a high degree of similarity to genes of *Arabidopsis*, rice, and tomato has been defined. Currently, the list comprises 27 potato orthologs of drought-responsive genes from tomato or rice. Nine of these sequences could be derived from genes belonging to gene families and thus may be only of limited applicability as COS markers. Preliminary results suggest that COS from tomato-*Arabidopsis*-coffee (made available by Cornell) are expected to provide 'universal' markers for Solanaceae, and possibly for dicots. The most promising COS identified across Solanaceae will be recommended for assessment in other dicots. For other dicots, a list of 287 candidate genes with possible involvement in drought tolerance has been compiled from *Arabidopsis* and soybean sequence databases. IITA, in collaboration with CIAT and University of California-Riverside, is using sequences from soybean databases and is currently designing putative COS primers for cowpea.

- **Algorithms for extraction of candidate sequences for conserved genes from EST databases are being tested and shared.** A computational approach under development at Cornell was shared with CIP for testing COS markers in potato toward general use in dicots in the GCP (Feinan Wu and Steve Tanksley, paper in preparation). Multiple species representing three plant families were used reciprocally as query and subject by BLAST, such that by screening tomato, potato, *Arabidopsis*, and coffee databases 12 query-subject pairs were obtained. For each species, a different number of best-matched groups were obtained, after which the common groups shared by the four sets of best matched groups were identified. Consensus sequences were obtained by first aligning DNA and inferred protein sequences using a multiple sequence alignment tool T_COFFEE, followed by manual editing.

- **Progress in producing and evaluating gene expression datasets for cross-species comparative analyses.** Research teams within SP 2 are exploring the use of different gene array platforms for gene expression analysis. The rice 22K oligo chip (a product of NIAS-Agilent collaboration) is being evaluated for its utility as a common expression platform for several cereals (rice, maize, wheat, and barley at IRRI, CIMMYT, and NIAS). Preliminary experiments showed good cross-hybridisation between rice oligos with genomic DNA from wheat but not with maize. RNA from the reproductive stage (panicle) of rice genotypes under contrasting water regimes (drought stress vs. control) was prepared and used for hybridisation with the 22K chip at NIAS. Also, RNA of parental lines of a rice recombinant inbred population segregating for stress tolerance (biotic and abiotic stresses) was used to hybridise to the 22K chip in preparation for genome-wide segregational analysis (IRRI, NIAS). Pilot experiments were conducted using RNA samples of rice genotypes challenged with pathogens. The up and down regulated genes are "binned" into disease QTL regions of rice consensus maps to identify candidate genes through the approach of convergent evidence.

In collaboration with Pioneer, CIMMYT has identified an initial set of genes (in thousands) through comparative microarray profiling across parental materials. A second set of analysis is in progress to compare contrasting genotypes from a segregating population. These are being studied in detail using more tissues and/or different time points with real time PCR. CIMMYT has also purchased publicly available maize microarrays and contracted the service facilities of the Mexican National University (UNAM) for the screening of materials (ears, silks and leaves) from different populations. A comparison across experiments should allow identification of a core set of genes for further study taking into account the pathways of importance and map position of QTLs identified for drought.

At CIAT, a search for genes related to stress-inducible traits (e.g., stomata closure) and for constitutive traits (e.g., root growth) from public databases was completed, leading to the identification of about 300 genes. About 150 genes were selected as potential key genes for each trait. Primers for these genes have been designed and ordered for gene expression analysis using real time PCR. The list of the genes has been made available to IITA for mapping experiments.

CIP has defined genes putatively involved in drought stress tolerance pathways of potato. These pathways include stress signalling, carbon metabolism, adaptation to osmotic stress, antioxidant production, and detoxification. The selection of pathways will be reviewed when data from high-throughput gene expression experiments is available. RNA has been prepared from selected potato genotypes and quantitative PCR experiments are being performed to detect expression changes in candidate genes in leaves of stressed and non-stressed native potato varieties. The gene functions tested comprise drought stress adaptation (e.g., dehydrins), antioxidant biosynthesis, and heat shock genes. Microarray experiments are planned in collaboration with Virginia Polytechnic Institute and TIGR.

- **EST libraries expanded for several species under stress conditions.** Two SSH libraries of *Musa* have been constructed starting from RNA from cryopreserved cellular embryogenic cell suspension. Two libraries (i.e., reciprocal subtraction) of 2000 cDNA each are now available (INIBAP). IITA will begin construction of cDNA library shortly using mRNA from seedlings of drought sensitive but high water use efficiency (WUE) *Musa acuminata* (AA). Drought-tolerant *Musa balbisiana* (BB genome) accessions and a *Musa balbisiana/ Musa textilis* interspecific hybrid have been water-stressed and RNA prepared for subtractive cDNA library construction.

- **Mapping population characterisation for drought QTL analysis.** A variety of population development and mapping experiments are in progress in multiple crops (e.g., sorghum, maize, potato, rice, *Musa*). These experiments provide the materials to apply COS markers to develop consensus QTL maps. In addition, the phenotypically-selected lines and advanced backcross progeny provide the materials for expression analysis or association tests with genetic variation (in coordination with SP1).

- **Brisbane meeting, 22-24 September, 2004**. SP2 organised three events to bring the participants together to discuss and review the scientific agenda relevant to comparative genomics research:
  1. Evening workshop on Gene Expression Analysis, 22 September.
     The workshop objective was to assess the current status of comparative gene expression analysis in other organisms, and discuss how the methodology and concepts could be applied to crops. The workshop was well attended (~40 people).
  2. Review of Year 1 commissioned research, 23 September.
     All contributors from Year 1 commissioned work were invited to give brief or collective presentations of the progress made in first year (up to September 2004).
  3. Brainstorming session, 24 September.
     An entire morning was devoted to discuss the overall research portfolio for the next 1-3 years and the potential commissioned research to fill gaps that may not be covered by the competitive grant programme. Participants discussed what was in progress outside the GCP and what potential projects were worthy of investment by the GCP. Discussion also focused on taking advantage of existing and new resources available from different species. The group (average 20 people throughout the session) was asked to survey and comment on a series of research topics and questions:

Genomic and genetic resources
- Specialised genetic stocks and designer germplasm and characterisation
  - Linkage, assembly and access
  - Develop needed resources
- Orthologous markers
  - How much more needed?
  - Focus on functional genes?
  - Can we apply them now?
- Comparative gene expression analysis (stress-focus)
  - Utility of subarrays—access and affordability
  - Cross-species comparison
- EST resources
  - Can the GCP make a difference?

Systematic phenotyping
- Parallel or comparative phenotyping
- enable gene identification and validation

Bioinformatics
- Orthologs identification and display, auto-pipeline
- Gene expression data centralised to enable comparative analysis data mining

The main conclusions were:
1. Specialised genetic stocks and resources are the foundation for gene discovery and represent a main comparative advantage of the institutions and labs participating in the GCP. SP2 can play a unique role in enhancing awareness, access and utilisation of existing genetic stocks (databases, curation, distribution), and promoting the development of future resources.
2. Genomic resources (sequence-related information, such as EST, BAC libraries) for many organisms are expanding at an exponential rate worldwide. The investment of GCP must be highly targeted to maximise the return and to avoid redundancy.
3. Genome-wide expression platforms are available albeit at relatively high cost. GCP should maximise the use of these platforms using unique biological materials in collaboration with technology-focused labs. We should strive to promote accessibility and affordability.
4. A high priority should be given to systematic characterisation of phenotypes in specialised materials (mutants, fine mapped QTL, and NIL) where phenotype-genotype relationship can be inferred.

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 a substantial commitment to create appropriate technologies for application of marker-assisted selection in national breeding programmes, to provide technical assistance for the rapid and effective uptake of molecular breeding in tropical staple crops and to foster the development of communities of practice supported by regional centres of excellence and state of the art technologies and approaches.

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. The recent developments in genomics and bioinformatics offer a real opportunity for dissecting drought tolerance into component traits and developing tools to manipulate the underlying genes. However, reconstructing effective drought traits will require considerable advances in whole plant physiology modelling as well as in the gene and trait manipulation technologies required for impact at the scale of international germplasm collections and modern plant breeding programmes. The GCP proposes to operate at all these R&D levels in the innovation-to-impact continuum.

The comparative genomics and biology theme of the GCP provides an operational structure for priority setting and focusing research activities within three crop groups: cereals, legumes, and clonal crops. Inevitably, global research progress in most of the cereals is sufficient for the development and application of gene-based marker systems for components of tolerance to drought and other abiotic stresses. Additional targeted investments will be required in millet (the most drought tolerant but least studied of the major cereal crops), though. Conversely, the critical mass of genomics researchers and resources in the legume and clonal crops is much less well developed. For this reason, careful prioritisation of crop focuses will be applied to ensure rapid and compelling proof-of-concept in key representatives of these crop groups. However, significant direct spillovers from sequence, gene, and trait analyses are expected to significantly impact progress in most other crops in each group. In addition, all crops are likely to be impacted by advances in generic facilitating technologies including: advances in the development of standardised phenotyping protocols, whole plant physiology modelling, molecular breeding simulation studies, and decision support tools, as well as procedures for creating low-cost trait diagnostics and high-throughput array-based genotyping systems. Most of these activities will be carried out through intensive collaboration with scientists in SP1, SP2, and SP4.

The selection of appropriate background genotypes is a critically important process for molecular breeding programmes to ensure widespread impact of new 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 plus farmer, processor, and consumer preference and trading potential. In addition, we are documenting appropriate baseline information for those varieties (including production and constraint mapping) that will be used in subsequent impact assessment studies. In this way, the GCP is emerging as a product-driven initiative with a strong value-chain-based approach to product development and delivery. We strive to move beyond just developing more productive crops to creating new varieties with enhanced stability (reduced vulnerability) and improved value (increased profitability), thus providing a real and sustainable impact on improving the livelihoods of our poorest stakeholders. This will inevitably demand the development of strong alliances with a much broader range of partners including NGOs and the indigenous private sector. 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 our capacity-building activities 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 genotype-by-environment interaction and whole-plant physiology modelling by their very nature require coordinated input from many scientists of different disciplines, eco-regions, and types of institution. 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, centralised validation and refinement of new technologies for routine application in national breeding programmes as well as

community support labs offering 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. In addition, such communities foster strong technology uptake and product delivery pathways.

The following is an update on SP3 activities and evolution of strategy in 2004.

Molecular Breeding Systems

The primary focus of SP3 lies in the application of genomics tools and the development of products based on outputs from the other subprogrammes. For this reason, first year activities in SP3 have been largely limited to the validation of pre-existing linked markers for drought tolerance as a means of establishing an effective operational framework in molecular breeding across each crop group. During 2005-2006, we envisage a rapid transfer of focus to gene-based markers for drought tolerance, as this is a fundamental pillar for the overall comparative biology philosophy of the GCP. However, some strategic activities such as the development of tools for the simulation of molecular breeding systems will in the short-term have to continue to rely on pre-existing linked markers for drought tolerance in cereal crops as the only available material. Thus, marker-assisted selection and marker-accelerated backcross breeding for drought tolerance during linked markers in rice, maize, sorghum and wheat is envisaged as an appropriate and necessary complementary activity during 2005-2006.

Markers for Drought Tolerance

A number of small additional research activities were commissioned for the first year only, to help synergise appropriate population development and QTL mapping of component traits of drought tolerance in a range of lesser-studied crops. However, from 2005 the development/identification of markers has been disaggregated into SP1 (association mapping) and SP2 (comparative mapping and genomics). As a consequence, conventional linkage mapping and MAS with linked markers will not be a major thrust from 2005 onwards. However, drought mapping associated with comparative studies is planned for rice, maize, sorghum and bean in SP2 during this period. Meanwhile, SP3 activities in this area will focus on the development of low cost assay technologies for the application of gene-based markers in NARS and SME breeding programmes across Africa, Asia, and Latin America.

Gene Isolation and Transgenic Products

During April, a workshop was held in Nairobi in coordination with CIP and NEPAD's BECA facility to address the following issues:

- Identify suitable varieties for improvement
- Determine the potential of existing gene technologies for engineering drought tolerance
- Develop information and tools for public awareness on transgenic crops
- Evaluate freedom to operate with gene technologies
- Outline research needs for the next 5 - 10 years

This group then went on to submit a number of cooperative preproposals for the GCP competitive grants programme based on priorities established during the workshop. This group was also mandated to develop a GCP vision and strategy document regarding the development and deployment of drought tolerant transgenic varieties (a draft of which is currently being revised by the broader communities). Three areas have now been highlighted for attention in the 2005-2006 commissioned grant programme: harmonised multilocational evaluation of various DREB constructs in a range of crops (across all three crop groups), a workshop on specific biosafety issues concerned with abiotic stress-tolerant transgenics, and a workshop on liability issues related to transgenic product development and deployment.

Background Genotypes

The foundation-building R&D activities described above have been supplemented by the development of a database of elite varieties that are considered the most appropriate candidate background genotypes for MAS or transgene introgression. Developing a substantial and comprehensive database for this purpose has not progressed as envisaged. Thus, medium-term activities in this area are being reformulated to facilitate a shift to a project-based strategy rather than the development of an all encompassing database. In this context, it is envisaged that all future competitive and commissioned grant proposals will be required to comprehensively demonstrate that any proposed background genotype has been selected in an appropriate product-driven way. A commissioned project on developing product development and deployment pathways will attempt to institutionalise this approach during 2005-2006. The GCP is also establishing an alliance with the Harvest Plus Challenge Programme with the aim of jointly developing seed-based products combining improved resilience and enhanced nutritional value.

Molecular Breeding Communities of Practice

Two major community capacity-building activities were also commissioned during the first year. A workshop was convened to synthesise the GCP research strategy and policy development regarding the application of transgenic solutions for complex traits such as drought tolerance. This has already resulted in several consortium-based proposals, while a synthesis and strategy paper will be released soon.

An intensive three-week molecular breeding training course was carried out in coordination with IITA and NEPAD's Biosciences Eastern and Central Africa (BECA) from 28 November to 18 December. This and future courses are aimed at launching and supporting molecular breeding communities of practice in Africa, Asia, and Latin America. Participants were selected from a wide range of countries in East, Central, Southern, and West Africa representing NARS, universities, and private sector research and breeding programmes on cereals, legumes, and clonal crops. Most participants have a working knowledge of DNA marker genotyping techniques and the training course is aimed to intensify and broaden their expertise so as to directly enhance the efficiency and impact of their current activities. The course had three broad goals:

- Provide advanced training to current genomics scientists in the region
- Establish functional relationships for technical backstopping and trouble shooting
- Empower practitioners in the region to make best use of the BECA hub

Periodic access to a high-throughput genotyping facility will help NARS and SME breeding programmes achieve cost-effective molecular breeding success stories that should in turn synergise sustainable national investments for infrastructural and capacity development in this area. Similarly, occasional access to a state-of-the-art genomics facility may have dramatic impacts on the pace and impact of national research projects.

The course attracted resource persons and invited speakers from across the GCP consortium members (both within and outside the CGIAR) plus representatives of donor and private sector communities. Finally, around 70% of the funding from this course came from a consortium of sponsors including private sector and foundation donors.

This training programme will now be scaled up during 2005-2006 to include training courses in East, Southern, and West Africa as well as key locations in Asia and Latin America. Thus, these capacity development and molecular breeding communities of practice themes will now be exclusively handled under SP5. This then leaves SP3 to focus on areas of product development (using pre-existing markers and the expected outputs from SP1 and SP2) that are critical to ensuring impact from GCP investments.

Evolving SP3 Strategy

This transition of focus areas reflects our attempts to differentiate clearer niches for each subprogramme and to better reflect the state-of-the-art that has evolved substantially since the original GCP framework was crafted. Thus, in essence (although not exclusively so), SP1 and SP2 have become the powerhouses of strategic research (supported by computational systems from SP4) while SP3 will focus on applied research areas critical to the development and effective application of gene-based product technologies generated by SP1 and SP2 (supported by SP4 and SP5). This is considered a critical but hitherto somewhat neglected area of public sector research that will require substantial levels of time, funds and innovation to ensure appropriate impact from GCP research investments. Appropriate orientation for product development and deployment activities will be fostered during 2005-2006 by a commissioned project on the development of product-driven, value-chain orientated pathways.

Inevitably, the portfolio of competitive grant projects left more gaps in this vision than could be filled by the available commissioned programme funds. Similarly, the competitive grant portfolio covers some areas more densely than others and deals with the historical to MTP transition in some areas better than others. It will clearly be critically important for the GCP competitive and commissioned calls for proposals during 2005-2006 to be highly explicit in order for us to maintain a healthy, focused and strategic critical mass in all areas essential for delivery of the GCP vision.

Highlights from Research Activities in Gene and Trait Introgression Technologies

Gene-based markers for blast disease resistance in rice have been used for the proof-of- concept pyramiding of a substantial number of QTL (up to 16) in a single genotype (in this case, up to 10 lines with good agronomic backgrounds and drought tolerance). These introgression lines are currently being evaluated under diverse water regimes at IRRI and at diverse national programme locations in India, the Philippines, and Indonesia.

QTL results from about 50 maize trials conducted using six segregating populations have been compiled on a consensus map, highlighting around 12 genomic regions of key importance for drought tolerance in maize. Within a given

segregating population QTL results seem quite stable across years and even across countries (Mexico and Zimbabwe). However, there was a large interaction of QTL by population. The primary objective in the construction of this drought consensus map was to develop and test novel MAS strategies that would focus on key regions "consistently" identified across genetic background, without having to map QTL in any new cross, a very time consuming and expensive step. However, results from this study on linked markers suggest that there are still major challenges related to the selection criteria to identify the target regions and the estimation of allelic effects at these regions within new segregating populations.

Similarly, single and flanking linked SSR markers for QTL contributing to terminal drought tolerance in sorghum and pearl millet are being tested through the phenotypic validation of products of MAS. In the case of sorghum, two different sources of the staygreen component of drought tolerance are being introgressed into elite varieties of economic importance in Latin America, Africa, and Asia. For pearl millet, QTL are being introgressed into a variety of popular hybrid variety maintainer lines and evaluated in diverse moisture regimes.

The development of effective molecular breeding tools for components of drought tolerance in legumes is being synergised by fostering large scale mapping efforts in common bean, cowpea, and chickpea. SSR markers in common bean linked to important QTL for drought tolerance from four diverse sources have been validated in multiple MAS backcross generations for three economically important varieties through phenotypic evaluation of material in Mexico and Brazil.

Several SSR markers have been identified for root trait components of drought avoidance in chickpea. Candidate gene markers (derived from a subtractive EST library) are now being tested on the same population following the development of EST-CAPS and EST-SNP markers. Meanwhile, following extensive evaluation of germplasm collections, a new more appropriate population has been rapidly developed for identification and validation of markers for root traits.

Similarly, intensive population development efforts are ongoing in cassava by IITA and CIAT to establish breeding populations for the effective pyramiding of drought tolerance with pest and disease resistance traits. Meanwhile, SSR mapping of drought tolerance in cowpea is progressing well.

Subprogramme 4: Information Network and Bioinformatics

Since the first three subprogrammes of the Generation Challenge Programme, concentrating on biology, genetics, and crop improvement produce tremendous amounts of data and rely on an effective and efficient access and analysis of these data, there is a fourth subprogramme that has made that access and analysis of data its objective.

The research institutes participating in the Generation CP consortium obviously all have their own facilities and procedures for managing and using data. This was a well-established basis upon which SP4 could build, but at the same time it formed a large barrier because of the low compatibility between the different approaches used in those institutes. The first year of SP4 therefore aimed to develop and begin implementing a strategy that would allow all Generation CP data to be accessed and shared by the consortium and by the rest of the world. A second objective was to determine the gaps in terms of capacity and tools, to decide what tools would have to be created, and what knowledge had to be generated to support the research in the first three subprogrammes. In its first year, SP4 has been quite successful in meeting these objectives. There now is a clear vision of where to go and how to get there, and the first steps have been taken.

The items listed below summarise the most important activities and their results of the first year of SP4.

- **Management structure for SP4 established.**
  Shortly after the appointment of Theo van Hintum as Subprogramme Leader, a Consultation Workshop was organised in Rome, where about 50 participants, both GCP partners and invited experts, discussed the content and planning for SP4. As input for this meeting, eight white papers were produced describing the general global status of following topics: 'Germplasm Information Systems;' 'Fingerprinting and Allele Data Systems;' 'Mapping Data and Analysis Systems;' 'Functional Genomic Information and Analysis System;' 'Laboratory Information Management Systems (LIMS);' 'Central Registry and User Needs;' 'Interoperability and Infrastructure;' and 'GRID Computing.' Based on the discussions at the meeting, the activities foreseen in the Year 1 workplan were regrouped and reformulated, and task-leaders were appointed to act as contacts to the SP4 leader. Based on inputs from the task-leaders, a detailed workplan was compiled. A virtual workspace was commissioned and is starting to be used for exchange of documents and as a discussion platform.

  Based on the outcome of the competitive granting process for 2005, a package of 12 projects for commissioned projects was compiled that will cover all necessary activities for 2005, complementary to the one project that was granted in the competitive process. The first draft of the structure of this package was discussed with the most relevant actors at the 2004 Annual Research Meeting and subsequently refined. Based on concept notes, the Principle Investigators have been invited to submit proposals that will be properly reviewed.

- **Design for Generation CP information exchange platform made, proof of concepts delivered.**
  From May 31st through June 4th, a combined GCP SP4 system design workshop convened at CIMMYT, involving a large range of Consortium partners with the addition of a significant number of non-Consortium invited bioinformatics experts, representing the most important players in the field of biological and bioinformatics databases. An outcome of this meeting was the decision to use web services technology at the basis of the Generation CP information exchange platform. This implies that each partner can continue to follow its own policy in the field of information management, provided that the data are made available via a web service. The structure (technology and data model) of that service will be defined by the Generation CP, and will be compatible with the current standards for data exchange. In this way the Generation CP will become a part of the global bioinformatics community.

  A smaller, follow-up workshop was convened at IRRI in July to undertake more detailed design and some prototyping of GCP systems.

  During the Annual Research Meeting, the technology was presented and a number of proof of concept cases were presented. The cases comprised a system that gives access to all passport data in both Singer and Eurisco (over eighty databases), prepared by IPGRI, a system that allowed browsing of IRIS, prepared by IRRI, and finally a system that allowed combined searches in the databases of INIBAP and CIRAD, prepared by INIBAP.

- **Plans for interoperability, infrastructure, and a central registry developed.**
  Collaborations between the GCP and a number of pertinent international initiatives were established to apply advanced data interoperability technology to the needs of the GCP:
  - SP4 was formally acknowledged as Plant Ontology Consortium Collaborator
  - Gene ontology consortium interactions were established
  - The principal BioMoby research scientists Mark Wilkinson (Genome Canada), Martin Senger (EBI/MyGrid), Gary Schiltz (NCGR) and Rebecca Ernst (PlaNet/MIPS) were directly involved in GCP design & implementation meetings (BioMoby web services technology is being incorporated into the ICIS Java platform by IRRI)
  - TAIR was visited to discuss collaboration.
  - MaizeGDB was invited to the GCP design meeting.
  - Some IRRI discussions with Gramene are ongoing concerning bilateral web services integration of germplasm and crop genomic information.

  The design, implementation, and deployment of the first generation infrastructure for expert curation of data standards (models, controlled vocabularies and ontology) was started by selecting the Generic Model Organism Database (www.gmod.org) "Chado" schema based database for commissioning a prototype GCP Controlled Vocabulary and Ontology (CVO) management framework. This schema is inspired by the designs of other public ontology development efforts like the Gene Ontology and Plant Ontology Consortia. In addition, the "Protégé" ontology management system has been adopted for its utility in representing semantic information in the GCP. A community process was initiated to extend the inventory of existing public data exchange standards to cover gaps relative to GCP platform needs and requirements starting with the compilation of public CVO's (e.g., Gene Ontology, Sequence Ontology) into the "Chado" schema.

  For the short-term solutions, criterion and priority issues of IP related to the Genetic Mapping Data Repository Task have been identified, discussed, and developed, particularly in relation to the use of Virtual Workspace Designs. The inventory listings of software have been broken down into those of three groups: GNU public license, author-restricted but open license, and commercial license. And finally, an extensible and flexible structural and functional repository design that can provide interoperability has been designed and implemented.

  For the central registry, IPGRI has prototyped database mirroring software for semi-automatic archiving of GCP data sets to a central location.

- **Integrated germplasm and crop information systems and LIMS reviewed.**
  Institutes involved in the development of the GCP Information System have reviewed existing systems and identified components which will be reused for CP data as well as components which must be developed or adopted. All institutes (IRRI, CIP, ICARDA, IITA, ICRISAT, CIAT, CIMMYT, and IPGRI-INIBAP) have suitable genetic resources information management systems, but most need to develop components to handle marker and genotype data. IRRI, CIP and INIBAP have investigated the Germinate schema from the Scottish Crops Research Institute (SCRI); ICARDA is testing the Gene Management System of the International Crop Information System (ICIS); and IITA, ICRISAT, and CIAT are extending existing in-house systems. A comparison of the Germinate and ICIS-DMS schemata at an IRRI-hosted implementation workshop in July has demonstrated remarkable similarities between the two and IRRI is now working to merge the best ideas of both into ICIS-DMS and then develop a marker/allele management system to link with genotype data in the DMS. IRRI also has an ongoing effort to port ICIS to a new Java language based architecture that includes advanced technologies such as life sciences identifiers (LSID), CVOs, and web services, as discussed within the SP4 design discussions.

  Concerning the development and deployment of LIMS, momentum has been created and various activities are taking place at various institutions ranging from an inventory of requirements to inclusion of LIMS output into the breeding database. A LIMS system is being commissioned at IRRI to capture SP2 activities for universal marker development. See also the web site created by CIAT demonstrating LIMSYS v3.0 (outsourced by CIAT to a local software developer: DATABIO located in Cali): http://gene4.ciat.cgiar.org/limsys3.0_demo

- **Capacity, tools, and databases to support SP1, 2, and 3 created.**
  CIP, ICRISAT, and IRRI (plus ILRI who was funded by another source) have purchased Paracel High Performance Computing clusters cross-linked into a global grid facility. Several software packages have been installed and tested. These include the Paracel BioView Workbench, R, and Structure. A temporary website has been created to give access to all consortium members (see http://hpc.cip.cgiar.org/webeval/). This capacity allows state of the art computing for both classical biometry and bioinformatics applications such as full genome blasts.

Based on Generation CP support, IRRI, CIP, ICARDA, IITA, ICRISAT, CIAT, IPGRI, and CIMMYT have hired and trained bioinformatics staff and initiated activities to improve the bioinformatics infrastructure in their institutes.

In the framework of support to the functional genomics activities (SP2), stress candidate gene discovery and characterisation schema options were reviewed, and it was decided to use the Generic Model Organism Database (GMOD; www.gmod.org) curation tools and "Chado" schema as a starting point for building a comparative gene catalogue. A prototype database is being commissioned this summer. An IRRI-hosted GCP site for SP2 data sets is under construction at http://www.iris.irri.org/generation.

The Stanford Microarray Database "Longhorn" open source microarray database system is being deployed as a repository for comparative gene expression profile data to capture Year 1 gene expression data (from SP2 experiments being undertaken at NIAS in Japan).

Tools are under development at EMBRAPA based on CORBA to experiment with the universal adaptors of well-known public domain packages that might be put together to store, visualise, and analyse genomic sequences and ESTs. This adaptation allowed for the evolution and the addition of new parts to the system.

Subprogramme 5: Capacity Building and Enabling Delivery

This subprogramme was the latest addition to the Challenge Programme and, as such, was not discussed as a separate subprogramme in the planning meeting held in Wageningen in August 2003. Because of that, a strategy document was prepared this year by the Capacity-building Coordinator, Carmen de Vicente, to describe the objectives of SP5 as well as the underlying principles that will guide the preparation of the workplan for the following years. The strategy document details:

- Who the beneficiaries of capacity-building activities in the GCP are
- Capacity-building schemes that will be used in the GCP
- Why needs assessment activities are the basis of our workplan
- Partnerships and alliances that will be sought to guarantee wider impact in our endeavour
- Coordination mechanisms that will be put in place to ensure coherence in capacity-building activities throughout the GCP
- Need for monitoring and measuring impact
- Plans for mobilising extra resources to fulfil our objectives in the subprogramme

During the Wageningen meeting, a few activities were embedded in Subprogramme 1 to be carried out in Year 1 as a means to prepare the development of a thorough capacity-building workplan for the duration of the GCP. One of these activities was the organisation of a workshop to assess the capacity/training needs of candidate partners of the GCP, representing a wide array of developing country institutions (mainly NARS and universities).

A Needs Assessment Workshop was held for National Agricultural Research Systems on 2-6 August 2004 in Costa Rica. Invitees were NARS representatives at the research director level or similar capacity and discussed their capacity-building needs and optimal Challenge Programme activities for meeting those needs. In order to select the best candidates, Generation CP Consortium contacts were requested to send nominations among current or prospective NARS partners. The questionnaire was prepared to assess the interest and suitability of the nominated institutions as potential partners of the GCP as well as to have a first grasp of the needs and offers of these partners. A questionnaire was sent to all nominees (approx. 120), and replies were received from 40 people. The subsequent selection was based on the independent analysis of the replies by the organisers, who tried to ensure a good representation of countries and regions. The final group was made up of representatives from National Research Institutions (18), universities (4), international networks (1), international research centres (1), and regional research centres (2). The representation per region was as follows: Latin America (10), Africa (7), Asia (7), and Eastern Europe (2). Staff from Cornell University that helped in the arrangements of the workshop attended. One resource person from IAC (Wageningen University, The Netherlands) was also invited because of her broad expertise in capacity building for developing-country scientists. The objectives of the workshop were:

1) Gain a better understanding of developing-country needs (as seen by leading organisations) and express them in actionable terms
2) Identify mechanisms and strategies to ensure that SP1 through SP4 outputs (knowledge, tools, products, and services) are oriented toward the identified needs
3) Advance a coherent plan that will justify donors' interest and support by linking needs and SP1 to SP4 outputs

Besides the outputs of the discussions, the workshop was meant as a start of a strong network of NARS scientists as Challenge Programme partners for product delivery. Several clear ideas emerged from the meeting: the need to establish regional hubs, the power of networks, the expectation of a virtual library and resource centre, a new mode of operation going beyond disciplines by linking specialists in different fields (also within institutions) and the great potential of a fellowship programme. The meeting ended with some explicit offers to the GCP to contribute to capacity building. There was also a request to the GCP to continue to be in touch through the implementation of regional or sub-regional communities of practice.

In addition, different capacity-building activities were included in the Year 1 workplan of the thematic subprogrammes and these have already been conducted in the course of 2004.

Courses/Workshops

Linked to Subprogramme 1:

- The 4th FAO/IAEA Interregional Training course on Mutant Germplasm Characterisation using molecular markers was held from 27 September to 22 October in Seibersdorf, Austria, in cooperation with IPGRI - INIBAP and within the framework of the Generation CP. Five trainees were funded by the GCP.
- A workshop on potato SSR analysis and database development was organised by CIP from October 25th to 29th. The course was attended by 25 participants from Argentina, Bolivia, Colombia, Ecuador, Peru, and Venezuela. Resource people from CIRAD participated.
- IRRI organised the workshop "Microarray and Bioinformatics: Applying Genomic Technologies to Identify Induced and Natural Variation in Stress-Response Genes" during the last week of February. Thirty-eight participants from Mali, Bangladesh, China, India, Indonesia, Iran, Korea, the Philippines, Syria, Thailand, and Vietnam attended, in addition to several IRRI staff.
- A Data Analysis Workshop was held in Zaragoza, Spain on 21-25 June to discuss the analysis of crop genotyping data. Recommendations for genotyping, analysis and definition of guidelines for the selection of germplasm to advance to SP2 and SP3 were among the basic outputs.
- A second workshop was held on phenotyping for drought stress tolerance during the week of July 5th in Montpellier, France. It brought together scientists from the CGs, ARIs, and NARS (40, 30 and 30% respectively). In addition to the technical conclusions, the workshop indicated opportunities for progress including exchange of scientists, PhD theses, and preparation of training courses.

Linked to Subprogramme 3:

- A workshop entitled "CAGT – Crops with Appropriate Gene Technologies"was held in Nairobi (ILRI) during the last week of April 2004. The workshop brought together for the first time all of the genetic transformation specialists in the CGIAR as well as several outside experts to discuss common approaches, challenges, and opportunities. The occasion was used to discuss ideas for joint preparation of pre-proposals.
- A course entitled "Intensive Training Programme in Molecular Breeding" was held at the end of November (28 November-18 December) at the Biosciences East and Central Africa (BECA) Centre (Nairobi), in collaboration with the GCP and NEPAD. The course aims at providing training tailored to the needs of the participants and effectively becoming a part of their research or breeding programmes. It is hoped that the training programme will become intimately linked with competitive research grant programmes to ensure a continuity of applications and to support a step-wise increase in national capacity in this area. The syllabus for the course will be the basis for the training plan in this subprogramme. Twenty-two participants have been selected by a panel composed of GCP and BECA staff. The Rockefeller, Pioneer, and Syngenta Foundations and the Kirkhouse Trust provided funds to match the total cost for the course.

Linked to Subprogramme 4:

Several workshops have been conducted in the framework of Subprogramme 4. In general, capacity-building components in these activities have focused on increasing competence within the Consortium.

- In February, IPGRI conducted a consultation workshop to assess all issues involved in the SP4 workplan, listing required actions and proposing task focal points and timeframes. Participants from all the Consortium members attended, except from CAAS, as well as a few external experts. No other NARS outside the Consortium were invited.
- The "Generation Challenge Programme Information Systems and Network Design Workshop" (SP4, Mexico, 31 May-4 June) gathered around 20 experts from within and outside the GCP to develop a comprehensive architectural blueprint for the GCP platform, network, and data registry. Following the workshop, a Paracel training course for the CGIAR GCP group on the high performance computing system took place in Pasadena, CA, from 7-9 June.
- IRRI organised a workshop on Information Systems Platform and Network Implementation from 3-23 July. The objective was to attempt to construct a first year full reference implementation of the GCP information platform and network reflecting design inputs discussed at CIMMYT in the previous workshop.
- A small workshop was conducted in the context of SP4 focusing on bioinformatics and genomic analysis of banana EST sequences with strong capacity-building components. It was organised by IPGRI-INIBAP in Montpellier, France, in October and attended by seven NARS participants (EMBRAPA and groups outside of the GCP), together with INIBAP staff.
- A survey was carried out among the Consortium member institutions to gather information concerning: a) the definition of areas of expertise related to SP4 (databasing, bioinformatics, platforms, analysis software, etc.), b) existing tools (training materials, etc.) and delivery mechanisms available, both within and outside the GCP Consortium, c) the available expertise within the GCP Consortium members for each of the areas of expertise identified, d) the existing gaps in expertise within the GCP Consortium as stated by the member's focal points and e) the identification of sources of expertise available outside the GCP Consortium.

Capacity Building Guidelines

It order to facilitate the organisation of capacity-building workshops in the coming years, a set of guidelines has been put together to ensure high quality in the preparation and delivery of training planned by the GCP. The guidelines include the definition of objectives, the curriculum and agenda design, the selection of participants, the identification of resource people, and the training materials to use. An application form, a training course evaluation form, and a set of criteria for evaluation of candidates complete the guidelines, available online at http://www.generationcp.org/latestnews.php?i=156&PHPSESSID=a26e9056f9c28128356e40596f921210.

Fellowships

The call for 8 GCP Fellowships was made at the end of September with the deadline of 30 November. These fellowships (2 per subprogramme) are meant to be awarded to scientists who carry out innovative research related to the running themes of the GCP and who want to benefit from collaboration with one of the Consortium members or a close partner. In addition, Pioneer and the GCP have agreed to promote PhD education in the areas of plant breeding and genetics in one of the GCP crops with one fellowship per year which will be contributed by the private sector.

Also, collaboration is ongoing between the International Foundation for Science (IFS) and the GCP to open a call for research grant applications for young scientists. The first call will target the participants in the GCP-BECA Molecular Breeding Training Course and will serve as a pilot test for increasing the endeavour to all courses in the Training Programme of the GCP in the future. These IFS fellowships are expected to help very much in the establishment of effective Communities of Practice of scientists in the different regions worldwide.

Travel Grants

On 11 November, the first call for applications for GCP Travel Grants was launched. It was established to cover the expenses of participation of NARS scientists, outside the Consortium, to the annual GCP meeting, or to visit a member institution of the Consortium with whom collaboration is ongoing. At least eight grants are planned per year, depending on the availability of funds.

Capacity-building Components Embedded in Research Activities

At the outset, we recognised that training and capacity building needs go beyond the transfer of tools and knowledge to NARS. The capacity-building activities of the GCP should involve expanding the expertise of CGIAR Centre researchers and enhancing the understanding by ARIs of the practical challenges and limitations confronting NARS and CGIAR staff. Thus, we have built in Year 1 activities to implement this "reciprocal" training process. An example of this activity is the on-going collaboration on gene expression between NIAS (an ARI) and IRRI. Experiments are being designed and executed to take advantage of the extensive experience of NIAS in gene chip technology. Three researchers from IRRI are currently working at NIAS (for 2-4 weeks each) to generate data on drought-response gene expression and test the utility of rice gene chips for heterologous hybridisation. Such a shuttle research arrangement is being planned for other GCP partners to work at NIAS as well.

Finally, a number of scientists from NARS outside of the Consortium have actively participated in the research activities planned for Year 1 by the different subprogrammes. Actual numbers of hands-on trainees in the different subprogrammes are: SP1=14 people, SP2=17 people, and SP3=6 people. While most of them are ongoing, a list of their activities may be found in the Year 1 Workplan, pages 12 to 15. A similar scheme will continue for the rest of the GCP, as the participation of NARS was introduced as a basic criterion for the selection of pre-proposals submitted to the first competitive call launched in April 2004.

One of the activities already started, an SP5 initiative, is the launching of the Interactive Resource Centre (a "helpdesk") by the Institute of Genomic Diversity at Cornell University to support scientists involved in the Challenge Programme. The impetus for this activity originated from one of the recommendations of the Working Group on Capacity Building at the Challenge Programme's Stakeholders Meeting in Alexandria, January 2003. In August of this year, participants at the Needs Assessment workshop with NARS in Costa Rica confirmed that this is a priority resource that needs to be developed.

Policy

Key policies issues within the GCP are: access and benefit sharing (ABS) and intellectual property rights (IPR). The GCP policy group deals with these issues both as a 'service issue' and as a 'researchable issue.' These are issues that are derived from international policies and agreements that are relevant to this Challenge Programme and to CGIAR (and other development-oriented) stakeholders that require the development of institutional policies and procedures.

During the first year, the policy group (which was, until recently, housed in SP1) concentrated on investigating relatively generic questions that are of immediate importance to the GCP. Draft reports have been produced on a number of pressing topics (final versions to be published early 2005):

- Overview of the international policy arena relevant to GCP
- Humanitarian licenses
- Liability and stewardship
- Other IP-mechanisms
- Benefit sharing
- Access legislation
- Impact of strengthened IPR on the breeding industry in developing countries
- Genetic Resource Policy Initiative

Scientists and consultants of the policy research group have also been instrumental in the development of the consortium agreement and a draft humanitarian license contract. These documents are in use/will be used by the GCP. Requests have been received from other international initiatives in the field of biosciences to use the GCP Consortium Agreement to develop their own agreements, given the fact that the GCP Agreement has been accepted by NARS, CG-Centres, and ARIs on the same terms.

Changes in SP5

As a result of the consultation with NARS at the Costa Rica workshop, and formal or informal discussions with contacts within the Consortium, a number of issues related to SP5 have been subject to modifications. This is not surprising given that when the GCP started, the programme of SP5 did not exist and had to be developed gradually.

- Regional Research Hubs: The idea of regional research hubs was considered an essential component to provide capacity or to facilitate access to state-of-the-art research facilities so that a wider number of partners outside the Consortium could participate and benefit from the GCP. While the relevance of this mechanism is generally acknowledged, it has been felt that not all regions may need the same scheme. The GCP is willing to give priority to the identification and support of RRH in Sub-Saharan Africa, while drawing partners in Latin America and Asia through different approaches. In SSA, the collaboration with NEPAD through the Biosciences East and Central Africa (BECA) will serve as a model for the other sub-regions within Africa.
- While different Consortium members have already engaged in training courses, the GCP is looking at the implementation of its own Training Programme. The Training Programme will consist of two workshops: Diversity-Breeding and Genomics-Bioinformatics. They are grouped together thematically to maximise theoretical and practical training. Depending on availability of funds, one complete training programme of two workshops (Diversity-Breeding and Genomics-Bioinformatics) will be held per year in three to four regions. Each workshop (Diversity-Breeding and Genomics-Bioinformatics) will have between 12 and 15 participants, for a total of 384 to 480 participants trained over four years. An important activity in 2005 will be the development of curricula and gathering of training materials as the basis for the workshops. The training materials will also be freely available on the Internet. Fundraising will be needed to fully implement the Training Programme as such and will target traditional and non-traditional donors, including the private sector.
- At the end of the meeting in Brisbane, it was felt that SP5 was the most suitable home for issues dealing with delivery, including policy. Based on that, the title of SP5 was changed to incorporate these aspects. The new title is "Capacity Building and Enabling Delivery."
- As a result of the new theme added to SP5, and in addition to activities already planned related to the assessment of needs through existing networks, other types of consultations are being designed at this point (Impact Initiative, see concept note: http://www.generationcp.org/sccv10/sccv10_upload/Concept_Note-Impact_Initiative_letterhead.pdf) to ensure that the GCP links with its beneficiaries to define research objectives that correspond to their needs. The goals are to produce a refined needs assessment for the target regions and crops in the context of our programme, and to provide guidance for additional activities that engage farmers and the crop research/production/delivery chain in the development of GCP products.

Year 2 Summary Workplan and Budget: Competitive and Commissioned Research

2005 Summary Competitive and Commissioned Research

Institution Type	Competitive (three-year average)	Commissioned Projects	TOTAL
CGIAR	1,740,091[1]	3,347,707	5,087,798
GCP ARIs	906,574	1,137,311	2,043,885
GCP NARS	650,815	524,976	1,175,791
non-GCP ARIs	844,725	369,270	1,213,995
non-GCP NARS	539,572	108,030	647,602
Estimate total	4,681,777[2]	5,487,294	10,169,071
Real 2005 TOTAL	**4,955,606[3]**	**5,736,000[4]**	**10,691,606**

Competitive 3-Year Total

Institution Type	Competitive Grants (total over 3 years)
CGIAR	5,220,272
GCP ARIs	2,719,721
GCP NARS	1,952,444
non-GCP ARIs	2,534,177
non-GCP NARS	1,618,716
TOTAL	**14,045,330**

1 Per year average of projects, for comparative purposes.
2 Estimate 2005 total is sum of yearly average.
3 Actual total amounts distributed in 2005. Differs from the estimate due to larger first year budgets in some projects.
4 Difference between real and estimate reflects uncommitted research funds to be allocated in 2005.

2005 Commissioned Research – GCP Consortium Members

(see Appendix C for full project details)

#	Cost (2005)	CIMMYT	CIP	IRRI	CIAT	IITA	IPGRI / INIBAP	WARDA	ICRISAT	ICARDA	CAAS	EMBRAPA	Cornell	JIC	NIAS	WUR	Agropolis (CIRAD, INRA, IRD)	Others
SP1																		
1	$445,000	$54,000							$148,620	$88,600	$111,890						$41,890	
2	$220,000	$40,000	$20,000	$20,000	$40,000	$30,000	$10,000		$30,000	$30,000								
3	$228,000		20,000			$45,000			$71,000	$30,000	$15,000	$3,000					$30,000	$14,000
4	$162,360			X	X		$38,940			X							$22,420	$101,000
5	$150,000			75,000													$75,000	
6	$254,730											$254,730						
7	$179,000																$179,000	
8	$277,536		$44,250		$44,250		$56,286										$88,500	$44,250
Total	$1,916,626																	
SP2																		
9	$250,000			$40,000	$40,000						$25,000				$40,000	$40,000	$40,000	$25,000
10	$60,000	$60,000																
11	$95,000				$95,000							x						
12	$100,300		$33,040															$67,260
13	$99,845			X	$23,010						$39,985				$36,850			
14	$99,560					$11,800			$25,220									$62,540
15	$200,000						x					x			$200,000		X	
16	$109,563		$31,152	X			$20,060			$28,320	$30,031							
17	$117,700				$44,500												$73,200	
Total	$1,131,968																	
SP3																		
18	$150,000	$58,200		$91,800													X	
19	$182,590	$46,610	$20,650	$58,690					$18,880									$37,760
20	$130,000	$85,000																$45,000
21	$67,850						$60,770											º$7,080
Total	530,440																	
SP4																		
22	$259,600		$45,430	$77,880			$45,430								$45,430		$45,430	
23	$180,000		$16,000	$16,000			$148,000											
24	$100,300		$7,080	$42,480			$7,080					$7,080			$7,080			$29,500
25	$80,000	38,700				$5,900	$5,900										$17,700	$11,800
26	$148,610	$11,695		$9,746		$8,771	$106,702										$11,696	
27	$150,000		$65,000	$46,000					$39,000									
28*	$350,000	$10,556	$10,556	$55,556	$10,556	$20,556	$10,555		$10,555	$10,555							$10,555	
29	$264,000	$33,000	$33,000	$33,000	$33,000	$33,000	$33,000		$33,000	$33,000								
30	$100,000						$2,430									$39,020	$58,550	
31	$100,000			$53,980					$5,900			$11,800					$28,320	
32	$100,000														$100,000			
33	$129,000	$15,500		$21,500					$92,000									
34	$40,120			$40,120														
Total	$2,001,630																	
Uncomm.	155,336																	
TOTAL	$5,736,000	$453,261	$346,158	$681,752	$330,316	$155,027	$545,153		$474,175	$220,475	$221,906	$276,610			$429,360	$79,020	$722,261	$445,190

x = collaborating institution

* additional $200,000 not yet assigned

Competitive Grants (3-year projects) – GCP Consortium Members (see Appendix B for full details of projects)

#	CIMMYT	CIP	IRRI	CIAT	IITA	IPGRI/ INIBAP	WARDA	ICRISAT	ICARDA	CAAS	EMBRAPA	Cornell	JIC	NIAS	WUR	Agropolis (CIRAD. INRA, IRD)	Others	TOTAL
1			489,360											106,200			304,440	
2			468,120														431,880	
3				226,949	100,207						272,379	172,138					95,472	
4	60,300														222,500		224,350	
5								276,120			238,695					59,400	324,020	
6					296,143												603,857	
7												64,900					35,100	
8			145,317									347,731					406,563	
9				409,342							140,066						345,498	
10				459,300			89,700				87,300	353,600					85,000	
11	105,000										150,000		185,000	85,000		235,000	140,000	
12			316,800							572,700							0	
13	473,180											155,760				42,480	227,632	
14	436,010				26,845					17,405						129,210	107,675	
15	289,100		160,480													194,700	254,406	
16											473,898	366,102					60,000	
17									392,000								507,000	
TOTAL	1,363,590		1,580,077	1,095,591	423,195		89,700	276,120	392,000	590,105	1,362,338	1,460,231	185,000	191,200	222,500	660,790	4,152,893	14,045,330

Competitive Budget per Year

#	Project Title	Yr1 2005	Yr2 2006	Yr3 2007	Yr4 2008	Total
1	Identifying Genes Responsible for Failure of Grain Formation in Rice and Wheat under Drought	305,836	295,768	298,396		900,000
2	Revitalising Marginal Lands: Discovery of Genes for Tolerance of Saline and Phosphorus Deficient Soils to Enhance and Sustain Productivity	312,300	342,244	245,456		900,000
3	Identifying the physiological and genetic traits that make cassava one of the most drought tolerant crops	298,540	294,883	273,722		867,145
4	An eco-physiological - statistical framework for the analysis of GxE and QTLxE as occurring in abiotic stress trials, with applications to the					
	CIMMYT drought stress programmes in tropical maize and bread wheat	169,550	175,050	162,550		507,150
5	Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools	390,311	277,589	230,335		898,235
6	Marker Development and Marker-Assisted Selection for Striga Resistance in Cowpea	300,000	300,000	300,000		900,000
7	Measuring linkage disequilibrium across three genomic regions in rice	100,000				100,000
8	Targeted discovery of superior disease QTL, alleles in the maize and rice genomes	294,297	291,386	313,928		899,611
9	Development of Low-Cost Technologies for Pyramiding Useful Genes From Wild Relatives of Cassava into Elite Progenitors	298,194	298,164	298,548		894,906
10	Exploring Natural Genetic Variation: Developing Genomic Resources and Introgression Lines for Four AA Genome Rice Relatives	331,700	337,800	325,200	80,200	1,074,900
11	Functional genomics of cross-species resistance to fungal diseases in rice and wheat (CEREALIMMUNITY)	387,000	327,000	186,000		900,000
12	Drought Tolerant Rice Cultivars for North China and South/Southeast Asia by Highly Efficient Pyramiding of QTL's fro Diverse Origins	296,500	296,500	296,500		889,500
13	Development of informative DNA markers through association mapping in maize to improve drought tolerance in cereals	268,080	293,420	337,552		899,052
14	Characterisation of genetic diversity of maize populations: Documenting global maize migration fro the centre of origin	305,620	183,490	228,035		717,145
15	Determination of a common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes	297,678	302,398	298,610		898,686
16	Isolation and Characterisation of Aluminium Tolerance Genes in the Cereals: An Integrated Functional Genomic, Molecular Genetic and					
	Physiological Analysis	300,000	300,000	300,000		900,000
17	Allele Mining Based on Non-Coding Regulatory SNPs in barley germplasm	300,000	300,000	299,000		899,000
	TOTAL	**4,955,606**	**4,615,692**	**4,393,832**	**80,200**	**14,045,330**

SP5: Capacity Building 2005 Budget[1]	Lead institute	TOTAL
Gathering or development of a set of training materials for a course in genetic diversity analysis of germplasm and design of course curriculum	CIRAD	$12,500
Development of a set of training materials for a course in genomics and comparative genomics and design of course curriculum	Cornell	$12,500
Gathering or development of a set of training materials for a course in marker-assisted selection and breeding and design of course curriculum	WUR	$12,500
Gathering or development of a set of training materials for a course in bioinformatics and design of course curriculum	IRRI	12,509
Development of reference molecular marker kits to analyse diversity of germplasm for the year 1 GCP crops CIRAD, IITA	ICARDA, CIAT, IRRI, CIMMYT, CIP, ICRISAT,	$69,300
Extra training activities embedded into GCP-relevant research projects • Cerealimmunity Research proposal: "Workshop "Cross-talk between biotic and abiotic stress"=98,000 • Course "Design and analysis of multi-environment trials: conventional and QTL-based methods"=9,300 • Core Project: Functional genomics to improve African crops=37,120		$144,420
A repository for GCP training materials is designed and made available to GCP consortium members and partners under UNCOMMITTED (4,920)	GCP Communications	0
A fellowship and travel grant scheme set up and implemented		280,000
A workshop based on genotyping results of the year 1 work plan including participation of germplasm managers/curators from the CG and NARS. Venue: Swaminathan Foundation	IPGRI, CIRAD	150,000
A seminar on policy, IPR issues and access and benefit sharing. In conjunction with workshop organised by CAAS in Beijing.	WUR, IPGRI	$42,000
Three courses held in Asia/Pacific, Africa and Latin America respectively with the participation of 12 regional scientists, representing a minimum of 6 countries, per course. (Two courses diversity-breeding, and one course genomics-bioinformatics)	ICRISAT, Cornell, CIMMYT	$300,000
A workshop on project proposal design and development, in collaboration with the other CPs, in Asia/Pacific, Africa, and Latin America.	IPGRI	$180,000
Help desk and interactive Resource Centre set up	Cornell	$51,000
Project delivery activities	CB Coordinator	$33,715
Develop policy-training courses for NARS	WUR	$35,000
Policy helpdesk & website + Online resource for CP CB and awareness (joined activities, remainder under UNCOMMITTED 52,960)		137,040
Analysis of access to materials and enabling technologies	WUR	$20,000
Expert Group	CB Coordinator	$30,000
Rainfed Lowland Rice-Breeding Network	IRRI	$247,661
BECA Genotyping		$339,365
Coordinator & Support		$120,000
Additional Enabling Delivery funds and uncommitted funds		$356,396
TOTAL		**$2,585,906**

[1] SP5 Strategy and priorities were developed later in the budget process to complement priorities and activities of the other subprograms. In future, the budget will be incorporated into commissioned activities.

FINANCIALS

The GCP has maintained a healthy and improving financial condition since its inception. This is due to timely provision of funds by donors, a significant rate of growth in the number of donors, very significant growth in the size of their contributions, and a declining US dollar value relative to the currencies of our major donors. We have been able to adequately fund the start up of our aggressive research programme as visualised in our original approved proposal. As of the end of 2004, we have $500,000 in reserves, and by the end of 2005, we expect to have US$1 M in reserves. This will cover all of our contractual commitments to personnel through the end of the project. Until the likelihood of a second phase of the GCP becomes clearer, we will not begin to draw down the reserves as Phase 1 nears its end. If, as planned, the GCP moves forward for a second phase, the reserves will remain at their current level, or increase as needed.

The summary financial reports (income and expenses) for 2003, 2004, and 2005 are shown in Tables 1-3. Details of 2005 expenses are shown in Appendix D. It is clear that by far the largest portion of our funds go to directly support the research and capacity-building efforts of the GCP and its partners.

Although approximately $7 M was committed to research and capacity-building activities in 2004, there still is a large carryover of $6.2 M to 2005. This reflects timing of some donor contributions that bridge years (e.g., DFID arrives in July and is to cover the March – April fiscal year).

Another significant reason for the large carryover is that a major activity in 2004 was to solicit externally-reviewed and then commissioned research projects. These could not be awarded until the PSC approved the GCP budget for 2005. The awards were approved by the PSC during the December 2004 Rome meeting. Thus, award letters were released immediately after the PSC meeting and funds will move in early 2005. Next year we look to complete the granting process earlier.

In 2005, we project total income (including the significant carry over from 2004) of $20.06 M.

Table 1.

2003 Income Vs Expenditures	**USD**	
		Actual Jun-Dec
Income		
Austria [1/]		54,482
Sweden [2/]		107,013
World Bank		3,000,000
Total Income		**3,161,495**
Expenditures		
Salaries & Benefits		
International Staff		15,827
Technical Start-up & Research Planning Workshop		117,188
Operational Travel	80,905	
Conferences & Technical Services	36,283	
Office Supplies & Services		17,730
Consulting		14,902
Overhead 4%		328,994[3/]
Sub-total		494,641
Capital		6,247
Total Expenditures		500,888
Balance		2,660,607

[1/] Equivalent to Eur 45,000
[2/] Equivalent to SEK 800,000
[3/] 4% of 3M from WB in 2003 and the EC 2003 contribution, received 14 January 2004

Table 2.

2004 Income Vs Expenditures	**USD**	
		Actual Jan-Dec
Income		
DIFD [1/]		4,675,625
EC [2/]		5,224,850
Pioneer Found		50,000
Syngenta [3/]		15,000
World Bank		1,000,000
Sub-Total		10,965,475
Carry - forward 2003		**2,660,607**
Total Income		**13,626,082**
Expenditures		
Salaries & Benefits		252,934
Operational Travel (GCP Management)		70,925
Conferences		304,205
Office Supplies & Services		27,223
Printing & Design		45,914
Vehicle Expenses		7,312
Consulting		39,513
Research		5,693,372
Genetic Diversity of Global Genetic Resources SP1	2,375,462	
Comparative Genomics for Gene Discovery SP2	1,018,511	
Trait Capture for Crop Improvement SP3	520,739	
Genetic Resources, Genomic & Crop Inf Systems SP4	1,778,660	
Capacity Building SP5		195,057
Indirect Costs 4%		236,085 [5/]
Sub-total		6,872,540
Capital		33,597
Reserve		500,000
Total Expenditures		7,406,137
Balance [4/]		**6,219,945**

[1/] Equivalent to £2.5m

[2/] 2003 Contribution received on Jan 14 04 equivalent to Eur 4.150m

[3/] Kirkhouse Trust & Rockefeller Foundation are supporting participants in the BECA MAS course at the equivalent of approximately $15k each.

[4/] Of carry over from 2004 to 2005, $515,000 is for capacity building in competitive grants programme awarded in 2004, but executed in 2005

[5/] 4% of 2004 income less the EC contribution (counted in 2003) plus the Austria/Sweden 2003 contributions

Table 3.

2005 Income Vs Expenditures USD

2005		Projection Jan-Dec
Income		
DIFD [1/]		4,250,000
EC [2/]		6,027,334
RF		855,000
Pioneer		50,000
Syngenta		50,000
Sweden [3/]		103,731
World Bank [4/]		2,500,000
Sub-Total		13,836,065
Carry - forward 2004		**6,219,945**
Total Income		**20,056,010**
Expenditures		
Salaries & Benefits		313,600
Operational Travel (GCP Management)		80,000
Conferences & PSC expenses		689,748
Office Supplies & Services		31,222
Printing & Design		50,000
Vehicle Expenses		23,000
Consulting (includes BECA Staff)		135,000
Research		15,030,776
Research Subprogrammes 1-4 Workplan Yr1 (2004 20%)	1,125,570	
Commissioned Research 2005	5,736,000	
Operational Support SPLs	400,000	
Sub-Programme Leaders (salary &benef compensation)	254,000	
Competitive Grants Yr1 - Round 1)	4,955,606	
Competitive Grants (Round 2) [5/]	2,000,000	
RF Grants	559,600	
Capacity Building SP5		2,585,906
Projects (MTP)	1,878,880	
Coordinator & Support	120,000	
East Africa & SA Projects	587,026	
Indirect Costs 4%		553,443
Sub-total		19,492,695
Capital		33,000
Reserve		500,000
Total Expenditures		20,025,695
Balance		30,315

[1/] Contribution expected in two instalments Jul & Dec equivalent £ 2.5m @ 1.700
[2/] 2004 Contribution equivalent Eur 4.6m
[3/] Equivalent SEK 0.683m
[4/] Contribution received 4 Feb
[5/] Awards to be made in Nov '05; 4 grants of $500k for 2 years; flexible in the event that financing projections are not met

In-Kind Contributions

Table 4. In-Kind Contributions in 2005-2007 GCP competitive grants awards.

Institution	N	3yr Budget	In-Kind	%
CGIAR	7	5,225,805	2,222,220	42.52%
Non-CG GCP	7	4,566,845	3,018,100	66.09%
Non-GCP	35	4,054,981	3,062,540	75.53%
T o t a l	49	13,847,631	8,302,860	
Non-CGIAR Institutions	42	8,621,826	6,080,640	70.53%

APPENDICES

Appendix A. Generation Challenge Programme Consortium Members and Partners

Consortium Members

Africa Rice Centre (WARDA)
Agropolis
Brazilian Agricultural Research Corporation (Embrapa)
Chinese Academy of Agricultural Sciences (CAAS)
Cornell University
International Centre for Tropical Agriculture (CIAT)
International Maize and Wheat Improvement Centre (CIMMYT)
International Potato Centre (CIP)
International Centre for Agricultural Research in the Dry Areas (ICARDA)
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
International Institute for Tropical Agriculture (IITA)
International Plant Genetic Resources Institute (IPGRI)
International Rice Research Institute (IRRI)
John Innes Centre (JIC)
National Institute of Agrobiological Sciences (NIAS-Japan)
Wageningen University

NARS Partners

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

ARI Partners

Australian Centre for Plant Functional Genomics Pty Ltd
Colorado State University (CSU), USA
Commonwealth Scientific & Industrial Research Organisation (CSIRO), Australia
Dart P/L, Australia
ETH-Zurich, Switzerland
Genaissance, France
Graingenes (CSIRO), Australia
Hebrew Univ. of Jerusalem, Israel
Institut für Pflanzenbau und Pflanzenzüchtung, Germany
Institute Agronomique Mediterranean de Montpelier (CIHEAM-IAMM), France
JIRCAS, Japan
Kansas State University, USA
Laboratory of Gene Expression, University of Aarhus, Denmark.
MOBY-S, Canada
Scottish Crop Research Institute (SCRI)
Sichuan Agriculture University, China
TIGR
United States Department of Agriculture, North Carolina State University (NCSU)
University of Queensland, Australia
Universita' di Udine, Italy
University of Adelaide, Waite Campus, Australia
University of California, Berkley, USA
University of California, Davis, USA
University of California, Riverside, USA
University of Tsukuba, Japan
University of Virginia, USA
VARTC, Vanuatu

Appendix B. Full List of Competitive Projects[1]

1. Identifying Genes Responsible for Failure of Grain Formation in Rice and Wheat under Drought (8)

Budget Summary by Partner	IRRI	CSIRO	NIAS	TNAU	NANJING	TOTAL
Total Direct Cost	414,712	198,000	90,000	30,000	30,000	762,712
Indirect Costs	74,648	35,640	16,200	5,400	5,400	137,288
Total Costs	**489,360**	**233,640**	**106,200**	**35,400**	**35,400**	**900,000**
In-Kind Contribution	**93,220**	**146,320**	**—-**	**—-**	**—-**	**239,540**

2. Revitalizing Marginal Lands: Discovery of Genes for Tolerance of Saline and Phosphorus Deficient Soils to Enhance and Sustain Productivity (9)

Budget Summary by Partner	IRRI	CSIRO/Graingene	UCD	Dhaka University	ICABGRRD	TOTAL
Total Direct Cost	384,712	105,000	125,000	76,000	72,000	762,712
Indirect Costs	69,248	18,900	22,500	13,680	12,960	137,288
Total Costs	**468,120**	**109,740**	**147,500**	**89,680**	**84,960**	**900,000**
In-Kind Contribution	**214,000**	**169,000**	**119,500**	**31,500**	**31,500**	**565,500**

3. Identifying the physiological and genetic traits that make cassava one of the most drought tolerant crops (17)

Budget Summary by Partner	EMBRAPA/ CNPMF	CIAT	IITA	Cornell University	SARI/Ghana	ARI, Tanzania	TOTAL
Total Direct Cost	221,830	201,330	165,830	145,880	45,900	45,900	745,761
Indirect Costs	39,929	36,239	29,849	26,258	1,836	1,836	121,384
Total Costs	**272,379**	**226,949**	**100,207**	**172,138**	**47,736**	**47,736**	**867,145**
In-Kind Contribution	**92,000**	**160,000**	**170,000**	**150,500**	**3,000**	**3,000**	**578,500**

4. An eco-physiological – statistical framework for the analysis of GxE and QTLxE as occurring in abiotic stress trials, with applications to the CIMMYT drought stress programmes in tropical maize and bread wheat (28)

Budget Summary by Partner	WUR	CSIRO	CIMMYT	INIA-URUGUAY	TOTAL
Total Direct Cost	445,000	412,200	102,000	36500	995,700
Indirect Costs			18,600		18,600
Total Costs	**222,500**	**206,100**	**60,300**	**18,250**	**507,150**
In-Kind Contribution	**105,000**	**102,767**	**240,000**	**—-**	**447,767**

5. Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools (31)

Budget Summary by Partner	EMBRAPA	UCB	ICRISAT-India	ICRISAT-Kenya	IBONE	CERAAS	Aarhus	CIRAD	TOTAL
Total Direct Cost	211,995	111,992	179,000	55,000	46,470	52,500	67,144	54,000	778,101
Indirect Costs	26,701	16,799	32,220	9,900	6,971	8,715	13,429	5,400	120,135
Total Costs	**238,695**	**128,791**	**211,220**	**64,900**	**53,441**	**61,215**	**80,573**	**59,400**	**898,235**
In-Kind contribution	**450,000**	**300,000**	**315,000**	**150,000**	**100,000**	**165,000**	**90,000**	**50,000**	**1,620,000**

6. Marker Development and Marker-Assisted Selection for Striga Resistance in Cowpea (36)

Budget Summary by Partner	IITA	CERAAS	UVA	TOTAL
Total Direct Cost	250,969	60,000	451,743	762,712
Indirect Costs	45,174	10,800	81,314	137,288
Total Costs	**296,143**	**70,800**	**533,057**	**900,000**
In-Kind Contribution	**60,000**	**30,000**	**31,188**	**121,188**

[1] There were no requirements for institutions to specify in-kind contributions. Those in-kind contributions that were provided are shown in the interest of completeness.

7. Measuring linkage disequilibrium across three genomic regions in rice (41)

Budget Summary by Partner	Cornell University	ICABGRRD	TOTAL
Total Direct Cost	55,000	29,746	84,746
Indirect Costs	9,900	5,354	15,254
Total Costs	**64,900**	**35,100**	**100,000**
In-Kind Contribution	**—-**	**—-**	**—-**

8. Targeted discovery of superior disease QTL alleles in the maize and rice genomes (42)

Budget Summary by Partner	Cornell University	IRRI	CSU	NCSU	Kari	TOTAL
Total Direct Cost	294,687	123,150	141,245	119,500	83,800	762,382
Indirect Costs	53,044	22,167	25,424	21,510	15,084	137,229
Total Costs	**347,731**	**145,317**	**166,669**	**141,010**	**98,884**	**899,611**
In-Kind Contribution	**—-**	**—-**	**—-**	**—-**	**—-**	**—-**

9. Development of Low-Cost Technologies for Pyramiding Useful Genes From Wild Relatives of Cassava into Elite Progenitors (45)

Budget Summary by Partner	CIAT	EMBRAPA/ CNPMF	NAARI	CRI	NRCRI	TOTAL
Total Direct Cost	346,900	118,700	110,737	110,737	110,736	797,810
Indirect Costs	62,442	21,366	4,429	4,429	4,430	97,096
Total Costs	**409,342**	**140,066**	**115,166**	**115,166**	**115,166**	**894,906**
In-Kind Contribution	**255,000**	**66,000**	**27,500**	**27,500**	**27,500**	**403,500**

10. Exploring Natural Genetic Variation: Developing Genomic Resources and Introgression Lines for Four AA Genome Rice Relatives (47)

Budget Summary by Partner	Cornell University	CIAT	FEDEARROZ	EMBRAPA	WARDA	TOTAL
Total Direct Cost	233,400	330,000	58,000	60,000	62,000	743,400
Indirect Costs	42,000	59,400	10,400	10,800	11,200	133,800
Total Costs	**353,600**	**459,300**	**85,000**	**87,300**	**89,700**	**1,074,900**
In-Kind Contribution	**400,800**	**380,000**	**32,000**	**32,000**	**288,000**	**1,132,800**

11. Functional genomics of cross-species resistance to fungal diseases in rice and wheat (CEREALIMMUNITY) (52)

Budget Summary by Partner	AGROPOLIS	CIMMYT	EMBRAPA	JIC	INRA RENNES	NIAS	UCD	TOTAL
Total Direct Cost	135,000	95,000	140,000	177,000	87,000	75,000	130,000	839,000
Indirect Costs	10,000	10,000	10,000	8,000	3,000	10,000	10,000	61,000
Total Costs	**145,000**	**105,000**	**150,000**	**185,000**	**90,000**	**85,000**	**140,000**	**900,000**
In-Kind Contribution	**140,000**	**100,000**	**100,000**	**200,000**	**80,000**	**90,000**	**140,000**	**850,000**

12. Drought Tolerant Rice Cultivars for North China and South/Southeast Asia by Highly Efficient Pyramiding of QTL's from Diverse Origins (54)

Budget Summary by Partner	CAAS	IRRI	TOTAL
Total Direct Cost	498,000	264,000	762,000
Indirect Costs	74,700	52,800	127,500
Total Costs	**572,700**	**316,800**	**889,500**
In-Kind Contribution	**—-**	**—-**	**—-**

13. Development of informative DNA markers through association mapping in maize to improve drought tolerance in cereals (64)

Budget Summary by Partner	CIMMYT	Cornell University	INRA	KARI	SAU	SIRDC	NSFCRC	Genaissance	TOTAL
Total Direct Cost	401,000	132,000	36,000	28,100	28,100	28,100	28100	95000	776,400
Indirect Costs	72,180	23,760	6,480	5,058	5,058	5,058	5058		122,652
Total Costs	**473,180**	**155,760**	**42,480**	**33,158**	**33,158**	**33,158**	**33,158**	**95,000**	**899,052**
In-Kind Contribution		**540,000**	**300,000**	**45000**	**45,000**	**45,000**	**45,000**	**—-**	**1,020,000**

14. Characterisation of genetic diversity of maize populations: Documenting global maize migration from the centre of origin (66)

Budget Summary by Partner	CIMMYT	INRA	KARI	IITA	Indian Ag.	Thailand	Indonesia	Phil DOA	CAAS	Vietnam	TOTAL
Total Direct Cost	369,500	109,500	22,000	22,750	22,750	14,750	14750	7000	14,750	10000	607,750
Indirect Costs	66,510	19,710	3,960	4,095	4,095	2,655	2655	1260	2,655	1800	109,395
Total Costs	**436,010**	**129,210**	**25,960**	**26,845**	**26,845**	**17,405**	**17,405**	**8,260**	**17,405**	**11,800**	**717,145**
In-Kind Contribution	**—-**	**—-**	**—-**	**—-**	**—-**	**—-**	**—-**	**—-**	**—-**	**—-**	**—-**

15. Determination of a common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes (67)

Budget Summary by Partner	CIMMYT	ACPFG-Australia	INRA	ETH-Zurich	IRRI	IGAU-India	SIRDC-Zimbabwe	TOTAL
Total Direct Cost	245,000	73,500	165,000	90,000	136,000	33,000	25,200	767,700
Indirect Costs	44,100	13,230	29,700	9,000	24,480	5,940	4,536	130,986
Total Costs	**289,100**	**86,730**	**194,700**	**99,000**	**160,480**	**38,940**	**29,736**	**898,686**
In-Kind Contribution	**—-**	**465,000**	**330,000**	**450,000**	**—-**	**75,000**	**75,000**	**1,395,000**

16. Isolation and Characterisation of Aluminium Tolerance Genes in the Cereals: An Integrated Functional Genomic, Molecular Genetic and Physiological Analysis (69)

Budget Summary by Partner	Cornell University	EMBRAPA Maize & Sorghum	EMBRAPA Wheat	EMBRAPA Rice and Beans	MOI University	TOTAL
Total Direct Cost	282,501	278,010	88,500	61,500	52,200	762,711
Indirect Costs	83,601	30,888	9,000	6,000	7,800	137,289
Total Costs	**366,102**	**308,898**	**97,500**	**67,500**	**60,000**	**900,000**
In-Kind Contribution	**—-**	**—-**	**—-**	**—-**	**—-**	**—-**

17. Allele Mining Based on Non-Coding Regulatory SNPs in barley germplasm (74)

Budget Summary by Partner	ICARDA	Adelaide	Udine	Tushreen University	TOTAL
Total Direct Cost	339,000	254,500	207,500	45,000	846,000
Indirect Costs	53,000				53,000
Total Costs	**392,000**	**254,500**	**207,500**	**45,000**	**899,000**
In-Kind Contribution	**—-**	**254,265**	**—-**	**—-**	**254,265**

Appendix C. Full List of Commissioned Projects

SP1

1a. Completing genotyping of composite germplasm set of barley

Budget summary by partner	ICARDA	CAAS/ Beijing Genomics Institute (BGI)	TOTAL
Total	$55,000	$70,000	$125,000
In-kind contribution	—-	—-	—-

1b. Completing genotyping of composite germplasm set of wheat

	CIMMYT	TOTAL
Cost (2005)	$54,000	$54,000
In-kind contribution	—-	—-

1c. Completing genotyping of composite germplasm set of sorghum

Budget summary by partner	Agropolis	ICRISAT	CAAS/ Beijing Genomics Institute (BGI)	TOTAL
Total	$41,890	$45,220	$41,890	$129,000
In-kind contribution	—-	—-	—-	—-

1d. Completing genotyping of composite germplasm set of chickpea

Budget summary by partner	ICRISAT	ICARDA	TOTAL
Total	$103,400	$33,600	$137,000
In-kind contribution			(see notes)

* The in-kind contribution from ICRISAT and ICARDA will be in terms of salaries of the scientists and technicians, equivalent to budget for salary/benefits available from CP.

2. Supporting distribution of reference germplasm

Budget summary by partner	CIMMYT	CIP	IRRI	CIAT	IITA	IPGRI/ INIBAP	ICRISAT	ICARDA	TOTAL
Total	$40,000	$20,000	$20,000	$40,000	$30,000	$10,000	$30,000	$30,000	$220,000
In-kind contribution	—-	—-	—-	—-	—-	—-	—-	—-	*not given

3a. Molecular characterisation of tier 2 (orphan) crops — Finger Millet

Budget summary by partner	ICRISAT	TOTAL
Total	$18,000	$18,000
In-kind contribution		(see notes)

* The in-kind contribution from ICRISAT will be in terms of salaries of the scientists and technicians, equivalent to budget for salary/benefits available from Challenge Programme.

3b. Molecular characterisation of tier 2 (orphan) crops — Pigeon Pea

Budget summary by partner	ICRISAT	TOTAL
Total	$30,000	$30,000
In-kind contribution		(see notes)

* The in-kind contribution from ICRISAT will be in terms of salaries of the scientists and technicians, equivalent to budget for salary/benefits available from Challenge Programme.

3c. Molecular characterisation of tier 2 (orphan) crops — Sweet Potato

Budget summary by partner	CIP	NAARI (Uganda)	TOTAL
Total	$20,000	$10,000	$30,000
In-kind contribution	—-	—-	—-

3d. Molecular characterisation of tier 2 (orphan) crops — Yam

Budget summary by partner	IITA	CIRAD	TOTAL
Total	$30,000	$0	$30,000
In-kind contribution	$25,000	$25,000	$50,000

3e. Molecular characterisation of tier 2 (orphan) crops — Lentil

Budget summary by partner	ICARDA	Institut für Pflanzenbau und Pflanzenzüchtung	TOTAL
Total	$30,000	$0	$30,000
In-kind contribution			(see notes)

* The in-kind contribution from ICARDA and U. of Kiel will be in terms of salaries of the scientists and technicians, equivalent to budget for salary/benefits available from CP.

3f. Molecular characterisation of tier 2 (orphan) crops — Groundnut

Budget summary by partner	ICRISAT	EMBRAPA	UCB	TOTAL
Total	$23,000	$3,000	$4,000	$30,000
In-kind contribution				(see notes)

* The in-kind contribution from ICRISAT, EMBRAPA, and UCB will be in terms of salaries of the scientists and technicians, equivalent to budget for salary/benefits available from CP.

3g. Molecular characterisation of tier 2 (orphan) crops – Coconut

Budget summary by partner	Agropolis	TOTAL
Total	$30,000	$30,000
In-kind contribution	—-	—-

3h. Molecular characterisation of tier 2 (orphan) crops — Soybean

Budget summary by partner	IITA	CAAS/ Beijing Genomics Institute (BGI)	TOTAL
Total	$15,000	$15,000	$30,000
In-kind contribution	—-	—-	—-

4. Assessing DArTs as a genome-wide scanning technology

Budget summary by partner	IPGRI/ INIBAP	Agropolis	Dart P/L	TOTAL
Total	$38,940	$22,420	$101,000	$162,360
In-kind contribution	—-	—-	—-	$48,000

* see proposal for specific in-kind details

5. Assessing Ecotilling as a methodology for targeted genotyping and SNP discovery (2)

Budget summary by partner	IRRI	Agropolis (CIRAD)	TOTAL
Total	75,000	$75,000	$150,000
In-kind	$75,000	$75,000	$150,000

6. Supporting emergence or reference drought tolerance phenotyping centres (3)

Budget summary by partner	EMBRAPA	TOTAL
Total	$254,730	$254,730
In-kind contribution	—-	—-

7. Whole-plant modelling (5)

Budget summary by partner	Agropolis (CIRAD and INRA)	CSIRO/UQ	TOTAL
Total	$179,000	$0**	$179,000
In-kind contribution	—-	—-	—-

** The distribution of Year 1 funds between Agropolis and CSIRO is dependent on placement of post doc – to be decided.

8. Association analysis in the course of varietal improvement (6)

Budget summary by partner	CIP	CIAT	IPGRI/ INIBAP	Agropolis/ CIRAD	CARBAP (subcon by Agropolis)	VARTC (subcon by Agropolis)	TOTAL
Total	$44,250	$44,250	$56,286	$88,500	$44,250	x	$277,536
In-kind contribution	—-	—-	—-	—-	—-	—-	—-

SP2

9. Systematic evaluation of rice mutant collections for conditional phenotypes with emphasis on stress tolerance

Budget summary by partner	IRRI	CIAT	CAAS/Beijing Genomics Institute (BGI)	NIAS	Wageningen (WUR)	Agropolis	Huazhong Agric. Univ.	TOTAL
Total	$40,000	$40,000	$25,000	$40,000	$40,000	$40,000	$25,000	$250,000
In-kind contribution	$100,000	$80,000	$50,000	$80,000	$80,000	$80,000	$50,000	$615,000

10. Wheat genetic stock assembly and utilisation

Budget summary by partner	CIMMYT	TOTAL
Total	$60,000	$60,000
In-kind contribution		$60,000

11. Legume mutant resource development

Budget summary by partner	CIAT	EMBRAPA	TOTAL
Total	$95,000	x	$95,000
In-kind contribution	—-	—-	—-

12. Tuber genetic stocks and gene function validation tools

Budget summary by partner	CIP	Hebrew Univ. of Jerusalem	SCRI	TOTAL
Total	$33,040	$27,730	39,530	$100,300
In-kind contribution	$20,000	$20,000	$20,000	$60,000

13. Crop gene expression profiles and stress-gene arrays

Budget summary by partner	IRRI	CIAT	CAAS/ Beijing Genomics Institute (BGI)	NIAS	TOTAL
Total	x	$23,010	$39,985	$36,850	$99,845
In-kind contribution	—-	—-	—-	—-	—-

14. Stress response-enriched EST resources for targeted species

Budget summary by partner	IITA	ICRISAT & CUoH	Univ. of Hyderabad (India)	TIGR	ICGEB - India	TOTAL
Total	$11,800	$25,220	x	$37,760	$24,780	$99,560
In-kind contribution	—-	—-	—-	—-	—-	—-

15. Targeted Musa genome sequencing and frame map construction *proposal pending*

Budget summary by partner	IPGRI/ INIBAP	EMBRAPA	NIAS	Agropolis	TOTAL
Total	x	x	$200,000	x	$200,000
In-kind contribution	—-	—-	—-	—-	—-

16. Validation of conserved orthologous markers

Budget summary by partner	CIP	IRRI	IPGRI/ INIBAP	ICARDA	CAAS/Beijing Genomics Institute (BGI)	TOTAL
Total	$31,152	x	$20,060	$28,320	$30,031	$109,563
In-kind contribution						(see notes)

* CAAS - 90% and 50% of two senior scientists respectively, 90% of one PhD student's time. High throughput robotics and genotyping. Bioinformatics platform.
CIP: 10 % of two senior scientists, HPC platform management. INIBAP: will contribute in kind contribution of 5% of the Global Musa Genomics Consortium coordinator
ICARDA: 10% each of the two senior staff.

17. Comparative QTL mapping for drought tolerance

Budget summary by partner	CIAT	Agropolis	CERAAS (Senegal)	TOTAL
Total	$44,500	$73,200	x	$117,700
In-kind contribution	—-	$158,000	—-	$158,000

18. Development of low tech gene-based trait assay technologies in rice and wheat

Budget summary by partner	CIMMYT	IRRI	TOTAL
Total	$58,200	$91,800	$150,000
In-kind contribution	—-	—-	—-

19. Evaluation and deployment of transgenic drought tolerant varieties

Budget summary by partner	CIMMYT	CIP	IRRI	ICRISAT	JIRCAS	University of Tsukuba	TOTAL
Total	$46,610	$20,650	$58,690	$18,880	$18,880	$18,880	$182,590
In-kind contribution	—-	—-	—-	—-	—-	—-	—-

20. Simulation of marker-assisted selection strategies for optimising molecular breeding systems for drought tolerance in cereals

Budget summary by partner	CIMMYT	CSIRO	Univ of Queensland	TOTAL
Total	$85,000	$25,000	$20,000	$130,000
In-kind contribution	—-	—-	—-	—-

21. Product delivery plans

Budget summary by partner	IPGRI/ INIBAP	IFPRI	TOTAL
Total	$60,770	$7,080	$67,850
In-kind contribution	—-	—-	—-

SP4

22. Development of GenerationCP data models

Budget summary by partner			CIP, CIRAD, IPGRI, NIAS	IRRI	TOTAL
Total	$45,430	$77,880	$259,600		
In-kind contribution	—-	—-	—-		

23. Implementation of web services technology in GenerationCP Consortium

Budget summary by partner	CIP	IRRI	IPGRI/ INIBAP	TOTAL
Total	$16,000	$16,000	$148,000	$180,000
In-kind contribution	—-	—-	—-	$28,000

24. Application of MOBY for GenerationCP Consortium

Budget summary by partner	CIP	IRRI	INIBAP	EMBRAPA	NIAS	MOBY-S	TOTAL
Total	$7,080	$42,480	$7,080	$7,080	$7,080	$29,500	$100,300
In-kind contribution	—-	—-	—-	—-	—-	—-	—-

25. Creation and maintenance of templates for GenerationCP data storage in repositories

Budget summary by partner	CIMMYT	IRRI	IITA	IPGRI/ INIBAP	CIRAD	SCRI	TOTAL
Total	38,700	0	5,900	5,900	$17,700	11,800	$80,000
In-kind contribution	—-	—-	—-	—-	—-	—-	—-

26. Creation and maintenance of GenerationCP Repository

Budget summary by partner	CIMMYT	IRRI	IITA	IPGRI/ SGRP	Agropolis	TOTAL
Total	$11,695	$9,746	$8,771	$106,702	$11,696	$148,610
In-kind contribution	—-	—-	—-	—-	—-	$16,500

27. Integration of the High Performance Computing (HPC)-facilities in the GenerationCP toolbox (25)

Budget summary by partner	CIP	IRRI	ICRISAT	TOTAL
Total	$65,000	$46,000	$39,000	$150,000
In-kind contribution	—-	—-	—-	—-

28. Improvement of quality of existing databases.

Budget summary by partner	CIMMYT, CIP, CIAT, IPGRI, ICRISAT, ICARDA, Agropolis	IRRI	IITA	CGIAR-unassigned	TOTAL
Total	$10,556	$55,556	$20,556	$200,000	$350,000
In-kind contribution					(see notes)

* IRRI will make in-kind contributions of platform design, code and software development for all modules of ICIS currently being worked on under World Bank and special projects (previous developments are already available since ICIS is an open project). IRRI will also supply working venue for the May development workshop.

29. Creation of institutional bioinformatics capacity

Budget summary by partner	CIMMYT	CIP	IRRI	CIAT	IITA	IPGRI/ INIBAP	ICRISAT	ICARDA	TOTAL
Total	$33,000	$33,000	$33,000	$33,000	$33,000	$33,000	$33,000	$33,000	$264,000
In-kind contribution	—-	—-	—-	—-	—-	—-	—-	—-	—-

30. Development of decision support systems for sampling germplasm

Budget summary by partner	IPGRI	WUR	CIRAD	TOTAL
Total	$2,430	$39,020	$58,550	$100,000
In-kind contribution				

* **CIRAD**-Agropolis: Personnel costs for scientists involved in methodological developments and validation activities; Molecular and phenotypic data on sorghum, rice, cocoa collections collected in other projects ; Darwin software; **IPGRI**: Personnel costs for database manager ; Access to germplasm databases (MGIS, SINGER, Eurisco); Software promotion via SP4 project and IPGRI network; **WUR:** GENEMINE methodology and software; Molecular and phenotypic data on lettuce (to be confirmed!)

31. Development of ortholog-function display tools (*see proposal for 2005/2006 budget differences)

Budget summary by partner	IRRI	ICRISAT	EMBRAPA	CIRAD	TOTAL
Total	$53,980	$5,900	$11,800	$28,320	$100,000
In-kind contribution	—-	—-	—-	—-	—-

32. Development of crop gene expression database and data mining tools (30)

Budget summary by partner	NIAS	TOTAL
Total	$100,000	$100,000
In-kind contribution	—-	—-

33. Development of decision support tools for MAS and MAB

Budget summary by partner	CIMMYT	IRRI	ICRISAT	TOTAL
Total	$15,500	$21,500	$92,000	$129,000
In-kind contribution	—-	—-	—-	—-

34. Use Cases

Budget summary by partner	IRRI	Total
Total	$40,120	$40,120
In-kind contribution	—-	—-

Appendix D. Detailed Budget for 2004

USD

Description	Expenses	Total
Salaries & Benefits		252,934
Mngm Int'l	226,048	
Mngm Admin Support	26,885	
Travel		70,925
Mngm Int'l	70,925	
Conferences		304,206
2003 Conferences & Technical Services	61,170	
PAG	6,916	
ARM	173,936	
External Review Meeting	19,389	
AGM	2,587	
PSC	21,604	
IP Workshop	15,938	
Stakeholders Meeting	292	
Others	2,374	
Office Supplies & Services		27,223
Office	11,374	
Shipping & Postage	9,298	
Maint & Repair	1,790	
Calls, Fax, CGNet	4,762	
Printing & Design		45,914
Printing & Design	34,227	
Web Page & Sofware	8,012	
Design Consortium Agreement	3,675	
Vehicle Expenses		7,312
Gasoline	1,297	
Maintenance	2,206	
Others	3,810	
Consulting		39,513
Management Consultants (Salary&Benefits, Travel)	39,513	
Research		2,375,462
SP1		
Phenotyping Workshop	100,000	
Research	2,105,488	
Operational support SPL	100,000	
Salary compensation SPL	69,974	
SP2		1,018,511
Research	850,109	
Operational support SPL	100,000	
Salary compensation SPL	68,402	
SP3		520,739
Research	358,879	
Operational support SPL	100,000	
CAGT Workshop	6,390	
Salary compensation SPL	55,471	
SP4		1,778,660
Research	1,633,660	
Operational support SPL	100,000	
Salary compensation SPL	45,000	
Capacity Building SP5		195,057
Coordinator - operating costs (travels & others)	63,600	
Helpdesk Initiation	50,150	
MAS course	50,000	
Int'l staff	27,807	
Visiting Scientific	3,500	
Overhead		236,085
Donors	236,085	
Capital		33,597
Vehicle	22,043	
Computers / printers	11,554	
Reserve		500,000
Reserve	500,000	
TOTAL EXPENSES		**7,406,137**

Appendix E. Detailed Budget for 2005

USD

	PROJECTION	
Description	**Expenses**	**Total**
Salaries & Benefits		313,600
Mngm Int'l	202,000	
Mngm Int Commun	47,000	
Mngm Admin Support	64,600	
Travel		80,000
RZ	50,000	
JN	30,000	
Conferences		689,748
PSC	200,000	
PAC	50,000	
Annual Research Meeting	200,000	
Stakeholders Committee (GFAR) (EC)	144,000	
AGM	10,000	
IT meeting	85,748	
Office Supplies & Services		31,222
Office	8,222	
Shipping & Postage	8,000	
Maintenance & Repair	3,000	
Calls, Fax, Cgnet	12,000	
Printing & Design		50,000
Printing & Design	30,000	
Software/Website	20,000	
Vehicle Expenses		23,000
Gasoline	10,000	
Insurance	3,000	
Maintenance	10,000	
Consultants (salary & benefits, travel)		135,000
Communications Consultant	15,000	
BECA /H - Salary & Benefits (50%) [1/]	60,000	
VI (Web content management)	20,000	
Legal consultant	30,000	
Consultant	10,000	
Research		15,030,776
Remaining 20% Work Plan Yr1	1,125,570	
Commissioned Research 2005	5,736,000	
Operational Support SPLs	400,000	
Sub-Programme Leaders (Salary Compensation)	254,000	
Competitive Grants (Yr1 - Round 1)	4,955,606	
Competitive Grants (Round 2)	2,000,000	
RF Grants	559,600	
Capacity Building (EC)		2,585,906
Projects	1,878,880	
SP5 Coordinator and Support	120,000	
RF Grants (Rainfed Rice, BECA)	587,026	
Overhead		553,443
DFID (4.250m 4%)	170,000	
EC ($6.027m 4%)	241,093	
Pioneer/Syngenta/Sweden	8,149	
RF	34,200	
WB ($2.5m 4%)	100,000	
Capital		33,000
Computer	10,000	
Printer	5,000	
Auto	18,000	
Reserve		500,000
TOTAL EXPENSES		**20,025,695**

[1/] Complemented by RF BECA for 3 years and Harvest Plus

Appendix F. GCP Outputs and Activities (based on the 2005-2007 Medium Term Plan)

GCP Goal: Improve livelihoods of resource-poor farmers and consumers in developing countries by accessing and utilizing the genetic potential of public genetic resources in plant breeding programs through the concerted generation, management, dissemination, and application of comparative biological knowledge

Objective 1: Develop a platform for, and conduct, analysis of genetic diversity in international crop genetic resources and apply this to improve major crops for drought tolerance and other related traits of importance to resource-poor farmers

Subprogramme 1	**Output 1.1:** Organise a rational access to sources of genes and alleles involved in key agricultural traits on the basis of coordinated surveys of molecular and phenotypic variation among the accessible germplasm collections for CG mandate crops.	**COMMISSIONED RESEARCH PROJECTS**	**Budget for 2005**	**COMPETITIVE GRANTS**	**Budget for 2005**
	Activity 1.1.1 Creating an improved understanding of the structure of the diversity for the major world food crops, diagnostic molecular markers for subsequent germplasm analysis identified, and a set of reference samples designed for integrated characterisation	1. Completing genotyping of composite germplasm set of barley, wheat, sorghum, and chickpea	$445,000	3. Identifying the physiological and genetic traits that make cassava one of the most drought tolerant crops	298,540
		3. Molecular characterisation of tier 2 (orphan) crops — pearl millet, finger millet, pigeon pea, sweet potato, yam, lentil, grass forage, legume forage, groundnut, coconut, and soybean (perhaps we won't have proposal for forages)	$228,000	10. Exploring Natural Genetic Variation: Developing Genomic Resources and Introgression Lines for Four AA Genome Rice Relatives (SP1&SP3)	165,850 (half of total of 331,700)
				14. Characterisation of genetic diversity of maize populations: Documenting global maize migration fro the centre of origin	305,620
	Activity 1.1.2 Develop a range of techniques accessible in key laboratories applied for high throughput molecular characterisation of germplasm	4. Assessing DArTs as a genome-wide scanning technology	$162,360	17. Allele Mining Based on Non-Coding Regulatory SNPs in barley germplasm	300,000
		5. Assessing Ecotilling as a methodology for targeted genotyping and SNP discovery	$150,000		
	Activity 1.1.3: Establish and implement a scientific and organisational framework to describe tolerance to drought	6. Supporting emergence of reference drought tolerance phenotyping centres (will probably be lumped back with below)	$254,730		
		7. Whole-plant modelling	$179,000		
	Activity 1.1.4: Associate molecular polymorphisms with higher tolerance to drought and integrate methodological improvements	8. Association analysis in the course of varietal improvement (SP1&SP3)	$277,536	7. Measuring linkage disequilibrium across three genomic regions in rice	100,000
		[Measuring linkage disequilibrium in sorghum and coconut (SPL budget)]	[$70, 000]	13. Development of informative DNA markers through association mapping in maize to improve drought tolerance in cereals (SP1&2)	134,040 (half of total of 268,080)
	Activity 1.1.5: Establish protocols and policy analyses to allow germplasm exchange with proper access and benefit sharing from the derivatives of the programme	2. Supporting distribution of reference germplasm (11 year one crops)	$220,000		
	Budget	TOTAL	$1,986,626		
Subprogramme 2	**Output 1.2**: Genes conferring stress tolerance, with emphasis in drought, in multiple crop species identified through the use of cross-cutting tools developed for comparative genomics and biology	**COMMISSIONED RESEARCH PROJECTS**	**Budget for 2005**	**COMPETITIVE GRANTS**	**Budget for 2005**
	Activity 1.2.1: Assembly of genomics and germplasm resources through consolidating existing (and developing new) specialised genetic stocks and framework genetic markers for target crops	10. Wheat genetic stock assembly and utilisation	$60,000	8. Targeted discovery of superior disease QTL, alleles in the maize and rice genomes (SP2&3)	294,297
		9. Systematic evaluation of rice mutant collections for conditional phenotypes with emphasis on stress tolerance	$250,000		
		11. Legume mutant resource development	$95,000		
		12. Tuber genetic stocks and gene function validation tools	$100,300		
	Activity 1.2.2: Develop comparative maps within and across species and deploy comparative mapping tools to CP partners, linked to the CP consensus map repository and major international plant databases	16. Validation of conserved orthologous markers	$109,563		
		17. Comparative QTL mapping for drought tolerance	$117,700		
	Activity 1.2.3: Assign genes and pathways to putative phenotypes through the convergence evidence of genome variation, expression patterns and phenotypic data	13. Crop gene expression profiles and stress-gene arrays	$99,845	11. Functional genomics of cross-species resistance to fungal diseases in rice and wheat (CEREALIMMUNITY)	387,000
		14. Stress response-enriched EST resources for targeted species	$99,560	16. Isolation and Characterisation of Aluminium Tolerance Genes in the Cereals: An Integrated Functional Genomic, Molecular Genetic and Physiological Analysis	300,000
				2. Revitalising Marginal Lands: Discovery of Genes for Tolerance of Saline and Phosphorus Deficient Soils to Enhance and Sustain Productivity (SP2&3)	156,150 (half of total of 312,300)
		15. Targeted Musa genome sequencing and frame map construction	$200,000	15. Determination of a common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes	297,678

	Activity 1.2.4: Validate genes and pathways through evaluation of under or over-expression constructs or variants (induced or natural) of the target genes			1. Identifying Genes Responsible for Failure of Grain Formation in Rice and Wheat under Drought	305,836
				13. Development of informative DNA markers through association mapping in maize to improve drought tolerance in cereals (SP1&2)	134,040 (half of total of 268,080)
	Activity 1.2.5: Disseminate genomic resources and information platform to NARES through networks and training (Links to Objective 2)				
	Budget	TOTAL	1,131,968		
Subprogramme 3	**Output 1.3:** Validation and application on elite varieties of gene-based markers for molecular-assisted breeding for tolerance to complex stresses (with emphasis on drought) in national and regional centres of excellence	**COMMISSIONED RESEARCH PROJECTS**	**Budget for 2005**	**COMPETITIVE GRANTS**	**Budget for 2005**
	Activity 1.3.1: Identification, agronomic evaluation and market appraisal of elite varieties suitable for conversion using marker assisted selection	[SPL research funds]	[30000]		
	Activity 1.3.2: Development, validation and refinement of gene and trait introgression technologies	18. Development of low tech gene-based trait assay technologies in rice and wheat	$150,000	5. Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools	390,311
		19. Evaluation and deployment of transgenic drought tolerant varieties	$182,590	2. Revitalising Marginal Lands: Discovery of Genes for Tolerance of Saline and Phosphorus Deficient Soils to Enhance and Sustain Productivity (SP2&3)	156,150 (half of total of 312,300)
		Association analysis in the course of varietal improvement (SP1&SP3)	$0 (SP1 funds)	6. Marker Development and Marker-Assisted Selection for Striga Resistance in Cowpea	300,000
				9. Development of Low-Cost Technologies for Pyramiding Useful Genes from Wild Relatives of Cassava into Elite Progenitors	298,194
				10. Exploring Natural Genetic Variation: Developing Genomic Resources and Introgression Lines for Four AA Genome Rice Relatives (SP1&SP3)	165,850 (half of total of 331,700)
	Activity 1.3.3: Design, implementation and improvement of molecular breeding programmes in NARS and GCP Consortium members	20. Simulation of marker-assisted selection strategies for optimising molecular breeding systems for drought tolerance in cereals	$130,000	12. Drought Tolerant Rice Cultivars for North China and South/Southeast Asia by Highly Efficient Pyramiding of QTLs fro Diverse Origins	296,500
	Activity 1.3.4: Establishment, support and promotion of molecular breeding communities of practice	See Activity 2.1.4			
	Activity 1.3.5: Development, deployment and impact assessment of improved seed-products	21. Product delivery plans	$67,850		
	Budget	TOTAL	$530,440		
Subprogramme 4	**Output (Subprogramme) 1.4:** A network of genetic resource, genomic and crop improvement information platforms supporting GCP research created and integrated with complementary resources in the global community and managed by a network of bioinformatics specialists in GCP members and their partners	**COMMISSIONED RESEARCH PROJECTS**	**Budget for 2005**	**COMPETITIVE GRANTS**	**Budget for 2005**
	Activity 1.4.1 Timely solutions for storage of, and access to, data currently generated in the GCP	22. Development of GenerationCP data models	$259,600		
		24. Application of MOBY for GenerationCP Consortium.	$100,300		
		25. Creation and maintenance of templates for GenerationCP data storage in repositories	$80,000		
		26. Creation and maintenance of GenerationCP Repository	$148,610		
	Activity 1.4.2: Improvement of quality of existing databases and analysis tools	27. Integration of the High Performance Computing (HPC)-facilities in the GenerationCP toolbox	$150,000		
		28. Improvement of quality of existing databases.	$350,000		
		29. Creation of institutional bioinformatics capacity	$264,000		
	Activity 1.4.3: Development of an information network of GCP data sources and analysis tools over the Internet and integration with international bioinformatics resources	23. Implementation of web services technology in GenerationCP Consortium.	$180,000		
	Activity 1.4.4: Develop new data processing and analysis tools that serve the needs of Sub Programmes 1, 2 and 3.	30. Development of decision support systems for sampling germplasm	$100,000	4. An eco-physiological - statistical framework for the analysis of GxE and QTLxE as occurring in abiotic stress trials, with applications to the CIMMYT drought stress programmes in tropical maize and bread wheat	169,550
		31. Development of ortholog-function display tools	$100,000		
		32. Development of crop gene expression database and data mining tools	$100,000		
		33. Development of decision support tools for MAS and MAB	$129,000		
		34. Use cases	$40,120		
	Budget		$2,001,630		
		Uncommitted	$155,336		
		Commissioned Research TOTAL	**$5,736,000**	**Competitive Research Total**	**4,955,606**

Objective 2: Strengthen the capacity of NARS and GCP consortium scientists to apply the tools of genomics, molecular biology and bioinformatics to the analysis of genetic diversity held in germplasm collections, and to use this knowledge to improve crop breeding programmes and to develop new stress-tolerant varieties

Subprogramme 5

Output 2.1: NARS scientists with capacity for full participation in CP	**COMMISSIONED RESEARCH PROJECTS**	**Budget for 2005**	**COMPETITIVE GRANTS**	**Budget for 2005**
Activity 2.1.1: Needs assessment conducted	SPL research funds	$30,000		
Activity 2.1.2: NARS capacity building components built into commissioned research programmes	Extra training activities embedded into GCP-relevant research projects	$144,420		
Activity 2.1.3: NARS capacity building built into competitive grants programme			Line item budgets in competitive grants	**[$562,617]**
Activity 2.1.4: Training courses or workshops on specific technologies and areas conducted	Gathering or development of a set of training materials for a course in genetic diversity analysis of germplasm and design of course curriculum	$12,500		
	Development of a set of training materials for a cours in genomics and comparative genomics and design of course curriculum	$12,500		
	Gathering or development of a set of training materials for a course in marker-assisted selection and breeding and design of course curriculum	$12,500		
	Gathering or development of a set of training materials for a course in bioinformatics and design of course curriculum	$12,509		
	Development of reference molecular marker kits to analyse diversity of germplasm for the year 1 GCP crops	$69,300		
	A fellowship and travel grant scheme set up and implemented	$280,000		
	A workshop based on genotyping results of the year 1 work plan including participation of germplasm managers/curators from the CG and NARS. Venue: Swaminathan Foundation	$150,000		
	A seminar on policy, IPR issues and access and benefit sharing. In conjunction with workshop organised by CAAS in Beijing.	$42,000		
	Three courses held in Asia/Pacific, Africa and Latin America respectively with the participation of 12 regional scientists, representing a minimum of 6 countries, per course. (Two courses diversity-breeding, and one course genomics-bioinformatics)	$300,000		
	A workshop on project proposal design and development, in collaboration with the other CPs, in Asia/Pacific, Africa, and Latin America.	$180,000		
Activity 2.1.5. Strengthen GCP internal capacity	On-line resource for internal CP capacity building and awareness on IP issues + policy helpdesk and website	$137,040		
Output 2.2: NARS Research Centres serve as Regional Research Hubs	**COMMISSIONED RESEARCH PROJECTS**	**Budget for 2005**		
Activity 2.2.1: Specific needs of NARS RRHs addressed	Help desk and interactive Resource Centre set up Develop policy-training courses for NARS	$51,000 $35,000		
Output 2.3: Crop improvement networks in place to incorporate novel alleles/traits	**COMMISSIONED RESEARCH PROJECTS**	**Budget for 2005**		
Activity 2.3.1: Meta analysis of existing and recent crop improvement networks with McKnight CCR and Harvest Plus	Project delivery evaluation	$33,715		
Activity 2.3.2: Development of regional improvement networks for multiple crops (in close cooperation with HarvestPlus and NGOs)	Eastern India Rainfed Lowland Rice Breeding Network (RF)	$247,661		
	BECA East Africa Genotyping of Cassava, Sorghum and Beans (RF)	$339,365		
Activity 2.3.3: Ex ante and longitudinal assessments of activities to maintain to relevance and focus on needs of resource poor farmers (Currently seeking supplemental funding for this)	Analysis of access to materials and enabling technologies	$20,000		
	Coordinator and support	$120,000		
	Uncommitted	$356,396		
	Capacity Building TOTAL	**$2,585,906**		

Generation

Cultivating Plant Diversity for the Resource Poor

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Consortium members

Agropolis • Brazilian Agricultural Research Corporation (Embrapa) • Chinese Academy of Agricultural Sciences (CAAS) • Cornell University • International Center for Tropical Agriculture (CIAT) • International Maize and Wheat Improvement Center (CIMMYT) • International Potato Center (CIP) • International Center for Agricultural Research in the Dry Areas (ICARDA) • International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) • International Institute for Tropical Agriculture (IITA) • International Plant Genetic Resources Institute (IPGRI) • International Rice Research Institute (IRRI) • John Innes Centre • National Institute of Agrobiological Sciences (NIAS-Japan) • Wageningen University • Africa Rice Center (WARDA)