Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE POOR

2005 Annual Report and Year Three (2006) Workplan

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Submitted by Jean-Marcel Ribaut, Director, and Jennifer Nelson, Communications Manager

Generation Challenge Programme
c/o CIMMYT
Apdo. Postal 6-641
06600 Mexico, D.F., Mexico
+52 55 5804 2004

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Dear Colleagues and Friends of the Generation Challenge Programme,

We are delighted to provide you with this report on our activities and outputs over the last 12 months, and we hope that, in reading it, you too will share in the sense of achievement we feel in looking back on our Programme's progress during 2005.

Last year, 2005, was the first year of "full speed" research activities for the GCP. With the initiation of 17 first round competitive grants and 50 new commissioned projects, we now have a rich portfolio of diverse and complementary activities conducted by an extensive network of experts. These activities and some very promising early results were highlighted at the GCP 2005 Annual Research Meeting in Rome in September. Many of the 2006 commissioned research projects took shape at this event, through animated and fruitful scientific discussions, which reflected the enthusiasm and commitment of the Generation community.

With all these projects rapidly progressing, the new challenge becomes the storage, analysis, and methods for sharing the data. If 2005 was characterised by the initiation of this large set of activities, I hope that 2006 will see a shift toward the release of research results from previous years to be made fully accessible via the GCP platform. During the last Annual Research Meeting, a colleague ventured that if the GCP can ensure that data generated by the different project teams all over the world could be made available to the community in a truly user-friendly format, the GCP would be a major success. I could not agree more.

Another important thrust this year was the initiation of a strategy paper to refine the objectives, and better define the operational framework, of the GCP. This is a necessary but complex task, as a strategy must allow the GCP to consolidate the research agenda around key topics, while at the same time remain sufficiently flexible to capture new ideas, approaches, and partners. With our dual funding system of competitive and commissioned grants, we are well-positioned to react promptly to compelling research opportunities and align with new partners or networks to achieve our objectives.

The explosion of capacity building activities and training efforts in 2005 and the tangible products that have already resulted from those endeavours are also critical GCP achievements. In 2006, we plan to embark on the next step toward making certain that potential users are able to deploy products from the GCP's research in plant breeding programmes. The GCP delivery strategy, articulated in 2005, has these principles at its heart, and firmly establishes the GCP's demand-driven mentality. As one GCP-funded molecular breeder stated simply in our 2005 Research Highlights publication about his partnership with Indian pearl millet breeder Om Yadav, "if he can't use it, there's no point in producing it."

Although the GCP is a young programme, it has already produced novel approaches and has generated useful tools—which are presented in this document—that can be directly applied in plant breeding programmes. I would like to reinforce here the major role of plant breeders as a critical sphere of users of GCP products and make a strong commitment to involve them even more at all levels of GCP activities. Henceforth, the GCP's mantra should be: "Take advantage of cutting-edge science and existing crop diversity to improve plant breeding for marginal environments."

The GCP is in healthy financial shape and there are encouraging signs of additional donor support to further consolidate our research agenda and implement product delivery. On behalf of all of our stakeholders I would like to thank our donors for their trust in and support for our Programme.

I would like to express my gratitude to Bob Zeigler, founding director of the GCP, who did a great job in successfully launching and establishing the GCP. My thanks also go to Theo van Hintum, who served as interim director during a three-month transition period. A special thanks goes to the GCP's Subprogramme leaders and headquarters staff, who did a terrific job over the entire year. I would also like to express my gratitude to former Subprogramme 3 leader Jonathan Crouch, who, unfortunately for the GCP, has left us to take up a new position. We wish him all the best in his new challenge.

Finally, I would like to thank the entire GCP scientific community for their contributions in making this programme a success. Today, looking at the GCP partner institutions, we can say that we have already achieved one of our major aims: to bring together scientists with a broad range of expertise but with common and complementary goals—working across 22 crops—to bridge the gap between basic and applied science.

In conclusion, allow me to say that it is an honour to be the Director of this innovative and dynamic programme, and I am looking forward to a very productive 2006.

Jean-Marcel Ribaut
Director

Introduction

After Building the Foundation, a Shift to Implementation

The completion of the Generation Challenge Programme's (GCP) second year was marked by a definitive shift from creating the underpinnings of the organisation to implementing activities. In 2004, operating procedures were defined, partnerships were formed, the vision and mission of this fledgling programme were articulated, and a path was formulated for meeting the GCP's objectives. In 2005, significant strides were made toward executing those well-laid plans.

Research activities commenced in January 2005 on the first round of competitive research grants—17 three-year projects of approximately US$ 1 million each. Early 2005 also saw the work begin on a fresh round of commissioned grants, which serve as the basis of the GCP platform of tools and technologies for genetic studies and applications. In total, the GCP initiated 67 competitive and commissioned research projects and capacity building activities in 2005.

Implementation of research and capacity building activities can also be seen in the healthy growth of the GCP's assemblage of partners, which now includes more than 30 national programmes from developing countries and over 25 advanced research institutes, in addition to the 18 GCP consortium members (nine Future Harvest Centres of the CGIAR, five advanced research institutions, and four national agricultural research systems [NARS]). Private sector involvement is also increasing. Hundreds of scientists around the world are now engaged in or affiliated with GCP research. In 2005, new mechanisms for interaction and project management were developed to support the new collaborations that the GCP incubated, thus enhancing the effective flow of funds, reporting, data, and project outputs.

Exemplifying the shift from planning to action in 2005 was the development of the GCP's delivery strategy. While in 2004 Generation focused on crafting an effective scientific strategy, in 2005 effort was directed to detailing how the Programme's science will substantially help plant breeders improve germplasm to ultimately benefit the resource poor. Full integration of the scientific and delivery strategies is now underway in the form of the overall GCP Strategy.

The GCP's second Medium Term Plan (MTP), articulated in mid-2005, further refined how the GCP organises its research toward medium- and long-term objectives. The 'projects' identified in the 2006-2008 Medium Term Plan under each subprogramme (SP) reflect a maturation of the objectives of each SP and Generation as a whole, as technologies develop, opportunities arise, and collaborations blossom. Also reflected in the plan is a profound commitment to ensuring that the GCP's research outputs can be accessed by the wider research community, especially scientists in developing countries. Producing the Medium Term Plan has proven to be a very useful annual exercise for the GCP Management Team, and it has become a crucial tool for planning, reporting, and identifying areas for improvement.

The 2005 Annual Research Meeting (ARM) in Rome was another important milestone. The ARM gives GCP scientists and partners the opportunity to hear firsthand about the research progress made by their colleagues during the preceding year. Discussions and Q&A sessions were notably lively following the numerous research presentations and plenaries. Partners were also offered many opportunities for face-to-face discussions to coordinate proposal development for new commissioned research projects, to start in January 2006. For the first time, mid-year reports of all ongoing projects were compiled and published as the ARM proceedings.

Finally, 2005 was also a year of administrative transition for Generation. Founding director Robert Zeigler, who oversaw the launch of the GCP, left in March to assume the position of Director General of the International Rice Research Institute (IRRI). Subprogramme 4 leader Theo van Hintum served as interim director until July 2005, when Jean-Marcel Ribaut, formerly Biotechnology Group Leader at the International Maize and Wheat Improvement Center (CIMMYT), was appointed GCP Director. In addition, Subprogramme 3 Leader, Jonathan Crouch, who was recently appointed head of the CIMMYT Genetic Resources Unit, departed the GCP. Recruitment for a new Subprogramme 3 Leader will begin in early 2006.

This 2005 Annual Report and 2006 Workplan summarises research progress and capacity building achievements in 2005 and presents an overview of the competitive and commissioned research portfolio and capacity building and delivery activities for 2006. This report was presented to and approved by the Programme Steering Committee meeting in November 2005.

Programme Structure

The governance and management structures established in 2004 continue to assure that GCP funds are managed efficiently and allocated in a transparent and orderly fashion. The governance structure consists of a Programme Steering Committee, who is advised by two panels, the Programme Advisory Committee (which provides input on scientific issues) and the Stakeholders Committee. The GCP director and five subprogramme leaders (SPLs) form the GCP Management Team. Management operations are run in accordance with a consortium agreement developed through extensive consultation with institutions inside and outside the consortium, and also through annual agreements (i.e., Commissioned Research Contracts) with consortium members, which establish reporting requirements.

Generation has two complementary research funding schemes—competitive grants and commissioned projects—that provide the means for keeping multiple research projects moving toward common objectives while providing flexibility to respond quickly and effectively to unforeseen circumstances or unique opportunities.

The GCP's five subprogrammes are the operative structure for allocating funds and managing research projects:

Subprogramme 1: Genetic Diversity of Global Genetic Resources

Characterises the diversity of crop germplasm collections held by the CGIAR and national programs, and assesses both the genetic structure of the collections and the phenotypic variation associated with that structure.

Subprogramme 2: Comparative Genomics for Gene Discovery

Identifies or develops genomic tools, technologies, and approaches for gene discovery and validation of gene function to improve an understanding of gene systems across crops.

Subprogramme 3: Trait Capture for Crop Improvement

Validates and refines molecular breeding systems and the resulting enhanced germplasm, with the purpose of increasing the efficiency, speed, and scope of plant breeding gains.

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

Integrates GCP information components and analysis tools into a coherent information gateway, and provides support for the data analysis needs of other subprogrammes.

Subprogramme 5: Capacity Building and Enabling Delivery

Provides fellowship and grant opportunities to developing country national programme scientists, designs and manages the GCP Training Programme, and coordinates the development and implementation of project delivery plans.

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

Generation pursues its mission through a package of three interlocking themes: *Discovering Genetic Diversity*, *Using Genetic Diversity*, and *Delivering Products* (as elucidated in Generation's *Research Highlights 2005*). *Discovering Genetic Diversity* entails organising access to the genetic diversity of the world's major food crops through an improved understanding of the structure of diversity and the creation of new sources of genetic diversity. *Using Genetic Diversity* involves tapping that diversity through the application of genomic tools and techniques—and the informatics systems required to sift through and analyse the data produced by those tools—to identify genes and alleles that control plant tolerance to stresses, and to then introgress favourable alleles into elite breeding material adapted to tropical and subtropical environments. *Delivering Products* represents the mechanisms the GCP employs to ensure that research outputs move efficiently through the product development pipeline and that their intended users are trained in the techniques needed to use GCP products in actual breeding conditions and programmes.

Strategic Overview

The Generation Challenge Programme was founded to harness the intersecting revolutions in molecular biology, bioinformatics, and communications, and bring together diverse institutions to nourish the biological knowledge base of genetic diversity and genomics, and from that, develop practical applications for plant breeding towards improved germplasm for marginal environments. Improving genetic gain under drought conditions has been identified as the area of focus for the GCP.

In its first year, the GCP cast its net wide to identify scientifically excellent projects that could lay a general foundation for meeting the GCP's technical objectives. In 2005, it became clear that a strategy was needed to guide the

integration of ongoing and new activities toward measurable medium- and long-term goals. A draft of the GCP Strategy was presented to the Programme Steering Committee at its November 2005 meeting. The draft GCP Strategy unveiled a new framework for GCP activities, visualised as a matrix of 'vertical' and 'horizontal' activities. On the matrix, horizontal activities address cross-cutting biological questions at different levels of plant architecture and across a broad set of crops, to promote the development and refinement of methodologies and resources. Vertical activities target a very limited number of traits in as few as one crop and are aimed at producing outputs to be used directly in plant breeding. As of the writing of this Annual Report, the GCP Strategy is undergoing revision and is expected to be published in mid-2006.

Perhaps foremost among the shifts in 2005 was an increased scrutiny and emphasis on product delivery, embodied by the development of the GCP's delivery strategy. One of the major tasks of the delivery strategy is to strictly define what GCP products are and who the users of those products are. There are many steps on the path from research and discovery in the areas of genetic diversity and genomics to applications in farmers' fields, and it is not feasible for the GCP to cover all of that territory on its own. Other institutions should and must actively participate in the development and delivery pipeline. Within that context, the GCP defined its products as "any output from any research stage, designed to meet the demands of an identified set of users." "Users" are defined as "anyone who uses a product developed by the GCP." Deceptively simple upon first glance, these definitions of "product" and "user" require a commitment by the GCP to identify and match specific products to specific users, thus ensuring that (i) projects are conceived and planned with a product and user in mind, and (ii) that the designated users contribute to the overall development and delivery pipeline by using GCP products to develop other products geared to farmers' needs.

In the delivery strategy, Generation also commits itself to capacity building for the first tier of users of GCP products, as those individuals often need training before they can effectively utilise GCP products. Although the GCP will not provide finished varieties to farmers, through capacity building it can help ensure ultimate benefits for farmers. Because the GCP is slated to close shop in 2013, the ability of collaborators to carry the work forward is essential for medium- and long-term impact.

First Products

Only two years into this Challenge Programme, the first GCP products are already being delivered. The GCP has 22 mandate crops[1] and, thanks to having established a network of committed partners, researchers now have access to the major sources of genetic diversity for all of them. The genotyping and analysis of these crops (up to 3,000 accessions of 21 crops were analysed with different sets of about 50 SSR markers) was a central GCP activity during 2004 and 2005 which produced a massive set of data representing the first large-scale look at the genetic diversity of so many staple crops. The data was generated using standardised protocols and the same set of markers for each crop, which the GCP calls 'Microsatellite Kits.' Once published (in 2006, online and in hard copy), the Microsatellite Kits will allow researchers at any institution anywhere in the world to evaluate the genetic diversity of their germplasm collections or breeding material and reference it with that of respective collections in CGIAR and other national gene banks. This has direct and important applications for plant breeding.

But even given the information now available from the GCP's work, many institutions that would like to better characterise their germplasm do not have access to the equipment or expertise needed for such endeavours. The GCP established a genotyping support service in late 2005 to facilitate this by providing training in genotyping methods and protocols and assistance with data production and analysis. Institutions using this service can evaluate their germplasm against the GCP reference germplasm, which yields benefits for them and the GCP: they can see where their collections are situated within the global scope of diversity for the crop; in turn, the data from the outside collections can help verify the diversity captured in the GCP global reference sets. Taken together, the Microsatellite Kits and the genotyping support service demonstrate that GCP 'products' can have direct impact on breeding activities within and outside the GCP.

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

Progress Report on Generation Challenge Programme 2005 Activities

Research and Capacity Building

In 2005, research activities accelerated greatly. Early in the year, letters of award for the 17 competitive grants and roughly 50 commissioned projects were issued to the principal investigating institutions. Initiating GCP research projects, with the many new partnerships and collaborations that were formed, was a considerable undertaking. Some projects got off to late or slow starts due to a range of problems: funds arriving late as a result of delays in delivering institutional financial reports, contracts, or subcontracts; changes in designated partners; or because 2005 work relied on as-yet-uncompleted 2004 work. A number of project management policies were developed or revised throughout the year to respond to these issues. Despite the unforeseen problems, the majority of projects started on schedule, and significant results were reported at the Annual Research Meeting in September 2005.

The GCP's competitive grants scheme is intended to attract the best science to the Programme, and in the first round of competitive grants this was achieved through a broad call for proposals that encouraged diverse ideas for scientific innovation. The second round of GCP competitive grants will open on 15 February 2006. The new call for proposals for competitive grants was based on the principles put forth in both the draft GCP Strategy document and the delivery strategy.

In accord with Generation's efforts to streamline its research portfolio, the second call for proposals is targeted toward five "thematic research areas." This should still attract the best science and scientists to the Programme—now that the GCP has established its reputation for quality—but will also narrow the GCP's research focus to a more manageable scope considering resources available. Each new competitive grant will be required, with the support of the GCP and external experts, to develop a detailed delivery plan, including capacity building activities needed for product delivery to the users.

The 2005 commissioned research portfolio provided cohesion to the GCP's agenda of scientific activities. Many of the new projects for 2006 grew out of the 2005 projects, and thus ensure continuity in the research while building linkages among projects. New 2006 commissioned projects include important and exciting research in the fields of allele mining, genomics, and gene discovery. The list of 2006 projects may be found in the appendices of this document. Scientific results and progress achieved in 2005 in the competitive and commissioned research projects is presented in detail in the Subprogramme Updates section of this report.

Capacity building embedded in the research activities is strongly encouraged in both the competitive and commissioned project schemes. A system for tracking the beneficiaries of project-based capacity building was implemented in 2005 in Subprogramme 5, and the fellowship and travel grant schemes of the GCP will target supporting more of such activities in 2006. The GCP Training Programme also began in earnest this year, with courses on plant genetic diversity and marker-assisted breeding offered in three regions (Asia, Africa, and Latin America) to NARS scientists, along with courses on project proposal development, also offered in the three regions.

The GCP Strategy: Integrating Scientific Strategy with a Delivery Orientation

Development of the GCP Strategy paper

The diversity in the GCP research portfolio is one of its unique assets. But the other side of this coin is that the Programme's focus and priorities can become diffused. The need to consolidate the research agenda around key topics in order to deliver real products in the short and long term is clear. Addressing this issue was an immediate and high priority for Generation's new director, Jean-Marcel Ribaut, when he came on board in mid-2005. The strategy document, which focused on this point, was developed by the GCP Management Team over the course of several months, culminating in a drafting meeting in Mexico in October 2005. The draft, submitted to the Programme Steering Committee at its November 2005 meeting, articulated the raison d'être of the GCP in the international agriculture context, defined how the research portfolio is organised around an activities matrix, and presented the criteria developed to ensure the application of GCP activities to plant breeding objectives. To aid in priority setting, the GCP is currently conducting a survey of the available resources in all of the GCP crops across the horizontal and vertical spectrums. Guided by the outputs of the survey, the strategy document is expected to be finalised at a Management Team meeting in April 2006.

Delivery strategy

Year 1 (2004) was a frenzy of organisational activities for the GCP: setting up the administrative and governance structures, developing the competitive grants programme, establishing the commissioned research scheme, and presenting the GCP concept to donors and partners to attract funds and the best scientific expertise to the consortium. In Year 2 (2005), discussions got underway to evaluate how well those structures work for furthering our research goals and how to sharpen the focus in the research portfolio to ensure impact during the life of the GCP. The delivery strategy began to take shape in April 2005, when an electronic forum was established with a group of willing volunteers (ranging from delivery experts, intellectual property specialists, economists, anthropologists, to research scientists) to discuss if and how the GCP should deliver products. The outputs of the e-forum fed into a workshop in Cali, Colombia, in July 2005, where principles for the GCP's delivery strategy were developed, including how the GCP defines "product," who the users of GCP products are, and the mechanisms necessary for ensuring delivery: product delivery plans and targeted training. Many outside observers and stakeholders, as well as the Management Team, reviewed the draft strategy and added their perspectives and refinements. The GCP delivery strategy and implementation plan documents were presented to the Programe Steering Committee in November 2005 and were approved.

Partnerships and Communications

Partnerships

Although interactions with potential new partners were limited this year, due in large part to the transitions the GCP underwent, some key alliances were identified:

- **Global Crop Diversity Trust.** Both the director of the Trust and the GCP see a win-win situation in aligning the Trust and the GCP in some way. The missions of the two institutions are complementary, as the Trust promotes the conservation and availability of crop diversity while the GCP promotes the use of the diversity using modern biotechnological tools. A formal alliance is under development.

- **International genomics initiatives.**
  - **Génoplante** is a major partnership programme in plant genomics, which links public research in France and several private partners. The identification of genes involved in drought tolerance is one of their major objectives. The GCP approached Génoplante about the possibility of a first phase of partnership entailing information exchange and links to our respective databases, and in the future, to seek opportunities to consolidate our research agendas when possible and mutually beneficial.

  - **Grain Legumes Integrated Project** (GLIP) is a large multinational project, co-funded by the European Commission FP6 Framework Programme, striving to develop new strategies to enhance the use of grain legume crops in food for human consumption and animal feed in Europe and beyond. Because GLIP and GCP share research objectives and are employing complementary approaches, there is clearly room for collaboration. The GCP plans to become a member of Grain Legume Technology Transfer Platform (GL-TTP) in 2006. Doing so will allow the GCP to participate in GL-TTP planning activities, identify new partners in the legume community, and have access to fresh sources of genomic information.

  - **US genomics initiatives** were represented by Dr. Larry Beach, USAID biotechnology expert, at the GCP Annual Research Meeting in Rome this year. Collaboration with one or more of those initiatives will be explored actively in 2006.

- **Regional molecular networks.** Several crop-specific biotech networks have been established in Asia, Africa, and Latin America. These represent a significant investment in terms of infrastructure and human resource development by national programmes as well as international funding agencies, and have resulted in a skilled cadre of national research scientists. These existing networks present an excellent mechanism for GCP efforts to validate and apply its new technologies in national breeding programmes. Representatives of several regional networks (AMMANET, AMBIONET, and ARBN) were invited to participate in our 2005 Annual Research Meeting to present their networks and learn more about the GCP. The desire of the GCP to build on these networks resulted in a commissioned project ("Molecular Breeding Communities of Practice") that will be initiated in 2006.

- **Provisional GCP Consortium members.** The Programme Steering Committee offered provisional membership[2] to four new organizations at its November 2005 meeting: INRA-Morocco, CINVESTAV-Mexico, BIOTEC-Thailand , and the Istituto Agronomico d'Oltremare (IAO) of Italy.

[2] Provisional membership provides all benefits of full membership except for membership on the Programme Steering Committee, because the GCP Consortium Agreement is under review and there is no document currently for new members to sign. Once any changes to the Consortium Agreement are ratified, the provisional members will be offered full membership and will then be able to participate fully in GCP activities, including PSC membership.

Communications

Communications plays a critical role in the operation and growth of the Generation Challenge Programme. A major communications objective that all members and affiliates of the GCP contribute to is establishing Generation as an important player and partner-of-choice in the global research community. To that end, the GCP sponsors a session at the Plant and Animal Genome (PAG) Conference every year and supports key symposia and workshops that relate to GCP areas of interest. The GCP director and subprogramme leaders participate in various international and national conferences, in addition to PAG, as GCP emissaries.

In 2005, the communications unit served as the project office of the GCP, drafting and distributing contracts, fielding queries from project offices at partner institutions, and proposing project management policies as needed. In 2006, these activities will be assigned to the new Project Officer.

The communications unit is responsible for several broad areas of activity. Objectives and outputs for 2005 in GCP communications are as follows:

Information flow within and outside the GCP

- E-newsletter: a periodic compilation of announcements of interest, GCP events, training opportunities, etc., was distributed to all GCP member scientists, partners, and many stakeholders (distribution list contains over 1,200 contacts)
- Contacts database: The communications unit developed and maintains a growing database of over 1,200 GCP affiliates, partners, potential collaborators, and others who have expressed an interest in the Programme.
- Point of contact: with few full-time staff at GCP headquarters, the communications unit is the logical entry point for newcomers as well as GCP members.

Public awareness for target audiences

- GCP Website: the communications unit is responsible for the development and maintenance of the Generation website (www.generationcp.org), which serves as the virtual library for GCP official documents as well as the public face of the GCP. The site receives over 4,000 hits per month.
- GCP in the news: the communications unit responds to requests for news bulletins, etc., and pursues opportunities for GCP features, interviews, and other mentions in various media outlets.
- GCP public awareness materials: the GCP brochure, folder, poster, bound reports, and other items were distributed to thousands of people in 2005.
- Targeted public awareness materials for international conferences, specific campaigns, etc.: the communications unit provides the service of developing materials about GCP themes or activities for outside events.

Packaging and communication of GCP products

- GCP products: the communications unit constructs web pages and publications to distribute and publicise GCP products such as informatics tools, training materials, protocols, and other useful information.
- Programme reports: the development of the Annual Report, Medium Term Plan, donor proposals and reports, and all other official GCP documents are coordinated by the communications unit.

Project and Product Management Policies

Several key achievements in the area of IP and policy were made in 2005:

- **Reporting requirements and templates established for all projects.** The GCP reporting schedule and templates for reports were developed and institutionalised in 2005. All projects must submit two technical updates per year (15 May and 15 October are the deadlines) for approval by the relevant subprogramme leader and must submit a final technical report upon completion of the project. All projects over $250,000 per year will also submit a yearly substantial technical report (31 December deadline). Financial reports are due up to 45 days after 31 December each year. Project funds for subsequent years will not be disbursed until technical and financial reports have been approved by the subprogramme leader.

- **Data production and availability.** Sharing data in a suitable and timely fashion is vital to the success of the GCP. Starting in 2006, all project proposals must include a section outlining what data is to be produced, in what format, and where it will be released upon the end of the project. A specific clause in the new contractual agreements requires the principal investigators to produce and share data as stated in the approved project proposal.

- **GCP Advisory and Review Panel.** To implement stringent quality control of the science conducted within the GCP, the Management Team identified the need for a consultative team of external reviewers to comment on the activities reported during the Annual Research Meeting and help reinforce the Management Team's strategic decisions about research. The Advisory and Review Panel is also the mechanism for the Management Team to bring in respected peers with outside perspectives to the strategic planning process and to employ them as reviewers of the commissioned project proposals.

- **Humanitarian use agreement.** The GCP consortium agreement provides that intellectual property developed by a GCP consortium member or supporting participant is the property of the institute that developed the IP. This is standard practice in joint research arrangements. However, in order to ensure that IP resulting from such research can be used for the purpose for which the work was funded, it is also a standard practice for the parties to agree that the resulting technology can be used for certain, specified purposes. Therefore, each Consortium Member has a non-exclusive, royalty-free right to use Challenge Programme IP for the activities with the aim to provide technology and products to the resource-poor on a royalty-free basis. The GCP Humanitarian Use agreement, approved by the Programme Steering Committee in 2005, will be used in developing new agreements with non-consortium members.

- **Contractual agreements streamlined.** A contract was developed to allow the GCP to enter into agreements with non-consortium members, which was necessitated by the second call for competitive grants that will allow non-GCP consortium member institutions to serve as principal investigator on projects. Subcontract templates that GCP members and non-members can use for their subcontracting needs were also developed, one for small amounts of funds (for "services") and one for larger amounts, both of which require the subcontracting party to adhere to the GCP's IP policies.

Subprogramme Updates

Subprogramme 1: Genetic Diversity of Global Genetic Resources

Introduction

Subprogramme 1 focuses on identifying novel, diversified, and superior variants of genes involved in target traits. Subprogramme 1 activities are closely linked to SP2 outputs, and like SP2, SP1 outputs are aimed at direct applications in Subprogramme 3. In accordance with the GCP's global priorities, particular emphasis is given to drought tolerance.

Objective

Access to sources of genetic diversity that may supply genes and alleles involved in key agricultural traits is essential to the mission and objectives of the GCP. Through our network of consortium members and partners, vast germplasm collections are available to the GCP, but to unlock the genetic diversity present in those collections, the structure of the collections must be understood through coordinated surveys of molecular and phenotypic variation. With hundreds of thousands of accessions across 22 crops collected in gene banks around the world, high-throughput molecular screening techniques must be developed to genotype the collections for fast results. Appropriate screening techniques to phenotype the collections for traits such as drought tolerance also need to be developed and applied to obtain reliable and analysable phenotype descriptions accompanied by the associated descriptions of environmental and weather conditions. Once the genotypes and phenotypes have been established, association studies and/or population genetics approaches must be conducted to illustrate their interactions.

Rationale

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

Characteristics/uniqueness

The GCP, and SP1 in particular, deals with the global genetic diversity of the main food crops, which hold a wealth of information important to all of humanity. This alone helps mobilise the interest of diverse research communities of the GCP's activities. SP1 coordinates an international network of laboratories, requiring development of and adherence to standards for data collection and analysis to ensure efficient communication and extrapolations from the data. Inevitably SP1 suffers tension between exhaustivity and focus, which requires fine-tuning. By covering a wide range of crops, it allows transversal approaches with high potential added value, by making use of homologies among orthologous genes, for example. By focusing on a single generic feature across a diversity of biological systems, SP1 enriches our understanding of the various mechanisms that translate to more tolerance to drought.

Major achievements

- *Genotyping of eighteen crops has progressed significantly*. Reference samples optimised for future integrated characterisation efforts are being profiled, which will enable identification of favorable genes, alleles, and chromosome segments for inclusion in breeding programmes.

- *Molecular characterisation methods developed*. These methods enable scientists from NARES to compare their own germplasm to an international reference.

- *Alternative molecular methods exhibit potential.* Assessment of alternative molecular methods identified the potential of using the simple agarose gel system for the application of EcoTILLing in SNP discovery/survey and the power of the DArT technology.

Activity report

Like the other subprogrammes, SP1 is composed of a number of contracted projects, including some commissioned in 2003 and started in 2004, and some initiated in 2005 after a competitive process. Most of the concrete results are derived from the projects initiated in 2004, whereas those started in 2005 have focused on organisational matters and production of specialised resources and have only started yielding outputs at the time of writing this report (November 2005). Therefore the outputs below outline a quantitative progress of projects started in 2004 and a quick, qualitative survey of the projects started in 2005.

Structure of the diversity in germplasm collections

SP1 has undertaken systematic work on the crops where the CGIAR has active breeding programmes. The work started in 2004 for eleven crops and in 2005 for another seven. The main initial undertaking in SP1 has been the genotyping with SSR markers of representative germplasm samples, which laid the foundation for the whole GCP. The data serve for identifying reference samples which will be the materials of choice for integrating further molecular and phenotypic characterisations.

For each crop, a first step consisted of collating information on various existing collections in order to apply a simple rationale for extracting a representative sample (the "composite set"); this is coordinated by the International Agricultural Research Centres in charge of each crop and has been completed for all 18 crops. The size of the sets depends on the number of resources globally available in the collections, ranging from several hundred accessions to a maximum of 3,000 for the most important crops.

A second step consists of characterising the composite set with molecular markers in order to reveal the structure of the diversity and to extract a reduced sample (the "reference sample") that will be made available for additional characterisation and evaluation in order to reveal functional correlations. This is in progress for 18 crops.

Given the variability of steps in the task, the heterogeneity of progress between crops, and the implications of including diverse partners, reporting on these activities has been a bit disorganised. It is planned to have a final report for all crops in the form of a collective publication with detailed standardised descriptions of polymorphism and its implications. This will be an important landmark and asset. Despite the shared difficulties to follow the planned calendar, very large amounts of data have been produced and will be sufficient for refining smaller germplasm samples with enhanced representativeness. These reference samples will be made available and distributed to collaborators worldwide.

In addition to the above mainstream activity, molecular characterisation of genetic diversity is being practised within several competitive projects. One example is that of a project led by CIMMYT called *Development of informative DNA markers through association mapping in maize to improve drought tolerance in cereals*, where both neutral markers (SSRs and SNPs) and candidate gene allelic sequences are being used on a set of tropical maize inbred lines. Another example is that of the project led by CIAT titled *Exploring natural genetic variation: Developing genomic resources and introgression lines for four AA genome rice relatives*, which uses both SSRs and SNPs for monitoring interspecific introgression. The latter is an example of additonal mobilisation of gene sources by broadening the genetic base of the pools accessible to recombination and breeding.

Molecular characterisation of composite sets in GCP crops

Crop	Lead institution and partners	year start – end	Core sample genotyping target N acc. x N loci	Genotyping % nov-2005
Rice	IRRI-CAAS-CIAT-WARDA-Agropolis	2004-2005	3000 x 50	70
Maize	CIMMYT-CAAS-IITA-Agropolis	2004-2005	1775 x 50	70
Wheat	CIMMYT-CAAS-ICARDA-Agropolis	2004-2006	(2600 + 400) x 50	60
Sorghum	ICRISAT-Agropolis-CAAS	2004-2006	(700 + 2300) x 50	50
Barley	ICARDA-CAAS	2004-2006	(500 + 2500) x 50	50
Common bean	CIAT-Embrapa	2004-2005	3000 x 50	60
Cowpea	IITA	2004-2005	2000 x 50	30
Chickpea	ICRISAT-ICARDA	2004-2006	286 + 2714	60
Cassava	CIAT-Embrapa-IITA	2004-2005	3000 x 36	60
Potato	CIP	2004-2005	1000 x 50	80
Musa	IPGRI-IITA-Agropolis	2004-2005	960 x 50	30
Finger millet	ICRISAT	2005-2006	1000 x 20	20
Groundnut	ICRISAT-Embrapa	2005-2006	1000 x 20	50
Pigeon pea	ICRISAT	2005-2006	1000 x 20	20
Lentil	ICARDA	2005-2006	1000 x 30	20
Yam	IITA	2005-2006	350 x 20	20
Coconut	Agropolis	2005-2006	1000 x 22	80
Sweet potato	CIP	2005-2006	500 x 50	20
Pearl millet	ICRISAT	2006	to be determined	-

Assessment of molecular characterisation methods
Other technologies that compliment standard molecular characterisation for elucidating germplasm structure (such as SSRs) will be very useful if proven efficient. Single Nucleotide Polymorphisms (SNPs) are the markers of choice for those crops where massive sequence data are available, such as ESTs from diverse germplasm. The quick evolution of SNP detection technologies and the present relative efficiency of resequencing versus setting up SNP detection suggest that it is wise that the GCP remain an observer of the technology for the time being. Contacts are being made to try to build alliances with high capacity partners, both for allele resequencing (SNP discovery) and for SNP detection (both as neutral markers or within candidate genes). Several competitive projects include work on SNP discovery and detection, both in rice, led by CIAT for monitoring interspecific introgression, and for maize, led by CIMMYT for developing association studies using candidate genes.

Along another line, work is ongoing in barley within a competitive project led by ICARDA called *Allele mining based on non-coding regulatory SNPs*. Reciprocal F1 hybrids are being produced to serve for testing the efficiency to identify cis-regulatory elements through allelic imbalance assays. A set of 70 stress responsive ESTs were identified and primers designed. SNPs were already identified and verified in 12 of them.

For the crops without much sequence information, SP1 is assessing EcoTILLing and Diversity Arrays Technology (DArT). EcoTILLing is used to identify SNPs in diverse germplasm pools without the need to sequence many genotypes. The pilot project is run by IRRI, which has advanced experience in rice, and adaptation work is being done at Agropolis for sorghum and banana (triploid). Primers were designed for a set of 16 tentative candidate genes given in the proposal; unlabelled primers have been obtained and the amplification efficiency was confirmed for 12 of them. Labeled primers for use on the LiCor have been obtained and verified for 6 genes. A modified procedure has been established that uses agarose gels and is therefore much more easily transferable. Ecotilling data have been generated for rice on 10 genes in over 330 accessions. Unfortunately the efficiency of the rice primers for amplification on sorghum (despite favourable homology) and *Musa* (no homology information) is poor, which will force the project partners to define species-specific primers.

DArT represents a potential platform for whole genome profiling in orphan crops. The work has several components, which have been completed at the end of 2005. A hundred accessions have been selected for each of sorghum, rice, and wheat, and existing DArT arrays are being hybridised. This is being analysed for testing the comparison of the diversity revealed with DArT to that revealed with SSRs; the data produced for sorghum and rice consist of matrices of 92 accessions and 516 polymorphisms out of 6144 clones spotted and 90 accessions x 519 polymorphic markers for rice also out of 6144 clones spotted, respectively. In cassava, the DArT technology has proven efficient to reveal numerous polymorphic markers using cultivars and wild relatives (Xia et al, 2005). A scientist from Thailand has started a nine-month stay at DArT Pty Ltd in Canberra, Australia, to prepare new libraries and extend the analysis to a large number of cultivars, focusing on accessions with large variation for dry matter content (DMC). Libraries are being expanded. The potential of the method is being explored on coconut and banana in collaboration with Agropolis, where a scientist from Sri Lanka (Coconut Research Institute) will spend six months conducting the testing. Several complexity reduction methods were tested and one promising method has been identified (PstI/BstNi). The work on banana started in early September when a scientist from France joined DArT for a three-month stay. Two arrays bearing 9216 clones have been built for coconut and four arrays bearing 3072 clones for banana. Initial diversity surveys for coconut (31 acc x 128 polymorphisms) and for banana (48 x 332) suggest high concordance with other types of markers.

Optimising the assessment of drought tolerance
The backbone of this activity consists of optimising access to efficient coordinated multilocal phenotyping platforms, supporting the evaluation by environment descriptions and whole plant modelling activities, and drawing experience from advanced physiological characterisation performed in crop-specific projects. *A Drought Tolerance Phenotyping Network*, coordinated by Embrapa, is being put in place and reinforced for integrating materials of international origin for evaluation. The initial phase of this project was used for purchasing or upgrading of various requisite equipment. The two groups involved in the Drought Phenotyping Network (coordinated by Embrapa) and in Whole Plant Modelling (coordinated by Cirad) met in May 2005 at Embrapa/Rice and Bean in Goiania, Brazil, in order to set the planned collaborations. They had further exchanges at the Annual Research Meeting in September. Priority crops considered by the project are upland rice, maize, and sorghum. The regions considered by the project will be: (i) Brazil, Piaui, Tocantins, Goias, Minas Gerais, and possibly Mato Grosso ; (ii) West Africa, sub-saharan region for sorghum and possibly upland rice crops ; (iii) Central America for maize crop (to be confirmed). Environmental analysis will be carried out in all these regions and for each crop, provided that the required data sets are available. A scientist from Embrapa is in charge and will collect necessary meteorological and soil data with support from all institutions participating, according to the site and country where they are stored. He will work in Cirad, Montpellier, from September 2005 to August 2006. He will spend two months at CSIRO in

Australia in 2006 in order to be trained on Apsim model and clustering tools. Another scientist from Embrapa will be trained at Cirad on SarraH model in November 2005 and will build a specific model for maize. Another scientist from Embrapa Meio Norte will also be trained in late 2005 or 2006, for specific adaptation of the model to cowpea and legume. At the end of the project, a general training course for Embrapa scientists will be organised by CIRAD, CSIRO, and Embrapa.

For fine phenotyping to be carried out, five accessions from the GCP reference samples will be selected. Different cases are identified:

- upland rice : complementary experiments conducted in Porangatu, Terezina, and Goiania during rainy and dry seasons
- maize : possibly (to be confirmed) complementary experiments in Terezina, Sete Lagoas, and Janauba
- sorghum : complementary experiments conducted in Janauba, Sete Lagoas, Goiania, and/or Porangatu during rainy and dry seasons. Existing data for West Africa will be exploited.

Numerous trials are going on and materials from the GCP reference samples can be integrated as they are identified and made available.

Meanwhile, a pioneering competitive project led by CIMMYT has started a large scale evaluation of over 400 hybrids of maize in relation to drought stress in diverse environments. In addition to the practical experience of widespread exchange and characterisation, the group performs assays of glucose and sucrose, ABA and ABA-glucose ester, as well as phaseic acid and dehydrin on leaf samples and silk samples.

Towards relating genotype to phenotype

Relating genotype at molecular markers (i.e., a molecular polymorphism) to phenotype for important traits can rest on direct functional involvement of the molecular polymorphism in the trait or on indirect association through linkage disequilibrium (LD) between the marker and the causal functional polymorphism. Therefore the extent of LD in a crop is essential for interpreting the meaning of statistical associations and for determining which populations can be used to map/reveal favourable genes and alleles through association studies. It is being monitored at the whole species level in two contrasting species, namely the annual autogamous sorghum and the perennial allogamous coconut, as well as in specific populations of rice in Indonesia. The study of 12 RFLP marker loci in a single region of about 5 cM in sorghum has revealed significant LD spanning 2 to 3 cM. It also exemplified how important it is to refine the reference sample before undertaking association studies. In coconut, a method has been refined to assess the level of LD in this highly heterozygous species. Two closely linked SSR markers (ca. 1 cM) display strong LD in populations (namely Mozambique, Panama, Vanuatu, and Brazil) where unlinked markers displayed none; data are being produced for another eight couples of SSR loci linked at 0 to 7 cM. In rice, the study focuses on three regions bearing disease resistance genes. A researcher from Indonesia came to Cornell for training for 4 months (April-July 2005). A total of 250 PCR primers have been designed, 60 in the *Xa7* region on chromosome 6, 60 around *Xa13* on chromosome 8, and 130 around the cluster *Xa4/Xa22/Xa26* on chromosome 11. Sequences from the 8 diverse Indonesian rice accessions have been generated for 215 primer pairs. Seventy five of the sequences from the 8 rice accessions have been aligned and SNPs have been called; 41 SNP detection primers have been designed.

Simultaneously, as an attempt to integrate association studies in the course of ongoing characterisation and breeding activities, similar exercises of LD assessment are ongoing for additional cases where accurate phenotypic data are available for materials amenable to LD-based mapping. These are: the cassava breeding programme at CIAT; the potato breeding programme at CIP; the banana breeding programme at CARBAP, Cameroon; the coconut breeding programme at VARTC, Vanuatu; and the yam (Dioscorea alata) germplasm evaluation programme at VARTC, Vanuatu. In the former three species, the possibilities for choosing the best materials have been analysed. Various options still exist; the assessment of the level of LD will be of primary importance. The case is more clearly defined in coconut, with materials consisting of 200 trees representing four generations of breeding materials. A total of 219 trees have been sampled in VARTC and DNA has been extracted. They are being analysed by a scientist from Sri Lanka during a training session in Montpellier in September-November 2005. A total of 31 loci will be surveyed, including 13 international reference markers and 9 couples of linked markers. In addition, a coconut breeder from Vanuatu will visit CIRAD in November for a three-week training session on DNA extraction, principles and applications of molecular breeding, and data management. For yam, the idea is that the insular history may have involved bottlenecks that have established strong LD in the well-characterised populations of Vanuatu; a mapping exercise is being undertaken to identify linked markers among the already used AFLPs for quick assessment of LD.

Coordination, planning, and capacity building

In August, SP1 held with SP5 a workshop on *Molecular markers for allele mining*. The workshop was held in Chennai, India, at the MS Swaminathan Research Foundation and gathered 39 participants, including 37 scientists. It was meant to review the progress of the various projects, explaining both scientific issues and managerial issues, providing the SP1 community a good opportunity for internal coordination while exhibiting scientifc discussions as well as a range of problems to three

groups of scientists: representatives of the System-wide Genetic Resources Programme (SGRP), which is composed of germplasm bank curators; experts in the fields covered by SP1 and coming from advanced laboratories outside the GCP; and senior scientists from various NARS, personally involved in SP1 related research field.

Several other workshops have been held within more specific topics, such as *SNP discovery through EcoTILLING* (15 trainees from NARES attended, from Asia), *DNA marker technology for crop improvement* including allelic imbalance assays (20 participants from West Asia and North Africa), and *Characterisation of genetic diversity of maize populations: documenting global maize migration from the center of origin*.

Lessons learned and conclusions

- SSR genotyping of large numbers of accessions is difficult. An initial target had been set for each crop and was often distributed among several partners. After two years of experience, it is clear that these targets will generally not be met in the planned calendar year, with expected completion rates between 50 and 100%. This is due to a range of diverse causes linked both with local supply and services difficulties and with transversal difficulties for exchanging biological materials and for comparing protocols and results. The lessons learned will help elaborate and promote a collective approach for optimising high throughput molecular characterisation in international agricultural research. Local difficulties for access to supplies and services would justify concentrating the work in a limited number of laboratories with critical mass and better negociating capacity.

- Exchange of biological materials has slowed down or hampered fluid processes. An important factor for initial delay, and ultimately incomplete data matrices, have been the restrictions on exchange of seeds, or even DNA, involving the NARS partners within the GCP. This suggests that the same problem will surely occur among a wider circle of NARS and requires both political action at the whole GCP level and beyond and adaptation of the proposed practices, keeping with the founding spirit of the GCP.

- Next to IP issues, the impact of constraints like the quarantine requirements on coordinated phenotyping perspectives needs to be assessed on a crop by crop basis.

Perspectives for 2006

The availability of reference samples will hopefully soon attract large integrated phenotyping initiatives. A mechanism for further enriching them from subsequent rounds of light molecular characterisation in global collections must be worked out.

The capacity for phenotyping in relation to drought will be surveyed and mobilised. The GCP is supporting the reinforcement of some capacities. Others exist throughout the GCP consortium and its partners, which need to be accurately inventoried for the best collective use.

Neutral markers are playing an important role in elucidating the structure of diversity. Their potential for connecting distinct batches of germplasm in different studies will help optimise access to global diversity. Moreover they may be very useful for LD-mapping. On the other hand, potentially functional markers will become more and more useful with the advent of longer lists of better candidate genes. Optimising the global capacity for genotyping is essential and must be centralised at high throughput facilities and regionalised at medium throughput facilities, and must provide mechanisms for access by the largest community of breeders and germplasm practitioners. Contacts have been taken with one high throughput public facility, the French National Genotyping Center (CNG), Evry, for allele resequencing at orthologous candidate genes in several crops and for large scale SNP detection.

The momentum in the GCP must be aimed toward field practitioners. The studies of materials within breeding programmes enable the determination of the best value of existing materials and phenotypic information. Their generalisation will be facilitated by the development of a genotyping support service, through which NARS partners will have quick access to genotyping capacities available in the GCP for characterising their information-rich germplasm populations.

The germplasm presently considered for analysis and for breeding can be widened by genetic base-broadening activities, which will help exploit previously untapped resources, assisted by the dissection power of molecular methods.

Subprogramme 2: Comparative Genomics for Gene Discovery

Introduction

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

Objective

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

To meet these objectives, Subprogramme 2 is designed to maximise the use of genomic and genetic resources available in the research community. We support the production of specialised stocks that will elevate the level of genetic research in different crops. We apply comparative approaches to leverage genetic knowledge from multiple plant species to investigate and validate gene functions important for stress tolerance. Multi-disciplinary teams are formed to apply the validated genes in breeding programmes.

Rationale

Since the inception of the GCP, there has been continued growth in sequence information across all plant species. The high-quality rice genome sequence is now complete, and the maize genome sequence is expected in the near future. Multiple genome-wide gene expression platforms in plants are available. It is increasingly feasible to use gene content (sequence information) rather than gene order as the entry point to identify orthologous genes and determine their functional relationships between species. Furthermore, from human and medical genetics, the power of SNP haplotypes and association genetics to identify functional genes is now well demonstrated. Subprogramme 2 strives to absorb the new knowledge gained in the wider research community and to adopt new approaches where appropriate.

Characteristic/uniqueness

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

Major achievements

- *Successful resource leveraging*. The assembly and development of specialised genetic and genomic resources have mobilised many players to contribute to the objective. This activity has brought together not only resources but also intellectual power from leading institutions. The rice mutant network is one concrete example where the GCP has linked multiple laboratories to apply the mutant resources developed by multi-million dollar investments in different countries. As information of flanking sequence tags (FST) continues to expand, it will eventually enable the identification of mutations of most plant genes.

- *Conserved markers to link different maps.* The use of orthologous markers to link different species maps has the dual benefit of integrating functionality and genomic positions (at least within a crop group), which will be an important long-term tool for using comparative genomics to identify common genome regions controlling target traits. The development of marker systems that can be used across several species would greatly strengthen the comparative framework.

  Despite initial difficulties, positive progress is seen in the development of conserved markers to link different species (within the dicots and the monocots). Currently two projects (*Validation of conserved orthologous markers* and *Targeted Musa genome sequencing and frame map construction)* are involved in the identification and testing of conserved orthologous markers. NIAS, leader of the *Musa* project, has a strong sequencing and informatics capacity that could help address some of the difficulties of developing COS markers. We expect more progress from the marker projects through use of information being generated by the research community at large and greater international linkages.

- *Genome-wide expression analysis reveals new candidate genes.* Positive results are seen from experiments using genome-wide expression as a means to identify candidate genes with contributions to target phenotypes. Such work seems particularly fruitful when integrated with mapping data. High-quality gene expression data have been generated using available rice oligo chips from NIAS (22K) and the Beijing Genomics Institute (60K) to correlate gene expression with genetic regions expressing QTL or mutant phenotypes. As gene chip technology becomes more robust and accessible for more species, integration of QTL and expression analyses will become routine for narrowing the choice of candidate genes and determining the causal relationships between expression and phenotypes.

- *Isolation of large QTL to give gene-based markers.* We expect early successes will come from the cloning of gene loci with relatively large phenotypic effects. Progress in the fine mapping and near-isolation of tolerance genes to aluminium toxicity, phosphorus-deficiency, and salinity are encouraging. Clearly the GCP is not the sole contributor to this research, but with its strong emphasis on turning good science into solutions, the GCP has accelerated the applications of the research and forged alliances among partners that may not have happened otherwise.

The cloning of the aluminium toxicity tolerance gene in sorghum will hasten the development of elite breeding lines. While waiting for validation of candidate genes, markers tightly linked to phosphorus uptake efficiency are being used in selection programmes to combine traits suitable for the drought-prone environments in Indonesia. This brings about at least two benefits. First, we can fast-track the delivery of useful genes to breeding programmes to address specific problems that are concomitant with stresses often associated with drought prone environments. Second, this will provide test cases to build the capacity of the community to apply marker-aided selection in breeding programmes.

Activity report

Results of SP2 activities between January to November 2005 are primarily derived from the implementation of the first round of competitive grants and commissioned research in 2005. In some cases, the results represent a continuation of Year 1 commissioned work in the later part of 2004. The work was organised under four main activities that are considered as Projects in the 2005 Medium Term Plan.

Assemble genomics and germplasm resources through consolidating existing (and developing new) specialised genetic stocks and framework genetic markers for target crops

Projects supported under this project focus on adding value to existing genetic and genomic resources and creating new ones when such investment would open new approaches and leverage collaboration. A project was initiated to assemble special wheat genetic stocks relevant for gene discovery and make them available for systematic phenotyping. A Wheat Genetic Stocks Utilisation Workshop was held from 5-7 April 2005 at CIMMYT. A preliminary list of wheat genetic stock candidates (with over 3,300 lines identified), available for distribution and characterisation by the workshop participants, was prepared. It was agreed that stocks currently available (30-50g of seed) will be sent to CIMMYT immediately for further multiplication and phenotypic characterisation.

A network of seven laboratories around the world (Wageningen University, CIRAD, NIAS, IRRI, CAAS, Huazhong Agricultural University, and CIAT) was formed to characterise rice mutants with insertions in candidate stress response genes. This network of laboratories collectively has produced the largest collection of rice mutants in the world providing flanking sequence tag (FST) databases for query of mutations in target genes. Currently, the OryGenes DB (http://orygenesdb.cirad.fr) developed at CIRAD has about 56,000 publicly available insertion sequences tagged by FST sequence on the rice genome sequence as annotated by TIGR. As of mid-2005, this DB was used to search for knockout inserts in candidate stress-associated genes and provided about 22% insertion coverage. These insertion lines have been categorised for phenotyping at CIAT.

Because of the growing evidence of potential roles of non-coding small RNA in regulation of many plant processes (including stress response), the group began a screen for genes controlling small RNA metabolism. Rice orthologs of seven *Arabidopsis* genes involved in the biogenesis of microRNA (miRNA) and short interfering RNA (siRNA) were identified. Insertion lines in these candidate genes were identified in Hirochika's Tos17 mutant collection in Japan as well as in Gyn An's T-DNA insertion collection in Korea. These lines have been assembled for phenotyping under different stress conditions. Using a population of EMS-induced IR64 mutants (about 2,200 lines), DNA pools (8 lines/pool) were produced to screen for mutations by TILLING. So far, from screening four small RNA related genes in 800 plants, a putative variant in SGS3 (*Suppressor of Gene Silencing)* has been identified.

Field-screening of random T-DNA insertion lines under drought stress conditions is underway at Huazhong Agricultural University. Drought stress was applied to rice plants at the vegetative stage (30-45 days after germination) in a sandy field. Within half a year, a total of 4,006 rice mutant families (20 plants each) were screened for drought tolerance at the vegetative stage in the field. Among them, 29 families showed segregation of drought sensitivity and one family showed segregation of drought tolerance. PCR analysis using the hygromycin resistance gene suggested that the mutant plants were positive for T-DNA insertion for all the 30 families. So far, flanking sequences of insertions were available for 10 mutant families. These putative mutants are now subject to a second round of evaluation of drought tolerance at both the vegetative and reproductive stages under well-controlled conditions.

Because plant growth hormones abscisic acid (ABA) and gibberellic acid (GA) play a major role in regulating gene expression during plant development and response to environmental stresses, IRRI has systematically identified mutants showing altered peduncle elongation, dormancy, and sensitivity to ABA during germination. So far 10 mutants with Elongated Uppermost Internode (*eui*) have been identified; the peduncles of these mutants elongate at the rate of 8-12 cm per day, compared to 4-5 cm per day in the wild type. The screen for the dormancy mutants yielded 11 mutants expressing a high level of dormancy (<50% seed germination compared to wild type). From a screen of 1,500 mutant lines for ABA insensitivity, 25 mutants were found to exhibit significant difference in germination, radicle, and shoot growth relative to the wild type. These mutants are now available for more detailed physiological analysis of drought-response traits in other GCP projects

In addition to rice, bean and a true-seed *Solanum* species were selected to produce mutant populations as a permanent resource for gene identification and validation. Multiple accessions of *S. verrucosum* available at CIP and the Scottish Crop Research Institute were examined for purity and homozygosity using molecular markers. The least heterozygous accessions were identified for seed increase and mutagenesis at CIP.

Bean genotype BAT93 was selected for mutagenesis. Pure seeds were produced at CIAT and provided to collaborators at Univ. of Geneva to conduct EMS mutagenesis. Mutagenesis protocol has been worked out at Univ. of Geneva and seed of M1 families were sent to CIAT. The first set of 800 M1:2 plants and the second set of 1,000 M1:2 plants have been or are being screened for phenotypic differences compared to the parental line BAT93. Phenotypic mutants (dwarfing, leaf fasciation, leaf variegation, spindly growth, etc.) have been documented and photographed. A database is being constructed with these photographs and characterisation data.

We expanded available gene/sequence information for stress-response pathways across selected species. Construction of EST libraries for millet (ICRISAT) and cowpea (IITA) was initiated to expand the genomic resources available for sequence comparison and expression analysis. Four cowpea lines, Vu7778 (drought susceptible), Tvu11986 (type I drought tolerance), Dan Ila (type II drought tolerance: stay green) and 12008D (fodder type), were subjected to drought stress and multiple tissue samples (root, stem, and leaf) were harvested for RNA extraction. Collaboration was extended to ILRI to expand the size of the EST dataset. For pearl millet, RNA was isolated from panicles and flag leaves of stressed and non-stressed plants of the two millet hybrids at nearly identical developmental stages. Stressed plants of the two genotypes had comparable levels of transpiration relative to their non-stressed counterparts. Differential EST library development is now underway.

The GCP supports a consortium effort to generate SNP data of multiple rice varieties. The project involves collaboration with Perlegen Sciences, a private company pioneering the use of chip-based technology to "re-sequence" whole genomes of human and other mammalian species. The first stage of this project targets 100 Mb of the rice genome across 15 diverse genotypes. Funding is being sought through partnerships under the International Rice Functional Genomics Consortium to complete the genome coverage and to expand the set of rice varieties to 20-30. As an example, Dr. Jan Leach at Colorado State University, together with TIGR and IRRI, has recently secured a USDA competitive grant to contribute to this effort, demonstrating the power of resource leveraging. All

data from this project will be in the public domain. Similar to the HapMap project (The International HapMap Consortium. 2005. *Nature* 437: 1299-1320), the SNP database will enable the application of association genetics in rice as well as other plant species.

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

Several groups (CIP, Cornell, CAAS, ICARDA, INIBAP, and the Musa Genomics Consortium) worked together on the development of conserved orthologous markers (COS) to facilitate comparative mapping and assignment of function to conserved genes across species. At CIP, 100 COS II (second generation COS markers) primers for candidate genes for disease resistance and drought tolerance were designed with aid from Cornell's SGN database. Primers were screened for polymorphism in subsets of 3 mapping populations of which 24 were polymorphic in at least one cross. DNA of bean (from CIAT) and sweet potato (CIP) were included in the screening and 30% gave clear PCR products. Genotypes of four wild and one cultivated potato species of known resistance phenotype were assembled toward application of COS to understand diversity in germplasm. Mapping and sequencing of products are in progress to validate the identity of the amplicons.

COS identification strategies were reviewed with support from SP4, using the custom BLAST from Paracel and genome annotation tool on the HPC. Further links with SP4 are established via collaboration on the common functional gene catalog. Available annotation tools for metabolic pathways and integration with sequence information were identified (BioCyc software) and are scheduled for evaluation and in the second half of 2005. Documentation on COS annotation strategies was initiated for publication on a website. In collaboration with Agriculture & Agri-Food Canada, SNPs have been identified in potato DNA sequences corresponding to 31 tomato-Arabiodposis COS based on comparisons with publicly available sequences. Six have detected polymorphism among potato genotypes.

At ICARDA, 50 abiotic stress-(drought, cold, and ABA) induced gene sequences from microarray experiments of Arabidopsis were used to identify putative orthologues and develop COS markers for legumes. Sequences were aligned with EST sequences of *Medicago*, soybean, and *Lotus*. Primer design at conserved regions is in progress. Amplification products of six COS markers with six legumes of ICARDA interest (faba bean, lentil, chickpea, and grasspea) are being investigated further by sequencing.

CAAS focused on the development of disease resistance EST-SSR markers across monocots, including wheat, rice, maize, and barley. From the public databases of NCBI and TIGR, a total of 48 SSR-containing ESTs were identified and 61 EST-SSR primers were designed based on wheat ESTs, of which 21 ESTs contain LRR or NBS-LRR domain, 21 contain PK or LRR-PK domain, and the other 6 ESTs were related to disease resistance. So far, 24 primers produced expected PCR products, of which 12 showed polymorphism in wheat varieties and have been used for genetic diversity analysis, and 6 primers used for genetic mapping in three mapping populations. Of 15 primers tested, 12 produced strong bands across the four monocots, and the other 3 primers did not get amplicons in maize.

Results from COS marker work on *Musa* coordinated by INIBAP suggested relatively few COS primers from the existing Cornell COS database could amplify orthologous products for *Musa*. Refinement of primer design, ideally based on EST comparisons, is required to obtain more useable primers for targeted genes. Using both ESTs from Musa and/or genes from other species could be generally effective in finding the genes conserved in banana.

The experience gained from the development of COS markers suggests that sequencing of orthologous genes is important to understanding the variation present between different species. While conservation of genes between species can be detected by bioinformatic approaches at the DNA or protein level, the identification of conserved regions for primer design and the amplification of the targeted regions have proven to be more difficult than expected. It is therefore important to share experience between groups to improve primer design, and to understand realistically to what extent conserved gene primers can be developed across all species.

A project on targeted sequencing of the *Musa* genome and frame map construction was launched to expand on the genomic resources for *Musa*. The project is led by NIAS and INIBAP and involves several labs from the *Musa* research community. *Musa* sequence and map data produced by this project will enable detailed comparative analysis with rice to span the range of monocots. Within half a year, the group has gathered around 32,000 EST clone sets from Syngenta and deposited them at the *Musa* Genome Resource Center (MGRC). A *Musa acuminata* cv. Tuu Gia BIBAC library was created at the MGRC. Three mapping populations containing at least 150 individuals were assembled. Diversity analysis was conducted using the six parents generating the three mapping populations. About 600 repetitive DNA sequences were isolated from *Musa acuminata* cv. Calcutta 4.

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

Activities under this Project consider target traits of common concern across more than a single species. The studies involve comparative analysis of phenotypes and genetic mapping, and often adopt a genome-wide approach to identify a pool of candidate genes for testing additional hypotheses and to validate gene function.

The project on *Determination of a common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes* (led by CIMMYT) emphasises precise phenotyping of tissue response across maize, rice, and wheat under drought stress. The phenotypic data will be co-analysed with expression data to identify common (or distinct) genes responsible for tissue growth under stress conditions.

In the first year, most of the work revolved around detailed characterisation of tissue/organ response in three crops. In maize, refined phenotyping was undertaken by the collaborative work between INRA-Agropolis and CIMMYT. Phenotyping methods were developed for analysing the responses of both leaves' and silks' growth to water deficit. The elongation rate of the sixth leaf of 120 RILs and environmental conditions were recorded in a greenhouse and a growth chamber over a period of drying. QTLs were detected for maximum growth under non stress conditions, as was response to soil water potential. These QTL colocalised with previous QTL for ASI under stress in the field, suggesting a common genetic mechanism for growth of silks and leaves (INRA).

CIMMYT's effort concentrates on characterisation of genetic variability for leaf elongation, leaf development under water stress, yields, and related traits in maize in field conditions. A population of RILs (P1xP2 - 220 genotypes) was planted in December 2004 and evaluated for a variety of characters under well-watered and stressed conditions. A parallel trial with two parental lines and six contrasting genotypes (three good and three bad) from the same segregating population was also evaluated to provide material for gene expression profiling.

For wheat, 100 lines were evaluated in the field under stress conditions and trait data collected. A subset was selected based on 2004 commissioned research and data for leaf and stem extension rate under stress and irrigated conditions collected. A subset of six pot-grown contrasting lines are currently being evaluated for leaf extension rate at known soil water potentials in controlled conditions. For rice, leaf emergence and elongation rate are being evaluated using 150 BC lines (Vandana x Moroberekan), under well-watered conditions in the field, and NILs (IR64 x Azucena) under well-watered and stressed conditions in the greenhouse (rainy season). These two populations will also be evaluated in the field during the dry season (January 2006).

Two projects involved comparative analysis disease resistance. The CerealImmunity project was initiated to identify genes responsible for cross-species, non-host resistance. The team conducted artificial inoculations under controlled greenhouse conditions to identify non-host and host specific isolates of blast fungus of rice and wheat. Fourteen wheat cultivars, one rice cultivar, and one barley cultivar were tested against 14 isolates of blast fungus collected from wheat, two from grasses (*Digitaria horizontalis* and *Eleusine indica*), and one each from barley and rice. All test isolates were virulent to wheat cultivars, including the rice, barley, and grass isolates, but showed differences in aggressiveness. The grass isolate from *D. horizontalis* was least aggressive on wheat cultivars. None of the isolates were virulent to the rice cultivar Bonança except the rice isolate. The most aggressive isolate (Py 5996) on wheat cultivars was selected for further studies on cytological characterisation of non-host interactions. It is proposed to test eight rice cultivars including IR64 with *P. recondita* races. The screening of disease susceptible rice mutants could provide useful materials for identifying non-host resistance. Linkage between the CerealImmunity project and the rice mutant network were discussed during the latest GCP Annual Research Meeting.

Working on disease resistance in maize, researchers at Cornell and North Carolina State University developed heterogeneous inbred families (HIF) as genetic materials to serve both purposes of gene discovery and practical breeding. F5 progeny from several maize crosses were tested by molecular markers to identify pairs of near-isogenic lines (with respect to specific candidate genes or chromosomal regions). The families will be analysed for Northern Corn Leaf Blight resistance and with SSRs to identify chromosomal regions conferring disease resistance. This approach is considered a means to achieve the dual purposes of gene identification and development of diverse breeding lines in local breeding programmes. The group also applied genome-wide expression analysis of rice advanced breeding lines with broad-spectrum resistance to reveal novel genes that mapped to chromosomal regions with significant disease QTL effects. Maize orthologs of these rice genes were identified from a maize sequence database to design markers for mapping in maize.

A series of gene expression experiments were conducted for selected phenotypes and crop genotypes to identify common and unique genes correlated with phenotypic expression across species. The newly released Affymetrix Barley array chips (22,840 elements/chip) were used to explore barley

drought tolerance genes between drought tolerance cultivars 'Tadmor' and sensitive cultivar 'WI2291.' The preliminary result showed that gene categories, including mainly the kinases, transcription, signal transduction, photosynthesis, heat shock, pathogen resistance-related, and transporters were putatively involved in the drought tolerance during the heading stage. The approach will be extended to additional barley germplasm and also to wheat using the recently available wheat Affymetrix chip. Comparative analysis will enable the identification of common or distinct genes correlated with similar or different drought tolerance mechanisms in different pedigrees.

NIAS, IRRI, and the Beijing Genomics Institute (BGI) collaborated to evaluate the utility of rice gene chips for analysing drought response in cereals. NIAS and IRRI first tested the Agilent rice gene chips for cross hybridisation with wheat and maize DNA. Moderate cross hybridisation was observed with wheat but not with maize. Gene expression during vegetative drought stress was further investigated in rice and wheat using the 60K oligo chips from BGI. Rice and wheat varieties of different levels of drought tolerance were used. Drought stress was imposed during the vegetative stage by withholding water until 20% field capacity or until the development of severe leaf wilting symptom. RNA were isolated from rice and wheat genotypes under different water stress regimes and hybridized to the BGI chip. Approximately 60% of features with significant hybridisation to rice also hybridised to wheat. By contrasting rice and wheat genotypes with different levels of tolerance to vegetative drought stress, we identified approximately 50 genes found in common rice and wheat that are correlated with drought tolerance phenotypes. Of these, 12 genes showed common expression patterns in both rice and wheat. A similar proportion of genes on the 22K Agilent chips showed significant hybridisation with wheat cRNA. The correspondence between the genes identified in Agilent and BGI chips is being examined. These experiments suggest that valuable information could be gained from using a common chip platform for wheat and rice.

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

Activities under this project have research components that are close to identifying specific candidate genes that can be subject to validation. Clearly, the distinction between the genome-wide discovery phase and gene function validation can be somewhat arbitrary. As more results are generated in other SP2 projects, more candidate genes will be available for functional validation.

The project on "Identifying genes responsible for failure of grain formation in rice and wheat under drought" aims at identifying opportunities to enhance reproductive-stage drought tolerance in rice and wheat through physiological, genetic, and molecular analyses of two yield determinants that are highly sensitive to field-level stress—panicle exertion and floret fertility. The team applied proteomics and microarray analysis to characterise the signal transduction pathways by which GA and ABA exert their effects on peduncle elongation. Chips from Agilent (with ~22K genes) and the Beijing Genomics Institute (with ~60K genes) have been hybridised with rice and wheat RNA. Hybridisations of the 22K array with three biological replications of peduncle RNA from well-watered, drought-stressed, and re-watered IR64 plants and well-watered plants of IR64 mutant (*eui10*) showing rapid peduncle elongation have been completed. Analysis of the data is underway. Detailed RT-PCR examination of the ABA-GA signal transduction pathways in peduncles has also been initiated, through examination of gene families of the ABRE-binding transcription factors and their post-synthetic modulators (the PKABA1-like protein kinases and protein phosphatases 2C). Of particular interest is the behavior of these genes at the base of the peduncle where cell division and elongation occur.

In the investigation of floret fertility, the team focuses on carbohydrate allocation to develop floral organs and cell- and tissue-types in wheat and rice. As in the peduncle, drought stress down-regulates all cell-wall invertases of the anthers and therefore disrupts the flow of carbon to anthers and pollen grains. RNA *in situ* hybridisation is used to identify which cell-wall invertases and hexose transporters operate in each of the tissues of rice and wheat showing drought-sensitive development. A segregating population of ~900 lines has been developed to the F4 stage for the cross IR64 x Moroberekan. These two parents differ significantly in their tolerance to drought at heading. In particular, under drought stress in the IRRI Phytotron, Moroberekan shows greater floret fertility in the top four rachis branches than IR64. This is correlated with clumping of the pollen in IR64. Pollen clumping can reduce the number of pollen grains released onto stigmatic surfaces for fertilisation or the ability of pollen to germinate on the stigmas. The segregating population is being used to test the hypothesis that the accumulation and breakdown of a particular anther glycoprotein governs the self-adhesion and stress tolerance of the floret.

Two projects are targeting traits controlled by QTL with large effects. The first project (led by IRRI) focused on the cloning of major QTL controlling tolerance to phosphorus-deficiency and salinity in rice. Through recombination analysis, the chromosomal region containing the *Pup1* gene (phosphorus uptake) was fine mapped, leading to the identification of two

putative candidates for further analysis. More recently, comparison of genome sequences indicated genomic rearrangements between *indica* and *japonica* genotypes in the *Pup1* region. The BAC clones in the *Pup1* region have now been identified in Kasalath, the original donor of the *Pup1* allele. Additional candidate genes in the Kasalath BAC clones are being examined. For salinity tolerance, a number of QTL derived from a salt-tolerant variety Pokkali have been fine mapped, including the QTL *SalTol* on chromosome I. Using information available in the databases, all the genes located in the *SalTol* region and the borders regions limiting *SalTol* in chromosome I have been identified and classified according to their putative functions. The group plans to apply genome-wide expression analysis to identify differentially expressed genes in contrasting advanced backcross lines or near-isogenic lines containing different QTL for salinity tolerance.

The second project (led by Cornell) aims at cloning aluminium toxicity tolerance in sorghum and subsequently in related cereals. High-resolution mapping led to the identification of two markers that flanked the aluminium tolerance (Alt_{SB}) and defined a 27 kb interval that spanned only three candidate ORFs. One of these ORFs encodes for a transporter-like protein that is implicated in organic acid efflux, and thus is a strong candidate for Alt_{SB}. Furthermore, elite Al tolerant sorghum hybrids have been developed from the Embrapa breeding programme.

Finally, we expect to make extensive use of available mutant populations as a community resource for gene function validation. The rice mutant network led by WUR has compiled a stress-associated gene (SAG) database based on several approaches, including expression induced by various abiotic stresses and overexpression of stress resistance genes. A panel of candidate genes has been established for searching knockout mutants in rice and other mutant collections. This is comprised of the following:

- 400 abiotic stress associated genes identified from publications
- 116 disease stress associated genes obtained from publications
- 260 (>1.5 fold) and 104 (>2 fold) BTH induced disease stress associated genes
- 48 putative rice orthologs of Arabidopsis genes revealed in a drought stress regulon
- 16 putative rice orthologs of Arabidopsis stress related RNAi mechanism genes.

Lessons learned and conclusions

- Better linkage between projects is needed. While each project within SP2 is advancing reasonably well, there has not been enough cross-linkage between projects. The Annual Research Meeting in Rome provided an opportunity to initiate collaboration, but this needs to be sustained throughout the duration of these projects. Developing joint experiments and sharing materials would be a good start.

- Converging QTL and expression analysis needs to be undertaken. There is a consensus among project investigators that serious attention should be given to the consolidation of QTL data and results from high-throughput experiments. For example, work on maize (CIMMYT and Cornell) has produced mapping data for traits related to drought and disease resistance. Similarly, work on gene expression (IRRI, NIAS, CAAS, Beijing Genomic Institute) has produced data using rice chip platforms. There are also good examples showing how integrative analysis of map and expression information can accelerate the identification of candidate genes (or at least narrow the number of candidates). It is urgent that the QTL data from multiple sources be systematically brought together with expression data (if available). In response, SP4 has commissioned research in 2006 to provide analytical power to help data analysis and their integration bring out the benefits of combining datasets across projects.

- Phenotyping capacity needs improvement. Community practice and standards for drought response/tolerant traits need to be widely known and practiced. Currently, there is not enough expertise across the programmes to evaluate drought-related traits. Although the methodologies are not necessarily inherently difficult, more researchers need to be trained to take up this function. Also, standard genotypes of individual crops should be nominated as a "common biological check" to be used in all phenotypic evaluation.

- Resource leveraging should increase. Leveraging existing research investment seems to be an appropriate strategy to accelerate progress, leading to early delivery and impact. Some SP projects in particular are attractive, as is competitive research that has a history of sponsorships by several donors. Questions are raised asking if the GCP rests too much upon previous investment. Can the GCP's investment be recognised in such projects? Also, are we supporting work that would be funded anyway? With our current research portfolio, it appears that even in cases with multiple supporters, the GCP has added value to the work, leading to early delivery of outputs.

- Cross-subprogramme questions need to be examined in detail. Are we focused? Is there too much non-drought work? What is the proper balance between cross-cutting (horizontal) activities and single crop (vertical), impact oriented research? These questions are actively discussed and debated within the Management Team and are being addressed in the GCP Strategic document.

Perspectives for 2006

A key to the success of this subprogramme is to continue to attract high-quality research groups to participate in the competitive and commissioned projects. This means we have to make use of the community's unique research and expertise to formulate impact-oriented yet interesting and hypothesis-testing research. Very often attractive projects are those with an element of uncertainty (high risk).

This subprogramme must be sufficiently agile to capture new breakthroughs and robust tools from emerging science to build into the research portfolio. A recent piece of work of high relevance to the GCP is the physiological analysis of the ERECTA gene which "controls" transpiration efficiency through its coordinated effects on the development and physiological processes. Such candidates should be continuously incorporated into our potential gene list.

The power of knowing what genes are involved in a "complex trait" is demonstrated by the recent cloning of "yield genes" in rice by Ashikari et al. 2005 (Science 309:741-745). The gene controlling grain number per panicle is a cytokinin oxidase (member of a gene family but with tissue-specific expression). A null mutation at this locus has led to higher grain yield. Apparently, such genetic variants have been independently selected and used in breeding programmes. This precise genetic knowledge of the gene function enables the construction of genotypes to yield the desired phenotypes. Another interesting observation from this and earlier studies on plant height and flowering time is that genes of high agronomic values are often variants of members of gene families that have diverged in terms of their expression patterns (in different tissues or organs). This could be instructive to our compilation of stress-related genes for functional tests or association genetic analysis.

While the initial gain will come from identification of genes with large effects, we expect that most phenotypic contribution to complex traits will come from genes with small but critical cumulative or interactive effects. It is therefore necessary to have a strategy to get at genes with small effects. We anticipate that whole-genome expression analysis will be increasingly used to reveal unexpected genes or gene interactions with significant contributions to phenotypes. We also expect to learn from the human HapMap project in applying genome-wide association analysis to address complex traits and to identify functional SNP. The GCP is in a position to benefit from the rapid advances in medical genetics and can adopt many of the methodologies in plants.

Subprogramme 3: Trait Capture for Crop Improvement

Introduction

The development of effective systems for breeding complex traits such as drought tolerance has eluded most practitioners despite a great deal of R&D investment which for some crops has spanned more than 50 years. However, the recent developments in genomics, computational systems, and biometrics offer a real opportunity for simultaneously manipulating the component traits of drought tolerance. Yet the greater challenge remains to use this knowledge and skill to develop products that will have significant impact on the livelihoods of farmers in resource-poor cropping systems. To create such projects will require a substantial change in how public sector scientists operate within multidisciplinary teams and across organisations.

Global research progress in many of the cereals is sufficient to begin the development and application of gene-based marker systems for components of tolerance to drought and other abiotic stresses (rice, maize, sorghum, wheat, barley). Thus, emphasis in these crops is more on the translation and/or application of pre-existing research outputs. However, additional targeted investments are required for example in pearl millet (the most drought tolerant but least studied of the major cereal crops).

Conversely, the global genomics researchers and resources in the legume and clonal crops are still well below critical mass. Unfortunately, the resources currently available to the GCP are insufficient to support a comprehensive programme in all crops. For this reason, careful prioritisation of crop focuses will be applied to ensure rapid and compelling proof-of-concept in key representative crops such as cowpea (legumes), groundnut (oilseeds), and cassava (clonal crops).

Objective

Subprogramme 3 strives to create product-driven teams that span all R&D levels in the innovation-to-impact continuum. In particular, we aim to bridge the gap between research outputs and product delivery. Alliances with the private sector (both multi-national corporations and small- to medium-size enterprises) will be especially critical to achieve these goals. In addition, significant direct spillovers from sequence, gene, and trait analyses in model species are expected to substantially impact progress in those closely related crops with a minimum of genomics resources and critical mass expertise. All crops are likely to benefit from generic advances in genomic platform technologies, low cost marker screening technologies, and molecular breeding simulation and decision-support systems.

Rationale

Subprogramme 3 aspires to populate the intellectual space between conventional upstream research outputs and practical product development. This is a greatly neglected and poorly credited area of public research, yet becomes a major rate limiting factor for the effective uptake and ultimate impact of applied research investments. Thus, SP3 fulfills the role of creating community linkages with plant breeding programme end-users that help orientate and set priorities while also being heavily involved in the evaluation, validation, and refinement of the molecular breeding technologies we are generating. Building these linkages with CGIAR, NARS, and SME breeding programmes are all equally important.

Beyond providing technologies that help breeders effectively manipulate beneficial genetic variation for drought tolerance, SP3 must also help in the selection of appropriate genetic backgrounds for gene function validation in SP2 and for products of marker-assisted selection. Finally, there is a range of facilitating technologies, such as simulation, modelling, and decision-support tools that will be essential facilitating tools for rapid and widespread adoption of molecular breeding technologies by conventional breeders. In the GCP's holistic perspective, these are all critically important supporting activities that will substantially influence the rate, extent, and quality of uptake and impact of outputs from SP1 and SP2.

Characteristics/uniqueness

Many activities in this subprogramme are highly dependent on an effective consortium approach: for example, dealing with the challenges of complex traits with high epistasis and genotype-by-environment interaction; building holistic simulation and decision-support tools; and evaluating transgenes in multiple genetic backgrounds, crop species, and mega-environments which require by their very nature coordinated input from many scientists.

At the same time, many allied activities in this subprogramme can capture substantial economies in time, cost, and efficiency through following a community-based approach: for example, centralised validation and refinement of new technologies for routine application in NARS and community support labs by developing low cost high-throughput genotyping services based on technologies beyond the reach of most national breeding programmes.

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

Major achievements

- *Progress in establishing holistic teams for the development of molecular breeding systems.* Subprogramme 3 projects have been successful in establishing strong collaborations across disciplines, crops, and types of institution. For example, the project *Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools* links advanced research institutions in Europe and the USA with a CGIAR centre and NARS in Africa, Asia, and Latin America. Similarly, the project *Development of Low-Cost Technologies for Pyramiding Useful Genes From Wild Relatives of Cassava into Elite Progenitors* brings together scientists in a number of NARS in Africa and Latin America, while the project *Development of low tech gene-based trait assay technologies in rice and wheat* brings together scientists in a number of NARS in Africa and Asia.

- *New paradigms in plant breeding being fostered.* GCP investments are already driving exciting new approaches to breeding lesser studied crops. For example, the project *Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools* is combining wide crosses and molecular marker analysis to drive a new paradigm in groundnut breeding that follows the dramatic success of using synthetics in the breeding of other complex polyploidy crops such as wheat and canola. Based on the narrow genetic base of groundnut varieties, this approach is likely to have dramatic impacts on groundnut breeding gains.

- *Pilot-testing of molecular breeding systems with simply inherited traits.* It is important for the less-studied crops that we move ahead with whatever technologies are already available. Thus, several SP3 projects focus on simpler inherited traits pending the availability of resources for drought tolerance. Thus, the proof-of-concept for use of synthetic germplasm in groundnut breeding is being carried out using disease resistances, while pest resistance is the focus for deploying MAS in cowpea. In both projects, efforts are simultaneously being made to generate the necessary resources for mapping and marker-assisted selection of drought tolerance in groundnut and cowpea.

- *Development of low-cost assay technology for NARS and SME breeding programmes.* Good progress is being made in the development of low cost assay technologies for gene-based marker-assisted selection of disease resistance in rice, grain quality in maize, and for linked markers for pest and disease resistance in cassava. These proof-of-concept activities provide essential methodological insight that will be critical for routine large-scale marker conversion activities once GCP gene-based technologies for drought tolerance begin to emerge.

Activity report

A summary of activities in 2005 for the SP3 competitive and commissioned research projects:

Drought tolerant rice Cultivars for North China and South/ Southeast Asia by highly efficient pyramiding of QTLs from diverse origins

This project started out with progeny testing of selected drought tolerant introgression lines (ILs) under stress and non-stress conditions and development of intercross populations for pyramiding QTL. The parental genotypes of these ILs have been screened with around 600 SSR markers, 100-200 of which are now being screened across the entire populations, while detailed phenotyping will be carried out during the coming season. Around 30 drought tolerant lines have already been identified that pyramid 30 or more drought tolerant QTLs. These will now be used for a large-scale backcross programme with a high yielding restorer line.

Identifying the physiological and genetic traits that make cassava one of the most drought tolerant crops

This project aims to find the best biological traits for improving drought tolerance by MAS in cassava whilst at the same time contributing to the improved understanding of the genetics and physiology of drought tolerance in cassava. Thus, this project aims to identify trait-marker associations for the development of a more cost-effective breeding process for drought tolerance in cassava. In particular, the project will assess the effect of the leaf retention gene for improving drought tolerance. Finally, the project will establish a strong network of institutions involved in the molecular breeding of drought tolerance in cassava.

Embrapa (Brazil) and CIAT (Colombia) breeding programmes identified 40 varieties with contrasting drought response phenotypes (broadly, 28 tolerant and 12 susceptible). These varieties were selected on the basis of 15 years of evaluation data and originated from Brazil, Colombia, Thailand, and Venezuela. These varieties have been multiplied up through *in vitro* micropropagation at CIAT for detailed evaluation at Embrapa and the University of Cornell.

Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools

Based on prior research, this group has published the first diploid A genome map of *Arachis* (Moretzsohn et al 2005). However, through this project it has been possible to augment this map and consolidate some linkage groups in order to reach the desired number of linkage groups. Using this map it

has also been possible to generate the first preliminary comparative map between *Arachis* and the model system *Lotus japonicus*. Meanwhile, efforts are ongoing to finalise a B genome map and an amphidiploid AABB genome map. Finally several repetitive element fragments from *Arachis* have been isolated and used to construct a pseudo-contig for fluorescent *in-situ* hybridisation. These maps and genomic tools will be especially valuable for marker-assisted introgression breeding using synthetic amphidiploids that facilitate the introgression of vast sources of genetic diversity from diploid species.

Root-knot nematodes are known to increase water stress in infected field conditions and, therefore, represent an important component of a holistic approach to developing drought tolerance in groundnut. Four thousand single read ESTs were produced from roots inoculated with root-knot nematodes (*Meloidogyne arenaria* race1) and from non-inoculated roots. Assembly of the ESTs produced 963 contigs and 2537 singlets. Homologues to transcripts involved in responses to biotic and abiotic stresses have been identified and candidate gene-based marker development is underway.

Based on prior research, a range of synthetic amphidiploids have been created with putative resistance to diseases. This material will be used for proof-of-concept while new synthetics are being generated and/or identified with putative drought tolerance. Thus, the project is currently screening the drought tolerance of a range of diploid species in Brazil and India.

Marker development and marker-assisted selection (for Striga resistance) in cowpea

Cowpea is a critically important source of protein-rich food and feed in the drier parts of Africa. Amongst the major legume crops, cowpea has the highest levels of drought tolerant germplasm yet national cowpea yields remain very low. This is partly due to the problem of retaining high levels of drought tolerance in breeding populations. But this is also due to the fact that where drought is a problem, so is *Striga*, insect pests, and other abiotic stresses. This project focuses on the development of efficient MAS systems for Striga resistance, which also offers a simpler trait for proof-of-concept.

The ability of cowpea genotypes to resist *Striga* parasitism depends on the geographic origin of the parasite. Based on the differential resistance reaction exhibited by various cowpea genotypes, six different races have been identified. Initial efforts have focused on the development of allele-specific (co-dominant) molecular markers for two sources of race-specific resistance. Two SCAR markers have been identified that are suitable for high-throughput screening. While mapping of a third source of resistance to *Striga* has been initiated using AFLP and SSR markers, mapping of resistance to a second parasitic weed (*Alectra*) has also been initiated. Studies are also underway to determine whether the SCAR and AFLP markers retain their selective power when applied in a different population. Most recently, around 1000 new cowpea genomic sequences were generated from which additional SSR markers will be generated. This project is also initiating some drought tolerance mapping studies.

This project has also identified a series of AFLP markers that discriminates among the different races of *Striga* that are parasitic on cowpea. These AFLP markers are now being converted in to SCAR markers to facilitate rapid identification of pathogen diversity in the field.

Development of low-cost technologies for pyramiding useful genes from wild relatives of cassava into elite progenitors

Wild *Manihot* germplasm are a wealth of useful genes for the cultivated species *M. esculenta* but their use in regular breeding programmes is restricted due the long reproductive breeding cycle of the crop and the deleterious linkage drag associated with the use of wild relatives in crop improvement. This project seeks to identify useful genes for pest and disease resistance and post-harvest deterioration in cassava as well as to develop low cost marker tools for their rapid introgression into cassava.

Previous research had identified a RAPD and SSR markers linked to resistance to the cassava mosaic disease (CMD). During the first year, this project has successfully converted the RAPD marker into a SCAR marker for high throughput low cost MAS applications. The project has now shifted attention to the development of markers for resistance to pests and diseases with phenotyping evaluation of mapping populations at NARS in Brazil, Uganda, Ghana, and Nigeria.

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

For marker-assisted improvement of rice for bacterial blight (BB) resistance, NARES collaborators from China, the Philippines, Indonesia, India, and Africa were surveyed for the germplasm materials serving as recipients in their national programme for improving resistance to BB. In each case, target disease resistant loci were sequenced in all germplasm.

For the parallel situation in maize for quality protein maize (QPM), eight QPM donor sources from diverse agroecological zones (mainly tropical lowland and subtropical) and nine non-QPM recipient sources from tropical highland, tropical lowland, and sub-tropical regions have been selected for sequence comparison of the alleles at the *opaqu2* locus.

This project has also initiated the development of an allele-specific dot-blot (gel-free) assay, using the rice bacterial blight system as a pilot test. Unfortunately initial tests were confounded by the high degree of sequence similarity between

resistant and susceptible alleles. However, this will be resolved when sequence data from all germplasm is available. A similar process has now also been initiated for the QPM system.

Evaluation and deployment of transgenic drought tolerant varieties
This project has brought together physiologists from across the CG system to refine a standard methodology for agronomic evaluation of DREB transgenics for drought tolerance. This includes rice (CIAT), wheat (CIMMYT), groundnut (ICRISAT), and potato (Univ Tsukuba/JIRCAS). Next steps in the project will include multilocational field evaluation and assessment of background genotype effect (through multiple genotype transformations or backcross programmes).

Simulation of marker-assisted selection strategies for optimising molecular breeding systems for drought tolerance in cereals
This project has been designed to present examples of many of the available options in utilising simulation to improve MAS. It is not a comprehensive study of any single approach, but general guidelines are also being developed. In particular, the aim is to develop some simulation examples that could be extended to other crops and different genetic models. The initial work is based on a study of an existing case study (wheat breeding at CSIRO) to combine known genes (using 'perfect' or near-perfect markers) into single genotypes for use as parents or further field screening. A population genetics model has been developed focusing on the efficient use of marker-based selection in plant breeding and a case study in wheat has been completed and a publication has been drafted. In addition, the QUCim breeding module is being modified to realise the linkage with physiological models. Future activities will include building case studies for rice and investigating options for maize.

Product development plans
The competitive grant projects that are involved in this study are: *Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools*/Embrapa; *Drought Tolerant Rice Cultivars for North China and South/Southeast Asia by Highly Efficient Pyramiding of QTL's from Diverse Origins*/CAAS; and *Revitalising Marginal Lands: Discovery of Genes for Tolerance of Saline and Phosphorous Deficient Soils to Enhance and Sustain Productivity*/IRRI. The commissioned grant projects that are involved in this study are: *Development of low tech gene-based trait assay technologies in rice and wheat*/IRRI and CIMMYT; *Development of low tech gene-based trait assay technologies in rice and wheat*/IRRI; and *Simulation of marker-assisted selection strategies for optimising molecular breeding systems for drought tolerance in cereals*/CSIRO.

It is hoped that this project will provide baseline examples for the GCP community to enable an efficient transition to all future proposals including a preliminary product development plan.

The strength of a conventional breeding programme will be a primary factor in the successful uptake and application of molecular marker technologies. This presents an additional constraint for tropical crop breeding programmes in developing countries. Thus, the GCP proposed to strengthen underlying breeding programmes through the application of modern plant breeding best practices in *Molecular Breeding Communities of Practice*. We believe that this is best achieved by an increase in functional proximity between breeding programmes in IARC's and those in NARS and SMEs. Thus, rather than developing training workshops for hand-over of knowledge, we envisage that the best approach to achieve this will be by establishing a functional overlap between national breeding programmes into IARC breeding programmes. This is highly congruent with the IARCs desire to increasingly focus

Commissioned Mega-Project for 2006-2007:
Proof-of-Concept "Molecular Breeding Communities of Practice"
Public sector breeding programmes have been slow to adopt molecular marker technologies mainly due to the following reasons:

Reasons why public sector breeders do not adopt marker-assisted selection	**How the GCP aims to address all these issues**
Many breeders feel that the loci targeted for marker development have been selected by molecular biologists rather than the breeders.	Allow breeders to select traits for application of MAS and give them a voice in planning future investments through *Molecular Breeding Communities of Practice.*
Absence of effective markers for complex traits with high genotype-by-environment interaction where MAS holds its greatest potential impact.	GCP central focus on development of tools for complex traits such as drought tolerance.
Low level of polymorphism for existing markers in breeding populations.	Use *Molecular Breeding Communities of Practice* to validate and select best markers.
Breeders would like diagnostic markers rather than markers at a large genetic (and potentially very large physical) distance from the gene of interest.	GCP central focus on gene-based technologies and tools.
Breeders are reluctant to redirect their current resources to marker screening and in many cases such redirection is not feasible.	Use *Molecular Breeding Communities of Practice* to provide funds for MAS pilot tests.
The long lead time for breeding means high risks to a breeding programme if it modifies its breeding strategies.	SP3 focus on development of robust and credible molecular breeding simulation tools for *in silico* redesign and testing of new breeding systems.

on the production of intermediate products rather than finished material, viz an increasing emphasis on the generation of international public goods through bioscience-enhanced germplasm enhancement.

Inevitably, it will be necessary in the proof-of-concept stage of this approach to work with the strongest NARS and the crops with the best genetic and genomics resources. However, the GCP retains its commitment to the three crop groups (cereals, legumes, and clonal crops) and will push ahead at this commissioned proof-of-concept stage with the best bet opportunities in all three crop groups. We also envisage major opportunities for all crops through competitive grant procedures and expect that the PI of this commissioned project will launch a major effort in this area towards the development of a donor consortium for the sustained funding of this initiative over the next 5-10 years. In this way, the GCP is committed to fostering self-reliance, enabling a shift of emphasis from major to minor crops.

Lessons learned and conclusions

The initiation of many Subprogramme 3 projects suffered delays due to problems experienced by consortium members negotiating sub-contractor arrangements and transferring funds. Other projects suffered start-up delays due to clearance delays for shipping germplasm between partners, or the unexpected time-consuming nature of bulking up large amounts of germplasm that was required to supply all the proposed partners of the project. Finally, a few projects have experience a slow initial implementation phase due to the time required to recruit project-dedicated staff. It is expected that based on this experience, most consortium members will be able to plan ahead more efficiently for future projects. However, it is also clear, particularly with commissioned projects, that more time spent on the development, review, and revision of proposals would surely have paid dividends.

Nevertheless, exciting progress has been made in many areas fundamental for the GCP's product development pathway or in actual application of marker-assisted selection for a variety of traits, including drought tolerance. Greater emphasis must now be given to validating and refining molecular breeding technologies in a range of national breeding programmes and it is hoped that the Molecular Breeding Communities of Practice will amply serve this purpose. Moreover, it is now time to move from generic MAS activities to greater emphasis on the application of technology outputs from SP1 and SP2.

Perspectives for 2006

The portfolio of activities in Subprogramme 3 has gone through a substantial evolution during its first two years of operation:

- **Year 1:** Seed funds were provided to augment a diverse range of on-going marker activities in CGIAR centres, from developing mapping populations to validating marker-assisted selection activities. These were predominantly associated with SSR markers for drought tolerance, provided a mixture of successes, and generally did not support the central pillar of the GCP regarding gene-based markers developed through comparative genomics with model systems. For these reasons, funding for all these activities was terminated.

- **Year 2:** Commissioned projects focused on the strategic theme of pilot testing distinct elements of the value chain that were considered key for applying gene-based markers for drought tolerance. These included the development of low cost assays for gene-based markers, agronomic evaluation of DREB transgenics, simulation and modelling of drought tolerance molecular breeding in various cereal crops, and mapping product development pathways for these three types of technologies (genomics, transgenics, bioinformatics). All these activities were scoped as two year seed projects with the expectation that PIs would generate mega-project proposals in these areas for funding thereafter.

  The portfolio of successful competitive grant projects followed a more pragmatic theme with a particular emphasis on orphan crops. These included the development of low cost markers in cassava (for disease resistance), marker-assisted selection in cowpea (for pest resistance), and molecular breeding of groundnut. There was also a project to investigate the physiological and genetic basis of drought tolerance in cassava plus a project to implement SSR-marker-assisted selection for drought tolerance in rice.

- **Year 3:** For the coming year, Subprogramme 3 has identified one single over-arching priority that it will concentrate all its new funds on: the coordinated support of marker-assisted selection applications in strong NARS through the formation of molecular breeding communities of practice. We envisage, based on two years of seed funds from the GCP, that it will be possible to establish a consortium of donors to scale-up and scale-out this concept more than ten-fold. It is believed that this will help establish a firm foundation for uptake and application of GCP drought tolerance outputs expected during the next 4-5 years depending on the crop.

  However, this focus on working with active breeding programmes to introduce, validate, and refine molecular breeding systems appears to be the most urgently required niche and natural focal theme for Subprogramme 3. Meanwhile, it remains an open question as to whether this subprogramme should pursue transgenic activities or whether these tools should be confined to gene function validation in Subprogramme 2. However, the recently drafted GCP statement on GMOs makes it clear that the GCP will withdraw from direct involvement in transgenic product development and deployment.

Subprogramme 4: Information Network and Bioinformatics

Introduction

Subprogramme 4 (SP4) addresses the challenge of linking and integrating the GCP information components and analysis tools into a coherent information gateway, and supporting GCP activities in terms of bioinformatics tools.

Objective

SP4 aims at implementing a strategy that allows all Generation data to be accessed and shared by the consortium and by the rest of the world. A second objective is to make sure that the components of the resulting platform are of sufficient quality, both in terms of the actual data and the tools to analyse and manage that data. A third and final objective is to create the necessary tools and generate the knowledge to support the research in the first three subprogrammes.

Rationale

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 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 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. SP4 therefore aims at implementing a strategy that allows all Generation data to be accessed and shared by the consortium and by the rest of the world. A second objective is to make sure that the components of the resulting platform are of sufficient quality, both in terms of the actual data and the tools to analyse and manage that data. A third and final objective is to create the necessary tools and generate the knowledge to support the research in the first three subprogrammes.

Characteristics/uniqueness

To achieve these goals, the GCP uses, as much as possible, the capacity within the consortium by creating teams across institutes. In that sense, SP4 is the subprogramme with the most collaboration in the GCP. To support this collaboration, facilities have been installed that allow the joint development of software (CropForge) and the joint development of documents (GCP Wiki). The collaborative teams try to involve as much as possible experts from outside of the consortium to ensure proper quality of the products as well as optimal use of existing knowledge and products. Our goals are ambitious, so we have to 'stand on the shoulders of giants.' Another distinctive feature of SP4 is the infrastructural nature of the products. Development of these products is therefore not suited for competitive granting. For example, if we need a facility for high capacity computing allowing CPU-intensive calculations such as whole genome blasts, this is not very suited to a call for proposals. The number of groups who can actually create such a facility is too limited. As a result, most of the activities are commissioned.

Major achievements

The second year of operation in SP4 was a successful one. The major achievement was, without doubt, the fact that the collaborative teams have proved to be productive. The planned strategy has been largely implemented; most of the foreseen outcomes have been delivered.

In terms of the establishment of the GCP platform, the major elements are all being produced as planned. The activities to develop and implement the technology for web services have made major achievements: appropriate tools have been created, staff has been trained, and web services have been implemented in a number of institutes. The development of the models on which the exchange of data and development of software will be based has resulted in a complete set of initial domain models. Since new types of data will emerge continuously, the implementation of the platform will never be completed. To facilitate the sharing of data irrespective of the availability of domain models and web-services, facilities have been created for uploading datasets to a central repository, based on relatively simple formats (implemented in spreadsheets). To create an overview of available and not-yet-available datasets, a central registry has been created and is populated with information of all data generated with GCP funds. Activities have been initiated that will ensure the availability of these data.

The improvement of the GCP platform components has seen a further investment in the building of bioinformatics capacity in a number of GCP institutes: the further development of the high performance computing (HPC) facilities, the development of an integrated (reference) information platform, and activities aimed at improving the quality of the data and their management per se.

Finally, the development of tools in support of other SPs has also seen much activity. Some initiatives are ongoing, i.e. the development of a computational tool to support MAS, as well as the development of an expression database and an ortholog database, both with tools for analysis. Others will end this year, such as the development of algorithms that allow the selection of germplasm for specific experiments, such as association mapping.

Activity report

When describing the main activities of SP4 in 2005, the division in the three projects, as described in the GCP Medium Term Plan, will be followed. These are:

- Establishment of the GCP Information Platform
- Improvement of the GCP Information Platform components
- Creation of software in support of GCP activities.

Establishment of the GCP information platform

This is the largest project in SP4 and aims at actually creating the platform needed for effective information exchange. The approach that was decided on in the GCPs first year, 2004, is that of web services. Web services allow wrapping local databases and software tools in such a way that they appear to be part of one system; they can be approached via a common protocol and a common language via the internet. The protocol can be interpreted by the wrapper, and the language can be translated by the wrapper in the language understood by the local database or software tool, which answers the query or does the analysis. The output is then translated back to the common language sent back to the one requesting it using the common protocol. Implementation of this approach has a number of components: the technology (software and protocol) should be available and the common language developed; the technology should be implemented by the consortium members requiring training; and the technology should be used. Since this can not be accomplished immediately, some short term solutions should be created that are compatible with the final solutions. In 2005 some major steps toward this goal have been realised. This involved a number of activities, each with their own outputs.

The first output is the development of the common language, based on models of the information-domain. To make sure that these models will form a good basis not only for data exchange but also for software development, it was decided to take a solid approach. In 2005 methodology was selected for the modelling, and the format for recording the models was also selected (Omondo EclipseUML). Editorial teams for the different sub-domains have been formed ("Generic Core Models," "Germplasm/Phenotype/Genotype Models," "Passport Models," "Functional Genomics Model"). These teams did the modeling resulting in version 1 models for all sub-domains. These models were consolidated into a single comprehensive model and posted into the GCP Middleware CropForge project at http://cropforge.irri.org/projects/gcpmiddleware/.

The second output is concerned with the training of staff and implementation of web services technology in the institutions. Several approaches and technologies for an easy deployment at the institutes have been considered. In June a workshop on "Web Services, its technical fundamentals and future implementations" was held to bring together experts on the different technologies that are to be used (DiGIR, BioCASE, and BioMOBY) with members of the GCP Consortium. This meeting aimed at providing a better understanding and promotion of web service technologies, but, most of all, it had to provide a clear implementation plan for the deployment and implementation of web services. A tool (Model Mapper Toolkit) for generating web services on site is expected to be ready before the end of the year.

The third output concerns the creation of a registry for links to the datasets (yellow pages) or datasets themselves that are not available as web services yet. For this purpose an inventory of all available data sets generated in GCP projects has been made and the PIs of these projects have been approached, asking for the data sets or information about the availability. A website has been created that will make this information available, including links to the actual data sets (if available). This site will also allow GCP management to monitor the availability of data.

The fourth output aims at improving the web services technology and applying it in a number of show cases to establish the GCP as a relevant player in the international arena. For this purpose several software tools have been developed. An important example is the new "MOBY Services Support" ("MOSES") framework to accelerate Java web services development. A number of GCP partners are now using this tool kit to develop MOBY web services in their projects. Also a "MOBY Dashboard" graphical user interface to facilitate the specification, registration, code generation, and testing of web services is being developed. GCP partners continue to register additional web service data types and services in BioMOBY central.

The fifth output concerns a solution to the short term issues that are not resolved yet by applying the web services technology: creating small applications for uploading and centrally storing data sets. Fur this purpose, templates for GCP passport data and fingerprinting data (SSR) have been developed and published. These templates are based on the GCP domain models (as described above). The mapping template is expected to be finalised by the end of November.

This will follow as much as possible the popular and well defined CMAP format. Phase 2 of the project is now expected to start in December with the development of templates for phenotyping, SNP, and DArT fingerprinting data. Tools to convert data in the templates to other popular formats, such as input files for analysis tools, are being developed.

The sixth and final output aims at properly capturing and analysing the wishes of the users and providing a platform for simultaneous software development, both of which facilitate effective software development. A web-based system for collaborative software development (http://cropforge.irri.org) has been created. Currently, there are 43 hosted projects and 93 registered users of this system. Many, but not all, of the projects currently hosted on CropForge are GCP related. Each project has its own administrator who is responsible for the project content, project resources configuration, and project team management. A web-based system for collaborative development of textual content, CGP Wiki (http://cropwiki.irri.org/gcp), has been in use since February 2005. Currently, there are about 280 pages that can be considered proper content pages. There have been a total of 23,689 page views, and 2,974 page edits since the Wiki was setup. There are 123 registered users, of which 12 users from 7 different institutions have administrator roles. Currently, most of the content of the site is related to SP4 according to the project proposal, but other subprograms have indicated their interest to use this platform in the near future.

Improvement of the GCP information platform components
The second project (in MTP terminology) has to do with the quality of the components that are to be part of the platform created in the first project. To ensure this quality of local curation of data, a number of issues have to be considered. There is the issue of institutional capacity needed to act as data supplier to the GCP, the issue of the quality of the data that are supplied, and finally the capacity needed by GCP scientists that cannot be supplied by one single centre.

Concerning institutional capacity, the CGP has the policy that consortium members are responsible themselves for creating appropriate capacity. However, where the GCP can create synergies, these opportunities will be used. In addition, the GCP aims to kick-start the development of institutional bioinformatics capacity by supporting the building of that capacity. The financial support provided by the GCP for this purpose is phased out from 50k$ in 2004 to 33k$ in 2005 to 17k$ next year. It is provided to all eight CGIAR institutions that have been in the consortium since the beginning (CIAT, CIMMYT, CIP, ICARDA, IITA, IPGRI, and IRRI). The funds have been used for a variety of activities, ranging from hiring and training bioinformatics staff to installing and/or improving the LIMS in the institute.

Concerning the quality of data and the systems they are managed and analysed with, a number of activities have been deployed. It became clear that the data quality issue required different approaches than the platform issue. In 2006 these activities will be separated. Guidelines were established during an SP4 meeting in February for conducting base-line quality surveys of data in GCP repositories. These guidelines were used as input for a meeting entitled Data Quality Workshop in August where base line quality surveys were reviewed from IPGRI-INIBAP, IRRI, CIP, ICRISAT, ICARDA, and IITA. The development of a Data Quality Strategy for the GCP was started. Concerning the platform development, a different approach was followed. Nine separate activities were organised ranging from the definition of a general platform architecture, to implementation of domain models in GCP middleware, further development of aspects of LIMS, to data warehousing and adaptation of functional genomics tools. These relatively small activities will form the building blocks in terms of components and experiences that will be used to create a versatile platform in the coming years.

The final element in improving the components of the GCP Information Platform is the creation of new joint institutional capacity, capacity that could not be established without the collaboration in the GCP. The creation, implementation, and integration into the GCP toolbox of a high performance computing (HPC) facility last year was the first step in that direction. In 2005 the primary emphasis of work has been upon the development of use cases by CIP, ICRISAT, and IRRI teams as the basis to facilitate and stimulate use of the HPCs by all GCP collaborators. Use cases implemented this year include automatic gene annotation, including COS using BLAST with custom scripts, simulation tools for linear models (statistics) implemented in R, association tests and population sub-structure analysis based on molecular markers (using Structure), construction of a pipeline of public domain tools for sequence assembly, and SNP detection and visualisation. Further, a large number of open source software tools have been structured and compiled for the cluster and have been installed on the Paracel HPC (these tools include MegaBlast from TGICL for EST clustering; PCAP and cap3, implemented using MPI and PBS for job scheduling). Web service access has been created to these and other tools (including Bio-Mirror of public sequence databases, EMBOSS, TIGR microarray analysis tools, and MAANOVA R Statistics package).

Creation of software in support of GCP activities
The third component of the SP4 activities is the one that will grow in importance once the first two have established themselves: the direct support to the GCP activities in terms of software tools and algorithms. The first three subprogrammes have data collection, curation, and analysis

needs that SP4 must address for optimal deployment of GCP outputs. Based on the needs formulated by the other SPs, five activities were articulated whose outputs would address those needs.

The first activity aims at facilitating germplasm sampling based on all available passport, phenotype, and genotype data, depending on the nature of the sample required. Algorithms have been developed for representative sub sampling (cluster analysis with dependent data and several approaches for joint analysis of molecular and phenotypic data), and 'structural' LD free sub sampling. The wide range of strategies that were developed and tested was implemented in an existing software package (DarWin). Next year, capacity will be made available to support the use of these algorithms by SP1 scientists.

The second activity aims at creating access to gene orthology relationships across species and related paralogy relationships within gene families. This is a two-year project that started in 2005 with some delay due to problems with the recruitment of staff. A GMOD Chado database is being deployed for the stress catalog. The "Apollo" genome sequence browser, now known to include the "JalView" multiple sequence and phylogenetic tree viewer, is being considered for GCP platform deployment in the activity. Next year there will be more results to report.

The third activity in this component of SP4 will create a crop gene expression database that will allow scientists to easily find and compare expression data across species. This is also a two-year project, but large achievements have already been made in the first year. A prototype of the crop gene expression database was constructed and will be made available in December 2005. It is based on the Rice expression database (http://red.dna.affrc.go.jp/RED). The unified Transcription Unit-based system (UTUS) was introduced to allow coverage of a wide spectrum of probes. A total of 62,617 TU were determined by mapping genomic (Predicted CDS) and transcript-based nucleotide sequences onto the rice genome (pseudomolecule rel. 3). For the description of the microarray experiments the MIAME-plant standard is used. A tool for the analysis of the clustered gene set and cis elements appearing in their promoter regions has been developed. The new database has been connected to the BioMOBY central registry and several web services have been started (including gene search). We expect that we currently have access to more than 200 microarray data sets (these will be mounted after publication).

The fourth activity aims at allowing breeders to more efficiently use markers in breeding programmes by integrating existing software in an integrated platform (iMAS). This two-year project has seen a very good start. Software for inclusion in the platform has been selected and largely tested. This involves following eight packages: IRRISTAT, GMendel (and possibly MapDisto), PlabQTL and Win QTL-Cartographer, Tassel, PopMin, and GGT. The Java-based development of the system is in progress according to the planning and a GUI has been developed and successfully tested. All software packages have been incorporated using Java-based open-source tools.

The fifth and final activity will create an eco-physiological – statistical framework for the analysis of GxE and QTLxE as occurring in abiotic stress trials, facilitating a better understanding of results of phenotyping experiments. This is the only 'competitive grant' project in SP4, and it started with a delay of five months. The work on wheat and maize has started. For wheat the work has focused so far on phenotypic and molecular data collation, preliminary analyses of phenotypic data, and the generation of the molecular map using various methods. For maize, a single-trait multi-environment mixed model was developed and evaluated using the historical data on a population for which alternative analyses have been performed in the past. The mixed model methodology will in the coming months be extended to allow for multi-trait multi-environment analysis.

Lessons learned and conclusions

After a first year of creating a strategy and an organisational framework, 2005 was the first 'production year.' From the perspective of the strategy this has been very successful; elements of the GCP information Platform are taking shape, tools are being developed, and nearly everything seems to fit.

Two forces could be observed in the process. One is the tendency to systematise, centralise, create standard methodology and procedures, document activities in a uniform way, etc. This is the way software companies would operate. On the other side is the pragmatic tendency to create solutions and not avoid taking short cuts. This is the way that scientists develop software. The first force has the danger of getting stuck in choosing the proper methodology and platforms without creating the product; the second in creating a product that has very limited applicability, flexibility, and compatibility. SP4 operates somewhere in between, taking a two-sided approach. The short term solutions are created pragmatically, with feedback from the centralised activities. In parallel, with a wider horizon, we invest in building a solid systematic basis for future development of the platform. It is only via the involvement of the same developers, or contacts between them, that the products of these parallel approaches 'fit.' This 'fit' is essential for the GCP Information Platform. The 'short term products' that are currently being developed will have to be submerged into the emerging platform. So far that is going very well. An example is the way the 'template' activities are tuned with the

'domain modelling' activities. This is only possible because of the willingness of the SP4 scientists to collaborate and communicate. The fact that this has taken shape is truly a remarkable achievement.

Perspectives for 2006

SP4 is now in the phase where the feedback of the user will become more important. The first products are ready to be presented to the user: the templates for data storage, the central registry for finding data sets, web service-enabled analytical tools and databases (including the HPC tools), algorithms for selecting germplasm, etc.

Next year SP4 will have a number of activities directly aimed at supporting the users; there will be support for SP1 scientists helping them to select germplasm and for SP2 scientists to analyse expression experiments and other genomic data. The HPC activities will be geared towards promoting and supporting the use of the facilities created so far.

This user orientation will not hinder the development of the solid basis; domain modelling and platform development will continue, as will the implementation and application of web services. These activities will start to have visible outputs, but the true value will be in the longer term.

The vision of the virtual database and toolkit—allowing any scientist anywhere to analyse any data with any tool without the hassle of data conversion—is not an exclusive GCP vision. The GCP is part of the global community and it is the vision of that community. At this stage, two years into its existence, the GCP is making major contributions in achieving this vision.

Subprogramme 5: Capacity Building and Enabling Delivery

Introduction

Subprogramme 5 is charged with developing and monitoring mechanisms that ensure outputs of GCP research activities are delivered to users and employed toward products that will positively impact resource-poor farmers. A priority task in Subprogramme 5 is providing the capacity building necessary to allow GCP institutions, partners, and potential collaborators to use GCP research outputs and to participate in the further development of products useful in plant breeding programmes.

Objective

Subprogramme 5 sponsors targeted training activities, fellowship and grant opportunities, and the development of learning resources for the GCP and other institutions, especially NARS. SP5 is also the home of policy research on intellectual property and access and benefit sharing.

Rationale

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

In the GCP, the focus on capacity building stems from the belief that education and knowledge form the basis for development. Capacity building efforts target NARS partners to both enable developing country scientists to collaborate in GCP research and to ensure sustainability of the research platform and toolbox of the GCP itself. The 'enabling delivery' component reflects the GCP's emphasis on developing the appropriate mechanisms for delivering the outputs of its research for maximum impact on farmer livelihoods.

Characteristic/uniqueness

Capacity building and enabling delivery activities are both embedded into ongoing GCP research projects as well as initiated outside the context of current projects to enhance scientific capacity of developing country researchers and to promote collaboration. By linking training to research, Subprogramme 5 helps foster a user orientation in the GCP as a whole. Capacity building is viewed as the primary vehicle for delivery in the GCP, since without targeted and thorough training, developing country researchers will not be equipped to employ GCP research products. Subprogramme 5 ensures that the GCP does not just pay lip service to these ideals by establishing systems for feedback and monitoring for all training courses, fellowships, and project-specific capacity building activities.

Major achievements

SP5 efforts in the second year of the GCP encompassed the three main areas of the subprogramme: training, policy research, and the development of a strategy for delivery of GCP products.

A significant number of scientists in NARS participated either in hands-on research in funded GCP projects, in regional training courses on subjects covering Subprogrammes 1 and 3, or in regional courses on project proposal development. Emphasis was placed on building linkages with NARS scientists for as much coverage outside the GCP as possible, while also strengthening links with traditional partners. In addition to the training sessions during the various courses, training events were used to inquire about the strengths and capacities of participants and their organisations to contribute to the aims of the GCP, in particular identifying possible roles for them in the delivery chain of GCP products. These opportunities were also used to identify more training and capacity building needs that the GCP could support under its mandate. It is important to highlight the role that the training courses and workshops have played in raising awareness about the GCP in general, the value of broad research partnerships, and the need to promote tighter linkages between laboratory and field scientists.

Eight fellowships for short research periods at GCP organisations, as well as a PhD fellowship and approximately 30 travel grants to attend GCP-related conferences or build linkages with Consortium scientists were also awarded.

Other activities were conducted in close collaboration with the technical subprogrammes. The contribution of SP5 in those events promoted sharing the benefits of the technical

knowledge generated in the GCP with NARS outside the Consortium involved in similar research at their home institutions.

In the policy area, 1) protocols were analysed and developed to facilitate germplasm exchange and proper access and benefit sharing from the derivatives of the GCP, in line with the published policies of the CBD and the FAO ITPGR; 2) reports were produced for generic questions of immediate importance to the GCP; and 3) a seminar was conducted to call the attention to policy issues that influence the operation of the GCP, in particular those related to the implementation of international policies for access to genetic resources and to institutional policies regarding intellectual property rights.

A Delivery Strategy was produced (http://www.generationcp.org/DRAFT_DELIVERY_sum.pdf), which lays out the mechanisms by which the GCP will ensure its products reach their intended users (who are most often "intermediate" users in the larger value chain of product development). The document defines the users of the outputs of GCP projects (who are they and how will they use these outputs?) and establishes that every GCP project will have a product delivery plan in place, developed in coordination with the appropriate set of users of the project outputs. The aim of the new Delivery Strategy is to ensure from conception to implementation to completion that the GCP is focused on the efficacy and efficiency of its products reaching the next level of users, who will then in turn be able to produce another product in the value chain, leading from lab to breeding programmes to farmers' fields.

Activity report

Training Programme

Three training courses on Project Proposal Development were conducted in Africa (Cotonou, Benin), Asia (Kuala Lumpur, Malaysia), and Latin America (Quito, Ecuador). The objective of these courses was to increase the capacity of the GCP African, Latin American, and Asian institutions as well as that of potential partners in developing high-quality project proposals, leading to more effective distribution of research outputs, results, and an increased fundraising ability. As a result of the courses, 69 scientists from NARS and CGIAR institutions and potential partners of the GCP were trained in planning and writing quality project proposals. They also acquired knowledge on donors' funding criteria (especially those for social impact and sustainability) and on how to respect them in the design of concept notes and project proposals. The participants represented 45 NARS institutions from 33 countries (9 countries in Africa, 11 in Asia, and 13 in Latin America).

Some exciting outcomes of the courses are: 1) several participants already used the course materials to teach colleagues upon return to their home institution, distributed the course CD, and already started its translation to Spanish; 2) a few participants working in the same crop decided to write a collaborative project proposal; 3) an interview of the course organisers was broadcasted in Radio Cotonou (Benin), and one column in the Espresso de Guayaquil was dedicated to the importance of the workshop in Ecuador.

Three regional training courses on Genetic Diversity and Molecular Breeding were conducted at the University of Pretoria-FABI in South Africa (Africa), Kasetsart University in Thailand (Asia), and INIA-La Platina in Chile (Latin America). The total number of participants that benefited from the course is 59. They represented 41 NARS institutions from 27 countries (10 in Africa, 10 in Asia, and 7 in Latin America). The objectives of this workshop were to provide both conceptual and hands-on training in the use of plant genetic diversity and molecular marker-assisted breeding, with emphasis on practical applied usage and improving the links between plant breeding, germplasm management and utilisation, and molecular biology methods. Participants' average evaluation scores of the courses ranged from 3.94 to 4.54 (0-5 scale).

Selected highlights of the courses are: 1) the selection of participants for the course in South Africa prioritised teams of molecular geneticists and breeders from the same institution; 2) instructors for courses included GCP Consortium scientists as well as regional scientists, and the evaluation of the latter were particularly high. This feature was deemed as extremely valuable to ensure good communication between participants and lecturers, helping the creation of links among scientists and promoting regional sustainability; 3) left-over funds from the training events were distributed among outstanding participants selected by the organisers to advance research in their home institutions in line with the learning experience gained during the course; 4) The participants in the course in Thailand formed AgBioAsia as a Yahoo Group (www.yahoogroups.com/groups/AgBioAsia) to foster collaborations with each other and with the GCP organisers as a mechanism for technical backstopping, re-training, and problem solving in the Asia region.

A special partnership was established with the International Foundation for Science (IFS) to link technical courses on molecular genetics/breeding organised by SP5 with their call for research grants for young scientists in developing countries. Selected participants for courses were encouraged to apply to the IFS call and course instructors offered guidance for the preparation of proposals to ensure competitiveness. IFS earmarked two grants for each of the GCP courses. A pre-

selection of suitable candidates will be made by the GCP followed by another evaluation by the standard IFS selection panel.

Linked to Subprogramme 1, a workshop titled Molecular Markers for Allele Mining was organised by IPGRI based on results from the GCP's year 1 genotyping efforts. The workshop, conducted at the MS Swaminathan Research Foundation (MSSRF) in Chennai, India, gathered participants representing: the System-Wide Genetic Resources Programme (SGRP, 5) of the CGIAR, the crops included in the SP1 genotyping activities of year 1 (10), crops involved in a SP1 commissioned project on association genetics (5), a number of experts in germplasm characterisation (3), NARS from developed countries (4), and NARS from developing countries (8, plus 6 Indian scientists). It was an opportunity for scientists involved in SP1 to exchange their experiences, successes, and difficulties, but also to have top scientists from NARS, advisers from advanced laboratories, and germplasm curators provide valuable ideas for improving activities. As a result of the workshop, the idea developed to open the platform of advanced laboratories to those NARS partners with information-rich germplasm. This could provide novel genetic information from *ad hoc* molecular marker genotyping.

Linked to Subprogramme 4, a workshop was co-organised with the Instituto Agronomico Mediterraneo de Zaragoza (IAMZ, Spain) on Design and Analysis of Multi-Environmental Trials: Conventional and QTL-based methods. The objective of the course was to provide the participants with working knowledge of statistical tools to be applied in breeding programmes requiring the use of multi-environmental trials to assess the responses of genotypes and their dependence on the environment. The programme covered the design of multi-environmental trials, the analysis and interpretation of genotype-by-environment interactions, the use of appropriate software, and the development of appropriate breeding strategies to better predict the genotypic responses. The course was attended by plant breeders, geneticists, and applied statisticians, all already involved in the subject matter presented. In total, there were 30 participants from 16 countries.

In most workshops, a questionnaire was circulated to assess the capacity building needs of potential GCP partners, requesting their perspectives on strengths and capacities of the institution to which they belong, their potential role in and contribution to the GCP, and the expectations they might have of the GCP. Common needs were the following: 1) to continue with the GCP fellowship programme and extend it for PhD candidates; 2) to further molecular breeding training; 3) to promote a small grant programme for NARS so that they can contribute to research in their own countries; 4) to upgrade a selected number of research facilities in the South; and 5) to train technical scientific staff in national programmes. A common wish was to host GCP activities in their countries and institutions.

Fellowships

A first call for the GCP fellowships was opened and 18 candidate applications were received. In a second call, 5 applicants competed. The full GCP Management Team evaluated and selected the winners as follows:

1. Chiedozie Egesi from the National Root Crops Research Institute (NRCRI) in Nigeria, to work on the project "Genetic mapping of resistance genes to major arthropod pests and delayed postharvest physiological deterioration (PPD) in Cassava" at the International Center for Tropical Agriculture (CIAT).
2. Daniel Fonceka from the Centre d'Etude Régional pour l'Amélioration de l'Adaptation à la Sécheresse (CERAAS) in Senegal went to the Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD) to work on "Drought tolerance related candidate genes in sorghum and their allelic diversity as revealed by Ecotilling."
3. Heru Kuswantoro, from the Indonesian Legume and Tuber Crops Research Institute (ILETRI), is at Cornell University working in the project "Characterising the genetic diversity of Indonesian soybean and groundnut landraces using microsatellite and SNP markers."
4. Kameswara Rao Kottapalli, from the Directorate of Oilseeds Development in India, went to the National Institute of Agrobiological Sciences (NIAS) to work on "Functional genome analysis for candidate gene discovery from a chromosomal region having mapped QTLs/loci for broad-spectrum bacterial blight disease resistance and submergence tolerance in rice."
5. Luis Carlos Rodríguez Zapata from the Centro de Investigacion Cientifica de Yucatan (Mexico) is working on the development of COS markers for drought tolerance for Musa germplasm, in collaboration with the International Plant Genetic Resources Institute (IPGRI)/International Network for the Improvement of Banana and Plantain (INIBAP).
6. Matthews M. Dida, from Maseno University in Kenya, is working on the project "From rice to finger millet: Comparative mapping of blast resistance genes" at Cornell University and the University of Georgia.
7. Suresh Kumar Sampath from Bharathiar University (India) works on "Enabling Biological Databases Interoperability to create an on-line integrated information resource on Banana and Plantain a worldwide access" at IPGRI/INIBAP.
8. Syed Sarfraz Hussein from the National Centre of Excellence in Molecular Biology at the University of the Punjab (Pakistan) is at the Australian Centre for Plant Functional Genomics (ACPFG) working on "Comparative Genomics of Drought Tolerance in Wheat."

The Pioneer-GCP Fellowship towards a PhD in a US University was also opened for applications in early 2005. A team composed of the GCP Director, SP3, and SP5 leaders, as well as the training officer at Pioneer, evaluated 12 applications. The award was given to Vinod Jakkula from India to conduct his dissertation research at the University of Georgia working on "Comparative and functional analysis of genes affecting plant height."

Travel grants

A travel grant programme to support NARS' visits to GCP member institutions or GCP-related meetings was initiated. Fourteen standard travel grants were awarded to scientists from the National Agricultural Research Organisation (NARO, Uganda), the Ethiopian Agricultural Research Organisation (EARO), the Rwanda National Agricultural Research Organisation (ISAR), the Kenya Agricultural Research Institute (KARI), Moi University (Kenya), the Hanoi University of Technology (Vietnam), Huazhong Agricultural University (China), the University of Namibia, the Indian Agricultural Research Institute (IARI), Tamil Nadu Agricultural University (India) and the Mtskheta Breeding Station (Georgia). Visits were paid to the National Institute of Agrobiological Sciences (NIAS, Japan), IRRI (The Philippines), Cornell University (USA), ICRISAT (India), CIP (Peru), ICARDA (Syria), CIRAD (France), and the African Centre for Gene Technologies (ACGT)/ FABI (South Africa). Other grantees will attend the 7th International Wheat Conference (Mar del Plata, Argentina) or the 5th International Rice Genetics Symposium and 3rd International Rice Functional Genomics Symposium at IRRI (The Philippines). In addition, 14 awards were given to scientists to attend InterDrought II in Rome (Italy). They represented national research organisations of Senegal, Russia, Uzbekistan, Iran, Bangladesh, Brazil, Turkey, Egypt, India, Pakistan, Tunisia, and China.

Learning materials

In 2005, the development of a series of training materials also got underway in the areas: genetic diversity analysis, plant genomics, molecular breeding, and bioinformatics. These are in addition to those prepared *ad hoc* to provide instruction in diverse workshops, either as part of the training programme (project proposal development and genetic diversity/ molecular breeding) or organised in the context of research projects. Each training workshop produced a CD-Rom with the course contents, presentations of instructors, software if applicable, and reference publications in PDF format. The basic set of learning materials will be finalised and ready in 2006, and will be stored in a training material repository accessible through the GCP web site.

Other

An Interactive Resource Center to offer online information and sustainable support to capacity recipients (http://irc.igd.cornell.edu) was created. The site offers links to plant databases, laboratory protocols, freely available literature, and funding and training opportunities. It is still under development and soon is expected to contain lists of suppliers of reagents, primers, other laboratory supplies, databases made for specific needs, workshops -real and virtual, and online tutorials.

A proposal was prepared in collaboration with BECA ("Tapping Crop Biodiversity for the Resource Poor in East and Central Africa") and submitted to the Rockefeller Foundation to match funds. The goals of the project are: a) to enable national researchers to apply genomics tools for characterisation and enhancement of major food crops in the ASARECA region, b) to empower a wider spectrum of stakeholders to link into regional and international research activities, c) to provide an operational framework for trainees from the GCP-BECA Molecular Breeding Training Programme to continue and intensify their training, d) to generate an active network of molecular breeders effectively using the BECA facility, and e) to develop an operational framework for collaboration on comparative genomics in Africa fostering multidisciplinary teams working across three African crops (sorghum, cassava and bean).

Capacity building activities within research projects

Providing hands-on capacity for NARS scientists outside the Consortium was a requirement of proposals submitted to the competitive call and highly encouraged in commissioned research activities in the technical subprogrammes. Mechanisms to follow-up on such activities were put in place in Subprogramme 5 in 2005. Beneficiaries of capacity building activities were requested to fill out a questionnaire to inform the GCP Management about progress, rating the learning experience, applicability to their home institutions, and suitability of the programme to fulfill their needs. Results are used to inform the placement of future trainees to research teams and to help better shape the activities. An interesting achievement of this endeavour has already been the increase of awareness of Consortium scientists of the importance and relevance of linking with outside NARS to reach the goals of the GCP. Up to date, ongoing research projects awarded through the competitive call in 2004 have engaged 23 scientists from developing country NARS in hands-on research. In addition, several training workshops have been organised with participation of as many as 138 scientists from 68 national institutions in 47 countries worldwide.

An activity closely related to SP1 was the development of microsatellite marker kits (reference molecular marker subsets to analyse diversity of germplasm and allow comparability across institutions and germplasm collections) for the crops genotyped in that subprogramme in year 1 of the GCP. The conversion into a capacity building activity was completed by means of selecting NARS scientists to participate in the development of the kits. Ten scientists from nine countries started work at a Consortium institution to carry out this activity: barley (Chao Lu, Yangzhou University, China), cassava (Luis Rodolfo Montes, Universidad de San Carlos, Guatemala), chickpea (SL Dwivedi, ICRISAT, India), common bean (Sandra Lorigados, INCA, Cuba), maize (Chaba Jampatong, National Corn and Sorghum Research Center, Thailand), Musa (Kouassi Koffi Simplice, CNRA, Ivory Coast), potato (Eliana Alba Alba, PROINPA, Bolivia), rice (Reflinur S.P., CABGRRD, Indonesia), sorghum (Mbaye Ndoye Sall, CERAAS, Senegal), and wheat (Genying Li, Shandong Academy of Agricultural Sciences, China).

Policy

Some achievements in the arena of policy research in 2005 are:

- A policy session was organised in the framework of the Symposium on Genomics-based Plant Germplasm Research, held in Beijing, China (25-28 April). The objectives of the session were two-fold: 1) to raise awareness of policy issues, particularly access and benefit sharing under the Convention of Biological Diversity and the International Treaty on Plant Genetic Resources, and their implications on the technical work of the Generation Challenge Programme, and 2) to get advice from National Programme officials and members of the Consortium on their vision of access to genetic resources relevant to the GCP. The session was also used to give partners a chance to participate in the conference. The session was well attended and had high-level participants. As a result of the session, there was clear advice from the Chinese participants on the processes for getting access to germplasm and materials. The publication "Access to plant genetic resources for genomic research for the poor: From global policies to target-oriented rules" by Niels P. Louwaars, Eva Thörn, José Esquinas-Alcazar, Shumin Wang, and Abebe Demissie was submitted for publication to "Genetic Resources Conservation and Utilisation."

- A publication compiling a series of white papers on policy issues relevant to the GCP was prepared and published: *Genetic Resource Policies and the Generation Challenge Programme*. It contains the following sections: a) the policy environment of the GCP regarding rights on biological materials, technologies, and knowledge; b) humanitarian licenses; c) the evolving international regime of liability and redress relating to the use of genetically modified organisms; d) open source mechanisms: the example of BIOS; e) issues on access to genetic resources; and f) impacts of strengthened intellectual property rights regimes on the plant breeding industry in developing countries.

- A number of projects were commissioned as follows:

1) Distant Policies is a distant learning module for scientists on Genetic Resources Policies and their implications for 'Freedom-to-Operate.' The objective of this product is to provide a basic and practical tool to help scientists of Generation Challenge Programme projects to understand the importance of rights associated with the access and use of plant genetic resources and tools, methods, and products protected by intellectual property rights (IPRs) and contracts when the results of research are to be used freely by smallholder farmers. It is addressed to GCP scientists who operate at a considerable distance from (inter)national PGR regulations and IPR, but also to scientists at NARS and other persons receiving GCP-products that need to be aware of possible strings attached to these (intermediary) products.
2) An Asset Inventory System for the Generation Challenge Programme to provide a service function to GCP scientists and administration, in order to facilitate product delivery, distribution, and uptake (technology transfer). The system is developing e-versions of asset/product identification and 3rd party materials and reporting forms, as well as an inventory database of GCP Products and 3rd party materials.
3) IP Matters is an Intellectual Property/Access and Benefit Sharing-Helpdesk, designed as an on-line resource for the GCP community, its partners, and stakeholders. It provides a practical on-line service desk for assistance, clearing-house activity, and feedback on topics concerned with intellectual property matters in the broadest sense.
4) Regional PGR courses, which will prepare learning materials and a course curriculum for NARS, to be tested in 2006 in a face-to-face workshop.

Enabling delivery

The understanding of the specific role of the GCP in delivering its products has significantly evolved since the GCP was established in 2003. With the progress of the Programme during its first year, it seemed clear that the GCP should develop a delivery strategy to ensure that indeed the GCP products reach the intended users and make impacts on the poor. Thus, an electronic forum was conducted among a number of experts (15) in relevant fields (agricultural economics, social sciences, intellectual property rights, bio-policies, agricultural geography, taxonomy, research planning, food technology, plant pathology, crop evolution, genetic resources, genetics-plant breeding) to the subject. Experts were drawn from within and outside the GCP Consortium,

and included the public and the private sectors. The forum was driven by selected questions addressing the significance of the involvement of the GCP in product delivery, the definition of intended users and GCP products, the mechanisms possible in the areas where the resource-poor live, and indicators of impact, among others.

Afterward, a face-to-face workshop was conducted to brainstorm about the delivery strategy in general and to discuss the important principles on which to base the drafting of the strategy document. It involved 17 participants: plant breeders, social scientists with backgrounds in rural innovation, agricultural economists with expertise in impact assessment, agricultural anthropologists, an intellectual property attorney, and farmer leaders from the three regions (Africa, Asia, and Latin America). The group represented perspectives of the CG Centres, NARS, ARIs, Harvest+ CP, donors, and stakeholders.

As a result, the GCP Management Team produced a final delivery strategy document with a supplementary text with details for its implementation.

The main thrust of this strategy is the adoption by the GCP of a value-chain based approach, in which it aims to catalyse the various players needed to bridge the gap between upstream strategic research in advanced laboratories and target user communities. In order to make it real, the GCP will require a delivery plan for every project proposal submitted and approved, and it will play an oversight role by ensuring that its products are inserted into existing delivery systems.

Lessons learned and conclusions

Several points for improvement were identified during this year, in particular in the area of training. One relates to the organisation of stand-alone training courses for technical themes. While it is indeed a type of activity always in demand and an important number of applications were received, the GCP should very much focus on impact. As a consequence, it was felt that the influence of training courses in our NARS partners would increase if they were first organised in the context of ongoing research projects and then targeted to those scientists and institutions already involved in the projects.

Another area that may benefit from past experience is the selection of fellows. It is expected that in the future a more restricted announcement will be circulated, limited to ongoing projects, with better defined requirements for application that will involve the agreement and commitment of the principal investigator of the project. With this, capacity of the fellows will be strengthened in the core subjects of the Programme and simultaneously they will support the progress of priority projects in our research agenda.

Perspectives for 2006

In 2006, SP5 will refocus as a result of the implementation of the delivery strategy. In the next call for competitive projects, the GCP will require delivery plans for every project proposal submitted and approved. The intent of delivery plans is to encourage scientists to explicitly explain how their results and products will be useful to intended users and how the use of these results/products will generate future products for farmers. SP5 will provide funds to conduct an initial workshop gathering research partners, intended users of the research products, and wider stakeholders (as appropriate). These workshops should facilitate scientific exchange, establish and strengthen partnerships as included in the delivery plan, distribute tasks, clarify roles, and also determine specific capacity building needs to ensure delivery. In consequence, most training activities will be identified and conducted within the projects.

Also related to the concentration on delivery and impact, SP5 will fund a number of projects based on the socio-economic analysis of some of the GCP products being generated now as a result of the competitive call in the previous year. While guiding the delivery of those products once ready, the results obtained should also serve to set priorities for the second phase of the Programme.

The Fellowship and Travel Grant programmes will continue, with emphasis on the selection of grantees to support ongoing competitive and commissioned projects.

Finally, policy activities will continue as planned and a number of new activities will be commissioned. These are: 1) the development of training materials for phenotyping and linkage disequilibrium and association mapping, 2) an international training course on phenotyping, and 3) a survey to assess the target level and criteria for involvement in the GCP of present NARS partners.

Year 3 (2006) Summary Workplan and Budget

2006 Summary Competitive and Commissioned Research

Institution Type	Competitive (three-year average)	Commissioned Projects	TOTAL
CGIAR	1,740,091 [3]	2,933,731	4,673,822
GCP ARIs	906,574	1,181,884	2,087,458
GCP NARS	650,815	591,644	1,242,459
non-GCP ARIs	844,725	571,628	1,416,353
non-GCP NARS	539,572	165,000	704,572
Partners to be identified	-	1,256,113	1,256,113
Estimate total[4]	4,681,777	6,700,000	11,381,777
Real 2006 TOTAL[5]	***4,615,692***	***6,700,0006***	***11,315,692***

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**

[3] Per year average of projects, for comparative purposes.

[4] Estimate 2006 total is sum of yearly average.

[5] Actual total amounts distributed in 2006. Differs from the estimate due to larger first year budgets in some projects.

[6] Difference between real and estimate reflects uncommitted research funds to be allocated in 2006.

2006 Commissioned Research – GCP Consortium Members

(see Appendix C for full project details)

#	2006 total	ACGT	Agropolis	Embrapa	CAAS	Cornell	CIAT	CIMMYT	CIP	ICARDA	ICRISAT	IITA	IPGRI	IRRI	JIC	NIAS	WUR	WARDA	Others
SP1																			
2005-06	178,430			178,430															
2005-07	396,720		239,720	157,000															
2006-01	109,386			12,744			12,980			6,490	19,470			57,702					
2006-02	573,000		87,200				27,600		88,000	12,600	64,600			15,000					278,000
2006-03	150,000		35,000											45,000					70,000
2006-04	51,000												51,000						
2006-05	35,400									35,400									
2006-06	20,000										20,000								
2006-29	50,150			4,720			15,340					30,090							
2006-30	25,016										25,016								
2006-31	60,042										60,042								
2006-32	30,000										30,000								
2006-33	15,000								15,000										
SP1 total	**1,694,144**																		
SP2																			
2005-09	250,000		40,000		25,000		40,000							40,000		40,000	40,000		25,000
2005-10	60,000							60,000											
2005-11	105,000						105,000												
2005-12	100,300								33,040										67,260
2005-13	99,845				39,985		23,010									36,850			
2005-15	200,000		40,000	40,000									40,000			80,000			
2005-17	82,300		26,800				55,500												
SP2 Total	**897,445**																		
SP3																			
2005-18	150,000							58,200						91,800					
2005-19	119,180						18,290	18,290	18,290		18,290			8,260					37,760
2005-20	130,000							80,000											50,000
2005-21	67,850												23,600						44,250
2006-07	300,300*							160,300											140,000
SP3 Total	**692,330**																		
SP4																			
2005-22	200,000	80,240	20,650						20,650				20,650	37,160		20,650			
2005-23	140,000								17,000				106,000	17,000					
2005-24	80,000		5,428				5,428						14,160	46,488		3,068	5,428		
2005-25	80,000	20,000						40,000					15,000	x					5,000
2005-26	120,950							10,620	10,620		3,540		90,270				5,900		
2005-27	100,000							8,614	40,764		21,004			21,004					8,614
2005-30	50,000		15,000														35,000		
2005-31	100,000		28,320	11,800							5,900			53,980					
2005-32	100,000															100,000			
2005-33	84,000							5,000			74,000			5,000					
2005-34	80,000								11,800					68,200					
2006-08	150,000							45,000	60,000					45,000					
2006-16	150,000	7,000	17,000	7,000				17,000	17,000	10,000	10,000			60,000		5,000			
2006-17	150,000													66,692					83,308
2006-18	16,500						16,500												
2006-19	16,500							16,500											

#	2006 total	ACGT	Agropolis	Embrapa	CAAS	Cornell	CIAT	CIMMYT	CIP	ICARDA	ICRISAT	IITA	IPGRI	IRRI	JIC	NIAS	WUR	WARDA	Others
2006-20	16,500								16,500										
2006-21	16,500									16,500									
2006-22	16,500										16,500								
2006-23	16,500											16,500							
2006-24	16,500												16,500						
2006-25	16,500													16,500					
2006-34	33,453										26,550	1,770							5,133
SP4 Total	**1,750,403**																		
Uncomm	**265,678**																		
SP1-4 Total	**5,300,000**																		
SP5																			
2005-CB15	67,745			2,575									10,300				54,870		
2005-CB16	76,220			5,150									60,770						10,300
2005-CB17	20,600										8,300		12,300						
2006-09	112,500		112,500																
2006-10	35,000																		
2006-11	12,500																12,500		
2006-12	500,000																		
2006-13	100,000																		
2006-14	100,000																		
2006-15	280,000																		
2006-26	25,000																		
2006-27	30,000																		
2006-28	25,000																25,000		
Uncomm	**15,435**																		
SP5 Total	**1,400,000**																		
TOTAL	**6,700,000**	**107,240**	**667,618**	**419,419**	**64,985**	**50,000**	**319,648**	**519,524**	**348,664**	**80,990**	**403,212**	**48,360**	**460,550**	**694,786**	**0**	**285,568**	**178,698**	**0**	**824,625**

Competitive Grants (3 year projects) – GCP Consortium Members

#	AGROPOLIS	EMBRAPA	CAAS	Cornell University	CIAT	CIMMYT	ICARDA	ICRISAT	IITA	IRRI	JIC	NIAS	WUR	WARDA	Others	TOTAL
1										489,360		106,200			304,440	
2										468,120					431,880	
3		272,379		172,138	226,949				100,207						95,472	
4						60,300							222,500		224,350	
5	59,400	238,696						276,120							324,020	
6									296,143						603,857	
7				64,900											35,100	
8				347,731						145,317					406,563	
9		140,066			409,342										345,498	
10		87,300		353,600	459,300									89,700	85,000	
11	235,000	150,000				105,000					185,000	85,000			140,000	
12			572,700							316,800					0	
13	42,480			155,760		473,180									227,632	
14	129,210		17,405			436,010			26,845						107,675	
15	194,700					289,100				160,480					254,406	
16		473,898		366,102											60,000	
17							392,000								507,000	
Total	**660,790**	**1,362,339**	**590,105**	**1,460,231**	**1,095,591**	**1,363,590**	**392,000**	**276,120**	**423,195**	**1,580,077**	**185,000**	**191,200**	**222,500**	**89,700**	**4,152,893**	**14,045,330**

First Round of Competitive Grants

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 for 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**

Financials

The GCP has maintained a healthy financial condition since its inception, thanks in large part to a donor community that generously supports the GCP. Our major donors are the European Commission (EC), the UK Department for International Development (DFID), and the World Bank (WB), contributing about 90% to our total income.

Compared to 2004 (US$ 10.9 M), our income increased in 2005 by about 28% (US$ 14 M). This overall increase was the result of growth in the size of the contributions from both the EC and the World Bank. The level of contribution from our major donors is anticipated to remain at the same level in foreign currency terms for 2006. However, income for 2006 is projected to decline to US$ 12.3M, reflecting the strengthening US dollar value relative to the currencies of our two major European donors. Budget projections have been based on a conservative exchange rate (5% below the lowest in December 2005) to anticipate some potential further increase in the US dollar value relative to European currencies during 2006.

A total of $6.2 M represented the carryover from 2004 to 2005, which reflected the delay in dispersing some funds due to a number of factors common to new programmes and the timing of some donor contributions that bridged years (e.g., DFID arrives in July and is to cover the March-April fiscal year). Resource allocation for research in 2005 and 2006 has deliberately exceeded income to help reduce and absorb this carryover. At the end of 2006 the total carry-forward is projected to be US$ 2.1 M, with a net carryover of US$ 0.8 M once 2006 remaining commitments (20% of the 2006 commissioned funds) have been removed. From 2007 on, the GCP will plan research activities according to our income status.

To clearly distinguish income versus expenditure and GCP assets, the presentation of the general financial tables in this report have been adjusted. The summary financial reports (income and expenses plus net assets) for 2005 and 2006 are shown in Tables 2 and 3. Details of 2005 and 2006 expenses are shown in Appendices D and E. Financial information presented for 2005 is based on actual year-end financial reports while the figure for 2006 is a projection based on anticipated income and expenditure. 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.

In 2005, an additional US$ 0.5 M was moved into the GCP reserves, which now total US$1 M. This reserve is shown as "Contingency Reserve" in the net assets section of the summary financial tables (Tables 2 and 3).

Although interactions with potential new donors were limited this year, due in large part to the transitions the GCP underwent, timely reporting to and good communication with our current donors has been maintained. Special attention will be dedicated during 2006 to diversifying the GCP's funding base to bring in additional funds for the purpose of further consolidating the research agenda and implementing GCP product delivery.

Table 1. In-Kind Contributions

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%
Total	**49**	**13,847,631**	**8,302,860**	'
Non-CGIAR Institutions	42	8,621,826	6,080,640	70.53%

Table 2. 2005 Summary Financials

USD

2005 Income vs Expenditures

			Actual
Income			
DFID [1/]			4,417,000
EC [2/]			6,027,334
Kirkhouse			15,000
Pioneer			20,000
RF			837,931
Sweden [3/]			189,495
World Bank [4/]			2,500,000
Sub-Total			**14,006,760**
Interest			186,361
Total Income			**14,193,121**
Expenditure			
Salaries & Benefits (Management)			262,090
Salaries & Benefits (SubProgram Leaders 1-5)			331,623
Operational Travel (GCP Management)			8,848
Conferences & PSC expenses			281,260
Office Supplies & Services			77,951
Printing & Design			37,393
Vehicle Expenses			7,751
Consulting			58,159
Research			13,647,004
Commissioned Research WorkPlan Yr1 (2004 20%)		1,041,338	
Commissioned Research WorkPlan Yr2 (2005 80%)		6,414,475	
Competitive Grants Yr 1 (2005 - Round 1)		4,931,956	
SP1	3,224,640		
SP2	3,225,289		
SP3	2,111,491		
SP4	2,084,172		
SP5	1,742,177		
Operational Support SPLs		435,000	
RF Grants		824,235	
Sub-total			**14,712,079**
Capital			23,221
Transfer to Reserve [5/]			500,000
Sub-Total			**15,235,301**
Indirect Costs 4% [6/]			324,330
Total Expenditure			**15,559,631**
Surplus /(Deficit) for year [7/]			**(1,366,510)**

[1/] Equivalent to GBP 2.5m
[2/] Equivalent Eur 4.6m
[3/] Contribution equivalent to SEK 0.683m received 24 Jan & Contribution equivalent to SEK .690m received 7 Dec
[4/] Contribution received 4 Feb
[5/] 2004 - 2005 target $1.0m
[6/] Includes adjustment for previous years (2003-2004)
[7/] See Note 1 in schedule of Statement of Changes in Net Assets

2005 Net Assets

	2003	2004	2005
Designated			
Opening balance	–	2,660,607	6,219,945
Net Surplus/(Deficit) for year	2,660,607	3,559,338	(1,366,510)
Closing Balance - Net Assets	**2,660,607**	**6,219,945**	**4,853,435** [1/]
Undesignated			
Contingency Reserve	–	500,000	1,000,000
Total Net Assets	**2,660,607**	**6,719,945**	**5,853,435**
Represented by:			
Cash held at CIMMYT	**2,660,607**	**6,719,945**	**5,853,435**

[1/] Carry-Forward breakdown:

84,000	2004 Commisioned Research commitment
1,280,000	2005 Commissioned Research remaining 20%
103,000	2005 Commissioned Research commitment
200,000	2005 Annual Research meeting commitment
3,186,435	2006 budget - carryover
4,853,435	Total

Table 3. 2006 Summary Financials

USD

2006 Income vs Expenditures

		Projection Jan-Dec
Income		
DFID [1/]		4,109,225
EC [2/]		5,196,367
Pioneer		25,000
RF		836,557
Pioneer		25,000
Sweden [3/]	-	
World Bank [4/]		2,000,000
Sub-Total		**12,192,149**
Interest	80,000	
Total Income		**12,272,149**
Expenditure		
Salaries & Benefits (Management)		315,000
Salaries & Benefits (SubProgram Leaders 1-5)		470,000
Operational Travel (GCP Management)		80,000
Conferences & PSC expenses		437,500
Office Supplies & Services		55,000
Printing & Design		50,000
Vehicle Expenses		21,000
Consulting		250,000
Research		12,702,779
Commissioned Research WorkPlan Yr2 (2005 20%)	1,280,847	
Commissioned Research Yr 3 (2006 80%) [5/]	5,583,455	
Operational Support SPLs	400,000	
Competitive Grants Yr2 (2006 - Round 1)	4,615,692	
RF Grants	822,785	
Sub-total		**14,381,279**
Capital		48,000
Sub-Total		**14,429,279**
Indirect Costs 4%	577,171	
Total Expenditure		**15,006,450**
Surplus/(Deficit) for year [7/]		**(2,734,301)**

[1/] Contribution expected in two installments Jul & Dec equivalent £ 2.5m (note 6)
[2/] Contribution equivalent Eur 4.7m.(note 6)
[3/] Contribution equivalent to SEK .690m received 7 Dec 2005
[4/] Estimated figure based on past average contribution
[5/] Commissioned Research projects under scheme 80/20%
2006 Budget $6.700m (80%) = 5.360m + 5 CR projects (100%) 223.4k
[6/] All foreign currency receipts subject to ExRate fluctuation
[7/] See note 1 in schedule of Statement of Changes in Net Assets

2006 Net Assets

	Projection 2006	
Designated		
Opening balance	4,853,435	
Net Surplus/(Deficit) for year	(2,734,301)	
Closing Balance - Net Assets	**2,119,134**	[1/]
Undesignated		
Contingency Reserve	1,000,000	
Total Net Assets	**3,119,134**	
Represented by:	**-**	
Cash held at CIMMYT	**3,119,134**	

[1/] Carry-Forward breakdown:
1,340,000 2006 Commissioned Research remaining 20%
779,134 2007 Budget - carryover
2,119,134

Appendices

Appendix A. 2005 Generation Challenge Programme Consortium Members and Partners

Consortium Members

Africa Rice Centre (WARDA)
African Centre for Gene Technologies (ACGT)
Agropolis
Brazilian Agricultural Research Corporation (Embrapa)
Chinese Academy of Agricultural Sciences (CAAS)
Cornell University
Indian Council on Agricultural Research (ICAR)
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 (WUR)

NARS Partners

Agricultural Biotechnology Research Institute of Iran (ABRII), Iran
Centre Africain de recherché sur bananas et plantains (CARBAP), Cameroon
Centre Research for Biotechnology, Bogor Agriculture University (IPB), Indonesia
Centre d'Etude Régional pour l'Amélioration de l'Adaptation à la Sécheresse (CERAAS), Senegal
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
Instituto Nacional de Investigación Agropecuaria (INIA), Uruguay
International Centre for Genetic Engineering and Biotechnology (ICGEB), India
Kenya Agriculture Research Institute (KARI), Nairobi, Kenya
Moi University, Kenya
Nakhon Sawon Field Crops Research Centre, Thailand
Namulonge Agricultural and Animal Production Research Institute (NAARI), Uganda
Nanjing Agricultural University (NAU), China
National Maize Research Institute, Vietnam
National Root Crop Research Institute (NRCRI), Umudike, Nigeria
New Partnership for African Development (NEPAD), Union of South Africa
Philippine Department of Agriculture
Scientific and Industrial Research and Development Centre (SIRDC), Zimbabwe
Tamil Nadu Agricultural University (TNAU), India
Tishreen University, Syria
Universidade Católica de Brasília (UCB), Brazil
University or Hyderabad, India
Universidad Autónoma Chapingo, Mexico

ARI Partners

Australian Centre for Plant Functional Genomics Pty Ltd, Australia
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
MOBY-S, Canada
National Center for Genome Resources, USA
Scottish Crop Research Institute (SCRI)
Sichuan Agriculture University, China
The Institute for Genomic Research (TIGR), USA
United States Department of Agriculture, North Carolina State University (NCSU)
Universita' di Udine, Italy
University of Aarhus, Denmark
University of Adelaide, Australia
University of California-Berkley, USA
University of California-Davis, USA
University of California-Riverside, USA
University of Queensland, Australia
University of Tsukuba, Japan
University of Virginia, USA
Vanuatu Agricultural Research and Training Centre (VARTC), Vanuatu

Appendix B. Full List of First Round Competitive Projects[7]

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

Principal Investigator: John Bennett, IRRI

Budget Summary by Partner	IRRI	CSIRO	NIAS	TNAU	NANJING	TOTAL
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

Principal Investigator: Abdelbagi Ismail, IRRI

Budget Summary by Partner	IRRI	CSIRO/Graingene	UCD	Dhaka University	ICABGRRD	TOTAL
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

Principal Investigator: Alfredo Alves, EMBRAPA

Budget Summary by Partner	EMBRAPA/ CNPMF	CIAT	IITA	Cornell University	SARI/Ghana	ARI, Tanzania	TOTAL
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

Principal Investigator: Fred van Eeuwijk, WUR

Budget Summary by Partner	WUR	CSIRO	CIMMYT	INIA-URUGUAY	TOTAL
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

Principal Investigator: Jose Montenegro Valls, EMBRAPA

Budget Summary by Partner	EMBRAPA	UCB	ICRISAT-India	ICRISAT-Kenya	IBONE	CERAAS	Aarhus	CIRAD	TOTAL
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

Principal Investigator: Festo Massawe, IITA

Budget Summary by Partner	IITA	CERAAS	UVA	TOTAL
Total Costs	296,143	70,800	533,057	900,000
In-Kind Contribution	60,000	30,000	31,188	121,188

7. Measuring linkage disequilibrium across three genomic regions in rice

Principal Investigator: Susan McCouch, Cornell University

Budget Summary by Partner	Cornell University	ICABGRRD	TOTAL
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

Principal Investigator: Rebecca Nelson, Cornell University

Budget Summary by Partner	Cornell University	IRRI	CSU	NCSU	Kari	TOTAL
Total Costs	347,731	145,317	166,669	141,010	98,884	899,611
In-Kind Contribution	—-	—-	—-	—-	—-	—-

[7] 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.

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

Principal Investigator: Anthony Bellotti, CIAT

Budget Summary by Partner	CIAT	EMBRAPA/CNPMF	NAARI	CRI	NRCRI	TOTAL
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

Principal Investigator: Joe Tohme, CIAT

Budget Summary by Partner	Cornell University	CIAT	FEDEARROZ	EMBRAPA	WARDA	TOTAL
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)

Principal Investigator: Pietro Piffanelli, CIRAD

Budget Summary by Partner	AGROPOLIS	CIMMYT	EMBRAPA	JIC	INRA RENNES	NIAS	UCD	TOTAL
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

Principal Investigator: Zhikang Li, CAAS

Budget Summary by Partner	CAAS	IRRI	TOTAL
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

Principal Investigator: Jean-Marcel Ribaut, CIMMYT

Budget Summary by Partner	CIMMYT	Cornell University	INRA	KARI	SAU	SIRDC	NSFCRC	Genaissance	TOTAL
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

Principal Investigator: Marilyn Warburton, CIMMYT

Budget Summary by Partner	CIMMYT	INRA	KARI	IITA	Indian Ag.	Thailand	Indonesia	Phil DOA	CAAS	Vietnam	TOTAL
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

Principal Investigator: Mark Sawkins, CIMMYT

Budget Summary by Partner	CIMMYT	ACPFG-Australia	INRA	ETH-Zurich	IRRI	IGAU-India	SIRDC-Zimbabwe	TOTAL
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

Principal Investigator: Leon Kochian, Cornell University

Budget Summary by Partner	Cornell University	EMBRAPA Maize & Sorghum	EMBRAPA Wheat	EMBRAPA Rice and Beans	MOI University	TOTAL
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

Principal Investigator: Michael Baum, ICARDA

Budget Summary by Partner	ICARDA	Adelaide	Udine	Tushreen University	TOTAL
Total Costs	392,000	254,500	207,500	45,000	899,000
In-Kind Contribution	—-	254,265	—-	—-	254,265

Appendix C. Full List of 2006 Commissioned Projects

SP1

2005-06. Supporting emergence of reference drought tolerance phenotyping centers

Budget summary by partner	EMBRAPA	TOTAL
Total	$178,430	$178,430

2005-07. Whole-plant modeling

Budget summary by partner	Agropolis	Embrapa	TOTAL
Total	$239,720	$157,000	$396,720

2006-01. Developing strategies for allele mining within large collections

Budget summary by partner	CIAT	EMBRAPA	ICRISAT	ICARDA	IRRI	TOTAL
Total	$12,980	$12,744	$19,470	$6,490	$57,702	$109,386

2006-02. A dataset on allele diversity at orthologous candidate genes in GCP crops (ADOC)

Budget summary by partner	Agropolis	CIP	ICRISAT	INRA-CNG	IRRI	ICARDA	CIAT	TOTAL
Total	$87,200	$88,000	$64,600	$278,000	$15,000	$12,600	$27,600	$573,000

2006-03. SNP analysis and the genetic diversity along the rice genome

Budget summary by partner	IRRI	CIRAD	INRA-CNG	TOTAL
Total	$45,000	$35,000	$70,000	$150,00

2006-04. Phenotyping in the field: global capacity accessible to the GCP—Inventory of phenotyping resources and capacity for the GCP

Budget summary by partner	IPGRI	TOTAL
Total	$51,000	$51,000

2006-05. Development of a composite collection and the genotyping of faba bean

Budget summary by partner	ICARDA	TOTAL
Total	$35,400	$35,400

2006-06. Genotyping composite collection of finger millet

Budget summary by partner	ICRISAT	TOTAL
Total	20,000	$20,000

2006-29. Preparing IITA-cassava reference germplasm for association mapping and distribution

Budget summary by partner	IITA	CIAT	EMBRAPA	TOTAL
Total	$30,090	$15,340	$4,720	$50,150

2006-30. Development of a composite collection and the genotyping of foxtail millet

Budget summary by partner	ICRISAT	TOTAL
Total	$25,016	$25,016

2006-31. Development of a composite collection and the genotyping of pearl millet

Budget summary by partner	ICRISAT	TOTAL
Total	$60,042	$60,042

2006-32. Development of a composite collection and the genotyping of pigeonpea

Budget summary by partner	ICRISAT	TOTAL
Total	$30,000	$30,000

2006-33. Development of a composite collection and the genotyping of potato

Budget summary by partner	CIP	TOTAL
Total	$15,000	$15,000

SP2

2005-09. Systematic evaluation of rice mutant collections for conditional phenotypes with emphasis on stress tolerance

Budget summary by partner	IRRI	WUR	CAAS/Beijing Genomics Institute (BGI)	NIAS	Agropolis	CIAT	Huazhong Agric. Univ.	TOTAL
Total	$40,000	$40,000	$25,000	$40,000	$40,000	$40,000	$25,000	$250,000

2005-10. Collection, distribution, phenytyping, and genotyping directed towards utilization of existing wheat genetic stocks to enhance tolerance/resistance of wheat cultivars to abiotic and biotic stresses with emphasis on drought

Budget summary by partner	CIMMYT	TOTAL
Total	$60,000	$60,000

2005-11. Legume mutant resource development

Budget summary by partner	CIAT	TOTAL
Total	$105,000	105,000

2005-12. A saturated potato mutant popluation for functional genomics among Solanaceae and tuber crops

Budget summary by partner	CIP	Hebrew Univ. of Jerusalem	SCRI	TOTAL
Total	$33,040	$27,730	39,530	$100,300

2005-13. Crop gene expression profiles and stress-gene arrays

Budget summary by partner	CIAT	CAAS/Beijing Genomics Institute (BGI)	NIAS	TOTAL
Total	$23,010	$39,985	$36,850	$99,845

2005-15. Musa genome frame-map construction and connection with the rice sequence

Budget summary by partner	IPGRI/ INIBAP	EMBRAPA	NIAS	CIRAD	TOTAL
Total	40,000	40,000	$80,000	40,000	$200,000

2005-17. Comparative QTL mapping for drought tolerance

Budget summary by partner	CIAT	Agropolis-IRD	TOTAL
Total	$55,500	$26,800	$82,300

SP3

2005-18. Development of low-cost gene-based trait assay technologies in cereals

Budget summary by partner	CIMMYT	IRRI	TOTAL
Total	$58,200	$91,800	$150,000

2005-19. Evaluation and deployment of transgenic drought tolerant varieties

Budget summary by partner	CIMMYT	CIP	IRRI	CIAT	ICRISAT	JIRCAS	University of Tsukuba	TOTAL
Total	$18,290	$18,290	$8,260	$18,290	$18,290	$18,880	$18,880	$119,180

2005-20. Optimizing marker-assisted breeding systems for drought tolerance in cereals through linkage of physiological and genetic models

Budget summary by partner	CIMMYT	CSIRO	Univ of Queensland	TOTAL
Total	$80,000	$30,000	$20,000	$130,000

2005-21. Planning for effective product development, delivery, and use

Budget summary by partner	IPGRI	IFPRI-ISNAR	TOTAL
Total	$23,600	$44,250	$67,850

2006-07. Molecular breeding communities of practice

Budget summary by partner	CIMMYT	Others (NARS TBD)	TOTAL
Total	$160,300	$140,000	$300,300

SP4

2005-22. Development of GenerationCP domain (data) models

Budget summary by partner	IRRI	NIAS	CIP	CIRAD	IPGRI/INIBAP	ACGT	TOTAL
Total	$37,160	$20,650	$20,650	$20,650	$20,650	$80,240	$200,000

2005-23. Implementation of web services technology in GenerationCP Consortium

Budget summary by partner	CIP	IRRI	IPGRI/ INIBAP	TOTAL
Total	$17,000	$17,000	$106,000	$140,000

2005-24. Application and development of web services technology

Budget summary by partner	IRRI	CIAT	CIRAD	IPGRI/INIBAP	NIAS	WUR	TOTAL
Total	$46,488	$5,428	$5,428	$14,160	$3,068	$5,428	$80,000

2005-25. Creation and maintenance of data templates

Budget summary by partner	CIMMYT	IRRI	ACGT	IPGRI	NGCR	KeyGene	TOTAL
Total	$40,00	$0	$20,000	$15,000	$5,000	$0	$80,000

2005-26. Management of GenerationCP Central Registry

Budget summary by partner	CIMMYT	IPGRI	CIP	ICRISAT	WUR	TOTAL
Total	$10,620	$90,270	$10,620	$3,540	$5,900	$120,950

2005-27. Integration of the High Performance Computing (HPC)-facilities in the GenerationCP toolbox

Budget summary by partner	CIP	CIMMYT	ICRISAT	ILRI	IRRI	TOTAL
Total	$40,764	$8,614	$21,004	$8,614	º$21,004	$100,000

2005-30. Data analysis support for existing projects in SP1 with emphasis on sampling germplasm

Budget summary by partner	WUR	CIRAD	TOTAL
Total	$35,000	$15,000	$50,000

2005-31. Development of ortholog-function display tools

Budget summary by partner	CIRAD	ICRISAT	IRRI	EMBRAPA	TOTAL
Total	$28,320	$5,900	$53,980	$11,800	$100,00

2005-32. Development of crop gene expression database and data mining tools

Budget summary by partner	NIAS	TOTAL
Total	$100,000	$100,000

2005-33. Development of an integrated decision support system for MAS and MAB

Budget summary by partner	IRRI	ICRISAT	CIMMYT	TOTAL
Total	$5,000	$74,000	$5,000	$84,000

2005-34. GCP software engineering and collaboration platform

Budget summary by partner	IRRI	CIP	TOTAL
Total	$68,200	$11,800	$80,000

2006-08. Data analysis support for existing projects in SP2 with emphasis on integrating results from microarray and mapping experiments

Budget summary by partner	CIMMYT	IRRI	CIP	TOTAL
Total	$45,000	$45,000	$60,000	$150,000

2006-16. Development of an integrated GCP information platform

Budget summary by partner	ACGT	EMBRAPA	CIMMYT	CIP	CIRAD	ICARDA	ICRISAT	IRRI	NIAS	TOTAL
Total	$7,000	$7,000	$17,000	$17,000	$17,000	$10,000	$10,000	$60,000	$5,000	$150,000

2006-17. GenerationCP data quality improvement and assurance

Budget summary by partner	IRRI	PARTNER 1(TBD)	TOTAL
Total	$66,692	$83,308	$150,000

2006-18. Creation of institutional bioinformatics capacity (CIAT)

Budget summary by partner	CIAT	TOTAL
Total	$16,500	$16,500

2006-19. Creation of institutional bioinformatics capacity (CIMMYT)

Budget summary by partner	CIMMYT	TOTAL
Total	$16,500	$16,500

2006-20. Creation of institutional bioinformatics capacity (CIP)

Budget summary by partner	CIP	TOTAL
Total	$16,500	$16,500

2006-21. Creation of institutional bioinformatics capacity (ICARDA)

Budget summary by partner	ICARDA	TOTAL
Total	$16,500	$16,500

2006-22. Creation of institutional bioinformatics capacity (ICRISAT)

Budget summary by partner	ICRISAT	TOTAL
Total	$16,500	$16,500

2006-23. Creation of institutional bioinformatics capacity (IITA)

Budget summary by partner	IITA	TOTAL
Total	$16,500	$16,500

2006-24. Creation of institutional bioinformatics capacity (IPGRI)

Budget summary by partner	IPGRI	TOTAL
Total	$16,500	$16,500

2006-25. Creation of institutional bioinformatics capacity (IRRI)

Budget summary by partner	IRRI	TOTAL
Total	$16,500	$16,500

2006-34. Installation and implementation of the ICRISAT LIMS at the Biosciences Eastern and Central Africa (BECA) facility and IITA-Ibadan

Budget summary by partner	ICRISAT	ILRI	IITA	TOTAL
Total	$26,550	$5,133	$1,770	$33,453

SP5

2005-CB15. Distance learning module for scientists on Genetic Resource Policies and their implications for Freedom-to-Operate.

Budget summary by partner	WUR	EMBRAPA	IPGRI	TOTAL
Total	$54,870	$2,575	$10,300	$67,745

2005-CB16. Intellectual Property and Access&Benefit Sharing-helpdesk and On-line-Resource for the GCP Community, Partners and Stakeholders

Budget summary by partner	IPRGI	EMBRAPA	Queen Mary IP Institute	TOTAL
Total	$60,770	$5,150	$10,300	$76,220

2005-CB17. Reporting for Product Distribution: An asset inventory system for the GCP

Budget summary by partner	IPGRI	ICRISAT	TOTAL
Total	$12,300	$8,300	$20,600

2006-15. Fellowships and travel grants

Budget summary by partner	TOTAL
Total	$280,000

2006-09. Training course on phenotyping

Budget summary by partner	INRA	TOTAL
Total	$112,500	$112,500

2006-10. Expanding partnership for delivery

Budget summary by partner	To be determined	TOTAL
Total	$35,000	$35,000

2006-11. Establishment of training materials for a course in association study/linage disequilibrium mapping (TM_AS)

Budget summary by partner	WUR	TOTAL
Total	$12,500	$12,500

2006-12. Support to competitive projects in development and implementation of delivery plans

Budget summary by partner*	TOTAL
Total	$500,000

2006-13. Competitive socioeconomic project

Budget summary by partner*	TOTAL
Total	$100,000

2006-14. Competitive socioeconomic project

Budget summary by partner*	TOTAL
Total	$100,000

2006-26. Translation of training materials

Budget summary by partner*	TOTAL
Total	$25,000

2006-27. Contribution to special conferences

Budget summary by partner*	TOTAL
Total	$30,000

2006-28. Regional PGR Courses

Budget summary by partner	WUR	TOTAL
Total	$25,000	$25,000

***Funds to be committed during 2006

Appendix D. Detailed Expenditure Schedule for 2005

USD

Description	Expenditures	Total
Salaries & Benefits		**262,090**
Mngm Int'l	179,889	
Mngm Int Commun	43,462	
Mngm Admin Support	38,739	
Salaries & Benefits SPLeaders (1-5) [1/]		**331,623**
SP1	73,773	
SP2	67,898	
SP3	53,393	
SP4	46,000	
SP5 [2/]	90,560	
Travel		**8,848**
RZ/JMR	3,530	
JN	5,318	
Conferences		**281,260**
PSC	47,829	
PAG (Plant&Animal Genome Conf)	1,268	
Annual Research Meeting	46,277	
Stakeholder's Committee (GFAR) (EC)	154,077	
AGM	4,182	
Others	27,628	
Office Supplies & Services		**77,951**
Office	11,764	
Shipping & Postage	15,992	
Maintenance & Repair	107	
Calls & Fax	5,361	
ICT Service (Inf & Comm. Tech) [3/]	11,333	
GCP Director Recruiting process [4/]	33,392	
Printing & Design		**37,393**
Printing & Design	30,472	
Software/Website	6,922	
Vehicle Expenses		**7,751**
Gasoline	2,081	
Insurance	1,695	
Maintenance	3,975	
Consultants (salary & benefits, travel)		**58,159**
Communications Consultant [5/]	1,730	
VI/KL (Web content management)	19,256	
Legal consultant	26,285	
Consultant	10,888	
Research		**13,647,004**
Commisioned Research - remaining 20% Work Plan Yr1 (2004)	1,041,338	
Commissioned Research 2005 (80%) [6/]	6,414,475	
Operational Support SPLs	435,000	
Competitive Grants 2005 (Yr1 - Round 1)	4,931,956	
RF Grants	824,235	
Competitive Grants (Round 2) [7/]		
Capital		**23,221**
Computer	2,724	
Printer	-	
Auto	18,283	
Office Addition equipment	2,214	
Transfer to Reserve		**500,000**
Indirect Costs [8/]		**324,330**
Adjustment prior years (2003-2004)	(271,401)	
4% on expenditures incurred	595,731	
TOTAL EXPENDITURE		**15,559,631**

[1/] Only moved from Research line item for administrative purpose
[2/] Includes cost of an Admin. Assistant to manage the Fellowships & Travel Grants
[3/] Service effective Jan 05
[4/] New commitment
[5/] Moved Mngm Int Commun
[6/] 20% carry forward 2006 $1.280m (Commissioned Research Projects under scheme 80/20%)
[7/] Project transferred to 2007
[8/] Includes adjustment for previous years (2003-2004)

Appendix E. 2006 Budget Details

USD

Description	Projection Expenditure	Total
Salaries & Benefits		**315,000**
Mngm Int'l	170,000	
Mngm Int Commun	50,000	
Mngm Admin Support	45,000	
Project Officer	50,000	
Salaries & Benefit SPLeaders		
Subprogram Leaders 1-5	470,000	**470,000**
Travel		**80,000**
JMR	50,000	
JN	15,000	
Project Officer	15,000	
Conferences		**437,500**
PSC	100,000	
PAG	15,000	
Annual Research Meeting	250,000	
Stakeholder's Committee (GFAR) (EC)	62,500	
AGM	10,000	
Office Supplies & Services		**55,000**
Office	10,000	
Shipping & Postage	11,000	
Maintenance & Repair	3,000	
Calls & Fax	6,000	
ICT Service (Inf & Comm. Technologies)	25,000	
Printing & Design		**50,000**
Printing & Design	30,000	
Software/Website	20,000	
Vehicle Expenses		**21,000**
Gasoline	6,000	
Insurance	5,000	
Maintenance	10,000	
Consultants (salary & benefits, travel)		**250,000**
Implementation (Quality Control & Delivery)	120,000	
(Web content management) - replacement	20,000	
Legal consultant	30,000	
Consultants / Facilitator	80,000	
Research		**12,702,779**
Remaining 20% Work Plan Yr2	1,280,847	
Commissioned Research 2006 (80%) [1]/	5,583,455	
Operational Support SPLs	400,000	
Competitive Grants (Yr2 - Round 1)	4,615,692	
RF Grants (Yr2)	822,785	
Capital		**48,000**
Computer	6,000	
Printer	2,000	
Cars (2)	40,000	
Indirect Costs		
Indirect Costs 4%		**577,171**
TOTAL EXPENDITURE		**15,006,450**

[1]/ Commissioned Research projects under scheme 80/20%
2006 Budget $6.700m (80%) = 5.360 m + 5 CR projects (100%) 223.4k

Generation

Cultivating Plant Diversity for the Resource Poor

For more information about the Generation Challenge Programme, please contact:
Jean-Marcel Ribaut, Director, or **Jenny Nelson**, Communications Manager
Apdo. Postal 6-641 06600 Mexico D.F., Mexico
Telephone: +52 55 5804 2004 x1312 or 1313 Fax: +52 55 5804 7558
Email: **j.ribaut@cgiar.org** or **j.nelson@cgiar.org**
Visit us on the web at **www.generationcp.org**

Consortium members

African Centre for Gene Technologies (ACGT) • Agropolis • Brazilian Agricultural Research Corporation (Embrapa) • Chinese Academy of Agricultural Sciences (CAAS) • Cornell University • Indian Council for Agricultural Research (ICAR) • 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)