



Generation Challenge Programme Medium-Term Plan: 2009–2011

**Compiled by
The GCP Management Team and Communications Manager**

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Generation Challenge Programme (GCP)

Hosted by CIMMYT

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Acronyms and abbreviations

ABA	abscisic acid
ABRII	Agriculture Biotechnology Research Institute of Iran
ACCI	African Centre for Crop Improvement, South Africa
ACGT	African Centre for Gene Technologies, South Africa
ACPFPG	Australian Centre for Plant Functional Genomics Pty Ltd
ADOC	allelic diversity for orthologous candidate genes
AGRA	Alliance for a Green Revolution in Africa
AICMIP	The All-India Coordinated Pearl Millet Improvement Project
Al	aluminium
<i>Alt_{SB}</i>	marker diagnostic for aluminium tolerance
ANR	L'Agence nationale de la recherche, France
ANR	Agence Nationale de la Recherche, France
AP2/ERF	Apetala 2/ Ethylene-responsive element binding factors
ARI	Agharkar Research Institute, India
ARI(s)	advanced research institute(s)
ARI-HAS	Agricultural Research Institute of the Hungarian Academy of Sciences, Hungary
ARI-Naliende	Agricultural Research Institute–Naliende Research Station, Tanzania
ARM	Annual Research Meeting
ART	Agricultural Research in Tanzania
ARTC	Agricultural Research and Technology Corporation, Sudan
ARTC	Agricultural Research and Technology Corporation, Sudan
ASR	ABA/water stress/ripening-induced
BAC	bacterial artificial chromosome
BC1	backcross1
BCMV	bean common mosaic virus
BGYMV	bean golden yellow mosaic virus
BINA	Bangladesh Institute of Nuclear Agriculture
BIOTEC	National Center for Genetic Engineering and Biotechnology, Thailand
Bioversity	Bioversity International
BLAST	Basic Local Alignment Search Tool
BLB	bacterial leaf blight
BMGF	Bill & Melinda Gates Foundation
BRRD	Bureau of Rice Research and Development, Rice Department, Thailand
BRRRI	Bangladesh Rice Research Institute
BSA	bulk segregant analysis
CAAS	Chinese Academy of Agricultural Sciences
CARBAP	Centre africain de recherche sur bananiers et plantains, Cameroon
CARDI	Cambodia Agricultural Research and Development Institute, Cambodia
CAZRI	Central Arid Zone Research Institute, India
CBF	C repeat_dehydration responsive element-binding factor
CBI	Crop Breeding Institute, Department of Research for Development, Zimbabwe
CBSD	cassava brown streak disease
cDNA	complementary DNA
CERAAS	Centre d'étude régional pour l'amélioration de l'adaptation à la sécheresse, Senegal
CGIAR	Consultative Group on International Agricultural Research
CGM	cassava green mites

CIAT	Centro Internacional de Agricultura Tropical (International Center for Tropical Agriculture)
CIMMYT	Centro Internacional de Mejoramiento de Maiz y Trigo (the International Maize and Wheat Improvement Center)
CIP	Centro Internacional de la Papa (International Potato Centre)
CIRAD	Centre de coopération internationale en recherche agronomique pour le développement, France
cM	centiMorgan
CMD	cassava mosaic disease
CMTV	Comparative Map and Trait Viewer
CoP	community of practice
COS	conserved orthologous sequence
CP	Challenge Programme (of the CGIAR)
CPU	central processing unit
CRI	Crops Research Institute, Ghana
CRRRI	Central Rice Research Institute, India
CRURRS	Central Rainfed Upland Rice Research Station, India
CSIRO	Commonwealth Scientific and Industrial Research Organisation, Australia
CSO	civil society organisation
CSSL	chromosome segment substitution line
DARS	Department of Agriculture Research Services, Malawi
DArT	diversity arrays technology
DArT P/L	Diversity Arrays Technology Pty Ltd
DNA	deoxyribonucleic acid
DP	Delivery Plan
DPI&F	Department of Primary Industries & Fisheries, Australia
DPKit	Delivery Plan Kit
DPKV	Dr Panjabrao Deshmukh Krishi Vidyapeeth (DPKV; Dr Panjabrao Deshmukh Agricultural University), India
DREB	drought-responsive element binding protein
DUAS	Dharwad University of Agricultural Sciences, India
DWR	Directorate of Wheat Research, India
DZARC	Debre Zeit Agricultural Research Centre, Ethiopia
ECABREN	Eastern and Central Africa Bean Research Network
Eger–Hungary	Department of Plant Sciences and Plant Physiology, Eszterházy Károly College, Eger, Hungary
EIAR	Ethiopian Institute of Agricultural Research
EMBRAPA	Empresa Brasileira de Pesquisa Agropecuária (Brazilian Agricultural Research Corporation)
EPMR	External Programme and Management Review
ERECTA	a leucine rich repeat receptor-like kinase
EST	expressed sequence tag
ETH	Eidgenössische Technische Hochschule, (Swiss Federal Institute of Technology), Zürich, Switzerland
ETH	Eidgenössische Technische Hochschule, (Swiss Federal Institute of Technology), Zürich, Switzerland
FL	a rice variety
FPP	field phenotyping platform
GCP	Generation Challenge Programme of the CGIAR
GIPB	Global Partnership Initiative for Plant Breeding Capacity Building
GIS	geographic information system(s)

GISH	genomic <i>in situ</i> hybridisation
GOST	GreenPhyl Ortholog Search Tool
GPL	General Public License
GSS	Genotyping Support Service
GxE	genotype by environment interaction
HAAS	Hebei Academy of Agricultural Sciences, Institute of Dry Farming, China
HPC	high-performance computing
HRD	an AP2/ERF-like transcription factor, identified by a gain-of-function Arabidopsis mutant hrd-D having roots with enhanced strength, branching, and cortical cells, exhibits drought resistance and salt tolerance, accompanied by an enhancement in the expression of abiotic stress associated genes
HZAU	Huazhong Agricultural University, China
ICABIOGRAD	Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development
ICARDA	International Centre for Agricultural Research in the Dry Areas
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
ICS–CAAS	Institute of Crop Science, Chinese Academy of Agricultural Sciences
IER	Institut d'économie rurale, Mali
IFPRI	International Food Policy Research Institute
IGKV	Indira Gandhi Krishi Vidyalaya, India
IIAM	Instituto de Investigação Agrária de Moçambique (Institute for Agricultural Research), Mozambique
IIAM	Instituto de Investigação Agrária de Moçambique (Institute for Agricultural Research), Mozambique
IIPR	Indian Institute of Pulses Research
IITA	International Institute of Tropical Agriculture
ILRI	International Livestock Research Institute
iMAS	Integrated Marker-Assisted Selection System
INCA	Instituto Nacional de Ciencias Agrícolas, Cuba
INCAE	INCAE Business School
INERA	Institut de l'environnement et de recherches agricoles, Burkina Faso
INIA–Chile	Instituto Nacional de Investigaciones Agropecuarias
INIA–Uruguay	Instituto Nacional de Investigación Agropecuaria, Uruguay
INIFAP	Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias, Mexico
INRA	Institut national de la recherche agronomique (France, Morocco)
INRAN	Institut national de recherches agronomiques du Niger
INTA	Instituto Nacional de Tecnología Agropecuaria (Argentina, Nicaragua)
INV	cell-wall invertase
IP	intellectual property
IPK	Leibniz Institute of Plant Genetics and Crop Plant Research, Germany
IPT	isopentenyltransferase (gene)
IRAD	Institut de la recherche agronomique pour le développement, Cameroon
IRD	Institut de recherche pour le développement, France
IRRI	International Rice Research Institute
ISRA	Institut sénégalais de recherches agricoles, Senegal
JCVI	James Craig Venter Institute, USA
JGI, DoE	Joint Genomics Institute, Department of Energy, USA
JIC	John Innes Centre, UK
JIRCAS	Japan International Research Center for Agricultural Sciences
KARI	Kenya Agricultural Research Institute

KSU	Kansas State University, USA
KUL	Katholieke Universiteit Leuven, Belgium
LAAS	Luoyang Academy of Agricultural Sciences, China
LD	linkage disequilibrium
LGPL	Lesser General Public License
LIMS	Laboratory Information Management System
LPP	local phenotyping platform
LZARDI	Lake Zone Agricultural Research and Development Institute, Tanzania
MAB	marker-assisted backcrossing
MAGIC	multiparent advanced generation inter-cross
MARC	Melkassa Agricultural Research Centre, Ethiopia
MARS	marker-assisted recurrent selection
MAS	marker-assisted selection
MAU	Marathwada Agricultural University, India
MB	molecular breeding
MBDT	Molecular Breeding Design Tool
MOSEL	Molecular Selection Tools
MPIDB	Max Planck Institute for Developmental Biology
MPIMPI	Max Planck Institute for Molecular Plant Physiology, Germany
MSA	multiple sequence alignments
MSV	maize streak virus
MTP	Medium-Term Plan
NAARI	Namulonge Agricultural Research Institute, Uganda
NaCRRI	National Crop Resources Research Institute, Uganda
NAFRI	National Agricultural and Forestry Research Institute, Laos
NAM	nested association mapping
NARS	national agricultural research system(s)
NCGR	National Center for Genome Resources, USA
NERICA	new rice for Africa
NGO	non-governmental organisation
NIAB	National Institute of Agricultural Botany, UK
NIAS	National Institute of Agrobiological Sciences, Japan
NIL	near-isogenic line
NIPGR	National Institute for Plant Genome Research, India
NPGRC	National Plant Genetic Resources Centre, Tanzania
NRCPB	National Research Centre on Plant Biotechnology, India
NRCRI	National Root and Tuber Crops Research Institute, Nigeria
NRCS	National Research Centre on Sorghum, India
NSFCRC	Nakhon Sawan Field Crops Research Center, Thailand
NU	Ningxia University, China
NWSUAF	Northwest Sci-tech University of Agriculture and Forestry, China
OFSP	orange-fleshed sweet potatoes
OPVs	Open-pollinated varieties
ORE	Organisation for the Rehabilitation of the Environment, Haiti
OSI	Open Source Initiative
OSU	Oregon State University, USA
PARC	Pakistani Agricultural Research Council
PAU	Punjab Agricultural University, India
PCR	polymerase chain reaction
PDA	Product Delivery Advisor
PDG	Project Development Guide

PDKV	Dr Panjabrao Deshmukh Krishi Vidyapeeth, India (Dr Panjabrao Deshmukh Agricultural University)
PhilRice	Philippine Rice Research Institute
PI	Principal Investigator
PROINPA	Promoción e Investigación de Productos Andinos, Bolivia
pSARK–IPT	IPT gene under control of SARK promoter
PSU	Pennsylvania State University, USA
<i>Pup1</i>	marker diagnostic for phosphorus uptake
PVT	participatory variety testing
QTL	quantitative trait locus
QTLxE	QTL by environment
R&D	Research and development
RAP	Review and Advisory Panel
RAU	Rajasthan Agricultural University, India
RCB–IPB	Research Center for Biotechnology, Bogor Agricultural University, Indonesia
RFLP	restriction fragment length polymorphism
RIKEN	Japanese abbreviation for ‘Rikagaku Kenkyūsho’: The Institute of Physical and Chemical Research
RIL	recombinant inbred lines
RNA	ribonucleic acid
RNAi	RNA interference
RYMV	rice yellow mottle virus
SAAS	Shanxi Academy of Agricultural Sciences, China
SABRN	Southern Africa Bean Research Network
<i>Saltol</i>	marker diagnostic for salt tolerance
SARI	Savannah Agricultural Research Institute, Ghana
SARK	senescence associated receptor protein kinase
SCRI	Scottish Crop Research Institute, UK
SGRP	System-wide Genetic Resources Programme of the CGIAR
SHN	gene responsible for brilliant, shiny green leaf surface of the gain-of-function mutant <i>shine</i>
SHW	synthetic hexaploid wheat
SMEs	small- and medium-sized enterprises
SNP	single nucleotide polymorphism
SP	Subprogramme
SPS	sucrose phosphate synthase
SPVD	sweet potato virus disease
SS	sucrose synthase
SSR	simple sequence repeat
TAMU	Texas A&M University
TBA	to be announced
TBD	to be determined
TF	task force; transcription factor
TLI	Tropical Legumes I Project
TLII	Tropical Legumes II Project
TNAU	Tamil Nadu Agricultural University, India
UAS	University of Agricultural Sciences, India
UC	University of California, USA
UCB	Universidade Católica de Brasília, Brazil
UGA	University of Georgia, USA
UK	United Kingdom

UKZN	University of KwaZulu–Natal, South Africa
UQ	University of Queensland Australia
USA	United States of America
USDA–ARS	United States Department of Agriculture–Agricultural Research Service
VBI	Virginia Bioinformatics Institute, Virginia Polytechnic Institute and State University, USA
Virginia Tech	Virginia Polytechnic Institute and State University, USA
WARDA	Africa Rice Center
WUR	Wageningen University and Research Centre, The Netherlands
YAAS	Yunnan Academy of Agricultural Sciences, China

Overview

Introduction

The Generation Challenge Programme (GCP) was launched in 2003 as a 10-year initiative in two five-year phases (2003–2008 and 2009–2013). This fifth Medium-Term Plan (MTP) therefore marks GCP's transition into Phase II.

In its four-year life, the Programme has made remarkable progress in intensive research and strategic planning. Two major developments in 2007–2008 are particularly noteworthy. These developments will have an impact on the GCP research strategy and on the sharing of responsibilities among GCP's governance, management and advisory groups.

The first event was the External Programme and Management Review (EPMR) commissioned by the Science Council of the Consultative Group on International Agricultural Research (CGIAR). The overall tone of the EPMR was quite positive and CGIAR Executive Committee (ExCo) during their May meeting in Ottawa, Canada, acknowledged GCP's good performance. This first-ever EPMR was very opportune for GCP, coming at a time when we ourselves were stocktaking and reassessing research priorities and recommendations on governance: the EPMR significantly helped accelerate ongoing governance reforms as well as crystallise research prioritisation. The objectivity and deep insights provided by the Panel were very useful. Detailed recommendations of the EPMR are in Appendix B. Of particular note is the EPMR recommendation for GCP to focus efforts on seven trait–crop combinations (challenge initiatives).

The second significant development was a fundamental reform in our governance structure, undertaken by the GCP Programme Steering Committee (PSC), which ushered in a new Executive Board (EB) effective 1 June 2008. The main purpose of this reform is to transfer several major responsibilities from the PSC to the EB; chief among these responsibilities is oversight of the scientific strategy of the Programme. This change in governance is to promote mainly both efficiency and objectivity. The Board comprises seven members with specific expertise, while the PSC has 22 members (including four provisional ones), each of them being the representative of a Consortium member. Transparency and objectivity are assured since the Board members are not at all involved in GCP research activities. These changes, the consequences and next steps, as well as the various bodies involved in GCP's governance and management, are discussed further in the section *GCP governance: reforms and background*.

As in previous years, a set of new research activities has been initiated this year that matches the evolution of our research strategy and increases interactions across Subprogrammes (SPs). Commissioned projects initiated in 2008—especially in SP3—build on the exploration and characterisation of diversity in major food crops conducted in SP1, and the gene discovery conducted in SP2. A large number of projects clearly add value to previous activities and encompass the validation on the ground of GCP's first products/outputs. In addition, the new round of competitive projects, selected in mid-2008, for initiation in the last quarter of the year, are structured by themes linked directly to SPs 1, 2, 3 and 4. Together, all these new projects initiated in 2007–2008 clearly build on our previous work, explore new and promising avenues of research to improve crops in drought-prone environments, but at the same time focus our overall research portfolio on key crops and selected target environments for impact on plant breeding to boost crop productivity.

In summation, 2009 will mark a major transition in GCP, not only into Phase II but also to a more sharply focused research portfolio, based on the EPMPR recommendations and assessment by the Management Team (MT). This refinement of the GCP research portfolio will remain high on the agenda of the MT and the Executive Board. One of the major recommendations of the EPMPR, endorsed by the GCP management Team (MT), was to define clear impact indicators at Programme level to evaluate the impact of GCP by 2013. These indicators should be identified over the coming months, and no later than June 2009 concomitant to refining our research portfolio, especially the seven challenge initiatives.

GCP's niche and network

GCP was created to undertake what is often referred to as 'upstream' research but with a clear mandate to link upstream and applied research ensuring the Programme is not technology pushed, but driven by specific (genetic and genomic resources) and local needs (markers for specific breeding traits). In more concrete terms, for GCP's case this means:

- characterising crop genetic diversity using molecular markers and trait-specific phenotypic approaches
- creating diversity by making wild crosses or creating mutant collections
- identifying favourable alleles for crop performance using comparative genomics, quantitative trait loci (QTL) analysis and 'omics' approaches
- testing and validating those alleles in adapted germplasm under local target conditions
- developing bioinformatic infrastructure and tools to conduct those studies in a suitable way ensuring data availability to the research community, and
- increasing the capacity of breeding programmes in target environments to ensure GCP products will be used by primary users.

To this end, GCP cultivates partnerships for innovative science and conducts research to better understand the genetic basis of GCP target traits (see *Collaborations and partnerships*). Linking basic research with applied science, GCP generates useful knowledge and develops practical tools such as molecular markers for target traits to complement phenotypic selection and impact crop breeding for adapted germplasm in target environments. In this way, GCP bridges the gap between high-tech bench scientists and the plant breeders and resource-poor farmers our research is supposed to help. It is this duality that defines GCP's particular niche within the CGIAR and the broader agricultural research-for-development community.

GCP was also assigned a trait of focus: drought tolerance, which affects almost all crops and all regions worldwide, thereby providing opportunities to apply useful discoveries across crops. As no single institution can command the breadth of expertise and resources necessary to achieve these objectives, GCP operates as a network that leverages significant resources—funds, skills, equipment, knowledge and social capital—through partnerships with a broad base of public and private institutions and initiatives. GCP partners are diverse and complementary in their skills. This ensures seamless continuity of activities all along the pipeline of GCP activities, starting from characterising and creating diversity, up to the delivery of value-added crops for marginal environments. A critical benefit of the network is that it provides access to vast stores of plant genetic resources, as well as to cutting-edge technologies and scientific expertise, bringing all the three together for crop improvement. GCP continues to engage with a vibrant community of more than 70 partners from universities, CG Centres and local breeding programmes—our main target users and stakeholders.

No doubt that this GCP community, in a broad sense, is the major asset of the Programme and in its 2008 report, the EPMPR Panel observed: "*Perhaps the most important value of GCP thus far,*

is the opportunities it has provided for people of diverse backgrounds to think collectively about solutions to complex problems, and, in the process, to learn from one another.”

Evolution of the GCP strategy and research trends

GCP, now in its fifth year, has achieved much. The Programme has developed an extensive consortium partnership and leveraged its resources to establish a broad network of R&D participants with extensive capability and capacity to support GCP objectives. As indicated in our recent [Strategic Framework](#),¹ by 2013, GCP is expected to have contributed to the following three main objectives:

1. Provide access to, and promote the use of, genetic diversity in plant improvement programmes.
2. Develop a public platform of genetic and genomic resources and tools, and support a global community that can use them.
3. Use genetic diversity and advanced science to develop products for plant breeding programmes to improve the livelihoods of resource-poor farmers in drought-prone environments.

As underscored in the recent EPMR report, analyses of diversity in several germplasm collections are nearly complete; and assembly of reference sets for these species represents a significant outcome from Phase I. The next step is to characterise—at the phenotypic level—specific subsets of those reference sets to boost access to new alleles to be used to improve GCP crop productivity in target environments. During Phase I, GCP has also contributed considerable scientific information on genetic diversity and genetic underpinnings of some important traits for drought-prone environments. As the Programme matures, gene and marker discovery must and is focusing more and more on drought tolerance as demonstrated clearly in the different research themes of the last two competitive calls in 2005 and 2008.

With regard to objective 2 above, GCP has developed genotyping, informatics and some genomics platforms for breeders to access modern marker technologies. The most recent objective of this effort is to develop a genomics platform focusing marker technology for less-studied crops, such as DArT arrays for potatoes, chickpeas, pigeonpeas and *Musa*. Significant effort has also been devoted to sequencing, such as sequence information through BAC end (*Musa* and groundnuts), sequencing for generating expressed sequence tags (ESTs) (for pearl millet), thus allowing the identification of microsatellite marker sets in several crops (chickpeas and beans) or Single Nucleotide Polymorphism (SNP) markers (rice or cowpeas). However, this effort to generate genomic resources *per se* will decrease over time, as urgent needs in this arena are progressively addressed.

In Phase II, GCP will pursue its current effort to facilitate access to reference sets of germplasm and markers for target traits. These represent useful products that can be used by breeders to identify new parental lines for further crosses, and to improve the efficiency of their breeding programmes through marker-assisted breeding. These are just two kinds of products developed so far that illustrate the progress made to achieve objective 3 above. However, as pointed out in the recent EPMR and by the Science Council, our research portfolio can be improved by greater focus. With our current approach, the Programme appears to be rather opportunity-driven, and the end-product orientation is not sufficiently clear. During Phase II, GCP needs to give more attention to prioritisation of Programme-level trait-crop opportunities, evaluate what the Programme can achieve, and more actively manage achievable high-priority product

¹ GCP's Strategic Framework and related strategy documents at <http://www.generationcp.org/brochure.php#strategy>

opportunities by ensuring a continuum of activities across the different Subprogrammes. Implementing this important strategy is described in the *Programme rationale and structure* section further below.

The year 2008 has seen a set of new commissioned projects initiated, and the nature of the new projects follows the logical evolution of the GCP research trends described above:

- SP1: After the characterisation of the reference sets for GCP crops, several new projects will focus on the phenotypic characterisation of those sets, and the development of new segregating populations with parental lines identified in the reference sets.
- SP2: A few projects will continue to focus on the development of genomic resources in less-studied crops, to complement and conclude efforts from GCP Phase I. However, it should be noted that these few projects are the last ones of this nature: SP2 now aims to focus exclusively on the discovery of drought tolerance genes and Quantitative Trait Loci (QTLs) towards breeding applications.
- SP3: Compared to previous years, this SP evolved significantly in 2008, in tune to products flowing from SPs 1 and 2. In this year, the budget allocation for SP3 commissioned projects rose by 50 percent as more markers identified (in SP2) and new populations developed (in SP1) needed validation in local target environments.
- SP4: The first priority for SP4 was to deliver a functional GCP informatics platform and database network for the GCP community, as well as providing tools and methods to store, analyse and exchange data within the GCP community. This platform and network should be fully functional by the end of Phase I. After this critical step, SP4 will focus on the development or adoption of research and breeding tools requested and required by GCP scientists. These tools will be accessible through the platform.
- SP5: The training and capacity-building component is increasingly oriented towards specific needs of ongoing projects, ensuring that products developed in GCP will be used by primary users and will have impact on breeding in GCP target environments and farming systems. Resources are now allocated to finalise products for distribution within and outside GCP. This finalisation involves ensuring that quality and packaging are adequate and appropriate for both segmented as well as broad distribution. The type of distribution will be determined by the nature of the product.

Products and Delivery Plan at the heart of GCP

Most, if not all, GCP activities aim at generating usable products—in both the short and long term—in the form of knowledge, materials and tools for plant breeders. In 2007, GCP launched its Delivery Plan Kit (DPKit) designed by a panel of experts in technology transfer, research management, impact assessment and marketing. For each new major project, a Delivery Plan is now required and potential users at different levels in the GCP delivery path (Figure 1) are involved in the development of these plans.

We are therefore clearly committed to promoting and disseminating GCP products among users that are ready to apply them, thus helping to further GCP's mission. GCP is a time-bound Programme that should ensure continued and sustainable use of its products after its lifespan. We continue to be strongly committed to establishing protocols by which GCP products can be maintained and distributed. To this end, and several initiatives were started in 2007 to implement this important element of our strategy for Phase II.

Given the foregoing, the need to start reflecting on, and developing, a clear and executable exit strategy over the next few years is a must. Many of the platforms developed—or improved—by GCP, are mainly coordinated by CGIAR Centres or by key partners. The full impact of GCP

products will require that these platforms have a ‘shelf-life’ beyond GCP’s predetermined lifetime. In addition, the platforms must be accessible by CGIAR Centres, NARS and some ARIs, and downstream breeding programmes and seed distribution networks. A top priority for GCP Phase II will be to have a functional quasi self-sustaining portal (from a financial point of view). This will facilitate reliable and user-friendly access by the breeding community to most GCP products.

Improving project monitoring and information exchange continue to be priority issues for GCP. In 2008, we are developing a customised GCP Workflow System, using MTP outputs (GCP projects) as the primary foundation. This web-based system will ensure easy and seamless access by our geographically distributed Management Team to both project progress reports, as well as financial and other administrative information. The system will further enhance GCP project monitoring and also promote transparency on GCP’s achievements since certain modules will be accessible to the entire GCP scientific community worldwide. In addition, through our website, some of the information for each GCP project, like timeline and specific outputs/products, will be publicly available.

In conclusion, we can confidently say that GCP is a healthy and fully functional challenge programme supported by a proactive and dedicated community. The Management Team is fully committed to continue implementing our strategy, so as to achieve our objectives by 2013. The research portfolio presented in this MTP shows increasing inter-Subprogramme cohesion and better end-product vision. And while the development of some platforms might target a large set of our [mandate crops](#),² specific research themes have been identified and will be pursued for important crops identified in GCP target farming systems. To ensure GCP is premised on a solid base, the Management Team committed to the following fundamentals:

- 1) data release and quality control (obligatory checkpoints and external reviews);
- 2) adding value to successful projects and building on partners’ existing infrastructure and expertise; and,
- 3) ensuring delivery, access to, and sustainability of, GCP products (eg, Genetic Resource Support Service and Molecular Breeding portal).

Context

Crop improvement for poverty alleviation

For the foreseeable future, public sector research on staple food crops, especially crops for marginal environments, will be indispensable for poor households in such environments. Economic alternatives to agriculture are often extremely limited in these areas. Yet to promote more rapid economic growth and improve the welfare of poor and marginalised populations, investments in agriculture are among the most solid and stable investments any nation can make, guaranteed to yield handsome returns. Operating at international level, GCP contributes to the goals of national and regional development strategies in our partner countries by adding value to local efforts to improve agriculture, through exchanging perspectives with other regions and countries, as well as sharing promising or working solutions.

The agricultural sectors of many developing countries are changing rapidly in response to a host of local and global factors. Farmers in more productive environments can now diversify beyond staple food crops and have increasing access to new global and domestic agricultural markets. Farmers in more challenging lands—areas typically characterised by high-risk crop production,

² GCP’s mandate crops are listed at <http://www.generationcp.org/gen.php?da=08128238>

poor agricultural yields and rampant poverty—are still isolated from markets, agricultural inputs and support services.

The global food crisis and drought

In the past year, global food prices have increased on average by more than 40 percent, according to the International Monetary Fund (IMF). It would appear that most experts believe that there is no single driver behind this unprecedented rise in the cost of food. Rather, there are numerous causal factors. However, what is abundantly clear is that the global food crisis threatens the food security and wellbeing of millions of people, particularly the poorest in the developing world. Therefore, while opinion may be divided on the relative importance of various factors in driving this food crisis, recurrent natural disasters such as drought are cited by many experts.

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

The quest for drought tolerance for food crops in GCP's aforementioned [target regions](#)³ continues to be our number one priority. Since its founding, GCP has worked on drought as the primary trait of focus in efforts to improve drought tolerance in food crops. We anticipate that this early investment will make an important contribution to the global fight against hunger and poverty.

GCP governance: reforms and background

Programme Steering Committee and Executive Board

GCP is legally a Partnership Consortium. For its functions, the Programme receives grants from funding agencies to establish, manage and finance projects in an integrated R&D programme to improve traits for crops grown by smallholder farmers in the developing world. Oversight, including legal and strategic guidance (collectively termed 'governance') has until June 2008 been provided by the [Programme Steering Committee](#) (PSC),⁴ essentially representing the institutional [Consortium partners](#).⁵

GCP operates under:

- a legal [Consortium Agreement](#)⁶ that circumscribes the legal and operational rights, as well as obligations of, institutional partners, including the host institution (CIMMYT; the International Maize and Wheat Improvement Center); and,
- a framework of contractual agreements covering the obligations of all Consortium and non-Consortium research partners for work funded, in whole or in part, by GCP.

Over the past two years, the PSC has undertaken the challenging task of reforming GCP's governance. As a result, during its December 2007 annual meeting in Beijing, China, the PSC

³ See summary document on GCP target regions at http://www.generationcp.org/UserFiles/File/gcp-target-systems_brief.pdf

⁴ PSC members listed at <http://www.generationcp.org/psc.php?da=0781307>

⁵ Consortium members and background at <http://www.generationcp.org/consort.php?da=0781248>

⁶ Consortium Agreement at: http://www.generationcp.org/UserFiles/File/Consortium_agreement_signed.pdf

approved the resolution to delegate most PSC responsibilities to a new governance body, the Executive Board (EB). The seven members of the new [Executive Board](#)⁷ were selected in April 2008 based on nominations by the broader GCP stakeholder community, including Consortium members and the GCP Management Team. Focus was placed on: (i) the independence of the Executive Board members, who must not have been involved in any GCP activities, and (ii) on sufficient capacity, and expertise for the tasks assigned to the Board. The Executive Board became effective on 1 June 2008.

However, the [current governance structure](#)⁸ is still less than ideal because, from a legal perspective, the Executive Board is only an advisory group to whose decisions the PSC has agreed to defer. This structure was adopted because amendments to the Consortium Agreement require the unanimous agreement of the signatories, and it was believed unlikely that sweeping reforms on governance would muster the unanimous vote required to make the reforms permanent. We are aware that this structure is not the most efficient from a process perspective and will likely mean that GCP will incur high transaction costs with two governance bodies. In fact the EPMP report “recommends that an attempt is made to further simplify and clarify the GCP governance by adapting the Consortium Agreement to the *de facto* status quo”. Consequently, a PSC Task Force (TF) has already been set up to redefine the role, function and *modus operandi* of the PSC in this new dispensation. The TF is now evaluating different possible scenarios on how the PSC and the Consortium should evolve, and is giving serious consideration to modifying the Consortium Agreement.

Stakeholders Committee

As reported in the last MTP, in this period when the entire GCP governance structure is under review, the EC, the Global Forum for Agricultural Research (GFAR) and GCP’s Management Team also plan to revamp and revitalise the GCP Stakeholders Committee (SHC). Consultations are already underway.

This critical advisory Committee was convened by GFAR in response to an EC recommendation. The SHC is conceived as a neutral platform for inter-stakeholder dialogue, and as a link between GCP and its various stakeholders. The rationale is to ensure better representation, in GCP decision-making, of regional and sub-regional agricultural fora and other stakeholders such as farmer groups, NGOs, civil society organisations (CSOs) and the local private sector. GCP is confident that a revamped functional SHC for Phase II will be in place by mid-2008.

Review and Advisory Panel

The [Review and Advisory Panel](#) (RAP)⁹ has a dual function. On the one hand, it provides scientific advice on Subprogramme-specific issues directly to Subprogramme Leaders. On the other hand, the RAP plays an active advisory and legitimisation function in the selection of commissioned grants. In light of these functions, and considering the fact that RAP members are chosen by GCP management, and also that no reporting relationship subsists between PSC and RAP, RAP is then more of an extension of management rather than a governance body.

RAP consists of five scientists, with one scientist assigned to each GCP Subprogramme. It has virtual and in-person meetings and consults frequently with the GCP management. In 2008, there was turnover in RAP members, reflecting, at least in part, the turnover within the GCP Management Team. In May 2008, Peter Langridge and Rose Rita Kingamkono, RAP members

⁷ Executive Board at <http://www.generationcp.org/whoweare.php?da=08124404>

⁸ Current governance structure at http://www.generationcp.org/pdg/?page_id=9#212

⁹ More on RAP at <http://www.generationcp.org/rap.php?da=0781418>

for SP2 and SP5 respectively, both stepped down. Peter will now be more directly involved in GCP research activities, while Rose will now focus more on her new, demanding, high-level responsibilities as Acting Director General at the Tanzania Commission for Science and Technology. In June 2008, Scott Jackson and Ana Mercedes Espinoza replaced Peter and Rose respectively. Scott is a professor at Purdue University (USA), specialising in plant genomics and genetics, while Ana is a professor at the University of Costa Rica, with expertise in capacity building for crop genetic improvement using biotechnology.

Programme rationale and structure

GCP's research, capacity-building and delivery activities are organised under five Subprogrammes and executed through three funding schemes: competitive grants, commissioned research projects and focus projects. The five Subprogrammes are the operational structure for allocating resources and managing research projects.

In conformity with the EPMR recommendations, GCP will continue focusing its research portfolio, starting with implementing one of the recommendations requiring the identification of seven trait-crops (challenge initiatives) to which half of the GCP research budget should be allocated. This notwithstanding, we will continue to work on other strategic projects not directly related to the seven challenge initiatives, building up mainly on investments already made, and focusing on consolidating and value-adding activities.

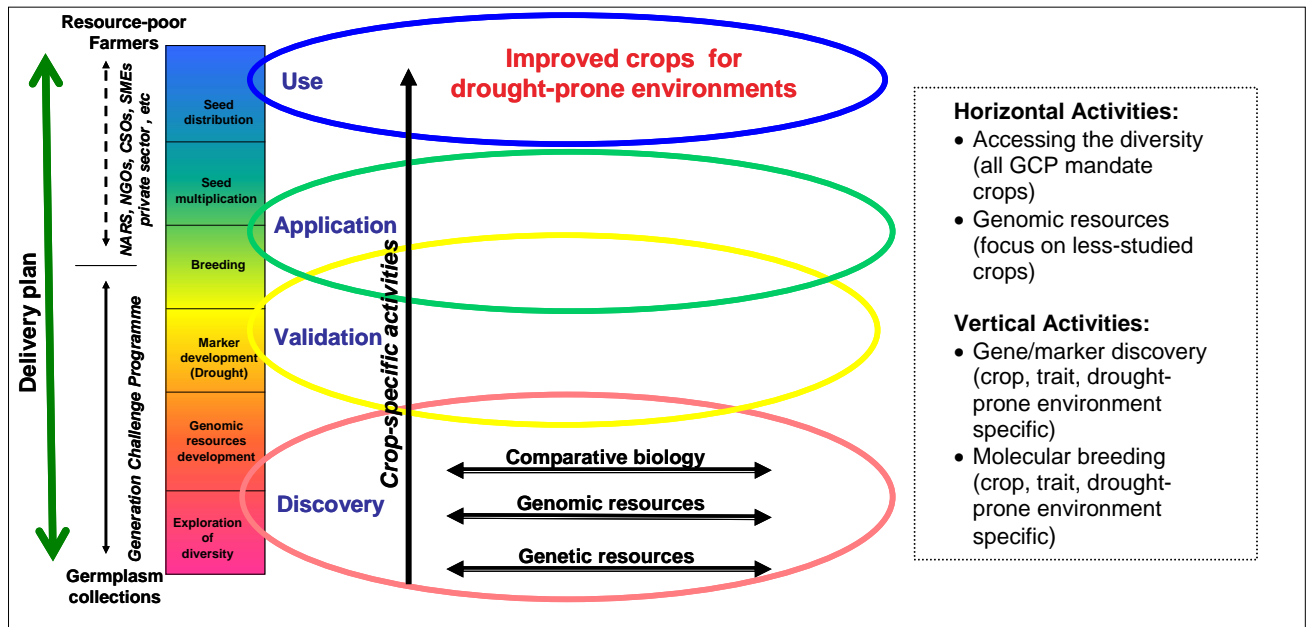
Even if the management of the challenge initiatives should evolve towards a two-dimensional matrix (Subprogramme and crop/trait platform dimensions), the Management Team will remain the ultimate body with decisional power in terms of scientific management and responsibility towards our stakeholders and funders. So, we do not question our current thematic Subprogrammes, which have thus far served well as an effective structure for effective management and resource allocation, but we fully agree that changes are indeed necessary in our management organogram if we want to deliver on products, and ensure their use by breeders in target environments (see *Implementation of the GCP Strategy*). The SPs ensure scientific and administrative coherence and integration of the various interdisciplinary approaches across the different types of projects and funding mechanisms.

Our five Subprogrammes are as follows:

- **Subprogramme 1: Genetic diversity of global resources**—Characterises the diversity of crop germplasm collections in the custody of the CGIAR and national programmes in terms of genetic structure and associated phenotypic variation
- **Subprogramme 2: Genomics towards gene discovery**—Uses or develops genomic tools and technologies and evaluates interdisciplinary approaches to better understand gene function and interaction, in order to improve knowledge of gene systems across crops
- **Subprogramme 3: Trait capture for crop improvement**—Validates gene function and refines molecular breeding systems and the resulting enhanced germplasm, so as to increase the efficiency, speed and scope of plant breeding
- **Subprogramme 4: Bioinformatics and crop information systems**—Integrates GCP information components and analysis tools into a coherent information gateway and provides support for data analysis to the other GCP Subprogrammes
- **Subprogramme 5: Capacity-building and enabling delivery**—Empowers scientists in developing country national programmes to use modern breeding approaches. SP5 also coordinates the development and implementation of project Delivery Plans and is responsible for intellectual property issues, and research in policy and impact assessment.

As illustrated in the GCP research approach (see Figure 1), on the research–development continuum, GCP’s direct engagement terminates at prebreeding. In conjunction with SP5, SP3 forges a vital link with breeders, and SP3-commissioned projects are particularly critical in promoting the use of molecular markers in national programmes.

Figure 1. GCP's research approach



Research framework

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

- 1) **Competitive grants:** Selected by an external review panel, the grant call is defined by the Management Team. Competitive calls stimulate scientific excellence and attract new projects/partners for GCP to achieve its objectives.
 - The 1st round of competitive grants comprised 17 projects, each with an annual budget of about US\$300,000. They were launched in January 2005 and were scheduled to end in January 2008. However, as is common with new programmes, a number of first-round projects started late, or had a slow start, meaning most of these 1st round projects are now on a no-cost extension until mid-2008, as had been anticipated in the last MTP.
 - The 2nd round of competitive grants had six two-year (2007–2008) projects of \$300–400,000 per year. The call went out in February 2006 and the six projects were selected in October 2006, with an expected start date in January 2007. However, due to delays in disbursement of EC funds, the projects were placed on hold and only commenced in late 2007.

- A call for the 3rd round of competitive projects was made in January 2008 as projected in the last MTP. A set of nine projects were selected across the four different thematic area of the call. In scrutinising the proposals, the external review panel laid a strong emphasis on the quality of the research and the relevance of the products in the context of the GCP strategy. This third set of competitive projects is for a three-year period. The annual budgetary support dedicated to these projects will range between USD 2.5 and 3 million. The projects are set to start within the last quarter of 2008. More details on the 3rd call are provided further on below.
- 2) **Commissioned research projects:** These are typically one- to two-year complementary projects with an annual budget ranging between US\$ 20,000–300,000. They are designed to add value to the array of genetic and genomic resources publicly available through GCP by addressing a specific need, or by collating outputs from research projects. Due to the delayed funding cited above, commissioned projects set to start in 2007 were only initiated towards the end of the year. To absorb the substantial 2007 EC contribution received in January 2008, a larger number of commissioned projects have been initiated and more resources allocated in 2008, compared to previous years.
 - 3) **Focus projects:** For these projects, budget and activities are developed in close collaboration with funders based on specific requirements. Currently, we have one large three-year focus project (2007–2010), funded by the Bill & Melinda Gates Foundation, on ‘Improving tropical legume productivity for marginal environments in Africa’, dubbed [Tropical Legumes I](#) (TLI).¹⁰ While TLI focuses on developing key genomic resources that are currently lacking, identifying molecular markers for important traits, and improving legume breeding capacity in sub-Saharan Africa, its ‘twin’ project, TLII led by the International Center for Research in the Semi-arid Tropics (ICRISAT), works on seed multiplication and dissemination, and is therefore a good conduit for the flow of products from TLI.

GCP management is cognisant of the fact that to optimise programme efficiency, it is imperative TO maintain a good balance between the three kinds of complementary projects above. We wish to continue to capture new ideas and approaches and bring in partners that fit our research priorities, while also retaining the flexibility of consolidating our project portfolio around the most important and most promising axes. Given this concerted and systematic consolidation, and the focus on seven trait–crops, GCP is likely to reassess the appropriateness of competitive calls in this redefined context. While competitive calls were a good mechanism for Phase I, Phase II might call for a different approach. It is significant, however, that the second and third calls are thematic, drawing from GCP’s Strategic Framework and outputs of the reference studies.¹¹

Update on 3rd round competitive project: August 2008

At the time of submitting this MTP in mid-August, of the 24 proposals submitted for the [third call](#)¹² for competitive research projects, nine proposals had been ranked in the top tier by the External Review Panel during a face-to-face meeting in Mexico towards the end of July 2008. The Management Team is therefore considering supporting all these projects. However, projects will first need to submit to a revised version of each proposal, taking into account Panel recommendations, as well as MT review comments, so as to better link the new projects with ongoing activities. The nine projects are as listed below.

¹⁰ More on TLI at <http://www.generationcp.org/gcptli/>

¹¹ Reference studies are used to identify impact targets in terms of farming systems, crops and traits. One such study, by Glenn Hyman et al, identified farming systems with the highest incidence of poverty, and the crops associated with those systems.

¹² More on the 3rd round of competitive projects at http://www.generationcp.org/research.php?da=0634417#3rd_call_for_compet_projects

- 1) ***Generating new wheat germplasm with enhanced drought/heat tolerance using AB genomes genetic diversity*** (SC Misra, ARI, India): This project will focus on developing diverse synthetic hexaploid wheat (SHW) lines as sources of variation that can be used to test for drought tolerance. The investigators will develop these lines and then propose to use DArT technology to genotype and phenotype the lines in various locations, primarily in South Asia, so as to identify new alleles for drought tolerance.
- 2) ***Improving grain yield on acid soils by the identification of genetic factors underlying drought and aluminum tolerance in maize and sorghum*** (PI—L Kochian, Cornell University/USDA—ARS): The PI and colleagues have already successfully identified a major sorghum Al tolerance gene in a previous project. The team now proposes moving towards identifying other Al tolerance genes in sorghum and maize, as well as drought stress-related genes in the same two crops. This objective will be attained through a combined approach using candidate gene and whole-genome association mapping.
- 3) ***Delayed senescence and drought tolerance in rice*** (PI—E Blumwald, UC—Davis): The project will explore a novel approach to increase drought tolerance in rice. It is premised on the development of rice lines (Indica and Japonica) overexpressing an isopentenyltransferase (IPT) gene under the control of a senescence activated receptor kinase (SARK). The approach is based on the finding that the IPT gene very efficiently confers drought tolerance to tobacco by regulating the cytokinin levels.
- 4) ***Drought from a different perspective: Improved tolerance through phosphorus acquisition*** (PI—S Heuer, IRRI): This project will aim to identify and isolate the *Pup1* gene in rice—a gene that promotes better root growth, even under phosphorous-deficient conditions. Two QTLs for drought tolerance will be combined with *Pup1* in a drought-sensitive background, in order to develop adapted germplasm with increased tolerance to drought, as well as improved efficiency in phosphorous uptake.
- 5) ***Discovery and development of alleles contributing to sorghum drought tolerance*** (PI—A Paterson, UGA): To improve drought resistance in sorghum, the investigators propose to identify more markers, as well as novel markers. Using a different set of germplasm, the additive effects and epistatic interactions of stay-green QTLs will be assessed with regard to their effects on terminal drought tolerance (ie, drought during the terminal phase of the crop cycle). RNA of selected parents (drought-stressed) of a MAGIC population will be sequenced to identify novel SNPs and to study the genomic organisation of selected gene families that might confer drought tolerance.
- 6) ***Targeting drought-avoidance root traits to enhance rice productivity under water-limited environments*** (PI—R Serraj, IRRI): This project will focus on one important aspect of drought tolerance in lowland rice—root growth to alleviate drought stress. Because root growth appears to be an area where little genetic gain has occurred, this project is expected to have impact on breeding by providing important basic understanding of the physiology and genetics of root function and plant adaptation under water-limited conditions.
- 7) ***Basal root architecture and drought tolerance in common beans*** (PI—J Lynch, PSU): The project proposes to address the problem of drought tolerance in common beans, a critically important protein source in Africa and Latin America. It deals with the key issue—in typical production environments—of how roots are to be manipulated genetically to meet the dual requirements of P uptake (shallow and intense rooting needed) and water uptake (deeper and much less intense rooting). The project will also identify traits that may affect both rooting depth and intensity.
- 8) ***Breeder-friendly high-throughput phenotyping tools to select for adaptive traits in drought environments*** (PI—F Ogbonnaya, ICARDA): The investigators propose to focus on developing breeder-friendly high-throughput phenotyping tools for wheat under contrasting drought environments (from summer to winter rain). The project will assesses

a large number of target traits, which have all been shown to contribute to drought tolerance in different related lines and cropping systems. The researchers will attempt to define the traits contributing to the high yield of ICARDA's elite drought lines, focusing on the important GxE relationship affecting wheat yield under different levels of drought.

- 9) ***Breeding drought tolerance for rainfed lowland rice in the Mekong region (PI—J Boonrat, BRRD)***: The investigators propose to test the hypothesis that drought tolerance in rainfed lowland rice is the result of adaptation to both anaerobic and aerobic growing conditions. The methods for testing the hypothesis through phenotypic evaluation of selected materials (rainout shelter and raised beds), identifying new traits and related QTLs, will be very useful for understanding drought tolerance in the Mekong region.

Implementing the GCP strategy

The implementation of the GCP strategy builds on the 2006 Strategic Framework and encompasses relevant recommendations from the various reviews GCP underwent during the past year, especially the EPMR. The recommendations resonate with the thinking of the MT to further focus our research agenda and concentrate on platform development to guarantee the distribution of GCP products in a user-friendly and sustainable way. Evolution of the platforms is elaborated in the section on *Product delivery plan and data management*. This brief therefore concentrates on research priorities that will have impact on breeding for selected crops and traits relevant to GCP target regions. Such implementation will require significant adjustments over the next 12 months in both the scientific content and management of our research portfolio, as underscored in a couple of recommendations from our recent EPMR:

- *Recommendation 3*: The review panel recommends that GCP deploy the majority (at least 50 percent) of its resources in pursuit of the seven highest impact Programme-level trait-in-crop products that it can achieve over the next five years.
- *Recommendation 9*: The review panel recommends GCP management adopt an end-product orientation for GCP activities, ie, the integration, alignment and prioritisation of product-oriented projects across Subprogrammes in line with high-priority Programme-level product objectives. To support this, the review panel recommends that GCP management acquire or develop a product project portfolio management system to help it plan, monitor and manage its best opportunities (achievable high-priority Programme-level objectives).

More focus in our research portfolio

To ensure impact by 2013, the Programme must further focus on a few crop-specific projects, at both the crop and trait levels. To make more educated decisions on the seven trait-crop challenge initiatives to be identified, in early 2008, the MT solicited 'GCP champions' to lead the development of strategic papers on 13 trait-crop potential challenge initiatives identified by the MT, considering mainly the quality and the potential impact of our ongoing projects, the quality of the partners involved, and potential bottlenecks in product delivery.

The purpose of the short papers was explicitly defined, designed to build on ongoing projects and existing outputs. For each of the trait-crops pre-selected, the MT requested:

- a. a general description of each activity proposed and technology to be used,
- b. the products that will be generated per activity,
- c. the NARS partners proposed in GCP target environments, and why,
- d. the impact indicators for the different activities, and
- e. the major challenges in delivering products, and contingency plans to overcome these challenges.

In May 2008, the MT comprehensively reviewed the strategic papers submitted and made a pre-selection of seven potential trait–crop challenge initiatives, following the same selection criteria described above.

Challenge initiatives

At the end of July 2008, the MT got approval from the new Executive Board to implement the GCP research strategy, following the EPMR and EC review recommendations to better focus the research agenda of the Programme. The seven challenge projects below were selected by the MT for implementation in GCP Phase II.

Cereals

1. Rice/drought–Africa
2. Wheat/drought–Asia
3. Sorghum/Drought–Africa
4. Rice/sorghum/maize/soil problem (Al toxicity (*Alt1*) and P deficiency (*Pup1*)–Asia and Africa

Legumes

5. Cowpeas/drought–Africa
6. Chickpeas/drought–Africa and Asia

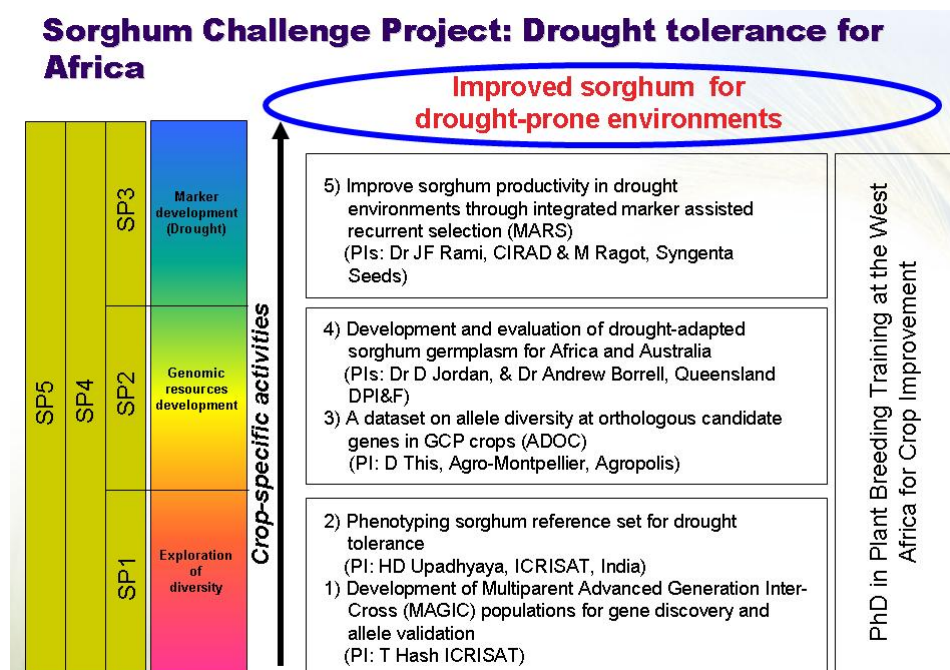
Root and tubers

7. Cassava/virus–Africa

As currently conceived, the challenge initiatives are a set of pre-existing GCP projects related to a given research topic. The challenge will be to coalesce and collate them into a coherent and cohesive set of activities over the next half year, with a global workplan and clear impact indicators at the challenge project level.

In illustration, below is a representation of the different existing GCP projects that can be ‘gouped’ under the sorghum challenge initiative, *Drought tolerance improvement for Africa*.

Figure 2. Illustrating the challenge initiative concept—the case of sorghum in Africa



A two-dimension management system

It is important to note that GCP is still revising and adjusting its management organogram and structure. Therefore ideas and concepts presented below may be adjusted as necessary, based on practical considerations that surface in the course of implementation.

The [current management structure](#)¹³ is oriented along Subprogrammes, favouring prioritisation of activities within Subprogrammes but not much across Subprogrammes. While this is a structure that supports excellence in scientific research by providing the possibility of selecting the highest-quality projects within each Subprogramme, it is challenging to support any integrated and harmonised approach across the different Subprogrammes with end-products of the whole Programme in mind.

Therefore, there is an increasing need to include a second dimension in our management matrix that will run across the Subprogramme dimension. This component must ensure that once our end-products at Programme level and their corresponding impact indicators have been identified, there is a management function that will ensure that activities and resources across Subprogrammes will deliver those end-products. This ‘product/crop’-specific complementary management function will be established through seven Product Delivery Advisors (PDAs) who will oversee the product delivery within each challenge initiative. PDAs will assist GCP management in operationalising and seamlessly integrating this complementary crop–farming system approach.

The main responsibility of the PDAs will be to manage and oversee the development and implementation of the delivery workplan within each challenge initiative, ensuring that the impact indicators for each initiative will be reached by 2013. PDAs will follow the progress of the different research activities across the Subprogrammes from a product delivery perspective and will interact with the MT on progress or adjustments to be made for each initiative to attaining its milestones.

It is anticipated that PDAs will champion their target trait–crop, and realistically be already involved in GCP activities, have a strong orientation towards breeding and have a very good knowledge of breeding programmes and partners in the target regions of the challenge project they will manage. We realise that potential candidates are already committed elsewhere timewise and that is why we need to consider scientists who are already engaged with GCP. The idea is to formally contract the PDAs to assume this management responsibility, and for them to contractually commit a portion of their time. The nature of this commitment will in turn be determined by the nature of each particular challenge initiative.

Implementation

The final list of the seven challenge initiatives will be communicated to the GCP community in September during the [Annual Research Meeting](#) (ARM).¹⁴ Preliminary discussions and contact with potential PDAs will also be during this same ARM. It is anticipated that the seven PDAs will be identified by the end of 2008, and that the strategic meetings for each of the seven challenge initiatives will be held before April 2009. The MT will lead these meetings, assisted by the PDAs. The meetings will involve key scientists as well as a cross-section of stakeholders.

¹³ GCP’s current management structure at http://www.generationcp.org/pdg/?page_id=9#212

¹⁴ Details on ARM at <http://www.generationcp.org/arm.php>

The major objective of these meetings will be for each challenge initiative to:

- develop a workplan with clear milestone taking into account ongoing work and the strategic papers, and
- develop the corresponding product Delivery Plan to ensure a cohesive effort and impact indicators to evaluate the performance of the challenge initiatives by 2013.

Product Delivery Plan and data management

In 2007, GCP launched its [Delivery Plan Kit](#) (DPKit),¹⁵ which was used by the seven projects initiated in 2007 (six competitive projects and one focus project). For every new major project (defined as projects with a budget of USD 250,000 or more), a [Delivery Plan](#)¹⁶ is now required. This Plan is formulated by researchers leading the projects, in direct consultation with the targeted users of their research products, to ensure product delivery and relevance.

We expect project development and reporting to be further streamlined by a new web-based tool for project design and management developed in collaboration with the Syngenta Foundation for Sustainable Agriculture and launched in early 2008, the [Project Development Guide](#) (PDG).¹⁷

The spectrum of GCP products is really broad and at almost every step along the GCP research pipeline, products generated can have direct impact on breeding efficiency, or can be used in the next step of the research pipeline. As an example, the upstream germplasm characterisation conducted by SP1 can not only lead to the identification of a new pool of diversity for prebreeding activities by local national programmes, but will also help identify contrasting lines for genetic studies in SP2, or lines with favourable alleles for desirable traits to be used as donor lines in marker-assisted selection experiments in SP3, using analytical tools developed by SP4 in partnership with breeders in national programmes supported by SP5.

GCP products can be classified into six broad categories:

- i. genetic resources
- ii. genomic resources
- iii. genes and related interactions for target traits
- iv. validated markers for breeding
- v. new tools and methodologies, and
- vi. training material.

Validation is central to product management and must precede delivery: it confirms the suitability and potential benefit of a given product in a given environment. Once validated, products can be widely disseminated.

One other key product that is implicit in the first four listed above is data. Data underpin effective and sustainable product delivery. As our projects mature and increasingly yield more concrete products, GCP management has been paying particular attention to data quality control and data release, all in the context of product management and product delivery.

In this regard, a number of concrete steps have been taken, as illustrated by an ongoing project on quality control for the GCP reference set. In this project, a subsample of the reference set generated in SP1 for the different crops will be re-genotyped by an external genotyping facility.

¹⁵ Delivery Plan Kit accessible at: http://www.generationcp.org/sp5/?da=08122719#dp_kit

¹⁶ See our rationale for Delivery Plans at: <http://www.generationcp.org/gen.php?da=0790433>

¹⁷ Project Development Guide at: <http://www.generationcp.org/pdg>

This exercise is to validate the quality of the molecular data generated for most crops using specific microsatellite kits. This will give both the scientists who generated the data, and the GCP Management Team the confidence that reference sets and related genotypic data can be distributed broadly for further genetic analysis.

GCP is also acutely aware of the need to make GCP products available to the community as indicated above, and to sustain this availability. In this regard, initiatives are being designed for initiation in late 2008 to make genetic resources and marker technology more widely available to the breeding community. These include the following initiatives:

1. *Genetic Resource Support Service (GRSS)*—The idea behind this concept is to build a critical mass of germplasm to be distributed to the breeding community for genetic studies, to ensure a certain level of quality, to harmonise the seed distribution and to reduce costs.
2. *Molecular Breeding Platform*—This project is at the heart of GCP and will be a cornerstone for Phase II. Pegged to the needs and priorities of breeding projects, the platform will provide facilitated access to: a) molecular techniques b) accurate phenotyping protocols c) information systems, and, d) data analysis tools. It will integrate these components into breeding workflows by providing flexible modular components which can be assembled in ways that match particular workflows.

Centre financial indicators

Original predictions for 2008 were quite positive and we were expecting support from our major funders at about the same level as in previous years. However, notification received at the end of June from the EC and DFID (therefore not accounted for in the GCP financial report submitted on 15 June 2008) obliged us to revise our strategy. The EC announced that their support will progressively reduce from EUR 4.6 million in the previous year to EUR 4.1 million in 2008, 3.5 million in 2009 and finally to 3.2 million in 2010. This translates to a reduction of about 30 percent in 2010. At the same time, DFID announced a 20 percent reduction in their support to GCP for the 2008–2009 fiscal year. However, from the explanation accompanying these budget notifications we understand that the adjustments are not related to the performance of the Programme *per se*. Rather, the reductions are driven by external factors. Nevertheless, this situation remains a concern from a management point of view as this reduction in our income for 2008 and over the coming years will affect our projected workplan and might jeopardise some of our Outputs. Therefore, adjustment at project level might be required starting at the end of July 2008 with a possible reduction of the budget to be allocated to our third round of competitive projects.

A major objective of the GCP Director in 2008 will be to seek new sources of funding to bridge this funding gap and get back on track with the projected budget for the coming years. The Programme should be in a position to achieve all of its objectives and deliver expected outputs with an annual income of about USD 15 million. The evolution of the exchange rate between the US dollar and the European currencies will also play a critical role in the budget balance of GCP over the coming years.

Collaboration and partnerships

GCP's newest venture in partnerships is helping establish crop and regional platforms to link NARS researchers working on the same crop and in the same region. These platforms use a new type of partnership closely linked to the validation phase in GCP research (Figure 1).

In addition, to fulfil its mission, GCP continues to forge and nurture dynamic R&D partnerships in research, breeding and delivery, and we are interacting increasingly with the private sector. The full list of GCP partners is in Appendix A.

The role of the private sector in GCP, though still modest, is also evolving, and growing. We recognise private organisations as key partners and we are identifying practical ways to involve them more actively in our research activities. Our goal is to tap the crop science technology and expertise of researchers and managers in large transnational seed companies. In working with the private sector, we take a case-by-case approach to reflect the nature of each partnership, and a few illustrations will suffice. The role of private sector foundations, such as the Syngenta Foundation for Sustainable Agriculture, play a critical role in enabling the public sector to access particular technologies, especially in molecular breeding.

GCP is also a good channel, in collaboration with crop Centres of the CGIAR, for the private sector to distribute some of their material for genetic studies. In 2008, Syngenta donated approximately 7,500 near-isogenic line (NIL) populations, 200 kernels of seed per line, and the SNP (single nucleotide polymorphism) marker data associated with the lines to the Maize Functional Diversity Group. This Group is a consortium of leading senior researchers at university and research centres devoted to improving knowledge of maize genetics. The germplasm will help accelerate the global knowledge of maize genetics for the ultimate benefit of growers worldwide, and will be distributed through GCP in collaboration with CIMMYT.

We also engage with the private sector in direct and active scientific collaboration. Over the last few years, scientists at Syngenta have successfully applied marker-assisted recurrent selection (MARS) to improve maize for polygenic traits like grain moisture content and precocity. A proposal is currently under discussion to apply this expertise to improve sorghum yield under water-stressed conditions in Africa. By drawing on Syngenta's expertise and genomic resources, this proposed project would illustrate a working example of how technology developed by the private sector can benefit plant breeding in the developing world. In such a scenario, scientists from Syngenta would be active project partners, working alongside breeders from Africa to improve sorghum.

Another subsector of interest is that of small- and medium-scale enterprises (SMEs). As a first step, representatives from several African seed companies and NGOs were invited to the 2007 Annual Research Meeting (ARM) to present their perspectives at the stakeholder session, thus providing pointers for exploring potential collaboration with GCP. With the 2008 ARM being held in Asia, we hope to use the same model to tune into local stakeholder issues in this equally important region.

These working partnerships validate the GCP model, which results in strengthened and diversified partnerships. We have demonstrated a capacity to evolve our structures and *modus operandi* in response to experience and feedback. As a result of these good partnerships, we are witnessing significant advances in the science that is our core business, enabling us to deliver on our commitment to the community of stakeholders that we serve, for the ultimate benefit of resource-poor farmers in drought-prone environments.

Alignment with CGIAR Systemwide Priorities

GCP's fundamental efforts to develop new knowledge and products support the United Nations Millennium Development Goal (MDG) of *halving, by 2015, the number of hungry people and those living on less than a dollar a day*. When these efforts result in superior crop varieties, they

offer potential for poor farm households to improve their food and nutritional security and income. They also offer the prospect of affordable food for poor consumers.

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

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

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

We would like to emphasise that in GCP, training and capacity-building are not stand-alone independent efforts. Rather, both are firmly embedded in our research projects. Therefore, every SP5 output contributes *directly* to the System Priorities listed above.

The project narrative section that follows provides a detailed analysis of GCP’s Subprogrammes, and outlines how Subprogramme Outputs fulfil these CG System Priorities.

Achievements in 2007

2007 impact highlights

- Completing molecular marker analysis of germplasm diversity for most GCP target crops, (all except faba bean and foxtail millet);
- Developing reference samples for the majority of GCP mandate crops;
- Generating novel information on gene flow related to crop domestication and implications for crop diversity distribution;
- Producing introgression materials with high genetic resolution for rice, and making them accessible for phenotypic evaluation and trait tagging;
- Developing first mutant populations for common beans and potato, and identifying ‘gain-of-function’ mutants in rice;
- Developing large-scale single nucleotide polymorphism markers (SNPs) for rice, drought expressed sequence tags (ESTs) for cowpeas and pearl millet, a novel set of simple sequence repeat markers (SSRs) for chickpeas, bacterial artificial chromosome (BAC) libraries for cowpeas and groundnuts and a functional illumina chip with 1,536 SNPs for cowpea;
- Generating a genetic map for *Musa* species with more than 500 marker loci, plus sequencing of some A- and B-genome BACs for *Musa* species;
- Identifying quantitative trait loci (QTLs) for multiple disease resistances and gene-based markers associated with QTLs for blast resistance in maize;
- Characterising and validating leaf growth QTLs in maize for genetic determinism of growth maintenance under water stress;
- Identifying, and transferring to national programmes, gene-based and linked markers diagnostic for salt tolerance (*Saltol*) and phosphorus uptake (*Pup1*) in rice;
- Identifying gene-based markers for aluminium tolerance in sorghum (AltSB) and validating SNPs/haplotypes for dissemination in Africa and South America;
- Developing near isogenic lines (NILs) for northern/southern leaf blight in maize, and for aluminium tolerance in sorghum;
- Transferring new sources of resistance to disease and of tolerance to drought from related species into cultivated germplasm of groundnut and cassava;
- Identifying recipient material for groundnuts, cowpeas, beans and chickpeas, including farmer- and consumer-preferred varieties in several African countries, forming the basis for marker-assisted selection (MAS) for simple traits and molecular breeding (MB) for complex traits for better performance in drought-prone environments;
- Developing models to improve MAS and MB strategies and favour their integration into conventional breeding schemes;
- Disseminating low-cost and high-throughput marker technologies developed by GCP to breeding programmes;
- Testing new markers for crop improvement in local environments and in adapted genetic backgrounds (eg, *Striga* resistance in cowpeas in West Africa);
- Using markers to select for biotic stress resistance and drought tolerance in several breeding programmes (eg, mosaic disease resistance for cassava in Nigeria, drought tolerance for rice in China);
- Establishing the GCP Central Registry for project datasets;
- Releasing iMAS (Integrated Marker-Assisted Selection System), a bioinformatics tool to help breeding programmes conducting MAS;
- Converting the Laboratory Information Management System (LIMS) developed at ICRISAT (International Crops Research Institute for the Semi-Arid Tropics) to open source and

installing it at BecA (Biosciences Eastern and Central Africa) and IITA (International Institute of Tropical Agriculture);

- Establishing a pipeline for gene expression analysis;
- Awarding ‘Capacity-building *à la carte*’ support to six national programmes;
- Implementing a fully-operational Genotyping Support Service (GSS);
- First meeting to establish the Rice Platform in Asia with regional partners to enhance uptake of products from GCP rice research;
- Establishing a large community to improve tropical legumes for Africa and coordination of initial activities; and
- Launching of the Delivery Plan Kit (DPKit) and formulating Delivery Plans for new projects.

Implications for future work

Overall, these results/achievements have the following implications for future work at the Subprogramme level.

- SP1 will finalise the development and delivery of its diverse products, and pursuing several research directions in continuity with past efforts. Fundamental work on securing the germplasm foundation will be completed in 2008. Reference samples will all be finalised, associated with characterisation data of validated quality and fully documented and published interpretations of diversity patterns. A global system will also be consolidated in order to ensure appropriate seed management and distribution of these samples.
- New SP2 projects will now focus exclusively on identifying genes/QTLs and gaining a better understanding of regulatory pathways involved in drought tolerance, exploring new approaches through comparative genomics, and taking advantage of the increasing number of genomic sequences available.
- The number of SP3 projects promoting the use of markers is increasing, commensurate with the knowledge generated in SP1 and SP2, as well as from research outside GCP. Thus, SP3 validates and adds value to the products and information generated by the other SPs. All SP3 projects will be geared towards crop improvement in drought-prone environments, focusing on [GCP target crops and regions](#).¹⁸
- For SP4, the basic infrastructure for information exchange within GCP has been developed. New development will focus on applying this infrastructure in specific research and breeding projects. The development of software, tools and methodology to sustain GCP’s science will continue as before, and support to GCP scientists on biological questions and on data handling and analysis will increase.
- The role of SP5 is becoming increasingly critical to ensure marketing and delivery of GCP products, while continuing to support capacity-building for target beneficiaries further down GCP’s delivery chain. We recently initiated *ex ante* analysis to evaluate the impact of key GCP products, and to help refine our target traits and regions based on local needs.

Changes in project composition from 2008–2010 MTP

The evolution through time, as well as future trends in GCP’s research portfolio in response to internal re-prioritisation and the recent EPMP have been reported in detail in earlier sections (see *Evolution of the GCP strategy and research trends*)

It is important, however, to underline that the identification of Output targets over three years represents a challenge for our Challenge Programme as the logframe presented here basically

¹⁸ http://www.generationcp.org/UserFiles/File/gcp-target-systems_brief.pdf

reflects our different research activities. So, and although we have a clear workplan within each Output, because of the rolling nature of our activity portfolio conducted through grants of between one and three years (competitive and commissioned research), in the current MTP, Output targets for a specific GCP activity might not be identified for all the three years of the logframe (ie, 2009–2011).

Unlike the previous years during which the set of projects to be initiated in following year was largely defined by the middle of the year, most of the commissioned projects to be initiated in 2009 will only be defined only towards the end of 2008. Indeed, we must first develop the workplans for each of our new challenge initiatives, clearly identifying gaps and bottlenecks constraining those projects. The set of new 2009 commissioned projects will then be designed to overcome these constraints and to complement the ongoing projects that will be embedded in the challenge initiatives as explained above. It will be critical for us to retain flexibility in resource allocation to implement our research strategy as underscored by the EPMR report. Given the foregoing, our logframe has a gap in terms of yet-to-be-defined projects, amounting to about USD 3–4 million.

Below is a summary of changes in project composition since the last MTP, reported by Subprogramme. For SPs 1–3, the reasons vary from funding difficulties at Programme level (as indicated above), Output refinement and strategic realignment and PI turnover. Detailed explanations on changes in project composition are provided in the Subprogramme narratives (see *Output descriptions and partnerships*).

SP1: Genetic diversity of global genetic resources

SP1: The 2008–2010 MTP had 26 Outputs, of which 12 will be completed by the end of 2008, and three were not concretised due to a shift in priorities, and lack of a solid proposal (details in SP1 Output descriptions). Progress has been slower than expected for the two Outputs below:

- **Output 1.3 (1.2 in current MTP). Seed of reference germplasm readily available for all crops:** Seed management appears to have been very diverse in the various CGIAR Centres. Departure from rigorous seed management which is necessary for founding genetic stocks is being assessed and will result in additional work, to be contracted later in 2008.
- **Output 1.7 (1.4 in current MTP). Methodology developed for resampling genetic diversity in large germplasm collections:** The project was launched in 2006 and was supposed to be based on genotyping data on rice. However, molecular data availability in rice was delayed and the methodology was slowed down due to lack of case studies. An Output target has been identified for 2009.

The current MTP reports 16 Outputs (compared to the 26 in the previous MTP), of which the five below are new.

- Output 1.1. Genotyping data validated for the reference samples and the reference markers for all GCP crops
- Output 1.4. DArTs developed as a genome-wide molecular characterisation technology for crops with little sequence information
- Output 1.10. Genetic factors underlying aluminium and drought tolerance in sorghum and maize identified
- Output 1.13. Linkage disequilibrium and patterns of selection in the genome of sorghum used for mapping useful genes
- Output 1.16. New wheat germplasm generated with broadened AB genome diversity

SP2: Genomics towards gene discovery

Seven of the 18 Outputs reported in the previous 2008–2010 MTP will be completed by the end of 2008, and progress has been slower than anticipated and/or adjustments made in nine Outputs. There are various reasons for this:

- *Administrative*: such as a delayed start and personnel changes (Outputs 2.1 and 2.7)
- *Strategic*: such as reprioritisation in line with the GCP renewed focus and target crops, resulting in scaling down Output targets for non-target crops (Outputs 2.8 and 2.9)
- *Technical*: such as non-polymorphic nature of existing DArT markers (Output 2.2), and BAC-library related issues (Output 2.4), and developing gene-based orthologous markers as a facilitative precursor to developing cross-species markers (Output 2.6)
- *Intellectual property (IP)*: such as impediments to sharing of BAC libraries (Output 2.4)
- *Adjusted Output targets*: For two of the Outputs, Output targets were adjusted for various reasons unrelated to the issues above. Outputs 2.11 had its Output targets adjusted to reflect new commissioned research within this Output, while Output 2.13 was adjusted based on results obtained to date, and taking into account the feasibility of achieving Output targets for 2009 and 2010.

For various reasons, new Output targets have also been defined or added for Outputs: 2.1, 2.2 and 2.3.

Detailed explanations for the slow progress and Output target adjustments and additions are outlined in the SP2 Output descriptions section. Overall, SP2 has reduced its emphasis on developing genomic resources and gene discovery and has intensified research activities on validation of genes/QTLs for transferring SP2 products to SP3.

In this MTP, SP2 presents 18 Outputs, including seven new ones. These are:

1. Output 2.10. Genomic resources (ESTs, markers and maps) developed for pigeonpea to enable trait/gene identification
2. Output 2.12. Discovery and development of alleles contributing to sorghum drought tolerance
3. Output 2.13. Examining natural variation in the transcriptional regulation of drought responses in wheat
4. Output 2.15. Drought from a different perspective: Improved tolerance through phosphorus acquisition
5. Output 2.16. Delayed senescence and drought tolerance in rice
6. Output 2.17. Validation of QTLs associated with drought tolerance traits in chickpea
7. Output 2.18. Enriching African sorghum varieties for stay-green using marker assisted selection

SP3. Trait capture for crop improvement

The 2008–2010 MTP described 23 Outputs. Of these, five will be completed in 2008 (3.1, 3.2, 3.13, 3.17 and 3.18 in the previous MTP).

One Output (3.8 in 2008–2010 MTP) has been split into two (3.8 and 3.9 in current MTP) to separate chickpeas and cowpeas in India and West Africa. Two network activities in the 2008–2010 MTP have since evolved into a community of practice approach and have therefore been transferred to SP5 (Output 3.17. *Quick conversion of popular rice varieties in the Mekong region*,

with emphasis on drought, salinity and grain quality improvement, and Output 3.22 MAS and dissemination of cassava varieties with resistance to pests and diseases).

Progress was slower than expected in six Outputs for different reasons. For five of them, the reason was a delayed start. This affected the following Outputs:

1. Output 3.2. Association mapping of downy mildew resistance in elite maize inbred lines in Thailand
2. Output 3.12. Integrating marker-assisted selection into the conventional breeding procedure for improvement of wheat in the drought-prone areas of Northern China
3. Output 3.13. Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco
4. Output 3.20. Integration of genomic tools with conventional screening for developing NERICA rice cultivars for West Africa
5. Output 3.21. Marker-assisted selection for sweet potato virus disease (SPVD) resistance in sweet potato germplasm and breeding populations

Output 3.27 (*Yield improvement of sorghum in Africa through marker assisted recurrent selection and a public-private partnership*) was delayed by staff turnover.

With the exception of the two Outputs transferred to SP5 for the reasons explained above, the 28 Outputs presented in the current MTP build upon those described for the Subprogramme in the 2008–2010 MTP.

The current MTP includes 20 new Outputs: four in Theme 1; eight in Theme 2; three in theme 3; and five in Theme 4. These are:

1. Output 3.1. Enhancing groundnut (*Arachis hypogaea* L) genetic diversity and speeding its utilisation in breeding for improving drought tolerance
2. Output 3.4. Making Latin America potato diversity available for Africa
3. Output 3.5. Field Evaluation of wheat-barley introgression lines under different water regimes
4. Output 3.6. Seed smoke treatment to favour germination under water stressed conditions
5. Output 3.7. Application of simulation models to pyramid multiple genes via MAS
6. Output 3.8. Linking genetic diversity with phenotype for drought tolerance traits through molecular and physiological characterisation of a diverse reference collection of chickpea
7. Output 3.9. Improving drought tolerance phenotyping in cowpea
8. Output 3.10. Development of a GCP phenotyping network
9. Output 3.11. Environmental assessment for phenotyping network
10. Output 3.12. Targeting drought-avoidance root traits to enhance rice productivity under water-limited environments
11. Output 3.13. Basal root architecture and drought tolerance in common bean
12. Output 3.14. Breeder-friendly high-throughput phenotyping tools to select for adaptive traits in drought environments
13. Output 3.17. Validation of *Alt_{SB}*, a major aluminium tolerance gene in sorghum
14. Output 3.18. Validation of *Saltol*, a major salinity tolerance gene in rice
15. Output 3.19. Application and validation of the major QTL Phosphate Uptake 1 (*Pup1*)
16. Output 3.24. Marker-assisted selection for resistance to *Striga gesnerioides* in cowpea
17. Output 3.25. Marker-assisted selection for resistance to streak virus in maize
18. Output 3.26. Dry bean improvement and marker-assisted selection for diseases and abiotic stresses in Central America and the Caribbean

19. Output 3.27. Yield improvement of sorghum in Africa through marker-assisted recurrent selection (MARS) and a public-private partnership
20. Output 3.28. Yield improvement of maize in Asia through marker-assisted recurrent selection (MARS) and a public-private partnership

SP4: Bioinformatics and crop information systems

There has been no major re-orientation. However, of the 21 Outputs in the last MTP, the following three are set for completion in 2008:

1. Output 4.18. An eco-physiological–statistical framework for GxE and QTLxE analysis developed
2. Output 4.20. Crop gene expression database and data mining tools developed
3. Output 4.21. Core collection methodology further developed and consolidated

Two Outputs were slowed down by delays in funding:

1. Output 4.10. Bioinformatics and data handling support to GCP scientists
2. Output 4.15. Methodology development for reconstruction of genealogies based on haplotypes related to geographic patterns

Nine Outputs (4.1, 4.3, 4.6, 4.7, 4.9, 4.11, 4.12, 4.13 and 4.15) have been modified to enhance efficiency, and/or clarify the Output/products, while Output 4.16 (*Large scale phylogenomic analyses tools developed for gene function prediction for GCP crops*) combines elements from Outputs 4.6 and 4.19 of the 2008–2010 MTP, with new Output targets.

This MTP features three new Outputs, of which Output 4.4 is in direct response to user needs. The new Outputs are:

1. Output 4.4. Quality and utility of GCP phenotyping data improved through the development of a data input template
2. Output 4.8. Quality management procedures in GCP research laboratories promoted
3. Output 4.17 Breeding drought tolerance for rainfed lowland rice in the Mekong region. This Output aims to identify traits for drought tolerance, as well as screening methods and genetic associations for those traits, develop methodology for using GIS and crop models to characterise drought environments and produce drought-tolerant germplasm for the region.

SP5: Capacity-building and enabling delivery

Of the 19 Outputs in the 2008–2010 MTP, two will have been completed by the end of 2008:

1. Output 5.3. Training materials for association studies/linkage disequilibrium mapping developed.
2. Output 5.16. Asset Inventory System for the GCP developed

Two Outputs were delayed:

1. Output 5.4 (5.3 in current MTP). Training materials for phenotyping developed: the Output took longer than expected to enhance the material with audio-visual aids.
2. Output 5.24. Targeting and impact analysis of GCP technologies. one of the collaborators was indisposed.

One Output was suspended.

1. Output 5.5. GCP training materials translated into selected languages (Spanish, French, Chinese, Portuguese and Arabic). This Output has been suspended, pending user-feedback on the English material to determine the need/viability for translation. Details on the delays and changes are explained in the SP5 Output description in the next section.

SP5 presents 27 Outputs in the current MTP for 2009–2011, of which 11 are new:

1. Output 5.5. Completed materials disseminated
2. Output 5.10. PhD in Plant Breeding Training at the West Africa Centre for Crop Improvement, University of Ghana
3. Output 5.12. Delivery Plan remote learning modules
4. Output 5.14. Improve cowpea productivity for marginal environments in Mozambique
5. Output 5.15. A cassava breeding community of practice in Africa for accelerated production and dissemination of farmer-preferred cassava varieties resistant to pests and diseases
6. Output 5.16. Establishment of and support to crop and regional platforms
7. Output 5.18. Validation of GCP products
8. Output 5.21. Toolbox of available molecular markers useful for marker assisted selection in GCP crops
9. Output 5.23. Development and implementation of a GCP Workflow And Repository System
10. Output 5.26. Getting the focus right: food crops and smallholder constraints
11. Output 5.27. A strategic assessment of the capacity to develop and adopt GCP technologies

Highlights of the 2008–2009 project portfolio

2008 highlights

Subprogramme 1: Genetic diversity of global genetic resources

In 2008, SP1 is finalising the development and delivery of its diverse products, and pursuing several research directions in continuity with past efforts. Fundamental work on securing the germplasm foundation will be completed in 2008. Reference samples will all be finalised and associated with characterisation data and fully documented and published interpretations of diversity patterns will be made available. Selected molecular data is being validated and a global system will be consolidated to ensure appropriate seed management and distribution of the reference samples. The genotyping platform is being managed to enable progress to be made along several lines. SSR markers are gradually being refined in order to sustain the GSS. Appropriate partnerships are being established in order to generalise the use of DARs, as well as to follow developments in model organisms, a responsibility shared with SP2 and SP3.

Subprogramme 2: Genomics towards gene discovery

In 2008, SP2 has begun delivery of a significant amount of genomic resources for crop species important in sub-Saharan Africa and Asia. Commissioned research has been initiated to develop genetic and genomic resources amenable to molecular breeding for some less-studied species (such as sweet potato and pearl millet). A commissioned project in coordination with the TLI project is generating sequence data and SNP arrays in cultivated groundnut to overcome the low diversity obstacle in molecular breeding. A critical and integrated approach using appropriate genomic tools and strategies with field-proven drought-tolerant genetic material is being amplified in rice and initiated in wheat to identify candidate genes for drought tolerance. In 2008 SP2 will validate and transfer some of its products to SP3 for molecular breeding. For instance, two new competitive projects dealing with validation of a QTL (*Pup1*) and a gene (*pSARK-IPT*) in rice for drought tolerance will be initiated. Collaboration with SP4 is being strengthened in genome analysis and gene expression studies.

Subprogramme 3: Trait capture for crop improvement

In 2008, SP3's activities are aligned to GCP's renewed strategy and refocused research priorities. All projects now address breeding issues in our target environment, for example, the project using *Oryza glaberrima* to improve drought tolerance in rice in Africa. Germplasm with enhanced tolerance to Al toxicity is being developed in sorghum, while salinity and phosphorus deficiency QTLs are being transferred to popular rice cultivars of Bangladesh and Indonesia, respectively. Other projects are developing cassava, potato and sweet potato germplasm with enhanced resistance to diseases for tackling the crippling factors limiting yield of these food crops in Africa's drought-prone environments. SP3 is collaborating with SP5 in capacity-building in MAS. Projects on drought tolerance for wheat in China and North Africa, for rice in Southeast Asia and for tropical legumes in Africa will benefit from the establishment of phenotyping networks and strengthened phenotyping capacity.

Subprogramme 4: Bioinformatics and crop information systems

The year 2008 opened with the basic infrastructure for the GCP information platform in place and gradually moving into a maintenance phase. This has released resources for more support to GCP scientists to help select and apply appropriate informatics tools to store and analyse their data. Anticipating an increase in demand for support, the initiative, envisioned in 2006, to create an

SP4 helpdesk improving access to all expertise and resources in SP4 was started in 2008. In response to concerns over the quality of some data, systematic quality assessment has been instituted, in parallel with efforts to evaluate existing data collections. Furthermore, the GCP tools for phylogenomic analysis are being refined and some new methods for LD and diversity analysis are being developed. Methodology for using GIS and crop models to characterise drought-prone environments and for breeding drought tolerance in rainfed lowland rice are being developed.

Subprogramme 5: Capacity-building and enabling delivery

GCP is generating a stream of concrete results and products, whose major impact can only be realised when they reach the intended users. This has direct consequences for SP5 including its delivery-enabling function. Capacity-building within SP5 in 2008 is building on the developments and advances arising from GCP research, and focusing on training excellence. Training is focusing in particular, on the use of markers for germplasm management and molecular breeding, phenotyping and data analysis. Tailored support is being offered to ensure continuity of downstream research. This includes addressing constraints identified in Delivery Plans, building ‘champion’ teams empowered by the Capacity-building *à la carte* Programme, and maximising complementarities with crop specific projects. SP5 is paying close attention to projects that promote delivery *per se* including a suite of support services, such as the GSS. To spread impact further, promote product delivery and assure sustainability, GCP is also helping to establish communities of practice and regional crop platforms.

2009 highlights

2009 selected highlights

- Establish reliable SSR fingerprints through validating genotyping data for the 21 crop reference sets. Corresponding seeds or clones generated and a cohesive institutional framework established for their distribution.
- DArT markers developed further to become available for all GCP crops that do not have advanced PCR based markers.
- Develop method to mine large collections for additional diversity.
- Analytical methods refined in collaboration with SP4 to reveal functional implications of genes and crop evolution.
- The best candidate genes for drought tolerance identified in SP2 resequenced within the reference samples of priority crops, to reveal the spectrum of allelic diversity for comparison with phenotypic diversity.
- Sorghum and maize used to analyse diversity for aluminium tolerance and address its relationship with drought tolerance.
- Development of specific introgression panels to be used in broader-based breeding and association mapping for rice, barley and wheat.
- New recombinant populations developed for rice and sorghum.
- Significant genomic resources associated with drought and biotic stress tolerance delivered for cassava, cowpeas, groundnuts, common beans and chickpeas.
- Basic genomic resources for molecular breeding for less-studied but important crops.
- Gene expression studies and transcriptome analyses for well-characterised cereals (eg, wheat, rice and sorghum) species to provide candidate genes and promising markers for drought tolerance.
- Validating and transferring SP2 products to SP3 for molecular breeding: mapping and validating of candidate QTL/gene (*Pup1* and *pSARK-IPT*) in rice and drought QTLs in sorghum and chickpea leading to marker-assisted introgression of the drought QTLs.

- Develop better methods for incorporating complex traits for more efficient breeding, focusing on drought and abiotic stress.
- Phenotyping platform established to identify potential phenotyping locations for GCP target crops.
- Phenotyping protocols for drought tolerance traits refined
- Validated markers for resistance to downy mildew in maize, diverse pests and diseases in potato, tolerance to Al toxicity in sorghum, salinity and phosphorus deficiency in rice, and drought in rice and wheat.
- Maize cultivars with enhanced resistance to downy mildew, cowpea cultivars with resistance to *Striga*, potato cultivars with better adaptation to Southeast African conditions, well-adapted rice varieties with enhanced tolerance to salinity and low phosphorus, and rice and wheat varieties with enhanced drought tolerance.
- Development of bioinformatics tools such as GOST (GreenPhyl Orthologous Search Tool) and Dayhoff: combination and expansion into a new major application.
- Improved efficiency in the analysis of genotypic data for LD analysis and genealogy reconstruction and in the exploration of QTLs.
- Adapt iMAS software to NARS requirements and train users.
- Helpdesk established for bioinformatics and biometrics.
- Optimise the quality, accessibility and usability of GCP data.
- Provide capacity to a focused group of NARS partners and collaborators
- Reach a wide community of users with GCP training, information and research products.
- High-quality degree training for African scientists.
- Mechanisms established to promote collaboration and synergy among NARS researchers to promote sharing of resources and adoption of GCP products
- Facilitate access to learning materials, a tool to assist in the preparation of Delivery Plans, a database on molecular markers, and the GSS.
- *Ex ante* impact studies to support decision-making at Programme and institutional level.

Subprogramme Highlights

Subprogramme 1: Genetic diversity of global genetic resources

After its first five years of activity, the main priority for SP1 is to translate a massive characterisation effort into products which will be broadly recognised and used by the scientific community and breeders. For each crop, a reference sample of germplasm has been selected to represent the diversity accessible to breeders; such samples must be managed as genetic stocks intended to be homogeneous, stable and available to all users. A genotyping data validation exercise will establish fingerprints with the most reproducible and resolute markers, seed will be generated and a cohesive institutional framework will be established for its distribution. DArT markers will be developed further to become available for all GCP crops that do not have advanced resources and cost-effective SNP assays. A method to use the information that has become available will be designed so that mining large collections remains an active source of additional diversity. Linkage disequilibrium assessment will continue as a key indicator to guide association studies.

The best candidate genes for drought tolerance identified with SP2 will be resequenced within the reference samples of the priority crops, in order to reveal the spectrum of allelic diversity to be compared with phenotypic diversity. Analytical methods refined in collaboration with SP4 will help reveal functional implications of the genes as well as throwing light on crop evolution.

Drought-related phenotyping will be conducted with reference samples of rice, sorghum, wheat and maize, as well as chickpea, common bean, cowpea and groundnut. Particular attention will be given to gathering records of and integrating outstanding genotypes in terms of drought-related behaviour. Association studies will be performed as soon as relevant phenotypic and genotypic data have been compiled, thus initiating a process that will gain in efficiency when additional data become available. Specific efforts will be devoted to sorghum and maize to highlight the architecture of aluminium tolerance in these species, focusing on the relationship with drought tolerance.

As a complement to association studies among representative materials, germplasm diversity will be explored further with other types of population which may also contribute to a better understanding of functional gene implication. Current work in rice and sorghum will be expanded to highlight specific patterns of introgression, and attempt admixture mapping.

Lastly, new recombinant populations will be developed for rice, sorghum, barley and wheat, combining multiple sources of alleles through hierarchical intercrossing or through wide interspecific crosses. They will broaden the genetic base of current breeding and produce materials that serve to resolve the contribution of genes and alleles to target phenotypes.

Subprogramme 2: Genomics towards gene discovery

The significant progress already made in SP2 to develop basic genomic resources will be expanded in 2009 to include less-studied crops and tropical legume species using next generation sequencing and high-throughput genotyping platforms. These projects are expected to generate resources amenable to molecular breeding in the crops. The availability of a 40K array in rice has prompted SP2 to amplify gene expression studies in rice for drought tolerance by using NILs. Similarly, transcriptome analysis is planned for identifying suitable alleles at candidate genes (transcription factors) and their combination to alleviate drought tolerance in wheat.

Several SP2 projects, already completed or to be completed by the end of 2008, have delivered promising practical outputs. We anticipate placing more emphasis in 2009 on validating and transferring these products to SP3 for molecular breeding. For instance, 2009 will see two new competitive research projects initiated. The new projects deal with understanding and validation of one QTL *Pup1* (results from earlier GCP competitive project¹⁹) and one gene in rice (*pSARK-IPT*, a promising candidate gene conferring drought tolerance in tobacco). Two more projects dealing with mapping and validation of drought QTLs in sorghum and chickpea have been initiated that will eventually lead to marker-assisted introgression of drought QTLs in these species. As well as planning to maximise the use of genomics research (using comparative and -omics approaches) in major crop species (eg, rice, wheat and sorghum) to identify QTLs/genes/alleles associated with drought tolerance, SP2 is interested in developing at least basic genomic resources for the less-studied but important crops such as sweet potato, pearl millet and pigeonpea in target environments. In 2009, delivery is also expected of a significant amount of genomic resources, eg, molecular markers, genetic and physical maps, ESTs, and markers associated with drought and biotic stress tolerance for cassava and four major tropical legumes (cowpeas, groundnuts, common beans and chickpeas) important in sub-Saharan Africa and Asia.

A critical and integrated approach using appropriate genomic tools and strategies with field-proven drought-tolerant genetic material is expected to deliver outputs for molecular breeding for drought tolerance. Focused investment and the appropriate combination of competitive and

¹⁹ Genes for tolerance of saline and phosphorus-deficient soils to enhance and sustain productivity in rice identified (G3005.02)

commissioned projects in 2009 will promote the achievement of research goals as well as build capacity in NARS for using SP2 products, in conjunction with SP5.

Besides this capacity-building link with SP5, several projects within SP2 already collaborate closely with projects within other GCP Subprogrammes and an even stronger integration of activities is foreseen in 2009 and beyond. For instance, collaboration with SP4 will be strengthened in genome analysis and gene expression studies, while work on validation of identified perfect markers, genes/QTLs and improved germplasm will strengthen ties between SP2 and SP3.

Subprogramme 3: Trait capture for crop improvement

As agreed at GCP's start-up meeting in 2003, the budget allocated to SP3 has proportionally increased over time relative to the other Subprogrammes, reflecting the fact that GCP is now emphasising activities under the responsibility of SP3, namely product validation and integration into breeding programmes. Activities have also evolved considerably within SP3; a greater proportion of resources are allocated to the validation and integration of new markers for crop breeding in target farming systems. There is a closer collaboration with other Subprogrammes for better use of the products that they deliver. There is emphasis on drought tolerance and more effort is being dedicated to the improvement of drought phenotyping quality. Three new competitive projects (on rice, bean and wheat) are aiming the refinement of drought phenotyping protocols and the use of large-scale phenotyping traits.

During GCP's first phase, most commissioned and competitive projects in SP3 focused on better methods for incorporating complex traits, including decision-support tools and technology development for more efficient breeding. This effort has been fruitful by generating, for example, low-cost and high-throughput markers, models and software to optimise MAB. Many of the products from these early years are now being used by ongoing and new projects. This effort will be maintained in 2009.

The increasing importance of drought and abiotic stress is reflected in the fact that all new projects address this issue. Previously, most activities focused on simply inherited traits. Of the 28 research projects within SP3 in 2009, 18 are focusing directly on drought and four on other abiotic stresses. A clear tendency to have a greater involvement of breeders and NARS in new projects will ensure more rapid and wider dissemination of markers in conventional breeding. Almost half of SP3 commissioned projects are now led by NARS.

To achieve its objectives, SP3 is helping establish a phenotyping platform which will include the identification of potential phenotyping locations for GCP target crops with adequate facilities and levels of expertise, and monitoring of germplasm exchange. Geographic information system (GIS) tools will play an important role in the deployment of this platform. They will help with the selection of testing locations that are representative of target environments and the identification of the extent to which phenotyping data collected in a given testing site can be used in other locations worldwide. They will also allow a better understanding of GxE and QTLxE interactions and better management of germplasm exchange.

Research products to be delivered in 2009 will include validated markers, new approaches and methodologies (to improve efficiency of marker-assisted breeding and drought phenotyping) and improved germplasm (prebreeding germplasm and germplasm to be directly disseminated to farmers). Validated markers will be concerned with resistance to downy mildew in maize, diverse pests and diseases in potato (late blight, potato tuber moth, *Diabrotica*, bacterial wilt, potato leaf

roll virus), and tolerance to Al toxicity in sorghum, salinity and phosphorus deficiency in rice, and drought in rice and wheat. Prebreeding germplasm will include introgression lines in groundnut and translocation lines in winter wheat. Other resources available to farmers will include maize cultivars with enhanced resistance to downy mildew, cowpea cultivars with resistance to *Striga*, potato cultivars with better adaptation to Southeast African conditions, well-adapted rice varieties with enhanced tolerance to salinity and low phosphorus, and rice and wheat varieties with enhanced drought tolerance.

An increasing number of activities will be conducted jointly with SP1 involving the evaluation of reference sets in target environments, and with SP2 regarding the identification and validation of genes/markers by NARS in target regions. Collaboration with SP4 will also increase as more data will be generated, thus increasing the need for efficient data storage and analysis. A close relationship with SP5 will ensure that breeders in NARS will have the capacity and expertise to conduct relevant work.

Subprogramme 4: Bioinformatics and crop information systems

SP4 has moved gradually from building the initial technical infrastructure for GCP, with relatively less emphasis on support to users of the infrastructure, to a Subprogramme aimed at supporting users by creating tools and methodologies applying the infrastructure. These changes over time are reflected in the budget and portfolio of activities in SP4. The building of the initial infrastructure in terms of, for example, the software architecture and basic data models, required large investments which are paying off. A good example is the development in 2007 of a fast and user friendly comparative genomic program, the GreenPhyl Orthologous Search Tool (GOST), allowing biologists to perform online phylogenomic analysis (this tool provides a reliable means of sequence annotation, gene functional analysis or candidate gene search across species). Another example is the 2008 product Dayhoff, a tool to document stress-response genes across plant species. This public resource is a compendium of protein families, phylogenetic trees, multiple sequence alignments (MSA) and associated experimental evidence, designed to elucidate orthologous and paralogous relationships between plant genes that may be involved in response to environmental stress, especially abiotic stress such as drought. Both of these products have been very well received by the bioinformatics community. In 2009 it is expected that they will have been combined and expanded into a new major application that will put GCP prominently on the map as a contributor to the bioinformatics toolkit.

SP4 aims to have significant impact in the biometrics arena. Research on the reconstruction of genealogies based on haplotypes related to geographic patterns should result in much more efficient analysis of genotypic data generated over the years by SP1, whereas research on the design and analysis of marker-trait association studies, with special attention for genetically challenging crops, is expected to improve the efficiency of the exploration of QTLs. In addition to these scientific innovations, SP4 will continue to work on its successful product iMAS (a software package for use by NARS to support MAS), adapting it to new user requirements and training more users. Direct support to GCP scientists will also be expanded; the helpdesk for all bioinformatics and biometrics questions will be developed further, acting as a broker between GCP scientists and SP4 expertise and products.

Continuing on the course pursued in recent years, the infrastructure of the GCP information platform, distributed web services, the underlying models, ontologies and tools will be maintained and where necessary further developed. Activities to increase the value of GCP data, defined by quality, accessibility and usability, will continue and, in some cases, expand. For example, to promote the application of quality management techniques in GCP partner institutes,

a series of workshops and consultancies will be organised, supported by activities in other related projects such as LIMS and the development of quality indicators.

Subprogramme 5: Capacity-building and enabling delivery

A significant part of the SP5 portfolio will follow the path of previous years. However increasing emphasis will be given to providing capacity to NARS partners and collaborators that are already engaged in GCP projects to enable them to further the research of GCP. Whilst this will result in SP5 focusing on a smaller number of direct beneficiaries from SP5 capacity-building activities, in compensation, emphasis will be given to distribution and dissemination of GCP outputs and products to reaching a wide community of users.

In past MTPs, SP5 has included Travel Grants for hands-on training and a Fellowship Programme. Both are being discontinued as separate activities from 2009 but comparable opportunities will exist for partners within the Capacity-building *à la carte* Programme. This Programme addresses priority research topics and capacity needs of selected teams that work to apply the results of upstream research undertaken in GCP's technical Subprogrammes.

The trend towards concentration on a more focused set of beneficiaries will be seen in other SP5 activities. High-quality degree training will be offered to those African crop communities in which GCP seeks to have greater impact. Research to improve cowpea productivity for marginal environments will create links to facilitate the application of results of the cowpea component of the TLI project in Mozambique. A cassava community of practice will be established building on the positive results obtained in past GCP projects involving several NARS working on the crop in Africa. The establishment of crop and regional platforms to link NARS researchers working in the same crop and region will promote sharing of new germplasm and protocols, and promote the use of new markers to enhance adoption and dissemination of GCP products. An online system will be developed to facilitate interaction between project PIs and GCP leaders and streamline management procedures. A thorough assessment will be carried out of existing capacity to adopt and use GCP technologies in target countries, ie those involved in GCP priority projects that will receive substantial funding in the second phase of the Programme.

Complementing these focused Outputs, SP5 will undertake activities to serve a wider community of beneficiaries through, for example, the completion and distribution of learning materials. A user-friendly tool will be provided for the preparation of Delivery Plans, covering understanding of delivery chains and impact pathways in the research-for-development continuum. Efforts will be made to validate GCP products and ensure that they are finalised in a format useful to intended users and disseminated as widely as possible. A database will be generated on available molecular markers for immediate use in all types of MAS scheme in breeding programmes working on GCP crops, and the GSS will be open to applications for assistance from all GCP partners and the wider scientific community in the developing world.

Research that will generate data about the relative importance of secondary breeding objectives of selected crops in GCP priority farming systems may qualify as helping focus GCP research, yet it also has wider implications through developing methodologies to identify constraints applicable to any crop and region. Its findings will support decision-making at the programme and institution level, with relevance also to funders.

Project narrative

Subprogramme 1: Genetic diversity of global genetic resources

Project overview and rationale

Access to genetic diversity is the foundation for breeding. GCP has devoted an entire Subprogramme to addressing this issue. Thus, SP1 seeks to provide the community of breeders and other scientists with germplasm samples gathered from various sources, selected for diversity and representativeness, and characterised as thoroughly as possible. It aims to establish standards that will serve as a reference for connecting and integrating future efforts within the global community, and thus intends to be able to mobilise a wide range of expertise and facilities.

A massive campaign of molecular characterisation of broad germplasm is coming to an end, and a subset of data to serve as a reference for the future is being validated within a complementary independent exercise. Seed is being purified for generating genetic stocks.

SP1 also undertakes activities that contribute data while consolidating capacity within GCP and providing access to external facilities. This covers exploration of new marker systems and development and optimisation of phenotyping capacities in relation to drought. Altogether, this integration should yield a biological understanding of diversity and of the genetic and functional architecture of adaptation. The diverse assessments that have come to a conclusion are providing directions for the future.

As a complement to exploitation of the representative reference samples, SP1 also orchestrates various exploratory approaches building on new types of population and new analytical angles that enable the production of genetic information and/or the contribution of pre-adapted germplasm for breeders. The choice of crops for this development is under consideration, in accordance with the current prioritisation exercise responding to the GCP.

Impact pathways

The mechanisms through which SP1 makes its contributions to the overall impact of GCP are described below, grouped by five themes.

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

Theme 1: Creation of an improved understanding of the structure of the diversity for the major world food crops

Access to genetic diversity available in large crop germplasm collections requires identification of representative samples of a smaller size to make them suitable for different surveys: screening of traits, evaluation of phenotypic diversity, evaluation of combining ability, assessment of molecular diversity, etc. Moreover, integrating diverse types of characterisation in the same

materials makes it possible to assess correlations among traits and investigate gene effects such as epistasis and pleiotropy. Passport data enable selection based on ecogeographic information; molecular markers offer means to further refine assessment of relatedness and to reduce sample size. Use of standardised methods yields data that can be compared across materials, laboratories and time, providing a durable momentum to enrich global understanding and representativeness.

The first phase of GCP will yield massive datasets featuring SSR diversity (12 to 50 loci) among large germplasm samples (300 to 3,000 accessions). This has served to identify reference samples of 50 to 500 accessions that are on the way to being handled as genetic stocks. Altogether, this led to a major GCP product: germplasm reference samples with validated data of reference markers, accessible as a global public good in a robust form. For each crop, the reference set was selected using all available genotyping data combined to phenotypic and passport information. Then a validation of the data was undertaken for this sample and the best 20 markers, which combine easy scorability and high resolution power. This should, *inter alia*, allow comparison of any new material with the international reference. Thus any novel diversity found in by newly accessed germplasm can be identified easily and used to enriching the global panel; conversely the global panel can be used to enrich the diversity accessible anywhere such as in a germplasm collection with a specific (eg, regional) mandate or any breeding programme. It is hoped that these samples will be shared widely and used, so that new data can be integrated to derive biological understanding useful for the management and use of germplasm diversity.

The primary users of these outputs are plant breeders. Trait donors can be identified by screening. However, donors with diverse trait genetic make-up are most easily accessed in samples which cover the whole spectrum of diversity, including for neutral molecular markers. Germplasm curators are also obvious beneficiaries, gaining a rationale for focusing characterisation efforts as well as methods for further mining the large collection. Other users are crop and trait specialists, who can invest their research efforts in materials which will also be studied by others with complementary expertise. This is an ideal situation for addressing the usual gaps in biology along the various operational scales: genome, transcriptome, proteome, metabolome, whole-plant and crop stand, and across environments.

In order to realise this potential, the following steps must be considered:

- germplasm curators are exposed to a range of biological situations that can broaden their understanding of germplasm characterisation opportunities
- germplasm curators are made aware of the value of comparative germplasm characterisation across collections using reference tools
- plant breeders are exposed to the potential of representative germplasm samples for accessing useful genetic diversity and broadening the genetic base of breeding populations
- opportunities are analysed for the distribution of GCP products through a global partnership involving germplasm curators and GCP-facilitated arrangements.

In order to realise this potential, it is imperative that the various partners share views and interests. To this end, a joint SP5–SP1 workshop will take place in November 2008. Participants will include scientists involved in GCP projects, who will present their work, as well as germplasm managers/curators and plant breeders from various institutions. This is being done in consultation with players that have a coordination and animation role in the field of germplasm management and use, such as the CGIAR System-wide Genetic Resources Programme (SGRP), the Global Crop Diversity Trust and the Global Partnership Initiative for Plant Breeding Capacity

Building (GIPB). This will set the stage for designing a cohesive key germplasm distribution system, and for specifying the role that GCP could play in this scheme.

Theme 2: Development of a range of flexible HTP genotyping techniques accessible in reference laboratories, and,

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

Accurate and high-throughput characterisation of materials is crucial to efficient germplasm exploitation, be it by genotyping with diverse markers or by evaluating materials for their behaviour when confronted to drought-related stresses. Within GCP, both fields converge when the two types of data are compared for association studies. Themes 2 and 3 were identified with the principal goal of serving the GCP community and helping it fulfill its obligation to mobilise the most efficient capacities within the GCP Consortium and beyond. In the meantime it was realised that this collective platform of proven capacities could serve a broader community. A global concept of plant breeding support service is being developed, which includes a genetic resource supply service, a genotyping support service (already running) and a phenotyping support service (to be refined). This would be accessible to all structured breeding programmes worldwide, thus hopefully multiplying the efficiency of the breeding community. This concept will be proposed to donors for potential implementation in 2009.

The GSS is already operational and is described elsewhere under SP5. Current effort on DArTs will expand the number of crops which benefit from this efficient and cost-effective marker system. Early efforts on allele resequencing have provided the basis for a community of practice with gene specialists essentially from outside the CGIAR, who look at orthologous genes across species, plus crop specialists within the CGIAR Centres, who look at diverse genes for their specific crops. The efficiency of this setup is under evaluation and, should it be satisfactory, is projected to continue along the same lines, focussing on new GCP priority crops and new candidate genes identified by SP2. The phenotyping capacity has been consolidated in the EMBRAPA network. However, its use is being opposed by phytosanitary constraints associated with intercontinental germplasm movement. GCP, with all the expertise located in the CGIAR Centres, is in a perfect position to anticipate and address such constraints. The initiative in phenotyping is being transferred to SP3.

Theme 4: Identification of favourable genetic factors (ie, potential genes or genome segments) and superior alleles (or haplotypes) through association studies

The objective of Theme 4 is to produce information which may serve for developing MAS; it is the core of the GCP. Users are primarily SP2 and SP3 scientists, the former for functional analysis of candidate genes, using cross-comparison between various types of evidence, aiming at gene identification and allele characterisation, the latter for the development and application of MAS tools. Occasionally, SP3 scientists can apply association study findings before identification of the causal polymorphism, thanks to LD. By construction, association studies are possible and productive when balanced materials have been carefully genotyped and extensively phenotyped. This is happening in maize in research ending in 2008. The next crops are likely to be rice and sorghum, then legumes. An effort on aluminium tolerance which successfully led to the identification of a major gene in sorghum is being extended in two directions and two crops; the characterisation of a complete association panel in sorghum and maize will give access to a broader range of alleles and is likely to highlight comparable and complementary mechanisms in the two crops; the characterisation of the materials for aluminium tolerance and drought tolerance will address the relation between both traits. SP3 is actively monitoring the breeding capacities which will make it possible to implement MAS in NARS. Such interaction among Subprogrammes—the essence of GCP—is ensured by internal coordination in programme

management and concertation among scientists in diverse relevant disciplines facilitated by events such as the Annual Research Meeting (ARM).

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

This Theme is the most upstream for its generic content. It is aimed at keeping germplasm research active beyond the release of reference samples and to ensure continuous input from germplasm collections. One approach is based on regular existing germplasm and consists of delineating subsets which will allow rigorous analyses powerful enough to point at novel sources of allele diversity at genes involved in target traits. Thus the scientists involved contribute information comparable to that which association studies can yield, following the same pathway as the results produced in Theme 4. This reflects part of GCP's identity in the appropriate application of analytical tools in germplasm science in order to sustain a flow of information and materials from genebanks to breeding programmes. The other approach is based on the production of specific new populations bearing higher allele richness rearranged in new combinations, either through multiple parent populations or through wide interspecific crosses. Here again, the results expected are comparable to those in Theme 4; yet the materials produced are likely to bear genetic gain making them ready for use in variety trials or in breeding schemes. This activity relates to prebreeding, which has long been the core of the CGIAR mandate. As a flagship for this type of analytically rich improvement approach, rice chromosome segment substitution lines developed at CIAT with the participation of Agropolis-IRD and EMBRAPA have started to be widely distributed among rice specialists and breeders worldwide.

Changes from 2008–2010 MTP

The MTP for 2008–2010 described 26 Outputs, of which the following 12 will have been completed by the end of 2008 and were therefore omitted from the MTP for 2009–2011:

- Output 1.1. Structure of genetic resources for the most advanced (tier-1) crops accurately described (including tools) and summarised in a reference sample
- Output 1.2. Structure of genetic resources for the less advanced (tiers 2 and 3) crops accurately described (including tools) and summarised in a reference sample
- Output 1.4. Global assessment of linkage disequilibrium in the genome of rice conducted
- Output 1.6. Detailed analysis conducted of maize diversity after migration out of America
- Output 1.8. DArTs validated as a genome-wide molecular characterisation technology
- Output 1.9. EcoTILLing assessed as a gene-targeted molecular characterisation technique
- Output 1.10. Methodology developed to assess SNPs with effect on allele expression (Non Coding SNPs)
- Output 1.13. Set of phenotyping facilities in Brazil made accessible for GCP germplasm evaluation
- Output 1.14. A crop and whole-plant modelling framework developed to support assessment of tolerance to drought
- Output 1.15. Phenotyping capacity accessible to the GCP is inventoried
- Output 1.17. Favourable genetic factors for drought tolerance in maize identified
- Output 1.24. Base broadened of current crop diversity in rice using related species

In addition, three other outputs were omitted for diverse reasons:

- Output 1.5. *Linkage disequilibrium assessed across several legumes along conserved gene stretches*. The proposal which was commissioned was not fully satisfactory. It is likely that the topic can be addressed more easily and more cost effectively when molecular resources

have advanced for legumes. Consequently, although not irrelevant, this Output, has been withdrawn from the new MTP.

- Output 1.20. *Ecogeographic/genetic clines related to drought identified for selection pattern analysis*. It had been anticipated that some activity along this line would emerge from the 2008 3rd competitive call. However; this was not the case.
- Output 1.23. *Diversity patterns in the genome of sweet potato used for mapping useful genes in relation to heterosis*. A shift in GCP priorities occurred this year, and sweet potato is no longer among the priority crops.

The MTP for 2009–2011 describes 16 Outputs, of which the following Outputs are new:

- Output 1.1. Genotyping data validated for the reference samples and the reference markers for all GCP crops
- Output 1.4. DArTs developed as a genome-wide molecular characterisation technology for crops with little sequence information
- Output 1.10. Genetic factors underlying aluminium and drought tolerance in sorghum and maize identified
- Output 1.13. Linkage disequilibrium and patterns of selection in the genome of sorghum used for mapping useful genes
- Output 1.16. New wheat germplasm generated with broadened AB genome diversity

Output descriptions and partnerships

The coverage of the germplasm surveyed within Theme 1 is meant to be as broad as possible. All GCP Consortium members participate, the CGIAR Centres bringing the collections that they manage, and NARS contributing complementary germplasm, although the latter material is not always readily accessible. ARIs bring germplasm, markers and access to genotyping facilities. Current Theme 1 projects recapitulate numerous earlier projects through the validation of selected genotyping data and the multiplication of reference germplasm seed. This is coordinated from the SP1 Leader's office, and it involves CGIAR Centres coordinated through the SGRP. Work aimed at mining large collections involves the same community.

DArT P/L is confirmed as an important private sector partner for genotyping within Theme 2. To date it has been a subcontractee, although its prominent role should be formalised within a global partnership agreement, together with laboratories which have established a DArT platform (currently ICRISAT). Phenotyping within Theme 3 is the priority area for partnership development. GCP has inventories of potential capacity and is running phenotyping projects with various CGIAR Centres, ARIs and NARS. The evolution towards a coordinated phenotyping support capacity requires appropriate investment, capacity validation and formalisation.

Association studies within Theme 4 require coordination of germplasm distribution, genotyping and phenotyping. Initiated under the leadership of ARIs that have primary experience on their selected crops, association studies are bound to become generalised and best be handled through close management within the GCP Consortium. Exploration of novel populational approaches within Theme 5 is an open area requiring the widest mobilisation of innovative potential through collaboration. It may become the main theme for competitive calls for new ideas in SP1.

In 2009–2011, SP1 will have 17 Outputs, distributed among five Themes as detailed below. All partners listed below by Theme and Output have a collaborative role in the research; the partner with principal responsibility (ie, where the PI is located) is underlined.

Theme 1: Creation of an improved understanding of the structure of the diversity for the major world food crops

- **Output 1.1. Genotyping data validated for the reference samples and the reference markers for all GCP crops:** The aim is to select and verify those data which will remain the reference for the future. Initially meant to assess data quality in various data batches coming from diverse partner laboratories, this Output was modified to become a verification of data for the reference samples using the best markers, which are easy to use and have a representative resolution power for describing germplasm structure. It involves collection of DNA and subcontracting to a service laboratory. Given the uncertainty of the management of the seed (see below), this exercise is coordinated with the production of founder seed for the reference samples, so that contingent within-accession heterogeneity is neutralised as a potential source of future discrepancies.
Partners: Agropolis-CIRAD, Bioversity, CIAT, CIMMYT, CIP, ICARDA, ICRISAT, IITA, IRRI
- **Output 1.2. Seed of reference germplasm readily available for all crops:** The activity was initially commissioned before the laboratories developed corrected realistic delivery calendars, which limited its efficiency. It had significant impact essentially for vegetatively propagated crops where germplasm exchange requires *in vitro* conditioning. Now that genotyping data are complete, the reference samples have been determined and must be ready for distribution. Seed management appears to have been very diverse in the various CGIAR Centres. Departure from rigorous seed management which is necessary for founding genetic stocks is being assessed and will result in additional work, to be contracted later in 2008.
Partners: Agropolis-CIRAD, Bioversity, CIAT, CIMMYT, CIP, ICARDA, ICRISAT, IITA, IRRI
- **Output 1.3. Methodology developed for resampling genetic diversity in large germplasm collections:** The objective is to provide a method to access new compartments of genetic diversity based on both existing molecular diversity patterns and external information (passport data or phenotyping data). The activity was started in 2006 and was supposed to be based on genotyping data on rice. However, as for Output 1.1, molecular data availability in rice was delayed and the methodology was slowed down due to lack of case studies. An Output target has been identified for 2009.
Partners: IRRI, EMBRAPA, ICARDA, ICRISAT

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

- **Output 1.4. DARts developed as a genome-wide molecular characterisation technology for crops with little sequence information:** This research includes expanding arrays developed in a previous GCP project for *Musa* and coconut, expanding arrays developed by DARt P/L (chickpea, pigeon pea, potato) and developing new arrays for yams, groundnut and pearl millet. The sets of germplasm used for marker discovery will be genotyped. In the case of coconut, groundnuts, yams and pearl millet, additional genotyping will be performed to explore the diversity in particular populations of interest. In the case of banana, this output will support high-density genetic mapping as a contribution to a *Musa* genome sequencing projects under consideration by the Agence Nationale de la Recherche (ANR), France.
Partners: (multiple PIs) Agropolis-CIRAD, Agropolis-IRD, CIP, CRI, DARt P/L, ICRISAT, IITA
- **Output 1.5. Database developed on allele diversity at candidate genes across species:** A project was launched in January 2006 in order to integrate diversity studies on seven target

crops (rice, barley, sorghum, beans, chickpeas, cassava and potatoes) and conduct molecular analysis on candidate genes for drought tolerance. Six genes or gene families were chosen: ERECTA, DREB, SS, SPS, ASR and INV. Specific and generic primers were designed and allelic sequencing is being performed on the different crop reference sets. The results will provide significant information on gene family evolution and crop genetic diversity organisation. Implication of the genes in drought tolerance will be possible with phenotyping data.

Partners: Agropolis–CIRAD, CIAT, CIP, ICARDA, ICRISAT, IRRI

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

- ***Output 1.6. Database established on field-proven drought-tolerant and drought-susceptible genotypes:*** Tolerance to drought can take various forms in various circumstances. Collecting genotypes which display outstanding behaviour allows capitalising on natural diversity. A database will be established in collaboration with SP3 to foster this type of collection, associated with accurate documentation and management of the seed as genetic stocks to promote exchange.

Partners: TBD

- ***Output 1.7. Drought-related phenotyping of specific populations with high quality molecular information implemented and Phenotyping Support Service consolidated:*** This is a group of projects which consist of phenotyping the GCP reference germplasm sets. They will provide information about the variation, under well-characterised drought conditions, of phenotypic traits, particularly those associated with drought tolerance. Depending on the crop, specific objectives include high quality seed multiplication, multi-location evaluation and generation of a set of hybrids from the GCP maize reference set, and a specific description of some traits based on the expertise of research partners. The current wave of projects covers sorghum, wheat, rice and maize. Pearl millet was initially included in the plan, but the reference germplasm set is not readily available.

Partners: (multiple PIs and partner teams): Agropolis–CIRAD; Agropolis–INRA; BIOTEC, CIMMYT, CRRI, ETH–Zürich, ICRISAT, IER, INRA–Morocco, ISRA/CERAAS, IGKV, IRRI, KARI, NPGRC, TNAU, UAS (Dharwad), WARDA.

Theme 4: Identification of favourable genetic factors (ie, potential genes or genome segments) and superior alleles (or haplotypes) through association studies

- ***Output 1.8. Favourable genetic factors for drought tolerance in rice identified:*** Phenotyping data will be analysed in conjunction with genotyping data that the rice community is currently developing using the Perlegen data. Up to several hundred thousand SNPs are expected; ultrafine association analysis will be possible, requiring innovative analytical approaches.
- Partners:* IRRI, Agropolis–CIRAD, WARDA, IGKV, CRRI, TNAU, BIOTEC
- ***Output 1.9. Favourable genetic factors for stress tolerance in four legume species identified:*** This focus project includes phenotyping of reference sets for drought tolerance and genotyping with the most advanced tools–SNP-based assay as well as DArTs–on groundnuts, cowpeas, chickpeas and common beans. Association analyses will be performed in a concerted manner.
 - ***Output 1.10. Genetic factors underlying aluminium and drought tolerance in sorghum and maize identified:*** This research proposed in the 3rd competitive call focuses on the genetic architecture of aluminium tolerance in sorghum and maize. Association panels will be phenotyped, first for aluminium tolerance, then for drought tolerance, with both field testing and high throughput root system imaging. Whole-genome SNP arrays will be developed for

sorghum and will be used together with existing maize arrays for characterising the panels. Maize candidate genes will also be monitored by re-sequencing. Association analyses will help characterise genetic factors for drought tolerance in relation to root system structure and the particular role of aluminium tolerance.

Partners: USDA-ARS, EMBRAPA, Cornell University, Moi University

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

- ***Output 1.11. Populations for multiple allelic segregation developed in rice and sorghum through multiple parent intercrossing:*** The overall goal of these projects is to develop populations suitable for localising multiple QTL for multiple traits to regions of 3 cM or less in populations targeted at specific agroecological environments. The Multiparent Advanced Generation Inter-Crosses (MAGIC) scheme theoretically enables this resolution to be reached. The current projects focus on rice and sorghum. In each case several populations will be developed, counting at least 1,000 inbred lines from each population. The process includes crude phenotyping and fingerprinting in order to ensure quality and to monitor progress of each breeding cycle. Recurrent selfing until 2011 will generate lines which can then be phenotyped and genotyped accurately.
Partners: (multiple PIs and partner teams) IRRI, NIAB, ICRISAT
- ***Output 1.12. Populations for multiple allelic segregation developed through nested intercrossing in rice:*** The project proposes to develop a nested association mapping population (NAM) in rice, following strategies developed in maize and sorghum. It will provide to much higher allelic diversity at the important QTLs than conventional mapping approaches do, enable fine mapping of QTLs (ie, localise them with high precision on the rice genome), and provide genetic materials (advanced lines) for direct introduction in breeding schemes. It will focus on African germplasm but also be of value for Latin America and the Caribbean, which share similar agroecosystems with Africa.
Partners: CIAT, Agropolis-IRD, WARDA
- ***Output 1.13. Linkage disequilibrium and patterns of selection in the genome of sorghum used for mapping useful genes:*** This project explores the potential of LD-based analysis in sorghum, both in a global representative sample of cultivar diversity and in a selected regional sample featuring introgression among cultivated races and spontaneous forms. The molecular characterisation involves whole-genome DArTs as well as allele resequencing at candidate genes. Phylogeographic approaches, admixture mapping and whole-genome mapping are being attempted.
Partners: Agropolis-CIRAD, DArT P/L, IER
- ***Output 1.14. Base broadened of current crop diversity in rice using interspecific bridges with African rice:*** This project aims to overcome an important obstacle to rice breeding: the interspecific sterility barrier separating the two cultivated rice species, *O sativa* and *O glaberrima*. New allelic diversity is expected to be incorporated in Asian rice germplasm from African germplasm, with emphasis on drought resistance and better water-use efficiency. However, because of a late start to the project, almost all Output targets have been redistributed over three years, up to 2010.
Partners: Agropolis-IRD, PhilRice, IER, Fedearroz, INERA, University of Arizona, CIAT, WARDA, Punjab Agricultural University
- ***Output 1.15. New alleles introgressed from wide crosses using crop wild relatives in barley:*** This project aims at resolving the potential of wild barley to contribute to improving drought tolerance in cultivated barley. It builds on the availability of 140 lines composed of an advanced elite background containing chromosome segments from a wild barley accession from the Fertile Crescent. Recombinant Segment Substitution Lines will be used for intensive

genotyping and phenotyping. Because of a late start of the project, almost all Output targets have been redistributed over three years, up to 2010.

Partners: SCRI, ICARDA, OSU, INIA–Chile, Universidad de Talca (Chile), UC–Riverside

- **Output 1.16. New wheat germplasm generated with broadened AB genome diversity:** This research proposed in the 3rd competitive call focuses on the expansion of the genetic base of bread wheat using emmer wheat. This group is thought to include valuable sources of tolerance to drought and heat. A reference set will be established and widely sampled for producing synthetic hybrids in combination with *Aegilops tauschii*. These in turn will be crossed with hexaploid bread wheats for starting recombination and selecting drought/heat tolerant genotypes. Derivatives will be genotyped with SSR and DArT for facilitating association studies.

Partners: ARI, CIMMYT, Sydney University, DUAS, PARC

International public goods

SP1 is delivering sets of germplasm with associated documentation that are a condensed representation of germplasm diversity for major food crops worldwide. These consist of germplasm reference samples with validated data on reference markers, accessible as a global public good in a robust form. The GCP partners contribute germplasm, markers, laboratories and capacity which, altogether, made the programme an extremely comprehensive initiative equipped to yield reference germplasm and reference markers of international value.

Subprogramme 2: Genomics towards gene discovery

Project overview and rationale

Plant traits for adaptation to environmental stresses are often controlled by complex genetic systems subject to influence by genotype by environment interactions. To combine the right complements of genes and alleles effectively in a breeding programme, sufficient understanding is needed of the genetic mechanisms underlying the adaptive processes, especially for traits like drought tolerance. Although advances in genomics tools and knowledge from model organisms are important for identifying potentially useful genes controlling complex traits like drought tolerance, translation of the new tools and approaches into agronomic improvement has been limited to a few species. Therefore, the main objective of this Subprogramme is to provide a scientific and collaborative environment so that interdisciplinary and integrated approaches can be used for gene discovery to dissect the genetic mechanisms underlying adaptive processes. Specifically, SP2 aims to: (i) develop cross-cutting research platforms for efficient application of genomic tools and knowledge to decipher genetic control of complex traits, and (ii) identify genes to alleviate target problems in the most efficient manner by pooling resources and expertise. To realise the full potential of these approaches requires capacity-building in the use of the new tools and creation of a pipeline to translate results into practice.

SP2 will continue to use (and develop, wherever required) genomics and genetic resources tools and technologies, and evaluate interdisciplinary approaches to enhance understanding of gene function and interaction to improve knowledge of gene systems across crops. Comparative approaches are applied to leverage genetic knowledge from multiple plant species to investigate and validate gene functions important to stress tolerance. Interdisciplinary teams are formed to apply the validated genes and/or superior alleles in breeding programmes. While the focus will be more on drought tolerance traits in the coming years, the genes and agronomic characteristics that improve crop resilience in difficult environments will be integrated with drought tolerance.

Impact pathways

The Outputs of SP2 are specialised genetic stocks (eg, mutants and advanced backcross lines) and genomic resources (molecular markers, ESTs, markers associated with abiotic and biotic stress tolerance, cloned genes for specific trait improvement, gene expression datasets, and desirable gene combinations in elite genetic backgrounds). While development of genomic resources in less studied crop species (like pearl millet, sweet potatoes, pigeonpeas) enables and encourages the crop community to undertake molecular mapping of traits of interest and eventually molecular breeding for crop improvement, generation and utilisation of specialised genetic stocks (like mutant populations, NILs) improves the efficiency of gene identification and validation so that appropriate allele combinations may be identified for the target environment. These genetic resources are used by the global research community, in general, and by researchers and breeders within GCP, interested in applying genomics to improve agriculture. For instance, developed prebreeding materials alleviate problems in resource-poor areas in Africa (eg, maize tolerant to Al toxicity in Kenya) and Asia (eg, rice tolerant to phosphorus deficiency in Indonesia and salinity in Bangladesh).

Another important aspect of SP2's approach is capacity-building for NARS as well as CGIAR research programmes in the area of modern genome biology through strong project components of training and partnerships among NARS, ARIs and CGIAR institutes. More detail is provided below on the impact pathways for work within SP2,s four Themes, which are:

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

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

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

In its first five years, GCP played a catalytic role by supporting the assembly of wheat stocks and the production of mutant collections in bean and true-seed potato. These start-up activities have stimulated interest from diverse institutions and research laboratories, thus increasing the likelihood that more specialised stocks in other crops will be shared or produced by other initiatives. Utilisation of a rice mutant collection with the candidate genes has identified 'gain-of-function' mutants for AP2/ERF transcription factor genes (CBF, SHN, HRD) with improved drought tolerance and water use efficiency phenotype in rice. The production and use of new genetic resources and development of tools will expand the research community's means for understanding gene function relevant to stress tolerance.

Just within the past year, new comprehensive genomic resources for several crops (sorghum, maize, cowpea and cassava) have been produced, or are in the pipeline. As sequencing and genotyping become less costly, whole genome genotyping, ultimately at the sequence level, is expected to be increasingly feasible. In this context, GCP has engaged its community of collaborators to produce genomic and genetic resources, particularly in crop species that are under-resourced eg, pearl millet, sweet potato and pigeonpea. Work within this first Theme will continue to take advantage of the large number of rice mutant collections around the world by supporting phenotyping of the mutants for stress tolerance. There will be greater focus on the mutant phenotyping work by linking it with the ADOC project. With the start of a focus project in 2007, significant efforts are being made in resource-building activities for four important African and Asian legume crops (common beans, chickpeas, cowpeas and groundnuts). For instance, 14 x genome coverage BAC libraries and more than six cDNA libraries to generate about 200,000 ESTs have been developed. Molecular markers are being developed in large numbers from SSR enriched genomic DNA libraries, ESTs and BAC-end sequences in almost all four legume species. Activities on these four legumes will create a permanent genomic resource base for each species, enabling the construction of genetic maps and marker-aided selection applications at various stages of genetic analyses and breeding. These activities will facilitate molecular breeding in legumes to develop improved cultivars with enhanced tolerance to drought and/or resistance to biotic stresses in Africa and Asia.

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

The second Theme of this Subprogramme aims at generating common markers and consensus maps across species, and at providing a framework for leveraging information across different crop species. GCP's investments in mapping orthologous genetic markers and genomic investigation of *Musa* are a modest attempt towards this aim. Indeed, inspired by progress made in developing the genome infrastructure in *Musa*, the GCP community is excited to interact with other genomic and funding initiatives like L'Agence nationale de la recherche (ANR; National Research Agency, France), Joint Genomics Institute, Department of Energy (JGI, DoE), USA, for sequencing the *Musa* genome. The development of cross-species markers for legumes, under the focus project, started in 2007, is another GCP initiative to develop and integrate gene-based orthologous markers into genetic maps of legume species, linked with Theme 1. This will help determine the relationship of the ancestral genome segments in these legumes and facilitate genomics-enabled legume breeding in Africa and Asia.

For cassava, a physical map with SNP markers will be produced by a team led by the University of Maryland. For sweet potato and pearl millet, an expansion of genome sequence data which will be aligned with genetic maps using mapping populations in breeding programmes is aimed for. A main emphasis in these activities is that the genomic resources should be anchored in well-used mapping or breeding populations. SP2's approach is to maximise the return on investment in a sequencing project by coupling it with SP1's development of genetic recombinant populations, so as to make use of the sequence data. By developing parallel genomic and genetic resources, benefits can be reaped in a relatively short time.

New activities will generate improved genetic maps for several species, including cassava, sweet potatoes, pearl millet and pigeonpeas. These efforts are expected to increase the genetic knowledge base of important crops that have thus far suffered under-investment. Outputs from these projects will promote mapping and genetic dissection of a suite of traits, particularly drought tolerance, and will eventually enable the respective communities to undertake molecular

breeding activities for developing improved crop cultivars for drought tolerance in the targeted regions of Africa, Asia and South America.

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

In the third Theme, emphasis is on the application of genome-wide tools such as gene chip technology to reveal the causal relationship between gene expression patterns and phenotypes. A unique feature of GCP's research is the use of agronomically relevant experimental conditions and genetic materials, such that the genetic knowledge generated from these experiments is relevant to researchers and breeders. The adoption of genome-wide approaches has proven to be fruitful in suggesting new genes or regulatory mechanisms for validation. Gene expression studies in the 1st round [competitive projects](#)²⁰ have shown that variation in gene expression (or expression-level polymorphisms) offers a new dimension of genetic diversity that can bridge the gap between genotypes and phenotypes. A whole-genome view of plant response to stress in relevant genotypes under realistic agronomic conditions will be important for identifying QTLs of large to moderate effects.

Two ongoing research projects that aim to discover genes and genomic regions controlling broad-spectrum disease resistance in maize, rice and wheat have already been completed, and another project dealing with models predicting the impact of different allelic combinations on growth rate in cereals should be completed by 2008. These projects have already delivered new markers associated with multiple disease resistance QTLs in cereals that have been taken further to develop NILs for resistance to diseases (eg Northern blight in maize) as well as to determine if expression patterns are causally related to target phenotypes. Results from these projects are important because disease resistance is often a requisite trait in drought-prone environments. New activities under this Theme will maximise the use of advanced genetic materials such as NILs. SP2 foresees the production of a multi-stage 'expression atlas' of genotypes with contrasting phenotypes in near-isogenic lines, followed by cosegregation analysis between expression patterns and relevant phenotypes. A project on rice transcriptome analysis by using drought NILs with a high-density microarray is continuing, and a new project has been planned to deal with identification of candidate genes/transcription factors that are known to increase drought tolerance when showing modified expression in wheat. A new project on discovery and development of alleles contributing to sorghum drought tolerance has been selected in the 3rd round of GCP's competitive research projects. New alleles will be identified at each of the candidate genes that show expression levels, correlated to drought tolerance and efforts will be made for introgression of the new alleles into cultivated germplasm. Parallel projects involving several crop species would be desirable as they will enable comparison between genes/pathways, hence providing support for orthologous candidate genes for validation. This approach, if proven successful, will provide an efficient way of assigning gene functions and identifying relevant pathways. Such efforts should provide candidate genes and promising markers for molecular breeding for a complex trait like drought tolerance to develop drought-tolerant varieties of wheat and rice in Asia and Africa.

²⁰ <http://www.generationcp.org/research.php?da=0634417#competitive>

Selection of the right genetic materials is crucial for gene identification and expression analysis. Moreover, to identify the right genetic material, methods to generate high-quality phenotypes with respect to drought tolerance are needed. It has been shown in several situations that drought tolerant/response phenotypes can be reliably measured provided that water stress is properly administered in the field or under equivalent agronomic conditions. Therefore, in conjunction with SP3, SP2 is interested in accelerating the progress in these proven systems and will also be sponsoring activities to improve current phenotyping methods with the aim of fast-tracking the identification of genotypes with relevant phenotypes.

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

Activities within this Theme aim to identify genes with useful functions and validate them for delivery to breeding programmes. While three Outputs concerning the identification of stress tolerance genes in wheat, rice, sorghum and maize have been or will be completed, two new Outputs dealing with mapping and validation of drought QTLs in sorghum in Africa and chickpea in Asia have been planned in the next phase. As a result of a completed project on the cloning of the gene that confers tolerance to Al toxicity in sorghum, allele mining in the crop has been initiated under SP3, and cloning of homologous Al-tolerance genes has been undertaken in other cereals. Similarly, the Output dealing with tolerance of salinity and P-deficiency in rice, has accomplished fine-mapping of the Saltol and Pup1 QTLs. As a result, SSR and gene-based diagnostic markers have been identified for tolerance to salinity and P-deficiency in rice. Based on these markers, marker-assisted backcrossing has been initiated to transfer Saltol into five Bangladeshi rice varieties and the Pup1 region into two common Indonesian rice varieties under the framework of SP3. The outcome of these activities will lead to development of improved rice varieties for saline and phosphorus-deficient soils in Asia. Furthermore, knowledge of the tolerance genes to counter soil problems in rice can be immediately used to identify similar genes in other cereals or legumes. Indeed, based on results from the Pup1 project, a new competitive research project was recently selected in the 3rd round of competitive grants. This new project will identify the candidate genes for Pup1 QTL, plus as other complementary genes that confer tolerance to P-deficiency as well as drought stress. Another project dealing with the identification of candidate genes responsible for failure of grain formation in rice and wheat under drought stress provided some further evidence on genes responsible for grain failure in these cereals. Recently, one more project has been initiated dealing with understanding and validating the role, in rice, of the *pSARK-IPT* gene—a most promising gene for conferring drought tolerance in tobacco. This will help to identify the key determinant genes in rice responsible for drought tolerance, as well as their corresponding knockout mutant lines.

Research is in progress to determine drought-adaptive mechanisms in bread and durum wheat aided by large-scale phenotyping methodologies. With improved phenotyping techniques, this project is expected to produce new wheat mapping resources for gene identification. Two new Outputs dealing with mapping and validation of drought QTLs in sorghum and chickpeas have been added to the MTP. In the case of sorghum, the stay-green QTLs identified in Australia will be validated and introgressed into drought-sensitive Africa sorghum lines. This Output will also enhance understanding of the association between plant height and stay-green, generating knowledge critical for the adoption of stay-green in Africa. In the case of chickpeas, a new Output linked with Theme 1 will engage the GCP community to map and validate both known and newly identified QTLs for drought traits eg, root traits, $\delta^{13}C$ and harvest index. Candidate drought QTLs will be used for marker-assisted breeding for drought tolerance to develop improved chickpea cultivars in Africa and Asia.

As GCP has moved to its second phase, more Outputs are foreseen dealing with validation of identified genes and QTLs so that the products of SP2 can continue to be transferred to the SP3 portfolio. Such efforts will be strengthened further in the coming years through formulation of new projects in conjunction with SP3 to evaluate the genes/markers from SP2.

The Outputs from these Themes are geographically neutral. The primary users of products from Subprogramme 2 will be researchers, plant biologists and breeders worldwide. Uptake of these products by researchers and breeders is expected to expand the capability and increase the efficiency of NARS breeding programmes, an outcome beyond the immediate users. At the global level, the resources and knowledge of gene function generated by SP2 activities are expected to be taken up by the plant biology community. The knowledge when applied to a range of crop systems can increase the potential of finding new genes from diverse plant species.

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

Changes from 2008–2010 MTP

The MTP for 2008–2010 described 18 Outputs, of which the following seven Outputs will have been completed by the end of 2008.

- Output 2.1. Systematic evaluation of rice mutant collections conducted for conditional phenotypes with emphasis on stress tolerance
- Output 2.11. Targeted discovery of superior disease QTL, alleles in the maize and rice genomes conducted
- Output 2.12. Functional genomics of cross-species resistance to fungal diseases in rice and wheat conducted
- Output 2.13. Common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes investigated and determined
- Output 2.15. Genes responsible for failure of grain formation in rice and wheat under drought identified
- Output 2.16. Genes for tolerance of saline and phosphorus deficient soil to enhance and sustain productivity in rice identified
- Output 2.17. Aluminium tolerance genes in the cereals identified and characterised

The MTP for 2009–2011 describes 18 Outputs, of which the following seven are new.

- Output 2.10. Genomic resources (ESTs, markers and maps) developed for pigeonpea to enable trait/gene identification
- Output 2.12. Discovery and development of alleles contributing to sorghum drought tolerance
- Output 2.13. Examining natural variation in the transcriptional regulation of drought responses in wheat
- Output 2.15. Drought from a different perspective: Improved tolerance through phosphorus acquisition

- Output 2.16. Delayed senescence and drought tolerance in rice
- Output 2.17 Validation of QTLs associated with drought tolerance traits in chickpea
- Output 2.18 Enriching African sorghum varieties for stay-green using marker assisted selection

Reflecting recent EPMR recommendations, SP2's research activities focus on drought tolerance, although significant achievements have been made over the last few years in the area of cloning and isolation of diagnostic markers for Al tolerance, salinity tolerance and phosphorus uptake efficiency in cereals. As GCP enters in its second phase, SP2 has reduced its emphasis on developing genomic resources and gene discovery and has intensified research activities on validation of genes/QTLs for transferring SP2 products to SP3.

Output descriptions and partnerships

SP2 strongly believes in partnerships in order to leverage information from multiple species to the target species and efficiently achieve the goals of the Subprogramme. In general, SP2 collaborates with ARIs to utilise their expertise in the area of modern genome biology, the CGIAR Centres for their rich genetic resources and role as the interface between ARIs and NARS, and NARS as its target users. SP2 works with private companies/service providers, eg, NCGR, JCVI and Perlegen to take advantage of the sequencing and gene expression services that they offer in a cost-effective manner. In almost all SP2 projects, NARS as well as CGIAR scientists benefit from the participation of ARIs through exposure to and training in modern genome biology applied to agriculture. A list of partners to achieve the 15 SP2 Outputs is given below.

All partners listed have a collaborative role in the research of the respective Output, and the partner with principal responsibility (ie, where the PI is located) is underlined.

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

- **Output 2.1. Bean genetic and genomic resources developed:** Genomic resources including ESTs, SSR, SNP and COS markers are being developed for identification of markers associated with drought tolerance and BCMV /bruchid resistance with a final goal of developing improved bean varieties with enhanced pest and disease resistance and tolerance to drought in Africa. Because of a late start, the scheduling of some Output targets eg, generating 20,000 ESTs has been postponed by one year. A new Output target has been added for 2011.
Partners: CIAT, ART, CBI, ECABREN, EIAR, Purdue University, RIKEN, SABRN, UC–Davis
- **Output 2.2. Chickpea genetic and genomic resources developed:** A larger number of molecular markers (DArT and SSR) are being generated to prepare a high density reference map of chickpea. These genomic resources will be used to identify molecular markers for drought tolerance and insect (*Helicoverpa*) resistance in chickpea to develop drought-tolerant and insect-resistant chickpea varieties in Asia and Africa. Because of the non-polymorphic nature of existing DArT markers, the Output target to develop polymorphic DArT arrays has been postponed by one year. A new Output target has been added for 2011.
Partners: ICRISAT, EIAR, LZARDI, DArT P/L, IIPR, NIPGR, UC–Davis, University of Frankfurt
- **Output 2.3. Cowpea genetic and genomic resources developed:** Genomic resources including cDNA libraries, BAC libraries, EST sequences and BAC-end sequences are being generated to develop SNP markers and place BAC contigs onto the genetic map. These

resources will be used to identify markers for drought tolerance and resistance to biotic stress (flower thrips, root nematode). A new Output target has been added for 2011.

Partners: UC–Riverside, IITA, INERA, IRAD, ISRA, UC–Davis

- **Output 2.4. Groundnut genetic and genomic resources developed:** Molecular markers (SSR and SNP) are being developed in large numbers from genomic and cDNA libraries to develop a genetic map for *Arachis*. In addition to identifying the markers for drought tolerance and foliar disease resistance, a linked genetic and physical map will be developed for the AA genome. Because of a late start of the project and some IP and technical issues relating to sharing the BAC library with project partners, almost all Output targets have been postponed by one year.

Partners: ICRISAT, University of Georgia, UCB, EMBRAPA, Dart P/L, Instituto Agronomico de Campinas, Chitedze Research Station, INRAN, ISRA, ARI–Naliendele

- **Output 2.5. Validation of drought-response/resistance pathways genes by phenotypic analysis of mutants):** After identification of mutant lines for drought response phenotypes, sib-lines will be characterised by physiological parameters (transpiration rate, stomatal conductance, root and water-use efficiency) using field screen and high-throughput phenotyping techniques. Subsequently, drought resistance/sensitive phenotypes will be identified for several candidate gene mutants in rice/*Arabidopsis* and datasets will be developed.

Partners: VBI, Virginia Tech, IRRI–Philippines, HZAU

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

- **Output 2.6. Cross-species resources developed for comparative biology in tropical crop legumes:** In order to develop cross-species markers for legume species, gene-based orthologous markers are being developed and mapped onto the genetic maps of bean, cowpea, chickpea and groundnut. This will help determine the relationships of the ancestral genome segments in these legumes and facilitate genomics-enabled legume breeding in Africa and Asia. Part of the original Output target for 2010 has been postponed to 2011.

Partners: UC–Davis, University of Georgia, UCB, UC–Riverside, ICRISAT, CIAT, IITA

- **Output 2.7. Genetic and physical mapping resources produced for drought breeding in cassava:** This Output plans to develop genome-wide BAC fingerprint contigs and the minimum tilling path to sequence several thousand BAC clones and develop a genome-wide SNP map that will be used to identify markers for drought tolerance. Because of a late start due to the PI's changing institute and the late signing of the GCP contract, all Output targets have been rescheduled by one year. Some minor editorial modifications have also been made in the Output targets.

Partners: University of Maryland; University of Pretoria; University of the Witwatersrand

- **Output 2.8. Genomic resources and mapping populations for sweet potato developed to enable trait/gene identification:** In order to develop genomic and genetic resources in under-resourced sweet potato, cDNA libraries, ESTs, EST-based markers and DArT arrays are being developed. In addition, a virus-free diploid mapping population is being generated *in vitro*. A medium density reference map developed based on these resources will be very useful for enabling trait mapping in the crop. Because sweet potato is not a target crop species for GCP (reflecting recent EPMR recommendations), only limited funds have been allocated to this work. As a result, the Output targets presented here have been scaled down from those listed in the MTP for 2008–2010.

Partners: CIP, IIAM, NAARI, INIA–Uruguay, EMBRAPA, DArT P/L

- **Output 2.9. Genomic resources and mapping populations developed and assembled for pearl millet to enable trait/gene identification:** To enrich the genomic resources in pearl millet, ESTs in large number are being developed for developing and integrating gene-based markers into existing pearl millet genetic maps. This will enable the pearl millet community to identify markers for terminal drought tolerance and grain and stover yield potential in Africa and Asia. Because pearl millet is not a target crop species for GCP (reflecting recent EPMR recommendations), again, only limited funds have been allocated to this work, and the Output targets here have been scaled down from those listed in the MTP for 2008–2010.
Partners: ICRISAT, AICPMIP, CAZRI, RAU–Beechwal, ILRI
- **Output 2.10. Genomic resources (ESTs, markers and maps) developed for pigeonpea to enable trait/gene identification:** In order to establish linkage between the TLI and TLII projects, development of genomic resources has been planned in pigeonpea since it is an important target crop in TLII. Next generation sequencing technologies and a high-throughput SNP genotyping platform are being established, in addition to SSR markers, to develop a linkage map of pigeonpea to enable trait mapping.
Partners: NCGR; NRCPB; ICRISAT; PDKV

Theme 3: Assignment of genes and pathways to phenotypes through the convergence evidence of genome variation

- **Output 2.11 Causal relationship between whole-genome expression patterns and stress tolerance determined in rice via analysis of near-isogenic lines:** In continuation of earlier work, this Output plans to develop and characterise NILs for drought tolerance. Use of a high-density microarray with the field-grown NILs will determine expression patterns for genes involved in drought tolerance. Subsequently, candidate chromosomal regions with expression signatures will be aligned with drought QTLs. Because new research has been commissioned within this Output, based on results from previous research and taking into account the feasibility of achieving objectives, the Output targets have been adjusted in this MTP.
Partners: NIAS, IRRI
- **Output 2.12. Discovery and development of alleles contributing to sorghum drought tolerance:**
This new output deals with exploitation of the stay-green QTLs in applied sorghum improvement. The output plans to generate all pairwise combinations of QTL introgression heterozygotes, as well as the double heterozygotes, to measure their epistatic interactions. Furthermore, high throughput genome sequencing (Solexa 1GB) of 10 genotypes involved in target (MAGIC, RIL and stay-green NILs) populations will provide the large number of SNPs for application of high-throughput genotyping approaches to MAGIC populations that will be key to both discovery research and product development.
Partners: University of Georgia, ICRISAT, SARI, MAU, NRCS, ARC
- **Output 2.13. Examining natural variation in the transcriptional regulation of drought responses in wheat:** Within this new Output, candidate genes/transcription factors that are known to increase drought tolerance when showing modified expression will be identified. Subsequently, new alleles will be identified at each of the candidate genes that show expression levels correlated to drought tolerance. Efforts will be made to introgress the new alleles into cultivated germplasm to develop drought-tolerant wheat varieties in Asia and Africa.
Partners: ACPFG, ICS–CAAS, CIMMYT

Theme 4: Validation of genes and pathways via evaluation of under- or overexpression constructs or variants (induced or natural) of target genes

- **Output 2.14. Drought-adaptive mechanisms in bread and durum wheat determined through large-scale phenotyping methodologies:** Within this Output, high-throughput precision phenotyping protocols are being developed that are characterised by good correlation to drought tolerance field screening and international trial performance. Subsequently, QTLs associated with drought-adaptive traits will be identified in bread and durum wheats. Markers identified in the target region will be useful for developing wheat cultivars with improved tolerance to drought, as well as understanding the syntenic relationship with rice. Based on results obtained to date, and taking into account the feasibility of achieving objectives, some minor modifications have been made in the Output targets for 2009 and 2010, and a new Output target has been added for 2011.
Partners: CIMMYT, ACPFG, DWR
- **Output 2.15. Drought from a different perspective: Improved tolerance through phosphorus acquisition:** This output is based on an earlier output where team showed maintenance of higher root growth rates of rice lines carrying P uptake QTL (*Pup1*) under P deficiency and *Pup1* locus was considered a prime target in improving P deficiency and drought tolerance in rice. This output plans to identify the gene(s) and understand the underlying physiological mechanisms; development of allele specific markers for MAS and develop the QTL pyramided lines.
Partners: UC-Davis, IRRI
- **Output 2.16. Delayed senescence and drought tolerance in rice:** This new output is based on the hypothesis (proved in tobacco) that drought-induced plant senescence is due to a type of cell death programme naturally activated during drought. Based on the success of overexpression of the IPT gene (mediating the synthesis of cytokinins) under the control of *SARK* promoter in tobacco, the team plans to test the efficacy of stress-induced cytokinin synthesis in conferring drought tolerance in upland and lowland rice varieties. If successful, the researchers will identify genes with significant roles in conferring drought tolerance in rice and generate drought-tolerant and water-use-efficient rice plants in different genetic backgrounds.
Partners: IRRI, University of Potsdam/MPIMPP, JIRCAS, ICABIOGRAD, Zhejiang University
- **Output 2.17. Validation of QTLs associated with drought tolerance traits in chickpea:** Identification and validation of QTLs for drought traits eg, root traits, $\delta^{13}\text{C}$ and harvest index have been planned within this Output. Candidate drought QTLs will eventually be used for marker-assisted breeding for drought tolerance so that improved chickpea cultivars with drought tolerance can be developed for Africa and Asia.
Partners: ICRISAT, DZARC, UAS–Bangalore
- **Output 2.18. Enriching African sorghum varieties for stay-green using marker-assisted selection:** Within this new Output, stay-green QTLs of sorghum identified in Australia will be validated and introgressed in drought-sensitive Africa sorghum lines. This Output will also enhance understanding of the association between plant height and stay-green, and generate knowledge critical for the adoption of stay-green in Africa.
Partners: DPI&F, MARC, ARTC

International public goods

The overall research portfolio of this Subprogramme focuses on drought-tolerance traits as well as genes and agronomic characters that improve crop resilience in difficult environments. The Outputs are primarily resources, knowledge and technologies that are international public goods consistent with the goals of the CGIAR System Priorities 2a and 2b. The key resources and tools

produced are specialised genetic stocks (eg, mutants and advanced backcross lines), gene expression data, cloned genes for specific trait improvement (tolerance to drought, soil problems and disease resistance) and desirable gene combinations in elite genetic backgrounds (prebreeding materials).

Subprogramme 3: Trait capture for crop improvement

Project overview and rationale

SP3 aims to create product-driven teams that span the innovation-to-impact continuum and bridge the gap between the development of research outputs and their actual use in breeding programmes. Ongoing commissioned projects focus on better methods for incorporating complex traits, including improved phenotyping approaches and protocols and MAS simulation, on the development of decision-support tools and markers for more efficient breeding, and on gene/marker validation and use in breeding programmes for target crops and regions.

Three new competitive projects will focus on the improvement of drought phenotyping by evaluating the accuracy of new traits or refining the use of already identified traits associated with drought tolerance. The overall objective of this research will be to provide innovative and efficient screening tools (for field and controlled environment) and their associated protocols, capable to better identify drought tolerant genotypes in segregating populations and large germplasm collections. New commissioned projects in 2008–2009 principally aim to accelerate validations of genes for tolerance to Al toxicity, salinity and phosphorus deficiency and resistance to *Striga*, and to favour the application of marker technologies in breeding programmes (eg, MAS for resistance to strike virus applied to maize breeding in Mozambique). Some will also contribute to active South–South exchanges and collaborations. For example, introgression and backcross lines will be developed from *Arachis* amphiploids generated by EMBRAPA, Brazil, to be evaluated and disseminated in Senegal, the main groundnut producer in Africa. Similarly, markers will be used in Latin American Southern Cone countries to select potato cultivars to be evaluated in Malawi and Mozambique.

Two new commissioned projects will contribute to improve drought phenotyping quality within GCP, through better characterisation of environments and better evaluation of facilities and expertise in the different phenotyping locations as well as the development of innovative large-scale phenotyping tools. Finally, two new projects will apply a marker-assisted recurrent selection (MARS) approach to sorghum in West Africa and to maize in Asia through a public–private partnership.

Impact pathways

The impact pathways that take the Outputs of SP3 through Outcomes to eventually have impact on the development goals of the CGIAR are described below by Theme. The SP Themes are:

- Theme 1: Characterisation of segregating populations and identification of genomic regions for plant breeding
- Theme 2: Development and evaluation of novel breeding or molecular technologies to better serve modern plant breeding
- Theme 3: Markers/alleles validation in adapted germplasm under target environments
- Theme 4: Application of molecular markers in breeding programmes

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

This Theme involves most of the ‘discovery’ activities of SP3. Work conducted under this Theme is expected to provide a better understanding of the genetic basis of drought tolerance in GCP target crops. They are generally conducted by or with NARS that already have a high level of expertise and facilities (eg, EMBRAPA in Brazil, BIOTEC in Thailand, NARS in the Southern Cone of Latin America etc) and in some cases through South–South collaborations. Products delivered under this Theme are mainly genomic regions associated with target traits, or prebreeding germplasm (eg, introgression lines of groundnut and wheat) that will be used by other SP3 projects (in Themes 3 or 4) before being delivered as products (markers or germplasm) to breeders. Even if, in most cases, products generated under this Theme are not expected to be used directly by breeders in the South, these final users are already associated with the projects (eg, breeding programmes in Senegal, Niger, and Malawi and Mozambique). This will ensure continuity of the pathway from research outputs to ultimate impacts on breeding.

Output 3.3. (Tailoring superior alleles for abiotic stress genes for deployment into breeding programmes: association analysis of *Alt_{SB}*, a major aluminium tolerance gene in sorghum) is quite representative of Theme 1. The PI of this project and his team have been able to identify one apparently improved version of *Alt_{SB}* in the framework of an SP2 competitive project. Through the present project, they are now applying association mapping to undertake a comprehensive scan for even better versions of this gene for deployment into sorghum breeding programmes. Through the use of cutting-edge genomics and statistical genetics approaches, this research is really bridging the gap between basic research on Al tolerance and applied breeding programmes, to develop the tools that plant breeders can use to breed for improved acid soil tolerance efficiently and effectively. To ensure continuity in the delivery chain and application in breeding, this project is linked with a commissioned project in Theme 3 (Output 3.17. Validation of *Alt_{SB}*, a major aluminium tolerance gene in sorghum). This is led by a sorghum breeder with the objective of validating *Alt_{SB}* alleles in West Africa (Niger and Mali) by transferring the gene into local backgrounds for cultivation in local acid soil conditions. This example, with a gene discovery phase in SP2, a refinement phase in SP3 Theme 1, and a validation/application phase in SP3 Theme 3, represents a typical example of GCP’s impact pathway from upstream research to breeding application.

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

In addition to the discovery of novel markers and the development of pre-breeding germplasm, there is also a need to develop and/or test new methodologies and tools to improve the efficiency of molecular breeding. This is the objective of activities under Theme 2. The new methodologies essentially cover two areas: the refinement and modelling of marker-assisted breeding strategies and the development of innovative phenotyping protocols. In the MTP for 2008–2010, the development of low-cost, high-throughput markers was also included in this Theme. However, this activity is now largely supported by the GSS, which falls within SP5, while the development of breeding methodologies remains a high priority for SP3.

As an output of the research conducted in SP3 and SP4 to improve the development of molecular breeding systems, MAB simulation models and corresponding software are now being developed. This exercise of molecular breeding simulation and monitoring is conducted in collaboration with ongoing SP1, SP2 and SP3 projects (particularly Output 3.15. Integrating marker-assisted selection into the conventional breeding procedure for improvement of wheat in the drought-prone areas of Northern China). MAS monitoring software, available for the entire molecular breeding community, will be developed in collaboration with SP4. The new breeding methodologies developed in Theme 2 also concern the application of innovative approaches developed by the private sector, to African crops. One example is research to develop sorghum

drought tolerant germplasm through marker-assisted recurrent selection, a molecular breeding methodology successfully applied to maize by the private sector.

Another component of Theme 2 is support to drought phenotyping activities. The objectives of the ongoing activities, conducted under both competitive and commissioned projects, are to develop better descriptions of the testing environments and to access innovative traits, either for large-scale or for precision phenotyping. A strategic network of GCP evaluation sites is being established for all GCP target crops. The geographic coordinates of these locations permit access to soil/climatic databases that provide information about the respective environment. These locations are being clustered according to their environmental characteristics, to estimate their representativeness and help to monitor germplasm exchange. A subset of locations, after evaluation of facilities and expertise, will become a phenotyping platform for large, high-quality drought phenotyping of GCP crops. Two other projects under this Theme deal with the use of innovative traits in drought phenotyping of two legumes, chickpeas and cowpeas. Since they aim to develop new methodologies and innovative support tools, activities under Theme 2 are generally led by CGIAR Centres or ARIs.

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

The objective of this Theme is to validate, under target environments, alleles that were identified or markers that were developed in Theme 1 or other Theme 3 Outputs, or in other GCP Projects (mainly SP2). Being closely related to SP3's product development activities, this Theme and Theme 4 together ensure the impact pathway from research outputs generated by SP1, SP2 and Theme 1 of SP3 to the ultimate impacts for achieving GCP's goals.

Product management activities create the conditions for a global and rationalised selection/management of validation projects. Projects in Theme 3 all are based on the concept of validation and value-adding of existing GCP products. They are all commissioned and defined on the basis of scientific quality (evaluated from reports, on-site visits and expert opinion), risk factors, alignment to the GCP strategic plan, competitive advantage for users (breeders, farmers), synergy with other projects and products, and feasibility and expectations for adoption. These projects that aim to transfer QTLs/genes identified by SP1, SP2 or SP3 in well adapted/adopted germplasm, involve breeders. As far as possible, they are led by NARS (eg, CAAS, China; INRA, Morocco; EMBRAPA, Brazil, for Outputs 3.15, 3.16, and 3.17 respectively). All of the genes/QTLs to be transferred concern drought or other abiotic stresses. Evaluation and impact assessments of the transferred genes/QTLs are done locally (eg, Northern China, Morocco, Niger and Mali, Bangladesh and Indonesia for Outputs 3.15, 3.16, 3.17, 3.18 and 3.19 respectively). All the validation projects will take advantage of the phenotyping platform developed through Theme 2 for better monitoring of testing conditions and management of germplasm exchange.

Research on the *Alt_{SB}*, *Saltol* and *Pup1* genes aims to validate products that have been generated under SP2. Consequently, these are good examples of upstream products generated by another GCP subprogramme, identified as having a large potential impact, and consequently validated for further use and dissemination. Importantly, in all these cases, there is also significant support from SP5 for training and enhancing the capacity of the NARS that are involved in the validation projects in Niger, Mali, Bangladesh and Indonesia. This ensures not only the delivery of germplasm, but also the transfer of MAB technologies.

Theme 4: Application of molecular markers in breeding programmes

This Theme targets the current application of markers developed by GCP (or by others) in breeding programmes via the most efficient approaches and represent the last step in the product delivery pathway. GCP is mainly focusing on the use of MAB for drought and other abiotic

stresses. However, due to the complexity of these traits, the use of markers in breeding programmes in many Theme 4 projects still involves disease resistance traits (eg, rice yellow mottle virus and bacterial leaf blight in rice, sweet potato virus disease, *Striga gesnerioides* in cowpea, streak virus in maize, bean golden yellow mosaic virus and root rot in bean). In contrast, activities on rice already address drought and many products (genes/QTLs) for abiotic stresses validated in Theme 3 are expected to be transferred into breeding activities through Theme 4 in the near future.

Work on MAS for resistance to *Striga gesnerioides* in cowpea is exploiting and disseminating the products of a previous SP3 project (MTP 2008–2010 Output 3.10, Markers developed for *Striga* resistance in cowpea). Efforts to fine-map four genes that reliably affect yield under both artificially imposed and natural drought, is taking advantage of large body of information delivered by several other projects. Its objective is to transfer these products to breeding, after having analysed the physiological basis of tolerance and confirmed their effects in farmers' environments in India and southern China, in collaboration with relevant NARS.

Changes from 2008–2010 MTP

The 2008–2010 MTP described 23 Outputs, of which the five below will have been completed by the end of 2008.

- Output 3.1. Physiological and genetic traits that make cassava one of the most drought-tolerant crops
- Output 3.2. Genetic diversity of groundnut's wild relatives unlocked with genomic and genetic tools
- Output 3.6. Low-cost technologies develop for pyramiding useful genes from wild relatives of cassava into elite progenitors
- Output 3.9. Drought-tolerant rice cultivars developed for North China and South/Southeast Asia by highly efficient pyramiding of QTLs from different origins
- Output 3.10. Markers developed for *Striga* resistance in cowpea.

In this MTP, SP3 has 28 Outputs which build upon those described for the Subprogramme in the 2008–2010 MTP, with the exception of two network activities. These two activities have evolved into a community of practice approach and have therefore been transferred to SP5 (Output 3.17. Quick conversion of popular rice varieties in the Mekong region, with emphasis on drought, salinity and grain quality improvement, and Output 3.22. MAS and dissemination of cassava varieties with resistance to pests and diseases).

Output descriptions and partnerships

Under Theme 1 which mainly covers discovery activities, partners are principally NARS institutions with relatively extensive facilities and expertise, such as EMBRAPA (Brazil), BIOTEC (Thailand), INIA (Uruguay) or the Hungarian Academy of Sciences. Several projects also include African partners with less extensive facilities (Malawi, Mozambique, Senegal). In some cases, the research is based on a South–South collaboration (eg, Output 3.4 involving collaboration between Argentina, Brazil, Chile, Malawi, Mozambique and Uruguay) or based on a large network involving a CGIAR Centre and countries from the North and the South (eg, Output 3.1, a partnership between ICRISAT, Bolivia, Brazil, France, Senegal and USA).

Activities under Theme 2 mainly involve ARIs (eg, Aberdeen University, Charles Sturt University, CSIRO, INRA, JIRCAS, Missouri University, Nagoya University, Pennsylvania State University, UC–Riverside, University of Texas, KUL) and CGIAR Centres (CIAT, CIMMYT, ICARDA, ICRISAT, IITA, IRRI, WARDA). Activities focusing on phenotyping in different

conditions also include NARS institutions (CAAS, EMBRAPA, INERA, ISRA, TNAU, University of Bangalore). Outputs 3.8 and 3.9 are linked to research on tropical legumes (TLI project) and contribute to reinforcing the phenotyping capacities and expertise of the African and Asian partners involved in this work.

Theme 3 groups together all activities focusing on product validation. Consequently, it mainly involves institutions from the South (BRRI, Dhaka University and BINA in Bangladesh, EMBRAPA in Brazil, CAAS, LAAS, HAAS, Ningxia University, NWSUAF and SAAS in China, ICABIOGRAD in Indonesia, INRA in Morocco, and INRAN in Niger). In some cases, projects are led by a NARS (CAAS for Output 3.15, INRA, Morocco for Output 3.16, EMBRAPA for Output 3.17), thereby ensuring validation of markers in the adapted/adopted background and the transfer of the associated MAS technologies.

The application of molecular markers in breeding programmes (Theme 4) concerns resistance to biotic stresses, tolerance to abiotic stresses, or both. Most activities are led by CGIAR Centres (WARDA, CIP, IRRI, ICRISAT/CIAT and CIMMYT for Outputs 3.20, 3.21, 3.22, 3.23 and 3.28, respectively), but some are led by NARS institution (Output 3.24 led by INERA, Output 3.26 led by INIFAP) or based on a South–South collaboration (Output 3.25: University of KwaZulu–Natal, South Africa and IIAM). Output 3.25 includes a non-governmental organisation (ORE-Haiti) and dissemination of the products will be ensured by different ways (through farmer organisations in Mexico, participatory breeding in Cuba, and through the non-governmental organisation in Haiti). Outputs 3.27 and 3.28 are notable in that they involve public–private partnerships.

All partners listed below have a collaborative role in the research; the partner with principal responsibility (ie, where the PI is located) is underlined.

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

- **Output 3.1: Enhancing groundnut (*Arachis hypogaea* L) genetic diversity and speeding its utilisation in breeding for improving drought tolerance:** Cultivated groundnuts have a narrow genetic basis and the first step for improving drought tolerance in this crop is by enhancing genetic diversity. This will be done by accessing the diversity of landraces from Bolivia (its centre of origin) and developing prebreeding germplasm from existing amphidiploids (generated through Output 3.2. in 2008–2010 MTP). Drought phenotyping capacity of the African partner (ISRA Senegal) will be improved to ensure accurate drought tolerance evaluation.
Partners: ISRA, PROINPA, USDA–ARS Plant Genetic Resources Unit, CIRAD, ICRISAT, EMBRAPA, UCB
- **Output 3.2. Association mapping of downy mildew resistance in elite maize inbred lines in Thailand:** A collection of maize lines is being used to identify markers associated to downy mildew resistance. The late approval of 2007 proposals created delays, now resolved, in the scheduling of commissioned research in this Output (as well as in Outputs 3.12, 3.13, 3.17 and 3.18).
Partners: BIOTEC, Kasetsart University, National Corn and Sorghum Research Center, NSFCRC
- **Output 3.3. Tailoring superior alleles for abiotic stress genes for deployment in breeding programmes—association analysis of *Alt_{SB}*, a major aluminium tolerance gene in sorghum:** *Alt_{SB}* alleles are being surveyed across diverse sorghum germplasm to identify superior *Alt_{SB}* haplotypes by association mapping. Haplotype-specific markers will be developed and used for introgression into African local landraces.

Partners: EMBRAPA, USDA–ARS, Cornell University, EMBRAPA, KSU

- **Output 3.4. Making Latin America potato diversity available for Africa:** Virus-free planting material (minitubers) from South America NARS and CIP will be sent to Malawi and Mozambique and selected locally, based on adaptation to local growing conditions (dormancy-maturity), consumer preferences and necessary resistances or tolerances (mainly virus and late blight). DArT markers will be used to characterise germplasm and PCR-based tools applied to identify and characterise genotypes for resistance to various pests/diseases. Partners: INIA–Uruguay, INIA–Chile, INTA–Argentina, EMBRAPA, IIAM, DARS, CIP
- **Output 3.5. Field evaluation of wheat-barley introgression lines under different water regimes:** Wheat/barley translocation, substitution and addition lines developed by the Molecular Cytogenetic Laboratory at ARI–HAS in Hungary will be analysed by *in situ* hybridisation (GISH). SSR and DArT markers will be used to better identify translocation breakpoints. Addition and translocation lines will be phenotyped for salt and Al toxicity tolerance in Hungary, and for drought tolerance in China, through a link with Output 3.12. Partners: ARI–HAS, CIMMYT, CAAS, Eger–Hungary
- **Output 3.6. Seed smoke treatment to favour germination under water stressed conditions:** Research activities are being conducted, through collaboration between Hungary and South Africa, to identify genes responsible for the action of smoke on crop germination. Partners: ARI–HAS, UKZN

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

- **Output 3.7. Application of simulation models to pyramid multiple genes via MAS:** Simulation tools are being developed and applied by CAAS and CIMMYT to facilitate effective implementation of QTLs in MAS for polygenic traits, such as drought tolerance. Activities will link with other ongoing projects using MAS (Outputs 3.12, 3.19 and 3.20). Partners: CIMMYT–CAAS, CSIRO, University of Queensland, CAAS, CIMMYT, INRA–France, IRRI, ICRISAT
- **Output 3.8. Linking genetic diversity with phenotype for drought tolerance traits through molecular and physiological characterisation of a diverse reference collection of chickpea:** A reference set of chickpea (300 accessions) identified as an output of the chickpea genotyping project of SP1 are being phenotyped for carbon isotope discrimination and other drought tolerance related traits and genotyped with DArT markers, through collaboration among ICRISAT, JIRCAS and the University of Bangalore. This Output and Output 3.9 are the result of splitting Output 3.8 in the 2008–2010 MTP that referred to drought phenotyping of two different crops (chickpea, cowpea) in two different target regions (India, West Africa). Partners: ICRISAT, JIRCAS, Univ of Agricultural Sciences, Bangalore
- **Output 3.9. Improving drought tolerance phenotyping in cowpea:** Cowpea varieties are compared for grain yield and drought tolerance-related physiological traits (including thermal imaging) in several environments in West Africa and California. This will provide baseline drought tolerance information for analysing GxE interactions and refine phenotyping protocols. Partners: UC–Riverside, TAMU, ISRA, INERA, IITA
- **Output 3.10. Development of a GCP phenotyping network:** A strategic network of field phenotyping sites for GCP target crops is being established. At least ten field locations will become centres of excellence in phenotyping for drought tolerance, while other locations will be supported to increase phenotyping capacity.
- **Output 3.11. Environmental assessment for phenotyping network:** The selection of sites for Output 3.11 is done on the basis of environmental data (assessed using geographic

information systems software, spatial overlay, and distance and proximity tools) and modelling tools.

Partners: CIAT, KUL, EMBRAPA, Waen Associates

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

- **Output 3.12. Targeting drought-avoidance root traits to enhance rice productivity under water-limited environments:** Screening tools and protocols are developed and refined for high-throughput phenotyping of dehydration-avoidance traits in rice
Partners: IRRI, WARDA, TNAU, Barwale Foundation, Aberdeen University, Missouri University, Nagoya University, Charles Sturt University
- **Output 3.13. Basal root architecture and drought tolerance in common bean:** Basal root whorl number and basal root growth angle measurement protocols are developed in bean and QTLs are identified for these two traits
Partners: Pennsylvania State University, CIAT, SABRN, IIAM
- **Output 3.14. Breeder-friendly high-throughput phenotyping tools to select for adaptive traits in drought environments:** Field-based, low-cost and high throughput phenotyping protocols are developed for crop water status and canopy size and functionality in wheat. The impact of selecting for those traits is estimated in several drought mega-environments.
Partners: ICARDA, CSIRO, CIMMYT, INRA Morocco, EIAR

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

- **Output 3.15. Integrating marker-assisted selection into the conventional breeding procedure for improvement of wheat in the drought-prone areas of Northern China:** Major drought tolerance QTLs identified previously are being introduced into cultivars largely cultivated in the main regions of Northern China (Hebei, Henan, Shanxi, Shanxi and Ningxia Provinces) and will be phenotyped in those same regions.
Partners: CAAS, Ningxia University, NWSUAF, SAAS, LAAS, HAAS
- **Output 3.16. Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco:** Contrasting bread and durum wheat genotypes are being characterised at both molecular and phenotypic levels. Markers are being used to screen for biotic stresses and are in development for abiotic stresses, mainly drought.
Partners: INRA–Morocco, ICARDA, Università di Bologna, Cornell University, University of Missouri, EMBRAPA, INRAN, ICRISAT–Niger), ICRISAT–Mali, Cornell University
- **Output 3.17. Validation of Alt_{SB} , a major aluminium tolerance gene in sorghum: assessment of the breeding value of superior haplotypes for Alt_{SB} , a major Al tolerance gene in sorghum: linking upstream genomics to acid soil breeding in Niger and Mali (ALTFIELD):** Elite Alt_{SB} haplotypes identified by association analysis within the ALTSORGHUM competitive project (Output 3.3. in the 2009–2011 MTP) will be validated on acid soils in West Africa. Technologies for evaluating and developing sorghum germplasm and cultivars with enhanced tolerance to Al toxicity will be transferred to NARS in Niger and Mali.
Partners: EMBRAPA, INRAN, ICRISAT–Niger), ICRISAT–Mali, Cornell University
- **Output 3.18. Validation of *Saltol*, a major salinity tolerance gene in rice:** IRRI scientists are collaborating closely with their counterparts at the BRRI, Dhaka University, and BINA to use MAB to introgress *Saltol*, a major QTL for salinity tolerance identified in a previous SP2 project (Output 2.16 in MTP 2009–2011) into popular varieties adapted to target environments.
Partners: IRRI, BRRI, University of Dhaka, BINA

- **Output 3.19. Application and validation of the major QTL Phosphate Uptake 1 (*Pup1*):** Phosphate uptake 1 (*Pup1*), a major QTL for tolerance to phosphorus deficiency identified in a previous SP2 project (Output 2.16, MTP 2009–2011) will be introgressed by MAB in three Indonesian varieties and two IRRI varieties, and the effect of *Pup1* on acid soils and under drought stress will be studied in detail to establish whether improved phosphorus nutrition confers drought tolerance.
Partners: IRRI, JIRCAS, ICABIOGRAD

Theme 4: Application of molecular markers in breeding programmes

- **Output 3.20. Integration of genomic tools with conventional screening for developing NERICA rice cultivars for West Africa: *Oryza glaberrima*** accessions and interspecific breeding lines with trait-improving alleles for drought tolerance are identified and screened for rice yellow mottle virus (RYMV) and bacterial leaf blight (BLB), using low-cost markers and supplied to NARS scientists for further evaluation and dissemination in West-Africa.
Partners: WARDA, IRD, IER
- **Output 3.21. Marker-assisted selection for sweet potato virus disease (SPVD) resistance in sweet potato germplasm and breeding populations:** Markers for resistance to SPVD are developed to be used to screen orange-fleshed sweet potatoes (OFSP) breeding populations (with high provitamin A content) and CIP germplasm.
Partners: CIP, NAARI
- **Output 3.22. Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-assisted breeding:** Quantitative trait loci (QTLs) with large effects on yield under stress, detected in a population derived from parents differing greatly in yield under drought (Vandana and Way Rarem) are being fine-mapped. Their impact on yield will be confirmed in India and China, and they will be introgressed into elite varieties via marker-assisted selection.
Partners: IRRI, TNAU, CRURRS, UAS, YAAS, University of Alberta
- **Output 3.23. Local germplasm enhanced via molecular breeding for target traits in tropical legumes (groundnuts, beans, cowpeas and chickpeas):** Backcross populations incorporating farmer/market preferences and disease resistance are being developed in the context of research funded by the Bill & Melinda Gates Foundation, that aims to increase yields in farmers' fields and increase incomes through the development and cultivation of improved local varieties.
Partner: ICRISAT
- **Output 3.24. Marker-assisted selection for resistance to *Striga gesnerioides* in cowpea:** INERA and IITA are jointly conducting rapid and reliable MAS screening of *Striga* resistant cowpea lines to generate well-adapted *Striga* resistant cowpea varieties available to farmers in Burkina Faso and Niger.
Partners: INERA, IITA
- **Output 3.25. Marker-assisted selection for resistance to streak virus in maize:** MAS technology is being used to rapidly introgress maize streak virus (MSV) resistance into Mozambican maize germplasm
Partners: University of KwaZulu–Natal, IIAM
- **Output 3.26. Dry bean improvement and marker-assisted selection for diseases and abiotic stresses in Central America and the Caribbean:** drought nurseries will be established for opaque black and small red seed classes by grouping the most drought-tolerant accessions from Mexico, Nicaragua, Cuba and Haiti. The nurseries will be screened for bean golden yellow mosaic virus (BGYMV) and root rot resistance. Segregating populations will be developed at Mexico and CIAT with the best accessions and selected for BGYMV and root-

rot resistance using MAS. The best lines will be distributed in Mexico, Nicaragua, Cuba and Haiti.

Partners: INIFAP, CIAT, INTA–Nicaragua, INCA, ORE–Haiti

- **Output 3.27. Yield improvement of sorghum in Africa through marker-assisted recurrent selection (MARS) and a public-private partnership:** An ARI (CIRAD), a private company (Syngenta) and an African NARS institution (IER, Mali) will work together to develop drought tolerant sorghum germplasm through MARS, an approach already successfully applied to maize by the private partner. The predecessor to this work presented in the 2008–2010 MTP (Output 3.23. Marker-assisted recurrent selection for drought tolerance in sorghum) suffered a one year delay because of the departure of the two African CoPIs, and difficulties in identifying other new breeding partners with sufficient facilities and expertise. The problem has now been resolved.

Partners: CIRAD, IER, Syngenta

- **Output 3.28. Yield improvement of maize in Asia through marker assisted recurrent selection (MARS) and a public-private partnership:** CIMMYT and NARS in Asia (China, India, Indonesia, Pakistan, Philippines, Nepal, Thailand and Vietnam), with the support of the private sector, will develop drought-tolerant lines and hybrids through MARS.

Partners: TBD

International public goods

SP3 is delivering marker technologies that are available as international public goods to generate germplasm with enhanced tolerance to drought, salinity or acid soils. Some germplasm with resistance to pests and diseases has also been delivered. The new approaches developed by SP3 to improve molecular breeding efficiency (development of low-cost, high-throughput markers, modelling for better monitoring of MAB strategies, development of innovative phenotyping protocols) are also international public goods, as well as the products generated from these approaches, technologies and protocols (eg, virus-resistant cassava and sweet potato, cowpea resistant to *Striga*, and rice resistant to bacterial blight). Finally, the development of a phenotyping platform, comprising experimental stations with adequate facilities and expertise, also constitutes a public good, available for germplasm evaluation and marker validation. This new venture into platforms will both generate and disseminate international public goods in collaboration with SP5.

Subprogramme 4: Bioinformatics and crop information systems

Project overview and rationale

The value of data is a function of their quality (are they reliable, interpretable and complete?), their accessibility (can they be found and used?) and their usability (are the necessary knowledge, tools and external datasources available?). SP4 aims to increase the value of the data generated by or relevant to GCP. As a result, the data will become available, not only to GCP, but also the rest of the world as international public goods. This calls for an infrastructure that ensures that the data be of sufficient quality and accessible, for tools to analyse the data and for users who are able to apply the tools.

A bioinformatics, biometrics and advanced data management system has been designed to support an integrated genetic resources, genomics and crop improvement information network. This platform provides access to the data generated within GCP, provides tools to analyse the data, and links GCP data and tools to global biodiversity and bioinformatics networks. Furthermore, the users of this infrastructure for data handling and analysis are supported through training and assistance in experimental design and in data handling, storage and analysis.

The development of such a platform has a number of components. Firstly numerous local systems are already in place. The challenge of integrating them into one system is daunting, given the very limited ability to dictate the architecture and organisation of existing systems, inside and outside the GCP Consortium. Secondly, the elements that already exist within the GCP Consortium must meet certain quality standards and be accessible. GCP believes that data are managed best when they are managed as closely as possible to where they are generated. This strategy allows proper data curation (in terms of corrections and additions to the data) and avoids ownership problems. However, making data management a local responsibility requires an appropriate level of skills and facilities—an issue also addressed in SP4. Thirdly, for all of the GCP Subprogrammes to function properly with respect to access to bioinformatics tools and databases, they need support in the selection of tools, identification of data sources, the integration of existing tools and databases, and the creation of new tools and information sources.

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

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

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

Work described in this MTP follows the course developed in earlier MTPs. Activities have been tuned according to the results of previous years and other inputs such as an external expert review of the GCP Data Platform. However, these did not call for any major reorientations, as is evident in the ‘Output descriptions and partnerships’ section.

Impact pathways

The logframe for SP4 pitches the impact of each Output at a level that reflects the service nature of the Project with respect to other components of GCP, especially SP1, SP2 and SP3. Thus, impacts relate, for example, to provision of higher quality data, more effective contributions of bioinformatics to crop improvement, or increased efficiency in molecular breeding programmes. These impacts are reached by way of outcomes involving users taking advantage of facilitated access to tools and data to achieve their research objectives. Other GCP Projects move further along the impact pathway towards increased crop productivity, particularly in marginal environments, and the contributions that that will have on human well-being and protection of the environment. At the strategic level, GCP’s synergistic internal (Subprogramme) design and its *modus operandi* with a heavy emphasis on capacity-building and partnership are conducive to the achievement of outcomes and broad impact.

Returning to SP4 *per se*, the impact pathways within each Theme are presented below. SP4’s three Themes are:

- Theme 1: Infrastructure—Facilitation of information flow of ongoing research, both in terms of data and in terms of communication between the researchers
- Theme 2: Improvement—Quality improvement of research data and bioinformatics applications in the GCP Consortium
- Theme 3: Support—Support to other GCP Projects in terms of methodology, software tools and data management

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

As described earlier, Theme 1 addresses the question: ‘How can the information flow between researchers in GCP be organised to maintain local curation of data and tools but also to allow optimal access?’ Theme 1 aims to create a platform for exchanging information. This has taken shape, and it can be observed that funding is decreasing to approach a maintenance level. The GCP data handling and analysis infrastructure is based on web services technology that allows the ‘wrapping’ of local databases and analysis tools and making them visible to the world via the Internet. The user needs an interface to access these web services. Also, a solution is needed to handle datasets that are not yet available as a web service, or need to be used outside of this infrastructure. This all implies that a number of elements are needed, implemented through the generation of five Outputs, as described below.

The first Output is the development of a common language for data exchange protocols. This is being created by first developing ‘GCP domain models’, as completed in the last two years, and then developing ontologies that can be used in these models. Ontology development involves a wide diversity of actors and requires clear prioritisation over the years. In 2009, eight ontologies (for rice, *Musa*, wheat, common beans, sorghum, chickpeas, groundnuts and maize) will become available. This activity is expected to decrease over the next two years to maintenance level.

The second Output is concerned with training staff and implementing web services technology in GCP member institutions. This started three years ago, and was to have been completed already. However, given the developments in web services technology, it will be continue for one more year, after which some remaining activities will probably be incorporated in Output 4.5.

The third Output delivers a short-term solution: templates for GCP data capture, storage and use, and a GCP Central Registry, a web portal where all GCP datasets are listed and made available as far as possible. The templates (usually in the form of Microsoft Excel spreadsheets) guarantee full interpretability of information and try to be as compliant as possible with the GCP Domain Model. The data in these templates are made centrally available, via the GCP Central Registry (but can also be maintained locally). For the GCP Central Registry, a list, based on GCP project descriptions is curated with all available and expected datasets, with descriptions and PIs responsible. As soon as the datasets are made available, they can be downloaded from the portal. The basic infrastructure has been established and is functioning. In 2009, the range of templates and the set of available datasets will be extended.

The fourth Output complements the third. Given the large amount of phenotypic data that are expected to become available in 2008, an additional activity was initiated to guarantee that the GCP Data Template for phenotypic data be tuned to the user needs and GCP expectations, and that the users be supported in using the template.

The fifth Output ensures that the technology underlying the GCP application of web services be up to date. It elaborates the GCP platform architecture for data transformation and data visualisation, and applies this architecture in the reference implementation of a search engine.

Furthermore, it allows for integration of bioinformatics workflow management into the GCP infrastructure. Finally it covers the technical backstopping of all developers involved in web services related software development. It is expected that Theme 1 will ultimately result in an infrastructure that allows central access to data maintained in a decentralised way, and the development of software that can access that information.

Theme 2: Improvement—Quality improvement of research data and bioinformatics applications in the GCP Consortium

The second Theme concentrates on improving data quality and handling, but is also concerned with the quality of data access and the tools to analyse data. The need to improve the quality of the data is clear, although GCP cannot enforce quality management procedures upon GCP Consortium members; this is an institutional responsibility. By creating the web services, it is hoped to increase the quality of data access.

The first Output within this Theme focuses on access to the data tools made available in the Theme. It has developed two interfaces with the GCP infrastructure: Koios, a web-based query engine and workbench, and Genomedium, a stand-alone software package that needs to be installed locally. Both packages allow access to the web services created by GCP, offering tools for analysis. These tools will be further developed in the coming years. In 2009, functionality will be created for each of SP1, SP2 and SP3 according to priority use cases as detailed earlier. The second Output deals with data quality and handling. It promotes and supports the use and installation of LIMS, develops methods to quantify aspects of data quality, and maintains a platform for collaborative software development (CropForge) and concept development (GCPWiki). The third Output takes up the challenge of promoting the use of quality management procedures in GCP institutes. Existing practices for selected laboratory methods will be reviewed, workshops will be organised for research and lab managers, and consultancies will be organised to give practical advice.

The fourth Output in this Theme provides access to high-performance computing (HPC) capacity to GCP scientists. An HPC facility has been created within the GCP Consortium and a range of software has been installed. In the coming years, the challenge will be integrating HPC functionality into the GCP platform. Also, the question of whether to upgrade the current hardware, or to outsource the function, will need to be addressed. Ultimately, Theme 2 will contribute to increasing the quality of the data produced and maintained by GCP, and will support the use of these data by providing better tools.

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

SP4 aims at accommodating the need for support in the handling and analysis of data by providing a central helpdesk that will match the question of the scientist with the solution (or expertise) from SP4. In addition to this, based on requests from the other Subprogrammes, a number of dedicated activities have been developed that create specific tools and methodologies. First is the SP4 helpdesk that will respond to email requests from GCP scientists within 48 hours, indicating the most appropriate contact for the support needed.

Specific questions concerning experimental design and data analysis are covered by two Outputs within this Theme. They deal with statistical support for experimental design and support for data analysis with emphasis on microarray and mapping experiments (mainly SP2) and bilateral support mainly to the GCP but also to NARS users of the GSS. The fourth Output also concerns service to NARS. In the last few years, a software package has been developed by integrating existing software into one platform (using web services technology) that allows users to use

markers more efficiently in breeding programmes. The product, called iMAS, was launched in 2007, and has been further developed in 2008. This will continue in 2009 with the addition of functionalities such as multi-location and multi-population analysis and the assurance of compatibility with the Comparative Map and Trait Viewer (CMTV). Also, every opportunity will be used to organise training workshops for (potential) users.

The next Output brings together the Outputs of two successful activities of previous years: GOST, a web-based, fast and user-friendly comparative genomics program, and Dayhoff, an online resource to document stress-response genes comparatively across plant species. Building on their success, it was decided to create a new activity that would aim at combining these tools and expanding the underlying database, to increase the quality and functionality of products.

The final Output is concerned with methodology for breeding drought tolerance in rainfed lowland rice. This involves identification of traits related to drought tolerance, development of screening methods and location of QTL as well as characterisation of drought stress environments using GIS and crop models. It is expected that Theme 3 will ultimately provide GCP scientists with additional solutions in the form of methodology and tools to properly manage and analyse their data.

Changes from 2008–2010 MTP

The MTP for 2008–2010 described 21 Outputs, of which the following three will be completed by the end of 2008:

4. Output 4.18. An eco-physiological–statistical framework for GxE and QTLxE analysis developed
5. Output 4.20. Crop gene expression database and data mining tools developed
6. Output 4.21. Core collection methodology further developed and consolidated.

There is no major reorientation in SP4 since the last MTP. Two Outputs (4.10 and 4.15) were slowed down by financial problems. This MTP features three new Outputs (4.4, 4.8 and 4.17), of which Output 4.4 is in direct response to user needs. Nine Outputs (4.1, 4.3, 4.6, 4.7, 4.9, 4.11, 4.12, 4.13 and 4.15) have been modified to enhance efficiency, and/or clarify the output/products, while Output 4.16 combines elements from Outputs 4.6 and 4.19 of the 2008–2010 MTP, with new Output targets.

Output descriptions and partnerships

In this MTP, SP4 has 17 Outputs. The partnerships in SP4 are presented by Output, corresponding to the MTP logframe. All partners listed have a collaborative role in the research of the respective Output, and the partner with principal responsibility (ie, where the PI is located) is underlined.

Scientists from Institutions of the National Agricultural Research System (NARS) at large (public and private research institutions, universities, and regional research centres and seed companies) are key partners in GCP for research, and main actors for delivery. Some NARS are directly involved in SP4 activities (eg, development of bioinformatics tools, data templates, etc). However, relative to the other GCP Subprogrammes, SP4 has less direct interaction with NARS scientists at this stage of infrastructure development.

Typically, bioinformatics tools and methods are developed in ARIs and CGIAR Centres, and made available to partners in ARIs, CGIAR Centres and NARS. SP4 largely operates through central ‘nodes’ or ‘hubs’ but the impact goes beyond the institute hosting the node and is of

relevance and benefit to NARS collaborators and associates. It should be noted that as SP4 increasingly shifts focus from infrastructure development to infrastructure release and use, NARS participation in SP4 activities is expected to increase. Several tools will be tested by a diverse set of NARS partners involved in breeding activities in GCP target environments, and feedback will be taken into account to improve the tools and identify new needs.

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

- **Output 4.1. GCP domain models developed:** Work within this Output aims to create the models required for software development in GCP. In the past few years it has concentrated on the domain models (describing the objects and their properties in the GCP domain); now it is shifting towards creating the ontologies that should be used in the domain. The methodology has been selected and teams have been set up to create the ontologies on a crop-by-crop basis, assuring proper user orientation. The Output is a continuation of the 2008–2010 MTP Output 4.1, within which the Output targets have not changed but have been made more specific.
Partners: [IRRI](#), Bioversity International, CIAT, CIMMYT, CIP, ICRISAT, Plant Ontology Consortium
- **Output 4.2. Web services technology implemented in the GCP Consortium:** In the first years of GCP, the predecessors of Output 4.2 resulted in instances of web services installation for most GCP Consortium members, development of tools to support the installation of web-service software, staff training, and the mapping of local domain models on the GCP domain model. The Output is a continuation of the 2008–2010 MTP Output 4.2, but has decreased in size. Currently it consists mainly of the software development component that, in time, could be merged with Output 4.5.
Partners: [Bioversity International](#), IRRI
- **Output 4.3. GCP Central Registry and templates for GCP data capture, storage and use created and maintained:** This combines the management of the GCP Central Registry with the creation and maintenance of the GCP Data Templates. As such, it is a combination of the 2008–2010 MTP Outputs 4.3 and 4.4. The Central Registry stores the data created in GCP activities in downloadable and fully interpretable files (Microsoft Excel spreadsheets) and makes them searchable. The format of these files, with examples and user guides are called GCP Data Templates. Output 4.3 ensures that data are uploaded by the PIs of GCP activities, and supports the PIs in so doing. The Output is a combination of the 2008–2010 MTP Outputs 4.3 (Templates) and 4.4 (Data Registry); the Output targets have not changed but have been made more specific.
Partner: [Bioversity International](#), CIMMYT, IRRI
- **Output 4.4. Quality and utility of GCP phenotyping data improved through the development of a data input template:** Because of the large amount of phenotypic data expected to become available in 2008, an additional activity was initiated to ensure that the GCP Data Template for phenotypic data be tuned to user needs and GCP expectations, and that users be coached in using the template. This is a new Output, not occurring in the 2008–2010 MTP.
Partners: [CropGen International](#), CIMMYT
- **Output 4.5. Web services tools and technology further developed:** Web-services technology is still under development and using this new technology appropriately within the GCP software architecture is not self-evident. Through this Output, GCP contributes to development of the technology, assuring adequate capacity to support the developers in other GCP projects. The Output is a continuation of the 2008–2010 MTP Output 4.5; the Output targets have not changed.
Partners: [IRRI](#), Bioversity International, EBI, NCGR

Theme 2: Improvement—Quality improvement of research data and bioinformatics applications in the GCP Consortium

- **Output 4.6. Integrated GCP Information Platform created:** Based on the GCP domain model defined in Output 4.1, a three-layer architecture has been defined and implemented in the GCP Information Platform. This Platform has been implemented in two main environments: Koios for web-based applications and Genomedium for client-based applications. Output 4.6 develops these further and creates a functionality for SP1 (GenDiversity, a tool for diversity analysis based on passport data and genotypic data), for SP2 (a workbench interface to query and cross-link gene data including gene annotation linked to phylogenomics, gene expression and QTL mapping data, and for SP3 (a Molecular Breeding Design Tool [MBDT] and Molecular Selection Tools (MOSEL) to support breeders in applying MAS/MAB. This is a continuation of the 2008–2010 MTP Output 4.8, with more specificity of Output targets.

Partners: IRRI, CIRAD, CIMMYT, EMBRAPA, ICRISAT, NCGR

- **Output 4.7. Data quality within the GCP further improved and assured:** Data quality has become increasingly important in GCP. This is the first of two SP4 activities aimed at addressing the issue and has a number of components. The first concerns the adaptation and adoption of ICRISAT’s LIMS system in other GCP institutes. The second component develops data quality indicators, best practice manuals, and a customised set of database/informatics and statistical tools for monitoring and improving data quality. The third component sets standards for GCP management to specify service-level agreements for data-producing projects. These three targets are a continuation of 2008–2010 MTP Outputs 4.7 and 4.9. The former is involved with the maintenance of the collaboration systems CropForge and CGPWiki. Output targets have not changed but have been made more specific.

Partners: IRRI, WUR, ICRISAT, CIP, CIRAD

- **Output 4.8. Quality management procedures in GCP research laboratories promoted:** This Output will promote the use of methods for quality management and assurance at the source, ie, the laboratories. Based on an inventory of existing approaches, a number of consultancies and workshops will be organised to raise the awareness of quality management in the GCP Consortium. This is a new Output.

Partners: TBD

- **Output 4.9. High-performance computing (HPC) facilities integrated in the GCP toolbox:** To allow the GCP community to conduct CPU-intensive analyses, such as whole-genome BLAST (Basic Local Alignment Search Tool) analysis and Structure, a facility has been set up consisting of three HPC clusters installed at IRRI, CIP and ICRISAT. The Output maintains this facility and installs software based on user demand. The possibility of using capacity of outside collaborators for this purpose will be actively explored and tested, to see if further investments to maintain functionality would be cost-effective. The Output is a continuation of the 2008–2010 MTP Output 4.10 in which the Output targets have been changed accommodate the possibility of outsourcing in the future.

Partners: CIP, ICRISAT, IRRI, NIAS

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

- **Output 4.10. Bioinformatics and data handling support to GCP scientists:** In the five years that SP4 has been running considerable expertise has been build up and a wide range of tools have been created. However, not all GCP scientists are aware of these resources. To bridge the gap, a helpdesk has been set up to act as a one-stop shop for the scientists. It will answer

any request for support within 48 hours, indicating which tool to use or which expert to consult. It corresponds to the 2008–2010 MTP Output 4.11 whose start was delayed due to financial problems that GCP faced in 2007. The Output targets remain unchanged.

Partner: WUR

- **Output 4.11. Statistical support provided for the design and data analysis of GCP projects:** Since the statistical components of experimental design and data analysis are frequently weaknesses in both GCP experiments and GSS proposals, a helpdesk has been set up to provide support in the preparation of proposals and the analysis of data. This support is backed up by a website giving access to additional information and resources. The Output is a continuation of the 2008–2010 MTP Output 4.12; its scope has been expanded to include non-SP1 scientists.
Partners: WUR, CIRAD, CIMMYT
- **Output 4.12. Data analysis support available for Project 2 with emphasis on microarray and mapping experiments:** Microarray and mapping technology are becoming increasingly important in GCP particularly in Project 2 (in MTP terminology; equivalent to GCP Subprogramme 2) which generates large volumes of data whose management and analysis are not straight forward. A pipeline for the analysis of this type of data has been set up in previous years and will now be applied in a number of named crops. This is a continuation of 2008–2010 MTP Output 4.13. The Output targets have been made much more specific to reflect the fact that 2009 is expected to result in the identification of candidate genes for rice, wheat, maize and chickpeas.
Partners: CIMMYT, IRRI, ICRISAT, CIP, NIAS, JIC
- **Output 4.13. Decision support tools for MAS and MAB further developed:** Over the last three years a package, iMAS, has been developed, bringing the best freeware for MAS and MAB together under one user interface. This product has been tested, improved, documented and workshops have been organised to train users. As a result of its success, new demands have been formulated in terms of the functionalities and the types of crop for which it can be used. A new version with extended possibilities will be released in 2009, and users will be trained. This is a continuation of the 2008–2010 MTP Output 4.14, with more specific Output targets.
Partner: ICRISAT
- **Output 4.14. Design and analysis of marker-trait association studies, with special attention for genetically challenging crops:** The methodology for marker-trait association studies for plants is still rather new, creating a demand within the GCP community. This activity will develop the methodology further and adapt it to GCP crops that are not all genetically simple diploid species in Hardy-Weinberg equilibrium. The Output is a continuation of some elements of the 2008–2010 MTP Output 4.15, and corresponds to 2008–2010 MTP Output 4.16 that was postponed due to financial difficulties that GCP faced in 2007. The Output targets have not been changed.
Partners: WUR, University of Hohenheim, Imperial College London, NIAB, SCRI, Leiden University Medical Center
- **Output 4.15. Methodology development for reconstruction of genealogies based on haplotypes related to geographic patterns:** Most methodologies to determine the structure of genetic diversity only rely on either passport or on genotypic data. Yet, GCP has access to a wide variety of data sources, leading to a demand for a methodology that could use both types of data simultaneously to reconstruct the genealogy of a crop, as covered by this Output. It corresponds to the 2008–2010 MTP Output 4.17 whose start was delayed due to the financial problems the GCP faced in 2007. There is more specificity at the Output target level.
Partners: CIRAD, CIP

- **Output 4.16. Large scale phylogenomic analyses tools developed for gene function prediction for GCP crops:** As part of the 2008–2010 MTP Output 4.6 a fast user-friendly web-based comparative genomic program, GreenPhyl Orthologous Search Tool (GOST) was implemented, allowing biologists to perform online phylogenomic analysis. In parallel, as 2008–2010 MTP Output 4.19, an online resource called Dayhoff was developed to document stress-responsive genes comparatively across plant species. Since both products have proven to be much appreciated by the plant genomic community, a new activity has been created to combine these tools and expand the underlying database, to increase the quality and functionality of the products. The Output is a combination of elements of the 2008–2010 MTP Outputs 4.6 and 4.19, with new Output targets.
Partners: Bioversity International, CIRAD, IIRI
- **Output 4.17. Breeding drought tolerance for rainfed lowland rice in the Mekong region:** This project will develop strategies and protocols for selection of drought-tolerant genotypes. It will start by using diverse populations to identify germplasm adapted to aerobic and anaerobic conditions which also have tolerance to vegetative stage and flowering stage drought. It will identify traits related to drought tolerance as well as screening methods and QTL for those traits and it will use GIS and crop modeling to characterize drought prone environments. Finally the project will select drought tolerant cultivars with appropriate grain and eating quality using farmer participatory selection.”
Partners: BRRD, Thailand; BIOTEC, Thailand; UQ, Australia; NAFRI, Laos; CARDI, Cambodia.

International public goods

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

Subprogramme 5: Capacity-building and enabling delivery

Project overview and rationale

SP5 fulfils its role by building technical capacity for the efficient implementation of GCP research and by facilitating the flow of GCP products through the research–delivery continuum. SP5 also conducts research in international and national policy questions to facilitate delivery and conducts *ex ante* impact studies to identify GCP research priorities (by crop, region and trait) to support decision-making and resource allocation. Thus, SP5 adds value to the activities of the other Subprogrammes.

As the quantity of GCP products increases, so the importance of efficiently managing and promoting these products to ensure a return on investments. Product delivery is not a given; it requires strategic and sustained effort, and cannot be realised without capacity-building. High-calibre researchers in target regions are best placed to guarantee dissemination and adoption of research products to and by efficient plant breeding programmes, to meet the needs of poor farmers effectively. To this end, GCP actively seeks collaboration with NARS to develop fruitful and meaningful partnerships, offering up-to-date training plus infrastructure and research support.

Capacity-building has entered a consolidation phase evolving to fewer more sharply focused activities, firmly embedded in and complementing GCP’s other Subprogrammes. This trend was recently reinforced by the recommendations of the 2007–2008 EPMP and is in line with GCP’s

new strategy—product delivery for real impacts on institutions and individual scientists within and outside the GCP community.

Impact pathways

SP5 plays a crucial role in promoting the impact of GCP as a whole, principally through enhancing the readiness of partners to participate in research-for-development and enhancing the take-up of the products that GCP generates among immediate partners and more widely. By promoting spill-over effects of GCP's research activities, SP5 broadens the impact of the Programme in scope and time. Complementing the capacity-building core of the Subprogramme, policy activities aid delivery, crop platforms and communities of practice promote sustainability and impact assessment studies support decision-making and resource allocation. Each Theme makes particular contributions to the overall impact as described below.

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

SP5 activities will primarily benefit researchers and institutions in GCP target regions, or whose work impacts farmers in those regions. Training course participants will also be selected on the same rationale, but in some instances, scientists beyond GCP's immediate scope may be invited. The goal is to strengthen and expand the pool of scientists able to conduct GCP-related research, thus providing GCP with strong and highly skilled collaborators, and more capable intermediaries for regional product delivery. At the end of 2008, a workshop is planned, in collaboration with SP1, on 'Reference sets of food crop germplasm for international collaboration'. This workshop is intended to present the reference markers in a robust form and accessible as a global public good to a selection of various players engaged in germplasm management in international programs. These samples will be widely shared and used, so that new data can be integrated in order to derive biological understanding useful for germplasm diversity management and use. In early 2009, a course will be offered for TLI project NARS partners to become acquainted and skilled with the concepts and practice of marker-assisted selection so that they can fully assume their tasks within the TLI workplan as it relates to using marker technologies in their breeding programmes.

Programme selection for training courses and learning materials is done in close consultation with the other Subprogrammes to ensure selection and training are relevant and in tandem with researchers' demand for additional knowledge and skills in areas of GCP expertise. SP5 also scans the external environment beyond GCP and carefully selects workshops on topical and relevant issues of interest to GCP. For instance, an online course will be conducted on IP issues, freedom-to-operate and genetic resources policies. The course, already successfully offered in 2007, helps GCP scientists and collaborators understand the importance of rights associated with the access to and use of plant genetic resources and related tools, methods and products protected by IPR, when the results of the research are to be used freely by smallholder farmers. In the selection of participants the GCP community is given priority but places are also reserved for outside applicants whose research interest relate to the core of GCP's work. This course will be offered online, with a tutor available to monitor results of exercises and to respond to questions. Beyond the official call for participation and consultation mechanism, the course materials are made freely available to promote a better understanding of the important underlying issues.

SP5 will engage with the Communications Unit of the GCP in a plan to disseminate as widely as possible training materials that have been produced so far to serve as self-teaching resources for those interested in getting baseline exposure to the research subjects of GCP. They can also be used for classroom teaching to undergraduate or graduate students in locations where up-to-date

material is difficult to obtain. A feedback form will be added in online versions of learning materials to elicit suggestions for improvement or translation.

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

This Theme supports NARS research and collaboration in priority GCP regions, with a three-pronged approach covering teams, individuals and institutions. Specific activities include the Capacity-building *à la carte* Programme, fellowships, travel grants, the professorship at the ACCI and PhD plant breeding training at WACCI. NARS in GCP target regions engaged in GCP projects are the frontline users of this Theme's Outputs since their role and active participation are critical ingredients for product delivery. The overall goal is to increase the use of GCP-generated products, by engaging target users directly involved in GCP research. The Capacity-building *à la carte* Programme will result in a core community of highly skilled researchers to advance GCP research. These champions will guarantee rapid uptake of GCP results and products, thus furthering GCP's mission and goals, and hopefully spilling over within their institutions and regions. This would help realise the product delivery goals of GCP's strategy framework and ensure that prebreeding materials, generated by SP3 from the outputs of SP1 and SP2, flow through the research-delivery pipeline.

In parallel with supporting teams, SP5 recognises individual training as equally important, providing hands-on research opportunities, contacts and collaborative opportunities. Support to the professorship in molecular breeding at the ACCI will help build a cadre of skilled plant breeders in Africa, resulting in stronger breeding programmes and better crop varieties for target farmers. Similarly, the PhD programme at WACCI will strengthen the breeding capacity of target crops and projects in Africa. The students will be identified in close consultation with SP3 and the Principal Investigators of ongoing projects in Africa selected for their higher expectations of impact at the end of the second phase of the GCP in 2013. The students will be able to benefit others within their home institutions, countries and regions once they graduate and engage in modern research in their NARS organisations.

Theme 3: Construction of systems for ensuring product delivery

Theme 3 is anchored in the GCP Delivery Strategy and focuses on capacity-building to meet project goals and ensure product uptake by targeted user groups. GCP's support to Delivery Plan development will promote a two-way flow of communication at different stages of the delivery chain with an anticipated impact of all GCP products being delivered to users, and each intermediate user developing additional products to improve farmer livelihoods. Identifying and promoting productive linkages is another mechanism for encouraging delivery. One such example is in Output 5.14 that seeks to link a promising national organisation in Mozambique with an ongoing project (TLI). The project focuses mainly on West Africa but would benefit from the integration of a research team in another area with contrasting environmental conditions. In support of this integration, the Mozambican partner will be enabled to engage in research, acquiring the capacity and expertise to participate at an adequate level, and the products from the upstream cowpea project will reach a new geographical area.

The community of practice is a mechanism that provides training opportunities for individuals (eg, MSc degree training), team-to-team technical backstopping and linkages between breeders in different countries within a framework that facilitates exchange of germplasm, information and know-how. This is conducive to both research and delivery, and is especially important for a crop such as cassava with its particular challenges as a clonally propagated crop. Crop and regional platforms similarly provide opportunities for partners to meet, present project results, offer products (eg, germplasm, markers, protocols), describe their capacity and identify needs. As well

as promoting research overall, this helps the GCP to identify suitable partners and to refine capacity-building to better address the needs of beneficiaries.

For effective and far-reaching product delivery, SP5 also looks beyond GCP, hence the efforts made to validate and distribute GCP products within the context of an expansive and inclusive strategy for product marketing and distribution. Intended users are not only GCP collaborators but also the wider community of beneficiaries who, once they access GCP products, continue improving them for an ever-widening range of end-users.

Theme 4: Development and implementation of support services

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

The GSS promotes the use of molecular markers to assess the potential value of germplasm and breeding materials for relevant agronomic traits. It helps GCP reach more national research programmes, bridging the gap between molecular laboratories and field practitioners. As a result of requests to GSS, the need emerged for a toolbox of available molecular markers for MAS in GCP target crops. The toolbox will be publicly and freely available via the Internet and in static (USB) format for potential users with limited connectivity. The toolbox should help researchers who wish to integrate modern tools into their breeding programmes, especially those in developing countries who may not have access to up-to-date information dispersed in restricted literature.

Theme 5: Ex ante impact analysis and impact assessment

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

This Theme aims to refine GCP's priorities in terms of regions, crops, traits, technologies and capacities, and to define indicators for future impact assessments. The primary user of this information will be GCP's Management Team. However, in keeping with GCP's tradition of transparency and in the spirit of capacity-building, the information will be publicly available for the benefit of other researchers and research managers in science and technology programmes for development. Output 5.26 in particular should provide the basis for an extended set of studies on other crops and priority geographical locations that could benefit the research-for-development strategy of a research organisation, and also could help target the allocation of funds by a donor.

Changes from 2008–2010 MTP

The MTP for 2008–2010 described 19 Outputs, of which the following will have been completed by the end of 2008:

- Output 5.3. Training materials for association studies/linkage disequilibrium mapping developed
- Output 5.16. Asset Inventory System for the GCP developed

Two Outputs were delayed for various reasons, outlined in the output descriptions:

- Output 5.4. Training materials for phenotyping developed
- Output 5.24. Targeting and impact analysis of GCP technologies

One Output was suspended:

- Output 5.5. GCP training materials translated into selected languages (Spanish, French, Chinese, Portuguese and Arabic)

The remaining Outputs will continue, representing activities such as training courses that are repeated annually in different subjects or formats, or activities that extend over more than one year such as the Tropical Legumes (TLI) project. Where they have been modified from the 2008–2010 MTP content, this is explained in the section on ‘Output descriptions and partnerships’ below.

Output descriptions and partnerships

In this MTP, SP5 has 27 Outputs, distributed among the SP’s five Themes. SP5 activities are all collaborative, involving Consortium member institutions as well as partners outside the Consortium. This partnership philosophy is at the heart of the GCP in general but is even more ingrained in SP5, which, by definition, begins by first building internal partnerships with the other GCP Subprogrammes. Outside the GCP management structure, SP5 deals with building capacity, creating links, building public knowledge platforms, providing services, supporting collaborators, disseminating knowledge, and much more. None of the Outputs would be possible without the complementary participation of a variety of external collaborators, who are carefully selected depending on the activity.

Within Theme 1, partnerships for the development of training materials rely mainly on ARIs. For example, Cornell University will finalise reference materials for modern breeding, including marker-assisted selection and basic concepts of conventional breeding, and Agropolis–INRA will finalise a set of teaching materials on phenotyping for drought. Courses are arranged in collaboration with competent partners usually in CGIAR Centres and ARIs.

Training activities within Theme 2 rely on partnerships with ARIs, CGIAR Centres and NARS at large, including academic institutions in the South. Capacity-building *à la carte* Programme awards go to research teams in institutions in the South who are engaged in an ongoing GCP projects. An example is the Bangladesh Rice Research Institute (BRRI), which collaborates on research with IRRI. SP5 has established a special partnership with ACCI at the University of Kwazulu–Natal in South Africa and with WACCI at the University of Ghana, both for training PhD students from the region.

A partnership within Theme 3 that deserves special mention is the project ‘Improving tropical legume productivity for marginal environments in sub-Saharan Africa’ (TLI) in which SP5 collaborates with all partners in both upstream as well as downstream research, overseeing the implementation of capacity-building in the different research components. The addition of a Mozambican University partner, as noted above, will bring in new synergies and opportunities for capacity building. SP5 is continuing to support the establishment of communities of practice, one for cassava in Africa offering a unique means of creating and maintaining close links between IITA, CIAT, and NARS breeding programmes, and building linkages with users, cassava breeding networks, international breeding programmes, and related GCP projects including GSS.

Crop and regional platforms use a new type of partnership closely linked to ‘vertical’ GCP research. The Rice in Asia Platform engages the main NARS partners involved in GCP rice projects in the region and will provide a mechanism for streamlining delivery and ensuring sustainability of GCP research products.

The launching of the Genotyping Support Service within Theme 4 represents a different type of partnership. It subsidises genotyping services for breeding programmes in the South (eg, the Coconut Research Institute (CRI) in Sri Lanka) and links them with providers in advanced institutions such as DArT P/L in Australia. Theme 5 develops novel approaches, brings in new partners and new ways of doing business. Impact targeting and assessment work has opened doors for collaboration with experts in different area that complement CGP research, such as Virginia Tech for *ex ante* impact analysis, CIMMYT to study secondary breeding objectives of GCP crops, and IFPRI for the evaluation of the capacity of local institutions and delivery pathways to farmers to realise the projected potential for GCP impact.

All partners listed below have a collaborative role in the research of the respective Output, and the partner with principal responsibility (ie, where the PI is located) is underlined.

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

- **Output 5.1. Selected training courses in molecular analysis of germplasm, genomics/molecular breeding, bioinformatics and phenotyping conducted:** Training courses are offered in areas related to the core research subjects of the GCP (not all every year). Their scope is diverse: (i) they address particular needs of national programme partners of ongoing GCP projects (eg, phenotyping for drought in the TLI project); (ii) they mean to convey the knowledge gathered in GCP research to a wide scientific community (eg, design and use of reference germplasm collections); or (iii) they target a broad audience that can benefit from up-to-date knowledge in subjects related to GCP research (eg, bioinformatics) and thereby be enabled to take up the GCP products. Past MTPs have referred to a range of courses within this Output.
Partners: (i) ICRISAT, CIAT, IITA, UC–Riverside, INRA/Montpellier Sup Agro; (ii) CIRAD, Global Crop Diversity Trust, SGRP, GIPB
- **Output 5.2. Online course on intellectual property, freedom-to-operate, and genetic resources policies, including the International Treaty on Plant Genetic Resources for Food and Agriculture:** GCP is founded on the use of genetic resources for modern breeding of crops for the resource poor. Short courses on IP, freedom-to-operate and genetic resources policies are offered to raise awareness about these issues among the GCP scientific community, to contribute to ensuring compliance with regulations, and to promote exchange of germplasm in the context of helping advance the agreement between GCP and the International Treaty.
Partners: WUR, Bioversity International
- **Output 5.3. Training materials for phenotyping developed:** GCP engaged from the outset in the development of training materials in core subjects to provide an appropriate baseline of up-to-date knowledge, in particular to partners in developing countries that may have difficulties to keep current with scientific advances. Use of advanced molecular marker technologies is only relevant if there is good knowledge and practice of crop and plant phenotyping. This is a clear bottleneck for the advancement of genomics and molecular biology. These learning materials will fill the gap for drought phenotyping. Materials will be amply distributed online and on CD-ROM. The Output has been delayed by ca. one year due to modifications in the plan to produce the materials. Enhancements such as audio comments and exercises have been added to provide a more effective and user-friendly product.

Partners: INRA/Montpellier Sup Agro, ICRISAT, IRRI, University of Queensland

- **Output 5.4. Training materials for modern plant breeding developed:** In an effort complementary to Output 5.3, materials will be developed for modern breeding, covering MAS in different breeding schemes and use of single-trait as well as quantitative trait genotyping. They will also tackle links with conventional breeding—an aspect usually forgotten by modern technologies when they practised only at the academic level.
Partner: Cornell University
- **Output 5.5 Completed materials disseminated:** This activity will deal with refinement of the quality of learning materials, packaging them in appropriate formats for wide distribution and use, and disseminating them as widely as possible within the GCP partner community and beyond. Originally Output 5.5 included translations. However, consultations at the 2007 GCP ARM with partners and the SP5 Review and Advisory Panel member led to a suspension of the activity pending feedback from online users of the materials (English version) to assess the demand for translation.

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

- **Output 5.6. Capacity-building à la carte Programme:** This Output aims to fill gaps in human resources and physical capacity to enable NARS partners that collaborate closely with GCP to take up the results of research and continue working with GCP products to push them along the delivery chain. Support to NARS teams is provided in the form of personnel training, small equipment (field, laboratory and computer), travel and technical backstopping. This Programme has increased relevance in the light of recent EPMR recommendations that it be offered through commissioning rather than competitively as was the case the past two years. Selected grantees will belong to priority GCP projects with clear impact indicators.

Partners:

- (i) KARI, INRA/Montpellier Sup Agro, ISRA, UCB, CIRAD, EMBRAPA
 - (ii) CRI-Ghana, CIMMYT
 - (iii) ABRII, IRRI, IPK
 - (iv) BRRRI, University of Dhaka, IRRI
 - (v) NRCRI, CIAT
 - (vi) ICABIOGRAD, IRRI, RCB-IPB
 - (vii) INERA, UC-Riverside IITA-Kenya, IITA-Nigeria
 - (viii) ISRA, UC-Riverside, IITA-Kenya, IITA-Nigeria
 - (ix) ISRA, CIRAD, UCB, EMBRAPA
- **Output 5.7. Fellowship Programme:** This Output, initiated in 2005, was reviewed at the 2007 GCP ARM. In response to concerns over the quality of applications, the subsequent call was targeted to particular Themes, instead of open to ad hoc proposals. This resulted in higher quality but a reduced number of applications, out of which five were awarded. The current awardees will complete their fellowships in 2009, after which the Programme will be discontinued as a separate entity, and will instead be embedded into GCP projects.
Partners:(Grantee underlined, host institution in italics) National Key Lab of Crop Genetics and Germplasm Enhancement (China) and *SCRI*; University of São Paulo, EMBRAPA and *WUR*; CIMMYT and *INRA-France*; PhilRice (Philippines) and *WUR*.
 - **Output 5.8. GCP Travel Grant Programme:** In the past this Output covered hands-on-training, participation in GCP-related conferences or workshops, and participation in the ARM. From 2009 onwards, travel grants will only cover participation in the ARM, as a very good opportunity to expose NARS partners to the wide range of research being conducted in

GCP, at the same time building linkages between the upstream and the downstream communities. Other travel opportunities will be offered within Output 5.6.

Partners: TBD

- **Output 5.9. Academic position in molecular breeding established and supported:** The University of Kwazulu–Natal will hire a professor to build capacity among sub-Saharan Africa scientists in molecular biology applied to food security and genetic diversity. The professor will teach a module on advanced technologies, genomics, and molecular markers to students at the African Centre for Crop Improvement (ACCI) and will mentor them for the incorporation of molecular breeding components into PhD research proposals. This Output has been delayed; ACCI was successful in recruiting a candidate for the position but because of difficulties in obtaining a working permit, the candidate declined. A new process had to open and interviews took place mid-May 2008. The final outcome is, as yet, unknown.

Partners: ACCI, Rockefeller Foundation

- **Output 5.10. PhD in Plant Breeding Training at the West Africa Centre for Crop Improvement, University of Ghana:** A critical mass of a new generation of plant breeders with knowledge in both traditional field-based selection methods and emerging laboratory-based tools and techniques is needed to develop and provide the necessary high yielding varieties to farmers, especially in Africa. The University of Ghana, through the West Africa Centre for Crop Improvement (WACCI) is dedicated to the training of plant breeders with skills in genetic improvement of the staple crops of the west and central Africa sub-region. Through this project, four PhD candidates will undertake two years of coursework at the University of Ghana and three years of field research in their local research institutions. The selection of candidates will be based on needs in crop teams closely engaged in GCP research.

Partners: WACCI, AGRA, Cornell University

Theme 3: Construction of systems for ensuring product delivery

- **Output 5.11. Capacity-building mechanisms and product pipelines established for tropical legume improvement in Africa:** This Output relates to the capacity-building objective of the focus project for legume improvement in Africa (TLI). It serves two main purposes: (i) the organisation of training activities and workshops to upgrade scientific knowledge of NARS partners to work adequately within the project; and (ii) the upgrading of field, computer and laboratory infrastructure so that partners can carry out the tasks assigned.

Partners: Chitedze Research Station, CBI, EIAR, INERA, IRAD, ISRA, LZARDI, ARI–Naliendele, SARI (*each partner takes the lead in their activity*)

- **Output 5.12. Delivery Plan remote learning modules:** GCP has found that agricultural research scientists are clear on how their innovations are expected to benefit resource-poor farmers, yet they are unclear on the process and mechanisms by which their innovations actually get to these farmers. This Output aims to develop a series of interactive tools to assist scientists involved in GCP activities to develop high-quality ‘Delivery Plans’. A series of interactive modules will provide guidance through all the steps of Delivery Plan development, to support the production of well-considered, high-quality Plans. The approach will be extremely cost-effective compared with bringing groups together for a residential course.

Partners: INCAE Business School, Cornell University

- **Output 5.13. Comprehensive support provided to competitive projects to define delivery and capacity-building plans:** This Output provides expert advice and support to research teams on the preparation, revision and monitoring of Delivery Plans, as a complement to Output 5.12.

- Output 5.14. Improve cowpea productivity for marginal environments in Mozambique:** This will build capacity in drought tolerance screening, offer training in analysing data for GxE interaction, provide baseline information on drought tolerance for cowpea varieties, and assess the importance of GxE interactions for grain yield under drought in Mozambique. The national partner in Mozambique will be linked with a mentor at UC–Riverside, to provide guidance in the design and implementation of a MAS-based programme. In addition to NARS strengthening, new breeding populations for the application of MAS and marker-assisted recurrent selection (MARS) will be produced.
Partners: Eduardo Mondlane University, UC–Riverside
- Output 5.15. A cassava breeding community of practice in Africa for accelerated production and dissemination of farmer-preferred cassava varieties resistant to pests and diseases:** This project builds on successful collaboration with cassava teams in Africa (linked through CIAT). It aims to develop a community of practice through breeder-to-breeder training in traditional and new methods of breeding, germplasm resource exchange, and web-based information sharing as ways of achieving set breeding goals and addressing common problems. It will facilitate the integration of MAS with field-based breeding by the transfer and implementation of effective strategies for breeding, primarily for disease and pest resistance in Nigeria, Ghana, Uganda and Tanzania. It will strengthen the capacity of NARS breeders through formal (MSc) and informal (exchange visits and workshops) training programmes and will build linkages with primary, secondary, and tertiary users of improved cassava varieties to ensure rapid uptake of technologies.
Partners: NRCRI, CIAT–Nigeria, CRI–Ghana; NaCRRI, ARI–Naliendele, IITA–Nigeria, CIAT–Colombia
- Output 5.16. Establishment of and support to crop and regional platforms:** To validate and disseminate GCP products, thereby intensifying delivery, GCP will work to establish crop and regional platforms to reinforce the idea of validating and promoting products and their adoption. These platforms will engage national programme teams, with active participation from CGIAR Centres and advanced research institutions working in ‘vertical’ ongoing projects. These projects will become flagships of GCP research, with a view to streamlining delivery and ensuring sustainability of the research.
Partners: Various—Rice in Asia Platform partners
- Output 5.17. A project development guide (PDG) designed and implemented:** The Project Development Guide is now available to the GCP scientific community and worldwide to all interested parties to learn how to prepare a good project proposal for GCP, complying with requirements and in line with the GCP vision and philosophy. This Output will ensure the PDG is now widely disseminated and its use will be monitored to refine the tool based on user feedback.
- Output 5.18. Validation of GCP products:** As GCP approaches the middle of its lifetime, its products are starting to become available. However, for research results to take the form of a product that can be passed to the intended users, either other partners in the GCP community or downstream links at the NARS level, they need to go through a validation process. Validation involves guaranteeing the quality (performance, suitability) of the products and packaging them appropriately so that they can be readily used. After validation, awareness will be raised through wide dissemination of information to potential users. Among the products given attention in 2008 and 2009 will be microsatellite marker kits and reference collections. The latter are a key GCP product of SP1, and were generated from wide collections using different approaches. Building on that experience, this Output will investigate various strategies to arrive at small but informative sets of genotypes and markers that should regenerate a large part of the relevant genetic variation with relatively little effort.
Partner: WUR

- **Output 5.19. GCP product distribution:** Some GCP products can be distributed as information only; this will be done in close collaboration with the GCP Communications Unit. Others will be distributed as tangible products (eg, reference collections in the form of seeds, or cuttings; microsatellite kits in the form of synthesised oligonucleotides and DNA; etc).

Partners: TBD

Theme 4: Development and implementation of support services

- **Output 5.20. Interactive Resource Centre established and maintained:** The Interactive Resource Centre (IRC) and Helpdesk is already fully functional and is now in a phase of improvement to increase awareness and add new items upon request. A team of scientists has been made available to answer questions addressed to the Helpdesk. Questions are answered on a same-day basis, providing personal responses to each query.

Partner: Cornell University

- **Output 5.21. Toolbox of available molecular markers useful for marker assisted selection in GCP crops:** This Output will develop a toolbox providing free and easy access to information on all publicly-available molecular markers ready for use for MAS in 19 food security crops. It will compile information available in Internet sources, public databases and papers, plus information gathered through communication with molecular crop breeding experts. Results will be made available via the Internet as a global public good and the features of the toolbox will be described in a peer-reviewed publication. By sharing the latest advances in molecular plant breeding, the toolbox is an important step into supporting modern agriculture for the benefit of the poor in developing countries.
- **Output 5.22. Genotyping Support Service:** The GSS is an ongoing activity that helps breeding programmes in the developing world gain access to molecular marker technologies for the analysis of germplasm. GSS hires competent high-throughput genotyping facilities and trains researchers in data analysis and in interpretation and implementation of the knowledge generated. The service covers 19 crops for plant breeding applications (eg, MAB/MAS) and genetic diversity analysis. Support and training for data analysis and interpretation is provided in close collaboration with the GCP Statistical Helpdesk within SP4.

Partners: [ICRISAT](#), [CIAT](#), [DArT P/L](#), [IRRI](#), [WUR](#), [KUL](#)

- **Output 5.23. Development and implementation of a GCP Workflow and Repository System:** This Output deals with the development of a project information and document management tool through a central online system. It is the extension of an existing Internet-based GCP system. Components that will be added are: project submission and reporting, applications to GSS, compilation of the GCP product repository content, compilation of publications, integration of the Asset Inventory System. The tool will facilitate interactions between project collaborators and the GCP Management Team and Project Office. It will facilitate collaborative work, provide traceability for project review processes, integrate different GCP activities in one location, and help exchange project information among Subprogrammes.

Theme 5: Ex ante impact analysis and impact assessment

- **Output 5.24. Targeting and impact analysis of GCP technologies:** This Output will produce data on crop-specific drought severity and type for GCP priority crops in priority farming systems. It will also analyse patterns of technology adoption at levels below the farming system. The output has been delayed by the ill health of a collaborator.

Partners: [CIAT](#), [CIMMYT](#), [IFPRI](#), [IRRI](#)

- **Output 5.25. Ex ante impact analysis of marker-assisted selection technologies supported by GCP:** This Output conducts an economic impact assessment of two of the first GCP projects. One deals with the discovery of genes for tolerance to saline and phosphorous-

deficient soils to enhance and sustain rice productivity, and the other develops low-cost technologies for pyramiding useful genes from wild relatives into elite progenitors of cassava. It will design a useful methodology for reporting on progress to GCP donors and identifying possible targets for research and delivery in the second phase of GCP.

Partner: Virginia Tech

- **Output 5.26. *Getting the focus right: food crops and smallholder constraints:*** Drought was identified as a major priority for GCP. However, it is generally accepted that a variety of other 'secondary' constraints limit productivity in good seasons, as well as in drought years. In recognition of the complexity of factors that affect the improvement of food crop yields and productivity under smallholder conditions in different farming systems throughout the developing world, this project will systematically tap into the tacit knowledge of experienced research and development practitioners to provide valuable information on the relative importance of different production constraints and traits. The results of the study will provide a checklist and guide to those involved in food crop breeding and crop systems research and development by prioritising key traits for improvement in each system.

Partners: CIMMYT, CIAT, IRRI, IITA, ICRISAT, ICARDA

- **Output 5.27. *A strategic assessment of the capacity to develop and adopt GCP technologies:*** Prior GCP studies identified priority crops and farming systems for GCP efforts, assuming that broadly-targeted GCP technologies will be successfully adapted by local breeding efforts and will then be adopted by local smallholders. Since these are both strong assumptions, GCP's initial target/focus areas will be subjected to a second phase evaluation that makes provision for the likely capacity of local institutions and farmers to realise the projected potential for GCP impact. This may be described as an assessment of the feasibility of achieving desired outcomes in high-priority (most attractive) focus areas.

Partners: IFPRI, CIAT

International public goods

All products generated in SP5—such as training materials, Delivery Plans, support services and impact studies—are intended to benefit not only Consortium members but the wider scientific community. They are always made available, without restriction, to the widest possible audience. SP5 also offers capacity-building opportunities, which strengthen institutions and individuals in target regions. While the activities benefit a selected group of collaborators in the first instance, they can truly be considered public goods in the sense that the spill-over effect through GCP's open policy on the availability of capacity-building materials is expected to influence a wider community of researchers in the countries and regions from which the collaborators come, supporting the collective effort to solve the needs of resource-poor farmers.

Logframe

Each Output is followed by the type of research activity/funding contributing to the Output (commissioned, competitive, focus, or discretionary); respective Project no(s); start and end dates; and the name and location of the PI(s) responsible for the Output (and its Output targets). Some Outputs are managed internally within GCP, in some cases involving coordination of a number of external PIs (PIs marked as ‘Various’).

Output	Output target	Intended user	Outcome	Impact
Project 1: Genetic diversity of global genetic resources				
Theme 1: Creation of an improved understanding of the structure of the diversity for the major world food crops				
Output 1.1. Genotyping data validated for the reference samples and the reference markers for all GCP crops <i>Commissioned: 4007-01, 2008–2009</i> <i>PI: Jean-François Rami, CIRAD, France</i>		Plant breeders and germplasm specialists worldwide	Users have opportunities to explore genetic diversity in breeding and in further characterisation for phenotypic and molecular traits	Better access to genetic diversity for breeding, resulting in more efficient crop improvement programmes
Output target 2008	A first set of validated genotyping data matrices for the reference samples and the reference markers generated for 10 priority crops			
Output target 2009	A second set of validated genotyping data matrices for the reference samples and the reference markers generated for 11 crops, thus completing all GCP crops			
Output 1.2. Seed of reference germplasm readily available for all crops <i>Commissioned:</i> • <i>G4005-02; 2005–2007</i> <i>PIs: Various</i> • <i>G4006-29; 2006–2008</i> <i>PI: D Dumet, IITA, Nigeria</i> • <i>Project no TBA; to start late 2008</i> <i>PI: TBD</i>		Plant breeders and germplasm specialists worldwide	For each crop, users have access to reference materials which will serve to represent wider collections and to compile information from diverse origins	Better access to genetic diversity for breeding, resulting in more efficient crop improvement programmes
Output target 2008	Reference germplasm samples implemented for all 21 priority crops, including <i>in vitro</i> propagated cassava			
Output target 2009	Reference sample implementation continued for 12 crops; distribution initiated for nine crops			
Output target 2010	Sustained distribution of reference samples for all crops			
Output 1.3. Methodology developed for resampling genetic diversity in large germplasm collections <i>Commissioned: G4006-01 2006–2009</i> <i>PI: R Sackville Hamilton, IRRI, The Philippines</i>		Germplasm specialists and plant breeders worldwide	Users are able to make use of available information optimally in order to further tap useful diversity in large collections	Better access to genetic diversity for breeding, resulting in more efficient crop improvement programmes
Output target 2008	An additional description of SSR diversity for 1,000 accessions of rice and chickpea			
Output target 2009	An algorithm developed for iteratively selecting accessions from a large, data-sparse collection given a data-rich subset of accessions			
Output 1.3. Methodology developed for resampling genetic diversity in large germplasm collections <i>Commissioned: G4006-01 2006–2009</i> <i>PI: R Sackville Hamilton, IRRI, The</i>		Tropical legume geneticists and breeders	Users have clear options for association studies in legumes	Increased efficiency in crop research and improvement

Output	Output target	Intended user	Outcome	Impact
<i>Philippines</i>				
	Output target 2008	An approach for LD assessment developed for four legumes		
	Output target 2009	LD assessed in legumes through extended molecular characterisation along targeted chromosome segments		
Output 1.4. Methodology developed for resampling genetic diversity in large germplasm collections <i>Commissioned: G4006-01 2006-2009</i> <i>PI: R Sackville Hamilton, IRRI, The Philippines</i>		Germplasm specialists and plant breeders worldwide	Users are able to make use of available information optimally in order to further tap useful diversity in large collections	Better access to genetic diversity for breeding, resulting in more efficient crop improvement programmes
	Output target 2008	An additional description of SSR diversity for 1,000 accessions of rice and chickpea		
	Output target 2009	An algorithm developed for iteratively selecting accessions from a large, data-sparse collection given a data-rich subset of accessions		
Theme 2: Development of a range of flexible HTP genotyping techniques accessible in reference laboratories				
Output 1.4. DArTs developed as a genome-wide molecular characterisation technology for crops with little sequence information <i>Commissioned: 4008-42 2008-2010</i> <i>PI: JC Glaszmann, GCP/Agropolis-Cirad, coordinator</i>		All germplasm specialists using molecular markers in GCP	Users have access to an inexpensive and rapid technique for mapping useful genes in progenies and more complex populations	Increased efficiency in genome mapping, thereby contributing to increased efficiency in plant breeding programmes
	Output target 2008	DArTs development and expansion undertaken for eight crops (<i>Musa</i> , coconut, chickpeas, pigeonpeas, potatoes, yams, groundnuts and pearl millet)		
	Output target 2009	DArTs made efficiently available for 8 crops (<i>Musa</i> , coconut, chickpea, pigeonpea, potato, yams, groundnut and pearl millet), with nucleus germplasm characterised		
Output 1.5. Database developed on allele diversity at candidate genes across species <i>Commissioned:</i> • <i>G4006-02; 2006-2008</i> <i>PI: D This, Agropolis-CIRAD, France</i> • <i>Project no TBA; to start late 2008</i> <i>PI: TBD</i>		Crop physiologists, geneticists and germplasm specialists on GCP crops and in the wider scientific community	Efficient comparative functional molecular diversity analysis available to users for translating results across crops	Improved understanding of adaptive value of molecular variation, contributing to increased efficiency in plant breeding programmes
	Output target 2009	An extended database developed; genes and crops to be decided according to GCP crop trait priorities		
	Output target 2010	An extended database developed; genes and crops to be decided according to GCP crop trait priorities		
Theme 3: Establishment and implementation of a scientific and organisational framework to describe tolerance to drought				
Output 1.6. Database established on field-proven drought-tolerant and drought-susceptible genotypes <i>Commissioned: Project no TBA; to start late 2008</i> <i>PI: TBD</i>		Crop scientists world-wide	Users have access to reference materials for assessment and dissection of drought tolerance in germplasm	Integration of most appropriate genotypes in analytical trials and in breeding programmes
	Output target 2009	A framework devised for collecting information on field-proven drought tolerance or susceptibility; transfer of new genotypes to other projects		

Output	Output target	Intended user	Outcome	Impact
Output target 2010	A sustained process established for collecting information on field-proven drought tolerance and supplying information to breeding and genetic studies			
Output 1.8. Drought-related phenotyping of specific populations with high quality molecular information implemented and Phenotyping Support Service consolidated <i>Commissioned:</i> <ul style="list-style-type: none"> • 4008-02; 2008–2011 Pi: H Upadhyaya, ICRISAT, India; • 4008-03; 2008–2010 Pi: S Dreisigacker, CIMMYT, Mexico • 4008-05 2008–2011 (also contributing to Output 1.9); Pi: J Cairns, IRRI, The Philippines • 4008-33; 2008–2010 Pi: J Gethi, KARI, Kenya 		GCP scientists; pearl millet, sorghum and other cereal geneticists and breeders	Users have access to the best drought tolerance screening facilities within GCP; more targets are available for MAS for improving drought tolerance in cereals	Increased efficiency in analysing the genetic control of tolerance to drought
Output target 2009	Phenotyping reference samples generated for four crops (rice, sorghum, wheat and maize)			
Output target 2010	Further phenotyping conducted after collective prioritisation; consolidation of a Phenotyping Support Service for GCP			
Output target 2011	Further phenotyping conducted after collective prioritisation; data used for conducting association studies			
Theme 4: Identification of favourable genetic factors (ie, potential genes or genome segments) and superior alleles (or haplotypes) through association studies				
Output 1.8. Favourable genetic factors for drought tolerance in rice identified <i>Commissioned: 4008-05) 2008–2011</i> (also contributing to Output 1.8 Pi: J Cairns, IRRI, The Philippines		Geneticists and breeders for rice and other cereal	Users have more targets available for MAS for improving drought tolerance in cereals	Increased efficiency in crop research and improvement
Output target 2009	Integrated phenotyping and association analysis carried out using whole-genome SNPs among 500 rice accessions			
Output target 2010	Integrated phenotyping repeated and identification of favourable alleles/haplotypes in rice carried out			
Output 1.9. Favourable genetic factors for stress tolerance in four legume species identified <i>Focus Project: G6007.05) 2007–2010</i> Pi: Carmen de Vicente, GCP, Mexico		Legume scientists world-wide	Users have more targets available for MAS for improving stress tolerance in legumes	Increased efficiency in crop research and improvement
Output target 2009	Reference samples evaluated in diverse environments for four legume species (groundnuts, cowpeas, chickpeas and common beans); first association studies performed; new recombinant populations created			
Output target 2010	Identification of favourable donors of drought tolerance and localisation of favourable alleles/haplotypes in target legumes			
Output 1.10. Genetic factors underlying aluminum and drought tolerance in sorghum and maize identified <i>Competitive: Project No TBA, 2008–2011</i> Pi:		Sorghum geneticists and breeders	Users have clearer options for association studies in sorghum	Increased efficiency in crop research and improvement

Output	Output target	Intended user	Outcome	Impact
Output target 2009	Association panels of sorghum and maize phenotyped for aluminium tolerance; whole-genome SNPs discovered in sorghum and genotyped in maize			
Output target 2010	Association panels of sorghum and maize genotyped with whole-genome SNPs, including candidate genes in maize; whole root systems digitally characterised for both association panels			
Output target 2011	Genetic architecture of aluminium tolerance determined in maize; panels of sorghum and maize phenotyped for drought tolerance and comparative genetic architecture of drought/aluminum tolerance described			
Theme 5: Development of novel populational approaches for relating genotypes to phenotypes				
Output 1.11. Populations for multiple allelic segregation developed in rice and sorghum through multiple parent intercrossing <i>Commissioned:</i> • 4008-01; 2008–2011 PI: H Leung, IRRI, The Philippines • Project no TBA; 2008–2011 PI: T Hash, ICRISAT, India		Rice and sorghum geneticists and breeders	Users have increased opportunities for mapping favourable genes and alleles in cereals	Increased efficiency in crop research and improvement
Output target 2009	Intercrossing and selfing generations advanced based on 1,000 S1 families for each of two sorghum populations for Asia and two rice populations; first sorghum hybrids for populations for Africa generated			
Output target 2010	Further intercrossing and advancement of selfing generations carried out			
Output target 2011	Further advancement of selfing generations carried out; materials used for phenotyping and genotyping for association analyses			
Output 1.12. Populations for multiple allelic segregation developed through nested intercrossing in rice <i>Commissioned: Project no TBA</i> 2008–2011 PI: M Lorieux, Agropolis–IRD/CIAT, Colombia		Rice geneticists and breeders	Users have increased and improved power and resolution for mapping favourable genes and alleles in rice	Increased efficiency in crop research and improvement
Output target 2009	Nested intercrossing and first selfing generation performed;			
Output target 2010	Selfing generations advanced through single seed descent for 4,000 lines			
Output target 2011	Seed stocks of 4,000 lines increased for distribution; a specific database established			
Output 1.13. Linkage disequilibrium and patterns of selection in the genome of sorghum used for mapping useful genes <i>Discretionary: Project no TBA</i> Timeframe ongoing PI: JC Glaszmann, GCP/Agropolis–CIRAD, France		Sorghum geneticists and breeders	Users have clearer options for association studies in sorghum	Increased efficiency in crop research and improvement
Output target 2008	Introgression patterns monitored between various cultivated and wild forms of sorghum using DArT markers			
Output target 2009	Patterns of selection monitored along the genome of sorghum; association analysis carried out using phenotyping data			

Output	Output target	Intended user	Outcome	Impact
Output 1.14. Base broadened of current crop diversity in rice using interspecific bridges with African rice <i>Competitive: G3007.01</i> <i>2007–2009</i> <i>PI: A Ghesquière, Agropolis/IRD, France</i>		Rice germplasm specialists and breeders	Novel rice germplasm tailored for genetic analysis of trait variation and innovative breeding available to users	Increased efficiency in crop research and improvement
Output target 2009	Genetic dissection of phenotypic contribution of African cultivated rice carried out			
Output target 2010	Favourable alien chromosome segments identified; a bridge established between Asian and African rices			
Output 1.15. Diversity patterns in the genome of sweet potato used for mapping useful genes in relation to heterosis <i>Commissioned:</i> • <i>G4008-09; 2008</i> • <i>2009; Project no TBA</i> <i>PI: TBD</i>		Sweet potato geneticists and breeders	Users have improved possibilities for association studies in sweet potato	Increased efficiency in crop research and improvement
Output target 2008	DArT markers developed with diverse germplasm of sweet potato			
Output target 2009	Patterns of molecular diversity and of heterosis compared			
Output 1.14. Base broadened of current crop diversity in rice using interspecific bridges with African rice <i>Competitive: G3007.01</i> <i>2007–2009</i> <i>PI: A Ghesquière, Agropolis/IRD, France</i>		Rice germplasm specialists and breeders	Novel rice germplasm tailored for genetic analysis of trait variation and innovative breeding available to users	Increased efficiency in crop research and improvement
Output target 2009	Genetic dissection of phenotypic contribution of African cultivated rice carried out			
Output target 2010	Favourable alien chromosome segments identified; a bridge established between Asian and African rices			
Output 1.15. New alleles introgressed from wide crosses using crop wild relatives in barley <i>Competitive: G3007-02, 2007–2009</i> <i>PI: R Waugh, SCRI, UK</i>		Barley germplasm specialists and breeders	Users have access to novel barley germplasm tailored for genetic analysis of trait variation and innovative breeding	Increased efficiency in crop research and improvement
Output target 2009	A range of recombinant genotypes generated that segmentally display introgression of the whole genome of wild barley			
Output target 2010	Genetic dissection of phenotypic contribution of wild germplasm in barley carried out; favourable introgressed materials identified			
Output 1.16. New wheat germplasm generated with broadened AB genome diversity <i>Competitive: Project No TBA</i> <i>2008–2011</i> <i>PI: SC Misra, ARI, India</i>		Wheat germplasm specialists and breeders	Users have access to novel synthetic wheat germplasm tailored for genetic analysis of trait variation and innovative breeding	Increased efficiency in crop research and improvement
Output target 2009	A range of 200 emmer-based synthetic hexaploid wheat generated using a diverse emmer wheat reference set			
Output target 2010	A range of 400 emmer-based synthetic back-cross lines developed			

Output	Output target	Intended user	Outcome	Impact
Output target 2011	Around 50 drought/heat tolerant emmer-based synthetic derivatives identified; a broad range of derivatives genotyped with SSR and DaRT markers			
Project 2: Genomics towards gene discovery				
Theme 1: Assembly of genomics and germplasm resources through consolidating and developing specialised genetic stocks				
Output 2.1. Bean genetic and genomic resources developed <i>Focus: G6007.03</i> <i>2009–2011</i> <i>PI: Mathew Blair, CIAT, Colombia</i>		Bean breeders in Africa and South America; legume genetics/genomics community world-wide	New markers for drought tolerance deployed in the bean research and breeding communities	Improved efficiency in developing adaptive bean varieties for the resource-poor
Output target 2009	Two subtractive root and shoot libraries (drought versus control) developed and 20,000 ESTs generated			
Output target 2010	200 new SSR, COS or SNP markers developed or mapped from EST, BAC and cross-legume sequences			
Output target 2011	At least five new markers developed for selection of BCMV and/or bruchid resistance			
Output 2.2. Chickpea genetic and genomic resources developed <i>Focus: G6007.04</i> <i>2008–2011</i> <i>PI: Rajeev Varshney, ICRISAT, India</i>		Chickpea breeders in Asia and Africa; legume genetics/genomics community worldwide	New markers for drought tolerance are used in the chickpea research and breeding communities	Improved efficiency in developing adaptive chickpea varieties for the resource-poor
Output target 2009	500 new SSR markers and DaRT arrays developed			
Output target 2010	Reference map with 1,000 marker loci developed			
Output target 2011	At least five molecular markers associated with drought-related component traits developed			
Output 2.3. Cowpea genetic and genomic resources developed <i>Focus: G6007.02</i> <i>2009–2011</i> <i>PI: Jeffrey Ehlers, UC–Riverside, USA</i>		Cowpea breeders in Africa; legume genetics/genomics community worldwide	Users have access to permanent genomic resources (including ESTs), a physical map, a source of SNPs, gene knowledge, the foundation of a high-density SNP map, and a high-throughput marker system	Improved efficiency in developing adaptive cowpea varieties
Output target 2009	14x genome coverage of cowpea BAC libraries produced; 200,000 ESTs generated			
Output target 2010	At least 10,000 BAC end sequences and BAC contigs placed onto the genetic map; 1000 SNP markers on map; 1,440 genotypes scored			
Output target 2011	At least five molecular markers associated with drought-related component traits developed			
Output 2.4. Groundnut genetic and genomic resources developed <i>Focus: G6007.01, G4008.06</i> <i>2008–2011</i> <i>PI: Vincent Vadez, ICRISAT, India</i>		Groundnut breeders in Africa, Asia and South America; legume genetics/genomics community worldwide	New markers being used by the groundnut research and breeding communities	Improved efficiency in developing adaptive groundnut varieties for the resource-poor
Output target 2009	20,000 ESTs, and 1,000 molecular markers established for <i>Arachis</i>			
Output target 2010	Existing RFLP and SSR maps of <i>Arachis</i> unified; one reference map developed for AA diploid genome			
Output target 2011	one linked physical and genetic map developed for AA diploid genome			

Output	Output target	Intended user	Outcome	Impact
Output 2.5. Validation of drought-response/resistance pathways genes by phenotypic analysis of mutants <i>Commissioned: G4007.02</i> 2007–2010 <i>PI: Andy Pereira, VBI Virginia Tech, USA</i>		Cereal crop genetics/genomics and breeding community worldwide	Existing mutant resources leveraged to generate supporting evidence for selecting high-confidence candidate genes for cross-species comparative studies	High-confidence drought responsive candidate genes used in cereal genetics and breeding
Output target 2009	At least 50 sib-lines characterised by physiological measurements of transpiration rate, stomatal conductance, root and water-use efficiency traits using field screen and high-throughput phenotyping techniques (eg, infrared imaging); drought resistant/sensitive phenotypes identified for 100 candidate gene mutants in rice/ <i>Arabidopsis</i> at vegetative and reproductive stage drought stress			
Output target 2010	Dataset on comparative rice/ <i>Arabidopsis</i> candidate drought related gene index developed with physiological mutant phenotypes			
Theme 2: Development of comparative maps within and across species and framework genetic markers for target crops				
Output 2.6. Cross-species resources developed for comparative biology in tropical crop legumes <i>Focus: G6007.05</i> 2008–2011 <i>PI: Douglas Cook, University of California–Davis, USA</i>		Legume genomics/genetics and breeding community worldwide	Knowledge of genomic information and agronomic traits across legume species leveraged, leading to increased use of molecular-genetic markers for legume improvement	General principles established for genomics-enabled breeding in tropical legumes; development of improved legume varieties based on MAS
Output target 2009	Integration of at least 300 orthologous markers into genetic maps for four legume crops (beans, cowpeas, chickpeas and groundnuts); linkage of at least 50 gene-based markers to biotic and abiotic stress tolerance determined			
Output target 2010	Relationship of ancestral genome segments in target legume crops determined; public repository of genetic marker data for crop legumes established; portal created for communication between researchers using common genetic marker resources			
Output target 2011	Marker platforms to use anchor markers in breeding programmes of target legume crops established; online navigation between legume genomes created			
Output 2.7. Genetic and physical mapping resources produced for drought breeding in cassava <i>Competitive: G3007.03</i> 2007–2011 <i>PI: Pablo Rabinowicz, University of Maryland, USA</i>		Cassava genomics/genetics and breeding community worldwide	Expanded cassava genomic resources offering opportunities for improvement of multiple traits in cassava	Cassava cultivars improved for multiple traits through molecular breeding
Output target 2009	At least 9,000 BAC clones sequenced from both directions; 1,000 SNP markers identified on a genome-wide scale			
Output target 2010	A genetic linkage map with 500 SNP markers constructed and SNP markers associated with at least five selected QTLs identified			
Output target 2011	Public database created for accessing mapping and SNP data of cassava through web interfaces			

Output	Output target	Intended user	Outcome	Impact
Output 2.8. Genomic resources and mapping populations for sweet potato developed to enable trait/gene identification <i>Commissioned: G4008.09 2008–2010 PI: Roland Schafleitner, CIP, Peru</i>		Sweet potato genomics/genetics and breeding community worldwide	Increased knowledge-base in under-resourced crops, opening up opportunities for genetic manipulation of various traits eg, drought tolerance and improving the crop	Improved sweet potato cultivars developed with enhanced drought tolerance
	Output target 2009	At least 20,000 ESTs, DArT arrays developed and a virus free diploid mapping population established <i>in vitro</i>		
	Output target 2010	A medium density reference map created		
Output 2.9. Genomic resources and mapping populations developed and assembled for pearl millet to enable trait/gene identification <i>Commissioned: G4008.07 2008–2010 PI: Tom Hash, ICRISAT, India</i>		Pearl millet genetics and breeding community and general cereal genetics/genomics community worldwide	Increased knowledge-base available to users on under-resourced crops, opening up opportunities for genetic manipulation of various traits eg, drought tolerance and improving the crop	Improved pearl millet cultivars with enhanced drought tolerance developed
	Output target 2009	Genome-wide sequence data (at least 60,000 ESTs) produced and new set of at least 200 markers developed for pearl millet		
	Output target 2010	Linkage map with at least 150 new markers developed and putative QTLs for terminal drought tolerance and grain and stover yield potential identified		
Output 2.10. Genomic resources (ESTs, markers and maps) developed for pigeonpea to enable trait/gene identification <i>Commissioned: Project no TBA 2008–2011 PI: Gregory D May, NCGR, USA</i>		Pigeonpea genetics and breeding community; general legume genetics/genomics community worldwide	Increased knowledge-base in under-resourced crops, opening up opportunities for genetic manipulation of various traits eg, drought tolerance and improving the crop	Improved pigeonpea cultivars developed using molecular breeding strategies
	Output target 2009	Genome-wide sequence data (at least 200,000 ESTs) generated; at least 1000 gene based SSRs and SNPs identified		
	Output target 2010	Linkage map of pigeonpea with at least 200 markers generated		
Theme 3: Assignment of genes and pathways to phenotypes through the convergence evidence of genome variation, expression patterns and phenotypic data				
Output 2.11. Causal relationship between whole-genome expression patterns and stress tolerance determined in rice via analysis of near-isogenic lines <i>Commissioned: G4008.08 2008–2010 PI: Shoshi Kikuchi, NIAS, Japan</i>		Rice genomics/genetics and breeding community worldwide	Gene expression polymorphisms serve to bridge the genotype–phenotype gap; providing users with a generalised method to assign gene functions to phenotypes in crop studies to improve drought tolerance in the crop	Increased knowledge about drought tolerance at gene level will aid rice improvement for drought tolerance
	Output target 2009	At least two pairs of near isogenic lines (NILs) developed and characterised for field performance under drought; Expression patterns determined for genes within at least two chromosomal regions corresponding to each of the large QTLs detected in NILs		
	Output target 2010	At least 10 regions of chromosomes with expression signatures identified in the		

Output	Output target	Intended user	Outcome	Impact
	genomes of two drought tolerant NILs; 10 candidate genes available with supporting evidence from expression pattern and QTL alignment			
Output 2.12. Discovery and development of alleles contributing to sorghum drought tolerance <i>Competitive: XXXX</i> 2009–2011 <i>PI: Andrew Paterson, University of Georgia, USA</i>		Sorghum genomics/genetics and breeding community worldwide	Large set of SNPs for high-throughput genotyping, and improved germplasm that combines enhanced drought tolerance with additional traits required for local adaptation in Western and Central Africa, Eastern and Southern Africa and South Asia	Enhanced genomic resources and genetic knowledge about drought tolerance at allele level will aid sorghum improvement for drought tolerance
Output target 2009	Pairwise combinations of homozygous stay-green QTLs developed and sequencing of 10 parental genotypes of different populations completed using Solexa 1G sequencing.			
Output target 2010	A large set of SNP identified useful for deterministic breeding in MAGIC populations, as well as developing a high-throughput genotyping platform for sorghum			
Output target 2011	Genetic maps of two RIL populations segregating for stay-green as well as host plant resistance to <i>Striga</i> and charcoal rot saturated with more molecular markers and identification of allele specific markers			
Output 2.13. Examining natural variation in the transcriptional regulation of drought responses in wheat <i>Commissioned: Project no TBA</i> 2009–2011 (on hold) <i>PI: Peter Langridge, ACPFG, Australia</i>		Wheat genomics/genetics and breeding community worldwide	Regulatory proteins isolated and evaluated to screen for natural variation in expression of regulatory genes shown to moderate the drought tolerance response in wheat	Increased knowledge about genomics for aiding wheat improvement through molecular breeding
Output target 2009	At least five genes isolated that are known to increase drought tolerance when showing modified expression			
Output target 2010	Two new alleles identified at each of the five target genes that show expression levels correlated to drought tolerance			
Output target 2011	Diagnostic markers developed for each of the new alleles			
Theme 4: Validation of genes and pathways via evaluation of under- or overexpression constructs or variants (induced or natural) of target genes				
Output 2.14. Drought-adaptive mechanisms in bread and durum wheat determined through large-scale phenotyping methodologies <i>Competitive: G3007.06</i> 2007–2011 <i>PI Mathew Reynolds, CIMMYT, Mexico</i>		Wheat breeding and genetics community worldwide; crop physiologists and biometrician in general	Users have access to new wheat mapping resources coupled with phenotyping techniques for improving wheat for drought tolerance	Increased knowledge about phenotyping coupled with genomics aids wheat improvement through molecular breeding
Output target 2009	QTLs associated with drought-adaptive traits identified in two bread wheat populations and one durum wheat population			
Output target 2010	At least 10 new markers available in each target region of around 10 cM and placed on high-resolution linkage map			

Output	Output target	Intended user	Outcome	Impact
Output target 2011	Target regions and markers arranged against the syntenic region of the rice genome sequence (pseudo-molecule)			
Output 2.15. Drought from a different perspective: Improved tolerance through phosphorus acquisition <i>Competitive: XXXX</i> <i>2009–2011</i> <i>PI: Sigrid Heuer, IRRI, The Philippines</i>		Rice genomics, breeding and genetics community worldwide; crop physiologists and agronomists in general	Function of <i>Pup1</i> candidate genes understood and novel regulatory genes for tolerance to P-deficiency and drought identified and validated and rice breeding lines developed by MAS with pyramided QTLs for drought and P-deficiency tolerance	Increased knowledge about cross-talking between P-deficiency and drought stress at molecular and physiological/phenological level and development of pyramided QTL lines will help rice improvement for drought tolerance and P-deficiency
Output target 2009	<i>Pup1</i> gene models within the <i>Pup1</i> locus validated <i>in silico</i> as well as by expression analysis and gene regulation assessed in <i>Pup1</i> NILs grown under P-deficiency and drought stress by using expression, RNAi and overexpression analyses; CSSLs of two target regions on chromosome 6 analysed under P deficiency and drought stress			
Output target 2010	<i>Pup1</i> haplotypes determined in IRRI breeding lines and GCP representative set; root growth parameters and characteristics of <i>Pup1</i> NILs evaluated under combined P stress and drought stress			
Output target 2011	Transcription factor (TF) differentially expressed under P-deficiency and drought stress in contrasting <i>Pup1</i> NILs identified and validated; nutrient x water interaction established; and at least two F3 pyramiding populations developed by MAS and screened under P-deficiency and drought stress			
Output 2.16. Delayed senescence and drought tolerance in rice <i>Competitive: XXXX</i> <i>2009–2011</i> <i>PI: Eduardo Blumwald, UC-Davis, USA</i>		Rice genomics, breeding and genetics community worldwide; crop physiologists in general	Function of <i>pSARK-IPT</i> gene tested in rice for drought tolerance and additional determinant key genes identified for identification of knockout mutant lines	Testing of <i>pSARK-IPT</i> gene in rice for drought tolerance and subsequently identification of key determinant genes and their knockout mutant lines will help breeding of commercial rice varieties for drought tolerance
Output target 2009	At least 25 independent lines of each rice variety showing overexpression of stress-induced cytokinin synthesis (<i>pSARK-IPT</i>) developed and characterised			
Output target 2010	At least 10 lines (showing overexpression) phenotyped under greenhouse and field conditions for drought and at least five lines selected and used for microarray analysis to identify the key genes playing significant			

Output	Output target	Intended user	Outcome	Impact
	roles during the adaptation to drought			
<i>Output target 2011²¹</i>	10 determinant candidate genes selected and lines for upland as well as lowland rice generated for overexpression of the selected determinant genes; knockout mutants identified and tested in field conditions			
Output 2.17. Validation of QTLs associated with drought tolerance traits in chickpea <i>Commissioned: Project no TBA 2009–2010</i> <i>PI: Pooran M Gaur, ICRISAT, India</i>		Chickpea breeding and genetics community in Asia	Validated QTLs for drought tolerance available to users for introgressing into drought sensitive lines for chickpea improvement	Chickpea with improved drought tolerance available in Asia and Africa
Output 2.18. Enriching African sorghum varieties for stay-green using marker assisted selection <i>Commissioned: Project no TBA 2009–2011</i> <i>PIs: David Jordan/Andrew Borrell, DPI&F, Australia</i>		Sorghum breeders in Africa and sorghum genetics community worldwide	Stay-green QTLs available to users for introgression into African sorghum lines for enhanced drought tolerance	Chickpea with improved drought tolerance available in Asia and Africa
Project 3: Trait capture for crop improvement				
Theme 1: Characterisation of segregating populations and identification of genomic regions for plant breeding				
Output 3.1. Enhancing groundnut (<i>Arachis hypogaea</i> L.) genetic diversity and speeding its utilisation in breeding for improving drought tolerance <i>Commissioned: Project no TBA</i> <i>PI: Ousmane Ndoye, ISRA, Senegal</i>		Groundnut breeders and breeding programmes in Bolivia (PROINPA), Brazil (EMBRAPA) and Senegal (ISRA)	New sources of diversity characterised and used as prebreeding sources of drought tolerance	More diversity and germplasm available for groundnut breeders
<i>Output target 2008</i>	At least 700 Bolivian landraces, two populations of chromosome segment substitution lines and backcross inbred lines available			
<i>Output target 2009</i>	Distribution of new sources of diversity to partners, and drought phenotyping in Senegal			
Output 3.2. Association mapping of downy mildew resistance in elite maize inbred lines in Thailand <i>Commissioned: G4007.04 2007–2009</i> <i>PI: Chalermpol Phumichai, BIOTEC, Thailand</i>		Maize breeding community in Thailand (Kasetsart University; Nakhon Sawan Field Crop Research Centre)	Backcross populations and new lines available for breeding, and new maize varieties resistant to powdery mildew developed	Maize varieties with improved resistance to downy mildew available to farmers in the Southeast Asia
<i>Output target 2008</i>	Maize inbred lines with resistance to powdery mildew identified; resistant maize inbred lines genotyped			
<i>Output target 2009</i>	Haplotypes for selected candidate genes identified; a set of indicative DNA markers available for allele discrimination and MAS			
Output 3.3. Tailoring superior alleles for abiotic stress genes for deployment in breeding programmes: association analysis of <i>Alt_{SB}</i>, a major aluminium tolerance gene in sorghum <i>Competitive: G3007.04 2007–2009</i> <i>PI: Jurandir Magalhaes, EMBRAPA, Brazil</i>		Sorghum breeders and breeding programmes in Niger and other countries facing soil acidity problems	Superior <i>Alt_{SB}</i> haplotypes identified by association mapping, and pre-breeding near-isogenic lines (NILs) carrying different <i>Alt_{SB}</i> haplotypes used in breeding programmes	Improvement of breeding efficiency in sorghum under acid soil conditions
<i>Output target 2008</i>	A diverse sorghum collection phenotyped for Al tolerance and genotyped at <i>Alt_{SB}</i> , superior <i>Alt_{SB}</i> haplotypes identified			

²¹ will be achieved in 2nd phase of the project

Output	Output target	Intended user	Outcome	Impact
Output target 2009	A set of <i>Al/Sb</i> haplotype-specific markers identified and easy-to-use SNP genotyping assays developed			
Output 3.4. Making Latin America potato diversity available for Africa <i>Commissioned: G4008.15</i> <i>2008–2009</i> <i>PI: Francisco Vilaro, INIA, Uruguay</i>		Potato breeders and breeding programmes in the Southern Cone of Latin America, and in Mozambique and Malawi	New breeding tools as DNA-based markers used in NARS in Latin America and Africa to select for key resistance traits, advanced germplasm disseminated to less developed countries, and capacity-building and expertise of breeding programmes improved	New and more sustainable varieties deployed to resource-poor farmers in Latin America and Africa
Output target 2008	Molecular markers used to monitor the presence of key resistance genes in elite breeding stocks; conversion of short-day adapted germplasm into long-day adapted; and germplasm resistant for known resistance genes exchanged			
Output target 2009	Elite germplasm phenotyped for drought tolerance and markers developed for priority resistance traits (eg, late blight, potato tuber moth, <i>Diabrotica</i> , bacterial wilt, potato leaf roll virus)			
Output 3.5. Field Evaluation of wheat-barley introgression lines under different water regimes <i>Focus: G4007.23</i> <i>2008–2009</i> <i>PI: Márta Molnár-Láng, ARI-HAS, Hungary</i>		Winter wheat breeders facing drought, salt or Al toxicity problems	Wheat-barley translocation lines with drought, salinity and Al toxicity tolerance available to winter wheat breeders	New sources of tolerance to drought, salt and Al tolerance for wheat breeding
Output target 2008	Wheat genetic stocks multiplied and made available to project partners			
Output target 2009	Wheat genetic stock (at least 20 addition, substitution and translocation lines) with chromosomes originating from barley identified using GISH and physically mapped using SSR markers; and effects on drought, salt and Al toxicity tolerance evaluated			
Output 3.6. Seed smoke treatment to favour germination under water stressed conditions <i>Focus: G4007.24</i> <i>2008–2010</i> <i>PI: Ervin Balazs, Academy of Sciences, Hungary</i>		Molecular geneticists and wheat molecular breeders	Genes responsible for the action of smoke compounds on germination identified, mode of action established, and active compound isolated and tested	Effects of smoke compounds on germination better understood and used for the development of molecular-based smoke technologies for crop germination and weed control
Output target 2009	Differentially expressed genes responsible for smoke action identified; pattern of smoke induced genes expressed in maize described			
Output target 2010	Genes involved in smoke action, amino acid sequence of the clones, domain organisation of the candidate proteins, and promoter sequences and organisation of the genes described			
Theme 2: Development and evaluation of novel breeding or molecular technologies to better serve modern plant breeding				
Output 3.7. Application of simulation models to pyramid multiple genes via MAS <i>Commissioned: G4007.06</i> <i>2008–2009</i>		MAS programmes in Asia and Africa	MAS models and software used in several breeding programmes in Asia and Africa	More efficient MAS strategies and protocols available for breeding programmes in Asia

Output	Output target	Intended user	Outcome	Impact
<i>PI: Jiankang Wang, CIMMYT-CAAS, China</i>				and Africa
Output target 2008	Simulation models developed and applied to several MAS projects in Asia and Africa			
Output target 2009	Simulation software developed			
Output 3.8. Linking genetic diversity with phenotype for drought tolerance traits through molecular and physiological characterisation of a diverse reference collection of chickpea <i>Commissioned: G4008.12 2008–2009</i> <i>PI: Junichi Kashiwagi, ICRISAT, India</i>		Chickpea breeding programmes in India	QTLs used for chickpea marker-assisted breeding in India	More efficient MAS strategies and protocols available for chickpea breeding programmes in Asia
Output target 2008	Chickpea reference collection phenotyped for carbon isotope discrimination and other drought tolerance traits and genotyped (using DArT markers)			
Output target 2009	QTLs identified for at least three drought tolerance traits in chickpea			
Output 3.9. Improving drought tolerance phenotyping in cowpea <i>Commissioned: G4008.13 2008–2010</i> <i>PI: Jeff Ehlers, UC–Davis, USA</i>		Cowpea breeding programmes in West Africa	Innovative phenotyping tools and protocols developed; phenotyping capacity and expertise for cowpea strengthened; drought-tolerant germplasm and efficient tools for drought tolerance screening identified in cowpea	Large-scale phenotyping facilitated for cowpea in Africa
Output target 2008	Innovative phenotyping methodologies implemented and phenotyping traits used in West African partner countries			
Output target 2009	Relationship established between canopy temperature depression, thermal imaging, speed of rooting and performance in field conditions			
Output target 2010	Genotype by environment interaction analysed for drought tolerance related traits			
Output 3.10. Development of a GCP phenotyping network <i>Commissioned: G4007.25 2009 (renewable)</i> <i>PIs: Abraham Blum; Greg Edmeades; John O'Toole (consultants),</i>		GCP projects and breeders of target crops in Africa, Asia and Latin America	At least 10 'hubs' used for high-quality and high-throughput drought phenotyping (complements Output 3.11)	Efficiency of drought phenotyping and germplasm deployment improved in GCP projects
Output target 2009	At least 10 suitable field phenotyping platform (FPP) 'hubs' drought phenotyping sites (and their candidate linked local phenotyping platform [LPP] sites) identified, along with recommended steps needed for FPP sites to attain the required GCP standards for uniformity, throughput and expertise			
Output 3.11. Environmental assessment for phenotyping network <i>Commissioned: G4008.34 2009–2010</i> <i>PI: Glenn Hyman, CIAT, Colombia</i>		Phenotypers and plant breeders of GCP target crops	At least 10 'hubs' used for high-quality and high-throughput drought phenotyping (Complementary to Output 3.10)	Efficiency of drought phenotyping and germplasm deployment improved in GCP projects

Output	Output target	Intended user	Outcome	Impact
Output target 2009	Reference FPP sites selected and characterised, relationships between testing sites described and map models of soil–water relationships delivered			
Output target 2010	Database of environmental and climate data, homologue maps, and drought stress indicators (soil–water balance modelling) available for GCP phenotyping locations			
Output 3.12. Targeting drought-avoidance root traits to enhance rice productivity under water-limited environments		Lowland rice phenotypers and breeders in India and Africa	Screening tools and high-throughput phenotyping protocols for drought-avoidance in lowland rice	A high-throughput phenotyping platform available for lowland rice
Output target 2009	Phenotyping protocols for root morphology and water uptake refined and root kinematics analysed			
Output target 2010	A collection of 300 accessions as well as NILs with and without major QTLs for yield under drought phenotyped for root morphology and water uptake, and under field conditions, for validation			
Output 3.13. Basal root architecture and drought tolerance in common bean		Common bean phenotypers and breeders in Latin America and Southern Africa	New phenotyping traits and protocols and markers available for tolerance to drought and low phosphorus availability in bean	Breeding efficiency improved for tolerance to drought and low phosphorus availability in bean
Output target 2009	288 accessions of the reference collection, 120 accessions of <i>Phaseolus coccineus</i> and <i>P. dumosus</i> evaluated for basal root whorl number			
Output target 2010	100 RILs from the cross DOR364xG19833 evaluated for basal root whorl number and basal root growth angle and QTLs identified			
Output 3.14. Breeder-friendly high-throughput phenotyping tools to select for adaptive traits in drought environments		Wheat breeders in drought-prone areas	Robust, field-based and non-invasive drought phenotyping tools and protocols available in wheat	Breeding efficiency improved for drought tolerance in wheat
Output target 2009	Eight phenotyping locations characterised and phenotyping protocols refined			
Output target 2010	Relative value of drought adaptive traits evaluated in the eight phenotyping locations			
Theme 3: Markers/alleles validation in adapted germplasm under target environments				
Output 3.15. Integrating marker-assisted selection into the conventional breeding procedure for improvement of wheat (<i>Triticum aestivum</i> L) in the drought-prone areas of Northern China <i>Commissioned: G4007.06 2007–2009</i> <i>PI: Ruilian Jing, CAAS, China</i>		Wheat breeders from Northern China (Ningxia, Shanxi, Henan and Hebei Provinces)	Drought-tolerant wheat germplasm disseminated and used in Northern China breeding programmes	Wheat breeding efficiency improved in several provinces of Northern China
Output target 2008	At least 8 major drought-tolerant QTLs validated and transferred into elite Chinese wheat backgrounds			
Output target 2009	At least 50 lines carrying target QTLs selected			
Output 3.16. Bridging genomics, genetic resources and breeding to improve wheat and barley production		Plant breeders, wheat and barley breeding programmes and,	Novel genes and alleles conferring tolerance to stresses	More efficient MAS strategies available for wheat and barley

Output	Output target	Intended user	Outcome	Impact
in Morocco <i>Commissioned: G4007.05</i> <i>2007–2009</i> <i>PI: Abbad Andaloussi Fouad, INRA, Morocco</i>		ultimately, small-scale farmers in resource-poor cropping systems of North Africa	and improving end use quality mined from the germplasm collections and used through MAS in breeding	improvement programmes under drought-prone environments
Output target 2008	Local and exotic germplasm evaluated under semi-arid conditions and contrasting accessions identified			
Output target 2009	Segregating populations developed for tagging loci involved in stress tolerance and new markers generated, including candidate gene/allele-based molecular markers			
Output 3.17. Validation of <i>All_{SB}</i>, a major aluminium tolerance gene in sorghum <i>Commissioned: G4008.10</i> <i>2008–2010</i> <i>PI: Robert Schaffert, EMBRAPA, Brazil</i>		Sorghum breeding programmes facing soil acidity constraints	Local germplasm carrying <i>All_{SB}</i> evaluated on acid soils, and available to West African scientists and breeders	Al toxicity genes/markers available for MAS in sorghum, and improved sorghum germplasm for acid soil conditions
Output target 2009	Comparison of performance, under acid soil conditions, of a set of prebreeding near-isogenic lines (NILs) carrying different <i>All_{SB}</i> haplotypes			
Output target 2010	<i>All_{SB}</i> transferred in sorghum African landraces			
Output 3.18. Validation of <i>Saltol</i>, a major salinity tolerance gene in rice <i>Commissioned: G4008.16</i> <i>2008–2009</i> <i>PI: Abdelbagi M Ismail, IRRI, The Philippines</i>		Rice breeding programmes facing salinity constraints	<i>Saltol</i> , a major salinity tolerance gene in rice validated in salinity conditions by an Asian NARS (Bangladesh) and available to breeders	Yield of rice varieties increased under saline conditions
Output target 2008	<i>Saltol</i> gene from Pokkali, FL378 and FL478 introgressed into wet and dry season rice varieties			
Output target 2009	Comparison of performance, under salinity conditions, of prebreeding NILs			
Output 3.19. Application and validation of the major QTL Phosphate Uptake 1 (<i>Pup1</i>) <i>Commissioned: G4008.41</i> <i>2008–2009</i> <i>PI: Sigrid Heuer, IRRI, The Philippines</i>		Asian rice breeding programmes facing phosphorus deficiency problems	<i>Pup1</i> , a major phosphorus deficiency tolerance gene in rice validated in acid soil conditions by an Asian NARS (Indonesia), and available to breeders	Yield of rice varieties increased under phosphorus deficient and acid soil conditions
Output target 2008	<i>Pup1</i> introgressed into upland and irrigated rice varieties			
Output target 2009	Seeds of the best <i>Pup1</i> lines disseminated for field screening in Laos and India within ongoing IRRI activities and made available to NARS partners within the GCP platform 'Rice in Asia' for further testing			
Theme 4: Application of molecular markers in breeding programmes				
Output 3.20. Integration of genomic tools with conventional screening for developing NERICA rice cultivars for West Africa <i>Commissioned: G4007.08</i> <i>2007–2009</i> <i>PI: Marie Noëlle Ndjondjop, WARDA, Benin</i>		Plant breeders, breeding programmes and, ultimately, small-scale farmers in resource-poor cropping systems	New improved germplasm combining African (<i>Oryza glaberrima</i>) and Asian (<i>O sativa</i>) sources developed and available to West African rice breeding programmes	Improved rice germplasm for Africa
Output target 2008	New segregating germplasm evaluated under abiotic stress			

Output	Output target	Intended user	Outcome	Impact
Output target 2009	MAS for target traits conducted, germplasm developed and links established with farmer communities			
Output 3.21. Virus resistance enhanced in sweet potato through exploration of heterosis <i>Commissioned: G4007.07 2007–2009</i> <i>PI: Wolfgang Grüneberg, CIP, Peru</i>		Plant breeders, breeding programmes and, ultimately, small-scale farmers in resource-poor cropping systems	Improved drought-tolerant and virus-resistant sweet potato lines available to users	Improved sweet potato germplasm for Africa
Output target 2008	Backcross populations developed, shared with NAARI Uganda and screened for virus resistance			
Output target 2009	Markers closely linked to SPVD resistance genes identified and MAS developed in two breeding populations			
Output 3.22. Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-assisted breeding <i>Competitive: G3007.05 2 years</i> <i>PI: Arvind Kumar, IRRI, Philippines</i>		IRRI, TNAU-Coimbatore, CRURRS–Hazariabag, and UAS–Bangalore (India); YAAS–Kunming (China)	Large-effect QTLs for yield under drought stress available for drought tolerance MAB in rice in India and China	Rice germplasm with improved drought tolerance disseminated in Asia; improved capacity to map and deploy drought yield QTLs developed in Asian NARS
Output target 2009	QTLs with consistent effects on drought yield across genetic backgrounds verified or disproved; effects of drought tolerance QTLs in other backgrounds evaluated			
Output target 2010	Low-cost system for detecting alleles with effects on drought tolerance across a range of backgrounds developed based on bulk segregant analysis (BSA); dissemination of advanced breeding lines			
Output 3.23. Local germplasm enhanced via molecular breeding for target traits in tropical legumes (groundnut, bean, cowpea, and chickpea) <i>Focus: G6007.05 2008–2010</i> <i>PIs: Rajeev Varshney, V Vadez (ICRISAT, India), M Blair (CIAT, Colombia), J Ehlers (UC–Riverside, USA)</i>		Breeding programmes and, ultimately, small-scale farmers in resource-poor cropping systems	New germplasm and improved breeding programmes for tropical legumes in Africa	Germplasm available for drought-prone areas, increased yields in farmers' fields and increased incomes due to improved local varieties
Output target 2009	New backcross populations developed incorporating farmer/market preferences and disease resistance			
Output target 2010	Diversified breeding populations developed with resistance to diseases and tolerance to drought and heat			
Output 3.24. Marker-assisted selection for resistance to <i>Striga gesnerioides</i> in cowpea <i>Commissioned: G4008.17 2008–2009</i> <i>PI: Jean-Baptiste Tignegre, (INERA, Burkina-Faso)</i>		Cowpea breeding programmes and, ultimately, small-scale farmers in resource-poor cropping systems in West Africa	MAS for resistance to <i>Striga gesnerioides</i> in cowpea implemented and <i>Striga</i> resistant cowpea available to farmers in Burkina Faso and Niger	New cowpea germplasm (with improved <i>Striga</i> resistance) widely available in West Africa
Output target 2008	<i>Striga</i> resistance markers used by INERA (Burkina Faso) to select <i>Striga</i> resistant cowpea germplasm			
Output target 2009	<i>Striga</i> resistance markers deployed in West African cowpea breeding programmes			
Output 3.25. Marker-assisted selection for resistance to streak virus in maize <i>Commissioned: G4008.19 2008–2009</i>		Maize breeding programmes and, ultimately, small-scale farmers in	MAS for maize streak virus developed in Southeast Africa; hybrids and OPVs with	New maize germplasm (with improved resistance to streak virus) for

Output	Output target	Intended user	Outcome	Impact
<i>PI: Mark Laing, UKZN, South Africa</i>		resource-poor cropping systems in Southeast Africa	streak virus resistance disseminated in Mozambique	Southeast Africa
Output target 2009	Resistant lines identified in the maize breeding programme of IIAM (Mozambique)			
Output target 2010	OPVs and hybrids with resistance to streak virus resistance developed using streak virus resistance markers deployed by UKZN			
Output 3.26. Dry bean improvement and marker-assisted selection for diseases and abiotic stresses in Central America and the Caribbean <i>Commissioned: G4008.11 2008–2010</i> <i>PI: Jorge A. Acosta-Gallegos, INIFAP, Mexico</i>				
Output target 2008	SCAR markers developed for BGYMV and root rot resistance traits	Bean breeders and farmers in Mexico, Nicaragua, Cuba and Haiti	Bean germplasm with improved BGYMV and root rot resistance and drought tolerance available to farmers in Central America and the Caribbean	Enhanced bean yield in Central America and the Caribbean
Output target 2009	40 root-rot-resistant and drought-tolerant accessions from worldwide collection identified			
Output target 2010	20 best advanced lines distributed in partner countries			
Output 3.27. Yield improvement of sorghum in Africa through marker-assisted recurrent selection (MARS) and a public-private partnership <i>Commissioned: Project no TBA 2009–2013</i> <i>PI: Jean-François Rami, CIRAD, France</i>		Sorghum breeding programmes in West Africa	Improved sorghum genotypes developed for marginal environments in Sahelian West African countries, and MARS protocols adapted to drought-prone environments	Sorghum yields enhanced in West Africa through a marker-assisted breeding approach developed by the private sector in the North and applied in the South
Output target 2009	Two populations of 400 individuals developed from well-adapted varieties			
Output target 2010	400 F3 individual of each population genotyped with 150 SSR markers and 400 F4 families of each population phenotyped in 4 different locations in Mali			
Output target 2011	QTLs involved in target traits and environments detected, F4 families genotyped for flanking markers of selected QTLs and improved lines from the material selected by MARS phenotyped in different locations			
Output 3.28. Yield improvement of maize in Asia through marker-assisted recurrent selection (MARS) and a public-private partnership <i>Commissioned: Project no TBA 2009–2013</i> <i>PI: M Bänziger, CIMMYT, Kenya</i>		Maize breeding programmes in China, India, Indonesia, Pakistan, Philippines, Nepal, Thailand and Vietnam	Drought-tolerant lines and hybrids identified and available to farmers	Maize yields enhanced in Asia through a marker-assisted breeding approach
Output target 2009	Top-crosses of BC1F2 and BC2F1 (derived from crosses between Asian inbred lines recipients and drought tolerance donor) generated			
Output target 2010	Top-crosses of BC1F2 and BC2F2			

Output	Output target	Intended user	Outcome	Impact
	phenotyped and genotyped			
Output target 2011	Double haploids extracted from BC1C2 and BC2C2			
Project 4: Bioinformatics and crop information systems				
Theme 1: Infrastructure—Facilitation of information flow of ongoing research, both in terms of data and in terms of communication between the researchers				
Output 4.1. GCP domain models developed <i>Commissioned: G4005-22</i> <i>Timeframe: ongoing; extension decided on an annual basis</i> <i>PI: Richard Bruskiewich, IRRI, The Philippines</i>		GCP software developers	Better integration of software and web services for use in germplasm conservation and crop improvement	More effective contribution of bioinformatics to crop improvement programmes
Output target 2009	Ontologies for eight crops (rice, <i>Musa</i> , wheat, common beans, sorghum, chickpeas, groundnuts and maize), published			
Output target 2010	All available ontologies further developed and maintained; new ones published			
Output target 2011	To be determined in response to user needs			
Output 4.2. Web services technology implemented in the GCP Consortium <i>Commissioned: G4005-23 2005–2009</i> <i>PI: Milko Skofic, Bioversity International, Rome</i>		GCP Consortium IT staff	Consortium members use web services to make data available	Increased efficiency in data analysis for crop research and improvement
Output target 2009	Needs-based implementation, training and support to tool development			
Output target 2010	Project will be merged with another related project (probably within Output 4.5)			
Output 4.3. GCP Central Registry and templates for GCP data capture, storage and use created and maintained <i>Commissioned: G4008–20</i> <i>Timeframe: ongoing; extension decided on an annual basis</i> <i>PI: Elisabeth Arnaud, Bioversity International, Rome</i>		Relevant bioinformatics and biodiversity scientists worldwide	Users have centralised access to all GCP-generated data	Better access to research data for crop researchers and improvement programmes promotes use of data for crop research and improvement
Output target 2009	GCP Central Registry is updated with all GCP datasets produced; new templates are developed (DART, SNP, QTL); all are maintained			
Output target 2010	Maintenance and further expansion of GCP Central Registry and templates, according to user needs			
Output target 2011	To be determined in response to the needs of the user community			
Output 4.4. Quality and utility of GCP phenotyping data improved through the development of a data input template <i>Commissioned: G4008-31 2008–2009</i> <i>PI: Robert Koebner, CropGen International, UK</i>		GCP phenotypers	Phenotypers' storage of phenotypic data is facilitated by availability of user-friendly template	Higher quality data for crop research
Output target 2009	Phenotyping template further developed, tested and implemented			
Output 4.5. Web services tools and technology further developed <i>Commissioned: G4007.12</i> <i>Timeframe: ongoing; extension decided on an annual basis</i> <i>PI: Martin Senger, IRRI, The Philippines</i>		Bioinformatics software developers within GCP and worldwide	GCP makes an enhanced contribution to the global bioinformatics community	Increased efficiency in data exchange and analysis for crop research and improvement

Output	Output target	Intended user	Outcome	Impact
Output target 2009	Maintenance of PANTHEON, TAVERNA and SOAPLAB; support to GCP software developers			
Output target 2010	To be determined based on the priorities set by software developers			
Output target 2011	To be determined based on the priorities set by software developers			
Theme 2: Improvement—Quality improvement of research data and bioinformatics applications in the GCP Consortium				
Output 4.6. Integrated GCP Information Platform created <i>Commissioned: G4006-16</i> <i>Timeframe: ongoing; extension decided on an annual basis</i> <i>PI: Graham McLaren, GCP/IRRI, The Philippines</i>		GCP informatics staff	GCP scientists have improved access to integrated tools and databases	More efficient bioinformatics research for crop improvement programmes
Output target 2009	GCP bioinformatics client developed; Subprogramme-specific functionalities further developed			
Output target 2010	To be determined based on user requirements			
Output target 2011	To be determined based on user requirements			
Output 4.7. Data quality within the GCP further improved and assured <i>Commissioned: G4006-17</i> <i>Timeframe: ongoing; extension decided on an annual basis</i> <i>PI: Thomas Metz, IRRI, The Philippines</i>		GCP informatics staff	Outputs facilitate improvement of data quality of existing data bases	Increased efficiency in application of GCP data for crop research and improvement
Output target 2009	LIMS use and installation promoted and supported; quality indicators for data developed; collaboration platform maintained			
Output target 2010	Further support to LIMS; development of best practices and maintenance of collaboration platform			
Output target 2011	To be determined based on remaining requirements to deliver Output			
Output 4.8. Quality management procedures in GCP research laboratories promoted <i>Commissioned: G4008-32</i> <i>Timeframe: ongoing; extension decided on an annual basis</i> <i>PI: TBD</i>		GCP laboratory staff	Quality of GCP data production better assured and managed at source	More reliable data and thus better crop research
<i>Output target 2009</i>	Existing practices for selected laboratory methods reviewed; three workshops and three consultancies organised to develop and build capacity in quality management			
Output 4.9. High-performance computing (HPC) facilities integrated in the GCP toolbox <i>Commissioned: G4005-27</i> <i>Time-frame: ongoing; extension decided on an annual basis</i> <i>PI: Anthony Collins, CIP, Peru</i>		GCP scientists	Access to fully functional HPC enhances GCP scientists' efficiency in analysis and use of data	Higher efficiency and effectiveness in application of data for crop research and improvement
Output target 2009	HPC functionality maintained, exploration of possibilities for outsourcing			
Output target 2010	HPC functionality maintained			
Output target 2011	HPC functionality maintained			
Theme 3: Support—Support to other GCP Projects in terms of methodology, software tools and data management				
Output 4.10. Bioinformatics and data handling support to GCP scientists <i>Commissioned: G4007-10</i> <i>Timeframe: ongoing; extension decided on an annual basis</i>			Better access to GCP Subprogramme 4 products and expertise enhances user bioinformatics	Increased efficiency in GCP crop research and improvement

Output	Output target	Intended user	Outcome	Impact
<i>PI: Theo van Hintum, GCP/WUR, The Netherlands</i>			capabilities	
Output target 2009	48-hour response helpdesk for GCP scientists created; website giving overview of products and expertise in the field of data handling and analysis developed			
Output target 2010	Helpdesk and website maintained			
Output target 2011	To be determined based on user demand and feedback			
Output 4.11. Statistical support provided for the design and data analysis of GCP projects <i>Commissioned: G4006-35</i> <i>Timeframe ongoing; extension decided on an annual basis</i> <i>PI: Marco Bink, WUR, The Netherlands</i>		Germplasm specialists and plant breeders within GCP; NARS collaborators reached through GSS	More efficiency in data handling and analysis for scientists involved in GCP and GSS activities	Increased efficiency in crop research and improvement
Output target 2009	Proactive support provided to GCP and NARS scientists for design and analysis; website maintained and expanded			
Output target 2010	To be determined based on user demand and feedback			
Output target 2011	To be determined based on user demand and feedback			
Output 4.12. Data analysis support available for Project 2 with emphasis on microarray and mapping experiments <i>Commissioned: G4006-08</i> <i>Timeframe: ongoing; extension decided on an annual basis</i> <i>PI: Guy Davenport, CIMMYT Mexico</i>		Crop geneticists and genomics specialists, especially those working with micro array technology	Users better able to analyse microarray and mapping experiments	Increased efficiency in crop research and improvement
Output target 2009	Analysis pipeline used for identifying candidate genes for 4 crops (rice, wheat, maize and chickpea)			
Output target 2010	To be determined based on user demand and feedback			
Output target 2011	To be determined based on user demand and feedback			
Output 4.13. Decision support tools for MAS and MAB further developed <i>Commissioned: G4007.11</i> <i>Timeframe: ongoing; extension decided on an annual basis</i> <i>PI: Jayashree Balaji (ICRISAT)</i>		Plant breeders, especially those in NARS wishing to work with MAS and MAB	More efficient use of markers by plant breeders	Increased efficiency in NARS molecular breeding programmes
Output target 2009	Functionalities extended (multi-location, multi-population, CMTV compatibility); users supported			
Output target 2010	To be determined based on user demand and feedback			
Output target 2011	To be determined based on user demand and feedback			
Output 4.14. Design and analysis of marker-trait association studies, with special attention for genetically challenging crops <i>Commissioned: G4007.09</i> <i>2008-2009</i> <i>PI: Fred van Eeuwijk, WUR, The Netherlands</i>		Germplasm specialists and crop geneticists within GCP and worldwide	Improved methodology enhances efficiency of LD-based phenotype analysis by GCP scientists	Increased efficiency in crop research and improvement
Output target 2009	Methodology and software developed for LD-based phenotype analysis			
Output 4.15. Methodology development for reconstruction of genealogies based on haplotypes related to geographic patterns <i>Commissioned: G4008.22</i> <i>2008-2009</i>		Germplasm specialists and crop geneticists within GCP and worldwide	Users achieve better insight in structure of gene pools	Increased efficiency in crop research and improvement

Output	Output target	Intended user	Outcome	Impact
<i>PI: Claire Billot, CIRAD, France</i>				
Output target 2009	Pipeline for analysis of sequences or SNPs established, including haplotype definition, network analysis and connection with external data, such as geographic origin, evolutionary history or genetic group assignment			
Output 4.16. Large-scale phylogenomic analyses tools developed for gene function prediction for GCP crops <i>Commissioned G4008.21 2008–2009</i> <i>PI: Mathieu Rouard, Bioversity International, France</i>		Bioinformaticians within GCP and worldwide	Users are better able to predict gene function	Increased efficiency in crop research and improvement
Output target 2009	MultiParanoid analysis integrated in software, web services implemented, workshop on protein family curation held			
Output target 2010	GOST and Dayhoff integrated, extended, documented and publicised			
Output 4.17. Breeding drought tolerance for rainfed lowland rice in the Mekong region <i>Competitive G4008 2009–2011</i> <i>PI: Boonrat Jongdee, Bureau of Rice Research and Development, Rice Department, Thailand</i>		Farmers in the Mekong Region, breeders in Thailand, Laos and Cambodia, scientists working on rainfed lowland rice	Improved methodology for drought screening in Rainfed Lowland Rice; Methodology for characterising drought-prone environments; Identification and screening for drought-related traits; Genetic maps and QTL for drought tolerance in rainfed lowland rice; Improved drought-tolerant germplasm for the Mekong region	Improved drought tolerant cultivars developed quickly and used by farmers in the Mekong region.
Output target 2009	Two populations selected for aerobic and anaerobic conditions, different soil properties and for drought tolerance in pot experiments and rainout shelters; GIS characterisation of drought environments for Savannakhet Province			
Output target 2010	Selected drought-tolerant lines screened under different conditions for drought at vegetative and flowering stage in multi-location trials; Identification of drought-related traits and genome regions affecting those traits; GIS characterisation of drought environments for Ubon, Kampong Cham, Vientiane and Champassak Provinces.			
Output target 2011	Effective field screening for drought tolerance demonstrated and adapted, drought-tolerant lines available and used in farmer participatory variety selection for grain and eating quality; GIS characterisation of drought environments for Khon Kaen and Takeo provinces and the rest of Laos.			

Output	Output target	Intended user	Outcome	Impact
Project 5: Capacity-building and enabling delivery				
Theme 1: Creation of a platform of training resources and a cadre of trained scientists to apply advanced technologies and add value to GCP products				
Output 5.1. Selected training courses in molecular analysis of germplasm, genomics/molecular breeding, bioinformatics and phenotyping conducted <i>Commissioned:</i> • 2005–2013 <i>Pls: Subcontracted to various institutions TBD</i> • G4008.27 <i>PI: Vincent Vadez, ICRISAT, India</i> • G4008.40 <i>PI: Jean Christophe Glaszmann, GCP/Agropolis-CIRAD, France</i>		Researchers collaborating directly or indirectly with GCP	Researchers in Africa, Asia and Latin America benefit from training through regional courses in subject matters of critical importance to furthering GCP goals	Increased capacity of NARS researchers in target countries to collaborate with GCP and conduct their own research towards improved crop varieties for farmers
Output target 2008	A training course on phenotyping for drought attended by at least 20 NARS researchers; a workshop on molecular analysis of reference collections to be attended by at least 15 NARS researchers			
Output target 2009	At least one training course conducted, with 15 researchers trained per course			
Output target 2010	At least one training course conducted, with 15 researchers trained per course			
Output target 2011	At least one training course conducted, with 15 researchers trained per course			
Output 5.2. Online course on intellectual property, freedom-to-operate, and genetic resources policies, including the International Treaty on Plant Genetic Resources for Food and Agriculture <i>Commissioned: G4005.53.01 2007–2010</i> <i>PI: Niels Louwaars, WUR, The Netherlands</i>		GCP Consortium and collaborating institutions, researchers, and staff; other potential stakeholders beyond the GCP community	Capacity on policy issues of major importance to GCP built in the GCP community at large	Increased compliance within GCP and among the wider scientific community with genetic resources policies and management of their implications for research
Output target 2008	Instructional materials made available on the Internet; partners' awareness of their availability raised			
Output target 2009	At least one online course conducted			
Output target 2010	Instructional materials continue to be available on the Internet; efforts to raise partners' awareness continue			
Output target 2011	To be determined according to partners feedback			
Output 5.3. Training materials for phenotyping developed <i>Commissioned: G4006-09 2006–2009</i> <i>PI: François Tardieu, INRA, France</i>		GCP researchers and collaborators, particularly crop geneticists and breeders	GCP researchers' and collaborators' capabilities enhanced in phenotyping, with emphasis on drought	NARS scientists in target countries better able to collaborate with GCP and conduct their own research to improve crop varieties for farmers
Output target 2008	Course materials completed			
Output target 2009	Course materials continue to be available online and on CD-ROM			
Output 5.4. Training materials for modern plant breeding developed <i>Commissioned: G4005.53.03 2009-1010</i> <i>PI: Theresa Fulton, Cornell University, USA</i>		GCP researchers and collaborators, particularly crop geneticists and breeders	GCP researchers' and collaborators' capabilities enhanced in the application of modern plant breeding techniques	NARS scientists in target countries better able to collaborate with GCP and conduct their own research to improve crop varieties for

Output	Output target	Intended user	Outcome	Impact
				farmers
	Output target 2008	Course materials developed		
	Output target 2009	Course materials completed and made available online and on CD-ROM		
	Output target 2010	Course materials continue to be made available online and on CD-ROM		
Output 5.5. Completed materials disseminated <i>Commissioned: Project no TBA 2009–2013</i>				
	Output target 2009	All completed training materials disseminated and their use monitored		
	Output target 2010	All completed training materials disseminated and their use monitored		
	Output target 2011	All completed training materials disseminated and their use monitored		
Theme 2: Cultivation of research and learning opportunities for GCP collaborators and NARS scientists to further the GCP mission and progress				
Output 5.6. Capacity-building à la carte Programme <i>Commissioned: G4007.13, G4008.39 2007–2013</i>		NARS in GCP target regions and their collaborators	Collaboration with GCP target NARS enhanced through support to targeted individuals and teams involving training opportunities, upgrading of facilities/ supplies and technical backstopping	GCP products more readily used by developing country researchers for crop improvement
	Output target 2009	At least eight grants provided to collaborating GCP researchers and their institutions for comprehensive capacity-building		
	Output target 2010	At least eight grants provided to collaborating GCP researchers and their institutions for comprehensive capacity-building		
	Output target 2011	At least eight grants provided to collaborating GCP researchers and their institutions for comprehensive capacity-building		
Output 5.7. GCP Fellowship Programme <i>Commissioned: G4007-14.1 2005–2009</i> <i>PI: Carmen de Vicente, GCP, Mexico</i>		GCP collaborators, particularly those engaged in ongoing projects	Research and capacity-building support provided to collaborators to boost capacity to participate in GCP research in their home institutions	Increased capacity of scientists in target countries to collaborate with GCP and conduct their own research toward improved crop varieties for farmers
	Output target 2008	Eight Fellowships awarded		
	Output target 2009	Eight Fellowships completed		
Output 5.8. GCP Travel Grant programme <i>Commissioned: G4007-14.2; G4008.38 2005–2013</i> <i>PIs: Various TBD</i>		GCP collaborators, particularly those from developing countries engaged in ongoing projects	Supportive relationships built between GCP scientists and collaborators; capacity of collaborators to participate in GCP research in their home institutions boosted	Increased collaborative and independent research activity and output by scientists in target countries towards improved crop varieties for farmers
	Output target 2009	10 travel grants awarded for participation in GCP's Annual Research Meeting		
	Output target 2010	10 travel grants awarded for participation in GCP's Annual Research Meeting		

Output	Output target	Intended user	Outcome	Impact
Output target 2011	10 travel grants awarded for participation in GCP's Annual Research Meeting			
Output 5.9. Academic position in molecular breeding established and supported <i>Commissioned: G4006-36</i> <i>2006-2011</i> <i>PI: Mark Laing, UKZN, South Africa</i>		PhD candidates in selected African countries and breeding programmes	A selected group of African plant breeders well-trained in modern plant breeding	Increased human capacity in national plant breeding programmes in Africa
Output target 2009	10 PhD candidates acquainted with topics on advanced technologies, genomics and molecular markers for breeding			
Output target 2010	10 PhD candidates acquainted with topics on advanced technologies, genomics and molecular markers for breeding			
Output target 2011	10 PhD candidates acquainted with topics on advanced technologies, genomics and molecular markers for breeding			
Output 5.10. PhD in plant breeding training at the West Africa Centre for Crop Improvement, University of Ghana <i>Commissioned: G4008-37</i> <i>2008-2013</i> <i>PI: Eric Y Danquah, University of Ghana, Ghana</i>		PhD candidates in selected African countries and breeding programmes	A selected group of African plant breeders well-trained in modern plant breeding	Increased human capacity in national plant breeding programmes in Africa
Output target 2009	Two PhD candidates registered and begin academic course requirements towards a graduate degree in modern plant breeding			
Output target 2010	Two PhD candidates continue their academic requirements towards a graduate degree in modern plant breeding; two PhD candidates registered and begin their academic requirements towards a graduate degree in modern plant breeding			
Output target 2011	Four PhD candidates continue their advanced training			
Theme 3: Construction of systems for ensuring product delivery				
Output 5.11. Capacity-building mechanisms and product pipelines established for tropical legume improvement in Africa <i>Focus: G6007.06</i> <i>2007-2010</i> <i>PI: Carmen de Vicente, GCP, Mexico</i>		African legume researchers and plant breeders	African researchers are enabled to apply modern plant breeding techniques and applications, through specialised training and updating of infrastructure in their institutions	Improved groundnut, bean, cowpea, and chickpea varieties delivered to resource-poor farmers
Output target 2009	A research workplan developed and Delivery Plans revised for projects on four crops (cowpeas, common beans, chickpeas and groundnuts) in Africa; equipment (field, laboratory and computer infrastructure) needs among sub-Saharan African partners fulfilled; at least 15 NARS scientists trained in MAS			
Output target 2010	Field and laboratory infrastructure improved in at least five African countries; implementation plan of research results in African partner institutions devised			
Output 5.12. Delivery Plan remote learning modules <i>Commissioned: Project no TBA</i> <i>2008-2009</i> <i>PI: Lawrence Pratt, INCAE, Costa Rica</i>		Project investigators of competitive grants, their collaborators, and NARS researchers	Two-way flow of communication activated from users to producers, and user capacity needs identified and fulfilled	Increased capacity in NARS to adopt GCP products; researchers use GCP products in developing improved crops

Output	Output target	Intended user	Outcome	Impact
	Output target 2009			
	Output target 2010			
Output 5.13. Comprehensive support provided to competitive projects to define delivery and capacity-building plans <i>Commissioned: G4006-12</i> <i>Timeframe: ongoing</i> <i>PI: Carmen de Vicente, GCP, Mexico</i>		Project investigators of competitive grants, their collaborators, and NARS researchers	Two-way flow of communication activated from users to producers, and capacity needs identified and fulfilled	Increased capacity in NARS to adopt GCP products; researchers use GCP products in developing improved crops
	Output target 2009			
	Output target 2010			
	Output target 2011			
Output 5.14. Improve cowpea productivity for marginal environments in Mozambique <i>Commissioned; Project no TBA</i> <i>2008–2010</i> <i>PI: Rogerio Chiulele, Eduardo Mondlane University, Mozambique</i>		Cowpea breeders in Mozambique	Mozambican researchers are enabled to apply modern plant breeding techniques and applications, through specialised training and research	Improved cowpea varieties delivered to resource-poor farmers in Mozambique
	Output target 2009			
	Output target 2010			
Output 5.15. A cassava breeding community of practice in Africa for accelerated production and dissemination of farmer-preferred cassava varieties resistant to pests and diseases <i>Commissioned: G4008.26</i> <i>2008–2011</i> <i>PIs: Chiedozie Egesi, NRCRI, Nigeria; Emmanuel Okogbenin, CIAT, Colombia</i>		Cassava breeders in Ghana, Nigeria, Tanzania, and Uganda	Users benefit through shared germplasm and information and training made available through the CoP involving cassava breeders, and primary, secondary and tertiary users	A new generation of NARS breeders trained in cassava field-based and MAS breeding working effectively to develop better varieties to respond to farmer's needs
	Output target 2008			
	Output target 2009			
	Output target 2010			

Output	Output target	Intended user	Outcome	Impact
	participating NARS: four MSc graduates trained in participating countries			
Output target 2011	At least 10 genotypes selected by MAS and conventional breeding approaches in each country; best five genotypes selected by farmers in participatory variety testing (PVT) trials for large-scale dissemination			
Output 5.16. Establishment of and support to crop and regional platforms <i>Commissioned: Project no TBA 2007–2013</i> <i>PI: Carmen de Vicente, GCP, Mexico</i>		GCP community and potential partner scientists and institutions	GCP understanding of partner needs enhanced and capacity-building activities refined to better address partner needs, enhancing probability of success in delivering GCP products	Increased capacity of scientists and institutions in target countries to collaborate with GCP, adopt GCP products and conduct their own research to improve crop varieties for farmers
Output target 2008	The Rice in Asia Platform established with partners from ongoing GCP rice projects in the region			
Output target 2009	Research, infrastructure and human resource capacity of collaborating NARS of at least three GCP research projects in GCP target regions assessed; information used to support partner capacity-building and assist medium to long term sustainability of GCP			
Output target 2010	Assessment and support continued; activities designed in response to partner feedback			
Output target 2011	Assessment and support continued; activities designed in response to partner feedback			
Output 5.17. A Project Development Guide (PDG) designed and implemented <i>Commissioned: Project no TBA 2007–2010</i> <i>PI: Vivienne Anthony, Consultant</i>		GCP Management Team, PIs and project team members, review teams for competitive grants, internal Review and Advisory Team, and external review teams reporting to donors	Systematic, unified, transparent approach to project management and planning within GCP	GCP's product-driven approach reinforced by better quality project plans; more products from research programmes being fully used; smooth and rapid handover of products; improved communication between project members and potential users
Output target 2008	A project management knowledge-based tool designed to maximise the delivery of GCP products on time and on budget			
Output target 2009	PDG disseminated and its use monitored			
Output 5.18. Validation of GCP products <i>Commissioned: G4008-23 2008–2013</i> <i>PI: Fred van Eeuwijk, WUR, The Netherlands (2008–2009)</i> <i>PI: TBD (2009–2013)</i>		GCP community and other stakeholders eg, germplasm curators, germplasm managers, crop breeders and crop geneticists	Users are better able to manage and use germplasm	Increased efficiency and effectiveness in crop improvement for development
Output target 2008	Reference lists of genotypes and markers for a selected set of crops developed and made available			
Output target 2009	Rules developed for choosing reference sets of genotypes and markers for crops; at least 10 microsatellite marker kits tested and validated: kits and information			

Output	Output target	Intended user	Outcome	Impact
	disseminated			
Output target 2010	To be determined based on GCP research progress and products available			
Output target 2011	To be determined based on GCP research progress and products available			
Output 5.19. GCP product distribution 2009–2013 <i>PI: Carmen de Vicente, GCP, Mexico</i>		GCP community and stakeholders in target regions	Users have facilitated access to and increasingly use GCP products	Increased efficiency and effectiveness in crop improvement for development
Output target 2009	At least two types of GCP product (eg, reference collections, reference samples for diversity analysis) distributed			
Output target 2010	To be determined based on GCP products validated			
Output target 2011	To be determined based on GCP products validated			
Theme 4: Development and implementation of support services				
Output 5.20. Interactive Resource Centre established and maintained <i>Commissioned: 2005-CB13 2005–2009</i> <i>PI: Theresa Fulton, Cornell University, USA</i>		Researchers worldwide working on plant genetic diversity and genomics	Users have access to a one-stop shop for information, references and advice	Increased access to information, resources and expertise enhances capacity, particularly in developing countries
Output target 2008	Interactive Resource Centre established and helpdesk function developed			
Output target 2009	Helpdesk function continued			
Output target 2010	To be determined depending on partner feedback			
Output 5.21. Toolbox of available molecular markers useful for marker-assisted selection in GCP crops <i>Commissioned: G4008.35 2008–2013</i> <i>PI: Veerle Van Damme, Consultant</i>		Crop breeders wishing to integrate molecular marker technologies	Users' implementation of molecular marker technologies facilitated	Enhanced processes of selection in crop variety development
Output target 2008	Database infrastructure developed			
Output target 2009	Database made available via Internet as a global public good on molecular markers useful for MAS in 19 food security crops			
Output target 2010	Database updated			
Output target 2011	Database updated			
Output 5.22. Genotyping Support Service <i>Commissioned: 2005-CB23 2006–2013</i> <i>PI: Humberto Gómez Paniagua, GCP, Mexico</i>		NARS researchers	Users in breeding programmes in developing countries have access to rapid and efficient genotyping of relevant germplasm	Enhanced understanding of genetic diversity and more efficient breeding processes
Output target 2009	Services (genotyping and data interpretation) provided for germplasm and routine MAS to NARS breeding programmes of selected crops			
Output target 2010	Services (genotyping and data interpretation) provided for germplasm or routine MAS to NARS breeding programmes of selected crops			
Output target 2011	Services (genotyping and data interpretation) provided for germplasm or routine MAS to NARS breeding programmes of selected crops			

Output	Output target	Intended user	Outcome	Impact
Output 5.23. Development and implementation of a GCP Workflow and Repository System <i>Commissioned: G4007.22</i> 2007–2009 <i>PI: Norbert Niederhauser, Cropster GmbH, Austria</i>		GCP community	Users are provided with facilitated procedures to store, manage and exchange project related information	Project management facilitated and Programme efficiency enhanced
Output target 2008	Workflow infrastructure developed and tested			
Output target 2009	Series of web-based modules to streamline management and monitoring of GCP projects validated; portal developed for GCP product distribution			
Theme 5: Ex ante impact analysis and impact assessment				
Output 5.24. Targeting and impact analysis of GCP technologies <i>Commissioned: G4006-13</i> 2006–2009 <i>PI: Glenn Hyman, CIAT</i>		GCP Management Team; wider scientific and development community; other decision makers	Users have access to detailed information about the potential impact of GCP research in target regions, crops and traits	Impact of GCP increased, contributing to reduced poverty and hunger
Output target 2008	Data available for impact targeting of crop-specific drought severity and type for GCP priority crops; analysis of patterns of technology adoption at disaggregated levels			
Output target 2009	GCP management Team incorporate learning into ongoing programme planning			
Output 5.25. Ex ante impact analysis of marker-assisted selection technologies supported by GCP <i>Commissioned: G4006-14</i> 2007–2009 <i>PI: George Norton, Virginia Tech, USA</i>		GCP Management Team; wider scientific and development community; other decision makers	Users have access to detailed information about the potential impact of GCP research in target regions, crops and traits	Impact of GCP increased, contributing to reduced poverty and hunger
Output target 2008	Economic analysis results available for cassava technologies; impact briefs produced to present the results of rice and cassava impact studies			
Output target 2009	Methods used for the economic impact assessment of GCP rice and cassava projects; manual produced describing the steps for a credible economic impact assessment of GCP projects			
Output 5.26. Getting the focus right: food crops and smallholder constraints <i>Commissioned: G4008.36</i> 2008–2009 <i>PI: John Dixon, CIMMYT, Mexico</i>		GCP Management Team; wider scientific and development community; other decision-makers	Users have access to detailed information about the potential impact of GCP research in target regions, crops and traits	Impact of GCP increased, contributing to reduced poverty and hunger
Output target 2008	Data produced for three crops (wheat, rice, sorghum) on relative importance of secondary traits			
Output target 2009	Methodology for identification of constraints and estimated losses for each constraint compiled for six food crops (wheat, rice, sorghum, cassava, cowpeas, chickpeas)			
Output 5.27. A strategic assessment of the capacity to develop and adopt GCP technologies <i>Commissioned: G4008.24</i> 2008–2010 <i>PI: Stanley Wood, IFPRI, USA</i>		GCP Management Team; wider scientific and development community; other decision makers	Users have access to detailed information about the potential impact of GCP research in target regions, crops and traits	Impact of GCP increased, contributing to reduced poverty and hunger

Output	Output target	Intended user	Outcome	Impact
Output target 2008	Methodology developed to assess the capacity of countries to undertake research and adopt GCP technologies			
Output target 2009	Methodology applied to the study of at least three selected countries			
Output target 2010	At least three validated country-specific case studies of the application of the revised GCP strategic priority-setting approach; maps, tabulations and interpretations of applying the validated method across all GCP focus regions, farming systems and crops			

Appendix A: Generation Challenge Programme Consortium members and partners—2008

Consortium members

Full members

1. Africa Rice Center (WARDA)
2. African Centre for Gene Technologies (ACGT)
3. Agropolis, France (incorporating CIRAD, IRD and INRA)
4. Bioversity International
5. Centro Internacional de Agricultura Tropical (CIAT; International Center for Tropical Agriculture)
6. Centro Internacional de la Papa (CIP; International Potato Center)
7. Centro Internacional de Mejoramiento de Maiz y Trigo (CIMMYT; The International Maize and Wheat Improvement Center)
8. Chinese Academy of Agricultural Sciences (CAAS)
9. Cornell University, USA
10. Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA; Brazilian Agricultural Research Corporation)
11. Indian Council of Agricultural Research (ICAR)
12. International Center for Agricultural Research in the Dry Areas (ICARDA)
13. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
14. International Institute of Tropical Agriculture (IITA)
15. International Rice Research Institute (IRRI)
16. John Innes Centre (JIC), UK
17. National Institute of Agrobiological Sciences (NIAS), Japan
18. Wageningen University and Research Centre (WUR), The Netherlands

Provisional members

19. Centro de Investigación y de Estudios Avanzados (CINVESTAV), Mexico
20. Institut national de la recherche agronomique (INRA), Morocco
21. Istituto Agronomico per l'Oltremare (IAO), Italy
22. National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand

NARS partners

1. African Centre for Crop Improvement (ACCI) at the University of KwaZulu–Natal, South Africa
2. Agharkar Research Institute, India
3. Agricultural Biotechnology Research Institute of Iran (ABRII)
4. Agricultural Research and Technology Corporation (ARTC), Sudan
5. Agricultural Research and Technology Corporation (ARTC), Sudan
6. Agricultural Research in Tanzania
7. Agricultural Research Institute (ARI–Naliendele), Naliendele Research Station, Tanzania
8. Agricultural Research Institute of the Hungarian Academy of Sciences (ARI–HAS), Hungary
9. Bangladesh Institute of Nuclear Agriculture (BINA)
10. Bangladesh Rice Research Institute (BRRI)
11. Bureau of Rice Research and Development (BRRD), Rice Department, Thailand

12. Cambodia Agricultural Research and Development Institute (CARDI), Cambodia
13. Central Rainfed Upland Rice Research Station (CRURRS), India
14. Central Rice Research Institute (CRRI), India
15. Centre d'étude régionale pour l'amélioration de l'adaptation à la sécheresse, (CERAAS), Senegal
16. Chitedze Research Station, Malawi
17. Crop Breeding Institute (CBI), Department of Research for Development, Zimbabwe
18. Crop Research Institute (CRI), Ghana
19. Debre Zeit Agricultural Research Centre (DZARC), Ethiopia
20. Department of Agriculture Research Services (DARS), Malawi
21. Dharwad University of Agricultural Sciences, India
22. Directorate of Wheat Research (DWR), India
23. Dr Panjabrao Deshmukh Krishi Vidyapeeth (DPKV; Dr Panjabrao Deshmukh Agricultural University), India
24. Eduardo Mondlane University, Mozambique
25. Ethiopian Institute of Agricultural Research (EIAR), Ethiopia
26. Fedearroz, Colombia
27. Hebei Academy of Agricultural Sciences, Institute of Dry Farming, China
28. Huazhong Agricultural University (HZAU), China
29. Indian Institute of Pulses Research (IIPR)
30. Indira Gandhi Krishi Vidyalaya (IGKV), India
31. Indonesian Centre for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD), Indonesia
32. Institut d'économie rurale (IER), Mali
33. Institut de l'environnement et de recherches agricoles (INERA), Burkina Faso
34. Institut de la recherche agronomique pour le développement (IRAD), Cameroon
35. Institut national de la recherche agronomique (INRA–Morocco)
36. Institut national de recherches agronomiques du Niger (INRAN)
37. Institut Sénégalais de Recherches Agricoles (ISRA), Senegal
38. Instituto Agronomico de Campinas, Brazil
39. Instituto de Investigação Agrária de Moçambique (IIAM; Institute for Agricultural Research), Mozambique
40. Instituto Nacional de Ciencias Agrícolas (INCA), Cuba
41. Instituto Nacional de Investigación Agropecuaria (INIA–Chile)
42. Instituto Nacional de Investigación Agropecuaria (INIA–Uruguay)
43. Instituto Nacional de Investigaciones Agropecuarias (INIA), Chile
44. Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias IINIFAP), Mexico
45. Instituto Nacional de Tecnología Agropecuaria (INTA–Argentina)
46. Instituto Nacional de Tecnología Agropecuaria (INTA–Nicaragua)
47. Kasetsart University, Thailand
48. Kenya Agriculture Research Institute (KARI)
49. Lake Zone Agricultural Research and Development Institute (LZARDI), Tanzania
50. Luoyang Academy of Agricultural Sciences (LAAS), China
51. Marathwada Agricultural University (MAU), India
52. Melkassa Agricultural Research Centre (MARC), Ethiopia
53. Moi University, Kenya
54. Nakhon Sawan Field Crops Research Center (NSFCRC), Thailand
55. Namulonge Agricultural and Animal Research Institute, Uganda (NAARI), Uganda
56. National Agricultural and Forestry Research Institute (NAFRI), Laos
57. National Center for Genome Resources (NCGR), USA
58. National Corn and Sorghum Research Center (NCSRC), Thailand

59. National Crop Resources Research Institute (NaCRRRI), Uganda
60. National Institute for Plant Genome Research (NIPGR), India
61. National Key Lab of Crop Genetics and Germplasm Enhancement, China
62. National Plant Genetic Resources Centre (NPGRC), Tanzania
63. National Research Centre on Plant Biotechnology (NRCPB), India
64. National Research Centre on Sorghum (NRCS), India
65. National Root and Tuber Crop Research Institute (NRCRI), Nigeria
66. Ningxia University, China
67. Northwest Sci-tech University of Agriculture and Forestry (NWSUAF), China
68. Organisation for the Rehabilitation of the Environment (ORE), Haiti
69. Pakistani Agricultural Research Council
70. Pakistani Agricultural Research Council (PARC), National Agricultural Research Center, Pakistan
71. Philippine Rice Research Institute (PhilRice)
72. Pohang University of Science and Technology, South Korea
73. Pontificia Universidad Católica de Valparaíso, Chile
74. Promoción e Investigación de Productos Andinos (PROINPA), Bolivia
75. Punjab Agricultural University (PAU), India
76. Research Center for Biotechnology, Bogor Agricultural University (RCB-IPB), Indonesia
77. Savannah Agricultural Research Institute (SARI), Ghana
78. Shanxi Academy of Agricultural Sciences (SAAS), China
79. Tamil Nadu Agricultural University (TNAU), India
80. Universidad de Talca, Chile
81. Universidade Católica de Brasília (UCB), Brazil
82. University of Agricultural Sciences, Bangalore, India
83. University of Agricultural Sciences, Dharwad, India
84. University of Dhaka, Bangladesh
85. University of Dhaka, Bangladesh
86. University of KwaZulu-Natal, South Africa
87. University of Pretoria, South Africa
88. University of the Witwatersrand, South Africa
89. West Africa Centre for Crop Improvement (WACCI), Ghana
90. Yunnan Academy of Agricultural Sciences (YAAS), China
91. Zhejiang University, China

ARI partners

1. Aberdeen University, UK
2. Agricultural Research Institute of the Hungarian Academy of Sciences (ARI-HAS), Hungary
3. Australian Centre for Plant Functional Genomics Pty Ltd (ACPFPG)
4. Centre de coopération internationale en recherche agronomique pour le développement (CIRAD), France
5. Charles Sturt University, Australia
6. Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia
7. Department of Plant Sciences and Plant Physiology, Eszterházy Károly College, (Eger-Hungary)
8. Department of Primary Industries & Fisheries (DPI&F), Australia
9. Eidgenössische Technische Hochschule (ETH), (Swiss Federal Institute of Technology), Zürich, Switzerland
10. European Bioinformatics Institute (EBI), UK

11. Imperial College London, UK
12. Institut de recherche pour le développement, France
13. Institut für Pflanzenbau und Pflanzenzüchtung, Germany
14. Institut national de la recherche agronomique (INRA–France)
15. Institute for Genomic Diversity (IGD), Cornell University, USA
16. Institute for Plant Genetics and Crop Plant Research (IPK), Germany (name in German?)
17. Institute of Crop Science, Chinese Academy of Agricultural Sciences (ICS–CAAS)
18. J Craig Venter Institute (incorporating TIGR, The Institute for Genomic Research), USA
19. Japan International Research Center for Agricultural Sciences (JIRCAS), Japan
20. Kansas State University, USA
21. Katholieke Universiteit Leuven (KUL), Belgium
22. L'Agence nationale de la recherche (ANR), France
23. Leibniz Institute for Plant Genetics and Crop Plant Research (IPK), Germany
24. Leiden University Medical Centre, The Netherlands
25. Max Planck Institute for Developmental Biology (MPIDB), Germany
26. Max Planck Institute for Molecular Plant Physiology (MPIMPI), Germany
27. McMaster University, Canada
28. Missouri University, USA
29. Nagoya University, Japan
30. National Center for Genome Resources (NCGR), USA
31. National Institute of Agricultural Biology (NIAB), UK
32. National Institute of Agrobiological Sciences (NIAS), Japan
33. Oregon State University (OSU), USA
34. Pennsylvania State University, USA
35. Purdue University, USA
36. RIKEN (Japanese abbreviation for 'Rikagaku Kenkyūsho': The Institute of Physical and Chemical Research)
37. Scottish Crop Research Institute (SCRI), UK
38. Sydney University, Plant Breeding Institute, Australia
39. Texas A&M University, USA
40. United States Department of Agriculture–Agricultural Research Service (USDA–ARS)
41. University of Alberta, Canada
42. University of Arizona, USA
43. University of California, Davis (UC–Davis), USA
44. University of California, Riverside (UC–Riverside), USA
45. University of Frankfurt, Germany
46. University of Georgia, Athens (UGA), USA
47. University of Hohenheim, Germany
48. University of Maryland, USA
49. University of Missouri, USA
50. University of Potsdam, Germany
51. University of Queensland, Australia
52. Virginia Bioinformatics Institute, Virginia Tech (Virginia Polytechnic Institute and State University), USA

Funders

1. Bill & Melinda Gates Foundation
2. Department for International Development (DFID), UK
3. European Commission (EC)
4. Pioneer Hi-Bred International, Inc

5. Swedish International Development Cooperation Agency (Sida)
6. Swiss Agency for Development and Cooperation (SDC)
7. Syngenta Foundation for Sustainable Agriculture
8. The Rockefeller Foundation
9. The World Bank

CGIAR Centres and Programmes

1. Challenge Program on Water and Food
2. HarvestPlus Challenge Program
3. International Food Policy Research Institute (IFPRI)
4. Sub-Saharan Africa Challenge Programme
5. System-wide Genetic Resources Programme (SGRP) of the CGIAR

Private sector

1. CropGen International
2. Diversity Arrays Technology Pty Ltd (DArT P/L), Australia
3. Syngenta
4. Waen Associates, Wales

Other partners

1. Alliance for a Green Revolution in Africa (AGRA)
2. Eastern and Central Africa Bean Research Network (ECABREN)
3. Global Crop Diversity Trust
4. Global Partnership Initiative for Plant Breeding Capacity Building (GIPB)
5. Plant Ontology Consortium
6. Program for African Seed Systems (PASS)
7. Southern Africa Bean Research Network (SABRN)

Appendix B: Progress report on implementation of external review recommendations

Name of CP: Generation Challenge Programme (GCP)

Dates of External Evaluation Report Presentation and Discussion:

Science Council: 31 March 2008, Nairobi, Kenya

Executive Council: 14 May 2008, Ottawa, Canada

CGIAR Annual General Meeting: *TBD*. December 2008

Recommendations as listed in the external review report	Response accepted or not accepted	Implementation		
		Milestones	Progress achieved	Target date of completion
1. The review panel recommends that GCP establish simple programme-level success criteria to provide GCP Management Team the means to focus, measure and monitor GCP programme effectiveness.	Accepted	<ul style="list-style-type: none"> Establish Programme-level impact indicators Develop a Programme logframe to better monitor Programme achievements 		End 2009
2. The review panel recommends that GCP management establish and apply a prioritisation process to identify the highest impact opportunities that GCP (Programme-level) can actually achieve and deliver to appropriate impact channels during its remaining six years.	Accepted	<ul style="list-style-type: none"> Focus on a few platforms that are easily accessible Prioritise a few challenge initiatives to focus the research of the Programme Milestones identified for recommendations 1 and 3 are also relevant to a certain extent to this recommendation 	Proposals under development for Genetic, Genomic and Molecular Breeding platforms	June 2009
3. The review panel recommends that GCP deploy the majority (at least 50 percent) of its resources in pursuit of the seven highest impact Programme-level trait-in-crop products that it can achieve over the next five years.	Accepted	Seven challenge initiatives identified and resources allocated accordingly	Partial. The seven initiatives identified, pending refinement and implementation in 2009	June 2009
4. The review panel recommends that GCP management in consultation with the curators of the source collections establish the protocols by which each GCP reference set will be maintained and distributed; and the means by which the current genotypic data and passport (catalogued) information on these reference sets will be maintained and augmented by current and future (non-GCP) discovery efforts that employ these collections.	Accepted	<ul style="list-style-type: none"> Protocols established for maintaining and distributing GCP's products after 2013 A Genetic Resource Support Service that should ensure quality, timely distribution and easy access to GCP breeding germplasm, with a specific attention to the reference sets, through standardised procedures 	<ul style="list-style-type: none"> Workshop in late 2008 to sensitise germplasm curators and breeders on research steps leading to the reference sets Recruitment of a Product Delivery Expert approved by the new Executive Board 	End 2011
5. The Review Panel recommends that GCP management revisit the skills training aspect of	Accepted	<ul style="list-style-type: none"> Greater participation by NARS in research 	By 2008, nine NARS applied	June 2009

Recommendations as listed in the external review report	Response accepted or not accepted	Implementation		
		Milestones	Progress achieved	Target date of completion
SP5 and focus skills training on the specific needs of the case studies and highest priority trait improvement projects.		through enhanced capacity <ul style="list-style-type: none"> Increased adoption of research results and more support to the 'Capacity-building à la Carte Programme', with a special focus on the seven new challenge initiatives 	research teams benefiting from tailored capacity building	
6. The review panel recommends that during setup of the Executive Board, a strong emphasis is placed on creating sufficient capacity and expertise for the Board to fulfill its duties, especially in: <ul style="list-style-type: none"> setting strategic direction for GCP; and, overseeing GCP finances and managing risks, also those relating to the host centre. 	Accepted	Executive Board established with relevant expertise	<ul style="list-style-type: none"> Seven-member Executive Board²² created as per PSC resolution²³, spanning the following professional fields: science, finance and corporate governance. The first meeting of the Executive Board took place towards the end of July 2008 	June 2008
7. The review panel recommends that an attempt is made to further simplify and clarify GCP governance by adapting the Consortium Agreement to the <i>de facto status quo</i> , and to clearly define the role and responsibilities of additional GCP governance bodies (the PSC, the PAC, the Stakeholder Committee).	accepted	<ul style="list-style-type: none"> Revise PSC status (organisation and <i>modus operandi</i>). Consortium Agreement²⁴ revised to reflect, among others, the transfer of some responsibilities from the PSC to the new Executive Board 	<ul style="list-style-type: none"> PSC Task Force to redefine PSC's new role established in December 2007 Recommendations of the TF to simplify GCP governance submitted to the PSC Chair by the end of July 2008 Liaison established with GFAR to revamp and redefine SHC role 	March 2009
8. The review panel recommends that GCP upgrade all Subprogramme Leader positions to fulltime positions for the next three years. Since SP3 and SP5 Leaders already have fulltime positions, this implies to move the leadership of	Accepted But to be implemented only when current half-	The three hafitime SPL positions converted to fulltime positions	SP4 Leader position already converted to fulltime position	Subject to current halftime SPLs (1 & 2)

²² Details on Executive Board at <http://www.generationcp.org/whoweare.php?da=08124404>

²³ PSC resolution at http://www.generationcp.org/UserFiles/File/final-resolution_executive-board-15Dec07_final.pdf

²⁴ Consortium Agreement at http://www.generationcp.org/UserFiles/File/Consortium_agreement_signed.pdf

Recommendations as listed in the external review report	Response accepted or not accepted	Implementation		
		Milestones	Progress achieved	Target date of completion
SP1, SP2 and SP4 from halftime to full time positions (in order to provide the necessary management capacity for programme-level management and the fulfillment of management duties in their respective SPs; and to avoid split responsibilities between the GCP and the SP Leaders' home institutions).	time SP Leaders, of their own volition, leave the Management Team			turnover, leaving of their own volition
9. The review panel recommends GCP management adopt an end-product orientation for GCP activities, ie, the integration, alignment and prioritisation of product-oriented projects across Subprogrammes in line with high-priority programme-level product objectives. To support this, the Review Panel recommends that GCP management acquire or develop a product project portfolio management system to help it plan, monitor and manage its best opportunities (achievable high-priority programme-level objectives).	accepted	<ul style="list-style-type: none"> • Product development crop manager identified, for each of the challenge initiative • Programme-level impact indicators defined • Two-dimension management matrix with a product-/crop-specific axis 	<ul style="list-style-type: none"> • Workflow system established to streamline portfolio management • Consultations underway on the seven trait-crop priorities, and associated products 	March 2009

Appendix C: Challenge Programme financial indicators

Already submitted to the CGIAR Science Council on 15 June. To be reproduced here for printed and e-version of MTP]