



Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE-POOR

**2008 Annual report and
year six (2009) workplan**

GCP's five Subprogrammes

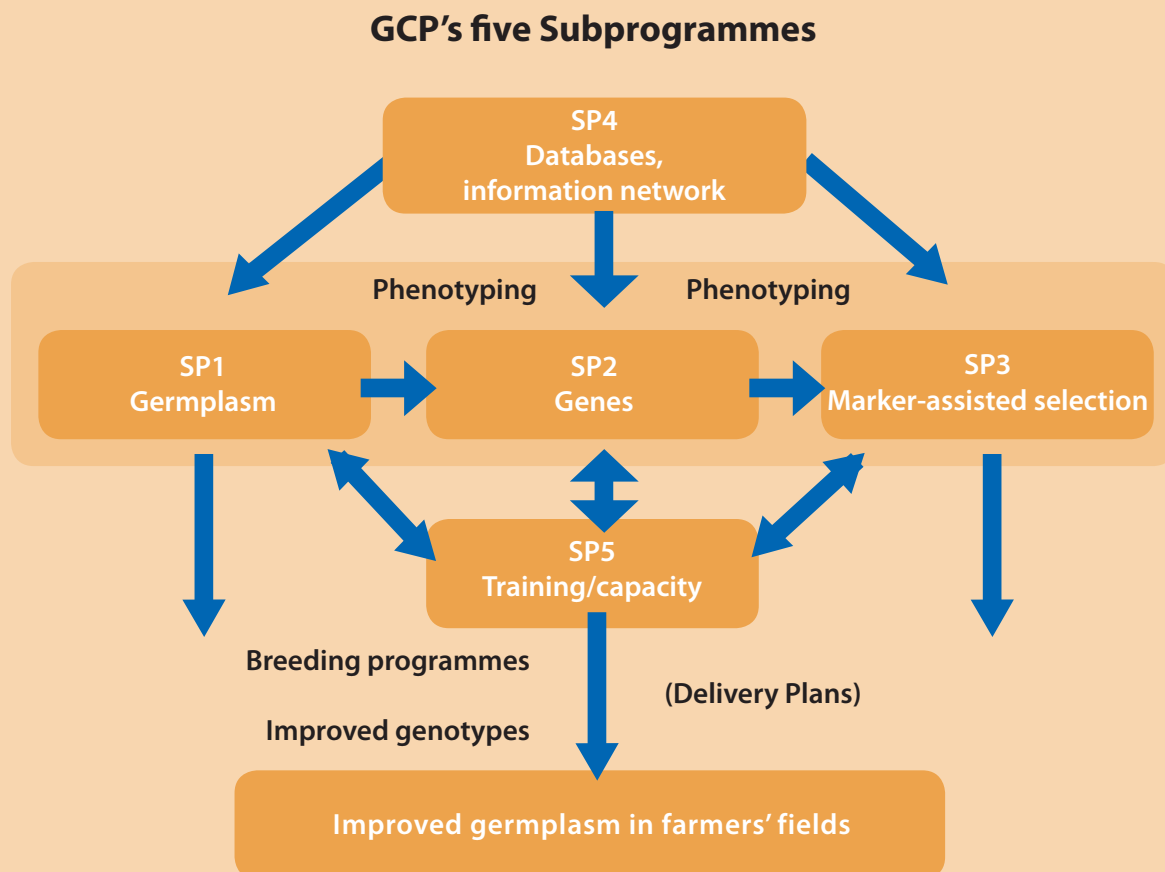
Subprogramme 1: Crop genetic diversity – Characterises the diversity of crop germplasm collections in the custody of the CGIAR and national programmes in terms of genetic structure and associated phenotypic variation

Subprogramme 2: Genomics towards gene discovery – Uses and designs 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 agricultural research programmes to use modern breeding approaches. SP5 also coordinates the design and implementation of project Delivery Plans and is responsible for intellectual property issues, and research in policy and impact assessment.





CGIAR Generation Challenge Programme

2008 Annual report and year six (2009) workplan

Generation Challenge Programme (GCP)

Hosted by CIMMYT

(Centro Internacional de Mejoramiento de Maíz y Trigo;
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Acronyms and abbreviations

ABC	Agricultural Biotechnology Center, Gödöllő, Hungary	CIMMYT	Centro Internacional de Mejoramiento de Maiz y Trigo (the International Maize and Wheat Improvement Center)
ABRII	Agriculture Biotechnology Research Institute of Iran	CIMS	Centro de Inteligencia sobre Mercados Sostenibles, INCAE Business School, Costa Rica
ACCI	African Centre for Crop Improvement, South Africa	CINVESTAV	Centro de Investigación y de Estudios Avanzados, Mexico
ACGT	African Centre for Gene Technologies, South Africa	CIP	Centro Internacional de la Papa (International Potato Centre)
ACPGF	Australian Centre for Plant Functional Genomics, Pty Ltd	CLDRI	Cuu Long Delta Rice Research Institute, Vietnam
AC–UT	Agricultural College, University of Tehran, Iran	CMTV	Comparative Map and Trait Viewer
ADOC	allelic diversity for orthologous candidate genes	CNG	Centre national de génotypage, Commissariat à l'énergie atomique, Evry, France
AGRA	Alliance for a Green Revolution in Africa	CNIRRI	China National Rice Research Institute
Agropolis–CIRAD	Centre de coopération internationale en recherche agronomique pour le développement, France	CoP	community of practice
Agropolis–IRD	Institut de recherche pour le développement, France	COS	conserved orthologous sequence
Agropolis–INRA	Institut national de la recherche agronomique, France	CP	Challenge Programme (of the CGIAR)
AICPMIP	All-India Coordinated Pearl Millet Improvement Project	CRI–Ghana	Crops Research Institute, Ghana
Al	aluminium	CRI–Sri Lanka	Coconut Research Institute, Sri Lanka
<i>Al</i> _{SB}	marker diagnostic for aluminium tolerance	CRIL	(CIMMYT–IRRI) Crop Research Informatics Laboratory
ANR	Agence nationale de la recherche, France	CRR1	Central Rice Research Institute, India
APSIM	Agricultural Production Systems Simulator	CRS	Chitedze Research Station, Malawi
ARC–Austria	Austrian Research Centers GmbH	CRURRS	Central Rainfed Upland Rice Research Station, India
ARC–Sudan	Agricultural Research Corporation, Sudan	CSIRO	Commonwealth Scientific and Industrial Research Organisation, Australia
ARI(s)	advanced research institute(s)	CSO	civil society organisation
ARI–Ghana	Agricultural Research Institute, Ghana	CSSL	chromosome segment substitution line
ARI–HAS	Agricultural Research Institute of the Hungarian Academy of Sciences, Hungary	CSU	Colorado State University, USA
ARI–India	Agharkar Research Institute, India	CU	Cornell University, USA
ARI–Naliendele	Agricultural Research Institute–Naliendele Research Station, Tanzania	$\Delta^{13}C$	Carbon isotope discrimination
ARM	(GCP) Annual Research Meeting	DAR	Department of Agricultural Research, Myanmar
ART	Agricultural Research in Tanzania	DARS	Department of Agriculture Research Services, Malawi
ARTC	Agricultural Research and Technology Corporation, Sudan	DArT	diversity arrays technology
ASR	ABA/water stress/ripening-induced (gene)	DArT P/L	Diversity Arrays Technology Pty, Ltd
BAC	bacterial artificial chromosome	DFID	Department for International Development, UK
BAU	Birsa Agricultural University, Ranchi, India	DMR	Directorate of Maize Research, India
BC, etc	backcross 1 etc	DNA	Deoxyribonucleic acid
BCMV	bean common mosaic virus	DoA–Indonesia	Department of Agriculture, Indonesia
BF	Barwale Foundation	DPI&F	Department of Primary Industries and Fisheries, Australia
BGYMV	bean golden yellow mosaic virus	DPKit	Delivery Plan Kit
BI	Bioversity International	DREB	drought-responsive element binding protein (gene)
BINA	Bangladesh Institute of Nuclear Agriculture	DWR	Directorate of Wheat Research, India
BIOTEC	National Center for Genetic Engineering and Biotechnology, Thailand	DZARC	Debre Zeit Agricultural Research Centre, Ethiopia
BLB	bacterial leaf blight	EARO	Ethiopian Agricultural Research Organization
BMGF	Bill & Melinda Gates Foundation	EB	(GCP) Executive Board
bp	base pairs	EBI	European Bioinformatics Institute, UK
BRRD	Bureau of Rice Research and Development, Rice Department, Thailand	EC	European Commission
BRR1	Bangladesh Rice Research Institute	ECABREN	Eastern and Central Africa Bean Research Network
CAAS	Chinese Academy of Agricultural Sciences	DPSPP–EKC	Department of Plant Sciences and Plant Physiology, Eszterházy Károly College, Eger, Hungary
CAPS	cleaved amplified polymorphic sequence (markers)	EgU	Egerton University, Kenya
CARDI	Cambodia Agricultural Research and Development Institute	EIAR	Ethiopian Institute of Agricultural Research
CAS–IP	CGIAR Central Advisory Service for Intellectual Property	EMBRAPA	Empresa Brasileira de Pesquisa Agropecuária (Brazilian Agricultural Research Corporation)
CAZRI	Central Arid Zone Research Institute, India	EPMR	External Programme and Management Review
CB	conventional breeding	ERECTA	a leucine rich repeat receptor-like kinase (gene)
CBI	Crop Breeding Institute, Department of Research for Development, Zimbabwe	EST	expressed sequence tag
cDNA	complementary DNA	ESU	Ebonyi State University, Nigeria
CERAAS	Centre d'étude régional pour l'amélioration de l'adaptation à la sécheresse, Senegal	ETH	Eidgenössische Technische Hochschule, (Swiss Federal Institute of Technology), Zürich
CGIAR	Consultative Group on International Agricultural Research	EURISCO	European Plant Genetic Resources Search Catalogue
CHF	Swiss francs	ExCo	CGIAR Executive Council
ChSU	Charles Sturt University, Australia	F ₁ etc	first filial generation etc
CI	Challenge Initiative	FABI	Forestry and Agricultural Biotechnology Institute, University of Pretoria, South Africa
CIAT	Centro Internacional de Agricultura Tropical (International Center for Tropical Agriculture)	Fedearroz	Federación Nacional de Arroceros, Colombia
CIFOR	Centre for International Forestry Research		
CIHEAM–IAMZ	Centro Internacional de Altos Estudios Agronómicos Mediterráneos–Instituto Agronómico Mediterráneo de Zaragoza, Spain		

FOFIFA–DRA	Foibem-Pirena Mombra ny Fikarohana Ampiharina Amin'ny Fampandrosoana ny eny Ambanivohitra (National Centre for Applied Research on Rural Development) Département de la recherche agronomique, Madagascar	IRC	Interactive Resource Center
GBP	British pounds	IRRI	International Rice Research Institute
GCDT	Global Crop Diversity Trust	ISABU	Institut des sciences agronomiques du Burundi
GCP	Generation Challenge Programme of the CGIAR	ISAR	Institut des sciences agronomiques du Rwanda
Genaisance	Genaisance Pharmaceuticals, Inc, France	ISRA	Institut sénégalais de recherches agricoles, Senegal
GFAR	Global Forum on Agricultural Research	JCVI	J Craig Venter Institute, USA
GIPB	Global Partnership Initiative for Plant Breeding Capacity Building	JIC	John Innes Centre, UK
GIS	geographic information system(s)	JIRCAS	Japan International Research Center for Agricultural Sciences
GISH	genomic in situ hybridisation	KARI	Kenya Agricultural Research Institute
GOST	GreenPhyl Ortholog Search Tool	kb	Kilobase
GRSS	Genetic Resources Support Service	KSU	Kansas State University, USA
GSS	Genotyping Support Service	KU	Kasetsart University, Thailand
GxE	genotype by environment interaction	KUL	Katholieke Universiteit Leuven, Belgium
HAAS	Hebei Academy of Agricultural Sciences, Institute of Dry Farming, China	LAAS	Luoyang Academy of Agricultural Sciences, China
HAKI	Research Institute for Fisheries, Aquaculture and Irrigation, Hungary	LD	linkage disequilibrium
HPC	high-performance computing	LIMS	Laboratory Information Management System
HZAU	Huazhong Agricultural University, China	LUMC	Leiden University Medical Center, The Netherlands
IAC	Instituto Agronomico de Campinas, Brazil	LZARDI	Lake Zone Agricultural Research and Development Institute, Tanzania
IAO	Istituto Agronomico per l'Oltremare, Italy	M&E	monitoring and evaluation
IARI	Indian Agricultural Research Institute	MAB	marker-assisted breeding
IA–Tápiószele	Institute for Agrobotany, Tápiószele, Hungary	MABC	marker-assisted backcrossing
IBONE	Instituto de Botánica del Nordeste, Argentina	MAGIC	multiparent advanced generation inter-cross
ICABIOGRAD	Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development	MahU	Mahidol University, Thailand
ICAR	Indian Council of Agricultural Research	MARC	Melkassa Agricultural Research Centre, Ethiopia
ICARDA	International Centre for Agricultural Research in the Dry Areas	MARI	Mikocheni Agricultural Research Institute, Tanzania
ICERI	Indonesian Cereals Research Institute	MARS	marker-assisted recurrent selection
ICIS	International Crop Information System	MAS	marker-assisted selection
ICL	Imperial College London, UK	MAU	Marathwada Agricultural University, India
ICRAF	World Agroforestry Centre	Mb	megabase
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics	MDG(s)	Millennium Development Goal(s)
ICS–CAAS	Institute of Crop Science, Chinese Academy of Agricultural Sciences	MMRI	Maize and Millets Research Institute, Pakistan
IER	Institut d'économie rurale, Mali	MPIMPP	Max Planck Institute for Molecular Plant Physiology, Germany
IFPRI	International Food Policy Research Institute	MPUAT	Maharana Pratap University of Agriculture and Technology, India
IFSSA	Indian Foundation Seed and Services Association	MSV	maize streak virus
IGD	Institute for Genomic Diversity, Cornell University, USA	MT	(GCP) Management Team
IGKV	Indira Gandhi Krishi Vishwa Vidyalaya (Indira Gandhi Agricultural University), India	MU	Moi University, Kenya
i-GOST	iterative version of GOST	N/A	not applicable
IIAM	Instituto de Investigação Agrária de Moçambique (Institute for Agricultural Research, Mozambique)	NAARI	Namulonge Agricultural and Animal Research Institute, Uganda
IIPR	Indian Institute of Pulses Research	NaCRRRI	National Crop Resources Research Institute, Uganda
IITA	International Institute of Tropical Agriculture	NAFRI	National Agricultural and Forestry Research Institute, Laos
ILRI	International Livestock Research Institute	NagU	Nagoya University, Japan
iMAS	Integrated Marker-Assisted Selection System (software)	NAM	nested association mapping
INCA	Instituto Nacional de Ciencias Agrícolas, Cuba	NARI	National Agricultural Research Institute, Eritrea
INCAE	INCAE (Instituto Centroamericano de Administración de Empresas) Business School, Costa Rica	NARS	national agricultural research system(s)
INERA–Burkina Faso	Institut de l'environnement et de recherches agricoles, Burkina Faso	NAU	Nanjing Agricultural University, China
INERA–DRC	Institut national pour l'étude et la recherche agronomique, Democratic Republic of Congo	NCE	no-cost extension
INIA–Chile	Instituto de Investigaciones Agropecuarias, Chile	NCGR	National Center for Genome Resources, USA
INIA–Uruguay	Instituto Nacional de Investigación Agropecuaria, Uruguay	NCSU	North Carolina State University, USA
INIFAP	Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias, Mexico	NDUAT	Narendra Deva University of Agriculture and Technology, India
INRA–Morocco	Institut national de la recherche agronomique, Morocco	NERICA	new rice for Africa
INRAN	Institut national de la recherche agronomique du Niger	NGO	non-governmental organisation
INTA–Argentina	Instituto Nacional de Tecnología Agropecuaria, Argentina	NIAB	National Institute of Agricultural Botany, UK
INTA–Nicaragua	Instituto Nacional de Tecnología Agropecuaria, Nicaragua	NIAS	National Institute of Agrobiological Sciences, Japan
INV	cell-wall invertase (gene)	NIL	near-isogenic line
IP	intellectual property	NIPGR	National Institute for Plant Genome Research, India
iPC	iPlant Collaborative	NKLCGGE	National Key Lab of Crop Genetics and Germplasm Enhancement, China
IPK	Leibniz Institute of Plant Genetics and Crop Plant Research, Germany	NMRI	National Maize Research Institute, Vietnam
IPT	isopentenyltransferase (gene)	No.	number
IRAD	Institut de la recherche agronomique pour le développement, Cameroon	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
		ORE	Organisation for the Rehabilitation of the Environment, Haiti
		OSU	Oregon State University, USA
		PABRA	Pan-African Bean Research Alliance
		PARC	Pakistani Agricultural Research Council
		PASS	Program for African Seed Systems
		PAU	Punjab Agricultural University, India
		PBI–UoS	Plant Breeding Institute, University of Sydney, Australia

PDC	Product Delivery Coordinator	SSA	sub-Saharan Africa
PDG	Project Development Guide	SSR	simple sequence repeat
PKV	Dr Panjabrao Deshmukh Krishi Vidyapeeth, (Dr Panjabrao Deshmukh Agricultural University) India	SUA	Sokoine University of Agriculture, Tanzania
PDL	Product Delivery Leader	TAMU	Texas A&M University, USA
PeU	Peking University, China	TBD	to be determined
PHI	Pioneer Hi-Bred International, Inc	TF	task force
PhilRice	Philippine Rice Research Institute	TLI	Tropical Legumes I Project
PI	Principal Investigator	TLII	Tropical Legumes II Project
POC	Plant Ontology Consortium	TNAU	Tamil Nadu Agricultural University, India
PROINPA	Promoción e Investigación de Productos Andinos, Bolivia	TPE	target population of environments
PSC	Programme Steering Committee	TU	Tishreen University, Syria
PSU	Pennsylvania State University, USA	UAC	Universidad Autónoma Chapingo, Mexico
PU	Purdue University, USA	UARI	Uyole Agricultural Research Institute, Tanzania
<i>Pup1</i>	marker diagnostic for phosphorus uptake	UAS	University of Agricultural Sciences, India
QTL	quantitative trait locus	UCB	Universidade Católica de Brasília, Brazil
QTLxE	QTL by environment interaction	UdB	Università di Bologna, Italy
R&D	research and development	UdT	Universidad de Talca, Chile
RAP	Review and Advisory Panel	UdU	Università di Udine, Italy
RAU	Rajasthan Agricultural University, India	UGA	University of Georgia, USA
RCB-IPB	Research Center for Biotechnology, Bogor Agricultural University, Indonesia	UK	United Kingdom
RF	The Rockefeller Foundation	UKZN	University of KwaZulu-Natal, South Africa
RFLP	restriction fragment length polymorphism	UEM	Universidade Eduardo Mondlane, Mozambique
RGDU	Rice Gene Discovery Unit, Thailand	UoA	University of Arizona, USA
RIKEN	Rikagaku Kenkyūsho (Institute of Physical and Chemical Research), Japan	UoAa	University of Aarhus, Denmark
RIL	recombinant inbred lines	UoAb	University of Aberdeen, Scotland
RNA	ribonucleic acid	UoAd	University of Adelaide, Australia
RYMV	rice yellow mottle virus	UoAl	University of Alberta, Canada
SAARI	Serere Agricultural and Animal Production Research Institute, Uganda	UoC	University of California, USA
SAAS	Shanxi Academy of Agricultural Sciences, China	UoD	University of Dhaka, Bangladesh
SABRN	Southern Africa Bean Research Network	UoF	University of Frankfurt, Germany
<i>SaltoI</i>	marker diagnostic for salt tolerance	UoH	University of Hohenheim, Germany
SARI-Ethiopia	South Agricultural Research Institute, Ethiopia	UoM	University of Maryland, USA
SARI-Ghana	Savannah Agricultural Research Institute, Ghana	UoMi	University of Missouri, USA
SARK	senescence associated receptor protein kinase	UoP	University of Pretoria, South Africa
SAU	Sichuan Agricultural University, China	UoPd	University of Potsdam, Germany
SciDev.Net	Science and Development Network	UoQ	University of Queensland, Australia
SCRI	Scottish Crop Research Institute, UK	UoS	University of Sydney, Australia
SDC	Swiss Agency for Development and Cooperation	UoV	University of Virginia, USA
SEK	Swedish krona	UotW	University of the Witwatersrand, South Africa
SFSA	Syngenta Foundation for Sustainable Agriculture	UoW	University of Washington, USA
SGRP	System-wide Genetic Resources Programme of the CGIAR	URU	Ubon Ratchatani University, Thailand
SHC	Stakeholder Committee	USA	United States of America
Sida	Swedish International Development Cooperation Agency	USD	United States dollars
SIRDC	Scientific and Industrial Research and Development Centre, Zimbabwe	USDA-ARS	United States Department of Agriculture-Agricultural Research Service, USA
SME	small- and medium-scale enterprise	USP	Universidade de São Paulo, Brazil
SNP	single nucleotide polymorphism	VBI	Virginia Bioinformatics Institute, VPI
SP	Subprogramme	Virginia Tech	see VPI
SP1, SP2 etc	Subprogramme 1, Subprogramme 2 etc.	VPI	Virginia Polytechnic Institute and State University, USA
SPL	Subprogramme Leader	WA	Waen Associates, UK
SPS	sucrose phosphate synthase (gene)	WACCI	West Africa Centre for Crop Improvement, University of Ghana
SPVD	sweet potato virus disease	WARDA	Africa Rice Center
SS	sucrose synthase (gene)	WMS	Workflow Management System
		WUR	Wageningen University and Research Centre, The Netherlands
		YAAS	Yunnan Academy of Agricultural Sciences, China
		YU	Yale University, USA
		ZU	Zhejiang University, China

Foreword

Dear friends and colleagues of the Generation Challenge Programme,

The year 2008 marks the end of Phase I (2004–2008) of the Generation Challenge Programme (GCP). It is, therefore, a fitting time for stocktaking and forward planning, as we embark on Phase II (2009–2013).

In the pages that follow, you will also read how this transition into Phase II is informed by several internal and external reviews,¹ of which the most comprehensive was the External Programme and Management Review (EPMR), commissioned by the Science Council of the Consultative Group on International Agricultural Research (CGIAR). The EPMR recommended the approval of GCP Phase II. For this positive outcome, on behalf of GCP's Management Team (MT), I would like to extend our sincere thanks to all the researchers and their support staff who participated in the review. It is their continued commitment and concrete contributions to science that brought about this good result, for which the MT is deeply grateful.

One key result of the internal and external reviews, strongly supported by our own critical self-appraisal, is greater focus in our work. As we continue to pursue the goals set out in our Strategic Framework² with the benefit of the review recommendations, we trust that this sharper focus will translate into even greater impact. To this end, we need well-defined impact indicators and milestones at Programme level, to clearly demonstrate achievements by 2013.

Another significant development that began in 2008 was the fundamental reform of our governance structure, in order to provide better support to our science. Undertaken by the GCP Programme Steering Committee (PSC), this reform ushered in a new Executive Board (EB) effective 1 June 2008. This change should eventually see the PSC converted into a Consortium Committee that will assume a primarily advisory scientific role in interacting with the MT.

Key results from Phase I

In the course of the last five years, GCP has made remarkable contributions to pushing forward the frontiers of scientific knowledge in crop science, as well as weaving together a dynamic R&D community collectively working towards solutions to some of the challenges facing food production and agricultural research today. Our major contributions to science in Phase I are summarised in this report.

Building the GCP community

During our first phase, we forged and nurtured an extensive consortium partnership, and leveraged resources to establish a broad network of R&D partners³ with diverse and extensive capabilities and capacity to support GCP objectives.⁴ To echo the words of one of our Phase I review reports, perhaps the most important value of GCP thus far is seen in the opportunities we have provided for people of diverse backgrounds to collectively reflect on, and formulate, solutions to complex problems in plant improvement and – in the process – learn from one another.

At the close of Phase I, GCP is supported by a vibrant community of researchers and stakeholders all along our pipeline of activities. These partners are from more than 200 different institutes including universities, the CGIAR, developing and developed country research programmes, and private sector and civil society organisations. Through this array of diverse partnerships, we are progressively achieving one of our major objectives – bridging the gap between fundamental and applied research.

At the crossroads . . .

The year 2008 was a watershed. In GCP's midlife, and marking the transition from Phase I to Phase II, we have made – and we expect to continue to make – several changes to enhance support to our science, and to rise effectively to the challenge of cultivating plant genetic diversity for the benefit of resource-poor farmers in GCP's priority areas.

¹ <http://www.generationcp.org/whoweare.php?da=08137524>

² http://www.generationcp.org/comm/gcp_framework_final.pdf

³ <http://www.generationcp.org/gcppartners.php?da=0646141>

⁴ <http://www.generationcp.org/index.php#objectives>

- **Dynamic management:** As would be expected, concepts and ideas at GCP's founding are now evolving into concrete products, tools, methodologies and firmer new directions as our projects mature and our project portfolio expands. Consequently, we began realigning our management structure in late 2008, bringing in a new dimension devoted to product delivery, to keep in step with the various stages in the implementation of our strategy. This realignment will continue into 2009 (see *A two-dimensional management structure in Introduction and highlights*).
- **Our challenges:** In keeping with our middle name, we have faced – and expect to continue to face – several challenges in realising our mission. The main ones include:
 - maintaining the motivation and momentum of the community we have built, while also being more focused in our research
 - maintaining effective communications in a virtual and widely distributed community
 - ensuring quality, release and exchange of data across different disciplines, institutions and capacities
 - moving rapidly forward in implementing our strategic plan, but without unduly rushing – or neglecting – critical steps
 - designing and implementing a viable and effective strategy to assure the sustainability of GCP products after 2013.
- **Proof and partners:** While we expect that the impact of the CIs will probably spill over beyond the target countries, having impact on breeding in the focus countries is what will constitute our proof of concept. GCP will continue to demonstrate that a research approach tapping into crop diversity and using modern biotechnology-based breeding can have impact on crop breeding in drought-prone environments. By so doing, we hope that R&D initiatives and national governments will be willing to further build on GCP achievements, and extend them based on the same – or largely similar – approaches.

To sum up, and taking into account the challenges we have faced and anticipate facing, five years on, the net balance from Phase I is, on balance, very positive: GCP has built a strong community, identified the most promising research trends and well-positioned partners, and is already delivering a significant set of products to improve crop genetic research and breeding. Therefore, we confidently approach the challenges of Phase II on a positive and optimistic note, with an added spring in our step. We also gratefully acknowledge the generosity, support and dedication of our Phase I funders (see *Appendix E*), without whom we would not be where we are today.

In Phase II, in parallel to research per se, our focus will also be on platform development to guarantee access to, and distribution of, GCP products in a user-friendly and sustainable manner. And because the original vision for GCP was time-bound to 2013, it is imperative that GCP ensure continued and sustainable use of Programme products after 2013. This objective on 'what next' in the 'after-GCP' era will, therefore, be at the core of our evolution strategy, which we shall be drafting in the course of Phase II.

And just like 2008 was, 2013 will be yet another watershed year – a clear crossing point and a time of transition, stocktaking, scoping and mapping in order to distil and build on promising and critically essential activities, and determine how such activities will be sustained after GCP.

No doubt, there are momentous and exciting times ahead!

Jean-Marcel Ribaut
Director

The road ahead . . .

- **Building on success and greater focus:** We have made some good strides forward in science, as demonstrated by the – overall – very positive feedback from the different reviews. But we are not resting on our laurels. The GCP MT, like the reports of the most recent reviews, recognises the need for GCP to focus its research agenda more sharply. It is to attain this objective that we have identified the set of seven Challenge Initiatives (CIs)⁵ that are crop- and trait-specific. In Phase II, a significant portion of GCP research funds will be dedicated to these CIs, with special attention to marker-assisted breeding (MAB).

⁵ http://www.generationcp.org/gen.php?da=08128238#gcp_challenge_initiatives

Introduction and highlights

GCP is an initiative of the CGIAR, and was launched in 2003 as a 10-year programme. The Programme was designed in two phases (2004–2008 and 2009–2013). Therefore, this Annual Report marks the end of Phase I and the transition into Phase II.

In these middle years, we continue to build on the foundations laid in the Programme's formative years, and to refine our Strategic Framework. This refinement has been complemented by a set of 'reference studies' that provide data on GCP's impact targets (farming systems and crops). It has also been informed by several external evaluations –including an External Programme and Management Review commissioned by the CGIAR Science Council – and our own critical self-appraisal. Accordingly, and for greater coherence with our strategy, the Management Team decided to sharpen the focus further on key areas to promote meaningful impact by the Programme's close at 2013. In 2008, this exercise resulted in the identification of seven Challenge Initiatives (CIs) that are crop- and trait-specific. From 2009, at least half of our research budget will be dedicated to the seven CIs.

Implementing the CIs, bringing our emphasis on product delivery to fruition, and establishing regional and crop communities of practice (CoPs) called for a revision of the GCP management organogram. In Phase II, GCP will pay particular attention to developing platforms as a channel for distributing GCP products in a sustainable and user-friendly manner, sensitive to client needs.

Another significant development in 2008 was the beginning of fundamental reform in our governance structure, for better support to our science. Undertaken by the GCP Programme Steering Committee, this reform brought in a new Executive Board in place as of 1 June 2008. With this change, the PSC should be converted into a Consortium Committee with a primarily scientific role, making for more meaningful engagement.

A set of new research activities was initiated in 2008, matching the evolution of our research strategy and increasing interactions across Subprogrammes. These activities include a new round of competitive projects selected in mid-2008 for initiation in the last quarter of the year. The

competitive projects are structured into four research themes corresponding to activities conducted across the five Subprogrammes, with several of them fitting directly into the new CIs. Together, all these new projects clearly build on our previous work, and explore innovative and promising avenues of research to improve crops in drought-prone environments. At the same time, they also focus our overall research portfolio on key crops and selected target environments for impact on plant breeding to boost crop productivity. Box 1 (overleaf) summarises our major achievements in 2008.

Among a range of achievements in our first phase, we have contributed considerable scientific knowledge on genetic diversity, established platforms and forged R&D partnerships to facilitate access to technology, and broadened the genetic base and fortified crops for drought tolerance. Projects to be conducted in Phase II will clearly build on – and add value to – our previous work, using favourable germplasm selected

through genetic studies to develop new populations, while testing new tools and validating alleles identified through genetic studies in breeding programmes.

GCP Subprogrammes

Subprogramme 1 (SP1): Crop genetic diversity
Subprogramme 2 (SP2): Genomics towards gene discovery
Subprogramme 3 (SP3): Trait capture for crop improvement
Subprogramme 4 (SP4): Bioinformatics and crop information systems
Subprogramme 5 (SP5): Capacity-building and enabling delivery

As Phase I comes to a close, GCP is supported by a vibrant community of researchers and stakeholders all along the pipeline of our activities. These partners are from more than 200 diverse institutes including universities, the CGIAR, and our main target users and stakeholders – developing country research programmes and civil society organisations. Through these partnerships, GCP is achieving one of its major objectives – to bridge the gap between fundamental and applied research.

Research activities

Alignment to CGIAR and global priorities

GCP has several means of establishing and maintaining its focus, relevance and applicability. The Programme's efforts to develop new knowledge and products contribute to the first 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 poor farm households the potential to improve their food and nutritional security and their income. They also offer poor consumers the prospect

Box 1. Scientific achievements

In 2008, key highlights included:

- Implementing a scheme for validating core characterisation data for genetic stocks of 11 GCP crops, and formulating guidelines to optimise seed multiplication practices
- Making available reference germplasm sets for most GCP crops and preparing seed for distribution
- Using reference samples to enhance understanding of factors involved in crop evolution, helping point to innovative pathways for germplasm characterisation and exploitation
- Completing molecular marker analysis for foxtail millet, focusing on data compilation and aggregation across laboratories and on data analysis
- Developing a significant quantity of molecular markers for four legumes to facilitate trait mapping
- Assembling physical maps for cowpeas and cassava to facilitate genome sequencing, and to provide the physical location of markers and genes for traits of interest
- Developing a high-throughput marker genotyping platform for cowpeas and using it for marker-assisted recurrent selection (MARS), and producing genetic maps
- Developing complementary DNA (cDNA) libraries for sweet potatoes, pearl millet, common beans, chickpeas and pigeonpeas, providing the first access to genic content in these species
- Establishing a 44K gene array in rice to undertake whole-genome expression and identify genes conferring tolerance to drought stress
- Identifying and validating markers for resistance to the major pests and diseases limiting crop yield in Africa's drought-prone environments, and using the markers in marker-assisted selection (MAS)
- Identifying and validating markers for tolerance to soil nutritional constraints in Africa and South Asia, including aluminium toxicity in sorghum, and salinity and phosphorus deficiency in rice
- Identifying and validating major QTLs for drought tolerance in rice (for India and China), wheat (for China), and legumes (for Africa)
- Developing and screening prebreeding germplasm for Africa and Asia, including translocation lines in winter wheat, and chromosome segment substitution lines in rice and groundnuts
- Implementing a phenotyping platform for GCP target crops, using geographic information system (GIS) tools to help select and characterise potential representative phenotyping locations
- Establishing a new helpdesk and support service to provide access to biometrics, bioinformatics and data management products and skills
- Implementing the GCP Informatics Platform providing access to rice crop information and to tools for quality checking, diversity analysis and functional genomics, as well as facilitating the integration of crop information to support future molecular breeding activities
- Releasing a new version of the Integrated Marker-Assisted Selection System (iMAS) with improvements including incorporation of the Comparative Map and Trait Viewer (CMTV)
- Developing the GreenPhylDB database for analysis of test sequences using the GreenPhyl Orthologous Search Tool (GOST) for phylogenomic analysis to facilitate comparative and functional genomics
- With the West Africa Centre for Crop Improvement (WACCI) at the University of Ghana, selecting and supporting two PhD candidates from among research communities working on GCP priority crops
- Enhancing the support offered to partners through the Genotyping Support Service (GSS) by establishing strong links to the new Bioinformatics and Biometrics Helpdesk
- Establishing a cassava community of practice (CoP) for Africa to create and maintain close links between developing country breeding programmes and the CGIAR Centres, other breeding activities and users
- Completing Phase I of the Workflow Management System (WMS) and initiating upgrades to enhance the integration, traceability and exchange of information on projects, collaborators, products and events
- Completing impact analysis research on rice improvement that reveals significant advantages of marker-assisted breeding (MAB) over conventional breeding approaches in terms of speed and cost

of affordable food. As well as supporting progress towards this first critical Goal, GCP contributes directly and indirectly towards the other MDGs.

At the level of the CGIAR, all GCP activities address one or more of the CGIAR System Priorities for 2005–2015.⁶ The characterisation of crop diversity is at the core of GCP's work, fulfilling System Priority 1A: *Promoting conservation and characterisation of staple crops*. This is fundamental to achieving Priority Area 2: *Producing more and better food at lower cost through genetic improvement*, which neatly describes GCP's own overall objective. GCP activities contribute to the overarching goal of Priority Area 2, particularly Priority 2A: *Maintaining and enhancing yields and yield potential of food staples*, and Priority 2B: *Improving tolerance to selected abiotic stresses*.

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 driven by technology, but rather by specific and local needs, be they for genetic and genomic resources, or for markers for specific breeding traits. In more concrete terms, during GCP Phase I, this has translated into the following key contributions to science:

- Analysing the diversity in germplasm collections for 21 CGIAR mandate crops, and assembling reference sets for these key food security crops.
- Incorporating genes from wild relatives to improve target traits in groundnuts and wheat, thus broadening the genetic base of cultivated varieties and increasing productivity.
- Developing new marker resources for less-studied crops, particularly legumes, and roots and tubers.
- Identifying several major genes to improve food crops, for example, genes for virus resistance in cassava, aluminium tolerance in sorghum and phosphorus uptake in rice.
- Identifying favourable alleles for crop performance using comparative genomics, quantitative trait loci (QTL) analysis and 'omics' approaches.
- Testing and validating elite alleles in adapted germplasm under local target conditions.
- Developing appropriate bioinformatics infrastructure, databases and analytical tools to facilitate data availability and access for the research community.
- Establishing genotyping, informatics and genomics platforms for breeders to access modern marker technologies.
- Increasing the capacity of breeding programmes in target environments to ensure GCP products will be adopted by primary users.

⁶ http://www.sciencecouncil.cgiar.org/fileadmin/user_upload/sciencecouncil/Reports/SCPriorities_prFinal_I-r_.pdf

To this end, GCP cultivates partnerships for innovative science and conducts research to improve understanding of the genetic basis of GCP target traits (see *Collaboration 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 have an impact on 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 that our research is intended 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 focal trait: drought tolerance, which affects almost all crops and all regions worldwide, thereby providing opportunities to apply discoveries across crops. As no single institution can command the breadth of expertise and resources necessary to achieve such a broad objective, 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 institutes and initiatives.

GCP partners are diverse and mutually complementary in their skills. This ensures seamless continuity of activities along the pipeline of GCP research, 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 three together for crop improvement.

Research in line with the GCP strategy

Evolution of Subprogramme activities through Phases I and II

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 internal and external 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,⁷ by 2013, GCP is expected to have contributed to achieving the following four 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. Generate and apply knowledge across crops, and demonstrate the potential of comparative genomics to contribute to plant improvement programmes.
4. 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 EPMP 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 the genetic diversity and genetic underpinnings of some important traits for drought-prone environments. As the Programme matures, gene and marker discovery is – as it should be – focusing more and more on drought tolerance, as clearly demonstrated in the different research themes of the last two competitive calls in 2006 and 2008.

With regard to the second objective above, GCP has developed genotyping, informatics and some genomics platforms for breeders to access modern marker technologies. The most recent target within this effort has been to develop a genomics platform, focusing on marker technology, particularly for less-studied crops. Such technology includes diversity arrays technology (DArT) for potatoes, chickpeas, pigeonpeas and *Musa*. Significant effort has also been devoted to sequencing, such as deriving information through bacterial artificial chromosome (BAC)-end sequencing (*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 for rice or cowpeas. However, this effort to generate genomic resources per se will decrease over time, as urgent needs in the area 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 applied by breeders to identify new parental lines for further crosses, and to improve the efficiency of their breeding programmes through marker-assisted breeding (MAB). These are just two kinds of product developed to date that illustrate the progress made towards achieving the third objective above. During Phase II, GCP will prioritise Programme-level trait–crop opportunities (see section below on *Seven Challenge Initiatives for more focus*), evaluate what the Programme can achieve,

⁷ <http://www.generationcp.org/brochure.php#strategy>

and more actively manage achievable high-priority product-oriented opportunities by ensuring a continuum of activities across the different Subprogrammes.

The implementation of this important strategy is already underway. For example, the year 2008 ushered in a set of new commissioned projects, whose design reflects the logical evolution of the GCP research trends described above.

Below are brief sketches on how this reorientation is being achieved within each Subprogramme:

- **SP1:** After the characterisation of the reference sets for GCP crops, several new projects will focus on phenotypic characterisation of those sets as well as developing new segregating populations with parental lines identified in the reference sets.
- **SP2:** A few projects will continue to focus on developing genomic resources in less-studied crops to complement and conclude efforts from Phase I. However, these are the last projects of this type; SP2 now aims to focus exclusively on discovering drought tolerance genes and QTLs for breeding applications.
- **SP3:** Compared to previous years, this Subprogramme evolved significantly in 2008, reflecting the flow of products primarily within – but also from – GCP. Thus, the SP3 budget allocation to commissioned projects rose by 50 percent to support the validation, in local target environments, of the increased number of markers identified by SP2, as well as new populations developed by SP1. With SP5, SP3 also undertakes capacity development to strengthen expertise for effective transfer of products and technologies to developing country programmes and breeders.
- **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 network infrastructure was fully functional by the end of Phase I in 2008. Individual partner databases are still being connected with the infrastructure to complete the platform. After this critical step, SP4 will focus on the development or adoption of research and breeding tools needed by GCP scientists. These tools – be they offered proactively by SP4 or requested by the scientists – will be accessible through the platform.
- **SP5:** The training and capacity-building component of this Subprogramme is increasingly oriented towards specific needs of ongoing GCP projects. To enhance impact on breeding in target environments and farming systems, SP5 ensures GCP products reach – and are deployed by – primary users. To help achieve this goal, a dedicated budget has been earmarked to finalise products for distribution within GCP and to the wider community. This involves ensuring that quality and packaging are adequate and

appropriate for targeted as well as broad distribution. The type of distribution will be determined by the nature of the product.

Seven Challenge Initiatives for more focus

As we approach Phase II, the clear need for us to more sharply focus our research portfolio is very timely. This is closely tied to improving the continuity and coherence of activities across Subprogrammes at both the design and implementation stage, all with the Programme vision in mind. In addition, this sharpened focus and renewed resolve both resonate well with the various reviews GCP underwent in the 2007–2008 period, especially the EPMR commissioned by the CGIAR Science Council. The central message on focus and impact from this first EPMR is encapsulated in two of its recommendations:

- **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).

These recommendations are very much in line with the thinking of the MT to further focus our research agenda on a few crop-and-region specific projects. These ‘mega-projects’ are termed Challenge Initiatives (CIs). The MT identified seven CIs through a consultative selection process. At the end of July 2008, the EB approved the implementation of the seven CIs that will receive a substantial portion of our research funds in Phase II. The initiatives will target the selected farming systems elaborated in the 2006 Annual Report, with specific focus on the following trait–crop combinations and regions:

Cereals

1. Improving drought tolerance in rice for Africa
2. Improving drought tolerance in wheat for Asia
3. Improving drought tolerance in sorghum for Africa
4. Comparative genomics to improve cereal yields in high-aluminium and low-phosphorous soils

Legumes

5. Improving drought tolerance in cowpeas for Africa
6. Improving drought tolerance in chickpeas for Africa and Asia

Root and tubers

7. Improving cassava yield in Africa's drought-prone environments

As currently conceived, each CI is a set of pre-existing GCP projects related to a given research topic. The challenge over the next half-year will be to collate and coalesce the projects across the Subprogrammes into a coherent and cohesive body of work, with a common workplan and clear impact indicators at the CI and Programme level. Such implementation will require significant adjustments over the next 12 months in both the scientific content and the management of our research portfolio (see *A two-dimensional management structure*). An example of a set of activities to be converted into a functional CI is illustrated in Figure 1 below. To further ensure focus for meaningful impact, each CI will have two or three pre-selected target countries, with anticipated spillover in the region beyond the actual CI target countries.

Better legumes for Africa: The Tropical Legumes I Project

In the first year of the Tropical Legumes I (TLI) project, considerable progress was made in building a legume research community in Africa, a very significant component being linking upstream researchers with those in the national programmes of target countries. TLI also has a website⁸ and a common landing page⁹ for the Tropical Legumes Project as a whole, developed in collaboration with Tropical Legumes II (TLII). As TLI's 'twin' project, TLII is primarily responsible for seed multiplication and distribution, thereby ensuring TLI research translates into products for breeding.

To reflect recommendations from the first project meeting in July 2008, activities on cowpeas, common beans and chickpeas were adjusted to develop populations for marker-assisted recurrent selection (MARS). Efforts were made to link with TLII

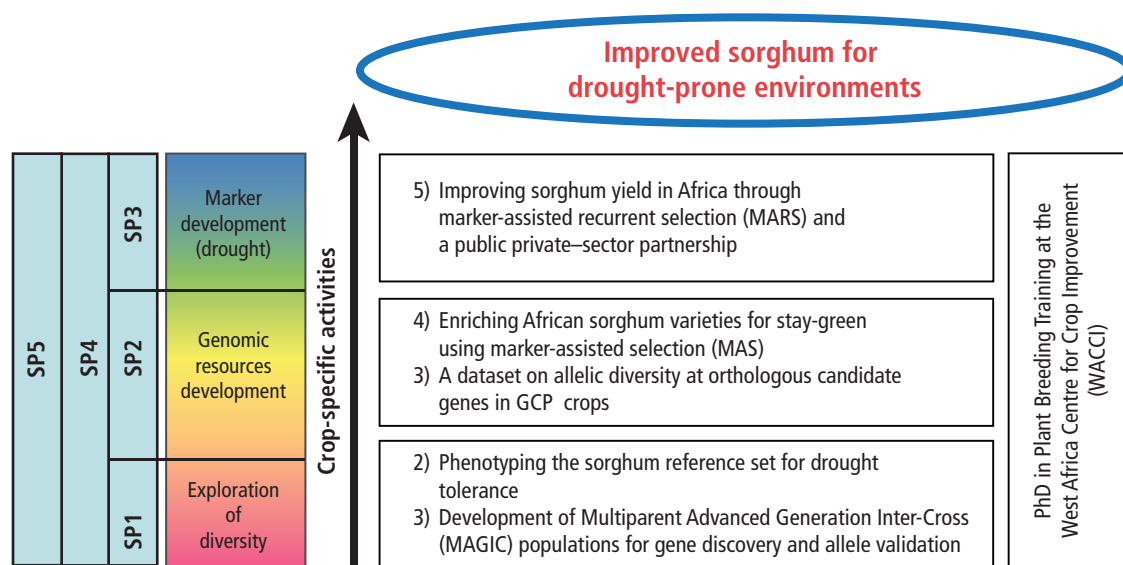
activities by encouraging communication between the PIs of both projects and, in particular, by encouraging TLII students to incorporate TLI research into their programmes.

Notable results achieved in 2008 include screening more than 300 groundnut genotypes for drought-related traits and disease resistance. To identify germplasm able to adapt to drought-prone sites in western Africa, 500 cowpea genotypes were characterised in Senegal, Burkina Faso, Nigeria and the USA (California). Several performed well under drought. For common beans, both the GCP reference collection and a set of regional and local varieties are being phenotyped for drought tolerance in eastern and southern Africa. Six new recombinant inbred line (RIL) populations were developed to evaluate drought tolerance in beans with an Andean background (ie, large-seeded). Analysis of 211 accessions in the ICRISAT core collection of chickpeas yielded a subset of genotypes with contrasting root traits. The GCP reference collection (305 lines) was evaluated for resistance to pod borer (*Helicoverpa armigera*) and about 25 genotypes were identified as less susceptible. These will be evaluated and selected for multi-site testing and breeding by national programmes.

Annual Research Meeting

The Annual Research Meeting (ARM) gathered together GCP project leaders, key partners and stakeholders to share experiences, compare notes and brainstorm on critical issues for the Programme to attain its objectives. The 2008 ARM was held in September in Bangkok, Thailand, kindly hosted by the National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand, with logistics superbly handled by Griselda Marquez, GCP's Executive Assistant.

Figure 1. Illustrating the Challenge Initiative concept – The case of sorghum in Africa



⁸ www.generationcp.org/gcptli

⁹ www.tropicallegumes.org

To reflect the stage that GCP has reached in terms of strategy implementation and focus, the theme of this year's ARM was, appropriately, 'Products and impacts'. Consequently, the presentations made at this ARM were designed to set the tone for discussions and interactions by having a more 'vertical' and pipeline-oriented emphasis. They were sequenced to trace the flow of products and research outputs within various GCP projects, and their ultimate impact – outside GCP – on developing country breeding programmes.

The 2008 ARM featured two brainstorming sessions on the two platforms that are to be established in 2009 – the Genetic Resources Support Service (GRSS) and the Molecular Breeding Platform (see *Establishing platforms for access, distribution and sustainability*). However, just as in Africa during the 2007 ARM, presentations were not limited to GCP research or researchers; this year's stakeholder session also brought in local voices and perspectives. GCP is particularly interested in engaging with small- and medium-scale enterprises (SMEs) in Asia to assure and enhance product delivery. Besides the regular poster session, the 2008 ARM also included a World Café to further enrich, deepen and broaden the discussions. This session was rated very highly by participants. The ARM presentations, poster abstracts, project updates and various rapporteur reports are all available online,¹⁰ and a summary of results from a participant survey will also be posted to the GCP website.

Resources and services

Bioinformatics: software and online services

GCP aims to provide strategic bioinformatic tools for data management. To this end, the Helpdesk on Bioinformatics and Biometrics¹¹ was launched in 2008. This online helpdesk provides expert support within two working days to scientists, linking them with the appropriate experts, tools or products from SP4. An informatics platform¹² for diversity analysis was also launched to support work in Subprogrammes 1 and 2. One other notable bioinformatic tool developed in 2008 was Version 1.4 of the software iMAS (Integrated Marker-Assisted Selection System). This version has been refined based on user feedback and enhanced with new features.

Capacity-building

In 2008, we continued our 'customer-adapted' approach to capacity-building, to harness the best of the diversity that characterises the GCP community and research portfolio.

¹⁰ <http://www.generationcp.org/arm.php>

¹¹ <http://www.generationcp.org/bioinformatics.php?da=08106902>

¹² <http://gendiversity.cirad.fr/Home>

¹³ <http://www.generationcp.org/sp5/>

¹⁴ <http://www.generationcp.org/sp5/?da=0794844>

¹⁵ http://www.generationcp.org/gen.php?da=08128238#gcp_mandate_crops

¹⁶ <http://www.generationcp.org/sp5/?da=08123058>

Three more developing country research teams benefited from the Capacity-building *à la carte* Programme,¹³ in addition to the six teams already on the programme.

Drawing on user feedback and lessons learnt from the pilot phase and the first call, we launched the second Genotyping Support Service¹⁴ (GSS) call in June. In so doing, we joined hands with the Global Crop Diversity Trust (the Trust) and the Global Partnership Initiative for Plant Breeding Capacity Building (GIPB), issuing a joint call for all three partners. The focus for the Trust was on phenotyping, for GCP on genotyping (extended to cover all the GCP mandate crops)¹⁵ and for GIPB on capacity-building. In this way, the three coordinated and complementary calls widened the scope of opportunities available to applicants since, together, they offer an all-round comprehensive programme.

Later in the year, SP5 also released three sets of learning materials on genetic resource policies, genomics and bioinformatics, all available on the GCP website¹⁶ as well as on CD-ROM. Four additional sets are in preparation on genetic diversity, marker-assisted selection (MAS), phenotyping and association genetics.

Product development and information management in the context of GCP products

Product validation and management

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 national programmes, but can also help identify contrasting lines for genetic studies in SP2. Similarly, it can point to lines with favourable alleles for desirable traits to be used as donor lines in MAS 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 seven 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 for molecular breeding
- vi) improved germplasm, and
- vii) learning materials.

Product management is essential to ensure optimal flow of upstream research outputs to more applied research within GCP. Several tools have been designed and implemented during Phase I to improve product management. New

templates have been developed to facilitate identification and further processing – as necessary – of outputs and products. A catalogue of products has been developed that now provides – for each product – background and other information necessary to take decisions about next steps, be they further processing within or outside GCP, transfer to other partners, validation or delivery. 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.

All of these product-related elements are now being embedded in a workflow system (see below) that facilitates access to information and its management. As a result, the flow of information and products, such as new protocols and technical tools, markers, germplasm, etc, across different GCP projects has been streamlined considerably. Based on this approach, there are now new connections between projects arising from the regional and thematic crop platforms. Product management activities have also allowed a global and rationalised selection and management of validation projects. Several commissioned projects are now conducted in collaboration with research programmes in Asia and Africa to evaluate and use markers, germplasm and protocols from upstream research projects.

Just as for project management, communication with research partners, follow-up of activities and product delivery, and on-site visits have proved to be key determinants of success, underpinning the capacity of GCP to generate, use, and disseminate research products. Product management has also further stimulated collaboration between Subprogrammes, which has in turn considerably enhanced product use. An increasing number of activities are conducted jointly between SP1 and SP3 for the evaluation of reference sets in target environments, and between SP2 and SP3 to identify and validate genes and markers by developing country programmes in target regions. Collaboration between SP3 and SP4 has also intensified for the collection, management and distribution of data that will be generated in increasing quantities. Finally, a close relationship between SP3 and SP5 has facilitated the incorporation of capacity-building components into projects to strengthen partner expertise and ensure the effective transfer of products and technologies to national programmes and breeders.

Establishing platforms for access, distribution and sustainability

GCP is acutely aware of the need to make GCP products available to the user community as indicated above, and to sustain their availability. In this regard, initiatives were designed to start in late 2008–early 2009 to make genetic resources

and marker technology more widely available to the breeding community. These include the following:

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, ensuring a certain level of quality, harmonising seed distribution and reducing costs.
2. **Molecular Breeding Platform:** This project is very central to 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: (i) molecular techniques; (ii) accurate phenotyping protocols; (iii) information systems; and, (iv) data analysis tools. It will integrate these components into breeding activities by providing flexible modular components that can be assembled in ways that match particular workflows.

In Phase II, GCP will continue its current effort to facilitate access to reference sets of germplasm and markers for target traits. These represent useful products that breeders can use to identify new parental lines for further crosses, and to improve the efficiency of their breeding programmes through MAB. The reference set and markers are just two kinds of product developed so far that illustrate the progress made towards achieving our objective to generate knowledge across crops, and to demonstrate the potential of comparative genomics for plant improvement.

The Project Development Guide

To complement and strengthen the Delivery Plan Kit (DPKit),¹⁷ in early 2008, we launched the Project Development Guide (PDG)¹⁸ – a web-based tool for project design and management. The development of the PDG was mainly funded by the Syngenta Foundation for Sustainable Agriculture.

Among the pioneer users of the PDG were applicants for our third competitive research call. Compared to previous calls, there was a notable increase in the quality of the proposals submitted, in terms of their relevance to GCP's mission. This improvement could be attributed to the PDG, in terms of the information, tools and checklists it provides. Also, in its very first year, the PDG appears to have already generated considerable user interest since, between the PDG's launch in early February and December 2008, the PDG website welcomed nearly 4,000 visits from 136 countries.

Workflow Management System

In 2008, we also began developing an information and workflow system to streamline our operations. This activity will continue into 2009. We anticipate that the Workflow Management System (WMS) will significantly increase

¹⁷ http://www.generationcp.org/sp5/?da=08122719#dp_kit

¹⁸ <http://www.generationcp.org/pdg>

internal efficiency in project reporting, while also enhancing information flow, knowledge sharing and knowledge management through a direct interface with the GCP website for information destined for the public domain. The WMS has six modules: proposal submission, project reporting, product repository, publications, contacts database and an events manager.

Data release and quality

One other key product that is implicit in the first six listed in the section above on *Product validation and management* 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 sets generated in SP1 for the different crops will be re-genotyped by an external genotyping facility. The exercise is to validate the quality of the molecular data generated using specific microsatellite kits. This will give both the scientists who generated the data and the GCP MT confidence that reference sets and related genotypic data can be distributed broadly for further genetic analysis.

GCP continues to meet its commitment to make available data from GCP-funded research as international public goods for public access at no cost. We do this through the online GCP Central Data Registry.¹⁹

Governance, management and staff

GCP governance: reforms and background Programme Steering Committee and Executive Board

Legally, GCP is 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 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),²⁰ essentially representing the institutional Consortium partners.²¹

GCP operates under:

- a legal Consortium Agreement²² that defines the legal and operational rights and obligations of institutional partners, including the host institute (CIMMYT);
- a Host Centre Agreement, to define and clarify the relationship between GCP and CIMMYT, and the respective responsibilities of each party; and,
- project contracts: a framework of contractual agreements covering the obligations of all Consortium and non-Consortium research partners for specific 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 approved the resolution to delegate most PSC responsibilities to a new governance body, the Executive Board²³ (EB). The seven members of the new EB were selected in April 2008 based on nominations by the broader GCP stakeholder community, including Consortium members and the GCP MT. Focus was placed on: (i) the independence of the EB 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 EB became effective on 1 June 2008, and members are listed in Box 2 below.

¹⁹ <http://gcpcr.grinfo.net/>

²⁰ <http://www.generationcp.org/psc.php?da=0781307>

²¹ See Appendix A and <http://www.generationcp.org/consort.php?da=0781248>

²² http://www.generationcp.org/UserFiles/File/Consortium_agreement_signed.pdf

²³ See Appendix B and <http://www.generationcp.org/whoware.php?da=08124404>

Box 2. GCP Executive Board members

No.	Name	Institute	Country	Expertise
1	Calvin Qualset (Chair)	University of California, Davis, USA	USA	Crop diversity, plant breeding
2	Andrew Bennett	Tropical Agricultural Association, UK	UK	Governance, intellectual property (IP), policies
3	Claudio Gonzalez-Vega	Ohio State University, USA	USA	Finance, rural development
4	Andreas Graner	Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany	Germany	Crop diversity, biotechnology
6	Jeff McElroy	Mendel Biotechnology, USA	USA	Plant breeding, seed enterprise
5	Esther Murugi Kahangi	Jomo Kenyatta University of Agriculture and Technology, Kenya	Kenya	Biotechnology, governance
7	Harold Roy-Macauley	World Agroforestry Centre (ICRAF)	Sierra Leone	Governance, plant physiology

On governance, despite establishing the EB, the current structure²⁴ is still not optimal because, from a legal perspective, the EB is only an advisory group to whose decisions the PSC has agreed to defer. This structure was adopted because, at the time, amendments to the Consortium Agreement required the unanimous agreement of the signatories, and it was believed unlikely that sweeping reforms on governance would muster the unanimous vote required to effect the reforms. In the meantime, the PSC retains the power to remove and replace any and all EB members.

It was also acknowledged that this governance structure still needs improvement from a process perspective and because it means that GCP will incur high transaction costs with two governance bodies. In fact, the EPMR 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”. In a similar vein, the European Commission (EC) review in 2008 supported the EPMR conclusions on governance, and went a step further to recommend that the process be speeded up, and the PSC dissolved.

Taking the foregoing into account, the PSC set up a Task Force (TF) to redefine its role, function and *modus operandi* in this new configuration. The TF evaluated several possible scenarios on how the PSC and the Consortium should evolve. In its report, presented at the December 2008 PSC meeting, the TF proposed that the PSC be replaced by a Consortium Committee. The TF also recommended, among other actions, modifying the Consortium Agreement to transfer all governance responsibilities to the EB.

The next step is for the PSC to revise the Consortium Agreement in the course of 2009 to align it with the actual current situation. A timeline for this revision was presented and approved by the PSC in its December 2008 meeting. Should the PSC approve the recommendation for its evolution into a Consortium Committee, this new committee will hold its first meeting in September 2009, around the dates of the ARM.

One recommendation, which the 2008 PSC meeting approved, was amending the unanimity clause. Prior to this amendment, any change to the Consortium Agreement required unanimity. However, this requirement has now been modified to approval by three quarters of the Consortium members, thereby providing more flexibility in amending the Consortium Agreement. This modification was a necessary facilitative step for revising the Consortium Agreement. The revised version of the Consortium Agreement needs to be approved by at least three quarters of the Consortium members. Institutes that

do not agree with the revised Agreement reserve the right to relinquish their Consortium membership, should they so wish.

Stakeholder Committee

In this period, while the entire GCP governance structure is under review, the EC, the Global Forum on Agricultural Research (GFAR) and GCP's MT also plan to revamp and revitalise the GCP Stakeholder 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 optimistic that a revamped functional SHC for Phase II should be in place in 2009.

Review and Advisory Panel

The Review and Advisory Panel (RAP)²⁵ has a dual function. On the one hand, it provides scientific advice on Subprogramme-specific issues directly to Subprogramme Leaders (SPLs). On the other, it plays an active advisory and legitimisation function in the selection of commissioned grants. In the light of these functions, and considering the fact that RAP members are nominated by GCP management, and also that no reporting relationship exists between RAP and the EB or PSC, RAP is then more of an extension of management than a governance body.

RAP consists of five scientists, with one assigned to each Subprogramme. It has virtual and in-person meetings and consults frequently with GCP management. In 2008, there was turnover in RAP membership reflecting, in part, turnover within the GCP MT. In May 2008, Peter Langridge and Rose Rita Kingamkono, RAP members for SP2 and SP5 respectively, both stepped down. Peter will now be more directly involved in GCP research activities, while Rose will focus more on her new, demanding, high-level responsibilities as Acting Director General of the Tanzania Commission for Science and Technology. We thank Peter and Rose for their dedication and service.

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.

²⁴ http://www.generationcp.org/pdg/?page_id=9#212

²⁵ See Appendix B and <http://www.generationcp.org/rap.php?da=0781418>

A two-dimensional management structure

Rationale

As pointed out in the recent EPMR and by the Science Council, our research portfolio can be improved by greater focus. With our original research approach, the Programme appeared to be rather opportunity-driven, and the end-product orientation not always sufficiently clear. Therefore, there is an increasing need to include a second dimension in our management matrix that will span the Subprogrammes. This new dimension must ensure that, once our end-products at Programme level and their corresponding impact indicators are identified, there is a management function that will guarantee that activities and resources across Subprogrammes will deliver those end-products.

Product Delivery Leader and Product Delivery Coordinators

The product- or crop-specific complementary management function above will be established through seven Product Delivery Coordinators (PDCs) who will oversee product delivery within each CI as a part-time responsibility. PDCs will report to the Product Delivery Leader (PDL), and will assist GCP management in operationalising and seamlessly integrating this complementary crop–farming system approach, since six of the seven CIs are both crop- and region-specific.

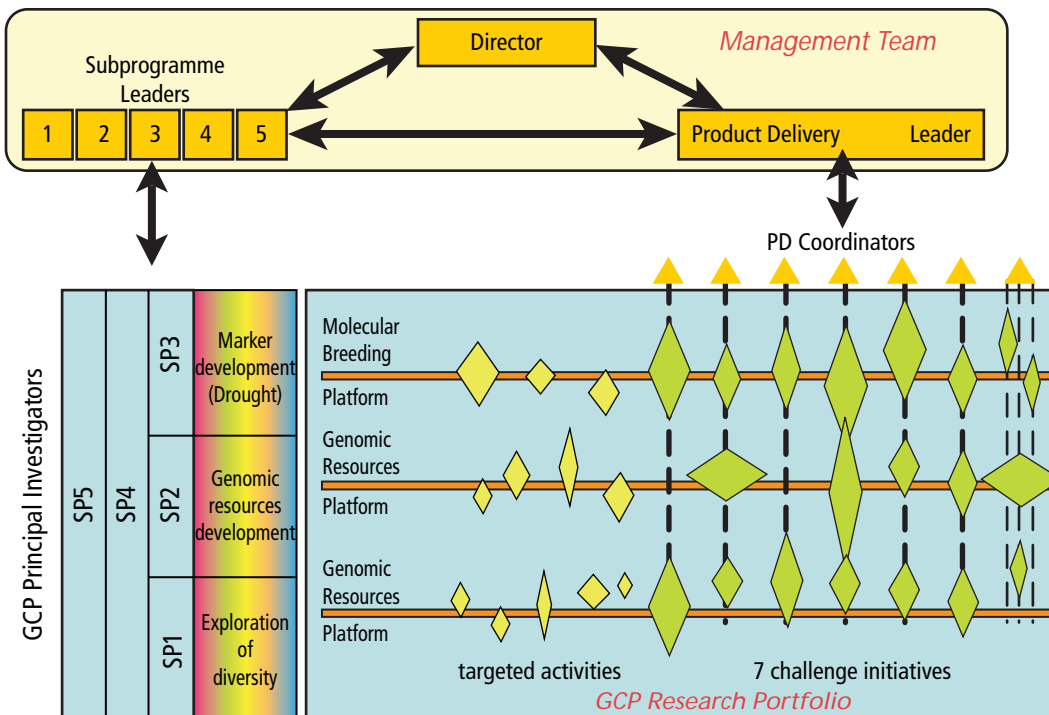
The PDL will provide leadership in the design and implementation of all GCP activities related to product delivery, ensuring the effective and sustainable marketing of

products, including packaging, promotion and dissemination to users. The main responsibility of the PDCs will be to manage and oversee the development and implementation of the delivery workplan within each CI, ensuring that impact indicators for each will be reached by 2013. PDCs will follow the progress of the different research activities across the Subprogrammes from a product delivery perspective, and both the PDL and the PDCs will interact with the MT on progress or adjustments to be made for each initiative to attain its milestones. In this two-dimensional matrix, the scientific management and the monitoring of GCP activities remain the responsibility of the five SPLs. The MT has a collective responsibility to stakeholders and funders regarding the scientific achievement and product delivery of the Programme (see Figure 2).

The PDL position is new, and we hope to have it filled by the second quarter of 2009. PDCs will champion their target trait–crop. Realistically, PDCs will ideally already be 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 CI they will manage.

The PDCs will be formally contracted to assume this management responsibility for approximately 10 percent of their time. All seven PDCs were identified by the end of 2008, and they are listed in Box 3 below. By April 2009, strategic meetings will be held for all the CIs. The MT will lead these

Figure 2. GCP's research management



meetings, assisted by the PDL (should the office-holder have been identified by then) and the PDCs. The major objective of these meetings between key scientists and a cross-section of stakeholders will be for each CI to:

- Draw up a workplan with clear milestone taking into account ongoing work within GCP, as well as in the external 'landscape' of the CI, beyond GCP. After review and approval by the MT, this workplan will be converted into a full proposal by mid-2009.
- Develop the corresponding product Delivery Plan in the second half of 2009 to ensure a cohesive concerted effort, with intermediate milestones and clear impact indicators to evaluate the performance of the CI before – and by – 2013.

Staff profile

In 2008, changes were made in our staff profile in keeping with the recommendations of the EPMR and the evolution of the Programme, and also due to natural staff turnover. A full listing of staff is provided in Appendix B.

Turnover

In June 2008, Theo van Hintum opted to step down from his position as SP4 Leader at the end of his term. Theo had steered SP4 in a half-time capacity since its founding in January 2004. Theo's departure was very much in the spirit and thinking – at GCP's founding – for SPLs to serve on a fixed-term tenure, and thus naturally facilitate periodic MT 'self-renewal', by rejuvenating the team with new blood and new ideas.

Theo now returns to resume full-time duties at Wageningen University and Research Centre (WUR) in The Netherlands. His dedication and high-quality service to the Programme over the last five years (2003–2008) were remarkable. As a pioneer member of the MT since the founding of GCP, his steadfast commitment to breaking new frontiers in building the GCP community and network went a long way in establishing and integrating a common channel of communication among the GCP bioinformaticians. Theo will continue to contribute his expertise as a GCP project PI.

Theo was replaced by Graham McLaren, who joined in September. Graham is not new to GCP: he is a senior scientist in bioinformatics previously working with IRRI and CIMMYT and was formerly Head of the joint IRRI–CIMMYT Crop Research Informatics Laboratory (CRIL). Graham brings a wealth of qualifications and experience in the field of international agricultural research and management, having headed biometrics and bioinformatics departments for the past 20 years.

Nosisa Mayaba, an Associate Scientist in SP5 and the TLI project, also left GCP in December 2008.

Strategic changes

The need for strong expertise in molecular breeding within the MT is becoming ever more apparent, given the increase in marker-assisted activities within our project portfolio, as well as the proposed Molecular Breeding Platform. This need will be addressed in the course of 2009.

Other changes in our staff profile to align with our strategy and priorities are presented in the previous section on *A two-dimensional management structure*, which outlines the roles of the new positions of a Product Delivery Leader and seven Product Delivery Coordinators.

Reviews and evaluations

External Programme and Management Review

The EPMR was commissioned by the CGIAR Science Council. The overall tone of the EPMR report, released in March 2008, was positive. Also, the CGIAR Executive Council (ExCo) reviewed the EPMR report at their May 2008 meeting in Ottawa, Canada and acknowledged GCP's good performance. The EPMR – GCP's first – was very opportune for the Programme, coming at a time when the Programme was stocktaking and reassessing research priorities and recommendations on governance. The objectivity and deep insights provided by the Review Panel were very useful, and the EPMR recommendations significantly helped accelerate ongoing governance reforms as well as crystallise research prioritisation.

Box 3. Product Delivery Coordinators

No.	Product Delivery Coordinator and home institute	Challenge Initiative
<i>Cereals</i>		
1	Nourollah Ahmadi, Agropolis–CIRAD, France	Improving drought tolerance in rice for Africa
2	Richard Trethowan, Plant Breeding Institute, University of Sydney, Australia	Improving drought tolerance in wheat for Asia
3	Oumar Niangado, Syngenta Foundation for Sustainable Agriculture, Mali	Improving drought tolerance in sorghum for Africa
4	Leon Kochian, USDA–ARS/Cornell University, USA	Comparative genomics to improve cereal yields in high-aluminium and low-phosphorous soils
<i>Legumes</i>		
5	Jeff Ehlers, University of California, Riverside, USA	Improving drought tolerance in cowpeas for Africa
6	Pooran Gaur, ICRISAT, India	Improving drought tolerance in chickpeas for Africa and Asia
<i>Root and tubers</i>		
7	Emmanuel Okogbenin, National Root Crops Research Institute, Nigeria	Improving cassava yield in Africa's drought-prone environments

In terms of research prioritisation it was recommended that, during Phase II, GCP needs to give more attention to prioritising Programme-level trait–crop opportunities, evaluate what the Programme can achieve, and more actively manage achievable high-priority product-oriented opportunities by ensuring a continuum of activities across the different Subprogrammes. How to implement this important strategy is described in the earlier section on *Evolution of Subprogramme activities through Phases I and II*.

Review by the European Commission

In their conclusion, the EC review team described GCP as “an exciting and worthwhile programme which has the potential to genuinely contribute to food security ... if its scientific objectives are achieved.” To this end, the review recommended a refocus on drought and scaling down of the initial scope of the Programme to specific crops and geographical regions. This review also endorsed EPMR recommendations on governance reform, with an additional recommendation that the reform be speeded up. The review recommended changes in management and reporting at project, Subprogramme and Programme level to more closely link technical outputs to product development, and ultimately to a Programme-level monitoring and evaluation (M&E) mechanism. GCP’s project-funding approach comprising commissioned, competitive and focus projects was described as having “promoted partnerships between public and private; developed and less-developed organisations that might not have been achieved using traditional funding mechanisms.”

The reports from both the EPMR and the EC reviews are online.²⁶

Communications

Given that one of GCP’s primary products is knowledge, the need for effective communication cannot be overemphasised, particularly as GCP increasingly turns to product promotion and dissemination in implementing the Programme’s strategy.

Operating as a virtual and global network presents both opportunities and challenges for GCP. Effective communication is vital, but we are also alive to the challenges that this poses, given that by nature and by definition, GCP is a diverse and highly geographically distributed community. Our broad spread and rich diversity do, however, have a downside in the challenge sometimes posed in terms of communication, and also in terms of the release and exchange of data. As a ‘learning organisation’, we meet this challenge in various ways. As one example, we design and disseminate resources, tools and templates for our researchers, and maintain an information-rich website.²⁷ We endeavour to keep the website up to date as a ‘living resource’ – a source and repository of information, resources and documents of interest to crop

scientists, the broader R&D community and the general public at large. In 2008, we augmented our online resources in collaboration with SP5, by adding the PDG and three sets of learning materials on genetic resource policies, bioinformatics and genomics. These materials²⁸ are also available offline on CD. We shall post additional learning materials online in the course of 2009.

Another way we tackle the challenge of distant communications is by aiming to provide very comprehensive information on the rights and obligations of researchers in GCP-funded projects at every stage of a project – and more so at the beginning through detailed contracts of agreement. A summary of GCP’s project management policies is online.²⁹

Publications presenting results from GCP-funded projects are a crucial indicator of research quality. They are important for the visibility of our work, while also serving as a useful independent criterion for evaluating the Programme. Regarding GCP publications, the EPMR report observed:

“It was apparent from the reviewed publications that the diverse partners are working together and recognise their respective contributions (through co-authorships). It is clear from the high quality of the journals in which most of the articles appear that the science being conducted under the auspices of the GCP is of a high quality and the outputs are recognised by peers.”

A notable website project in 2008 was tracking and compiling a list of GCP publications since the Programme’s inception, with the good support of our scientists. The full list of GCP publications tracked to date is online,³⁰ and a list of selected 2008 publications is provided in Appendix D. Where permissible, publications are also made available through our website.

The next step will be integrating publications into the Workflow Management System (WMS) under development, so that publications are linked to their ‘parent’ projects, and are also searchable by various fields such as geographical area, crop and trait, and not just by the traditional author–date categorisation.

Collaboration and partnerships

As we enter an era of concerted consolidation and continuity, and begin to reflect on what next after 2013 in terms of ensuring the sustainability of GCP’s research products, our newest venture in partnerships is to help establish crop and

²⁶ <http://www.generationcp.org/whoweare.php?da=08137524>

²⁷ <http://www.generationcp.org>

²⁸ <http://www.generationcp.org/sp5/?da=08123058>

²⁹ <http://www.generationcp.org/gen.php?da=0642324>

³⁰ <http://www.generationcp.org/research.php?da=0642451>

regional platforms to link national researchers working on the same crop and in the same region. These platforms are premised on a novel type of partnership closely linked to the validation phase in GCP research. In addition, to fulfil its mission, GCP continues to build and foster dynamic R&D partnerships in research, breeding and delivery, and we are interacting increasingly with the private sector. The full list of GCP partners in 2008 is provided in Appendix A. All GCP projects are collaborative efforts, and the majority involve multiple partnerships within and beyond the GCP Consortium. The full breadth of GCP's collaborations is evidenced in the boxes listing projects and partners in each Subprogramme report in the pages that follow (and also in Appendix C), while the PIs leading the projects are listed in Appendix B.

In collaboration with crop Centres of the CGIAR, GCP serves as a good channel for the private sector to distribute some of their material for genetic studies. To illustrate the point, in 2008, Syngenta donated to the Maize Functional Diversity Group approximately 7,500 near-isogenic line (NIL) populations, 200 kernels of seed per line, and the SNP marker data associated with the lines. This Group is a consortium of leading senior researchers in academia and research institutes, 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.

The role of the private sector in GCP, although still modest, is 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 for the benefit of the public sector.

In working with the private sector, we take a case-by-case approach to reflect the nature of each partnership. We 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, precocity and, ultimately, grain yield. In follow-up, so that public-sector research can also benefit from this breakthrough, a joint GCP–Syngenta project has already been initiated to apply this expertise to improve sorghum yield under water-stressed conditions in Africa. By drawing on Syngenta's expertise and genomic resources, the project will be an exemplar on how technology developed by the private sector can enhance public research and plant breeding in the developing world. In this scenario, scientists from Syngenta are active project partners, working alongside sorghum breeders in Africa.

Our engagement with Syngenta is not limited to the company. We also partnered with the Syngenta Foundation for Sustainable Agriculture (SFSA) on several initiatives in 2008. The role of private-sector foundations, such as SFSA, is critical for enabling the public sector to access particular technologies, especially in molecular breeding. As an example, SFSA facilitated access to Syngenta technology for the sorghum MARS project above. The Foundation also facilitated the sharing and exchanging of complementary information between Syngenta and GCP researchers. Our collaboration included designing and co-funding the PDG. In addition, the partnership has also resulted in yet another in-kind contribution in terms of staff-time for the PDC for the sorghum CI (see *A two-dimension management structure* above).

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 ARM to present their perspectives at the stakeholder session and provide pointers for exploring potential collaboration with GCP. In 2008, we used the same model to tune into local stakeholder issues in Asia – an equally important region. The niche of SMEs is quite different, and the idea behind the collaboration is to more widely disseminate GCP tools and value-added germplasm.

SMEs are an excellent channel for reaching small scale-farmers. In India, through the Barwale Foundation, contact has already been established with the Indian Foundation Seed and Services Association (IFSSA), which the Foundation supports. Significantly, the Barwale Foundation participated in, and made a presentation at, the 2008 ARM. With this engagement, and through the contacts initiated and sustained, we expect GCP to have an impact on seed production in India. In addition, GCP's third call in 2008 for competitive research ushered new partners into our network, particularly in Asia. These included the Agharkar Research Institute (India) and the Bureau of Rice Research and Development (BRRD, Thailand) who are each leading a new competitive project.

In the area of partnerships, as elsewhere, we continue to demonstrate a capacity to adapt our structures and *modus operandi* in response to experience and feedback. The working partnerships illustrated above validate the GCP model, which results in strengthened and diversified collaboration. 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.

Subprogramme summaries

Subprogramme 1: Crop genetic diversity

SP1 explores the genetic and phenotypic diversity in the vast pool of crop germplasm available globally, to provide breeders and crop researchers with information on, and access to, that diversity. The work places particular emphasis on collections managed by CGIAR Centres and national programmes. In 2008, the first of SP1's five Themes addressing the structure of diversity saw the completion of molecular characterisation for all but one of the GCP crops. The data were used to identify germplasm reference sets to be made available as a global public good in the form of stabilised genetic stocks. To this end, SP1 formulated plans for future production of seed of reference sets and for distributing key germplasm. Theme 2 concerns the high-throughput genotyping techniques essential for optimal use of gene pools. In 2008, work focused on expanding the use of DArT marker technology, providing insights into the evolution and gene pool structure of target crops. The third Theme aims to develop a platform for describing drought tolerance. The platform's phenotyping sites were upgraded in 2008. SP1 also adapted and tested crop models to support phenotyping and held a workshop to review application of the models and plan follow-up work. Progress was made in phenotyping eight crop reference sets for drought-related traits. Theme 4 provides genetic information that will help identify favourable alleles at target loci to facilitate molecular breeding, with notable advances in 2008 in association studies on maize. Finally, Theme 5 explores novel approaches to promote the continued contribution of collections to crop improvement, making particular progress in developing interspecific base-broadening populations for several crops.

Subprogramme 2: Genomics towards gene discovery

SP2 aims to provide an environment within which genomic tools and knowledge can be used to dissect the mechanisms governing adaptation – especially to drought – and improve knowledge of gene systems across crops. The first of SP2's four Themes supports the assembly and development of genetic stocks. There was particular progress with tropical legumes in 2008, including the development of a large number of ESTs, SSRs, SNPs and BAC libraries, and creation of genetic and physical maps. These are being used to identify markers for stress tolerance or resistance. Theme 2 takes a cross-species approach to developing common markers, genetic maps and genome-wide infrastructure, with a focus on neglected

crops such as *Musa*, cassava, pearl millet, sweet potatoes and pigeonpeas. Among the achievements recorded in 2008, about 500 orthologous genes were identified in tropical legumes and almost 30,000 BACs were fingerprinted to develop a physical map for cassava. Theme 3 applies genomic tools to understanding genotype–phenotype links, and has established a transcript profiling platform. The resources developed include a 44K gene array in rice to identify genes conferring drought tolerance. The final Theme in SP2 focuses on identifying and validating useful genes/QTLs, such as those for salt tolerance and phosphorus uptake, for delivery to breeding programmes. A number of activities were initiated late in 2008, including work to validate and introgress stay-green QTLs identified in Australia into drought-sensitive African sorghum lines, and to validate root-trait QTLs in chickpeas to help develop drought-tolerant varieties in Africa and Asia.

Subprogramme 3: Trait capture for crop improvement

SP3's objectives are to validate candidate genes on genomic regions of interest in target environments and adapted germplasm, to develop means of optimising MAS (simple traits) and MAB (complex traits), and to expand and support phenotyping. The Subprogramme aims to build teams to link research innovations to developing country breeding programmes, through work structured around four Themes. The first Theme focuses on characterisation to help understand the genetic basis of disease resistance and drought tolerance in GCP crops. Products include genomic regions associated with target traits and prebreeding germplasm for delivery to breeders, such as groundnut backcross populations and introgression lines obtained through collaboration between Agropolis–CIRAD and ISRA. Theme 2 aims to develop and evaluate new breeding technologies. Accordingly, SP3 has supported the development of a phenotyping network, and has developed and applied simulation tools to facilitate the use of QTLs in MAS for several cereals. This Theme also promotes novel approaches to evaluation, such as work carried out in 2008 to phenotype the chickpea reference set and genotype it with DArT markers. The third Theme seeks to validate alleles and markers in adapted germplasm, thereby adding value to existing GCP products. Achievements in 2008 include identifying markers for tolerance to salinity and phosphorus deficiency in rice, and initiating their validation in Bangladesh and Indonesia, respectively. The final SP3 Theme promotes the application of molecular markers in breeding

programmes, with increasing emphasis over time on abiotic stresses, especially drought. Work in 2008 applied MAB to rice and wheat in Asia, and to rice, maize, sweet potatoes and tropical legumes in Africa.

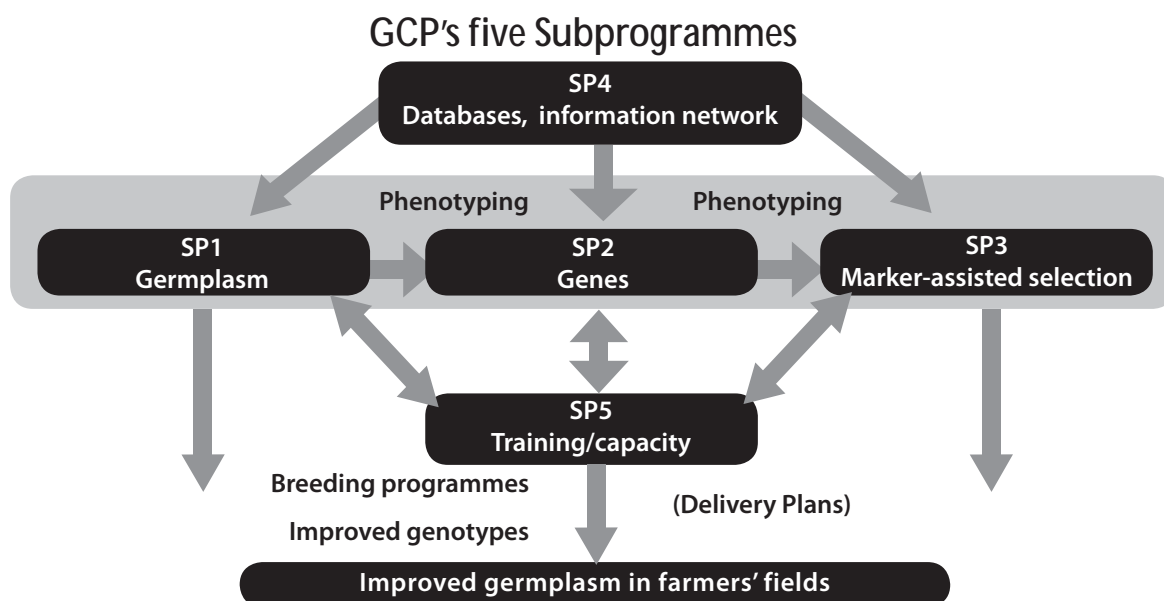
Subprogramme 4: Bioinformatics and crop information systems

SP4 aims to ensure the effective management of GCP data through linking and integrating information and tools into a coherent information platform. The work of SP4 falls into three Themes, the first of which addresses infrastructure, including standards, guidelines and facilities. A GCP domain model covering all relevant data types was completed and published during 2008. Progress was achieved in providing methodologies for developing and maintaining ontologies, as well as developing ontologies for four crops. Work continued on training GCP scientists in the use of the Central Registry and in providing templates for data entry. Theme 2 is concerned with data quality and the accessibility of data and tools. Analyses of GCP project data confirmed the need for quality improvement. In 2008, development of the GCP Informatics Platform focused on improving efficiency in accessing data sources and enhancing the workbench of query, visualisation and analytical tools. There was progress in making high-performance computing available to GCP scientists, and ICRISAT's Laboratory Information Management System (LIMS) was upgraded to support high-throughput genotyping services. Two collaboration platform tools, CropForge and the GCPWiki, were also maintained and supported. Theme 3 focuses on services to GCP and the wider community. A helpdesk was launched in 2008 to provide access to informatics tools and expertise in bioinformatics and biometrics. Specific support was also provided on experimental design and statistical analysis, and on comparative genomics and

expression array analysis. In addition, a new version of the software Integrated Marker-Assisted Selection System (iMAS) was issued during the year.

Subprogramme 5: Capacity-building and enabling delivery

SP5's work to build technical capacity and facilitate the flow of products from research to delivery falls under five themes. The first Theme aims to develop training resources and create a cadre of trained scientists. Two training courses and one workshop were held in 2008. Three sets of training materials were completed and made available to users, with progress on several others. Theme 2 focuses on building capacity among developing country scientists to further GCP's aims. In 2008, five research fellowships were awarded and five travel grants enabled recipients to train in advanced laboratories. Twelve travel grants supported participation by Asian scientists in the 2008 ARM in Thailand and by Latin American scientists in the TLI annual meeting in Senegal. Three awards were made within the Capacity-building *à la carte* programme, which endeavours to strengthen developing country partner teams. Advanced training in African universities was furthered through selecting and supporting four PhD students, as well as financing a professor position in molecular breeding. Within SP5's third Theme on product delivery, 2008 saw the testing and launching of the Project Development Guide, the initiation of a project to support Delivery Plan development, and the launching of a community of practice for cassava. Theme 4 provides support services and, during the year, continued to assist GCP partners through helpdesks, the Genotyping Support Service and the development of a molecular marker toolbox for use in MAS. The final Theme is on Programme-level impact and, in 2008, studies of rice and cassava improvement demonstrated the advantages of MAB over conventional breeding.



Subprogramme reports

Subprogramme 1: Crop genetic diversity

Rationale

SP1 is devoted to exploring the genetic structure and associated phenotypic variation in the vast range of crop germplasm available through GCP's network of Consortium members and partners. Particular emphasis is placed on the germplasm collections in the custody of the CGIAR and national programmes. In this way, SP1 seeks to provide the community of breeders and other scientists with germplasm samples selected for diversity and representativeness, and characterised as thoroughly as possible, recognising that access to such diversity is the foundation for all breeding activities. In addition, SP1 aims to establish standards that will serve as a reference for connecting and integrating future efforts within the global community, thereby mobilising a wide range of expertise and facilities. As GCP moves from Phase I to Phase II, an extensive molecular characterisation effort is coming to an end, its results complemented by validation of a subset of data to serve as a reference for the future. SP1 is also purifying seed for producing genetic stocks. An organisational and institutional arrangement is being established that will be part of a Genetic Resources Support Service (GRSS), integrated into the GCP Molecular Breeding Platform (see *Introduction and highlights*).

In parallel with this research, SP1 undertakes activities that contribute data and simultaneously consolidate capacity within GCP, as well as providing access to external facilities. This includes the exploration of new marker systems, integrated with developing and optimising phenotyping capacities in relation to drought. The research will yield a biological understanding of diversity and of the genetic and functional architecture of adaptation.

SP1 also coordinates various exploratory approaches, building on new types of population and new analytical methods that enable the production of genetic information or the contribution of adapted germplasm for breeders. Products range from interspecific hybrids to incorporate – or finely introgress – new genes (alleles) into crop varieties, to multiparental populations among cultivars made in order to reshuffle allelic associations. The choice of crops for this activity is closely linked to ongoing Programme-level prioritisation.

Major achievements in 2008

During 2008, SP1's most significant achievements were as outlined below.

- **Molecular marker analysis of germplasm diversity:** This analysis was completed for foxtail millet; work on faba beans is still pending due to inadequate marker quality. The effort focused on data compilation and aggregation across laboratories, and on data analysis. Data quality was assessed using global methods proposed by SP4; these methods highlighted uneven standards of data curation and scoring precision. Nevertheless, data analysis resulted in coherent descriptions of germplasm structure in agreement with established features of the species. In most cases, novel information was retrieved, highlighting new features and yielding new insights on crop domestication.
- **Setting the foundation for certified genetic stocks:** A scheme for validating core data was implemented; representative materials were selected and used to set the basis for reference genetic stocks, and to extract DNA for data validation. By the end of 2008, eleven crops had been characterised using this scheme. Current schemes of seed multiplication were reviewed and guidelines were formulated for rigorously developing genetic stocks, in order to minimise seed heterogeneity and maximise comparability between distinct characterisation efforts. Depending on the crop, the review confirmed current practices, or indicated a need for new extraction of genotypes for founding the stocks.
- **Distribution of reference sets:** Reference germplasm sets were developed for most GCP crops and made available or prepared for seed distribution. Depending on the individual user perspective, the reference sets serve to represent the main components of the germplasm, to analyse multiple correlations as a window on the broader collections, to assess diversity in representative comparable panels for access to favourable alleles, or to diversify the crop through prebreeding. A wide cross-section of the user community was consulted in order to define partner expectations of the potential value of these reference sets, and to discuss their distribution.

- **Use of reference samples for exploring novel populational approaches:** Several studies contributed to an enhanced understanding of factors involved in crop evolution, such as emergence of crop neodiversity during domestication, evidence for admixture and introgression in some compartments, and comparison between allele phylogenies and population structure. These will help provide the basis for innovative pathways for germplasm characterisation and exploitation.
- **Base-broadening through distant crosses:** Projects in rice, barley and groundnuts continued to advance, producing progenies with breeding value and high information content. A project on wheat has just started involving the use of emmer and, within a narrower base, efforts to produce multiparental progenies among cultivars in rice and sorghum are beginning to yield results.

Activity report

The activities conducted within SP1 are organised in five Themes, each divided into several projects. These are shown in Box 4, along with a listing of partners involved in SP1 activities during 2008.

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

SP1 has led the production of massive datasets featuring simple sequence repeat (SSR) diversity (12 to 50 loci) among large germplasm samples (300 to 3,000 accessions). Molecular characterisation has been completed for all crops except faba beans. Data have been delivered and, in most cases, used for identifying reference sets. These data are being assessed for quality with a view to releasing 'GCP-certified' datasets, using the best easy-to-use markers that also have a representative resolution power for describing germplasm structure. This has led to a major GCP product, namely the germplasm reference sets, accessible as a global public good in a robust form. These sets are meant to 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. Seed management requirements for founding stable genetic stocks were assessed during the year, and a roadmap was drawn up for producing seed of reference germplasm for subsequent distribution.

A joint SP1–SP5 workshop took place in November 2008 involving partners in GCP projects, plus germplasm managers and plant breeders from various institutes. This has set the stage for designing a cohesive distribution system for key germplasm, with a specified role for GCP. At the same time,

methodologies for accessing genetic diversity in large collections have been explored involving geographic studies in maize and linkage disequilibrium (LD) assessment in rice. For the latter, single nucleotide polymorphism (SNP) data have been produced (1,446 SNPs x 839 accessions) and made available to various data analysis teams analysing introgression patterns between different germplasm compartments.

Theme 2: Development of a range of flexible high-throughput genotyping techniques accessible in reference laboratories

Accurate and high-throughput characterisation is crucial for efficient germplasm exploitation, either by genotyping with diverse markers, or by evaluating material for behaviour under drought stress. These two aspects converge when the two types of data are compared for association studies. Current efforts are expanding the number of crops that benefit from diversity arrays technology (DART) markers; they include expanding arrays for bananas, coconuts, chickpeas, pigeonpeas and potatoes, and developing new arrays for yams, groundnuts and pearl millet. In the case of bananas, this research is supporting high-density genetic mapping as a contribution to a *Musa* genome sequencing project initiated by the Agence nationale de la recherche (ANR), France. Sorghum has been used for an accurate comparison among markers, showing the respective advantages of DARTs versus SSRs versus restriction fragment length polymorphisms (RFLPs).

Early efforts on allele resequencing have led to the formation of a community of practice (CoP) with gene specialists looking at orthologous genes across species, plus crop specialists looking at diverse genes for their specific crops. A project launched in 2006 conducted sequence analysis on six candidate genes for drought tolerance and seven target crops (rice, barley, sorghum, beans, chickpeas, cassava and potatoes). Several types of gene (*ERECTA*, *DREB*, *SS*, *SPS*, *ASR* and *INV*) were surveyed using specific and generic primers. In 2008, some 16Mb of sequence were produced across 80 genes, providing insights into gene family evolution and crop phylo-ecogeographic organisation. Some significant patterns await comparison with phenotypic data. This approach could be applied to new GCP priority crops and new candidate genes identified by SP2.

Box 4. SP1 Themes, projects and partnersLead partner(s) underlined, where applicable. Full names of partners in *Acronyms and abbreviations***Theme 1.** Creation of an improved understanding of the structure of the diversity for the major world food crops

1. Structure of genetic resources for the most advanced (tier-1) crops accurately described (including tools) and summarised in a reference sample
Agropolis–CIRAD, BI, CAAS, CIAT, CIMMYT, CIP, ICARDA, ICRISAT, IITA, IRRI (multiple PIs)
2. Structure of genetic resources for the less advanced (tier 2- and 3-) crops accurately described (including tools) and summarised in a reference sample
ICRISAT
3. Global assessment of linkage disequilibrium in the genome of rice conducted
IRRI, Agropolis–CIRAD, Agropolis–INRA, CNG
4. Detailed analysis conducted of maize diversity after migration out of America
CIMMYT, Agropolis–INRA, CAAS, DoA–Indonesia, IARI, ICAR, IITA, KARI, NMRI, NSFRCRC
5. Genotyping data validated for the reference samples and the reference markers for all GCP crops
Agropolis–CIRAD, ADNid (service provider/collaborator), BI, CIAT, CIMMYT, CIP, ICARDA, ICRISAT, IITA, IRRI
6. Seed of reference germplasm readily available for all crops
Agropolis–CIRAD, BI, CIAT, CIMMYT, CIP, ICARDA, ICRISAT, IITA, IRRI
7. Methodology developed for resampling genetic diversity in large germplasm collections
IRRI, EMBRAPA, ICARDA, ICRISAT

Theme 2. Development of a range of flexible high-throughput genotyping techniques accessible in reference laboratories

8. DARts validated as a genome-wide molecular characterisation technology
Agropolis–CIRAD, BI, DARt P/L (service provider/collaborator) (multiple PIs)
9. Ecotilling assessed as a gene-targeted molecular characterisation technique
IRRI, Agropolis–CIRAD
10. Methodology developed to assess SNPs with effect on allele expression
ICARDA, TU, UdU, UoAd
11. DARts developed as a genome-wide molecular characterisation technology for crops with little sequence information
Agropolis–CIRAD, Agropolis–IRD, CIP, CRI–Ghana, DARt P/L (service provider/collaborator), ICRISAT, IITA (multiple PIs)
12. Database developed on allelic diversity at candidate genes across species (ADOC)
Agropolis–CIRAD, Agropolis–INRA, CIAT, CIP, CNG, ICARDA, ICRISAT, IRRI

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

13. Set of phenotyping facilities in Brazil made accessible for GCP germplasm evaluation
EMBRAPA
14. A crop and whole-plant modelling framework developed to support assessment of tolerance to drought
Agropolis–CIRAD, CSIRO, Pioneer, UoQ (multiple PIs)
15. Phenotyping capacity accessible to the GCP is inventoried
BI
16. Drought-related phenotyping of specific populations with high-quality molecular information implemented and Phenotyping Support Service consolidated (rice, sorghum, wheat, maize)
Agropolis–CIRAD, Agropolis–INRA, BIOTEC, CIMMYT, CRRI, ETH, ICRISAT, IER, INRA–Morocco, ISRA/CERAAS, IGKV, IRRI, KARI, NPGRC, TNAU, UAS (Dharwad), WARDA (multiple PIs and partner teams)

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

17. Favourable genetic factors for drought tolerance in maize identified
CIMMYT, Agropolis–INRA, CU, Genaisance (service provider/collaborator), KARI, NSFRCRC, SAU, SIRDC (multiple PIs and partner teams)
18. Favourable genetic factors for drought tolerance in rice identified
IRRI, Agropolis–CIRAD, WARDA, IGKV, CRRI, TNAU, BIOTEC
19. Favourable genetic factors for stress tolerance in four legume species identified
(*synthesis activity, with various lead partners*) *UoC (Davis), ARI–Naliendele, ART, CBI, CIAT, CRS, ECABREN, EgU, EIAR, EMBRAPA, EMU, ICRISAT, IIPR, IITA, INERA–Burkina Faso, INRAN, IRAD, ISRA, LZARDI, SARI–Ethiopia, SABRN, UCB, UGA, UoC (Riverside)*
20. Genetic factors underlying aluminium and drought tolerance in sorghum and maize identified
USDA–ARS, EMBRAPA, CU, MU

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

21. Base broadened of current crop diversity in rice using related species
CIAT, Agropolis–IRD, CU, EMBRAPA, Fedearroz, WARDA
22. Populations for multiple allelic segregation developed in rice and sorghum through multiple parent intercrossing
IRRI, ICRISAT, NIAB (multiple PIs and partner teams)
23. Populations for multiple allelic segregation developed through nested intercrossing in rice
CIAT, Agropolis–IRD, WARDA
24. Linkage disequilibrium and patterns of selection in the genome of sorghum used for mapping useful genes
Agropolis–CIRAD, DARt P/L, IER
25. Base broadened of current crop diversity in rice using interspecific bridges with African rice
Agropolis–IRD, CIAT, Fedearroz, IER, INERA–Burkina Faso, PAU, PhilRice, UoA, WARDA
26. New alleles introgressed from wide crosses using crop wild relatives in barley
SCRI, ICARDA, INIA–Chile, OSU, UdT, UoC (Riverside)
27. New wheat germplasm generated with broadened AB genome diversity
ARI–India, CIMMYT, PARC, UAS (Dharwad), UoS

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

Phenotyping for drought tolerance is a major challenge, both in terms of facilities and expertise and in terms of integrative phenotypic modelling. Facilities have been upgraded in Brazil's network of breeding and agronomy stations at EMBRAPA (Empresa Brasileira de Pesquisa Agropecuária; the Brazilian Agricultural Research Corporation). This Brazil platform encompasses two centres of excellence and five reference sites, for which climatic conditions and soil physical and chemical properties have been carefully characterised, and the soil spatial variability of the site-specific areas has been determined. Irrigation systems have also been installed and evaluated, along with water flow rate and water management monitoring devices.

Phytosanitary constraints to germplasm movement have hampered broad use of the platform; the first trials hosted were done with local materials and designed to support the development of models. A detailed target population of environments (TPE) characterisation has been completed for rice and maize in the Brazilian cerrados. Trials have helped improve crop models in the APSIM (Agricultural Production Systems Simulator) platform, thus making it possible to virtually explore the effect of QTLs on yield across a wide range of drought patterns. The whole-plant growth model ECOMERISTEM has been adapted and successfully tested for its capacity to assist high-throughput phenotyping on rice. The results were discussed in detail at a workshop hosted by Pioneer Hi-Bred International, Inc in February 2008, and have generated recommendations for follow-up work. In order to expand the range of capacities, drought tolerance experts visited existing phenotyping sites and reported on the potential role of the sites in a global platform, the coordination of which has been transferred to SP3.

Practical drought-related phenotyping of GCP germplasm reference sets has been undertaken for chickpeas, cowpeas, groundnuts and common beans within the framework of the Tropical Legumes I (TLI) project. Other crops for which this has been initiated – with respective activity coordinators in brackets – are: sorghum (ICRISAT), rice (IRRI), and wheat and maize (both coordinated by CIMMYT).

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

Theme 4 aims to provide information to support the development of molecular breeding. Association studies on maize concluded in 2008. Two years of field data and

metabolite data are now available, and 350 inbred lines have been analysed for 1,536 SNPs, half of which are borne by candidate genes. Many associations involving some 30 genes were unearthed and are being finely analysed. Similar studies will be undertaken rice and sorghum, followed by legumes. Rice 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. An effort on aluminium tolerance, which led to the successful identification of a major gene in sorghum, is being extended. Characterising a complete association panel in sorghum and maize for aluminium tolerance and drought tolerance will give access to a broader range of alleles, and is likely to highlight comparable and complementary mechanisms in the two crops and the two traits.

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

This Theme carries germplasm research beyond the release of reference samples, and will ensure continuous input from germplasm collections. One approach, based on existing germplasm, consists of delineating subsets with high LD, which will contribute information comparable to that from association studies. LD has been assessed in sorghum using physically mapped DArT markers and global germplasm, as well as regional germplasm from Mali. LD only appears to be strong at the 10kb scale and to completely disappear beyond 1Mb. Phylogeographic analysis reveals the existence of neodiversity that emerged during domestication.

Another approach consists of producing new populations bearing higher allele richness rearranged in new combinations, either through multiple parent populations, or through wide interspecific crosses. First generation crosses have been made for producing multiple parent segregating progenies rice and sorghum, counting at least two populations with 1,000 inbred lines each. In addition, first generation hybrids have been produced through nested intercrossing in rice; the focus is on African germplasm but the findings are also relevant to Latin America and the Caribbean.

As a flagship activity, rice chromosome segment substitution lines (CSSLs) developed at CIAT (Centro Internacional de Agricultura Tropical; International Center for Tropical Agriculture) with the participation of Agropolis-IRD (Institut de recherche pour le développement, France) and EMBRAPA are at the initial stages of distribution to rice specialists and breeders worldwide. CSSL production was most advanced with *O glaberrima*, consisting of 4,200 individuals

representing 54 BC₄F₂ families. Progenies with *O meridionalis*, *O rufipogon*, *O barthii* and *O glumaepatula* are at the BC₂ or BC₃ generation. Genotyping and field testing will continue in 2009. Other rice interspecific hybrids as well as barley interspecific backcrosses are being advanced further. The production of new wheat germplasm with broadened AB genome diversity began in late 2008.

Lessons learnt

The main product of SP1 activities is the reference sets offered to the global community as material for compiling information through integrated characterisation efforts in the future. The large body of data that was used for identifying these reference sets contains a wealth of information, but these data also have certain limitations. They are of uneven quality, as detected by simple coherence indicators within genotyping data. In most cases, this could be corrected by proper curation but it demonstrates, yet again, the time pressure that most scientists work under, making it difficult for them to devote sufficient time to analysing their own data. With the help of SP4, GCP has mobilised scientists through workshops to establish mechanisms for data quality management in their laboratories. Also, analyses are currently being repeated and GCP-certified data on the GCP Central Registry are being distinguished from unscreened data deposited directly by the source laboratory. To complement these efforts, SP1 is promoting data analysis by providing scholarships for students to work under the supervision of senior scientists whose time is also being funded.

Management of the seed of reference GCP materials requires very close attention and sustained commitment. This will involve parties who will undertake the mission of verifying, conserving, multiplying and distributing the seed, while applying the highest standards of quality control. All materials are heterogeneous at the starting point and, generally, can only be made more homogeneous by selfing. Moreover, diversity arises over time by mutation. Thus, from the outset, it would be unrealistic to expect pristine purity or total stability. However, notwithstanding these realities, the resources need careful curation in order to minimise drift, screen the best data, and incorporate complementary diversity when it is identified.

Difficulties in attaining the goal of quality data have, in some instances, delayed important research. One such example is the work aimed at using the reference set descriptions to provide pointers for further enrichment through targeted exploration of the wider collections. Sometimes, the achievement of research milestones is also hampered and delayed by the management complexities of mutually

dependent cross-institutional projects, which are part and parcel of the collaborative research and community-building that typify the GCP approach.

Conclusions, and perspectives on 2009 and Phase II

In 2008, progress was recorded across the range of activities within SP1, with especially significant advances in the first massive association study in maize and the development of genetic base-broadening populations, which is advancing for several crops. A major priority for SP1 remains the validation, management and use of the reference sets identified for each crop. These reference sets are meant to help 'READ' germplasm, that is, to ensure Representation of genetic structure, and to help Enter the broader collections, Assess donors of genes and alleles, and Diversify the foundation of the crop.

The experience and lessons learnt during the course of Phase I make it clear that, understandably, mobilising a broad range of partners in an effort that includes several steps and diverse technical capacities yields an invaluable – yet imperfect – product. Given the essence of biological diversity, perfect representativeness is an unattainable ideal. All the same, we realise that the germplasm reference sets identified and validated through SP1 constitute a valuable resource that both requires and merits curation.

Several joint studies with SP4 have shed light on data quality and have provided guidelines for priority activities. A collective discussion facilitated by SP5 has helped refine future perspectives by setting priorities, prescriptions and directions. Thus, the reference sets:

- Fill a clear gap in global germplasm management, in coordination with partners such as the Global Crop Diversity Trust, and with initiatives such as the Global Public Goods Phase 2 project of the GCIAR System-wide Genetic Resources Programme (SGRP).
- Require a collective approach for efficient and effective distribution.
- Need curation to optimise quality.

The GCP community concurs with the EPMR estimate of three years as an adequate timeline for establishing a service to ensure accessibility, distribution and use of the reference sets. It is also clear that the reference sets require further characterisation and adaptation so as to fully meet the expectations of breeders who do not want to use donors that will compromise the value of their breeding material. Therefore, breeders require that the widest possible range of traits be described. The more finely characterised the

material is, the better, with emphasis on phenology. Breeders also expect to have prebred materials building on the reference sets, which corresponds well with several SP1 projects initiated in 2008. Efforts on phenotyping and base-broadening will both involve very close collaboration with SP3.

The global genotyping capacity must be managed to enable access by a broad community of decentralised users. Current partnerships will help generalise the use of DArTs as well as SNP-based systems. This task, initially shared with SP2 and SP3, will now be done in concert with all Subprogrammes.

Subprogramme 2: Genomics towards gene discovery

Rationale

Plant traits for adaptation to environmental stresses are often controlled by complex genetic systems that are subject to the influence of genotype by environment (GxE) interactions. To combine the right complement of genes and alleles effectively in a breeding programme, sufficient understanding is needed of the genetic mechanisms underlying the adaptive processes, especially for complex traits like drought tolerance. Although advances in developing genomic tools and knowledge gained from model organisms are important for identifying potentially useful genes controlling such traits, translating 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 in which interdisciplinary and integrated approaches can be used for gene discovery to dissect the mechanisms governing adaptation.

Specifically, SP2 aims to: (i) develop cross-cutting research platforms for the 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. Realising the full potential of these approaches requires capacity-building in the use of the new tools, and creating a pipeline to translate results into practice – aims that SP2 shares with SP5.

SP2 is continuing to use – and develop, wherever required – genomic and genetic resources, tools and technologies. The Subprogramme also evaluates interdisciplinary approaches to enhance understanding of gene function and interaction to improve knowledge of gene systems across crops. Comparative methods are being applied to leverage genetic knowledge from a range of plant species to investigate and validate gene functions important to stress tolerance. SP2 brings together interdisciplinary teams to apply the validated genes or superior alleles in breeding programmes. While the focus will principally be on drought tolerance traits in the coming years, the various genes and agronomic characteristics that improve crop resilience in difficult environments will be integrated with drought tolerance.

Major achievements in 2008

In the course of GCP Phase I, SP2 has both assembled and developed specialised genetic resources in a number of crops such as wheat, rice, common beans and potatoes. Major

emphasis has been put on use of the resources. For instance, rice mutant lines were used in 2008 to identify ‘knock-out’ mutants for several candidate genes. However, although significant amounts of genomic resources were developed for most GCP crops in Phase I, they are still lacking for a few. These include crops of regional importance such as pearl millet in Africa, pigeonpeas in Asia and sweet potatoes in South America. Following the initiation of the TLI focus project in 2007, impressive progress was made during 2008 in developing genomic resources for groundnuts, cowpeas, common beans and chickpeas, as well as cross-species markers in these crops.

With the objective of establishing the causal relationship between gene expression patterns and phenotypes, transcript profiling projects were initiated in 2008 for rice, wheat and sorghum. Finally, a number of projects were launched in 2008 on sorghum, rice and chickpeas to validate the cloned or identified genes or QTLs for stress tolerance. The main outputs of all of these efforts during the year are as described below.

- **Molecular markers and genetic maps developed:**

A significant number of molecular markers have been developed for four tropical legumes. For groundnuts they include longer SSR markers and the first 4X cultivated genetic map. For cowpeas, information has been generated on some 6,000 SSRs. For common beans, information on SSRs has been derived from BAC-end sequences, and more than 1,500 novel SSR markers have been developed for chickpeas. In addition, about 500 orthologous gene markers have been developed that will align different legume genome maps. The markers and maps will provide the necessary infrastructure for undertaking trait mapping in these legumes that had previously been bypassed by the genome revolution.

- **Physical map assembled:** Two BAC libraries with 17X genome coverage (70,000 clones) were generated for cowpeas. Based on fingerprinting of 60,000 BACs, a physical map has been assembled for the crop. Similarly, a physical map has been developed for cassava after fingerprinting 29,952 BACs. Linking genetic maps with physical maps in these species will eventually provide the physical location of markers and genes for traits of interest in the genome. Physical maps will also provide the basic infrastructure to undertake genome sequencing.

- **High-throughput marker genotyping platform developed:** High-throughput and cost-effective marker genotyping are prerequisites for association genetics as well as for marker-assisted breeding (MAB). Accordingly, a high-density SNP (1,536) genotyping platform (Illumina GoldenGate assay) has been developed for cowpeas. This is being used to develop genetic maps as well as for marker-assisted recurrent selection (MARS) in collaboration with SP3.
- **Transcriptomic resources and transcript profiling platform established:** A number of cDNA libraries have been developed for sweet potatoes, pearl millet, chickpeas and pigeonpeas, while a full-length cDNA library has been developed for common beans. Some of these libraries have already been used for Sanger and/or 454/FLX sequencing to generate the ESTs that are providing the first access to genic contents in these species. In addition, a 44K gene array has been established in rice to undertake whole-genome expression to identify genes conferring tolerance to drought stress.

SP2 is already working closely with SP3 and this collaboration will grow even more in the future, so that identified QTLs or genes can be validated and transferred to SP3 for molecular breeding. Collaborative work will include mapping and validating drought QTLs in sorghum and chickpeas, leading to marker-assisted introgression of the drought QTLs. Collaboration between SP2 and SP4 is providing useful analytical tools for comparative genomics and expression analysis.

Activity report

The activities conducted within SP2 are organised according to four Themes, each divided into several projects. These are shown in Box 5, along with a listing of partners involved in SP2 activities during 2008. The four SP2 Themes – genomic resources, comparative mapping, genetic pathway analysis, and gene validation – represent a progression in gene discovery through the use of genomics.

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

This Theme recognises the importance of genetic resources (including mutants, isogenic lines, cytogenetic stocks and chromosome substitution lines) and genomic resources as tools for identifying gene functions. However, with a few exceptions, most crops have little specialised germplasm available to support gene identification and confirmation. Therefore, in its first four years, GCP played a catalytic role by supporting the assembly and development of genetic stocks for several crops.

In 2008, this has been followed by significant progress in developing genomic resources, particularly in tropical legumes. For example, a large number of SSRs (3,000 detected, 800 primers ordered), cleaved amplified polymorphic sequence (CAPS) markers (50) and conserved orthologous sequence (COS) markers (40) have been developed for common beans, to identify the markers associated with drought tolerance and resistance to bean common mosaic virus (BCMV) and bruchids.

In the case of chickpeas, the development of about 1,500 new SSR markers has extended the SSR repertoire to about 2,300, with the development of DArT/SNP arrays in progress. These markers are being used to develop inter- and intra-specific genetic maps and identify molecular markers for drought tolerance and insect (*Helicoverpa*) resistance.

Significant progress has also been made in developing cDNA libraries, BAC libraries, EST sequences and BAC-end sequences to develop SNP markers, and place BAC contigs onto the genetic map in cowpeas. A high-density SNP genotyping platform (GoldenGate assay of Illumina) and a BAC-based physical map have also been developed during 2008. They are being used to identify markers for drought tolerance and resistance to biotic stress (eg, to flower thrips and root nematodes).

In the case of groundnuts, pilot BAC-hybridisations for 315 microarrays have been carried out in order to develop a physical map for the AA genome. The first genetic map for cultivated groundnuts and longer SSR-enriched libraries have also been developed. These genomic resources will be very useful for identifying markers for drought tolerance and foliar disease resistance. The development of genomic resources for these legumes is making it possible to create genetic maps and identify markers associated with tolerance or resistance to abiotic or biotic stress. This work will continue in 2009, with emphasis on identifying markers linked with drought resistance and tolerance to targeted biotic stresses. The markers will be useful for developing improved cultivars for Africa and Asia.

Rice provides an example of the effective utilisation of existing genetic resources and those developed by GCP. After identifying ERECTA sequences on chromosome 6 (7693bp genomic DNA sequences with a coding sequence of 2937bp encoding 978 amino acids), four independent insertion mutants were identified from Hirochika's *Tos17* collection.³¹ These mutants will be characterised in 2009.

³¹ Hirochika H (2001) Contribution of the Tos17 retrotransposon to rice functional genomics. *Current Opinion in Plant Biology* 4:118-22.

Box 5. SP2 Themes, projects and partners.Lead partner(s) underlined, where applicable. Full names of partners in *Acronyms and abbreviations***Theme 1.** Assembly of genomics and germplasm resources through consolidating and developing specialised genetic stocks

1. Bean genetic and genomic resources developed
CIAT, ART, CBI, ECABREN, EIAR, PU, RIKEN, SABRN, UoC (Davis)
2. Chickpea genetic and genomic resources developed
ICRISAT, DArT P/L (service provider), EIAR, IIPR, LZARDI, NIPGR, UoC (Davis), UoF
3. Cowpea genetic and genomic resources developed
UoC (Riverside), IITA, INERA–Burkina Faso, IRAD, ISRA, UoC (Davis)
4. Groundnut genetic and genomic resources developed
ICRISAT, ARI–Naliendele, CRS, DArT P/L (service provider), EMBRAPA, INRAN, IAC, ISRA, UCB, UGA
5. Validation of drought-response/resistance pathways genes by phenotypic analysis of mutants
VBI, HZAU, IRRI, VPI

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

6. Cross-species resources developed for comparative biology in tropical crop legumes
UoC (Davis), CIAT, ICRISAT, IITA, UCB, UoC (Riverside), UGA
7. Genetic and physical mapping resources produced for drought breeding in cassava
UoM, UoP, UotW
8. Genomic resources and mapping populations for sweet potato developed to enable trait/gene identification
CIIP, DArT P/L (service provider), EMBRAPA, IIAM, INIA–Uruguay, NAARI
9. Genomic resources and mapping populations developed and assembled for pearl millet to enable trait/gene identification
ICRISAT, AICPMIP, CAZRI, ILRI, RAU
10. Genomic resources (ESTs, markers and maps) developed for pigeonpea to enable trait/gene identification
NCGR (collaborator/service provider), ICRISAT, NRCPB, PDKV

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

11. Causal relationship between whole-genome expression patterns and stress tolerance determined in rice via analysis of near-isogenic lines
NIAS, IRRI
12. Discovery and development of alleles contributing to sorghum drought tolerance
UGA, ARC–Sudan, ICRISAT, MAU, NRCS, SARI–Ghana
13. Examining natural variation in the transcriptional regulation of drought responses in wheat
ACPFG, CIMMYT, ICS–CAAS

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

14. Drought-adaptive mechanisms in bread and durum wheat determined through large-scale phenotyping methodologies
CIMMYT, ACPFG, DWR
15. Drought from a different perspective: Improved tolerance through phosphorus acquisition in rice
IRRI, ICABIOGRAD, JIRCAS, UoPd/MPIMPP, ZU
16. Delayed senescence and drought tolerance in rice
UoC (Davis), IRRI
17. Validation of QTLs associated with drought tolerance traits in chickpea
ICRISAT, DZARC, UAS (Bangalore)
18. Enriching African sorghum varieties for stay-green using marker-assisted selection
DPI&F, ARTC, MARC

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

This Theme aims to generate common markers and consensus maps, and provide a framework for leveraging information across different crops. The TLI project is developing a significant quantity of cross-species markers for legumes and is integrating gene-based orthologous markers into genetic maps in collaboration with Theme 1. Outputs from Theme 2 projects will promote mapping and genetic dissection of a suite of traits, particularly drought tolerance, and will eventually enable the user community to undertake molecular breeding activities to develop improved cultivars for drought tolerance in target regions in Africa, Asia and South America.

In order to develop cross-species markers in legumes, based on genome and transcript sequence data of soybeans, *Medicago* and *Lotus*, a set of about 500 gene-based orthologous markers were developed in 2008. These markers will be used in 2009 for integration into the genetic maps of common beans, cowpeas, chickpeas and groundnuts.

With the aim of establishing genome-wide BAC fingerprint contigs (physical map) in cassava, 29,952 BACs have been fingerprinted and, as a result, 1,877 contigs and 1,890 singletons have been identified. SNP discovery is in progress to develop a genome-wide SNP map that will be used to identify markers for drought tolerance.

In the case of sweet potatoes, several cDNA libraries have been developed for producing expressed sequence tags (ESTs), and work on DArT arrays is in progress. A virus-free diploid mapping population is also being generated *in vitro*. A medium-density reference map based on these resources will be produced for trait mapping.

Similarly, in order to enrich the genomic resources of pearl millet, four cDNA libraries were developed during 2008 for generating ESTs using 454/FLX sequencing technology. EST resources will be used to produce SSR and SNP markers for integration into existing 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. Another activity initiated in late 2008 will generate ESTs and marker resources using Solexa³² sequencing technology.

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

The emphasis in this Theme is on applying genome-wide tools such as gene chip technology to reveal the causal relationship between gene expression patterns and phenotypes. A unique feature of GCP research is the use of agronomically relevant experimental conditions and genetic materials. As a result, the genetic knowledge gained benefits both researchers and breeders. Selecting the right genetic materials is crucial for gene identification and expression analysis. Moreover, to identify the right genetic material, methods are needed to generate high-quality drought-tolerant phenotypes.

With the objective of determining expression patterns for genes involved in drought tolerance using field-grown NILs (for drought tolerance), a 44K gene array covering whole-genome expression in rice has been established. RNA samples for transcriptome analysis have been collected from spikelet, leaf and root tissues of IR644/Aday Sel NILs. In 2009, the relationship between phenotypes under controlled conditions and field performance (specifically as yield under stress) will be established by matching expression and QTL maps.

A new activity, which started in late 2008, deals with exploiting stay-green QTLs to improve sorghum. The activity aims to generate all pairwise combinations of QTL introgression heterozygotes, as well as double heterozygotes, to measure their epistatic interactions. In parallel, a high-

throughput SNP genotyping platform will be developed to genotype multiparent advanced generation inter-cross (MAGIC), recombinant inbred line (RIL) and stay-green NIL populations for discovery research and product development. Another new activity is identifying candidate genes and/or transcription factors known to increase drought tolerance when showing modified expression. New alleles will then be identified at each of the candidate genes that show expression levels correlated to drought tolerance.

Theme 4: Validation of genes and pathways through evaluation of under- or over-expression 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. Most of the work under the Theme started in late 2008. Thus, efforts made during the year will provide a basis for more significant progress in 2009 and onwards.

Research to determine drought-adaptive mechanisms in bread wheat and durum wheat through large-scale phenotyping methodologies has examined three mapping populations (DH1 = Kukri x RAC875, DH2 = Excalibur x Kukri, and DIC = Atil x *Triticum dicoccum*). These have been phenotyped under multiple environments in Mexico, Australia and India for many traits including crop establishment, canopy temperature, water-use efficiency, stem carbohydrates and yield components. Subsequently, genetic mapping of DH1 (495 markers) and DH2 (430 markers) has provided QTLs for yield and yield components in several field locations. Glasshouse experiments have also been designed to assess drought-adaptive traits in a controlled environment.

Four new SP2 activities were initiated in late 2008. One is based on earlier research wherein maintenance of higher root growth rates under phosphorus deficiency was found in rice lines carrying the phosphorus uptake QTL (*Pup1*). The aim is to identify the gene or genes at the *Pup1* QTL to understand the underlying physiological mechanisms, as well as developing allele-specific markers for MAS and QTL pyramided lines. The second activity is based on the hypothesis, as proved in tobacco, that drought-induced plant senescence is due to a type of programmed cell death that is naturally activated during drought. Based on the success of over-expression of the *IPT* gene that mediates the synthesis of cytokinins under the control of the *SARK* promoter in tobacco, the next step is testing the efficacy of stress-induced cytokinin synthesis in conferring drought tolerance in upland

³² <http://www.illumina.com>

and lowland rice varieties. The third activity involves identifying and validating QTLs for root traits, $\Delta^{13}\text{C}$ (carbon isotope discrimination) and harvest index. Candidate QTLs will eventually be used for MAB to develop improved chickpea cultivars with drought tolerance for Africa and Asia. Finally, the fourth new activity deals with validation and introgression of stay-green QTLs identified in Australia into drought-sensitive African sorghum lines to develop superior cultivars and enhance understanding of the association between plant height and stay-green.

Lessons learnt

A number of lessons were learnt in the course of carrying out SP2 activities during 2008. These will inform research management and resource allocation in 2009 and beyond. At a general level, SP2 will move from working on a range of stresses, as was done in Phase I, to a greater focus on drought tolerance.

Since it has proved difficult to secure the necessary institutional commitment to maintain and distribute specialised genetic stocks, a decision has been made for SP2 not to make any further investment in developing genetic resources. However, the Subprogramme will continue to place emphasis on use of the stocks by the GCP community through a coordinated approach.

As a result of advances in sequencing and genotyping technologies, sequence data generation, fingerprinting of BACs and SNP genotyping can be done faster and at a lower cost when outsourced to reliable service providers. SP2 is taking advantage of this trend by establishing relationships and negotiating costs between GCP partners and service providers including Everogen (Russia), J Craig Venter Institute (JCVI; USA), Macrogen (Korea) and NCGR (USA).

When undertaking gene expression analysis, appropriate genetic material (eg, NILs) and plant material (eg, field-grown) is critical. Therefore, SP2 is encouraging partners to undertake transcript profiling only with suitable material.

A final lesson learnt is that, in addition to identifying and cloning the gene of interest, it is also very important to identify superior haplotype or allele combinations for a particular trait. SP2 is working with SP3 in this direction.

Conclusions, and perspectives on 2009 and Phase II

Progress was recorded across the range of activities within SP2 during 2008, with especially notable advances in developing genomic resources in legumes. The year also saw the initiation of a number of new activities, mainly in Themes 3 and 4; these are expected to deliver significant outputs in 2009. Important progress was made throughout Phase I in developing basic genomic resources for most GCP crops. SP2 does not anticipate any further such investment in Phase II, with emphasis now shifting to technical outputs directly linked to product delivery.

The larger part of SP2's efforts in Phase II will be vertically oriented through seven crop Challenge Initiative (CIs; see *Introduction and highlights: Seven Challenge Initiatives for more focus*). These will include initiating projects on gene discovery, or on gene or QTL validation in target crops. One of the CIs that will deal with the comparative genomics of salinity and aluminium tolerance will have the majority of its components linked to SP2. This CI will provide candidate genes or markers for soil health problems in cereals, for transfer to SP3, as well as helping to understand genome architecture and comparative genome evolution. To achieve the goal of this CI, SP2 is working very closely with SP4 to develop and deploy analytical tools for comparative genomics and transcriptome analysis.

Several SP2 projects initiated in 2003 or 2004 have been completed recently, and some new projects with major emphasis on drought tolerance were initiated in 2008. More results are anticipated in 2009 and 2010 on validating and transferring SP2 products to SP3 for molecular breeding. SP2 will continue to maximise the use of genomics research – using comparative and omics approaches – to identify the QTLs, genes and alleles associated with drought tolerance. 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.

Focused investment and collaboration with appropriate partners, including developing country programmes, will be critical for achieving the goals of SP2 in the coming period. Also, integrating SP2 activities even more strongly with those of other Subprogrammes is foreseen in future years. For example, collaboration with SP4 will be strengthened in genome analysis and gene expression studies, while validation of identified gene-based markers, genes, QTLs and improved germplasm will strengthen ties with SP1 and SP3. In Phase II, SP2 will further enhance links with SP5 in training developing country and CGIAR scientists at developed country institutes.

Subprogramme 3: Trait capture for crop improvement

Rationale

Most developing countries – with the notable exception of a few with large advanced plant breeding programmes – have limited access to the new technologies and skills that have enhanced the effectiveness of plant breeding in industrialised countries. SP3 aims to create product-driven teams that span the innovation-to-impact continuum and bridge the gap between generating research outputs and using them in developing country breeding programmes. The Subprogramme capitalises on the latest advances in germplasm characterisation, genomics, information technology and bioinformatics, to accelerate genetic progress in simple traits such as resistance to biotic stresses. But more importantly, SP3 strives to develop, validate and use markers to improve complex traits for impact on crop productivity in drought-prone environments.

SP3 has three main objectives. First, it seeks to validate candidate genes in target environments and adapted germplasm. Tremendous progress has been made in understanding the genetic basis of key regulatory pathways in plants grown under drought-prone environments in terms of gene function and allele value. However, before any molecular breeding applications can be considered, many such discoveries must be extrapolated and validated in a suitable biological context. Thus, the quantification of favourable genetic effects at loci of interest in adapted germplasm under target field conditions is a major goal. Second, the Subprogramme aims to develop better means of optimising MAB, such as decision-support tools and protocols, and MAB simulation models and software. SP3's third objective is to expand and support phenotyping. Drought tolerance phenotyping remains difficult because of limited capacity, inadequate protocols, extensive diversity, and problems in the design of controlled stress experiments. Therefore, particular attention is being given to establishing, supporting and strengthening phenotyping networks, as well as defining robust protocols.

SP3 activities are aligned to GCP's renewed strategy and refocused research priorities, with an increasing number being conducted jointly with other Subprogrammes. SP3

has – together with SP5 – played a major role in developing crop platforms. These platforms have reinvigorated and also stimulated collaboration and the exchange of germplasm, information and skills. The platform approach has also contributed to the basis for CI 'mega-projects'. Other collaborative activities include evaluating reference sets in target environments with SP1, identifying and validating genes and markers by developing country partners in target regions with SP2, and developing decision-support tools with SP4.

Major achievements in 2008

Research products to be delivered by the end of 2008 or early 2009 include validated markers, new approaches and methodologies to improve efficiency of MAB and drought phenotyping, and improved prebreeding germplasm for distribution to breeders. A huge impact is expected from the further dissemination of these products. For example, introducing major drought-tolerance QTLs will influence rice production in large areas in India, while QTLs for improved wheat cultivars should significantly increase production in Northern China where wheat is cultivated on 10 million hectares. MAB would also significantly increase breeding efficiency of rice, maize, sorghum, cowpeas, groundnuts, chickpeas, beans, potatoes and sweet potatoes in Africa.

Marker-assisted selection (MAS) and marker-assisted breeding (MAB)

MAS involves using DNA-based markers associated with traits of interest to increase the effectiveness of selection within a breeding programme and thereby accelerate variety development. MAB differs from and builds upon MAS in that *de novo* mapping is done on each breeding population. MAB feeds into marker-assisted recurrent selection (MARS) for maximum advantage.

The most significant outputs generated by SP3 during 2008 are outlined below.

- **Validating markers for disease and pest resistance:** Validated markers for disease resistance will help tackle crippling factors limiting food-crop yield in Africa's drought-prone environments. In 2008, attention was given to resistance to the major pests and diseases affecting yield in drought-prone conditions, such as downy mildew in maize, yellow mottle virus and bacterial leaf blight in rice, *Striga* in cowpeas, golden yellow mosaic virus and root rot in beans, and late blight, tuber moth, *Diabrotica*, leaf roll virus, and bacterial wilt in potatoes. Markers for these traits have been identified, or are already in use for MAS.

- **Validating markers for tolerance to soil constraints:** In many developing countries, crops are cultivated on acid or saline soils, whose nutritional constraints usually exacerbate drought-related problems. Markers for tolerance to poor soils in Africa and South Asia were identified, including aluminium toxicity in sorghum, and salinity and phosphorus deficiency in rice. These markers are now being validated in Kenya and Niger, and in Bangladesh and Indonesia, respectively.
- **Drought QTLs identified:** SP3 has also validated and used markers to improve complex traits like drought tolerance. Major QTLs for this trait have been identified and validated in rice (for India and China), in wheat (for China), and in tropical legumes (for Africa). Markers developed for cowpeas, groundnuts, chickpeas and beans are being used extensively in the TLI project. Their application in breeding programmes is expected to have impact on crop productivity in drought-prone environments.
- **Screening germplasm:** Prebreeding germplasm that has been developed for Africa and Asia is being screened for drought tolerance and disease resistance. Examples include translocation lines for winter wheat, and chromosome segment substitution lines for rice and groundnuts.
- **Phenotyping platform:** In 2008, SP3 took the first steps to establish, with partners, a phenotyping platform for GCP target crops. This includes potential phenotyping locations with adequate facilities and levels of expertise. GIS tools have played an important role in setting up this platform. These tools served to accurately select and characterise test locations that are representative of target environments, and to identify the extent to which phenotyping data collected in a given site can be used in other locations worldwide. This will enhance understanding of GxE and QTLxE (QTL by environment) interactions, and improve management of germplasm exchange.

Activity report

The activities conducted within SP3 are organised under four Themes, with each Theme having several projects. All these are shown in Box 6 along with partners involved in SP3 activities during 2008.

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

This Theme aims to provide a better understanding of the genetic basis of disease resistance and drought tolerance in GCP mandate crops. Another objective is to enhance genetic diversity and accelerate its utilisation in breeding. Products include identifying genomic regions associated with target

traits, as well as prebreeding germplasm to be used by other SP3 projects or to be delivered to breeders. Generally, the work has been conducted by or with developing country partners that have relatively extensive facilities and expertise (eg, EMBRAPA, Brazil; BIOTEC, Thailand), or has been based on a large network involving a CGIAR Centre and both developed and developing country national programmes.

Association mapping has helped identify useful markers in maize and sorghum. In maize, markers associated with downy mildew resistance have been identified by scientists from BIOTEC using a large collection of maize lines, while in sorghum, superior *Alt_{SB}* haplotypes have been identified by EMBRAPA. In this latter case, haplotype-specific markers have been developed and are being used for introgression into local African landraces.

Wheat–barley translocation, substitution and addition lines developed in Hungary have been analysed by genomic *in situ* hybridisation (GISH) and some have been phenotyped for tolerance to drought and aluminium toxicity. The lines will now be used in wheat breeding. A collaboration between Agropolis–CIRAD and ISRA (Institut sénégalais de recherches agricoles, Senegal) has produced BC₁ and BC₂ populations and introgression lines in groundnuts that will also be valuable in improving the crop. Results expected for 2009 include two sets of chromosome segment substitution lines obtained through marker-monitored backcross introgression, two populations of BC inbred lines obtained through selfing, and a molecular map derived from two interspecific BC₁ populations. In addition, improved potato germplasm has been selected for testing in Malawi and Mozambique. The germplasm is from national programmes in South America and from CIP.

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

In addition to discovering novel markers and developing prebreeding germplasm, there is also a need to develop and test new methodologies and tools to improve the efficiency of molecular breeding. Accordingly, Theme 2 covers two areas – refining and modelling MAB strategies, and improving phenotyping.

The first area includes developing models to support MAB and gene pyramiding. Simulation tools have been developed through collaboration between the Chinese Academy of Agricultural Sciences (CAAS), CIMMYT and the Commonwealth Scientific and Industrial Research Organisation, Australia (CSIRO). These tools help to compare genetic gain for different traits and in different environments,

Box 6. SP3 Themes, projects and partners.Lead partner(s) underlined, where applicable. Full names of partners in *Acronyms and abbreviations*.**Theme 1.** Characterisation of segregating populations and identification of genomic regions for plant breeding

1. Enhancing groundnut (*Arachis hypogaea* L) genetic diversity and speeding its utilisation in breeding for improving drought tolerance
ISRA, Agropolis-CIRAD, EMBRAPA, ICRISAT, PROINPA, UCB, USDA-ARS
2. Association mapping of downy mildew resistance in elite maize inbred lines in Thailand
BIOTEC, KU
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
EMBRAPA, CU, INRAN, KSU, USDA-ARS
4. Making Latin American potato diversity available for Africa
INIA-Uruguay, CIP, DARS, EMBRAPA, IIAM, INIA-Chile, INTA-Argentina
5. Field evaluation of wheat-barley introgression lines under different water regimes
ARI-HAS, CAAS, CIMMYT, DPSPP-EKC
6. Seed smoke treatment to favour germination under water-stressed conditions
ARI-HAS, UKZN

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

7. Breeding for drought tolerance with known gene information
CIMMYT, CAAS, CSIRO, ICRISAT, Agropolis-INRA, IRRI, UoQ
8. Linking genetic diversity with phenotype for drought tolerance traits through molecular and physiological characterisation of a diverse reference collection of chickpeas
ICRISAT, JIRCAS, UAS (Bangalore)
9. Improving drought tolerance phenotyping in cowpeas
UoC (Riverside), IITA, INERA-Burkina Faso, ISRA, TAMU
10. Development of a GCP phenotyping network
CIAT, EMBRAPA, KUL, WA
11. Environmental assessment for the GCP phenotyping network
CIAT, EMBRAPA, KUL, WA

Theme 3. Marker/allele validation in adapted germplasm under target environments

12. Integrating marker-assisted selection into the conventional breeding procedure for improvement of wheat in the drought-prone areas of Northern China
CAAS, HAAS, LAAS, NU, NWSUAF, SAAS
13. Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco
INRA-Morocco, CU, CIMMYT, ICARDA, UdB, UoMi
14. Validation of *Alt_{SB}*, a major aluminium tolerance gene in sorghum: assessment of the breeding value of superior haplotypes: linking upstream genomics to acid soil breeding in Niger and Mali (ALTFIELD)
EMBRAPA, CU, ICRISAT, INRAN
15. Validation of Saltol, a major salinity tolerance gene in rice
IRRI, BINA, BRRI, UoD
16. Application and validation of the major QTL phosphate uptake 1 (*Pup1*)
IRRI, ICABIOGRAD, JIRCAS

Theme 4. Application of molecular markers in breeding programmes

17. Integration of genomic tools with conventional screening for developing NERICA rice cultivars for West Africa
WARDA, IER, Agropolis-IRD
18. Marker-assisted selection for sweet potato virus disease (SPVD) resistance in sweet potato germplasm and breeding populations
CIP, NAARI
19. Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-assisted breeding
IRRI, CRURRS, TNAU, UAS (Bangalore), UoAI, YAAS
20. Local germplasm enhanced via molecular breeding for target traits in tropical legumes (groundnuts, beans, cowpeas and chickpeas)
ICRISAT, CIAT, UoC (Riverside), ARI-Naliendele, DARS, DZARC, IIPR, IITA, INERA-Burkina Faso, ISRA, LZARDI, UCB, UGA, UoC (Davis)
21. Marker-assisted selection for resistance to *Striga gesnerioides* in cowpea
INERA-Burkina Faso, IITA
22. Marker-assisted selection for resistance to streak virus in maize
UKZN, IIAM
23. Dry bean improvement and marker-assisted breeding for diseases and abiotic stresses in Central America and the Caribbean
INIFAP, CIAT, INCA, INTA-Nicaragua, ORE
24. Yield improvement of sorghum in Africa through marker-assisted recurrent selection (MARS) and a public-private partnership
Agropolis-CIRAD, IER, Syngenta
25. Yield improvement of maize in Asia through marker-assisted recurrent selection (MARS) and a public-private partnership
CIMMYT, DMR, ICERI, MMRI, MPUAT, NMRI, YAAS

to build a genetic model for drought tolerance traits, to optimise crossing and selection strategies to pyramid major genes in wheat and to develop a breeding-by-design approach and software tools. These tools have been applied to facilitate the use of QTLs in MAB for polygenic traits in wheat, rice, sorghum and maize.

The second area concerns improving phenotyping quality within GCP. For this purpose, SP3 has projects to stimulate innovative approaches to tackling drought tolerance. New phenotyping tools and protocols such as carbon isotope discrimination ($\Delta^{13}\text{C}$) and thermal imaging have been used to evaluate legume germplasm for drought tolerance. The chickpea reference set (an SP1 output) has been phenotyped for $\Delta^{13}\text{C}$ and other drought tolerance-related traits, and genotyped with DArT markers. The drought tolerance phenotyping in cowpeas will provide baseline information for analysing GxE interactions and refining phenotyping protocols.

Other projects have been implemented to improve characterisation of environments and phenotyping facilities, and enhance expertise in testing locations. A strategic network of field phenotyping sites for GCP target crops has been established. GIS tools and soil water balance models have been used to describe the drought scenario faced by the crops in different environments, and to compare and cluster the phenotyping locations involved in GCP projects. The facilities and expertise in the different locations have been evaluated, and a subset will become reference locations for large, high-quality drought phenotyping. The development of this phenotyping network is expected to have a positive impact on phenotyping in most GCP projects, increasing understanding of GxE interactions and enhancing monitoring of germplasm exchange and distribution.

Theme 2 activities mainly involve ARIs and CGIAR Centres, with other developing country partners also included in activities focusing on phenotyping under different conditions.

Theme 3: Marker/allele validation in adapted germplasm under target environments

The objective of this Theme is to validate, under target environments, alleles identified or markers developed in GCP projects, and to integrate MAB into conventional breeding procedures. Closely related to SP3's product development activities, this Theme promotes the impact pathway from research outputs generated by GCP through to their application in breeding. Theme 3 projects are all based on the concept of validating and adding value to existing GCP products. They all involve institutes from developing countries, and some projects are led by a developing country

partner, thereby ensuring validation of markers in the adapted or adopted background and the transfer of the associated MAB technologies.

Under this Theme, major drought tolerance QTLs have been introduced into cultivars grown in the main regions of Northern China (Hebei, Henan, Ningxia, Shaanxi and Shanxi provinces) and phenotyped in the same regions. Contrasting bread and durum wheat genotypes have been characterised at the molecular level and phenotyped under different conditions in Morocco. They have also been screened for biotic stresses using MAS. In sorghum, the breeding value of superior *Alt_{SB}* haplotypes with putative tolerance to aluminium toxicity is being evaluated in acid soils. Elite *Alt_{SB}* haplotypes will be validated in acid soils in Niger and Mali, and the technologies used will be transferred to national partners.

In rice, *Saltol*, a major QTL for salinity tolerance, has been validated in Bangladesh and is being introgressed by IRRI into popular varieties adapted to target environments, in collaboration with Bangladeshi scientists. Phosphate uptake 1 (*Pup1*), a major QTL for tolerance to phosphorus deficiency, has been introgressed into three Indonesian varieties and two IRRI varieties. The effect of *Pup1* on performance in acid soils and under drought stress is being investigated.

Theme 4: Application of molecular markers in breeding programmes

This Theme promotes the application of markers developed by GCP, or by others, in breeding programmes via the most efficient approaches. It represents the last step in the product delivery pathway. Most of the projects are still on disease resistance traits but are now increasingly focusing on drought and other abiotic stresses. Many markers validated in Theme 3 are expected to be transferred into breeding activities through Theme 4 in the near future. Activities are led by CGIAR Centres or developing country partners, with some being based on South–South collaboration, and some involving public–private partnerships, or NGOs.

In Africa, *Oryza glaberrima* accessions and interspecific breeding lines for national partners have been screened for drought tolerance, and resistance to rice yellow mottle virus (RYMV) and bacterial leaf blight (BLB). Cowpea germplasm has been screened for *Striga gesnerioides* resistance using MAS, to generate well-adapted resistant cowpea varieties and make them available to farmers in Burkina Faso and Niger. MAS technology has been used to rapidly introgress maize streak virus (MSV) resistance into Mozambican maize germplasm. Groundnut, bean, cowpea and chickpea germplasm is being enhanced via molecular breeding for target traits. Backcross populations have been developed incorporating farmers' preferences and disease resistance.

Markers for resistance to sweet potato virus disease (SPVD) have been developed for sweet potatoes to screen orange-fleshed, high provitamin A content breeding populations. In Asia, QTLs with large effects on yield under stress were fine-mapped. Their impact is being verified in India and China, after which they will be introgressed into elite varieties via MAS. In Central America and the Caribbean, drought-tolerant bean germplasm is being screened for resistance to bean golden yellow mosaic virus (BGYMV) and root rot. Segregating populations have been developed from the best accessions. Lines selected for the target traits using MAS will be distributed through farmer organisations in Mexico, through NGOs in Haiti, and via participatory breeding in Cuba.

Two Theme 4 projects aim to improve yield using MARS through public–private partnerships. One partnership involves a developing country institute, a private company and an African partner, all working together to develop drought-tolerant sorghum germplasm for Ethiopia and Mali. Another partnership involves CIMMYT and national programmes in Asia (China, India, Indonesia, Pakistan, Philippines, Nepal, Thailand and Vietnam). With private sector support, they will develop drought-tolerant lines and hybrids through MARS.

Lessons learnt

The increasingly concerted interactions and collaboration among GCP projects and the resulting synergies, stimulated by the crop platforms that have been established, have spurred progress along the research–delivery continuum. More and more developing country partners are involved in validating and refining molecular breeding technologies. This is despite the fact that having a strong involvement of developing countries in MAB projects is not always easy, due to the diverse problems that these partners face. Experience has highlighted the importance of having a good definition and understanding of the needs of GCP's research partners and also of the technical and material constraints affecting their access to GCP tools or services. In this context, communication, follow-up of activities, and visits have proved to be crucial success factors. Particularly essential has also been the development of crop platforms that stimulate collaboration and favour the exchange of information and products between groups.

The deliberate user-driven approach adopted by SP3 has proved to be efficient in creating a community of developed country institutes, CGIAR Centres and developing country partners working together to facilitate access by breeders in developing countries to new genomic technologies and skills. Private sector organisations and NGOs are also now part of this community. Although GCP's clients, mandate

and objective are clearly different from those of the private sector, collaboration with this sector can help develop new approaches and methodologies, and improve the efficiency of GCP's product management activities.

These lessons will be essential for GCP Phase II, particularly in building up the CIs: CIs will require an excellent knowledge of needs and constraints, effective communication among partners, willingness to collaborate actively, and the vision to identify gaps and design ambitious yet realistic objectives for the next five years.

Conclusions, and perspectives on 2009 and Phase II

For GCP, the increasing importance of drought and abiotic stress as selection objectives and target traits is reflected in the fact that more and more SP3 projects address this issue whereas, previously, many activities focused on simply inherited traits. Of the 27 SP3 research projects in the 2009 portfolio, six are on biotic stresses while 17 focus directly on drought, and four on other abiotic stresses. All the projects address breeding issues in GCP target regions and cropping systems. A deliberate tendency to increase the involvement of breeders from national partner institutes in target regions in new projects – almost half of the SP3 commissioned projects are now led by developing country partners – will ensure more rapid deployment and wider dissemination of markers in conventional breeding.

During 2008, exciting progress has been made in many areas fundamental to GCP's product development pathway, and in particular in applying molecular breeding to a variety of traits, including tolerance to salinity, drought, phosphorus deficiency and aluminium toxicity. SP3's position is pivotal in GCP's research–delivery pathway, being primarily responsible for applying technical outputs flowing from SP1 and SP2.

During GCP's first phase as a whole, SP3 has contributed significantly to a better understanding of the genetic basis of drought tolerance and to important genetic gains in GCP target crops. These contributions stand on the shoulders of progress in identifying genomic regions associated with target traits, developing and evaluating novel breeding or molecular technologies, establishing, supporting and strengthening phenotyping networks, and delivering prebreeding germplasm to be used by other SP3 projects or transferred to breeders.

New markers have been disseminated in several developing country breeding programmes. In many cases, marker transfer has required capacity-building to strengthen molecular

breeding expertise for partners. This has been ensured through close collaboration with SP5. SP3 has also significantly contributed to developing support tools that improve breeding efficiency for complex traits such as drought, and has contributed to developing innovative approaches, such as MARS, that are currently being applied to maize breeding in Asia and sorghum breeding in West Africa. Efforts to improve phenotyping approaches and practices should be maintained or reinforced during Phase II.

At the end of Phase I, SP3 has a substantial number of projects and activities that are well-aligned to its mandate, and to GCP's renewed strategy and refocused research priorities. Through its product management activities, SP3 has participated in the identification of several 'flagship' projects. Together with SP5, SP3 has made a strong contribution to developing the crop platforms that represent a proof-of-concept and foundation for the CIs to be implemented during Phase II.

Subprogramme 4:

Bioinformatics and crop information systems

Rationale

The value of the data generated in Subprogrammes 1, 2 and 3 largely depends on how those data are captured, stored, managed, analysed and made accessible to GCP Consortium members and the rest of the world as international public goods. How the data are analysed depends, in turn, on the analytical tools and other information sources available. SP4 addresses the challenge of linking and integrating information components and analytical tools into a coherent information platform. Thus, a bioinformatics, biometrics and advanced data management system is being created to support an integrated information network for genetic resources, genomics and crop improvement. This platform will provide access to the data generated in GCP and will provide tools to analyse them. Furthermore, it will link GCP data and tools to global biodiversity and bioinformatics networks. Finally, SP4 supports the users of this infrastructure through training and assistance in experimental design, and in data handling, storage and analysis.

The information platform has a number of components. First, there are the numerous local systems already in place. The challenge of combining these into one integrated system has been quite daunting, given that GCP has very limited latitude in dictating the architecture and organisation of existing systems, whether within or outside the GCP Consortium. Secondly, there are the elements that already exist within the GCP Consortium which 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 have been generated. This strategy allows proper data curation in terms of making corrections and additions to the data, and clarifies ownership. Thirdly, to ensure proper data handling in all of the Subprogrammes, GCP scientists need support in selecting and integrating tools and data sources, in creating new tools and information sources and, importantly, in using the tools.

Major achievements in 2008

At the end of 2008, which also marks the end of GCP Phase I, SP4 offers an impressive portfolio of information resources, software applications and methodologies to support GCP scientists and others working in agricultural research, as summarised below.

- **SP4 Helpdesk on Bioinformatics and Biometrics:** A new helpdesk and support service³³ was established in 2008 to provide access to SP4 products and informatics skills. GCP scientists can scan the web portal for tools or information on biometrics, bioinformatics or data management issues. They can also email the helpdesk³⁴ with queries, which will be passed to appropriate experts and responded to within 48 hours. Helpdesk support will expand during Phase II in order to strengthen the linkages between SP4 products and the impact of GCP research.
- **GCP Informatics Platform:** The GCP Informatics Platform has been implemented for diversity analysis³⁵ and for access to rice crop information.³⁶ This is a major step in the integration of diverse data sources from SP1 and SP2 research. The platform also gives access to analysis tools for quality checking, diversity analysis and functional genomics. It will also form the basis for integration of crop information to support molecular breeding activities in Phase II.
- **New version of the Integrated Marker-Assisted Selection System:** The year 2008 saw the release of Version 1.4 of the Integrated Marker-Assisted Selection system (iMAS). Improvements include its extension to multiple population mapping datasets and multi-environment evaluation datasets, as well as inclusion of the Comparative Map and Trait Viewer (CMTV).
- **Phylogenomic analysis to facilitate comparative and functional genomics:** GreenPhylDB is a large-scale phylogenomic database of gene families across twelve genomes that has been developed for analysis of test sequences using the GreenPhyl Orthologous Search Tool (GOST).³⁷ Sequence data from several species have been added to the database and a web portal was developed in 2008 for community annotation of gene families.

Activity report

The activities conducted within SP4 are organised according to three Themes, each divided into several projects. These are shown in Box 7, along with a listing of partners involved in SP4 activities during 2008.

³³ <http://www.generationcp.org/bioinformatics.php?da=08106902>

³⁴ sp4helpdesk@generationcp.org

³⁵ <http://gendiversity.cirad.fr/Home>

³⁶ <http://seeds.irri.org>

³⁷ <http://greenphyl.cirad.fr/cgi-bin/greenphyl.cgi>

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

This Theme addresses how information flow between GCP researchers can be organised to maintain local curation of data and tools, while also ensuring optimal access. The aim is to establish the infrastructure for integrating and exchanging data and information. An agreed set of standards for structure and semantics in data integration across GCP's different crops and disciplines is being developed through a project led by Richard Bruskiewich (IRRI). This involves a domain model that is well advanced and now only requires maintenance, plus ontologies to provide the semantics for extending and enriching the domain model for specific crops and data types. Following work in 2007 on passport and genotyping data, Rosemary Shrestha, Guy Davenport (CIMMYT), Elizabeth Arnaud, Adriana Alercia (Bioversity International), Reinhard Simon (CIP) and Jayashree Balaji (ICRISAT) have convened

community teams to work on plant and trait ontologies for rice, maize, wheat, *Musa*, potatoes, chickpeas and sorghum. These ontologies can be viewed at the project's website i) for developers of ontology;³⁸ and ii) for scientific end-users of ontology.³⁹

Milko Škofič (Bioversity) is leading efforts to use the domain model and ontologies to 'wrap' existing databases and thus make the data they contain available as BioMOBY⁴⁰ web services. This has created a virtual network where scientists from all over the world can access and share data across distant locations. In 2008, Milko Škofič worked with Martin Senger (IRRI), to develop a prototype toolkit that can be used to select appropriate BioMOBY services and wrap relevant databases, thereby connecting data structures to domain model concepts and ontology terms.

³⁸ <http://pantheon.generationcp.org>

³⁹ <http://mcclintock.generationcp.org>

⁴⁰ <http://www.biomoby.org/>

Box 7. SP4 Themes, projects and partners.

Lead partner(s) underlined, where applicable. Full names of partners in *Acronyms and abbreviations*.

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

1. GCP domain models and ontologies developed
IRRI, BI, CIMMYT, CIP, ICRISAT, POC
2. Web services technology implemented in the GCP Consortium
BI, CIMMYT, IRRI
3. GCP Central Registry and templates for GCP data capture, storage and use created and maintained
BI, CIMMYT
4. Quality and utility of GCP phenotyping data improved through the development of a data input template
CropGen International, CIMMYT, IRRI
5. Large-scale phylogenomic analyses tools developed for gene function prediction for GCP crops
BI, Agropolis-CIRAD, IRRI

Theme 2. Tools – Quality improvement of research data and bioinformatics applications in the GCP Consortium

6. Integrated GCP Information Platform created
IRRI, Agropolis-CIRAD, CIMMYT, EBI, ICRISAT, NCGR
7. Web services tools and technology further developed
IRRI, BI
8. Data quality within the GCP further improved and assured
IRRI, WUR, ICRISAT, CIP, Agropolis-CIRAD
9. High-performance computing (HPC) facilities integrated in the GCP toolbox
CIP, ICRISAT, IRRI, NIAS

Theme 3. Services – Support to other GCP projects in terms of methodology, software tools and data management

10. Bioinformatics and data handling support to GCP scientists
WUR
11. Statistical support provided for the design and data analysis of GCP projects
WUR, Agropolis-CIRAD, CIMMYT
12. Data analysis support available for SP2 with emphasis on microarray and mapping experiments
CIMMYT, CIP, ICRISAT, IRRI, JIC, NIAS
13. Decision support tools for MAS and MAB further developed
ICRISAT, CIMMYT, IRRI, *breeders in developing country agricultural research programmes*
14. Design and analysis of marker-trait association studies, with special attention for genetically challenging crops
WUR, ICL, LUMC, NIAB, SCRI, UoH
15. Methodology development for reconstruction of genealogies based on haplotypes related to geographic patterns
Agropolis-CIRAD, CIP

A project led by Elizabeth Arnaud (Bioversity) is finalising templates for passport, genotyping, mapping and expression data, training GCP scientists in the use of the templates, and managing the Central Registry⁴¹ of GCP datasets. The Registry contains metadata describing the datasets. It also contains the datasets themselves in template format if they are not publicly available from another source. A related project led by Robert Koebner (CropGen International)⁴² is creating a template and wizard for phenotyping data in anticipation of an increase in this type of data during GCP Phase II. This reflects a need for greater emphasis and support to PIs on proper documentation of GCP data, to complement the helpdesks and training materials.

Another project, jointly coordinated by Mathieu Rouard (Bioversity), Matthieu Conte (IRRI) and Christophe Périn (Agropolis–CIRAD), has extended the GreenPhyl database of orthologous gene families by clustering 12 plant genomes into protein gene families using a phylogenomic approach. GOST, which predicts phylogenomic relationships between a particular gene and the species represented in GreenPhyl, has been integrated into the Taverna⁴³ workflow system for ease of use by researchers. An iterative version, i-GOST, has been developed to integrate several protein sequences into a gene family.

Theme 2: Tools – Quality improvement of research data and bioinformatics applications in the GCP Consortium

This theme is concerned with improving the quality, handling and accessibility of data as well as access to analysis and visualisation tools. A project coordinated by Graham McLaren (IRRI) aims to develop a GCP Informatics Platform. In 2008, it focused on access to the data and tools specifically required by researchers in Subprogrammes 1, 2 and 3. To improve efficiency, Martin Senger and the back-end team at IRRI completely refactored the platform middleware layer to access different data sources. The workbench of query, visualisation and analytical tools for analysis of genetic diversity was enhanced by Manuel Ruiz (Agropolis–CIRAD), with additional facilities to access new data types and databases, filter data, assess data quality, check for duplicates and compute linkage disequilibrium (LD). The general web query engine and interface, Koios, was improved and deployed as the basis of a new workbench for functional genomics in rice by Richard Bruskiwich (IRRI). Jayashree Balaji (ICRISAT) and Guy Davenport (CIMMYT) made progress on stand-alone tools to support molecular breeding.

A second project to develop tools and technology to increase the functionality of the GCP Informatics Platform is led by Martin Senger (IRRI). The main focus has been on providing

several data sources as Java-based components allowing access to data resources, especially covering the International Crop Information System (ICIS) database. Other data sources covered include databases run by Bioversity, especially EURISCO⁴⁴ (the European Plant Genetic Resources Search Catalogue), which contains passport data on European *ex situ* genetic resource collections, and the rice mutant database run at IRRI. Another important task was to create the software 'Pantheon Validator' to validate and check the quality of individual data sources. A pedigree viewer was developed for the platform, and existing third-party tools – Soaplab⁴⁵ and BioMOBY – were supported and extended.

A third project coordinated by Thomas Metz (IRRI) that deals with data quality management and improvement delivered several products in 2008. The ICRISAT Laboratory Information Management System (LIMS) was upgraded to support the high-throughput genotyping service laboratory at ICRISAT, and seven users in developing country national programmes, ARIs and a private company were assisted in its use. Algorithms to assess the quality of data were developed and applied to GCP genotyping datasets. The results indicate that quality is very variable and needs to be documented and, in some cases, improved if the datasets are to provide reliable assessments of genetic structure. Two collaboration platform tools were maintained and supported during 2008. CropForge,⁴⁶ a software engineering and collaboration platform for open source software development and support, hosts 82 projects, 25 of which are related to GCP, and has 225 registered users. The GCPWiki⁴⁷ platform for collaboration within GCP has 50 registered users and includes about 800 content pages.

Anthony Collins (CIP) has continued to lead a project to make high-performance computing available to GCP scientists. The computing clusters at CIP, ICRISAT and IRRI have been upgraded with new operating systems and grid-enabled so that future applications can simultaneously use any or all of the computing resources at the same time, and can be launched from any GCP partner institute. New applications on the clusters include a climate interpolator at CIP, a genomic synteny-based marker identification pipeline for less-studied crops (managed by Jayashree Balaji, ICRISAT) and an improved microarray data analysis pipeline (managed by Ramil Mauleon, IRRI). The CIP team continues to provide helpdesk and support services and is investigating access to global grid computing resources for when the in-house facilities become obsolete.

⁴¹ <http://gcpcr.grinfo.net/>

⁴² <http://www.cropgeninternational.com/>

⁴³ <http://taverna.sourceforge.net/>

⁴⁴ <http://eurisco.ecpgr.org/>

⁴⁵ <http://sourceforge.net/projects/soaplab>

⁴⁶ <https://cropforge.org/>

⁴⁷ http://cropwiki.irri.org/gcp/index.php/Main_Page

Theme 3: Services – Support to other GCP projects in terms of methodology, software tools and data management

GCP has invested in bioinformatics and crop information systems since its inception, and has produced many applications and developed considerable capacity. A project was started in 2008 to make these tools and skills available to partners within GCP and the wider research community to support their work on bioinformatics and data handling. The project has developed a web portal⁴⁸ that provides access to informatics tools, and has compiled a list of GCP personnel expertise in bioinformatics and biometrics to help meet the commitment to respond within 48 hours to requests for assistance.

Marco Bink (WUR) continues to lead a project providing statistical support to GCP scientists. As well as organising well-received workshops, this project gave one-on-one support on issues such as experimental design, phenotypic and genotypic data curation, quality control and diversity analysis. Specific consultations were undertaken with researchers from CIP on association mapping in potato, with Bioversity, IITA and Agropolis–CIRAD on diversity in *Musa* germplasm, and with Diversity Array Technology Pty Ltd (DART P/L), to compare the effectiveness of DART markers with that of SSR markers for elucidating genetic structure in germplasm collections. Assistance has also been provided to the GCP Genotyping Support Service⁴⁹ (GSS), through training and consultations.

Another project, coordinated by Guy Davenport (CIMMYT) with participation from teams at IRRI, NIAS (National Institute of Agrobiological Sciences, Japan), JIC (John Innes Centre, UK), ICRISAT and CIP, concentrates on supporting SP2 scientists working on comparative genomics and expression array analysis. This project has continued to adapt or develop and apply tools for the analysis of gene expression and QTL data. A GCP implementation of the genomics informatics system Ensembl⁵⁰ is being used to manage GCP maize sequence data for analysis of SNP data collected through the Solexa system of Illumina Inc.⁵¹ The project also provides direct support to GCP projects generating gene expression and mapping data such as the SP2 project on 'Determination of a common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes'. Support to projects in identifying common factors for abiotic and biotic stress responses across species has included implementation of next-generation sequencing analysis tools to analyse high-throughput Solexa sequences.

A project coordinated by Jayashree Balaji (ICRISAT), has continued to develop iMAS for use by developing country partners. Based on user feedback from testing workshops, iMAS has been refined and Version 1.4 of the system has been released and distributed to end-users, and the user manual has been updated. Currently, iMAS consists of six modules: data validation, including multiple location datasets and multiple population mapping datasets; phenotyping, including analysis of multi-environment datasets; linkage map building; QTL analysis with selective viewing and printing options; genome display; and sample size determination for marker-assisted backcrossing (MABC). Map outputs are now compatible with the CMTV mapping tool.

Fred van Eeuwijk (WUR) leads a project on the design and analysis of marker–trait association studies, with special attention to genetically challenging crops. The project reviewed the state of the art in LD mapping at a workshop in Wageningen, and will now build on this knowledge to develop a new methodology for polyploid species.

Lessons learnt

There is scope for increasing the coherence of the portfolio of commissioned projects in SP4, and for enhancing connections to research activities in other Subprogrammes. One underlying factor prompting this direction is the extent to which attention was given to building infrastructure in GCP Phase I, and a second is the dispersed nature of the SP4 team. Efforts have begun to consolidate projects into more meaningful units, for example, the merging of templates and Central Registry tasks in Output 3. This will continue in 2009 with a refocusing of SP4 Themes to cover infrastructure, data curation and quality, biometrics and bioinformatics support, and methodology development. Increasing the connection and relevance of SP4 projects to research activities in other Subprogrammes is being achieved by placing greater emphasis on helpdesk and service projects.

Some products identified in SP4 commissioned projects are delayed or are not being delivered at all. This can be attributed in part to overoptimistic proposals and underestimation of the resources required for developing tools and methodologies. Another cause is the overextension of team members who all have other institutional and research commitments. A determined attempt will be made to align future commissioned work more closely to the institutional responsibilities of team members and to help partners arrive at realistic estimates of the resources and time required to deliver products.

⁴⁸ <http://www.generationcp.org/bioinformatics.php>

⁴⁹ <http://www.generationcp.org/sp5/?da=08122824>

⁵⁰ <http://www.ensembl.org/index.html>

⁵¹ <http://www.illumina.com>

Conclusions, and perspectives on 2009 and Phase II

The year 2008 has seen the maturing of SP4 activities with the delivery of some basic infrastructure for integrating dispersed data sources and for facilitating comparative genomics. As SP4 moves into Phase II, increased attention is also being given in the transition period to the service aspects of SP4's mandate.

Two factors will influence the direction of SP4 activities during this new phase. The first is the implementation of the iPlant Collaborative⁵² (iPC) in the USA that proposes to invest USD 50m in cyber infrastructure for plant biology. SP4 will need to integrate with this effort, which coincides closely with the Subprogramme's upstream ambitions. Much of the basic

infrastructure should be developed by the large iPC initiative, with SP4 activities tending to support the crop improvement dimension of informatics, particularly molecular breeding.

The second factor is the anticipated shift in emphasis of GCP activities from basic research to deployment of products. Thus, the move into Phase II is seeing information and technology generated in Phase I being applied in crop improvement. The informatics constraints to implementing molecular breeding in development agriculture include requirements for much more precise sample and pedigree tracking, and integration of data from different sources – laboratory and field. Also, new procedures are needed to analyse genotypic and phenotypic data, and present the results in ways that are useful for crossing and selection decisions. Finally, it will be necessary to integrate local breeding data with other public datasets collected by GCP and other partners in development agriculture.

⁵² <http://iplantcollaborative.org/>

Subprogramme 5: Capacity-building and enabling delivery

Rationale

This Subprogramme is cross-cutting and is mandated to build capacity as the means of securing delivery of products from GCP's technical Subprogrammes. SP5 fulfils its role not only by building technical capacity for the efficient implementation of research activities in the other Subprogrammes, but also by facilitating the flow of GCP products through the research–delivery continuum by addressing international and national policy questions. In addition, SP5 engages in selected socio-economic studies at the Programme level to inform GCP's research focus in terms of crops, regions and traits for better decision-making, and to guide prioritisation and resource allocation. In this way, SP5 adds value to the activities of the other Subprogrammes.

As well as supporting delivery, capacity-building is crucial for the long-term sustainability of the GCP research platform. The end of 2008 marks the completion of the first phase of GCP. This conveys a sense of urgency to the Programme as a whole, and especially to SP5. When research projects terminate, delivery of their outputs and products should also be completed. As the quantity of products increases, so too does the importance of promoting these products efficiently to ensure fulfilment of GCP's goal of having impact in farmers' fields. This impact is directly proportional to the ability of partners in developing country national programmes to take up the technical outputs and use them in crop improvement in target regions. Therefore, successful delivery depends heavily on there being high-calibre researchers who can ensure the adoption of the research outputs, and their assimilation into efficient plant breeding programmes.

In building the capacity of national collaborators, SP5 directly serves GCP's mission. Following the recommendations of the 2007–2008 EPMR, SP5 is evolving to a pattern of fewer but more sharply focused activities that are firmly embedded in GCP's other Subprogrammes.

Major achievements in 2008

- **Support to PhD candidates at the West Africa Centre for Crop Improvement (WACCI):** In April 2008, GCP negotiated an agreement with WACCI at the University of Ghana to support four PhD candidates. The candidates were to be selected from among research communities working on the crops prioritised by GCP for Phase II of the Programme, giving priority also to the target countries in

which GCP aims to have its greatest impact in this second phase. Two students – Ruth Thompson from the Crops Research Institute (CRI) in Ghana, and Dramane Sako from the Institut d'économie rurale (IER) in Mali – will start their graduate studies in January 2009, with two additional students in January 2010.

- **Enhancing the Genotyping Support Service with a bioinformatics helpdesk:** The GSS has continued to serve the needs of teams in developing country research institutes. In 2008, 16 teams representing nine countries (Bolivia, Brazil, China, Ethiopia, Ghana, Iran, Kenya, Sri Lanka and Tanzania) benefited from support in the application of molecular markers in germplasm management and MAB. To enhance support to partners, strong links were established between the GSS and the new Helpdesk on Bioinformatics and Biometrics.⁵³ The GSS is demonstrating that the adoption of molecular marker technologies by developing country researchers will only increase when there is the necessary support to access genotyping facilities and conduct data analysis.
- **Establishing a cassava community of practice for Africa:** The community of practice (CoP) mechanism is conducive to both research achievement and delivery, and is especially important for cassava, with its particular challenges as a clonally propagated crop. The newly established cassava CoP in Africa is offering a unique mechanism for creating and maintaining close links between developing country breeding programmes and the CGIAR Centres, while also building links with users, cassava breeding networks, international breeding programmes and related GCP projects. The CoP aims to become the avenue of choice for empowering cassava researchers, operating as the crucial adoption and transfer factor in the delivery path from upstream research products to developing relevant varieties for the intended user community.
- **Developing and implementing a GCP Workflow Management System:** SP5 is developing a tool to assist project information and document management through a central online system. This tool consists of six modules: proposal submission, project reporting, product repository, publications, contacts database and an events manager. It aims to enhance interactions between project collaborators and the GCP Management Team (MT) and Project Office, as well as encouraging information exchange among Subprogrammes.

⁵³ <http://www.generationcp.org/bioinformatics.php?da=08106902>

Activity report

The activities conducted within SP5 are organised according to five Themes, each divided into several projects. These are shown in Box 8, along with a listing of partners involved in SP5 activities during 2008.

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

Three sets of training materials were made available on the GCP website and on CD-ROM in 2008. The materials cover: the 'Genetic resource policies course'⁵⁴ a distance learning module; 'Genomics and comparative genomics';⁵⁵ and the 'Crop bioinformatics course'.⁵⁶ Additional materials are at different stages of completion and are expected to be released in 2009. These materials are on 'Dynamics of diversity of cultivated plants', 'Modern breeding', 'Drought phenotyping' and 'Association genetics'.

Three training events were conducted in 2008 targeting priority topics and trainees identified in consultation with GCP technical Subprogrammes. The first, held in February, was a course on 'Applied statistical methods in plant genomics', organised by the Centro Internacional de Altos Estudios Agronómicos Mediterráneos–Instituto Agronómico Mediterráneo de Zaragoza (CIHEAM–IAMZ), Spain, and co-funded by GCP. It targeted plant breeders seeking to update their statistical skills to take full benefit of new genomics tools.

The second, a 'Phenotyping course for drought-related traits across tropical legumes – concepts and practices', was held at ICRISAT in India in March. It registered 24 participants including 10 scientists, seven technicians from the TLI project, two scientists and one technician from TLII, as well as four scientists from the rest of the GCP community at large.

The third event held in November was a workshop on 'Reference sets of food crop germplasm for international collaboration'. This was jointly convened by Agropolis–CIRAD and GCP in Montpellier, France, to introduce the broader GCP scientific community to the Programme's germplasm reference samples. It is hoped that these samples will be widely distributed and used, so that new data can be integrated in order to derive and share biological understanding useful for germplasm diversity management and use. Various players engaged in germplasm management in international programmes contributed to the workshop, including the SGRP, the Global Crop Diversity Trust, and the Global Partnership Initiative for Plant Breeding Capacity Building (GIPB).

Theme 2: Cultivating research and learning opportunities for GCP collaborators and developing country scientists to further the GCP mission and progress

A number of approaches were used to achieve the aims of this Theme in 2008. Research topics for fellowships were proposed by GCP project PIs. Screening was then done based on the closest match with ongoing GCP research, thereby using the fellowships to not only enhance individual capacity but also boost selected Programme-level research priorities. In response to a call made in December 2007, five fellowships were awarded as detailed in Box 9.

The 2008 call for GCP Travel Grants was oriented towards hands-on training. Five awards were made to applicants from India, Nigeria, Tanzania and Thailand. In addition, 10 researchers were awarded grants to participate in GCP's 2008 Annual Research Meeting (ARM) in Bangkok, Thailand. The travel grants to the ARM mainly targeted researchers working in national programmes in the region (Asia), particularly those involved in the 'Rice in Asia Platform' or the Rice CoP in the Mekong Region, as well as African and Asian recipients of Capacity-building *à la carte* grants. Two more Travel Grants were awarded to researchers from the Bolivian national programme, PROINPA, to attend a workshop to initiate an SP3-funded groundnut project. This workshop followed the TLI annual meeting in Dakar, Senegal. Training travel grants are listed in Box 10, while ARM and groundnut workshop travel grants appear in Box 11 and Box 12, respectively.

The 2008 competitive call for Capacity-building *à la carte*⁵⁷ awards went out in December 2007. The main purpose of this programme is to strengthen developing country partner teams heavily involved in GCP projects in applying newly gained knowledge and outputs in their home countries. The awards provide training, equipment and technical backstopping. The two partner-led African teams and one Asian team detailed in Box 13 were selected for their close fit with the expectations of the call.

As noted in the 2007 Annual Report, the candidate originally selected for the professorship in molecular breeding at the African Centre for Crop Improvement (ACCI) at the University of KwaZulu–Natal (UKZN) declined the position, and recruitment recommenced. After a fresh round of advertising and interviews, a molecular plant breeder, Dr Jedidah Danson from Kenya, was appointed and took up the post in November 2008.

⁵⁴ <http://www.generationcp.org/distantpolicies/>

⁵⁵ <http://www.generationcp.org/genomics/>

⁵⁶ <http://mcclintock.generationcp.org/>

⁵⁷ <http://www.generationcp.org/capcorner.php?da=0775534>

Box 8. SP5 Themes, projects and partners.

Lead partner(s) underlined, where applicable. Activities led from GCP Headquarters are marked 'GCP'. Full names of partners in *Acronyms and abbreviations*.

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

1. Selected training courses in molecular analysis of germplasm, genomics/ molecular breeding, bioinformatics and phenotyping conducted
CIHEAM-IAmZ, WUR; ICRISAT, CIAT, IITA, UoC (Riverside), Agropolis-CIRAD, GCDT, GIPB, SGRP
2. Training materials for phenotyping developed
Agropolis-INRA, ICRISAT, IRRI, UoC
3. Training materials for modern plant breeding developed
CU
4. Learning materials completed and disseminated
GCP, WUR, IRRI, IGD-CU

Theme 2. Cultivating research and learning opportunities for GCP collaborators and developing country scientists to further the GCP mission and progress

5. Capacity-building à la carte Programme
Grantee institutes underlined and followed by the respective mentoring partner(s).
2008 awards: BRRI, IRRI, UoD; INERA-Burkina Faso, IITA, UoC-Riverside; ISRA, IITA, UoC-Riverside
2007 awards: (ongoing) ABRII, IPK, IRRI; CRI-Ghana, CIMMYT; ICABIOGRAD, IRRI, RCB-IPB; ISRA, Agropolis-CIRAD, EMBRAPA, UCB; KARI, Agropolis-INRA; NRCRI, CIAT
6. Fellowship Programme
Grantee institute underlined and followed by the respective host institute/s: NKLCGGE, SCRI; USP, EMBRAPA and WUR; CIMMYT, Agropolis-INRA; PhilRice, WUR
7. GCP Travel Grant Programme
See:
 - Box 10. Travel grants awarded for training
 - Box 11. Travel grants awarded to attend the 2008 GCP Annual Research Meeting
 - Box 12. Travel grants awarded to attend the groundnut workshop
8. Academic position in molecular breeding established and supported
ACCI, RF
9. PhD in plant breeding at the West Africa Centre for Crop Improvement, University of Ghana
WACCI, AGRA, CU

Theme 3. Constructing systems for ensuring product delivery

10. Capacity-building mechanisms and product pipelines established for tropical legume improvement in Africa
Lead institute N/A: each takes the lead in their activity:
ARI-Naliendele, ART, CRS, CBI, EIAR, INERA-Burkina Faso, IRAD, ISRA, LZARDI, SARI-Ethiopia

11. Delivery Plan remote learning modules

CIMS-INCAE, CU

12. Comprehensive support provided to competitive projects to define delivery and capacity-building plans

GCP

13. Improve cowpea productivity for marginal environments in Mozambique

UEM, UoC (Riverside)

14. A cassava breeding community of practice in Africa for accelerated production and dissemination of farmer-preferred cassava varieties resistant to pests and diseases

CIAT, NRCRI, ARI-Naliendele, CRI-Ghana, IITA, NaCRRI

15. Establishment of and support to crop and regional platforms

Barwale Foundation, Rice in Asia Platform partners

16. A project development guide (PDG) designed and implemented

N/A

17. Validation of GCP products

WUR

18. GCP product distribution

GCP

Theme 4. Developing and implementing support services

19. Interactive Resource Centre established and maintained

IGD-CU

20. Toolbox of available molecular markers useful for marker-assisted selection in GCP crops

Veerle van Damme (consultant)

21. Genotyping Support Service

Beneficiaries: AC-UT, ARI-Ghana, CNRRI, CRI-Ghana, CRI-Sri Lanka, KARI, EMBRAPA, INIA-Chile, MARI, PROINPA, SARI-Ethiopia, UARI
Service providers: CIAT, DaT P/L, ICRISAT, IRRI, KUL, WUR

22. Development and implementation of a GCP Workflow and Repository System

GCP assisted by Cropster GmbH (service provider)

Theme 5. Ex ante impact analysis and impact assessment

23. Targeting and impact analysis of GCP technologies

CIAT, CIMMYT, IFPRI, IRRI

24. Ex ante impact analysis of marker-assisted selection technologies supported by GCP

VPI

25. Getting the focus right: food crops and smallholder constraints

CIMMYT, CIAT, ICARDA, ICRISAT, IITA, IRRI

26. A strategic assessment of the capacity to develop and adopt GCP technologies

IFPRI, CIAT

Box 9. Fellowships awarded in 2008.

Name	Institute	Country	Topic	Host
1. Zhengzhi Zhang	NKLCGGE, NAU	China	Translation of SNPs underlying drought tolerance in wild barley into high-throughput low-technology markers	SCRI, UK
2. Priscilla Sabadin	USP	Brazil	Multi-trait multi-environment QTL analysis for agronomical performance of sorghum on acid soils	EMBRAPA Maize and Sorghum, Brazil and WUR, The Netherlands
3. Caroline Marques Castro	EMBRAPA Clima Temperado	Brazil	The use of relatedness information in linkage disequilibrium mapping: pedigree information versus molecular marker information	WUR, The Netherlands
4. Mateo Vargas Hernández	CIMMYT	Mexico	Data analysis of a network of field trials involving a population of recombinant inbred lines: dissecting the genotype x environment interaction	Agropolis-INRA
5. Dindo A Tabanao	PhilRice	Philippines	The use of relatedness information in linkage disequilibrium mapping: pedigree information versus molecular marker information	WUR, The Netherlands

Given the importance of relying on strong crop breeding teams in Africa during GCP Phase II, SP5 negotiated the admission of four GCP-funded candidates into the PhD programme at WACCI. This is a five-year programme, of which the first two years are devoted to academic courses, the next two to research in the home institution, and the final year to dissertation writing and defence. Two candidates were selected to commence studies in January 2009. Another two others will be selected later in 2009 to start in January 2010. The PhD programme is co-funded by the Alliance for a Green Revolution in Africa (AGRA).

Theme 3: Constructing systems for ensuring product delivery

The Project Development Guide (PDG),⁵⁸ a tool for information and guidance on best practice for GCP-funded projects, was tested by a number of collaborators. Feedback was incorporated and the tool made publicly available online prior to GCP's third competitive call for research proposals made in March 2008.

An SP5-funded project with emphasis on product delivery, namely the 'Delivery Plan remote learning modules', started in 2008. This project will formulate a series of interactive

modules to guide trainees through all of the steps of designing Delivery Plans, and thus ensure that the inherent concept and objectives are internalised.

In the context of Objective 6 of the TLI project – 'Training and capacity-building for sub-Saharan African scientists' – SP5 provided 10 collaborating national programmes with computers and equipment for drought phenotyping. The support was identified through an infrastructural needs assessment.

Funding was provided in 2008 for a project linked to TLI on improving cowpea productivity for marginal environments in Mozambique. The project aims to add Mozambique to the TLI network, which will also enhance national capacity in drought tolerance screening. This is being achieved through training in data analysis for GxE interactions and, importantly, in the design and implementation of a MAS-based programme, in close collaboration with mentors at the University of California, Riverside (USA).

⁵⁸ <http://www.generationcp.org/pdg/>

Box 10. Travel grants awarded for training

Name	Institute	Country	Topic	Host
1. Sarkar Ramani Kumar	CRRRI	India	Molecular markers	IRRI
2. Afiukwa Celestine Azubuikwe	Ebonyi State University	Nigeria	Molecular markers	FABI, South Africa
3. Triwitayakorn Kanokporn	Mahidol University	Thailand	Phenotyping for drought	Cornell University, USA
4. Jude Obidiegwu	NRCRI	Nigeria	Phenotyping for drought	CSIRO, Australia
5. Geoffrey Mkamillo	ARI-Naliende	Tanzania	Marker-assisted selection	CIAT, Colombia

Box 11. Travel grants awarded to attend the 2008 GCP Annual Research Meeting

Name	Institute	Country
1. Shailaja Hittalmani	UAS (Bangalore)	India
2. Kongpanh Kanyavong	NAFRI	Laos
3. Issa Drabo	INERA	Burkina Faso
4. MA Salam	BRRRI	Bangladesh
5. Nguyen Thi Lang	CuuLong Delta Rice Research Institute	Vietnam
6. Ndiaga Cissé	ISRA	Senegal
7. Khin Than Nwe	DAR	Myanmar
8. Sabariappan Robin	TNAU	India
9. Habibul Bari Shozib	University of Dhaka	Bangladesh
10. Lalith A Perera	Coconut Research Institute	Sri Lanka

Box 12. Travel grants awarded to attend the groundnut workshop

Name	Institute	Country
1. René Maita	PROINPA	Bolivia
2. Jorge Rojas	PROINPA	Bolivia

Box 13. Capacity-building à la carte awards for 2008

Team Leader	Institute	Country	Project
1. MA Salam	BRRRI	Bangladesh	Enhancing MAS capacity for salt-stress rice breeding in Bangladesh
2. Issa Drabo	INERA	Burkina Faso	Improving capacity for phenotyping for abiotic and biotic stress in Burkina Faso
3. Ndiaga Cissé	ISRA	Senegal	Improving capacity for phenotyping for abiotic and biotic stress in Senegal

During the year, SP5 became involved in a new concept of validating GCP products for use by the wider research community, especially in developing countries. The first project under this umbrella is supporting a developing country scientist to work under the supervision of statisticians and molecular geneticists at WUR. The outputs will consist of rules and protocols for constructing reference sets of genotypes and markers to be used for all GCP crops, plus defined reference sets for a number of crops.

The CoP for rice in the Mekong Region went into its second year, and the model was used to establish the new 'Cassava breeding community of practice in Africa' to accelerate production and dissemination of farmer-preferred cassava varieties resistant to pests and diseases. This project will provide a framework for breeder-to-breeder training in traditional and new breeding methods, for germplasm resource exchange, and for web-based information sharing to achieve breeding goals and address common problems. It will facilitate the integration of molecular breeding into field-based breeding by transferring and implementing effective strategies for breeding primarily for disease and pest resistance in target countries. It will contribute to capacity-building for breeding teams in developing countries through formal mechanisms (MSc) and informal training involving exchange visits and workshops. It will also build links with primary, secondary and tertiary users of improved cassava varieties to ensure rapid uptake of technologies.

Two projects initiated and completed in 2008, in collaboration with SP1, contributed to the training of Hungarian scientists in characterisation procedures using SSR markers. They characterised Hungarian maize and bean germplasm and compared it with the respective GCP reference sets. Finally, following on from the first meeting of the 'Rice in Asia Platform' in 2007, SP5 provided support to seven scientists to participate in the 2008 'International workshop-cum-training on marker-assisted selection' organised by the Barwale Foundation.

Theme 4: Developing and implementing support services

The 2007 Annual Report presented three operational helpdesks, namely, the Interactive Resource Center (IRC)⁵⁹ supported by SP5 in collaboration with Cornell University, USA, the Intellectual Property Helpdesk⁶⁰ supported by SP5, and the Data Templates Helpdesk⁶¹ (supported by SP4 and linked to SP1, SP2 and SP3). These helpdesks continued to assist GCP projects and partners in 2008 and the new Helpdesk on Bioinformatics and Biometrics,⁶² which is managed by SP4 and linked to SP5 and the GSS⁶³ in particular, became fully operational in 2008. It provides advice on

experimental design and data analysis from the stage of selecting appropriate methods through to the use of results in applicants' research projects.

Following the pilot phase, the first call for GSS applications was made in 2007 and implemented in 2008. A total of 33 applications were received, of which 19 were successful. They covered potatoes (with five applications), cassava (with four), rice (with three), sweet potatoes (with two), and maize, chickpeas, coconuts, yams and *Musa/Ensete* (one application each). The successful applications were from Tanzania (four), Kenya and Ghana (three each), Brazil (two), and Bolivia, Chile, China, Ethiopia, India, Iran and Sri Lanka (one each). Fourteen of the applications aim to conduct molecular characterisation of germplasm, while five address plant breeding issues such as MAS, gene tagging or genetic map development. The completion workshop for participants in the 2007 call is planned for January 2009.

During 2008, based on experience, user feedback and lessons learnt, efforts were made to continually improve GSS administrative and technical procedures, particularly contracts with service providers. Also improved were the 'Genotyping Support Service Request Form', the applicants' DNA quality requirements and data quality control. A second GSS call went out in July 2008. It attracted 49 proposals, of which 31 have been accepted for implementation starting in 2009.

After completing the first phase of the Workflow Management System (WMS) in early 2008, the decision was made to expand and upgrade its functions in terms of user integration. During 2008, significant advances were made in the new system that should now be able to integrate external project collaborators and executors (eg, PIs) in a more direct manner. It will provide traceability for project proposal review processes, serve as a one-stop-shop to document different GCP activities and integrate and exchange information about projects among different Subprogrammes. The tool will streamline project and report submission, support calls for applications and assist in organising events. It will also serve as a repository of GCP-related publications and automatically input information into the GCP products database.

Finally, a new project to be completed in 2009 is developing a toolbox of available molecular markers. This will provide easy access to information on all publicly available molecular markers that are ready for use in MAS and MAB for 19 food

⁵⁹ <http://irc.igd.cornell.edu/>

⁶⁰ <http://www.generationcp.org/iphelpdesk.php?da=0629604>

⁶¹ <http://www.generationcp.org/bioinformatics.php?da=0782837>

⁶² <http://www.generationcp.org/bioinformatics.php?da=08106902>

⁶³ <http://www.generationcp.org/capcorner.php?da=0794844>

security crops. The activity will compile information available through Internet sources, public databases and published papers, as well as gathered through communication with molecular crop breeding experts. The toolbox will be available via the Internet as a global public good. In a bid to reach yet more target users, the tool and what it offers will be described in a peer-reviewed publication.

Theme 5: *Ex ante* impact analysis and impact assessment

SP5 *ex ante* impact analysis activities are intended to support GCP in decision-making, priority-setting and resource allocation. An ongoing CIAT-led project initiated in 2006 targets broad-scale but high-resolution global impact assessment for GCP. It comprehensively reviews priority farming systems, including detailed poverty evaluation in priority areas. It assesses the implications of drought for each GCP crop, with in-depth evaluation of constraints and opportunities related to crop production, thus teasing out factors that could impede, or greatly enhance, the end use of GCP technologies.

A second project led by the Virginia Polytechnic Institute and State University (VPI), USA, was completed in 2008. It examined GCP-supported research on discovering genes for tolerance to saline and phosphorous-deficient soils to enhance rice productivity, and on developing low-cost technologies for pyramiding genes from wild relatives into elite progenitors of cassava. The results predicted economic benefits based on the situation with and without the new traits, and considered: (i) the area planted to crops affected by target stresses and production in specific countries; (ii) the nature of relevant markets; (iii) projected changes in yields and costs; (iv) the time required to develop and deploy the DNA marker technologies; (v) the time required to develop and disseminate new cultivars; and, (vi) the discount rate.

The economic surplus analysis has been completed for rice and cassava, and presented in two MSc theses. Results indicate that MAB in rice will save at least 3–6 years compared to conventional breeding (CB). MAB also yields significant incremental benefits. These range from USD 50–500 million, depending on the country, the abiotic stress and the lag for CB under base assumptions. For cassava, benefits of using MAB to incorporate resistance to cassava mosaic disease, green mites, white flies, and post-harvest deterioration vary between USD 34m and USD 817m, depending on the country. Although the costs of using MAB exceed those of CB, the financial benefits of its use are such that it is clearly the more cost-effective approach. A third thesis on gender impacts of improved cassava varieties in Nigeria is still underway. A household survey has been completed and the data obtained are currently being analysed for presentation in an MSc thesis.

Two new projects started in 2008. The first, led by IFPRI, is entitled 'From attractiveness to feasibility: a strategic assessment of the capacity to develop and adopt GCP Technologies'. This project will subject GCP's initial target/focus areas to an evaluation of the likely capacity of local institutions and farmers to realise the projected potential on GCP impact. Three to five countries will be selected in which GCP has significant ongoing collaborations and with promising impact in Phase II. The second project, led by CIMMYT and entitled 'Getting the focus right: food crops and smallholder constraints', will systematically tap into the tacit knowledge of experienced R&D practitioners to provide valuable information on the relative importance of different production constraints and traits in addition to drought. It will concentrate on six crops (wheat, rice, sorghum, cassava, chickpeas and cowpeas). The study should provide a checklist and guide to those involved in crop breeding and crop systems R&D by prioritising key traits for improvement in each of the systems.

Lessons learnt

Experience from Phase I proves that downstream sustainability of GCP research will depend on a stable critical mass of trained, networked and well-equipped researchers. These researchers must link with broader regional and international networks. Equally important is maintaining interactions with peers and/or mentors, who will help assess new capacity needs and identify interventions to provide mentoring support as the researchers mature in their capabilities and progressively advance to working on their own.

Notwithstanding SP5's efforts to date to enhance capacity among partners, it is also important to sustain support to build and maintain effective teams in downstream research. The challenge is to confront the weakness in most developing country plant breeding programmes resulting from insufficient institutional support coupled with inadequate funds for breeding activities. Thus, it is important not to overestimate the capacity or presuppose the readiness of developing world researchers and, instead, assess partnerships carefully and give special consideration to building capacity tailored to the constraints identified in project Delivery Plans.

Conclusions, and perspectives on 2009 and Phase II

All aspects of SP5's work saw significant progress in 2008. Support was provided to priority teams and individuals, training partnerships were consolidated, and complementary resources and mechanisms extended the reach of GCP's capacity-building efforts to a wider community of users.

In parallel with these efforts to help build a critical mass of skilled practitioners, SP5 also made strides forward in developing tools to streamline access to information on GCP's processes and products, and in understanding the pathways to achieving impact.

The rationale for SP5 as a whole, and for capacity-building in particular, is founded on GCP's philosophy on delivery. The concrete results and products that GCP has generated in Phase I will only have major impact when they reach the intended users. Therefore, capacity-building efforts will be based on the developments and advances arising from GCP research, and will continue to focus firmly on users.

The success of the GCP project portfolio and research management approach in Phase II will, similarly, depend greatly on the capacity of the institutions selected as recipients and promoters of GCP products. Where there are capacity shortfalls, SP5 will endeavour to fill the gap to ensure that the expected impact of the new initiatives and projects can be realised, thereby contributing to the success of GCP as a whole.

Generating products is essential but products alone are not impact. They have to respond to user demand and be appropriately tailored and packaged. Often, capacity-building provides the only bridge for GCP products to reach intended users and intended applications. This emphasises

the key role of SP5 in targeting the right partners in the user community, and fostering supportive and dynamic relationships with them.

Lessons and actions from SP5 in Phase I will be instructive in implementing the CIs in 2009 and beyond. More than ever before, the majority of the SP5 interventions will be through the Capacity-building *à la carte* programme. Interventions will be complemented by activities that follow the model of CoPs or regional crop platforms. SP5 will also support projects that promote delivery per se. These will include a suite of support services such as the ongoing GSS, the concept of which will be extended to other GCP products in the near future.

Finally, SP5 will continue its innovative socio-economic investigations into factors that influence the impact of GCP's work upon target beneficiaries. Results to date show the dramatic benefits that can follow in terms of the speed of crop improvement and reduced costs when molecular breeding is applied to staple crops in priority farming systems. The studies are also providing important diagnostic information that will guide the planning and implementation of future crop improvement initiatives. Thus, not only will these studies serve to validate GCP's strategic approach, they will sharpen priority-setting and targeting of resources. This will maximise the Programme's impact on the livelihoods of poor people throughout the developing world.

Financial report

Summary

GCP is grateful to the funder community for its generous support. Agencies and foundations who supported our Programme in 2008 include the European Commission (EC), the UK Department for International Development (DFID), the Bill & Melinda Gates Foundation (BMGF), the World Bank (WB), the Swiss Agency for Development and Cooperation (SDC), and the Swedish International Development Cooperation Agency (Sida). We are also grateful to INRA–Morocco and the Government of Hungary for providing matching funds for specific GCP research activities.

In 2008, our major funders continued to support GCP at about the same level as in previous years, with the exception of the European Commission. At the end of June, EC announced that their support would 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. 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, including the support to a new CGIAR Challenge Programme. However, this reduction in the EC contribution had been anticipated, and we had cautiously projected an income of EUR 4 million for 2008.

The major factor that affected the 2008 income was a volatile exchange rate between the United States dollar (USD) and the Euro and Pound Sterling. Consequently, GCP effectively lost approximately USD 1.5m (1.0m from DFID and 0.5m from EC) due to unfavourable exchange rates in 2008. In terms of the projection, this results in a loss of USD 0.5m, since we had already projected income in foreign currencies at 10 percent below the exchange rate prevailing at the time of writing the 2007 report.

We recently received DFID's 2009–2010 notification, and are very pleased to report that this contribution will remain at GBP 2.5m. Otherwise, projections for 2009 are affected by both the actual reduction of the EC contribution and continuing uncertainties regarding exchange rates. Our net projection for income in 2009 is USD 11.0m, or USD 17.7m if we include delayed 2008 payments and USD 100,000 in interest (see below). But we have used a very conservative exchange rate at 25 percent below January 2009 values, in view of the significant

exchange rate fluctuations in 2008. In this scenario, GCP would have a projected deficit of USD 2.4m at the end of 2009, resulting in total net assets of USD 4.4m.

2008 budget

Financial figures for 2008 are presented in the following tables:

- Table 1. 2008 Summary financial report: Income versus expenditure
- Table 2. 2008 research budget by category of project and expense
- Table 3. 2008 detailed expenditure schedule

The actual income received by the end of December 2008 amounted to USD 8.9m in donations (Table 1), comprising 2008 funds from the World Bank, DFID (80 percent of the 2008 funding), the Bill & Melinda Gates Foundation and SDC. Ninety percent of the 2008 EC contribution, and the remaining 10 percent of the 2007 EC contribution were received in January 2009, as well as a supplementary payment of GBP 0.5m from DFID. Therefore, these delayed disbursements (amounting to USD 6.7m) are all reported under income in 2009 (Table 6). Summing up the income for 2008 reported in Table 1 and Table 6, the total income for the year is USD 15.7m.

Interest generated in 2008 amounted to USD 188,000 – slightly lower than had been projected due to the sharp drop in US interest rates payable on fixed-term deposits.

In 2008, expenditure reached USD 17.6m. This is USD 4.7m less than had been projected in our 2007 Annual Report (USD 22.3m, Table 9). The difference mainly resulted from the non-disbursement in 2008 of USD 4.1m worth of committed funds (due to delays in contracting, some partners' non-compliance with administrative requirements, and withheld balances of 20 percent in the final year to be paid once final technical and financial reports have been approved). These funds will be disbursed during the first quarter of 2009. In addition, a conservative approach in our operational expenditures resulted in a saving of about USD 0.6m.

Comparing income versus expenditure, the result is a deficit of USD 8.5m for 2008, but is reduced to USD 1.9m if we consider the total 2008 income (USD 15.7m) received in 2008 and 2009. If we add to this amount the USD 4.1m for 2008

commitments carried forward to 2009 (see explanation below), we arrive at a net deficit of USD 6.0m, which exactly corresponds to our projection (USD 6.0m, 2007 Annual Report Table 9).

The deficit of USD 8.5m for 2008 has been covered by the 2007 designated reserve carryover of USD 12.3m (the delays in disbursement by some of our funders has been a recurrent trend through the years, and explains the history of large carryovers at year-end). Therefore, at the end of 2008, GCP had a balance of designated reserves amounting to USD 3.8m (see Table 1) which will be used to cover outstanding contractual obligations of USD 4.1m.

By the end of 2008, the total contingency reserve stood at USD 3.0m and is intended to cover the following two potential contingent expenditures:

- a) staff costs in the event of closure of programme activities (USD 1.0m); and
- b) funds for research activities in 2009–2010 (USD 2.0m).

GCP spent USD 15.2m in 2008 to support research activities (details in Table 2). To meet our research objectives, resource allocation across the Subprogrammes is evolving, in step with implementing our strategy. Compared to 2007, the major trend is a decrease in resources allocated to SP1 and SP4, and increases for SP2 and SP5.

Details on our operational expenditures are presented in Table 3. Starting in 2008, salaries for Subprogramme Leaders (SPLs) are now reported under 'Research management' – a new expense category. In 2009, support to the Product Delivery Coordinators, as well as some planning fora will also be reported under this new expense category. The expenses to support conferences decreased in 2008 because, for the first time, we requested Principal Investigators (PIs) to charge ARM travel to their research projects, since these costs are budgeted for in every new project. In 2008, the cost for 'Offices supplies and services' includes costs for a professional recruitment firm hired to assist in recruiting the Product Delivery Leader.

2009 projected budget

Projected financial figures for 2009 are presented in the following tables:

- Table 6. 2009 projected income versus expenditure – summary
- Table 7. 2009 projected research budget by category of project and expense
- Table 8. 2009 projected expenditure schedule – details

Income for 2009 is projected at USD 17.6m, which takes into account a conservative reduction of USD 2.0m before an eventual loss of 25 percent on the EC and DFID contributions due to unfavourable exchange rates. As explained in the previous section, USD 6.7m of the income is from late disbursement of some 2008 contributions. Taking into account our current commitments, expenditures will be USD 20.1m, resulting in a projected deficit of USD 2.4m (Table 6). Designated carryover from 2008 (USD 3.8m) will absorb this deficit to reflect a balance of designated reserves of USD 1.4m at the end of 2009 (Table 6). Our net assets are projected to be USD 4.4m at the end of 2009.

Although it will not change the overall financial picture, we would like to underscore that 20 percent of the funds for the 2009 commissioned projects will be paid in 2010 to ease cash flow. It is also expected that the 2009 and 2010 EC contributions will be received during the respective fiscal years, given the current three-year EC–GCP contract. Under these circumstances: i) GCP should be able to disburse committed funds in early 2010, and, ii) the pressure to maintain a high carryover to bridge project funding early during the fiscal year and delayed disbursements from funders should be reduced.

In 2009, GCP will devote USD 16.3m to research activities (details in Table 7). The detailed projection of our operational expenditure for 2009 is presented in Table 8, with line item allocation largely similar to 2008.

List of financial tables and charts

Unless otherwise indicated, currencies in the financial tables are in USD.

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Table 1. 2008 Summary financial report: Income versus expenditure

	Actual
Income	
Bill & Melinda Gates Foundation (BMGF)	3,143,579
DFID ^{1/}	3,283,900
Sida ^{2/}	61,093
SDC ^{3/}	436,506
World Bank	2,000,000
Subtotal	8,925,078
Interest ^{4/}	188,293
Total income ^{5/}	9,113,371
Expenditure	
Salaries and benefits	486,329
Travel	77,795
Conferences	102,067
Programme Steering Committee	20,096
Executive Board	43,736
Office supplies and services	126,648
Vehicle expenses	9,987
Publications	32,693
Consultants	138,450
Research grants (refer to Table 2)	15,175,562
Research management (SPLs 1–5)	491,873
Capital equipment	29,466
Indirect costs ^{6/}	849,297
Total expenditure	17,583,998
Surplus/(deficit) for year ^{7/}	(8,470,627)

^{1/} Equivalent to GBP 2.0m^{2/} Equivalent to SEK 0.5m^{3/} Equivalent to CHF 0.45m^{4/} Includes interest credit for DFID USD 57,000; and BMGF USD 6,000^{5/} Commitments for matching funds in the amount of USD 121,500; USD 100,000 INRA–Morocco contribution and USD 21,500 Government of Hungary contribution^{6/} 18% direct costs, and 4% on services and pass-through funds^{7/} See 'Statement of changes in net assets' below**Statement of changes in net assets**

	2007	2008
Designated		
Opening balance	7,341,035	12,287,524
Net surplus/(deficit) for year	4,946,489	(8,470,627)
Closing balance – net assets	12,287,524	3,816,897
Undesignated		
Contingency reserve	3,000,000	3,000,000
Total net assets	15,287,524	6,816,897
Represented by:		
Accounts receivable	12,121,979	
Funds held at CIMMYT	2,165,545	3,816,897
Cash held at CIMMYT	1,000,000	3,000,000
Total net assets	15,287,524	6,816,897

Table 2. 2008 research budget by category of project and expense

Particulars	Actual January–December
Commissioned and competitive projects	11,807,029
Research commitments prior years	165,395
Commissioned research Year 4 (2007 – 20%) ^{1/}	158,891
Commissioned research Year 5	7,913,732
Competitive grants Round I (2007 – 20%) ^{2/ 3/}	157,460
Competitive grants Round II ^{2/}	869,043
Competitive grants Round III ^{2/}	2,542,508
Operational support SPLs	350,000
Focus projects	3,018,533
TLI Project Years 1 and 2 (2007–2008)	3,018,533
Total	15,175,562

^{1/} 20% of annual project funds withheld pending approval of financial and technical reports

^{2/} Round I: 2005–2007; Round II: 2007–2009; Round III: 2008–2011

^{3/} 20% of final year funds withheld pending approval of final financial and technical reports

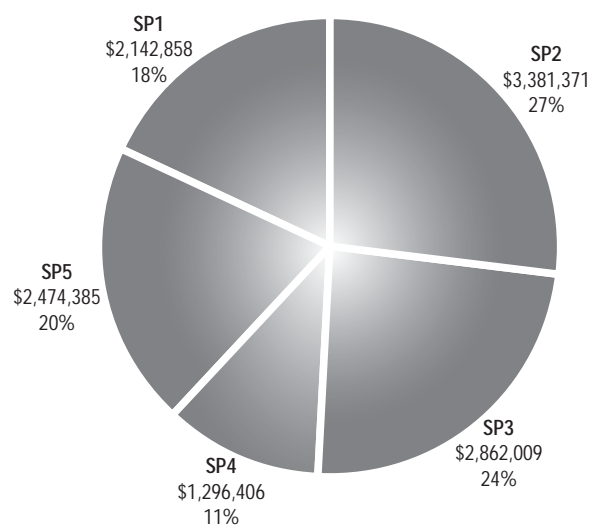
Chart 1. 2008 research budget allocation by Subprogramme

Table 3. 2008 detailed expenditure schedule

Description	Actual	
	Expenditure	Total
1. Salaries and Benefits		486,329
1.1 International staff	381,584	
1.2 National staff	104,744	
2. Travel		77,795
Fares and subsistence – GCP staff	77,795	
3. Conferences		165,898
GCP Programme Steering Committee	20,096	
GCP Annual Research Meeting ^{1/}	96,710	
Executive Board	43,736	
CGIAR Annual General Meeting	5,356	
4. Office Supplies and Services		126,648
Stationery and other consumables	11,753	
Shipping and postage	6,585	
Maintenance and repair	25	
Calls and fax	13,123	
ICT Service (Information and communication technologies)	38,251	
Subscriptions	378	
Recruitment	56,534	
5. Vehicle Expenses		9,987
Fuel		4,208
Insurance	1,751	
Maintenance	4,027	
6. Publications		32,693
Production and design	16,623	
Software/Website	16,070	
7. Consultants		138,450
Science and quality control	46,868	
Web programming and design	32,645	
Legal consultant	25,502	
Facilitators/others	33,435	
8. Research grants (details in Table 2)		15,175,562
Commissioned, competitive and focus projects	15,175,562	
9. Research management ^{2/}		491,873
Support to SPLs (salaries, benefits and discretionary funds)	491,873	
10. Capital equipment		29,466
	29,466	
Indirect costs ^{3/}		849,297
Indirect costs – 18% (Items 1, 2, 3, 4, 5, 8 and 9)	239,952	
Indirect costs – 4% ^{4/} (Items 6, 7, 8, 9 and 10)	586,885	
Indirect costs – 15% TLI project	22,460	
Total expenditure		17,583,998

^{1/} Costs partially absorbed by satellite workshops around Annual Research Meeting

^{2/} SPLs 1, 2 and 4 half-time; SPLs 3 and 5 full-time. SPL 4 full-time as of September 2008

^{3/} Indirect costs: 18% on direct costs and 4% on services and pass-through funds including a focus project

^{4/} Research grants to GCP's host institution not subject to indirect costs of 4%

Table 4. 2008 research budget summary by type of partner and project

Institute type	Grant type			Total	%
	Competitive	Commissioned	Focus		
CGIAR Centres	1,476,059	3,633,303	1,327,150	6,436,512	40
Developed country partners	1,738,967	2,311,001	824,997	4,874,965	30
Developing country partners	1,300,468	1,958,429	866,431	4,125,328	26
Service providers	0	550,940	125,000	675,940	4
Total	4,515,494	8,453,673	3,143,579	16,112,746	100

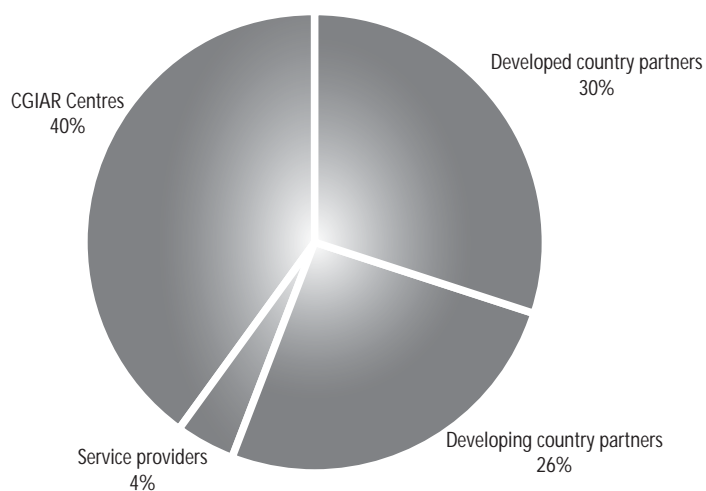
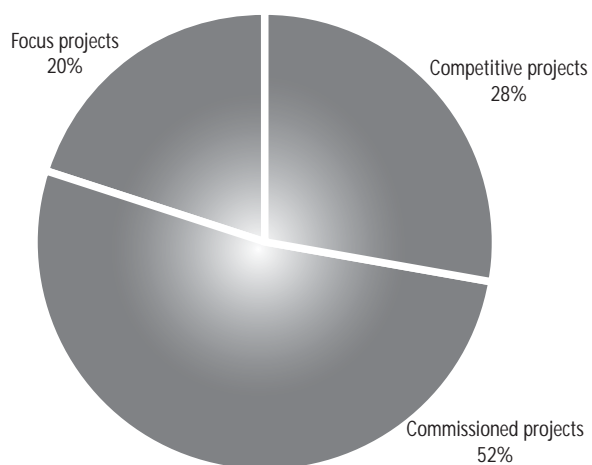
Chart 2. 2008 research budget by type of partner**Chart 3. 2008 research budget by category of research**

Table 5. 2008 research budget summary by Consortium members and research category

No.	Institute	Competitive	Commissioned	Focus	Total
1	ACGT	0	0	0	0
2	Agropolis	0	781,906	0	781,906
3	BIOTEC*	0	98,689	0	98,689
4	Bioversity International	0	178,968	0	178,968
5	CAAS	0	70,800	0	70,800
6	CIAT	194,400	234,980	514,009	943,389
7	CIMMYT	295,200	836,370	0	1,131,570
8	CINVESTAV*	0	0	0	0
9	CIP	0	416,598	0	416,598
10	Cornell University	37,172	88,966	0	126,138
11	EMBRAPA	224,400	32,540	0	256,940
12	IAO*	0	0	0	0
13	ICAR	0	0	0	0
14	ICARDA	187,901	0	0	187,901
15	ICRISAT	73,900	815,499	691,193	1,580,592
16	IITA	0	96,132	95,751	191,883
17	INRA–Morocco*	18,000	100,000	0	118,000
18	IRRI	635,765	698,591	0	1,334,356
19	JIC	0	0	0	0
20	NIAS	0	20,400	0	20,400
21	WARDA	72,700	203,730	0	276,430
22	WUR	0	231,028	0	231,028
Total – Consortium		1,739,438	4,905,197	1,300,953	7,945,588
Total – Non-Consortium		2,776,056	3,548,476	1,842,626	8,167,158
Grand total		4,515,494	8,453,673	3,143,579	16,112,746

*Provisional Consortium members

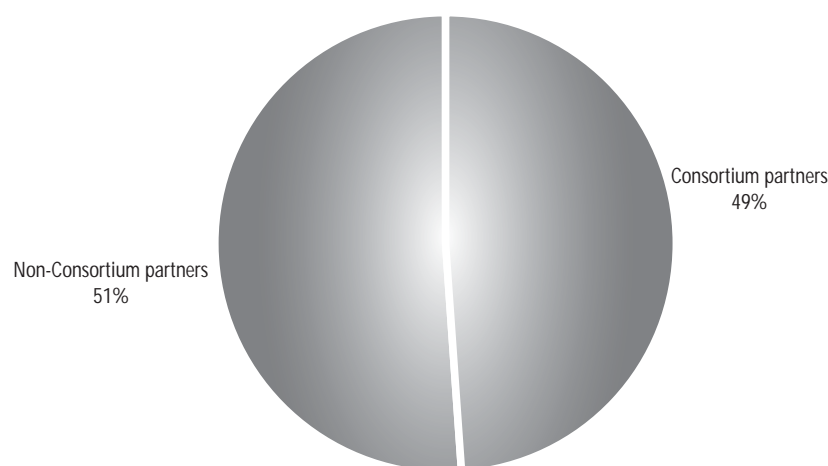
Chart 4. 2008 research budget by Consortium and non-Consortium partners

Table 6. 2009 projected income versus expenditure – summary

	2009 Projection
Income	
Bill & Melinda Gates Foundation	2,966,279
DFID ^{1/}	3,317,088
European Commission ^{2/}	8,928,421
Pioneer Hi-Bred International, Inc	25,000
SIDA ^{3/}	90,208
SDC ^{4/}	294,295
World Bank	2,000,000
Sub-Total	17,621,290
Interest	80,000
Total income	17,701,290
Expenditure	
Salaries and benefits	770,000
Travel	150,000
Conferences	300,000
Executive Board	150,000
Office supplies and services	120,000
Vehicle expenses	30,000
Publications	70,000
Consultants	250,000
Research grants (Refer to Table 2)	16,262,040
Research management ^{5/}	940,000
Capital equipment	55,000
Indirect costs ^{6/}	1,045,782
Total	20,142,821
Surplus/(deficit) for year ^{8/}	(2,441,531)

^{1/} Equivalent to GBP 0.5m receivable in January 2009; and equivalent to GBP 2.5m in two instalments July and December 2009 (Note 7)

^{2/} Equivalent to EUR 0.9212m receivable in January 2009, retention 2007 (10%); 2008 contribution equivalent to EUR 4.095m expected in two instalments: 1st instalment EUR 3.685m (90%) in January 2009; and, 2nd instalment, retention (10%) EUR 0.409m receivable in 2010; 2009 contribution equivalent to EUR 3.503m expected in two instalments: 1st instalment EUR 3.153m (90%) receivable in 2009; and, 2nd instalment, retention (10%) EUR 0.35m receivable in 2011 (Note 7)

^{3/} Equivalent to SEK 1.0m (Note 7)

^{4/} Equivalent to CHF 0.45m (Note 7)

^{5/} SPLs 1–5, Product Delivery Coordinators, and strategic events

^{6/} 18% on direct costs, and 4% on services and pass-through funds

^{7/} All outstanding foreign currency receipts subject to exchange rate fluctuations (due to exchange rate fluctuations, income projection is at a rate of 25% below prevailing exchange rate in January 2009)

^{8/} See 'Statement of changes in net assets' below

Statement of changes in net assets

	2008	2009
Designated		
Opening balance	12,287,524	3,816,897
Net surplus/(deficit) for year	(8,470,627)	(2,441,531)
Closing balance – net assets	3,816,897	1,375,366
Undesignated		
Contingency reserve	3,000,000	3,000,000
Total net assets	6,816,897	4,375,366
Represented by:		
Funds held at CIMMYT	3,816,897	1,375,366
Cash held at CIMMYT	3,000,000	3,000,000
Total net assets	6,816,897	4,375,366

Table 7. 2009 projected research budget by category of project and expense

Particulars		Projection
Commissioned and competitive projects		13,249,244
Commissioned research prior years	748,923	
Commissioned research Year 5 (2008 – 20%) ^{1/}	1,464,476	
Commissioned research 2009	7,118,621	
Competitive grants Round III ^{2/}	2,840,477	
Competitive grants Rounds I and II ^{2/} (2008 – 20%) ^{3/}	1,076,747	
Operational support SPLs		200,000
Challenge Initiatives		210,000
Operational support Product Delivery Coordinators	210,000	
Focus projects		2,602,796
TLI Project Years 2 and 3 (2008–2009)	2,602,796	
Total		16,262,040

^{1/} 20% of annual project funds withheld pending approval of financial and technical reports

^{2/} Round I: 2005–2007; Round II: 2007–2009; Round III: 2008–2011

^{3/} 20% of final year funds withheld pending approval of final financial and technical reports

Table 8. 2009 projected expenditure schedule – details

Description	Projection	
	Expenditure	Total
1. Salaries and benefits		770,000
1.1 International staff (Headquarters)	640,000	
1.2 National staff	130,000	
2. Travel		150,000
Fares and subsistence – GCP staff	150,000	
3. Conferences		450,000
Annual Research Meeting	285,000	
Executive Board	150,000	
Consortium Committee	15,000	
4. Office supplies and services		120,000
Stationery and other consumables	18,000	
Shipping and postage	10,000	
Maintenance and repair	5,000	
Calls and fax	18,000	
ICT Service (Information and communication technologies)	45,000	
Subscriptions	9,000	
Recruitment	15,000	
5. Vehicle expenses		30,000
Fuel	12,000	
Insurance	6,000	
Maintenance	12,000	
6. Publications		70,000
Production and design	35,000	
Software/website	35,000	
7. Consultants		250,000
Science and quality control	100,000	
Web programming and design	40,000	
Legal consultant	35,000	
Facilitators/others	75,000	
8. Research grants		16,262,040
Commissioned, competitive and focus projects	16,262,040	
9. Research management		940,000
Support to SPLs (salaries, benefits and discretionary funds)	640,000	
Product Delivery Coordinators	150,000	
Strategic events	150,000	
10. Capital equipment		55,000
	55,000	
Indirect costs ^{1/}		1,045,782
Indirect costs – 18% (Items 1, 2, 3, 4, 5, 8 and 9)	420,782	
Indirect costs – 4% ^{2/} (Items 6, 7, 8, 9 and 10)	600,000	
Indirect costs – 15% TLI project	25,000	
Total expenditure		20,142,821

^{1/} Indirect costs: 18% on direct costs and 4% on services and pass-through funds including a focus project

^{2/} Research grants for GCP host institution not subject to indirect costs of 4%

Table 9. Competitive projects Round II: Total budget

Project No.	Title	SP	Year 1: 2007	Year 2: 2008	Total
G3007.01	iBridges: Interspecific bridges that give full access to the African rice allele pool for enhancing drought tolerance of Asian rice	1	340,000	329,000	669,000
G3007.02	Genomic dissection of tolerance to drought stress in wild barley	1	343,154	224,450	567,604
G3007.03	Development of genomic resources for molecular breeding of drought tolerance in cassava	2	434,215	323,843	758,058
G3007.04	Tailoring superior alleles for abiotic stress genes for deployment into breeding programmes: a case study based on association analysis of <i>Alt_{Sb1}</i> , a major aluminium tolerance gene in sorghum	3	299,598	303,503	603,101
G3007.05	Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-aided breeding	3	284,458	314,132	598,590
G3007.06	Genetic dissection of drought adaptive mechanisms in bread and durum wheat through large-scale phenotyping methodologies	2	301,000	301,000	602,000
Total			2,002,425	1,795,928	3,798,353

Table 10. Competitive projects Round III: Total budget

Project No.	Title	SP	Year 1: 2008	Year 2: 2009	Year 3: 2010	Total
G3008.01	Generating new wheat germplasm with enhanced drought/heat tolerance using AB genome's genetic diversity	1	259,940	259,940	259,940	779,820
G3008.02	Improving grain yield on acid soils by the identification of genetic factors underlying drought and aluminium tolerance in maize and sorghum	1	406,521	257,248	193,597	857,366
G3008.03	Delayed senescence and drought tolerance in rice	2	264,108	281,873	305,915	851,896
G3008.04	Drought from a different perspective: improved tolerance in rice through phosphorus acquisition	2	300,000	300,000	300,000	900,000
G3008.05	Discovery and development of alleles contributing to sorghum drought tolerance	2	246,880	250,167	259,178	756,225
G3008.06	Targeting drought-avoidance root traits to enhance rice productivity under water-limited environments	3	300,000	300,000	300,000	900,000
G3008.07	Basal root architecture and drought tolerance in common bean	3	292,667	300,667	306,666	900,000
G3008.08	Breeder-friendly high-throughput phenotyping tools to select for adaptive traits in drought environments	3	300,050	303,327	293,696	897,073
G3008.09	Breeding drought tolerance for rainfed lowland rice in the Mekong region	4	269,200	287,200	291,200	847,600
Total			2,639,366	2,540,422	2,510,192	7,689,980

A note on commissioned projects

For details on commissioned projects, please see *Appendix C: Ongoing projects in 2008 by category and Subprogramme*.

Table 11. Focus projects: Total budget**Improving tropical legume productivity for marginal environments in sub-Saharan Africa**

Project No.	Objective No.	Objective	Year 1: 2007	Year 2: 2008	Year 3: 2009	Total
G6007.01	1	Improving groundnut (<i>Arachis hypogaea</i> L) productivity for marginal environments in sub-Saharan Africa	1,075,446	1,014,030	948,036	3,037,512
G6007.02	2	Improving cowpea (<i>Vigna unguiculata</i> L) productivity for marginal environments in sub-Saharan Africa	928,623	544,374	479,011	1,952,008
G6007.03	3	Improving common bean (<i>Phaseolus vulgaris</i> L) productivity for marginal environments in sub-Saharan	625,384	628,009	613,934	1,867,327
G6007.04	4	Improving chickpea (<i>Cicer arietinum</i> L) productivity for marginal environments in sub-Saharan Africa	357,348	364,800	351,978	1,074,126
G6007.05	5	Developing cross-species resources for comparative biology in tropical crop legumes	256,402	295,166	316,120	867,688
G6007.06	6	Training and capacity-building for sub-Saharan African scientists	297,200	297,200	257,200	851,600
Total			3,540,404	3,143,579	2,966,279	9,650,262

Appendixes

Appendix A: GCP Consortium members and partners – 2008

1. Consortium members¹

Full members

1. Africa Rice Center (WARDA)
2. African Centre for Gene Technologies (ACGT), South Africa
3. Agropolis, France (incorporating CIRAD, INRA and IRD)
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 Maíz 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

2. Developing country partners

1. African Centre for Crop Improvement (ACCI) at the University of KwaZulu–Natal, South Africa
2. African Centre for Gene Technologies (ACGT), South Africa*
3. Agharkar Research Institute, India
4. Agricultural Biotechnology Research Institute of Iran (ABRII)
5. Agricultural College, University of Tehran, Iran
6. Agricultural Research and Technology Corporation (ARTC), Sudan
7. Agricultural Research Institute, Ghana
8. Agricultural Research Institute (ARI), Naliende Research Station, Tanzania
9. All-India Coordinated Pearl Millet Improvement Project (AICPMIP)
10. Bangladesh Institute of Nuclear Agriculture (BINA)
11. Bangladesh Rice Research Institute (BRRI)
12. Barwale Foundation, India
13. Birsa Agricultural University, Ranchi, India
14. Bureau of Rice Research and Development (BRRD), Rice Department, Thailand
15. Cambodia Agricultural Research and Development Institute (CARDI)
16. Central Arid Zone Research Institute (CAZRI), India
17. Central Rainfed Upland Rice Research Station (CRURRS), India
18. Central Rice Research Institute (CRRI), India
19. Centre d'étude régional pour l'amélioration de l'adaptation à la sécheresse, (CERAAS), Senegal
20. Centro de Inteligencia sobre Mercados Sostenibles (CIMS), INCAE Business School, Costa Rica
21. China National Rice Research Centre
22. Chinese Academy of Agricultural Sciences (CAAS)*
23. Chitedze Research Station, Malawi
24. Coconut Research Institute (CRI), Sri Lanka
25. Crop Breeding Institute (CBI), Department of Research for Development, Zimbabwe
26. Crop Research Institute (CRI), Ghana
27. Cuu Long Delta Rice Research Institute, Vietnam
28. Debre Zeit Agricultural Research Centre (DZARC), Ethiopia
29. Department of Agricultural Research (DAR), Myanmar
30. Department of Agriculture Research Services (DARS), Malawi
31. Department of Agriculture, Indonesia

¹ In the partner lists from category 2 onwards, Consortium members are also included, and denoted by an asterisk*, and provisional members by †

32. Directorate of Maize Research (DMR), India
33. Directorate of Wheat Research (DWR), India
34. Dr Panjabrao Deshmukh Krishi Vidyapeeth (PDKV; Dr Panjabrao Deshmukh Agricultural University), India
35. Ebonyi State University, Nigeria
36. Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA; Brazilian Agricultural Research Corporation)*
37. Ethiopian Agricultural Research Organization (EARO)
38. Ethiopian Institute of Agricultural Research (EIAR)
39. Fedearroz, Colombia
40. Foibem-Pirenena Mombra ny Fikarohana Ampiharina Amin'ny Fampandrosoana ny eny Ambanivohitra (National Centre for Applied Research on Rural Development) Département de la recherche agronomique (FOFIFA–DRA), Madagascar
41. Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, South Africa
42. Hebei Academy of Agricultural Sciences, Institute of Dry Farming, China
43. Huazhong Agricultural University (HZAU), China
44. Indian Agricultural Research Institute (IARI)
45. Indian Council of Agricultural Research (ICAR)*
46. Indian Institute of Pulses Research (IIPR)
47. Indira Gandhi Krishi Vidyalyaya (IGKV; Indira Gandhi Agricultural University), India
48. Indonesian Centre for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD)
49. Indonesian Cereals Research Institute (ICERI)
50. Institut d'économie rurale (IER), Mali
51. Institut de l'environnement et de recherches agricoles (INERA), Burkina Faso
52. Institut de la recherche agronomique pour le développement (IRAD), Cameroon
53. Institut des sciences agronomiques du Burundi (ISABU)
54. Institut des sciences agronomiques du Rwanda (ISAR)
55. Institut national de la recherche agronomique (INRA) Morocco[†]
56. Institut national de la recherche agronomique du Niger (INRAN)
57. Institut national pour l'étude et la recherche agronomique (INERA), Democratic Republic of Congo
58. Institut sénégalais de recherches agricoles (ISRA), Senegal
59. Institute of Crop Science, Chinese Academy of Agricultural Sciences (ICS–CAAS)*
60. Instituto Agronomico de Campinas, Brazil
61. Instituto de Botánica del Nordeste (IBONE), Argentina
62. Instituto de Investigação Agrária de Moçambique (IIAM; Institute for Agricultural Research), Mozambique
63. Instituto de Investigaciones Agropecuarias (INIA–Chile)
64. Instituto Nacional de Ciencias Agrícolas (INCA), Cuba
65. Instituto Nacional de Investigación Agropecuaria (INIA), Uruguay
66. Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias (INIFAP), Mexico
67. Instituto Nacional de Tecnología Agropecuaria (INTA), Argentina
68. Instituto Nacional de Tecnología Agropecuaria (INTA), Nicaragua
69. Kasetsart University, Thailand
70. Kenya Agricultural Research Institute (KARI)
71. Lake Zone Agricultural Research and Development Institute (LZARDI), Tanzania
72. Luoyang Academy of Agricultural Sciences (LAAS), China
73. Maharana Pratap University of Agriculture and Technology (MPUAT), India
74. Mahidol University, Thailand
75. Maize and Millets Research Institute (MMRI), Pakistan
76. Marathwada Agricultural University (MAU), India
77. Melkassa Agricultural Research Centre (MARC), Ethiopia
78. Mikochei Agricultural Research Institute, Tanzania
79. Moi University, Kenya
80. Nakhon Sawan Field Crops Research Center (NSFCRC), Thailand
81. Namulonge Agricultural and Animal Research Institute (NAARI), Uganda
82. Nanjing Agricultural University (NAU), China
83. Narendra Deva University of Agriculture and Technology (NDUAT), India
84. National Agricultural and Forestry Research Institute (NAFRI), Laos
85. National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand[†]
86. National Crop Resources Research Institute (NaCRRI), Uganda
87. National Institute for Plant Genome Research (NIPGR), India
88. National Key Lab of Crop Genetics and Germplasm Enhancement, China
89. National Maize Research Institute (NMRI), Vietnam
90. National Plant Genetic Resources Centre (NPGRC), Tanzania
91. National Research Centre on Plant Biotechnology (NRCPB), India
92. National Research Centre on Sorghum (NRCS), India
93. National Root and Tuber Crop Research Institute (NRCRI), Nigeria
94. Ningxia University, China
95. Northwest Sci-tech University of Agriculture and Forestry (NWSUAF), China
96. Organisation for the Rehabilitation of the Environment (ORE), Haiti
97. Pakistani Agricultural Research Council (PARC)
98. Peking University, China
99. Philippine Rice Research Institute (PhilRice)
100. Pohang University of Science and Technology, South Korea

101. Promoción e Investigación de Productos Andinos (PROINPA), Bolivia
102. Punjab Agricultural University (PAU), India
103. Rajasthan Agricultural University (RAU), India
104. Research Center for Biotechnology, Bogor Agricultural University (RCB–IPB), Indonesia
105. Rice Gene Discovery Unit, Thailand
106. Savannah Agricultural Research Institute (SARI), Ghana
107. Scientific and Industrial Research and Development Centre (SIRDC), Zimbabwe
108. Serere Agricultural and Animal Production Research Institute (SAARI), Uganda
109. Shanxi Academy of Agricultural Sciences (SAAS), China
110. Sichuan Agricultural University (SAU), China
111. Sokoine University of Agriculture, Tanzania
112. South Agricultural Research Institute (SARI), Ethiopia
113. Tamil Nadu Agricultural University (TNAU), India
114. Tishreen University, Syria
115. Ubon Ratchatani University, Thailand
116. Universidad Autónoma Chapingo, Mexico
117. Universidad de Talca, Chile
118. Universidade Católica de Brasília (UCB), Brazil
119. Universidade de São Paulo (USP), Brazil
120. Universidade Eduardo Mondlane, Mozambique
121. University of Agricultural Sciences (UAS), Bangalore, India
122. University of Agricultural Sciences (UAS), Dharwad, India
123. University of Dhaka, Bangladesh
124. University of Ghana
125. University of KwaZulu–Natal (UKZN), South Africa
126. University of Pretoria, South Africa
127. University of the Witwatersrand, South Africa
128. Uyo Agricultural Research Institute, Tanzania
129. West Africa Centre for Crop Improvement (WACCI), Ghana
130. Yunnan Academy of Agricultural Sciences (YAAS), China
131. Zhejiang University, China
9. Centre national de génotypage (CNG), France
10. Charles Sturt University, Australia
11. Colorado State University, USA
12. Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia
13. Cornell University, USA*
14. Department of Plant Sciences and Plant Physiology, Eszterházy Károly College, Eger, Hungary
15. Department of Primary Industries and Fisheries (DPI&F), Australia
16. Eidgenössische Technische Hochschule (ETH; Swiss Federal Institute of Technology)
17. European Bioinformatics Institute (EBI), UK
18. Imperial College London, UK
19. Institut de recherche pour le développement (IRD), France*
20. Institute for Agrobotany, Tápíószele, Hungary
21. Institute for Genomic Diversity (IGD), Cornell University, USA*
22. Japan International Research Center for Agricultural Sciences (JIRCAS)
23. John Innes Centre (JIC), UK*
24. Kansas State University, USA
25. Katholieke Universiteit Leuven (KUL), Belgium
26. Leibniz Institute for Plant Genetics and Crop Plant Research (IPK), Germany
27. Leiden University Medical Centre, The Netherlands
28. Max Planck Institute for Molecular Plant Physiology (MPIMPP), Germany
29. Nagoya University, Japan
30. National Center for Genome Resources (NCGR), USA
31. National Institute of Agricultural Botany (NIAB), UK
32. National Institute of Agrobiological Sciences (NIAS), Japan*
33. North Carolina State University (NCSU), USA
34. Oregon State University (OSU), USA
35. Pennsylvania State University, USA
36. Plant Breeding Institute, University of Sydney, Australia
37. Purdue University, USA
38. Research Institute for Fisheries, Aquaculture and Irrigation (HAKI), Hungary
39. Rikagaku Kenkyusho (Institute of Physical and Chemical Research), RIKEN, Japan
40. Scottish Crop Research Institute (SCRI), UK
41. Texas A&M University, USA
42. United States Department of Agriculture–Agricultural Research Service (USDA–ARS)
43. Università di Bologna, Italy
44. Università di Udine, Italy
45. University of Aarhus, Denmark
46. University of Aberdeen, UK
47. University of Adelaide, Australia
48. University of Alberta, Canada

3. Developed country partners

1. Agence nationale de la recherche (ANR), France
2. Agricultural Biotechnology Center (ABC), Gödöllő, Hungary
3. Agricultural Research Institute, Hungarian Academy of Sciences (ARI–HAS)
4. Australian Centre for Plant Functional Genomics Pty Ltd (ACPGF)
5. Austrian Research Centers GmbH
6. Agropolis–Centre de coopération internationale en recherche agronomique pour le développement (CIRAD), France*
7. Agropolis–Institut de recherche pour le développement (IRD), France*
8. Agropolis–Institut national de la recherche agronomique (INRA), France*

49. University of Arizona, USA
50. University of California, Davis, USA
51. University of California, Riverside, USA
52. University of Frankfurt, Germany
53. University of Georgia (UGA), USA
54. University of Hohenheim, Germany
55. University of Maryland, USA
56. University of Missouri, USA
57. University of Potsdam, Germany
58. University of Queensland, Australia
59. University of Virginia, USA
60. University of Washington, USA
61. Virginia Bioinformatics Institute (VBI), Virginia Polytechnic Institute and State University (VPI), USA
62. Wageningen University and Research Centre (WUR), The Netherlands*
63. Yale University, USA

4. Funders

1. Bill & Melinda Gates Foundation
2. Department for International Development (DFID), UK
3. European Commission (EC)
4. Swedish International Development Cooperation Agency (Sida)
5. Swiss Agency for Development and Cooperation (SDC)
6. The World Bank

5. CGIAR Centres and Programmes

1. Africa Rice Center (WARDA)*
2. Bioversity International*
3. Centro Internacional de Agricultura Tropical (CIAT; International Center for Tropical Agriculture)*
4. Centro Internacional de la Papa (CIP; International Potato Center)*
5. Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT; The International Maize and Wheat Improvement Center)*
6. CGIAR Central Advisory Service for Intellectual Property (CAS-IP)
7. Challenge Program on Water and Food
8. HarvestPlus Challenge Program

9. International Center for Agricultural Research in the Dry Areas (ICARDA)*
10. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)*
11. International Food Policy Research Institute (IFPRI)
12. International Institute of Tropical Agriculture (IITA)*
13. International Livestock Research Institute (ILRI)
14. International Rice Research Institute (IRRI)*
15. Sub-Saharan Africa Challenge Programme
16. System-wide Genetic Resources Programme (SGRP) of the CGIAR

6. Private sector

17. Diversity Arrays Technology Pty Ltd (DArT P/L), Australia
18. Biogemma, France
19. Genaissance Pharmaceuticals, Inc, France
20. Pioneer Hi-Bred International, Inc
21. Syngenta
22. Waen Associates, UK

7. Service providers

1. ADNid Montpellier, France
2. CropGen International
3. Cropster GmbH
4. Everogen (Russia)
5. J Craig Venter Institute, USA
6. Macrogen (Korea)
7. National Center for Genome Resources (NCGR), USA
8. Perlegen, USA

8. Other partners

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

Appendix B: Who's who in GCP?

This Appendix lists the people behind GCP in 2008, arranged in terms of their function as follows:

- | | |
|---------------------------------------|---|
| 1. Executive Board (EB) | 4. Product Delivery Coordinators (PDCs) |
| 2. Programme Steering Committee (PSC) | 5. Principal Investigators (PIs) |
| 3. Review and Advisory Panel (RAP) | 6. Staff |

For more information, please visit our 'Who we are' page at <http://www.generationcp.org/whoweare.php>

1. Executive Board

Effective 1 June 2008, the Executive Board replaced the PSC as GCP's apex governing body.

Board chair	
1. Calvin Qualset	Professor Emeritus, Department of Plant Sciences, University of California, Davis, USA
Board members	
2. Andrew Bennett	President of the Tropical Agricultural Association (UK) and Chair of the Boards of Trustees of the Centre for International Forestry Research (CIFOR) and Science and Development Network (SciDev.Net)
3. Claudio Gonzalez-Vega	Director of the Rural Finance Program and Professor of Agricultural, Environmental and Development Economics, Ohio State University, USA
4. Andreas Graner	Acting Director, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany
5. Jeff McElroy	Vice-President, BioEnergy Seeds, Mendel Biotechnology, Inc, USA
6. Esther Murugi Kahangi	Professor, Department of Horticulture and Deputy Vice-Chancellor for Research Production and Extension, Jomo Kenyatta University of Agriculture and Technology, Kenya
7. Harold Roy-Macauley	Representative, Guinea Node, West and Central Africa the World Agroforestry Centre (ICRAF)

Profiles of EB members at: <http://www.generationcp.org/whoweare.php?da=08124404>.

2. GCP Programme Steering Committee

Prior to the formation of the EB, the PSC provided programme guidance to GCP research activities. PSC members are drawn from member institutions of the GCP Consortium as listed below. In 2008, the PSC set up a Task Force to redefine its role in line with the governance reforms approved in December 2007.

Chair	
1. Eugene Terry	
Consortium member	
Consortium member's representative on the PSC	
Full members	
2. African Centre for Crop Improvement, South Africa (ACGT), South Africa	E Jane Morris
3. Agropolis, France (incorporating CIRAD, INRA and IRD)	Yves Savidan
4. Bioversity International	Emile Frison
5. Chinese Academy of Agricultural Sciences (CAAS), China	Gong Xifeng
6. CIAT	Douglas Pachico
7. CIMMYT	Masa Iwanaga (left 2008)
	Thomas Lumpkin (joined March 2008)
	Charles Crissman
	Steve Kresovich
	José Geraldo Eugénio de França
	Rajeev Kumar Jain
8. CIP	Maarten van Ginkel
9. Cornell University, USA	Dyno Keatinge (left 2008)
10. Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA), Brazil	David Hoisington (joined February 2008)
11. Indian Council of Agricultural Research (ICAR)	Paula Bramel
12. ICARDA	Bob Zeigler
13. ICRISAT	John Snape
	Takuji Sasaki
14. IITA	Ton den Nijs
15. IRRI	Marco Wopereis
16. John Innes Centre, (JIC), UK	
17. National Institute of Agrobiological Sciences (NIAS), Japan	
18. Wageningen University and Research Centre (WUR), The Netherlands	
19. WARDA	
Ex-officio member	
20. GCP Director	Jean-Marcel Ribaut
Provisional members	
21. Centro de Investigación y de Estudios Avanzados (CINVESTAV), Mexico	Victor Villalobos
22. Institut national de la recherche agronomique (INRA), Morocco	Mohamed Badraoui
23. Instituto Agronomico per l'Oltremare (IAO), Italy	Alice Perlini
24. National Center for Genetic Engineering and Biotechnology, (BIOTEC), Thailand	

More on the PSC and GCP Consortium at: <http://www.generationcp.org/psc.php?da=0781307>.

3. Review and Advisory Panel

RAP comprises a group of five experts who work with the Management Team, providing an objective perspective on GCP activities at SP level.

Name	Subprogramme	Home institute
Dario Grattapaglia	SP1	EMBRAPA, Brazil
Peter Langridge	SP2	Australian Centre for Plant Functional Genomics Pty Ltd (ACPFPG) and University of Adelaide, Australia
Scott Jackson		
Michel Ragot	SP3	Syngenta, France
David Marshall	SP4 and RAP Chair	Scottish Crop Research Institute, UK
Rose Rita Kingamkono	SP5	Tanzania Commission of Science and Technology, Tanzania
Ana M Espinoza Esquivel		

Profiles of RAP members at: <http://www.generationcp.org/rap.php?da=0781418>.

4. Product Delivery Coordinators

Following an extensive External Programme and Management Review (EPMR) in late 2007, in its 2008 report, the EPMR panel recommended that half of GCP's resources be devoted to seven trait–crop combinations, now termed 'Challenge Initiatives' (CIs). In 2008, a PDC was assigned to each of the seven CIs, on a 10 percent shared time basis with their home institute. The seven PDCs are:

Name	Challenge Initiative	Home institute
Cereals		
Nourollah Ahmadi	Improving drought tolerance in rice for Africa	Agropolis–CIRAD, France
Richard Trethowan	Improving drought tolerance in wheat for Asia	Plant Breeding Institute, University of Sydney, Australia
Oumar Niangado	Improving drought tolerance in sorghum for Africa	Syngenta Foundation for Sustainable Agriculture, Mali
Leon Kochian	Comparative genomics to improve cereal yields in high-aluminium and low-phosphorous soils	USDA–ARS/Cornell University, USA
Legumes		
Jeff Ehlers	Improving drought tolerance in cowpeas for Africa	University of California, Riverside, USA
Pooran Gaur	Improving drought tolerance in chickpeas for Africa and Asia	ICRISAT
Roots and tubers		
Emmanuel Okogbenin	Improving cassava yield in Africa's drought-prone environments	National Root and Tuber Crops Research Institute (NRCRI), Nigeria

5. Principal Investigators

Below are the PIs leading GCP projects in 2008.

* denotes that (a) project led by PI is on a no-cost extension into 2008

Name	SP	Home institute
1. Fouad Abbad Andaloussi	SP3	Institut national de la recherche agronomique, (INRA), Morocco
2. Jorge Acosta-Gallegos	SP3	Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias, (INIFAP), Mexico
3. Alfredo Augusto Cunha Alves*		SP3 EMBRAPA–Cassava and Tropical Fruits, Brazil
4. Elizabeth Arnaud	SP4	Biodiversity International
5. Jayashree Balaji	SP4	ICRISAT
6. Ervin Balazs	SP3	Agricultural Research Institute of the Hungarian Academy of Sciences, (ARI–HAS)
7. Michael Baum*	SP1	ICARDA
8. Anthony Bellotti*	SP3	CIAT
9. John Bennett (left 2008) *	SP2	IRRI
10. David Bertoli*	SP3	Universidade Católica de Brasília (UCB), Brazil
11. Claire Billot	SP4	Agropolis–CIRAD, France
12. Marco Bink	SP4	Wageningen University and Research Centre (WUR), The Netherlands
13. Matthew Blair	SP2	CIAT
14. Abraham Blum	SP3	Consultant
15. Eduardo Blumwald	SP2	University of California, Davis, USA
16. Richard Bruskiewich	SP4	IRRI
17. Masdiar Bustaman	SP5	Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD)
18. Jill Cairns	SP1	IRRI
19. Manuela Cereza (left 2008)	SP5	Centro Internacional de Altos Estudios Agronómicos Mediterráneos–Instituto Agronómico Mediterráneo de Zaragoza (CIHEAM–IAMZ), Spain
20. Scott Chapman*	SP3	Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia
21. Rogerio Chiulele	SP5	Universidade Eduardo Mondlane, Mozambique
22. Julapark Chunwongse	SP3	National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand
23. Ndiaga Cissé	SP5	Institut sénégalais de recherches agricoles (ISRA), Senegal
24. Anthony Collins	SP4	CIP
25. Douglas Cook	SP2	University of California, Davis, USA
26. Eric Danquah	SP5	University of Ghana
27. Guy Davenport	SP4	CIMMYT
28. Carmen de Vicente	SP5	GCP
29. John Dixon	SP5	CIMMYT
30. Issa Drabo	SP3, SP5	Institut de l'environnement et de recherches agricoles (INERA), Burkina Faso
31. Susanne Dreisigacker	SP1	CIMMYT
32. Gregory Edmeades	SP3	Consultant
33. Chiedozi Egesi	SP5	CIAT–National Root and Tuber Crops Research Institute (NRCRI), Nigeria
34. Jeffrey Ehlers	SP2, SP3	University of California, Riverside, USA
35. Morag Ferguson	SP5	IITA
36. Martin Fregene*	SP3	CIAT
37. Theresa Fulton	SP5	Institute for Genomic Diversity (IGD), Cornell University, USA

Name	SP	Home institute
38. James Gethi	SP1, SP5	Kenya Agricultural Research Institute (KARI)
39. Alain Ghesquière	SP1	Agropolis–IRD, France
40. Jean Christophe Glaszmann	SP1, SP5	Agropolis–CIRAD, France/GCP
41. Humberto Gómez Paniagua	SP5	GCP
42. Reinaldo Gomide*	SP1	EMBRAPA–Maize and Sorghum, Brazil
43. Wolfgang Gruneberg	SP3	CIP
44. Michael Halewood	SP5	Bioversity International
45. Tom Hash	SP1, SP2	ICRISAT
46. Sigrid Heuer	SP2, SP3	IRRI
47. David Hoisington (left 2008)	SP4, SP5	ICRISAT
48. Ghasem Hosseini Salekdeh	SP5	Agriculture Biotechnology Research Institute of Iran (ABRII)
49. Glenn Hyman*	SP3, SP5	CIAT
50. Abdelbagi Ismail*	SP2, SP3	IRRI
51. Ruilian Jing	SP3	Chinese Academy of Agricultural Sciences (CAAS)
52. Boonrat Jongdee	SP4	Bureau of Rice Research and Development (BRRD), Rice Department, Thailand
53. Junichi Kashiwagi	SP3	ICRISAT
54. Shoshi Kikuchi	SP2	National Institute of Agrobiological Sciences (NIAS), Japan
55. Steven J Knapp	SP2	University of Georgia (UGA), USA
56. Leon Kochian*	SP1, SP2	USDA–ARS/Cornell University, USA
57. Robert Koebner	SP4	Consultant
58. Arvind Kumar	SP3, SP5	IRRI
59. Mark Laing	SP3, SP5	University of KwaZulu–Natal (UKZN), South Africa
60. Hei Leung	SP1	IRRI
61. Zhi-Kang Li	SP5	Institute of Crop Sciences, Chinese Academy of Agricultural Sciences (CAAS)
62. Mathias Lorieux	SP1	Agropolis–IRD/CIAT, France/Colombia
63. Delphine Luquet*	SP1	Agropolis–CIRAD, France
64. Jonathan Lynch	SP3	Pennsylvania State University, USA
65. Jurandir Magalhaes	SP3	EMBRAPA–Maize and Sorghum, Brazil
66. Gregory May	SP2	National Center for Genome Resources (NCGR), USA
67. Graham McLaren	SP4	GCP
68. Kenneth McNally*	SP1	IRRI
69. Thomas Metz	SP4	IRRI
70. SC Misra	SP1	Agharkar Research Institute, India
71. Márta Molnár-Láng	SP3	Agricultural Research Institute of the Hungarian Academy of Sciences, Hungary (ARI–HAS)
72. Philippe Monneveux	SP3	GCP
73. Jean-Benoit Morel*	SP2	Agropolis–INRA, France
74. Satoru Muranaka*	SP3	IITA
75. Marie Noelle Ndjiondjop	SP3	WARDA
76. Ousmane Ndoye	SP3, SP5	Institut sénégalais de recherches agricoles (ISRA), Senegal
77. Rebecca Nelson*	SP2	Cornell University, USA
78. Norbert Niederhauser	SP5	Consultant
79. George W Norton	SP5	Virginia Polytechnic Institute and State University (VPI), USA
80. Francis Ogonnaya	SP3	ICARDA
81. Emmanuel Okogbenin	SP5	CIAT
82. Allen Oppong	SP5	Crops Research Institute (CRI), Ghana

Name	SP	Home institute
83. Peter Papp	SP5	Agricultural Biotechnology Center (ABC), Gödöllő, Hungary
84. Andrew H Paterson	SP2	University of Georgia, USA
85. Andy Pereira	SP2	Virginia Bioinformatics Institute (VBI), Virginia Polytechnic Institute and State University, USA
86. Chalermpol Phumichai	SP3	National Center for Genetic Engineering and Biotechnology, Thailand (BIOTEC)
87. Laurence Pratt	SP5	Centro de Inteligencia sobre Mercados Sostenibles (CIMS), INCAE Business School, Costa Rica
88. Pablo Rabinowicz	SP2	University of Maryland, USA
89. Jean-François Rami	SP1, SP3	Agropolis–CIRAD, France
90. Matthew Reynolds	SP2	CIMMYT
91. Mathieu Rouard	SP4	Bioversity International
92. Ruairaidh Sackville Hamilton	SP1	IRRI
93. MA Salam	SP5	Bangladesh Rice Research Institute (BRRI)
94. Robert Schaffert	SP3	Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA)–Maize and Sorghum, Brazil
95. Roland Schafleitner	SP2	CIP
96. Martin Senger	SP4	IRRI
97. Rachid Serraj*	SP2, SP3	IRRI
98. Ibolya Simon-Kiss	SP1	Research Institute for Fisheries, Aquaculture and Irrigation (HAKI), Hungary
99. Milko Škofič	SP4	Bioversity International
100. François Tardieu*	SP2	Agropolis–INRA, France
101. Dominique This	SP1	Agropolis–CIRAD, France
102. Jean-Baptiste Tignegre	SP3	Institut de l'environnement et de recherches agricoles, (INERA), Burkina Faso
103. Joe Tohme	SP1	CIAT
104. Theerayut Toojinda	SP5	National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand
105. Hari Upadhyaya	SP1	ICRISAT
106. Vincent Vadez	SP2, SP5	ICRISAT
107. José Valls*	SP3	EMBRAPA–Genetic Resources and Biotechnology, Brazil
108. Veerle van Damme	SP5	Consultant
109. Fred van Eeuwijk	SP4, SP5	Wageningen University and Research Centre (WUR), The Netherlands
110. Theo van Hintum	SP4	Wageningen University and Research Centre (WUR), The Netherlands
111. Rajeev Varshney	SP2	ICRISAT/GCP
112. Francisco Vilaró	SP3	Instituto Nacional de Investigación Agropecuaria, Uruguay (INIA), Uruguay
113. Jiankang Wang	SP3	CIMMYT/Chinese Academy of Agricultural Sciences (CAAS)
114. Marilyn Warburton*	SP1	CIMMYT
115. Robbie Waugh	SP1	Scottish Crop Research Institute (SCRI), UK
116. Stanley Wood	SP5	IFPRI
117. Yunbi Xu*	SP5	CIMMYT
118. Jianbing Yan*	SP1	CIMMYT
119. PH Zaidi	SP3	CIMMYT

More details on PIs and projects can be found at: <http://www.generationcp.org/whoweare.php?da=09137417> and Appendix C in this report on GCP projects.

6. GCP staff

Name	Function	Location	Joined
1. Jean-Marcel Ribaut	Director	GCP HQ, Mexico	2005
2. Jean Christophe Glaszmann	SP1 Leader	Agropolis–CIRAD, France	2004
3. Rajeev Varshney	SP2 Leader	ICRISAT, India	2007
4. Philippe Monneveux	SP3 Leader	GCP HQ, Mexico	2006
5. Theo van Hintum	} SP4 Leader	WUR, The Netherlands	2004 (left 2008)
6. Graham McLaren		GCP HQ, Mexico	2008
7. Carmen de Vicente	SP5 Leader	GCP HQ, Mexico	2004
8. Nosisa Mayaba	Associate Scientist, SP5	GCP HQ, Mexico	2007 (left 2008)
9. Antonia Okono	Communications Manager	GCP HQ, Mexico	2007
10. Kate Durbin	Communications Assistant	GCP HQ, Mexico	2007
11. Adriana Santiago	Project Officer	GCP HQ, Mexico	2004
12. Imelda Rosas	Accounting/Administrative Assistant	GCP HQ, Mexico	2006
13. Paula Maria de León	Administrative Coordinator	GCP HQ, Mexico	2007
14. Griselda Marquez	Executive Assistant	GCP HQ, Mexico	2004
15. Laura Ruiz	Programme Assistant (SP3 and SP5)	GCP HQ, Mexico	2007
16. Sandra Insignares	Consultant	GCP HQ, Mexico	2008
17. Aida Martínez	Programme Assistant	GCP HQ, Mexico	2007

Appendix C:

Ongoing projects in 2008 by category and Subprogramme

NB. Project duration and budgets extracted from project proposals and grant agreements

Competitive projects

Subprogramme 1: Crop genetic diversity

No.	Duration	Total budget (USD)	Collaborating institutes in 2008	Crop(s), trait(s), region(s)
Current projects				
1	<i>G3005.10 Exploring natural genetic variation: developing genomic resources and introgression lines for four AA genome rice relatives</i> (PIs: Mathias Lorieux, Agropolis-IRD and Joe Tohme, CIAT) January 2005–December 2008	1,074,900	CU, EMBRAPA, WARDA, Fedearroz	rice drought tolerance various regions
2	<i>G3007.01 Interspecific bridges that give full access to the African rice allele pool for enhancing drought tolerance of Asian rice</i> (PI: Alain Ghesquière, Agropolis-IRD) August 2007–July 2009	669,000	CIAT, Fedearroz, IER, INERA–Burkina Faso, PAU, PhilRice, UoA, WARDA	rice drought tolerance Africa, Asia
3	<i>G3007.02 Genomic dissection of tolerance to drought stress in wild barley</i> (PI: Robbie Waugh, SCRI) August 2007–July 2009	567,604	ICARDA, INIA–Chile, OSU, UoC (Riverside), UdT	barley drought tolerance various regions
4	<i>G3008.01 Generating new wheat germplasm with enhanced drought/heat tolerance using AB genomes genetic diversity</i> (PI: SC Misra, Agharkar Research Institute, India) November 2008–October 2011	779,820	CIMMYT, PARC, PBI–UoS, UAS (Dharwad)	wheat drought tolerance various regions
5	<i>G3008.02 Improving grain yield on acid soils by the identification of genetic factors underlying drought and aluminium tolerance in maize and sorghum</i> (PI: Leon Kochian, USDA–ARS/Cornell University) November 2008–October 2011	857,366	CU, EMBRAPA, MU	maize, sorghum Acidity sub-Saharan Africa
Projects on no-cost extension (NCE) into 2008 or beyond				
6	<i>G3005.13. Development of informative DNA markers through association mapping in maize to improve drought tolerance in cereals</i> (PI: Marilyn Warburton, to June 2008; Jianbing Yan, effective June 2008, CIMMYT) January 2005–December 2007 NCE: December 2008	899,052	Agropolis–INRA, CU, Genaisance, KARI, NSFCRC, SAU, SIRDC	maize drought tolerance, low soil fertility various regions
7	<i>G3005.14: Characterisation of genetic diversity of maize populations: Documenting global maize migration from the centre of origin</i> (PI: Marilyn Warburton, CIMMYT) January 2005–December 2007; NCE: December 2008	717,145	Agropolis–INRA, CAAS, DoA–Indonesia, IARI, ICAR, IITA, KARI, NMRI, NSFCRC	maize drought tolerance various regions
8	<i>G3005.17: Allele mining based on non-coding regulatory SNPs in barley germplasm</i> (PI: Michael Baum, ICARDA) January 2005–December 2007; NCE: June 2008	899,000	TU, UdU, UoAd	barley tolerance to drought, frost, cold and salinity various regions
Subprogramme 2: Genomics towards gene discovery				
Current projects				
9	<i>G3007.03: Development of genomics resources for molecular breeding of drought tolerance in cassava</i> (PI: Pablo Rabinowicz, UoM) August 2007–February 2010	758,058	UoC (Davis), UoP, UotW	cassava drought tolerance Africa, Asia, Latin America

Subprogramme 2: Genomics towards gene discovery (cont'd...)

No.	Duration	Total budget (USD)	Collaborating institutes in 2008	Crop(s), trait(s), region(s)
10	<i>G3007.06: Genetic dissection of drought adaptive mechanisms in bread and durum wheat through large-scale phenotyping methodologies</i> (PI: Matthew Reynolds, CIMMYT) August 2007–July 2009	602,000	ACPGF, DWR	wheat drought tolerance Latin America, Asia
11	<i>G3008.03: Delayed senescence and drought tolerance in rice</i> (PI: Eduardo Blumwald, UoC (Davis)) November 2008–October 2011	851,896	IRRI	rice drought tolerance various regions
12	<i>G3008.04: Drought from a different perspective: Improved tolerance through phosphorous acquisition</i> (PI: Sigrid Heuer, IRRI) November 2008–October 2011	900,000	ICABIOGRAD, JIRCAS, UoPd/MPIMPP, ZU	rice drought tolerance, phosphorus deficiency various regions
13	<i>G3008.05: Discovery and development of alleles contributing to sorghum drought tolerance</i> (PI: Andrew H Paterson, UGA) November 2008–October 2011	756,225	ARC–Austria, ICRISAT, MAU, NRCS, SARI–Ghana	sorghum drought tolerance Africa, Asia

Projects on NCE into 2008 or beyond

14	<i>G3005.01: Identifying genes responsible for failure of grain formation in rice and wheat under drought</i> (PIs: John Bennett, to December 2008; Rachid Serraj, effective December 2008, IRRI) January 2005–December 2007; NCE: June 2009	900,000	CSIRO, NAU, NIAS, TNAU	rice, wheat drought tolerance Asia
15	<i>G3005.02: Revitalising marginal lands: discovery of genes for tolerance of saline and phosphorus deficient soils to enhance and sustain productivity</i> (PI: Abdelbagi M Ismail, IRRI) January 2005–December 2007 NCE: June 2008	900,000	ABRII, ICABIOGRAD, JIRCAS, NIAS, UoC (Davis), UoD	rice salinity and phosphorus deficiency Asia
16	<i>G3005.08: Targeted discovery of superior disease QTL alleles in maize and rice genomes</i> (PI: Rebecca Nelson, CU) January 2005–December 2007; NCE: December 2008	899,611	CSU, ICABIOGRAD, RCB–IPB, IRRI, KARI, NCSU	maize, rice disease resistance various regions
17	<i>G3005.11: Functional genomics of cross-species resistance to fungal diseases in rice and wheat (cereal immunity)</i> (PI: Jean-Benoit Morel, Agropolis–INRA) January 2005–December 2007; NCE: October 2008	900,000	CIMMYT, EMBRAPA, JIC, NIAS, UoC (Davis)	rice, wheat disease resistance various regions
18	<i>G3005.15: Determination of a common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes</i> (PI: François Tardieu, Agropolis–INRA) January 2005–December 2007; NCE: December 2008	898,686	ACPGF, Biogemma, CIMMYT, ETH, ICAR, IRRI, KARI	various crops drought tolerance various regions
19	<i>G3005.16: Isolation and characterisation of aluminium tolerance genes in the cereals: An integrated functional genomic, molecular genetic and physiological analysis</i> (PI: Leon V Kochian, USDA–ARS/Cornell University, USA) January 2005–December 2007 NCE: December 2008	900,000	EMBRAPA, MU	sorghum, maize, rice, <i>Triticum</i> aluminium tolerance various regions

Subprogramme 3: Trait capture for crop improvement

Current projects

20	<i>G3007.04: Tailoring superior alleles for abiotic stress genes for deployment into breeding programmes: a case study based on association analysis of <i>Alt_{Sb}</i>, a major aluminium tolerance gene in sorghum</i> (PI: Jurandir Vieira Magalhaes, EMBRAPA) August 2007–July 2009	603,101	IGD–CU, KSU, INRAN, USDA–ARS	sorghum aluminium tolerance Africa and other developing regions
21	<i>G3007.05: Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-aided breeding</i> (PI: Arvind Kumar, IRRI) August 2007–July 2009	598,590	CRURRS, TNAU, UAS (Bangalore), UoAI, YAAS	rice drought tolerance Asia
22	<i>G3008.06: Targeting drought-avoidance root traits to enhance rice productivity under water-limited environments</i> (PI: Rachid Serraj, IRRI) November 2008–October 2011	900,000	BF, ChSU, Drought Breeding Network (CRRI, CRURRS, IGKV, NDUAT, UAS [Bangalore]), NagU, SUA, TNAU, UoAb, UoMi, WARDA	rice drought tolerance Asia

Subprogramme 3: Trait capture for crop improvement (cont'd...)

No.	Duration	Total budget (USD)	Collaborating institutes in 2008	Crop(s), trait(s), region(s)
23	G3008.07: <i>Basal root architecture and drought tolerance in common beans</i> (PI: JP Lynch, PSU) November 2008–October 2011	900,000	CIAT, IIAM, SABRN	beans drought tolerance Africa
24	G3008.08: <i>Breeder-friendly high-throughput phenotyping tools to select for adaptive traits in drought environments</i> (PI: Francis Ogonnaya, ICARDA) November 2008–October 2011	897,073	Agropolis–INRA, CIMMYT, CSIRO, EIAR	wheat drought tolerance Africa, Asia
Projects on NCE into 2008 or beyond				
25	G3005.03: <i>Identifying the physiological and genetic traits that make cassava one of the most drought-tolerant crops</i> (PI: Alfredo Alves, EMBRAPA) January 2005–December 2007; NCE: December 2008	867,145	ARI–Naliendele, CIAT, CU, IITA, KARI, SARI–Ghana	cassava drought tolerance Africa, Latin America
26	G3005.05: <i>Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools</i> (PIs: José Valls, EMBRAPA and David Bertoli, UCB) January 2005–December 2007; NCE: June 2008	898,235	Agropolis–CIRAD, CERAAS, IBONE, ICRISAT, TAMU, UAS (Bangalore), UoAa	groundnuts drought tolerance and disease resistance Africa, Asia
27	G3005.06: <i>Marker development and marker-assisted selection for Striga resistance in cowpeas</i> (PI: Satoru Muranaka, IITA) January 2005–December 2007; NCE: October 2008	900,000	CERAAS, ISRA, UoV	cowpeas Striga resistance Africa
28	G3005.09: <i>Development of low-cost technologies for pyramiding useful genes from wild relatives of cassava into elite progenitors</i> (PIs: Anthony Bellotti and Martin Fregene, CIAT) January 2005–December 2007; NCE: December 2008	894,906	CRI–Ghana, EMBRAPA, NAARI, NRCRI	cassava disease resistance Africa, Latin America

Subprogramme 4: Bioinformatics and crop information systems

Current projects

29	G3008.09: <i>Breeding drought tolerance for rainfed lowland rice in the Mekong region</i> (PI: Boonrat Jongdee, BRRD) November 2008–October 2011	847,600	BIOTEC, CARDI, NAFRI, UoQ	rice drought tolerance Asia
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Projects on NCE into 2008 or beyond

30	G3005.04: <i>An eco-physiological–statistical framework for the analysis of GxE and QTLxE as occurring in abiotic stress trials, with applications to the CIMMYT drought stress programmes in tropical maize and bread wheat</i> (PI: Fred van Eeuwijk, WUR) January 2005–December 2007; NCE: July 2008	507,150	CIMMYT, CSIRO, UAC	maize, wheat drought tolerance various regions
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Commissioned projects

Subprogramme 1: Crop genetic diversity

Current projects

31	G4006.01: <i>Developing strategies for allele mining within large collections</i> (PI: NR Sackville Hamilton, IRRI) January 2006–July 2008	200,000	EMBRAPA, ICARDA, ICRISAT	various
32	G4006.02: <i>A dataset on allele diversity at orthologous candidate genes in GCP crops (ADOC)</i> (PI: Dominique This, Agropolis–CIRAD) January 2006–December 2008	860,000	Agropolis–INRA, CIAT, CIP, CNG, ICARDA, ICRISAT, IRRI	various crops drought tolerance various regions
33	G4007.01: <i>Genotyping validation of the GCP reference sets</i> (PI: Jean-Francois Rami, Agropolis–CIRAD) January 2007–December 2008	379,280	ADNid, Bioversity, CIAT, CIMMYT, CIP, ICARDA, ICRISAT, IITA, IRRI	various
34	G4008.01: <i>Population development to underpin gene discovery and allele validation in rice: the Multiparent Advanced Generation Inter-Crosses (MAGIC)</i> (PI: Hei Leung, IRRI) January 2008–December 2009	113,994	ICRISAT, NIAB	various
35	G4008.02: <i>Phenotyping sorghum reference set for drought tolerance</i> (PI: HD Upadhyaya, ICRISAT) January 2008–December 2010	473,650	IER, ISRA/CERAAS, KARI, NPGRC, UAS (Dharwad)	sorghum drought tolerance Africa, Asia
36	G4008.03: <i>Precision phenotyping of the GCP spring wheat reference sample for drought</i> (PI: Susanne Dreisigacker, CIMMYT) January 2008–December 2010	153,600	INRA–Morocco	wheat various traits and regions

Subprogramme 1: Crop genetic diversity (cont'd...)

No.	Duration	Total budget (USD)	Collaborating institutes in 2008	Crop(s), trait(s), region(s)
37	<i>G4008.05: Connecting performance under drought with genotypes through phenotype associations</i> (PI: Jill Cairns, IRRI) January 2008–December 2010	467,676	Agropolis–CIRAD, BIOTEC, CRRI, IGKV, TNAU, WARDA	rice drought tolerance Asia
38	<i>G4008.33: Drought tolerance phenotyping of the GCP maize inbred line reference set</i> (PI: James Gethi, KARI) January 2008–February 2011	257,301	Agropolis–INRA, CIMMYT, ETH	maize drought tolerance Africa
39	<i>G4008.42: Developing DArT markers for several crops in the GCP</i> (PI: JC Glaszmann, Agropolis–CIRAD/GCP) January 2008–December 2009	337,600	CIP, CRI–Ghana, DArT P/L, ICRISAT, IITA	various
40	<i>G4008.45: A nested association mapping (NAM): Laying the bases for highly efficient QTL characterisation population of rice</i> (PI: Mathias Lorieux, Agropolis–IRD/CIAT) August 2008–July 2010	226,010	WARDA	rice drought tolerance various regions
41	<i>G4008.46: Sorghum MAGIC: Multiparent advanced generation inter-cross development for gene discovery and allele validation</i> (PI: Tom Hash, ICRISAT) August 2008–July 2010	92,286	NIAB, NRCS	sorghum various traits Africa
42	<i>G4008.52: Genetic Resources Support Service (GRSS – Implementation feasibility work programme)</i> (PI: JC Glaszmann, Agropolis–CIRAD/GCP) September 2008–December 2008	15,000	N/A at this stage of the project	various
Projects on NCE into 2008 or beyond				
43	<i>G4005.01.03 Genotyping of composite germplasm set – sorghum</i> (PI: Tom Hash, ICRISAT) January 2005–December 2005; NCE: September 2008	129,000	Agropolis–CIRAD, CAAS	sorghum various traits and regions
44	<i>G4005.05: Assessing Ecotilling as a methodology for targeted genotyping and SNP discovery</i> (PIs: Kenneth McNally, IRRI and Claire Billot, Agropolis–CIRAD) January 2005–December 2005; NCE: Sep 2008	150,000	N/A	rice, sorghum various traits and regions
45	<i>G4005.06: Supporting emergence of reference drought tolerance phenotyping centers</i> (PI: Reinaldo L Gomide, EMBRAPA) January 2005–December 2007; NCE: June 2008	581,590	N/A	cereals (maize, sorghum, rice, wheat); legumes (common beans, cowpeas) drought tolerance various regions
46	<i>G4005.07: Whole-plant physiology modelling of drought tolerance in cereals</i> (PI: Delphine Luquet, Agropolis–CIRAD) January 2005–December 2006; NCE: May 2008	575,720	CSIRO, PHI, UoQ	various
47	<i>G4006.30: Development and genotyping of composite collection of foxtail millet (<i>Setaria italica</i> (L) Breaux)</i> (PI: HD Upadhyaya, ICRISAT) January 2006–December 2006; NCE: July 2008	25,016	N/A	foxtail millet various traits Asia, Europe, North America
48	<i>G4006.31: Development and genotyping of composite collection of pearl millet (<i>Pennisetum glaucum</i> (L) R Br)</i> (PI: HD Upadhyaya, ICRISAT) January 2006–December 2006; NCE: July 2008	60,042	N/A	pearl millet various traits Africa, Asia, Latin America

Subprogramme 2: Genomics towards gene discovery

Current projects

49	<i>G4007.02: Validation of drought-response/resistance pathway genes by phenotypic analysis of mutants</i> (PI: Andy Pereira, VBI–VPI) August 2007–July 2009	200,543	HZAU, IRRI, VPI	rice drought tolerance various regions
50	<i>G4008.06: Single Nucleotide Polymorphism discovery, validation, and mapping in groundnut</i> (PI: Steven J Knapp, UGA) January 2008–December 2008	152,543	ICRISAT, NCGR, USDA–ARS	groundnuts various traits and regions
51	<i>G4008.07: Improving molecular tools for pearl millet</i> (PI: C Tom Hash, ICRISAT) January 2008–December 2009	296,429	AICPMIP, CAZRI, ILRI, RAU	pearl millet various traits Africa, Latin America, Asia
52	<i>G4008.08: Transcriptome analysis of near-isogenic rice lines to identify expression signatures and gene combinations conferring tolerance to drought stress</i> (PI: Shoshi Kikuchi, NIAS) January 2008–December 2009	305,400	IRRI	rice drought tolerance various regions

Subprogramme 2: Genomics towards gene discovery (cont'd...)

No.	Duration	Total budget (USD)	Collaborating institutes in 2008	Crop(s), trait(s), region(s)
53	<i>G4008.09: Development of genetic and genomic resources for breeding improved sweet potato varieties</i> (PI: Roland Schafleitner, CIP) January 2008–December 2009	299,540	DaRT P/L, EMBRAPA, IIAM, INIA–Uruguay, NAARI	sweet potatoes drought and disease resistance sub-Saharan Africa
54	<i>G4008.47: Developing genomic resources for pigeonpeas using next generation sequencing technologies</i> (PI: Gregory D May, NCGR) August 2008–July 2010	292,200	ICRISAT, NRCPB, PDKV	pigeonpeas drought and disease resistance various regions

Subprogramme 3: Trait capture for crop improvement

Current projects

55	<i>G4007.04: Association mapping of downy mildew resistance in elite maize inbred lines in Thailand</i> (PIs: Chalermphol Phumichai and Julapark Chunwongse, BIOTEC) August 2007–July 2009	60,464	KU	maize mildew resistance Asia
56	<i>G4007.06: Integrating marker-assisted selection into the conventional breeding procedure for improvement of wheat (Triticum aestivum L) in the drought-prone areas of Northern China</i> (PI: Ruilian Jing, CAAS) August 2007–July 2010	150,590	HAAS, LAAS, NU, NWSUAF, SAAS	wheat drought tolerance Asia
57	<i>G4007.07: Marker-assisted selection for sweet potato virus disease (SPVD) resistance in sweet potato germplasm and breeding populations</i> (PI: Wolfgang Grüneberg, CIP) August 2007–July 2010	379,800	NaCRR1	sweet potatoes SPVD resistance various regions
58	<i>G4007.08: Integration of genomic tools with conventional screening for developing NERICA rice cultivars for West Africa</i> (PI: Marie Noelle Ndjiondjop, WARDA) August 2007–July 2009	304,440	Agropolis–IRD, IER	rice drought tolerance Africa
59	<i>G4007.25: Development of drought phenotyping network</i> (PIs: Gregory Edmeades and Abraham Blum, Consultants) December 2007–February 2008	22,500	CIAT, EMBRAPA, KUL, WA	various
60	<i>G4008.10: 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)</i> (PI: Robert Schaffert, EMBRAPA) January 2008–December 2010	205,200	CU, ICRISAT, INRAN	sorghum aluminium tolerance Africa
61	<i>G4008.11: Dry bean improvement and marker-assisted selection for diseases and abiotic stresses in Central America and the Caribbean</i> (PI: Jorge A Acosta-Gallegos, INIFAP) January 2008–December 2010	382,590	CIAT, INCA, INTA–Nicaragua, ORE	beans drought and disease resistance Latin America and the Caribbean
62	<i>G4008.12: Linking genetic diversity with phenotype for drought tolerance traits through molecular and physiological characterisation of a diverse reference collection of chickpea</i> (PI: Junichi Kashiwagi, ICRISAT) January 2008–December 2009	156,215	JIRCAS, UAS (Bangalore)	chickpeas drought tolerance various regions
63	<i>G4008.13: Improving drought tolerance phenotyping in cowpea</i> (PI: Jeff Ehlers, UoC–Riverside) January 2008–December 2010	450,836	IITA, INERA–Burkina Faso, ISRA, TAMU	cowpea drought tolerance Africa
64	<i>G4008.14: Breeding for drought tolerance with known gene information</i> (PI: Jiankang Wang, CIMMYT) January 2008–December 2009	300,000	Agropolis–INRA, CAAS, CSIRO, ICRISAT, IRRI, UoO	various
65	<i>G4008.15: Developing potato cultivars adapted to Southern Africa countries</i> (PI: F Vilaró, INIA–Uruguay) January 2008–December 2009	209,868	CIP, DARS, EMBRAPA, IIAM, INIA–Chile, INTA–Argentina	potato various traits Africa
66	<i>G4008.16: Speeding the development of salt-tolerant rice varieties through marker-assisted selection and their dissemination in salt-affected areas of Bangladesh</i> (PI: Abdelbagi M Ismail, IRRI) January 2008–December 2009	223,768	BINA, BRRI, UoD	rice salt tolerance Asia
67	<i>G4008.17: Application of marker-assisted selection for Striga resistance in cowpea</i> (PI: Jean Baptiste Tignegre, INERA–Burkina Faso) January 2008–December 2009	199,986	IITA	cowpea Striga resistance Africa

Subprogramme 3: Trait capture for crop improvement (cont'd...)

No.	Duration	Total budget (USD)	Collaborating institutes in 2008	Crop(s), trait(s), region(s)
68	<i>G4008.19: Incorporation of an MSV resistance gene in Mozambican maize varieties, mediated by use of MAS</i> (PI: Mark Laing, UKZN) January 2008–December 2010	240,000	IIAM	maize MSV resistance Africa
69	<i>G4008.30: Development of a GCP Phenotyping Network</i> (PIs: Abraham Blum and Greg Edmeades, Consultants) February 2008–February 2009	117,000	CIAT, KUL	various
70	<i>G4008.34: Environmental assessment for phenotyping network</i> (PI: Glenn Hyman, CIAT) January 2008–December 2009	279,403	EMBRAPA, KUL, WA	various
71	<i>G4008.41: Application and validation of the major QTL phosphate uptake 1 (Pup1)</i> (PI: Sigrid Heuer, IRRI) January 2008–December 2009	166,550	ICABIOGRAD, JIRCAS	rice salt tolerance Asia
72	<i>G4008.48: Improve sorghum productivity in semi-arid environments of Mali through integrated MARS</i> (PI: Jean-François Rami, Agropolis–CIRAD) August 2008–July 2013	678,600	IER, Syngenta	sorghum drought tolerance Africa
73	<i>G4008.49: Enhancing groundnut (Arachis hypogaea L) genetic diversity and speeding its utilisation in breeding for improving drought tolerance</i> (PI: Ousmane Ndoye, ISRA) August 2008–July 2009	81,600	Agropolis–CIRAD, EMBRAPA, ICRISAT, PROINPA, UCB, USDA–ARS	groundnuts drought tolerance Africa, Latin America
74	<i>G4008.55: GCP phenotyping book</i> (PI: Philippe Monneveux, GCP) July 2008–December 2008	15,000	N/A	various
75	<i>G4008.56: Drought-tolerant maize for Asia</i> (PI: PH Zaidi, CIMMYT) November 2008–October 2013	1,500,000	DMR, ICERI, MMRI, MPUAT, NMRI, YAAS	maize drought tolerance Asia

Projects on NCE into 2008 or beyond

76	<i>G4005.20: Optimising marker-assisted breeding systems for drought tolerance in cereals through linkage of physiological and genetic models</i> (PIs: Scott Chapman, CSIRO and Jiankang Wang, CIMMYT) January 2005–December 2006; NCE: May 2008	260,000	Agropolis–INRA, PHI, UoQ	various cereals drought tolerance various regions
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Subprogramme 4: Bioinformatics and crop information systems

NB: By its nature, SP4 work is applicable across multiple crops, traits and regions

Current projects

77	<i>G4005.22: Development of Generation CP domain models ontology</i> (PI: Richard Bruskiwich, IRRI) January 2005–December 2008	704,174	BI, CIMMYT, CIP, ICRISAT, POC	various
78	<i>G4005.23: Implementation of web services technology in the Generation Challenge Programme Consortium</i> (PI: Milko A Skofic, BI) January 2005–December 2008	507,000	CIMMYT, IRRI	various
79	<i>G4005.27: High-performance computing facilities for the Generation CP</i> (PI: Anthony Collins, CIP) January 2005–December 2008	384,000	ICRISAT, IRRI, NIAS	various
80	<i>G4006.08: Data analysis support for existing projects in SP2 with emphasis on integrating results across gene expression and QTL mapping experiments</i> (PI: Guy Davenport, CIMMYT) January 2005–December 2008	412,300	CIP, ICRISAT, IRRI, JIC, NIAS	various
81	<i>G4006.16: Development of an integrated GCP Information Platform</i> (PI: Graham McLaren, GCP/IRRI) January 2006–December 2008	463,050	Agropolis–CIRAD, CIMMYT, EBI, ICRISAT, NCGR	Global
82	<i>G4006.17: Generation CP data quality improvement and assurance</i> (PI: Thomas Metz, IRRI) January 2006–December 2008	474,289	Agropolis–CIRAD, WUR, CIP, ICRISAT	various
83	<i>G4006.35: Support for existing projects in SP1 on germplasm data analysis (GDA)</i> (PI: Marco Bink, WUR) January 2006–December 2008	205,000	Agropolis–CIRAD, CIMMYT	various
84	<i>G4007.09: Design and analysis of marker–trait association studies, with special attention for genetically challenging crops</i> (PI: Fred van Eeuwijk, WUR) August 2007–December 2008	300,000	ICL, LUMC, NIAB, SCRI, UoH	various
85	<i>G4007.10: Support to GCP scientists regarding issues related to bioinformatics and data handling</i> (PI: Theo van Hintum, WUR) August 2007–July 2009	116,640	N/A	Global
86	<i>G4007.11: Further development and support for use of iMAS by NARS and other user communities</i> (PIs: Jayashree Balaji, effective June 2008; David Hoisington, up to June 2008, ICRISAT) January 2007–December 2008	164,000	CIMMYT, IRRI, breeders in developing country agricultural research programmes	various
87	<i>G4007.12: Development of tools and technology to increase the functionality of the GCP Information Platform</i> (PI: Martin Senger, IRRI–CRIL) February 2007–December 2008	186,441	BI	Global
88	<i>G4008.20: Management of the GCP Central Registry and the creation and maintenance of templates for data storage in repositories</i> (PI: Elizabeth Arnaud, BI) May 2008–December 2008	140,000	CIMMYT	Global

Subprogramme 4: Bioinformatics and crop information systems (cont'd...)

No.	Duration	Total budget (USD)	Collaborating institutes in 2008	Crop(s), trait(s), region(s)
89	<i>G4008.21: Large-scale phylogenomic analyses to gene function prediction for GCP crops</i> (PI: Mathieu Rouard, Bioversity) January 2008–December 2009	240,567	Agropolis–CIRAD, IRRI	Global
90	<i>G4008.22: Methodology development for reconstruction of genealogies based on haplotypes related to geographic patterns (HaploPhyle: Graphical haplotype network in the light of external data)</i> (PI: Claire Billot, Agropolis–CIRAD) January 2008–December 2008	152,540	CIP	Global
91	<i>G4008.31: Upgrading the quality and utility of GCP phenotyping data through the development of a data input template to facilitate the storage of data in cross-specific databases</i> (PI: Robert Koebner, CropGen International) February 2008–January 2009	72,000	CIMMYT, IRRI	Global
92	<i>G4008.32: Promotion of quality management procedures in GCP research laboratories</i> (PI: TBD) July 2008–June 2009	192,000	TBD	Global
93	<i>G4008.54: Implementation—Molecular Breeding Platform</i> (PI: Graham McLaren, GCP) September 2008–December 2008	30,000	N/A at this stage of the project	Global

Projects on NCE into 2008 or beyond

94	<i>G4005.24: Application and development of web services technology</i> (PIs: Mathieu Rouard, BI, effective 2007; Richard Bruskiwich, IRRI, 2005–2006) January 2005–December 2007 <i>NCE: October 2008 (continued from January 2008 under project G4008.21, No. 89 on this table)</i>	260,300	Agropolis–CIRAD, EMBRAPA, NIAS	Global
95	<i>G4005.25: Creation and maintenance of templates for Generation CP data storage in repositories</i> (PI: Guy Davenport, CIMMYT) January 2005–December 2007 <i>NCE: October 2008</i>	240,000	N/A for 2008	Global

Subprogramme 5: Capacity-building and enabling delivery

Current projects

96	<i>G4005.53 (CB03): The use of molecular markers in efficient crop improvement: Marker-assisted breeding – A learning module</i> (PI: Theresa Fulton, IGD–CU) January 2005–December 2005 and August 2007–July 2008	32,500	N/A	various
97	<i>G4005.63 (CB13): The Interactive Resource Center and Helpdesk</i> (PI: Theresa Fulton, IGD–CU) January 2005–July 2009	109,587	N/A	various
98	<i>G4006.14: Ex ante impact analysis of marker-assisted selection technologies supported by GCP</i> (PI: George W Norton, VPI) December 2006–December 2008	148,618	N/A	various
99	<i>G4006.36: Capacity-building and research project</i> (PI: Mark Laing, ACCI–UKZN) January 2007–December 2011	500,312	RF	various
100	<i>G4007.03: The 'Community of Practice' concept applied to rice production in the Mekong region: Quick conversion of popular rice varieties with emphasis on drought, salinity and grain quality improvement</i> (PI: Theerayut Toojinda, BIOTEC) January 2007–December 2008	120,000	CARDI, DAR, NAFRI, RGDU, URU	rice drought and salinity tolerance, grain quality Asia
101	<i>G4007.13: Capacity-building à la carte 2007</i> (PI: Carmen de Vicente, GCP) July 2007–July 2008	400,000	See sub-projects below	
101.01)	<i>G4007.13 (01): Capacity-building à la carte 2007 – Capacity-building for characterising maize for water stress tolerance at KARI–Katumani</i> (PI: James Gethi, KARI) July 2007–July 2009	48,943	Agropolis–INRA	maize water stress tolerance Africa
101.02)	<i>G4007.13 (02): Capacity-building à la carte 2007 – Marker-aided development of nutritionally enhanced cassava for Nigeria</i> (PI: Chiedozi Egesi, NRCRI) July 2007–July 2009	97,644	CIAT	cassava various traits Africa
101.03)	<i>G4007.13 (03): Capacity-building à la carte 2007 – Application of molecular tools for controlled wild introgression into peanut cultivated germplasm in Senegal</i> (PI: Ousmane Ndoye, ISRA) July 2007–July 2009	133,809	Agropolis–CIRAD, EMBRAPA, UCB	groundnuts drought and disease resistance Africa
101.04)	<i>G4007.13 (04): Capacity-building à la carte 2007 – Characterisation of maize germplasm found in Ghana, using the bulking technique</i> (PI: Allen Oppong, CRI–Ghana) July 2007–July 2009	72,500	CIMMYT	maize drought tolerance, streak virus disease Africa

Subprogramme 5: Capacity-building and enabling delivery (cont'd...)

No.	Duration	Total budget (USD)	Collaborating institutes in 2008	Crop(s), trait(s), region(s)
101.05)	<i>G4007.13 (05): Capacity-building à la carte 2007 – An integrated proteomics and genomics approach to discover salt tolerance genes</i> (PI: Ghasem Hosseini Salekdeh, ABRIL)			
	July 2007–July 2009	48,970	IPK, IRRI	rice salinity resistance Asia
101.06)	<i>G4007.13 (06): Capacity-building à la carte 2007 – Enhancing capacity of ICABIOGRAD in phenotyping and molecular analysis to develop elite rice lines suitable to Indonesian uplands</i> (PI: Masdiar Bustammam, ICABIOGRAD)			
	July 2007–July 2009	79,709	IRRI, RCB-IPB	rice blast resistance Asia
102	<i>G4007.14: Fellowships and travel grants 2007</i> (PI: Carmen de Vicente, GCP)			
	One year fellowships, between January 2007–December 2008 (various start and end dates)	160,000	<i>Sending institutes:</i> EMBRAPA, NRCRI <i>Host institutes:</i> CSIRO, UoW (Project start deferred from 2007 to 2008)	various
103	<i>G4007.17.02: GCP Project Development Guide – system and implementation</i> (PIs: Andreas Idl and Norbert Niederhauser, Cropster GmbH)			
	June 2007–January 2008	7,200	N/A	Global
104	<i>G4007.20: Managing the Generation Challenge Programme in a post-International Treaty world: A proposal for a technical training workshop and related materials</i> (PI: Michael Halewood, Bioversity)			
	August 2007–July 2008 <i>NCE: December 2008</i>	34,100	CAS-IP, EMBRAPA, IRRI	Global
105	<i>G4007.21: Genotyping Support Service 2007</i> (PI: Humberto Gómez Paniagua, GCP)			
	August 2007–February 2009	400,000	<i>Beneficiaries:</i> AC-UT, ARI-Ghana, CNRRI, CRI-Ghana, CRI-Sri Lanka, KARI, EMBRAPA, INIA-Chile, MARI, PROINPA, SARI-Ethiopia, UARI <i>Service providers:</i> CIAT, DArT P/L, ICRISAT, IRRI, KUL, WUR	Global
106	<i>G4007.22: GCP Workflow and Repository System</i> (PI: Norbert Niederhauser, Cropster GmbH)			
	August 2007–December 2008	116,980	N/A	Global
107	<i>G4008.23: Statistical rules for defining characteristic genotype and marker sets</i> (PI: Fred van Eeuwijk, WUR)			
	January 2008–December 2008	30,000	N/A	Global
108	<i>G4008.24: From attractiveness to feasibility: A strategic assessment of the capacity to develop and adopt GCP technologies</i> (PI: Stanley Wood, IFPRI)			
	January 2008–December 2009	261,112	CIAT	various
109	<i>G4008.25: Advanced course on 'Applied statistical methods in plant genomics', Zaragoza, 18–29 February 2008</i> (PI: Manuela Cereza, CIHEAM-IAMZ)			
	January 2008–December 2008	25,000	WUR	Global
110	<i>G4008.26: A cassava breeding Community of Practice in Africa for accelerated production and dissemination of farmer-preferred cassava varieties resistant to pests and diseases</i> (PIs: Emmanuel Okogbenin, CIAT and Chiedozie Egesi, NRCRI)			
	January 2008–December 2010	651,525	ARI-Naliende, CRI-Ghana, IITA, NaCRRI	cassava disease and pest resistance Africa
111	<i>G4008.27: Phenotyping course for drought-related traits across tropical legumes – Concepts and practices</i> (PI: Vincent Vadez, ICRISAT)			
	January 2008–December 2008	118,776	CIAT, IITA, UoC (Riverside)	various crops drought resistance Africa
112	<i>G4008.35: Toolbox of available molecular markers useful for marker-assisted selection in GCP crops</i> (PI: Veerle Van Damme, Consultant)			
	March 2008–March 2010	41,000	N/A	various
113	<i>G4008.36: Getting the focus right: Food crops and smallholder constraints</i> (PI: John Dixon, CIMMYT)			
	January 2008–December 2009	145,800	CIAT, ICARDA, ICRISAT, IITA, IRRI	various
114	<i>G4008.37: PhD in plant breeding training at the West Africa Centre for Crop Improvement</i> (PI: Eric Y Danquah, University of Ghana)			
	March 2008–February 2014	667,054	AGRA, CU	various crops and traits Africa
115	<i>G4008.38: Fellowships and travel grants 2008</i> (PI: Carmen de Vicente, GCP)			
	Between January 2008–December 2008 (various start and end dates)	160,000	<i>Sending institutes:</i> ARI-Naliende, BRRI, CIMMYT, CLDRI, CRI-Sri Lanka, CRRI, DAR, EMBRAPA, ESU, INERA-Burkina Faso, ISRA, MahU, NAFRI, NAU, NRCRI, PhilRice, PROINPA, TNAU, UAS (Bangalore), UoD, USP <i>Host institutes:</i> Agropolis-INRA, CIAT, CU, FABI, IRRI, SCRI, WUR	various
116	<i>G4008.39: Capacity-building à la carte 2008</i> (PI: Carmen de Vicente, GCP)			
	April 2008–April 2010	195,541	See sub-projects below	See sub-projects below
116.01)	<i>G4008.39 (01): Capacity-building à la carte 2008 – Enhancing MAS capacity for salt-stress rice breeding in Bangladesh</i> (MA Salam, BRRI)			
	April 2008–March 2010	119,778	IRRI, UoD	rice salt tolerance Asia
116.02)	<i>G4008.39 (02): Capacity-building à la carte 2008 – Improving capacity for phenotyping for abiotic and biotic stress in Burkina Faso</i> (PI: Issa Drabo, INERA-Burkina Faso)			
	April 2008–March 2010	76,383	IITA, UoC-Riverside	cowpeas various traits Africa

Subprogramme 5: Capacity-building and enabling delivery (cont'd...)

No.	Duration	Total budget (USD)	Collaborating institutes in 2008	Crop(s), trait(s), region(s)
116.03	<i>G4008.39 (03): Capacity-building à la carte 2008 – Improving capacity for phenotyping for abiotic and biotic stress in Senegal</i> (PI: Ndiaga Cissé, ISRA) April 2008–March 2010	79,232	IITA–Kenya, IITA–Nigeria, UoC (Riverside)	cowpeas various traits Africa
117	<i>G4008.40: Workshop on 'Reference sets of food-crop germplasm for international collaboration'</i> (Pis: MC de Vicente and JC Glaszmann, Agropolis–CIRAD/GCP) January 2008–December 2008	120,000	GCDT, GIPB, SGRP	Global
118	<i>G4008.43: Improve cowpea productivity for marginal environments in Mozambique</i> (PI: Rogério Chiulele, UEM) July 2008–June 2010	68,592	UoC (Riverside)	cowpeas drought tolerance Africa
119	<i>G4008.44: GCP Learning Materials</i> (PI: Carmen de Vicente, GCP) January 2008–December 2008	15,000	IRRI, IGD–CU, WUR	Global
120	<i>G4008.50: Delivery Plan remote learning modules</i> (PI: Laurence Pratt, CIMS–INCAE Business School) August 2008–July 2009	246,620	CU	Global

Projects on NCE into 2008 or beyond

121	<i>G4006.13: Targeting and impact analysis of Generation Challenge Programme (GCP) technologies</i> (PI: Glenn Hyman, CIAT) November 2006–October 2007; NCE: December 2008	149,742	CIAT, CIMMYT, IFPRI, IRRI	Global
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Focus projects

Current projects

122	<i>G6007: Tropical Legumes I (TLI): Improving tropical legume productivity for marginal environments in sub-Saharan Africa</i>			
122.01	<i>G6007.01 Improve groundnut (Arachis hypogaea L) productivity for marginal environments in sub-Saharan Africa</i> (Pis: Vincent Vadez, effective June 2008; David Hoisington, September 2007–May 2008, ICRISAT) May 2007–April 2010	3,037,512	ARI–Naliendele, CRS, DaRT P/L, EMBRAPA, IAC, ICRISAT, INRAN, ISRA, UCB, UGA	groundnuts drought and disease resistance Africa
122.02	<i>G6007.02: Improve cowpea (Vigna unguiculata L) productivity for marginal environments in sub-Saharan Africa</i> (PI: Jeff Ehlers, UoC–Riverside) May 2007–April 2010	1,952,008	UEM, IITA, INERA–Burkina Faso, IRAD, ISRA, UoC (Davis)	cowpeas drought and disease resistance Africa
122.03	<i>G6007.03: Improve common bean (Phaseolus vulgaris L) productivity for marginal environments in sub-Saharan Africa</i> (PI: Matthew Blair, CIAT) May 2007–April 2010	1,867,327	ART, CBI, ECABREN, EIAR, PU, RIKEN, SABRN, UoC (Davis)	beans drought and disease resistance sub-Saharan Africa
122.04	<i>G6007.04: Improve chickpea (Cicer arietinum L) productivity for marginal environments in sub-Saharan Africa</i> (Pis: Rajeev Varshney, GCP/ICRISAT, effective June 2008; David Hoisington, September 2007–May 2008, ICRISAT) May 2007–April 2010	1,074,126	DaRT P/L, EIAR, IIPR, LZARDI, NIPGR, UoC (Davis), UoF	chickpeas drought and disease resistance Africa
122.05	<i>G6007.05: Develop cross-species resources for comparative biology in tropical crop legumes</i> (PI: Doug Cook, UoC–Davis) May 2007–April 2010	867,688	UCB, UGA	groundnuts, cowpeas, beans, chickpeas drought and disease resistance sub-Saharan Africa
122.06	<i>G6007.06: Provide training and capacity-building for SSA scientists</i> (PI: Carmen de Vicente, GCP) May 2007–April 2010	851,600	ARI–Naliendele, ART, CBI, CRS, ECABREN, EMBRAPA, EIAR, IIPR, INERA–Burkina Faso, INRAN, IRAD, ISRA, LZARDI, TLII partners, SABRN, SARI–Ethiopia, UCB	groundnuts, cowpeas, beans, chickpeas drought and disease resistance Africa
123	<i>G4005.69.01 (CB19a/RF–FS022): Developing and disseminating resilient and productive rice varieties for drought-prone environments in India</i> (PI: Arvind Kumar, IRRI) March 2005–February 2008; NCE: February 2009	120,000	BF, BAU, CRRI, CRURRS, IGKV, NDUAT, TNAU, UAS (Bangalore)	rice drought tolerance Asia
124	<i>G5005.69.02 (CB19b/RF–FS029): Pathway dissection and candidate gene identification of drought tolerance in rice by a forward genetics approach</i> (PI: Zhi-Kang Li, ICS–CAAS) March 2005–February 2008	120,000	IRRI, PeU, YU	rice drought tolerance Asia
125	<i>G4005.70 (CB20a & CB 20b/RF–FS091 & RF–FS092): Tapping crop biodiversity for the resource-poor in East and Central Africa (ICRISAT and IITA)</i> (Pis: David Hoisington, ICRISAT, and Morag Ferguson, IITA) ICRISAT: July 2005–June 2008; NCE: October 2008 IITA: July 2005–June 2008; NCE: June 2009	276,000 (ICRISAT and IITA combined)	ICRISAT-led team: ARI, ARTC, EARO, ISABU, ISAR, KARI, NARI, SAARI IITA-led team: ARI–Naliendele, FOFIFA–DRA, IIAM, INERA–DRC), ISAR, KARI, NAARI	sorghum various traits Africa

Focus projects cont'd...

No.	Duration	Total budget (USD)	Collaborating institutes in 2008	Crop(s), trait(s), region(s)
126	<i>G4007.05: Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco</i> (PI: Abbad Andaloussi Fouad, INRA–Morocco) January 2007–December 2008	200,000	CIMMYT, CU, ICARDA, UdB, UoMi	wheat, barley various traits Africa
127	<i>G4007.23: Field evaluation of wheat–barley introgression lines under different water regimes</i> (PI: Márta Molnár-Láng, ARI–HAS) December 2007–November 2010	144,000	CAAS, CIMMYT, DPSPP–EKC	wheat; barley drought, salt and aluminium tolerance various regions
128	<i>G4007.24: Seed smoke treatment to favour germination under water-stressed conditions</i> (PI: Ervin Balazs, ARI–HAS) December 2007–November 2009	24,000	UKZN	various
129	<i>G4008.28: Characterisation of maize diversity in Central Europe</i> (PI: Peter Papp, ABC–Gödöllő) January 2008–December 2008	18,000	CIMMYT, IA–Tápiószele	maize various traits and regions
130	<i>G4008.29: Characterisation of bean diversity in Central Europe</i> (PI: Peter Papp, ABC–Gödöllő) January 2008–December 2008	18,000	CIAT, IA–Tápiószele	beans various traits and regions
131	<i>G4008.51: Use of molecular marker and physiological tests to characterise Hungarian rice diversity and new sources of blast resistance</i> (PI: Ibolya Simon-Kiss, HAKI) April 2008–October 2008	13,500	Agropolis–CIRAD	rice blast resistance various regions
Projects on NCE into 2008 or beyond				
132	<i>G4005.69.03 (CB19c/RF–028): Innovative and integrated approaches to improve the tolerance of maize to water-limited environments</i> (PI: Yunbi Xu, CIMMYT) April 2005–March 2007; NCE: June 2008	80,000	CAAS, SAU	maize drought tolerance Africa, Asia

Appendix D:

Selected publications – 2008

In the interests of space, the list below is limited to books, book chapters, journal articles and Programme-wide publications only. For the full list of all GCP publications in 2008, please see: <http://www.generationcp.org/research.php?da=0642451>

Programme publications

Book chapters

Ribaut J-M, Monneveux P, Glaszmann JC, Leung H, van Hintum T and de Vicente C (2008). International programs and the use of modern biotechnologies for crop improvement. In: *Genomics of tropical crop plants* (Moore P and Ming R, eds). Part of series *Plant genetics and genomics: Crops and models*, Volume 1. Springer, New York, USA, pp 21–63. ISBN: 978-0-387-71218-5 (DOI: 10.1007/978-0-387-71219-2_2). <http://www.springerlink.com/content/hw6867421475n4n2/>

Annual Report and Medium-Term Plan

Generation Challenge Programme (2008). *CGIAR Generation Challenge Programme 2007 Annual report and year five (2008) workplan*. Generation Challenge Programme, Texcoco, Mexico, 64 pp. http://www.generationcp.org/UserFiles/File/GCP_2007-Annual-Report-and-2008-workplan.pdf

Generation Challenge Programme (2008). *CGIAR Generation Challenge Programme Medium-Term Plan 2009–2011*. Generation Challenge Programme, Texcoco, Mexico, 118 pp. <http://www.generationcp.org/UserFiles/File/GCP-MTP-2009-2011.pdf>

Brochures

Generation Challenge Programme (2008). *The CGIAR Generation Challenge Programme. Reflecting on Phase I and looking ahead to Phase II*. Generation Challenge Programme, Texcoco, Mexico, 5 pp. http://www.generationcp.org/UserFiles/File/GCP-Phase-I-to-Phase%20II_Ver%203.pdf

Generation Challenge Programme (2008). *The CGIAR Generation Challenge Programme – Cultivating plant diversity for the resource-poor*. Generation Challenge Programme, Texcoco, Mexico, 2 pp. <http://www.generationcp.org/UserFiles/File/GCP-brochure-2008.pdf>

Project updates

Generation Challenge Programme (2008). *CGIAR Generation Challenge Programme 2008 project abstracts*. Generation Challenge Programme, Texcoco, Mexico, 207 pp. http://www.generationcp.org/UserFiles/File/2008_Project_abstracts.pdf

Project briefs

Generation Challenge Programme (2008). *Generation Challenge Programme 2007 project briefs*. Generation Challenge Programme, Mexico DF, Mexico, 74 pp. http://www.generationcp.org/UserFiles/File/2007_Project_briefs.pdf

Learning materials

Generation Challenge Programme (2008). *Genetic resource policies course*. A distant learning module for scientists on genetic resource policies and their implications for freedom to operate. *GCP Learning Materials No. 1*. Developed by GCP in collaboration with WUR. Available on CD-ROM and online. <http://www.generationcp.org/distantpolicies/>

Generation Challenge Programme (2008). *The McClintock crop bioinformatics course*. This self-study introductory online course targets scientists with a reasonable background in germplasm, biology and genetics, and their application in plant and agricultural sciences. *GCP Learning Materials No. 2*. Developed jointly by GCP and IRRI (2008). Available on CD-ROM and online. http://mcclintock.generationcp.org/index.php?option=com_content&task=section&id=19&Itemid=170

Generation Challenge Programme (2008). *Genomics and comparative genomics tutorial*. For use as basic class material or self-tutorial by scientists and advanced students with a strong background in biology and genetics. *GCP Learning Materials No. 3*. Material developed in collaboration with IGD. Available on CD-ROM and online. <http://www.generationcp.org/genomics/>

Posters

Programme-wide scope

Generation Challenge Programme (2008). Defining and refining priorities: our strategy through time. Poster presented at the *2008 CGIAR Annual General Meeting*, 1–5 December 2008, Maputo, Mozambique. http://www.generationcp.org/UserFiles/File/Our-strategy-through-time_Dec08.pdf

Generation Challenge Programme (2008). Introducing the CGIAR Generation Challenge Programme. Poster presented at the *2008 CGIAR Annual General Meeting*, 1–5 December 2008, Maputo, Mozambique. http://www.generationcp.org/UserFiles/File/Introducing-the-CGIAR-Generation-Challenge-Programme_Dec08.pdf

- Generation Challenge Programme (2008). Looking back on Phase I and moving on to Phase II and the future. Poster presented at the *2008 CGIAR Annual General Meeting*, 1–5 December 2008, Maputo, Mozambique.
http://www.generationcp.org/UserFiles/File/Phase-I-Phase-I_Dec-08.pdf
- Generation Challenge Programme (2008). Tapping crop diversity to provide new tools for breeders. Poster presented at the *2008 CGIAR Annual General Meeting*, 1–5 December 2008, Maputo, Mozambique.
http://www.generationcp.org/UserFiles/File/Tapping-crop-diversity-to-provide_Dec08.pdf
- Generation Challenge Programme (2008). The CGIAR Generation Challenge Programme at a glance. Poster presented at the *2008 CGIAR Annual General Meeting*, 1–5 December 2008, Maputo, Mozambique.
http://www.generationcp.org/UserFiles/File/The-CGIAR-Generation-Challenge-Programme-at-a-glance_Dec-08.pdf
- Generation Challenge Programme (2008). The CGIAR Generation Challenge Programme in Asia. Poster presented at the *GCP Annual Research Meeting*, 16–20 September 2008, Bangkok, Thailand.
<http://www.generationcp.org/UserFiles/File/2008-ARM-03-The-CGIAR-Generation-Challenge-Programme-in-Asia.pdf>
- Generation Challenge Programme (2008). The GCP Mission. Poster presented at the *2008 CGIAR Annual General Meeting*, 1–5 December 2008, Maputo, Mozambique.
http://www.generationcp.org/UserFiles/File/The-GCP-Mission_Dec08.pdf
- Generation Challenge Programme (2008). The GCP R&D community. Poster presented at the *2008 CGIAR Annual General Meeting*, 1–5 December 2008, Maputo, Mozambique.
http://www.generationcp.org/UserFiles/File/The-GCP-R-and-D-community_Dec-08.pdf

Abstracts for project-level posters

- Generation Challenge Programme (2008). *Poster abstracts: 2008 Annual Research Meeting*, 16–20 September 2008, Bangkok, Thailand. Generation Challenge Programme, Texcoco, Mexico, 76 pp.
http://www.generationcp.org/UserFiles/File/2008_Poster-abstracts_final.pdf

Reviews and evaluations

- Consultative Group on International Agricultural Research (2008). *Report of the first external review of the Generation Challenge Programme* (Beverdors WD, Palenberg MA and Thomson JA, reviewers). 98 pp.
http://www.generationcp.org/UserFiles/File/Report-of-the-EPMR-to-the-GCP_March08.pdf
- European Commission (2008). *Report of the EU-commissioned review of the Generation Challenge Programme - 'Cultivating plant diversity for the resource poor'* (Bennett C and Hillocks R, reviewers). 58 pp.
http://www.generationcp.org/UserFiles/File/Final-report_EC-review-2008.pdf

For responses to, and commentary on, the above report, please visit our Reviews and Evaluations webpage at <http://www.generationcp.org/whoware.php?da=08137524>

Project publications

Book chapters

- Kikuchi S (2008). High-throughput transcriptome analysis in rice from a genome perspective. In: *Rice biology in the genomics era* (Hirano HY, Hirai A, Sano Y and Sasaki T, eds). *Volume 62* in series: *Biotechnology in agriculture and forestry* (Nagata T, Lörz H and Widholm J, eds). Springer–Verlag, Berlin Heidelberg, Germany, pp 53–67. ISBN: 978-3-540-74248-7 (DOI: 10.1007/978-3-540-74250-0_5). <http://www.springerlink.com/content/k5w75x43043u1653/?p=0e3b20139dc245b180048c803f3f8a99&pi=4>
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<http://www.springerlink.com/content/h3656h2r765xvg64/>
- Xu Y and Crouch JH (2008). Genomics of tropical maize, a staple food and feed across the world. In: *Genomics of tropical crop plants* (Moore PH and Ming R, eds). Springer, New York, USA, pp 333–370. ISBN: 978-0-387-71218-5 (DOI: 10.1007/978-0-387-71219-2_14).
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Journal articles

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http://www.generationcp.org/UserFiles/File/Ali-et-al-Genetic-studies-Pakistan_from-web.pdf
- Balaji Jayashree, Rajgopal S, Hoisington D, Prasanth VP and Chandra S (2008). Webstructure and VisualStruct: web interfaces and visualization for structure software implemented in a cluster environment. *Journal of Integrative Bioinformatics* 5:89 (DOI 10.2390/biecoll-jib-2008-89).
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Appendix E:

GCP's funders in the course of Phase I (2004–2008)

We gratefully acknowledge the support of the following funders in Phase I, listed in alphabetical order:

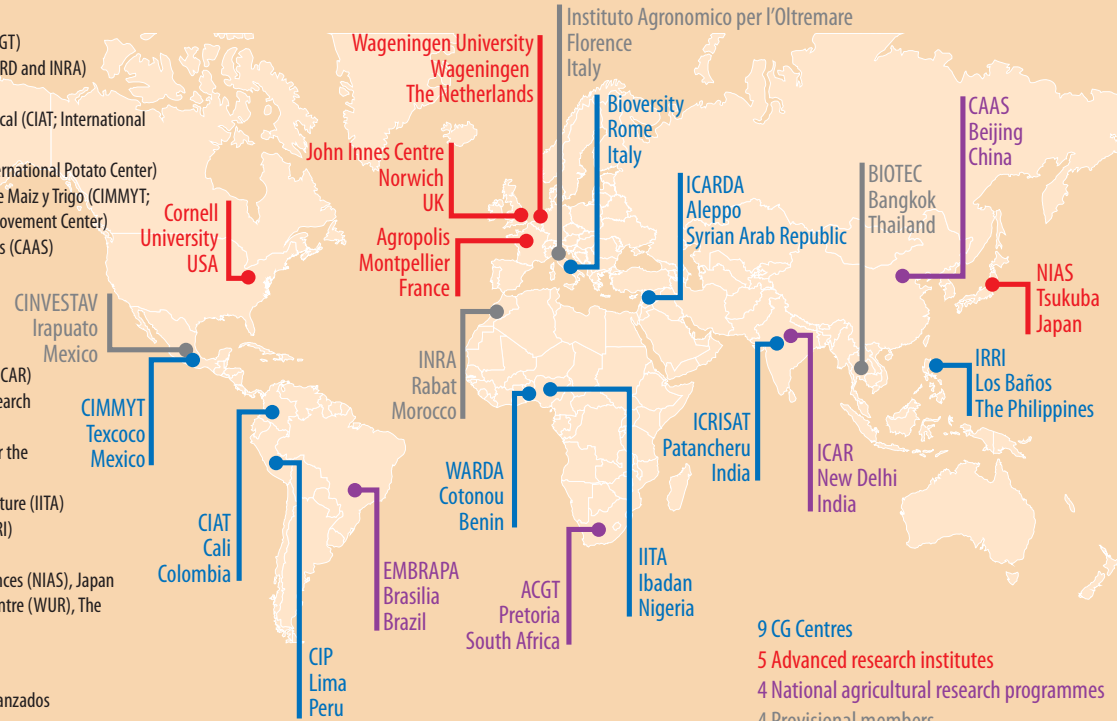
1. Austrian Research Centers GmbH
2. Bill & Melinda Gates Foundation
3. Department for International Development (DFID), UK
4. European Commission (EC)
5. Kirkhouse Trust
6. Pioneer Hi-Bred International, Inc
7. Swedish International Development and Cooperation Agency (Sida)
8. Swiss Agency for Development and Cooperation (SDC)
9. Syngenta
10. Syngenta Foundation for Sustainable Agriculture
11. The Rockefeller Foundation
12. The World Bank

For a full list of GCP's funders by year, please visit: <http://www.generationcp.org/funders.php?da=0783830>

The GCP Consortium

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

Where in the world is GCP? The GCP network in 2008

In 2008, GCP worked with more than 200 partners spread across 64 countries:

Central and West Asia and North Africa

1. Iran
2. Morocco
3. Syria

Latin America and the Caribbean

4. Argentina
5. Bolivia
6. Brazil
7. Chile
8. Colombia
9. Costa Rica
10. Cuba
11. Haiti
12. Mexico
13. Nicaragua
14. Peru
15. Uruguay

South and Southeast Asia

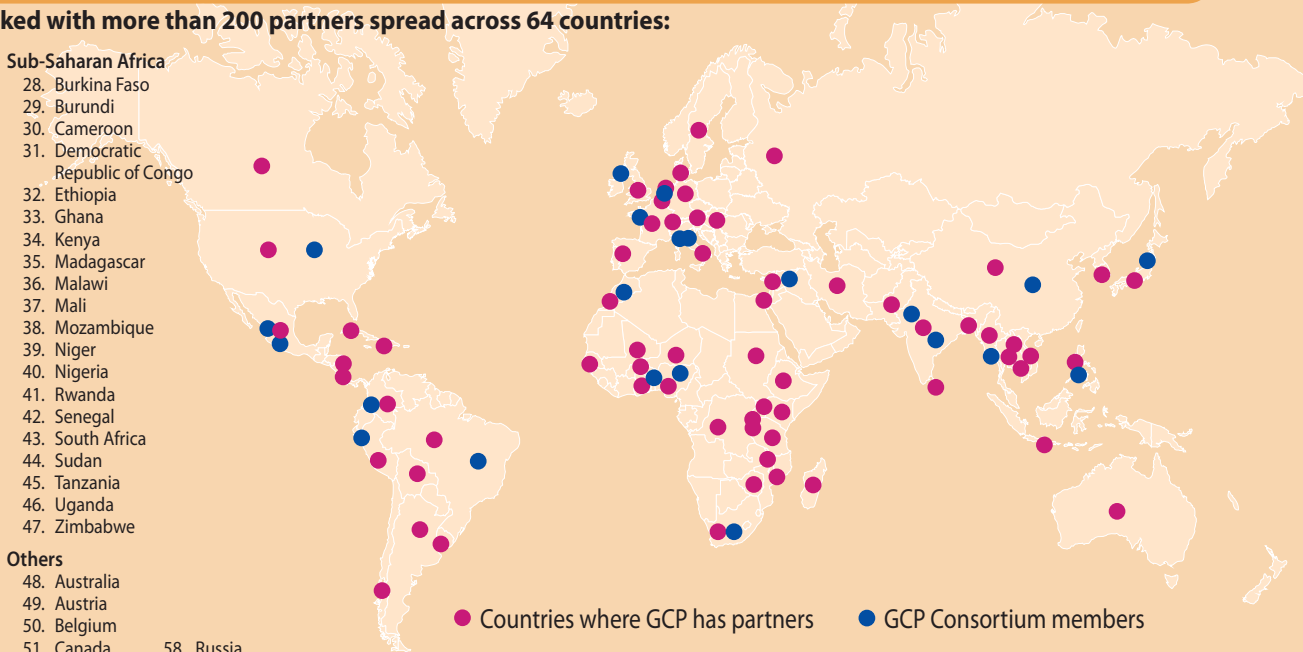
16. Bangladesh
17. Cambodia
18. China
19. India
20. Indonesia
21. Laos
22. Myanmar
23. Pakistan
24. Sri Lanka
25. Thailand
26. The Philippines
27. Vietnam

Sub-Saharan Africa

28. Burkina Faso
29. Burundi
30. Cameroon
31. Democratic Republic of Congo
32. Ethiopia
33. Ghana
34. Kenya
35. Madagascar
36. Malawi
37. Mali
38. Mozambique
39. Niger
40. Nigeria
41. Rwanda
42. Senegal
43. South Africa
44. Sudan
45. Tanzania
46. Uganda
47. Zimbabwe

Others

48. Australia
49. Austria
50. Belgium
51. Canada
52. Denmark
53. France
54. Germany
55. Hungary
56. Italy
57. Japan
58. Russia
59. South Korea
60. Sweden
61. Switzerland
62. The Netherlands
63. UK
64. USA





GCP Annual Research Meeting participants, September 2008, Bangkok, Thailand