



# Medium-Term Plan 2010–2012

December 2009

**Generation**  **Challenge programme**

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE-POOR

[www.generationcp.org](http://www.generationcp.org)

## GCP's five Subprogrammes

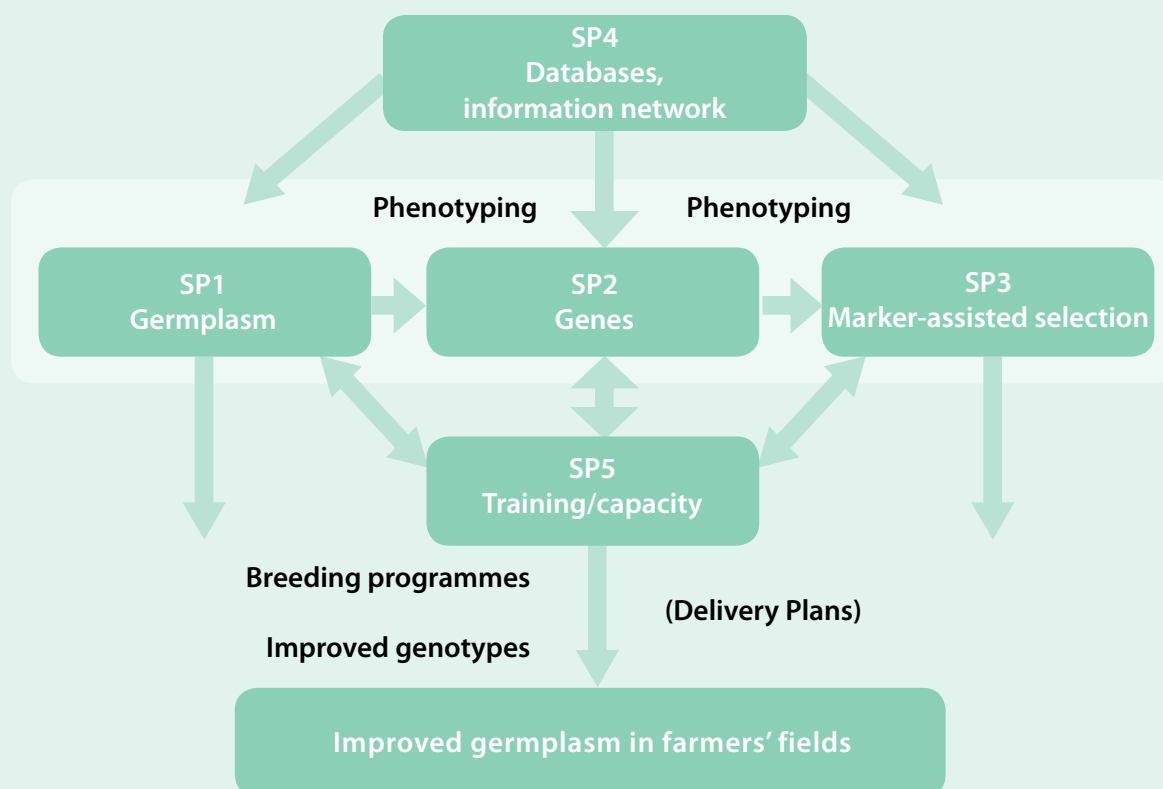
**Subprogramme 1: Crop genetic diversity** – Characterises the diversity of crop germplasm collections in the custody of the CGIAR and national programmes in terms of genetic structure and associated phenotypic variation

**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 Medium-Term Plan: 2010–2012

December 2009<sup>1</sup>

**Generation Challenge Programme (GCP)**

Hosted by CIMMYT

(Centro Internacional de Mejoramiento de Maíz y Trigo;  
the International Maize and Wheat Improvement Center)

*Mailing address:*

c/o CIMMYT, Apdo Postal 6–641  
06600 Mexico, DF, Mexico

*Physical address:*

c/o CIMMYT Km 45 Carretera México–Veracruz  
El Batán, Texcoco, México, CP 56130

Tel: +52 55 5804 2004

Fax: +52 55 5804 7558

Email: [generationcp@cgiar.org](mailto:generationcp@cgiar.org) or [info@generationcp.org](mailto:info@generationcp.org)  
[www.generationcp.org](http://www.generationcp.org)

Available online at: <http://www.generationcp.org/brochure.php#MTPs>

---

<sup>1</sup> Submitted to the CGIAR Science Council on 15th June 2009, with minor editorial changes being carried out in December 2009

© The Generation Challenge Programme of the Consultative Group on International Agricultural Research.  
**Fair use:** you are free to quote from, or reproduce, sections of this publication without further permission, provided the Generation Challenge Programme (GCP) of the Consultative Group on International Agricultural Research (CGIAR) is acknowledged as the source. We would also appreciate receiving a copy of the publication.

**Correct citation:** Generation Challenge Programme (2009). CGIAR Generation Challenge Programme Medium-Term Plan: 2010–2012. Generation Challenge Programme, Texcoco, Mexico, 113 pp.

**Edited by:** Catherine Durbin

**Art direction:** Eliot Sánchez P, Miguel Mellado E, CIMMYT.

**Available online at:** <http://www.generationcp.org/brochure.php#MTPs>

# Contents

<b>Acronyms and abbreviations</b> .....	<b>vii</b>
<b>Overview</b> .....	<b>1</b>
Introduction.....	1
Executive summary.....	1
GCP at a glance .....	1
Who we are.....	1
What is GCP's core business?.....	1
Trends.....	1
Where we are.....	1
Where we've come from, and where we're going.....	2
Realignment towards Challenge Initiatives and platforms.....	2
New research in the context of CIs, platforms and Subprogrammes.....	3
Challenges.....	3
GCP's niche and network.....	3
Context.....	4
Crop improvement for poverty alleviation.....	4
The global agenda: agriculture, drought and climate change.....	4
GCP governance.....	5
Reforms and background.....	5
Programme Steering Committee and Executive Board.....	5
Stakeholders Committee .....	6
Review and Advisory Panel.....	6
Programme rationale and structure.....	6
Research framework.....	7
GCP research strategy: evolution and management.....	9
Evolution of the GCP strategy and research trends.....	9
Challenge Initiatives .....	10
Delivery platforms.....	11
Managing our research strategy.....	13
Product Delivery Leader and Product Delivery Coordinators.....	13
Product management and delivery.....	14
Data release and quality.....	15
Product management .....	15
Financial indicators .....	15
Collaboration and partnerships.....	16
Alignment with CGIAR Systemwide Priorities .....	17
Achievements in 2008.....	18
Implications for future work.....	19
Slower than expected progress.....	19
<b>Highlights of the 2009–2010 project portfolio</b> .....	<b>21</b>
2010 selected highlights.....	21
Subprogramme 1: Crop genetic diversity (Project 1 in the MTP).....	21
2009 highlights.....	21
2010 highlights.....	22
Subprogramme 2: Genomics towards gene discovery (Project 2 in the MTP).....	22
2009 highlights.....	22
2010 highlights.....	22
Subprogramme 3: Trait capture for crop improvement (Project 3 in the MTP).....	23
2009 highlights.....	23
2010 highlights.....	23

Subprogramme 4: Bioinformatics and crop information systems (Project 4 in the MTP) .....	24
2009 highlights .....	24
2010 highlights .....	24
Subprogramme 5: Capacity-building and enabling delivery (Project 5 in the MTP) .....	24
2009 highlights .....	24
2010 highlights .....	25
<b>Project 1 – SP1: Crop genetic diversity.....</b>	<b>27</b>
Project narrative .....	27
Project overview and rationale .....	27
Impact pathways.....	27
Theme 1: Creation of an improved understanding of the structure of the diversity for the major world food crops.....	27
Theme 2: Establishment and implementation of a scientific and organisational framework to describe tolerance to drought .....	28
Theme 3: Development of novel populational approaches for relating genotypes to phenotypes.....	29
Theme 4: Assembly of global elite materials as reservoirs for enhancing mobilisation of genetic diversity.....	29
Changes from previous MTP.....	29
Output descriptions and partnerships.....	30
Overview .....	30
Output descriptions.....	31
International public goods.....	35
Elaboration of partner roles.....	35
Project 1 logframe – SP1: Crop genetic diversity.....	36
Theme 1: Creation of an improved understanding of the structure of the diversity for the major world food crops .....	36
Theme 2: Establishment and implementation of a scientific and organisational framework to describe tolerance to drought.....	36
Theme 3: Development of novel populational approaches for relating genotypes to phenotypes.....	38
Theme 4: Assembly of global elite materials as reservoirs for enhancing mobilisation of genetic diversity.....	40
<b>Project 2 – SP2: Genomics towards gene discovery .....</b>	<b>41</b>
Project narrative .....	41
Project overview and rationale .....	41
Impact pathways.....	41
Theme 1: Assembly of genomics and germplasm resources through consolidating and developing specialised genetic stocks.....	41
Theme 2: Development of comparative maps within and across species and framework genetic markers for target crops.....	42
Theme 3: Assignment of genes and pathways to phenotypes through the convergence evidence of genome variation, expression patterns and phenotypic data .....	42
Theme 4: Validation of genes and pathways through evaluation of under- or overexpression constructs or variants (induced or natural) of the target genes .....	42
Changes from previous MTP.....	43
Output descriptions and partnerships.....	44
Overview .....	44
Output descriptions.....	44
International public goods.....	49
Elaboration of partner roles.....	49
Project 2 logframe – SP2: Genomics towards gene discovery.....	50
Theme 1: Assembly of genomics and germplasm resources through consolidating and developing specialised genetic stocks.....	50
Theme 2: Development of comparative maps within and across species and framework genetic markers for target crops.....	51

Theme 3: Assignment of genes and pathways to phenotypes through the convergence evidence of genome variation, expression patterns and phenotypic data.....	52
Theme 4: Validation of genes and pathways through evaluation of under- or over-expression constructs or variants (induced or natural) of the target genes.....	54
<b>Project 3 – SP3: Trait capture for crop improvement.....</b>	<b>57</b>
Project narrative .....	57
Project overview and rationale.....	57
Impact pathways.....	57
Theme 1: Characterisation of segregating populations and identification of genomic regions for plant breeding.....	57
Theme 2: Development and evaluation of novel breeding or molecular technologies to better serve modern plant breeding.....	58
Theme 3: Markers/alleles validation in adapted germplasm under target environments .....	58
Theme 4: Application of molecular markers in breeding programmes.....	59
Changes from previous MTP.....	59
Output descriptions and partnerships.....	60
Overview .....	60
Output descriptions.....	61
International public goods.....	65
Elaboration of partners roles.....	65
Project 3 logframe – SP3: Trait capture for crop improvement.....	66
Theme 1: Characterisation of segregating populations and identification of genomic regions for plant breeding.....	66
Theme 2: Development and evaluation of novel breeding or molecular technologies to better serve modern plant breeding.....	66
Theme 3: Markers/alleles validation in adapted germplasm under target environments.....	69
Theme 4: Application of molecular markers in breeding programmes .....	70
<b>Project 4 – SP4: Bioinformatics and crop information systems .....</b>	<b>73</b>
Project narrative .....	73
Project overview and rationale.....	73
Impact pathways.....	73
Theme 1: User support – Ensure that all GCP scientists have access to advice and tools to facilitate data management, analysis and publication.....	73
Theme 2: Data curation and quality – Provide access to fully documented GCP data of certified quality for GCP partners and other interested researchers Output 4 to Output 6 .....	74
Theme 3: Methodology development – Bioinformatics research required to provide the methodology and informatics tools needed for GCP and MBP activities.....	74
Theme 4: Informatics infrastructure – Provide facilities for data integration and sharing among GCP and MBP partners .....	74
Changes from previous MTP.....	75
Output descriptions and partnerships.....	75
Overview .....	75
Output descriptions.....	76
International public goods.....	79
Elaboration of partner roles.....	79
Project 4 logframe – SP4: Bioinformatics and crop information systems .....	79
Theme 1: User Support–Ensuring that all GCP scientists have access to advice and tools to facilitate data management analysis and publication .....	79
Theme 2: Data Curation and Quality - Provide access to fully documented GCP data of certified quality for GCP partners and other interested researchers .....	80
Theme 3: Methodology Development – Bioinformatics research required to provide the methodology and informatics tools needed for GCP and MBP activities.....	81
Theme 4: Informatics Infrastructure – Provide facilities for data integration and sharing among GCP partners .....	83

<b>Project 5 – SP5: Capacity-building and enabling delivery .....</b>	<b>85</b>
Project narrative .....	85
Project overview and rationale .....	85
Impact pathways .....	85
Theme 1: Creation of a platform of training resources and a cadre of trained scientists to apply advanced technologies and add value to GCP products .....	85
Theme 2: Cultivation of research and learning opportunities for GCP collaborators and NARS scientists to further the GCP mission and progress .....	86
Theme 3: Construction of systems for ensuring product delivery .....	86
Theme 4: Development and implementation of support services .....	87
Theme 5: <i>Ex ante</i> impact analysis and impact assessment .....	87
Changes from previous MTP .....	87
Output descriptions and partnerships .....	88
Overview .....	88
Output descriptions .....	88
International public goods .....	93
Elaboration of partner roles .....	93
Project 5 logframe – SP5: Capacity-building and enabling delivery .....	94
Theme 1: Creation of a platform of training resources and a cadre of trained scientists to apply advanced technologies and add value to GCP products .....	94
Theme 2: Cultivation of research and learning opportunities for GCP collaborators and NARS scientists to further the GCP mission and progress .....	94
Theme 3: Construction of systems for ensuring product delivery .....	96
Theme 4: Development and implementation of support services .....	98
Theme 5: <i>Ex ante</i> impact analysis and impact assessment .....	99
 <b>Annexes .....</b>	 <b>101</b>
Annex A: GCP Consortium members and partners – 2009 .....	101
1. Consortium members .....	101
Full members .....	101
Provisional members .....	101
2. Developing country partners .....	101
3. Developed country partners .....	103
4. Funders .....	103
5. CGIAR Centres and Programmes .....	103
6. Private sector .....	104
7. Service providers .....	104
8. Other partners .....	104
Annex B: Progress report on implementation of external review recommendations .....	105
Annex C: Financing plan .....	107
Table 1: Allocation of project costs by Priority Area and Priorities, 2010 .....	107
Table 2: Allocation of project costs to CGIAR Priorities, 2008–2012 .....	107
Table 3: Summary of project costs, 2008–2012 .....	108
Table 4: Summary of priority costs, 2008–2012 .....	108
Table 5: Investments by undertaking, activity and sector, 2008–2012 .....	108
Table 6: Project investments by developing region, 2008–2012 .....	109
Table 7: Summary of investments by developing region, 2008–2012 .....	109
Table 8: Expenditure by object, 2008–2012 .....	109
Table 9: Member and non-member unrestricted grants, 2008–2010 .....	110
Table 9a: Member and non-member unrestricted and restricted grants, 2008–2010 .....	110
Table 10: Allocation of member, non-member grants and other sources to projects, 2008–2010 .....	111
Table 11: Internationally and nationally recruited staff, 2008–2012 .....	111
Table 12: Currency structure of expenditure, 2008–2010 .....	111
Table 13: Statement of Financial Position (SFP), 2008–2010 .....	112
Table 14: Statement of activities (SOA), 2008–2010 .....	113



# List of figures

Figure 1. GCP's research approach.....	7
Figure 2. GCP's research management.....	14

# List of boxes

Box 1. Timeline: Revisions on the Consortium Agreement.....	5
Box 2. The seven Challenge Initiatives.....	11
Box 3. Challenge Initiative target countries.....	11
Box 4. Timeline for drafting CI proposals.....	11
Box 5. Product Delivery Coordinators.....	13

# Acronyms and abbreviations

AAFC–SPARC	Agriculture and Agri-Food Canada, Semiarid Prairie Agricultural Research Centre	CRURRS	Central Rainfed Upland Rice Research Station, India
ABRII	Agricultural Biotechnology Research Institute of Iran	CSIR	Council for Scientific and Industrial Research, South Africa
ACCI–UKZN	African Centre for Crop Improvement–University of KwaZulu–Natal, South Africa	CSIRO	Commonwealth Scientific and Industrial Research Organisation, Australia
ACPGF	Australian Centre for Plant Functional Genomics, Pty Ltd	CSSL	chromosome segment substitution line
ADOC	allelic diversity for orthologous candidate genes	CSU	Charles Sturt University, Australia
AfricaRice	Africa Rice Center	CU	Cornell University, USA
AGRA	Alliance for a Green Revolution in Africa	DARS	Department of Agriculture Research Services, Malawi
Agropolis–CIRAD	Centre de coopération internationale en recherche agronomique pour le développement, France	DArT	diversity arrays technology
Agropolis–INRA	Institut national de la recherche agronomique, France	DArT P/L	Diversity Arrays Technology Pty, Ltd
Agropolis–IRD	Institut de recherche pour le développement, France	DFID	Department for International Development, UK
AICMIP	The All-India Coordinated Pearl Millet Improvement Project	DMR	Directorate of Maize Research, India
Al	aluminium	DNA	deoxyribonucleic acid
<i>Alt<sub>5g</sub></i>	marker diagnostic for aluminium tolerance	DPI&F	Department of Primary Industries & Fisheries, Australia
ARC	Agricultural Research Corporation, Sudan	DREB	drought-responsive element binding protein (gene)
ARI(s)	advanced research institute(s)	DZARC	Debre Zeit Agricultural Research Centre, Ethiopia
ARI–Naliendele	Agricultural Research Institute–Naliendele Research Station, Tanzania	EC	European Commission
ARS	Agricultural Research Station, Durgapura, Rajasthan, India	ECABREN	Eastern and Central Africa Bean Research Network
ART	Agricultural Research in Tanzania	EIAR	Ethiopian Institute of Agricultural Research
BAC	bacterial artificial chromosome	EMBRAPA	Empresa Brasileira de Pesquisa Agropecuária (Brazilian Agricultural Research Corporation)
BC <sub>1</sub> etc	Backcross population <sub>1</sub> etc	EPMR	External Programme and Management Review
BC <sub>1</sub> F <sub>4</sub>	F <sub>4</sub> progenies derived from BC <sub>1</sub>	EST	expressed sequence tag
BC–NAM	back-Cross Nested Association Mapping	ETH	Eidgenössische Technische Hochschule, (Swiss Federal Institute of Technology), Zürich, Switzerland
BecA	Biosciences Eastern and Central Africa, Kenya	FERA	Food and Environment Research Agency, UK
BF	Barwale Foundation	EgU	Egerton University, Kenya
BCKV	Bidhan Chandra Krishi Viswavidyalaya, India	Fedearroz	Federación de productores de arroz, Colombia
BCMV	bean common mosaic virus	FPP	field phenotyping platform
BI	Bioversity International	GCP	Generation Challenge Programme of the CGIAR
BIOTEC	National Center for Genetic Engineering and Biotechnology, Thailand	GIPB	Global Partnership Initiative for Plant Breeding Capacity Building
BMGF	Bill & Melinda Gates Foundation	GIS	geographic information system(s)
BRRD	Bureau of Rice Research and Development, Rice Department, Thailand	GOST	GreenPhyl Ortholog Search Tool
BRRRI	Bangladesh Rice Research Institute	GPL	General Public Licence
CAAS	Chinese Academy of Agricultural Sciences	GSS	Genotyping Support Service
CARBAP	Centre africain de recherche sur bananiers et plantains, Cameroon	GxE	genotype by environment interaction
CARDI	Cambodia Agricultural Research and Development Institute, Cambodia	HAAS	Hebei Academy of Agricultural Sciences, Institute of Dry Farming, China
CBI	Crop Breeding Institute, Department of Research for Development, Zimbabwe	HPC	high-performance computing
CBSD	cassava brown streak disease	HUJ	Hebrew University of Jerusalem, Israel
CDP	common donor parent	HZAU	Huazhong Agricultural University, China
CDT	Global Crop Diversity Trust	IAC	Instituto Agronomico de Campinas, Brazil
CSS lines	chromosome segment substitution lines	IARI	Indian Agriculture Research Institute, India
CERAAS	Centre d'étude régional pour l'amélioration de l'adaptation à la sécheresse, Senegal	ICABIOGRAD	Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development
CGIAR	Consultative Group on International Agricultural Research	ICAR	Indian Council of Agricultural Research, India
CGM	cassava green mites	ICARDA	International Centre for Agricultural Research in the Dry Areas
CIAT	Centro Internacional de Agricultura Tropical (International Center for Tropical Agriculture)	ICERI	Indonesian Cereals Research Institute, Indonesia
CIMMYT	Centro Internacional de Mejoramiento de Maíz y Trigo (the International Maize and Wheat Improvement Center)	ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
CIP	Centro Internacional de la Papa (International Potato Centre)	ICS–CAAS	Institute of Crop Science, Chinese Academy of Agricultural Sciences
CI(s)	Challenge Initiative(s)	IER	Institut d'économie rurale, Mali
CMD	cassava mosaic disease	IIAM	Instituto de Investigação Agrária de Moçambique (Institute for Agricultural Research), Mozambique
CoP	community of practice	IFPRI	International Food Policy Research Institute
COS	conserved orthologous sequence	IGD	Institute for Genomic Diversity, Cornell University, USA
CP	Challenge Programme (of the CGIAR)	IGKV	Indira Gandhi Krishi Vidyalaya, India
CRI	Crops Research Institute, Ghana	IIPR	Indian Institute of Pulses Research
CRISL	Coconut Research Institute of Sri Lanka	IITA	International Institute of Tropical Agriculture
CRS	Chitedze Research Station, Malawi	ILRI	International Livestock Research Institute
		iMAS	Integrated Marker-Assisted Selection System
		INCA	Instituto Nacional de Ciencias Agrícolas, Cuba
		INCAE	Instituto Centroamericano de Administración de Empresas, Costa Rica
		INERA	Institut de l'environnement et de recherches agricoles, Burkina Faso

INIA—Chile	Instituto de Investigaciones Agropecuarias, Chile	OSU	Oregon State University, USA
INIA—Uruguay	Instituto Nacional de Investigación Agropecuaria, Uruguay	P-efficiency/ acquisition	Phosphorus uptake efficiency/acquisition
INIFAP	Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias, Mexico	PARC	Pakistani Agricultural Research Council
INRA—Morocco	Institut national de la recherche agronomique, Morocco	PASS	Program for African Seed Systems
INRAN	Institut national de recherches agronomiques du Niger	PAU	Punjab Agricultural University, India
INTA—Argentina	Instituto Nacional de Tecnología Agropecuaria, Argentina	PBI	Plant Breeding Institute, University of Sydney
INTA—Nicaragua	Instituto Nacional de Tecnología Agropecuaria, Nicaragua	PDC	Product Delivery Coordinator
IP	intellectual property	PDG	Project Development Guide
IPGR	Institute for Plant Genetic Resources, Bulgaria	PDKV	Dr Panjabrao Deshmukh Krishi Vidyapeeth, India (Dr Panjabrao Deshmukh Agricultural University)
IPK	Institute for Plant Genetics and Crop Plant Research, Germany	PhD	Philosophy Doctor
IRAD	Institut de la recherche agronomique pour le développement, Cameroon	PhilRice	Philippine Rice Research Institute, Philippines
IRRI	International Rice Research Institute	PI	Principal Investigator
ISRA	Institut sénégalais de recherches agricoles, Senegal	POC	Plant Ontology Consortium
JIRCAS	Japan International Research Center for Agricultural Sciences	PROINPA	Promoción e Investigación de Productos Andinos, Bolivia
KARI	Kenya Agricultural Research Institute	pSARK—IPT	IPT gene under control of SARK promoter
KSU	Kansas State University, USA	PSU	Pennsylvania State University, USA
KU	Kasetsart University, Thailand	PU	Purdue University, USA
KUL	Katholieke Universiteit Leuven, Belgium	<i>Pup1</i>	marker diagnostic for phosphorus uptake
LA	Latin America	QDPI	Queensland Department of Primary Industries
LAAS	LuoYang Academy of Agricultural Sciences, China	QTL	quantitative trait locus
LD	linkage disequilibrium	QTLx	QTL by environment
LI	lead institute	R&D	research and development
LIMS	Laboratory Information Management System	RAKCA—Sehore	RAK College of Agriculture—Sehore (RAKCA—Sehore), Madhya Pradesh, India
LPP	local phenotyping platform	RAP	Review and Advisory Panel
LZARDI	Lake Zone Agricultural Research and Development Institute, Tanzania	RARS	Regional Agricultural Research Station, Nandyal, India
MAB	marker-assisted breeding	RAU	Rajasthan Agricultural University, India
MABC	marker-assisted backcrossing	RCB—IPB	Research Center for Biotechnology, Bogor Agricultural University, Indonesia
MAGIC	multiparent advanced generation inter-cross	RF	The Rockefeller Foundation
MARC	Melkassa Agricultural Research Centre, Ethiopia	RIKEN	Japanese abbreviation for 'Rikagaku Kenkyusho': The Institute of Physical and Chemical Research
MARS	marker-assisted recurrent selection	RFLP	restriction fragment length polymorphism
MAS	marker-assisted selection	RIL	recombinant inbred lines
MATE	multidrug and toxic compound extrusion	RNA	ribonucleic acid
MB	molecular breeding	RP	recurrent parent
MPIMPP	Max Planck Institute for Molecular Plant Physiology, Germany	RYMV	rice yellow mottle virus
MBDT	Molecular Breeding Design Tool	SA	South Asia
MBP	Molecular Breeding Platform	SAAS	Shanxi Academy of Agricultural Sciences, China
MMRI	Muhammad Saleem Shaheen Yusufwala Maize and Millets Research Institute, Pakistan	SABRN	Southern Africa Bean Research Network
MOSEL	Molecular Selection Tools	<i>Saltol</i>	marker diagnostic for salt tolerance
MRP	MRP University of Science and Technology, India	SARK	senescence associated receptor protein kinase
Ms3 male sterility	Male sterility gene 3	SARI	Savannah Agricultural Research Institute, Ghana
MSV	maize streak virus	SARI—Ethiopia	South Agricultural Research Institute, Ethiopia
MTP	Medium-Term Plan	SDP	Specific donor parent
MU	Moi University, Kenya	SF	Syngenta Foundation for Sustainable Agriculture
NAARI	Namulonge Agricultural and Animal Research Institute, Uganda	SGRP	System-wide Genetic Resources Programme of the CGIAR
NaCRRRI	National Crop Resources Research Institute, Uganda	SINGER	System-wide Information Network for Genetic Resources
NagU	Nagoya University, Japan	SNP	single nucleotide polymorphism
NAM	nested association mapping	SP	Subprogramme
NAFRI	National Agricultural and Forestry Research Institute, Laos	SPVD	sweet potato virus disease
NARS	national agricultural research system(s)	SSA	Sub-Saharan Africa
NCGR	National Center for Genome Resources, USA	SCRI	Scottish Crop Research Institute, UK
NIAB	National Institute of Agricultural Botany, UK	SFSA	Syngenta Foundation for Sustainable Agriculture
NIAS	National Institute of Agrobiological Sciences, Japan	SSR	simple sequence repeat
NERICA	new rice for Africa	StraP	Strategic Project
NIL	near-isogenic line	TAMU	Texas A&M University
NIPGER	National Institute for Plant Genome Research, India	TBA	to be assigned
NKLCGGE	National Key Lab of Crop Genetics and Germplasm Enhancement, China	TBD	to be determined
NMRI	National Maize Research Institute, Vietnam	TF	task force; transcription factor
NPGRC	National Plant Genetic Resources Centre, Tanzania	TLI	Tropical Legumes I Project
No.	number	TLII	Tropical Legumes II Project
NRCPB	National Research Centre on Plant Biotechnology, India	TNAU	Tamil Nadu Agricultural University, India
NRCRI	National Root and Tuber Crops Research Institute, Nigeria	TSL	The Sainsbury Laboratory, Norwich, UK
NRCS	National Research Centre on Sorghum, India	UAS	University of Agricultural Sciences, India
NU	Ningxia University, China	UCB	Universidade Católica de Brasília, Brazil
NWSUAF	Northwest Sci-tech University of Agriculture and Forestry, China	UdB	Università di Bologna, Italy
OFSP	orange-fleshed sweet potatoes	UdT	Universidad de Talca, Chile
OPVs	Open-pollinated varieties	UEM	Universidade Eduardo Mondlane, Mozambique
ORE	Organisation for the Rehabilitation of the Environment, Haiti		

UES	University of Ebonyi State, Nigeria	UotW	University of the Witswatersrand, South Africa
UGA	University of Georgia, USA	UPLB–CSC	University of The Philippines Los Baños–Crop Science Cluster
UK	United Kingdom	USA	United States of America
UKM	Universiti Kebangsaan Malaysia, Malaysia	USD	United States dollars
UKZN	University of KwaZulu–Natal, South Africa	USDA–ARS	United States Department of Agriculture–Agricultural Research Service
UNALM	Universidad Nacional Agraria La Molina, Peru	USDA–ARS PGRU	United States Department of Agriculture–Agricultural Research Service, Plant Genetic Resources Institute, USA
UoA	University of Arizona, USA	USP	Universidade de São Paulo, Brazil
UoAb	University of Aberdeen, UK	VBI	Virginia Bioinformatics Institute, VPI
UoAl	University of Alberta, Canada	VPI	Virginia Polytechnic Institute and State University
UoC	University of California, USA	WACCI	West African Centre for Crop Improvement, University of Ghana
UoD	University of Dhaka, Bangladesh	WB	The World Bank
UoF	University of Frankfurt, Germany	WMS	Workflow Management System
UoG	University of Ghana	WUR	Wageningen University and Research Centre, The Netherlands
UoM	University of Maryland, USA	YAAS	Yunnan Academy of Agricultural Sciences, China
UoMi	University of Missouri, USA	ZmMATE	MATE gene of maize ( <i>Zea mays</i> )
UoP	University of Pretoria, South Africa	ZU	Zhejiang University, China
UoPd	University of Potsdam, Germany		
UoS	University of Sydney, Australia		
UoQ	University of Queensland, Australia		

# Overview

## Introduction

The Generation Challenge Programme (GCP) of the Consultative Group on International Agricultural Research (CGIAR) was launched in 2003 as a 10-year initiative in two five-year phases (2004–2008 and 2009–2013). This first Medium-Term Plan (MTP) of our second phase lays out the plans for 2010 to 2012.

## Executive summary

To sum up the net balance from Phase I is, overall, very positive: GCP has built a strong and dedicated 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 entered Phase II on a positive and optimistic note, with an added spring in our step. The Management Team is fully committed to continue implementing the GCP strategy, so as to achieve Programme objectives by 2013. And while the development of some platforms might target a large set of our mandate crops,<sup>2</sup> specific research themes have been identified and will be pursued through seven Challenge Initiatives for important crops and traits identified in GCP target farming systems. Our revised strategy emphasises product management and delivery as crucial cornerstones of GCP's work in the coming years: concepts and ideas at GCP founding are increasingly evolving into useful GCP products, and we remain committed to delivering practical and relevant products to end-users,<sup>3</sup> and – ultimately – to farmers by improving crop productivity. Because the original vision for GCP was time-bound to 2013, it is imperative that GCP ensures 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 will be drafting in the course of Phase II.

## GCP at a glance

### *Who we are*

The Generation Challenge Programme (GCP) is a broad network of partners from the developing and the developed world, collectively working to improve crop productivity in drought-prone environments. GCP partners draw on plant

diversity and new technologies to improve crops with desired traits, focusing on drought tolerance. Through this wide range of partners, GCP links basic science with applied research and helps to weave an effective and interactive community of crop researchers at both global and regional level. GCP is a programme of the Consultative Group on International Agricultural Research (CGIAR).

### *What is GCP's core business?*

We selectively characterise the diversity of the most important crop germplasm for agriculture, including collections stored in gene banks under the custody of the CGIAR as well as national research programmes. Using this diversity, GCP applies genomic tools and interdisciplinary approaches to better understand gene function and their interactions. This understanding of gene systems across crops helps to identify and tag genes which contribute desired agronomic traits. Selection of favourable alleles at those genes increases the efficiency, speed and scope of plant breeding.

GCP also integrates information components and analytical tools into a coherent information gateway, and provides support for data storage and analysis. To ensure impact, GCP empowers scientists in developing country national programmes to use modern breeding. Having completed Phase I (2004–2008) and now embarking on Phase II (2009–2013), our new strategy emphasises product management and delivery as crucial cornerstones of GCP's work in the coming years.

## Trends

### *Where we are*

The year 2008 was one of intensive research and strategic planning, while 2009 will see the implementation of our revised research strategy and continued governance reforms. This MTP illustrates how GCP concretely addressed recommendations from two recent reviews: i) the External Programme and Management Review (EPMR) commissioned by the CGIAR Science Council in 2007–2008, and, ii) the review conducted by the European Commission in June 2008. These recommendations resonated well with – and augmented – the strategic conceptualisation and planning of

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

<sup>3</sup> See GCP's definition of users in our Delivery Strategy at: [http://www.generationcp.org/UserFiles/File/FINAL%20Delivery%20Strategy-Nov%202005\\_logo.pdf](http://www.generationcp.org/UserFiles/File/FINAL%20Delivery%20Strategy-Nov%202005_logo.pdf)

the GCP Management Team, and resulted in solid and realistic workplans for the second phase of the Programme. These plans, presented in this MTP, are undergirded by the following key principles:

- a clear focus on three pre-determined levels: crop, trait and target countries
- value-adding and building on key achievements in Phase I
- shifting from discovery to more applied activities
- enhancing existing infrastructure and expertise
- working with partners who have demonstrated they can deliver
- ensuring delivery, access to, and sustainability of, GCP products
- a forward perspective beyond 2013 into the 'after GCP'

#### ***Where we've come from, and where we're going***

GCP's foundation work is now yielding concrete products, tools, methodologies and firmer new directions as our projects mature following the principles presented above. Consequently, we began realigning our management structure in late 2008 and 2009, bringing in a new dimension devoted to product delivery, to keep in step with the various stages in the implementation of our strategy. This new dimension must ensure that, once our end-products 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. One way to assess impact will be on the basis of adoption of GCP products. Towards the end of 2009, the Management Team will define impact indicators at both the research theme and Programme level.

#### ***Realignment towards Challenge Initiatives and platforms***

Two major developments in 2008–2009 are particularly noteworthy from a research perspective: the establishment of seven research Challenge Initiatives and the development of two platforms to ensure access and distribution of some of GCP's products (eg, germplasm, markers, protocols) and technologies for molecular breeding to our partners and stakeholders.

##### ***i) Challenge Initiatives***

The shift from a broad set of activities towards a more focused agenda with seven Challenge Initiatives that will receive at least 50 percent of our research budget represents a major crossing point in our research strategy and organisation, and fully addresses the limited research focus pointed out by the recent reviews as well as by the Science Council in response to our MTP in previous years. Six of those CIs will each focus on a single crop, primarily address drought and target 2–3 countries maximum. The seventh CI is based

on comparative genomics for two major genes across three crops: taking advantage of knowledge in some model crops to facilitate gene discovery in other genomes was one of the challenges GCP is supposed to address. The core of activities for the seven CIs will be in the 2010–2013 period.

The MT fully supports and is excited about clustering a significant number of our research activities in the CI model, and planning activities at the CI level definitely increases interactions across Subprogrammes (SPs). But we also realise that such evolution in our research structure will have consequences on our operational dynamics and partnerships. Although no final decision has yet been taken at this point, it appears that a competitive approach may not find a fit with the CI model. Rather, a hybrid between competitive and commissioned approaches might be adopted to create healthy competition among potential grantees. Shifting from open competitive calls and broad sets of commissioned activities towards more focus via the CIs, plus establishing delivery platforms (see below) has implications on the composition of the GCP community. The benefits and challenges of this shift from a partnership perspective are described in more detail in *Collaboration and Partnerships*.

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.

##### ***ii) Platforms***

In Phase II, focus will also be on platform development to guarantee access to, and distribution of, GCP products in a user-friendly and sustainable manner. In this regard, we are designing initiatives scheduled to start in 2009 to make genetic resources (Platform 1) and marker technology (Platform 2) more widely available to the breeding community. The full impact of GCP products will require that these platforms be sustainable beyond GCP's predetermined lifetime. In addition, the platforms must be accessible by all potential users: CGIAR Centres, developing country agricultural research programmes, academia, small and medium-sized enterprises (SME), and downstream breeding programmes and seed distribution networks.

### ***New research in the context of CIs, platforms and Subprogrammes***

As in previous years, a set of new research activities should be initiated in 2009 that matches the evolution of our research strategy. This set will be reduced compared to the previous years owing to two reasons:

- Firstly, a large number of new commissioned projects were initiated in 2008 to absorb the double contribution received from the EC. Those projects are generally 2–3 year projects and therefore the level of commitments for our ongoing projects is high in 2009, meaning the MT has limited flexibility in allocating new resources.
- Secondly, 2009 is in essence a year of planning, conceptualisation and contract preparation. Therefore, the core of CI activities is set to start in early January 2010. Meantime, a few 'bridging' activities will start in 2009 to support critical activities within each CI, so as not to jeopardise or compromise future plans and to help prepare the terrain for upcoming activities (eg, making new crosses) in a timely and efficient manner. We project that approximately USD\$ 6m per year will be allocated to CIs effective 2010.

The launch of our two platforms will represent the most significant set of new activities for 2009. If our proposal for the Molecular Breeding Platform is approved, in 2009, approximately USD 3.5m will be allocated to establish and start up both platforms.

This MTP marks a clear and significant transition for GCP, towards a more sharply focused research portfolio, based on the EPMR recommendations and assessment by the Management Team. The research portfolio presented in the logframes shows increasing inter-Subprogramme cohesion and better end-product vision. This refinement of the GCP research portfolio and the implementation of a good monitoring and evaluation system will remain high on the agenda of the MT and the Executive Board throughout GCP Phase II.

### ***Challenges***

In keeping with our middle name, we have faced – and will 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 injecting greater focus into 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;
- given our timeframe, moving on rapidly with our strategic planning without overlooking critical steps in the product delivery pathway; and,

- designing and implementing a viable and effective strategy to assure the sustainability of GCP products after 2013.

### **GCP's niche and network**

GCP was created to undertake what is often referred to as 'upstream' research, but with a clear mandate to link upstream and applied research ensuring the Programme is not technology push, but driven by specific (genetic and genomic resources) and local needs (markers for specific breeding traits).

In more concrete terms, for GCP's case this means:

- characterising crop genetic diversity using molecular markers and trait-specific phenotypic approaches;
- creating diversity through crosses with wild relatives or by creating mutant collections;
- conserving and distributing plant genetic resources, including genomic resources;
- identifying favourable alleles for crop performance using comparative genomics, quantitative trait loci (QTL) analysis and 'omics' approaches;
- testing and validating those alleles in adapted germplasm under local target conditions;
- developing bioinformatic infrastructure and tools to conduct studies above in an appropriate manner, and to ensure data availability to the research community; and,
- increasing the capacity of breeding programmes in target environments to ensure GCP products will be used by primary users.

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

GCP was also assigned a trait of focus: drought tolerance, which affects almost all crops and all regions worldwide, thereby providing opportunities to apply useful discoveries across crops. As no single institution can command the breadth of expertise and resources necessary to achieve

these objectives, GCP operates as a network that leverages significant resources – funds, skills, equipment, knowledge, biological resources and social capital – through partnerships with a broad base of public and private institutions and initiatives. GCP partners are diverse and complementary in their skills. This promotes seamless continuity of activities all along the pipeline of GCP activities, starting from characterising and creating diversity, to the delivery of value-added crops for marginal environments. A critical benefit of the network is that it provides access to vast stores of plant genetic resources, as well as to cutting-edge technologies and scientific expertise, bringing all the three together for crop improvement. GCP continues to engage with a vibrant community of more than 170 partners mainly from universities, CG Centres and developing country breeding programmes – our main target users and stakeholders.

## Context

### Crop improvement for poverty alleviation

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

The agricultural sectors of many developing countries are changing rapidly in response to a host of local and global factors. Farmers in more productive environments can now diversify beyond staple food crops and have increasing access to agricultural markets in the new global and domestic arena. However, farmers in more challenging lands – areas typically characterised by high-risk crop production, poor agricultural yields and rampant poverty – are still isolated from markets, agricultural inputs and support services.

### The global agenda: agriculture, drought and climate change

Modelling studies published in *Science* in 2008 and 2009 predict that by the end of the 21<sup>st</sup> century, growing season temperatures in the tropics and subtropics will exceed the

most extreme seasonal temperatures recorded between 1900 to 2006. In temperate regions, the hottest seasons on record will represent the future norm in many locations. The studies predict that, due to climate change, southern Africa could lose more than 30 percent of its main crop – maize – by 2030, while in South Asia, losses of many regional staples, such as rice, millet and maize could exceed 10 percent.

So global climate models are predicting more extended – and more extreme – weather events. For instance, a dry and cold winter followed by a heat wave in August were key factors contributing to an estimated fall of 25 million tons (or 12 percent) in cereal production in the European Union in 2003–2004. Among the effects of climate change, the spectre of more prolonged and intense droughts is particularly disturbing. Today, even favourable and irrigated environments are at greater risk from drought.

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

The prediction is that sub-Saharan Africa is likely to suffer most from the combined effects of higher temperature and reduced rainfall, which imply a higher frequency of drought conditions during the crop growing season. Crop improvement on its own cannot mitigate the full economic loss caused by drought, but it can play a key role in at least maintaining production levels in drought-prone areas.

Based on this rationale, the quest for drought tolerance for food crops in GCP's target regions<sup>4</sup> continues to be our number one priority. Since its founding, GCP has worked on drought as the primary trait of focus in efforts to improve drought tolerance in food crops. We anticipate that this early investment will make an important contribution to the global fight against hunger and poverty, in the context of adaptation to climate change.

<sup>4</sup> Summary document on GCP target regions accessible via [http://www.generationcp.org/gen.php?da=08128238#gcp\\_target-crops](http://www.generationcp.org/gen.php?da=08128238#gcp_target-crops)



## 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 traits for crops grown by smallholder farmers in the developing world. Oversight, including legal and strategic guidance (collectively termed 'governance') has until June 2008 been provided by the Programme Steering Committee (PSC),<sup>5</sup> essentially representing the institutional Consortium partners.<sup>6</sup>

GCP operates under:

- a legal Consortium Agreement<sup>7</sup> that defines the legal and operational rights and obligations of institutional partners, including the host institution (CIMMYT; the International Maize and Wheat Improvement Center);
- 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 three 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 Board<sup>8</sup> (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.

Despite this significant step, more remains to be done: the current structure<sup>9</sup> 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 (CA) 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. 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 as 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 (see box below) for this revision was presented and approved by the PSC in its December 2008 meeting. Parallel to the CA revision, CIMMYT is also reviewing its Host Agreement with GCP, which could have implications on the Consortium Agreement since the Host Agreement is part of the Consortium Agreement. However, we remain optimistic that revisions on the Consortium Agreement will be finalised by mid-2009, in keeping with the approved timeline below.

#### **Box 1. Timeline: Revisions on the Consortium Agreement**

1 January 2009	Draft language to implement items discussed at PSC December 2008 meeting
31 January 2009	Peer review by three volunteers completed
1 March 2009	Interactions completed between Legal Counsel and the three volunteers above on comments
8 March 2009	Send draft to Consortium members
30 April 2009	Feedback from Consortium members
31 May 2009	Incorporate changes from Consortium members
30 June 2009	Signature of final amendments

<sup>5</sup> <http://www.generationcp.org/psc.php?da=0781307>

<sup>6</sup> See Annex A and <http://www.generationcp.org/consort.php?da=0781248>

<sup>7</sup> [http://www.generationcp.org/UserFiles/File/Consortium\\_agreement\\_signed.pdf](http://www.generationcp.org/UserFiles/File/Consortium_agreement_signed.pdf)

<sup>8</sup> See Annex A and <http://www.generationcp.org/whowere.php?da=08124404>

<sup>9</sup> Current governance structure at [http://www.generationcp.org/pdg/?page\\_id=9#212](http://www.generationcp.org/pdg/?page_id=9#212)

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 GCP Annual Research Meeting.

One recommendation, which the 2008 PSC meeting approved, was amending the unanimity clause in the Consortium Agreement. Prior to this amendment, any amendment of 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.

#### *Stakeholders Committee*

In this period when 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 the course of 2009.

#### *Review and Advisory Panel*

The Review and Advisory Panel (RAP)<sup>10</sup> consists of five scientists, with one assigned to each Subprogramme. It has virtual and in-person meetings and consults frequently with the GCP management.

The RAP 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 and workplan development 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 rather than a governance body.

## Programme rationale and structure

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

In Phase II, GCP is focusing its research portfolio, starting with implementing seven trait-crops Challenge Initiatives to which a substantial portion of the GCP research budget will be allocated. This notwithstanding, we will continue to work on other strategic projects (StraPs) not directly related to the seven Challenge Initiatives, building up mainly on investments already made, and focusing on consolidating and value-adding activities.

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

Our five Subprogrammes are as follows:

- **Subprogramme 1: 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

<sup>10</sup> <http://www.generationcp.org/rap.php?da=0781418>

- **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.

Through adaptive management, we redefine our approach in response to experience and lessons learnt; the external 'landscape'; reality on the ground and results achieved; and in line with our projected objectives and strategy for the future.

Our current research approach (see Figure 1 below) is oriented towards 'vertical' activities that are more crop-specific, targeting genetic gains for drought-prone target environments. This vertical axis, mainly the CIs from now on, will be complemented by 'horizontal' activities across commodities that are mostly 'platform-oriented' (by which we primarily mean focusing on generating and sharing genetic

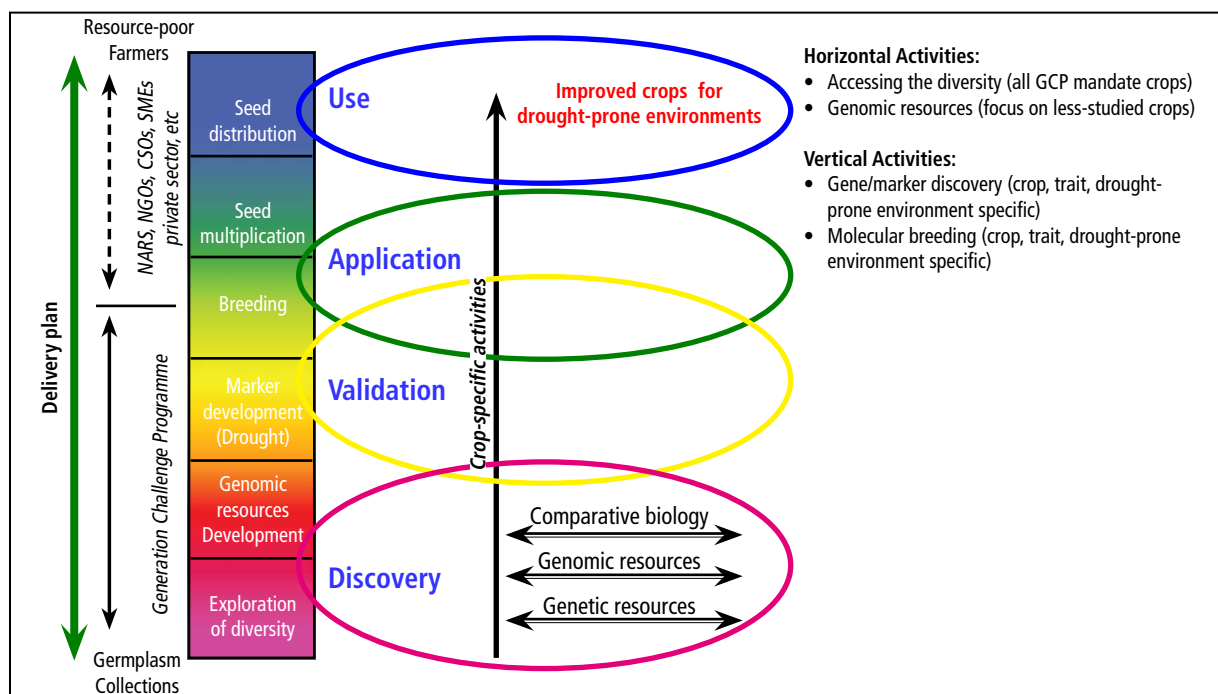
and genomic resources, and related services). Therefore, on the agricultural research–development continuum, GCP focuses on prebreeding, with SP3 forging a vital link between breeders and outputs from Subprogrammes 1, 2 and 4. In this regard, SP3 projects are particularly critical in testing the allelic value of selected genes in target environment, and promoting the use of molecular markers in developing countries. This last activity is conducted in close collaboration with SP5 to ensure that breeding programmes have the necessary human resources and infrastructure to use modern breeding technologies.

## Research framework

GCP's research framework combines three complementary funding mechanisms – competitive grants, commissioned research projects and focus projects. Until recently, these three mechanisms were an appropriate and agile funding system, and the logframe identifies the funding mechanism for each Output. However, as indicated further below, our funding mechanism as well as the classification of our projects might be revisited for a better fit with evolution of our research strategy. More details on funding mechanisms are as follows.

- 1) **Competitive grants:** Selected by an external review panel, the grant call is defined by the Management Team. Competitive calls stimulate scientific excellence and attract new projects and partners for GCP to achieve its objectives.

**Figure 1. GCP's research approach**



- The 1st round of competitive grants comprised 17 projects, each with an annual budget of about USD 300,000. They were launched in January 2005 and were scheduled to end in January 2008. However, as is common with new programmes, a number of first-round projects started late, or had a slow start, meaning most of these first-round projects were on a no-cost extension during 2008. However, all 1st-round projects have now been completed.
  - The 2nd round of competitive grants had six two-year projects of USD 300–400,000 per year. The call went out in February 2006 and the six projects were selected in October 2006, with an expected start date in January 2007. However, due to delays in disbursement of EC funds, the projects were placed on hold and only commenced in late 2007–early 2008. Therefore, all of them are expected to have output targets for 2010 and are reported in this MTP.
  - A call for the 3rd round of competitive projects was made in January 2008. A set of nine projects were selected across the four different thematic areas<sup>11</sup> of the call. In scrutinising the proposals, the external review panel laid a strong emphasis on the quality of the research and the relevance of the products in the context of the GCP strategy. This third set of competitive projects is for a three-year period. The annual budgetary support dedicated to these projects will range between USD 2.5 and 3 million. The projects were set to start within the last quarter of 2008. However, a few of them had their start delayed to early 2009 due to administrative issues related to project contracts. The list of the 3rd round competitive projects and a brief summary description were presented in the previous MTP.
- 2) **Commissioned research projects:** These are typically one- to two-year complementary projects with an annual budget ranging between USD20,000 and 300,000. They are designed to add value to the array of genetic and genomic resources publicly available through GCP by addressing a specific need, or by collating outputs from research projects. Commissioned projects consolidate our work, or fill gaps identified in the GCP competitive research portfolio, ensuring that our research objectives will be met. Commissioned projects are therefore the natural home for most projects under SP4 and SP5 that typically offer research support services. No doubt, with a more focused research agenda geared to achieve specific objectives and with clear impact indicators, most of our research in Phase II will be commissioned.
- 3) **Focus projects:** For these projects, budget and activities are developed in close collaboration with funders based on specific requirements. Currently, we have one large three-year focus project (2007–2010), funded by the Bill & Melinda Gates Foundation, titled Improving tropical legume productivity for marginal environments in Africa. The project is dubbed Tropical Legumes I (TLI).<sup>12</sup> While TLI focuses on developing key genomic resources that are currently lacking, identifying molecular markers for important traits, and improving legume breeding capacity in sub-Saharan Africa, its ‘twin’ project, TLI2 led by the International Center for Research in the Semi-arid Tropics (ICRISAT), works on seed multiplication and dissemination, and is therefore a good conduit for the flow of products from TLI.
- During Phase I, the GCP management strived to maintain a good balance between the three kinds of complementary projects listed above, to optimise programme efficiency. The idea was to capture new ideas and approaches and bring in appropriate partners for our research priorities, while also retaining the flexibility of consolidating our project portfolio around the most important and most promising axes. Given this concerted and systematic consolidation, and the focus on seven trait–crops, GCP is likely to reassess the appropriateness of competitive calls in this redefined context. While competitive calls were a good mechanism for Phase I, Phase II might call for a different approach.
- The current project nomenclature might also be revisited to better reflect the dynamics of our research portfolio. For example, should the Molecular Breeding Platform be approved for funding, it will be difficult to classify it in any one of the current project categories. Indeed, since we are requesting for the start-up of this platform to be supported mainly by the Bill & Melinda Gates Foundation, it would mean that grantees will have to comply with both the GCP and the Foundation requirements in terms of contracts and project monitoring, which are all hallmarks of a focus project. However, the idea of a plant breeding support service was conceived in GCP a few years ago and is really at the core of what GCP plans to accomplish in Phase II. The Foundation was approached to co-finance the initiative. Undoubtedly, the Foundation’s support would provide critical leverage for GCP’s effort: it would greatly broaden the scope, perspective and potential of this initiative. But in case we do not obtain Foundation’s support, GCP will still pursue this initiative, albeit on a lower scale and with the workplan adjusted accordingly. Given the foregoing, the Molecular Breeding

<sup>11</sup> [http://www.generationcp.org/research.php?da=09139804#3rd\\_call\\_for\\_compet\\_projects](http://www.generationcp.org/research.php?da=09139804#3rd_call_for_compet_projects)

<sup>12</sup> <http://www.generationcp.org/gcptli/>

Platform initiative is also – in spirit at least – really a set of commissioned projects.

Considering that it is improbable that GCP will have another call for competitive projects along the lines of the three previous calls, a possible project structure and nomenclature for our work in Phase II might be:

- CIPro: CI projects – for all projects embedded in a Challenge Initiative
- MBP: for all projects embedded in the Molecular Breeding Platform initiative
- GRSS: for all projects embedded in Genomic Resource Support Service initiative
- TLI: for all projects embedded in the Tropical Legume I initiative, and
- Strategic projects (StraPs): for projects that address a specific critical strategic issue, but do not however fall into any of the clusters above.

While CIs were identified at Programme level, strategic projects can be identified at either the Subprogramme level (for example, a socio-economic impact study under SP5), or at Programme level. An example of the latter is a plant breeding issue (in the broad sense) not already covered by the seven CIs, such as the project *Drought Tolerant Maize for Asia*. This project serves as a good illustration of our concept on StraPs. While the MT recognises improving drought tolerance in maize as a critical issue, the maize proposal requested by the MT in 2008 was not advanced to a CI. The main reason was the external environment: the Bill & Melinda Gates Foundation is already allocating significant resources to address this issue at a level that surpasses GCP's entire annual budget. In view of this, the MT decided that this issue was already adequately covered. However, drought is also a major issue in Asia, and this has not yet been addressed by the Foundation. There are very good sources of drought-tolerant germplasm in Africa, and research institutes in Asia generally have good phenotyping facilities for drought. Given all the foregoing, the MT approved a five-year pilot project to demonstrate that it is possible to improve drought tolerance in maize for Asia through molecular breeding. The idea is to introduce genes for drought tolerance from African germplasm into elite and popular lines grown in Asia. In this way, we address crucial research for maize, building on the Foundation's work in Africa.

## GCP research strategy: evolution and management

The implementation of the GCP strategy builds on the 2006 Strategic Framework and encompasses relevant recommendations from the various reviews GCP

underwent during the past year, especially the EPMR. The recommendations resonate with the thinking of the MT to further focus our research agenda and concentrate on platform development to guarantee the distribution of GCP products in a user-friendly and sustainable way. Implementing our research strategy will require significant adjustments in 2009 in both the scientific content and management of our research portfolio.

## Evolution of the GCP strategy and research trends

GCP, now in its sixth year, has achieved much. The Programme has developed an extensive consortium partnership and leveraged its resources to establish a broad network of R&D participants with extensive capability and capacity to support GCP objectives. As indicated in our recent Strategic Framework,<sup>13</sup> by 2013, GCP is expected to have contributed to 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

The previous MTP described the various research activities conducted to achieve the different objectives. As we start our second phase, it is clear that the achievement of the first two objectives will no longer exclusively depend on research activities, and a clear shift in resource allocation will be required to achieve Objective 2.

However, under Objective 1, it is critical to characterise – at the phenotypic level – specific subsets of reference sets identified by SP1 in Phase I to boost access to new alleles to improve crop productivity in GCP's target environments. Similarly, Phase II will see the development and evaluation under different water regimes of a Multiparent Advanced Generation Inter-Cross (MAGIC) population for different cereals and legumes, and Nested Association Mapping (NAM) founder lines for sorghum and rice, allowing whole genome association studies based on haplotype information. The early

<sup>13</sup> GCP's Strategic Framework and related strategy documents at <http://www.generationcp.org/brochure.php#strategy>

years of Phase II will also see the development of genomic resources for less-studied crops, focusing on legumes such as groundnuts, chickpeas and pigeonpeas. These studies will complement the massive effort in Phase I: since 2004, GCP has actively undertaken developing genomic resources for less-studied crops, while also facilitating phenotype–genotype links for genomic resources available for the relatively well-studied crops. As a result, several hundred microsatellite markers, several thousand DArT markers, hundreds of thousands of ESTs, several BAC libraries, dense genetic maps and genome-wide physical maps have been produced for GCP target crops. The complementary studies projected for early Phase II mean GCP will be in a position to report a major milestone to be achieved in the course of Phase II, ie, that through SP2, within a few years, all GCP target crops will have sufficient molecular markers for meaningful genetic studies.

We will therefore still have several activities serving Objectives 1 and 2, but the bulk of resources will now be allocated to establishing appropriate platforms and services to facilitate the delivery of genetic and genomic resources from the first phase of the Programme. Delivery vehicles include the Genomic Resource Support Service and the Molecular Breeding Platform, presented in more detail further below (see *The Molecular Breeding Platform*).

In Phase II, most of the research and support activities will serve Objective 4, and, to a lesser extent, Objective 3. Impact on plant breeding in developing countries will be the major overall objective for GCP in Phase II.

As stated in Objective 3, testing comparative genomic approaches is a pillar of GCP's research, with the aim of transferring knowledge for well-studied crops to identify new target gene or genomic regions in other crops. In this context, a two-year sequence analysis of six candidate genes for drought tolerance has borne fruit in seven target crops: barley, bean, cassava, chickpea, rice, sorghum and potato. In 2008, a large sequencing effort was conducted across 80 genes, providing insights into gene family evolution and crop phylo-ecogeographic organization. Some significant patterns await comparison with phenotypic data to identify strong candidate genes for drought tolerance. But overall, it is fair to acknowledge that achievements in this area of comparative genomics have been limited and have not met original expectations in the discovery–application pathway: while significant information is now available, the major missing link continues to be how to convert this information into knowledge for application in breeding programmes.

The conclusion of the MT is that comparative genomics to identify drought genes remains a major challenge at this stage,

mainly due to the genetic complexity of drought. In this regard, GCP should focus on identifying orthologous genes for major genes that express a large percentage of the plant phenotype. Consequently, comparative genomics in Phase II will be embedded in the CI *Comparative genomics to improve cereal yields in high-aluminium and low-phosphorous soils*. Phase I saw the characterisation of two major genes. The first gene was *Alt1* for sorghum tolerance to aluminium toxicity – a problem encountered in acid soils. The second was a gene (*Pup1*) to improve phosphate uptake in rice in poor soils. The main objective of this CI is therefore to build on the Phase I characterisation of *Alt1* and *Pup1* to identify orthologous gene(s) for aluminium tolerance in rice and sorghum, and better P uptake efficiency in sorghum and maize. We are also quite confident that in the course of Phase II, elite alleles for those orthologous genes will be tested in adapted germplasm in local conditions, and gene-based or linked markers for breeding will be available for most genes.

The other six CIs will focus on Objective 4. During Phase I, GCP contributed considerable scientific information on genetic diversity and genetic underpinnings of some important traits for drought-prone environments. As the Programme matured, gene and marker discovery focused more and more on drought tolerance as demonstrated clearly in the different research themes of the last two competitive calls in 2006 and 2008. Phase II will see a clear shift from the discovery to the application of biotechnologies to better serve plant breeding. This shift began in 2009 and will be even more pronounced when CI activities commence in 2010, as demonstrated by the large number of SP3 Outputs, relative to other SPs. A large proportion of the CI projects will be housed in SP3 and it is also anticipated that SP3 and SP5 will have the largest budget in GCP's closing years. Testing and pyramiding elite alleles at major genes in popular germplasm and discovering and stacking favourable alleles in elite by elite crosses through Marker-Assisted Recurrent Selection (MARS) will represent the main core of SP3 activities. This shift towards application implies also that we will work more closely with developing country breeders for them to adopt and use the new approaches proposed by GCP. Meeting this objective will require appropriate and focused capacity building, closely embedded in the research activities and customised to local needs.

### ***Challenge Initiatives***

At the end of July 2008, the MT got approval from the new Executive Board to implement seven Challenge Initiatives (CIs) that are crop-, trait- and country-specific. The initiatives will

target selected countries falling within GCP's priority farming systems<sup>14</sup> and specifically focus on the following trait–crops and regions (details on target countries further below):

CI were initially a set of pre-existing GCP projects related to a given research topic. In early 2009, in two separate workshops in March and April, the CIs were officially launched. These workshops brought together all existing partners in the projects, drawn from academia, CGIAR Centres and national programmes. For each CI, the diverse partners collectively defined:

- specific objectives;
- proposed activities to realise the objectives defined; and
- a five-year workplan with clear milestones and outputs.

Each CI is composed of a few projects, each with its own specific objective(s), and the number of projects will vary from one CI to another. Each CI project has a PI and an SP home. Impact indicators to evaluate performance and achievements of the CI by 2013 as well as Delivery Plan will be drawn up in September 2009, once CI workplans have been reviewed by the GCP Management Team.

To both ensure focus and maximise impact on plant breeding by 2013, each CI will focus on ideally two countries, with three as the absolute maximum. These countries are listed below in Box 3.

#### Box 2. The seven Challenge Initiatives.

##### Cereals

1. Improving drought tolerance in rice for Africa (CI 4)
2. Improving drought tolerance in wheat for Asia (CI 6)
3. Improving drought tolerance in sorghum for Africa (CI 5)
4. Comparative genomics to improve cereal yields in high-aluminium and low-phosphorous soils (CI 7)

##### Legumes

5. Improving drought tolerance in cowpeas for Africa (CI 3)
6. Improving drought tolerance in chickpeas for Africa and Asia (CI 2)

##### Root and tubers

7. Improving cassava yield in Africa's drought-prone environments (CI 1)

#### Box 3. Challenge Initiative target countries

CI 1	CI 2	CI 3	CI 4	CI 5	CI 6	CI 7
Cassava	Chickpeas	Cowpeas	Rice	Sorghum	Wheat	Al/low P
Nigeria Tanzania	Ethiopia India	Burkina Faso Senegal	Mali Nigeria Burkina Faso	Ethiopia Mali Sudan	China India	Indonesia Kenya Zambia

#### Implementing the CIs

In late April 2009, the MT reviewed the seven CI proposals, meticulously going through each workplan. The MT then drafted recommendations for every project falling within a CI. The recommendations were thereafter shared with the respective Product Delivery Coordinators (PDCs) for their input and reactions. PDC feedback was taken on board, and revised workplans finalised in mid-May.

The next step is for SP Leaders and PDCs to:

- send specific recommendations and comments on the research projects to the respective CI communities,
- collate input from the different projects in the CI, and
- coordinate writing the full proposals.

The timeline for CI proposals is as presented in Box 4 below.

#### Delivery platforms

A major goal for GCP in the coming years is to create a set of plant breeding support services as sustainable public goods. This will facilitate access by plant breeders in the South to modern plant science technologies, at optimal cost and with logistical and technical support. Activities supported by a Molecular Breeding Platform (MBP) will address specific needs identified by developing country breeders. The MBP will include several breeding services, which address germplasm, markers and traits. The services are all related and complementary, but each component (service) can also be used independently. The Genetic Resource Support Service (GRSS) will supply the germplasm requested through the MBP.

The MT acknowledges that genomics resources are a major output of GCP activities, as described in detail in the Project 2 narrative, and to some extent in Project 1. As indicated under GCP's Objective 2, (Develop a public platform of genetic and genomic resources and tools, and support a global community that can use them), it is GCP's responsibility to ensure that these genomic resources will be available in a sustainable and user-friendly way during and after GCP's lifetime. However, the

#### Box 4. Timeline for drafting CI proposals

July 17 2009	1st draft of full CI proposals submitted to MT
August 21	Full proposal reviewed by MT and Review and Advisory Panel (RAP); additional external review, if necessary
Last week of August	Compile feedback and consult with PDCs
August 28	Send revisions on proposals to project PIs in each CI.
Late September (during ARM)	Discuss and clarify revisions
October 9	Submission of the final CI proposals, with a separate document to indicate how the revisions have been addressed
October 10–22	Final review by SPLs and PDCs
October 23	Proposals approved
December 15	Contracts signed
January 15 2010	Funds disbursed

<sup>14</sup> [http://www.generationcp.org/gen.php?da=08128238#gcp\\_target-crops](http://www.generationcp.org/gen.php?da=08128238#gcp_target-crops)

MT believes there is no need for GCP to develop a distribution platform as such, since there are already several established and efficient distribution channels for these genomic resources. To mention a few, the BAC libraries are distributed through the service established at the University of Arizona, the results of sequencing efforts are available in public databases specialising in sequence information (eg, the J Craig Venter Institute, USA) and most genetic markers are available through crop databases or service providers.

A list describing the genomic resources generated so far in GCP will be posted to our website, with a link to the appropriate sources responsible for distribution. That way, interested users can access these resources.

The MT would like to guarantee that platform services are sustained beyond GCP's lifetime. GCP believes that eventually, beneficiaries and recipients should make a contribution rather than receive goods and services completely free of charge. These user contributions also enhance sustainability. The MT is considering chargebacks for GCP products distributed through the platforms (eg, germplasm, markers, etc). However, access to databases and information will remain free for all. Under the Product Delivery Leader's guidance (see *Product Delivery Leader and Product Delivery Coordinators*), business plans will be drafted for both platforms, which will – among other issues – address the following crucial questions:

- Creating incentives for plant scientists – particularly breeders in developing countries – to access the platforms
- Creating incentives for users to release their data (genotypic and phenotypic) and make their material accessible through the platforms
- Cultivating a sense of ownership among the different user communities
- Developing an appropriately flexible chargeback system for the broad set of potential users.

The delivery platforms are seen as a major legacy of GCP that will outlive the Programme and continue to harness the best of modern technologies to enhance crop breeding in developing countries.

### ***The Genetic Resource Support Service (GRSS)***

This service aims at providing appropriate germplasm to support breeders. It is founded on the idea that any breeding programme needs to constantly or periodically monitor the genetic base of their programme and possibly broaden it by using the most appropriate alternative sources. The GRSS is envisioned as dedicated to providing this service.

The panel of genetic resource available will be from GCP products primarily stemming from research by CGIAR Centres, but could also be external products endorsed by GCP.

The material to be distributed through the GRSS includes:

- reference sets of representative germplasm from gene banks;
- collections of mutants;
- introgression lines;
- mapping populations; and,
- near-isogenic lines.

The potential resources and derived genetic stocks will be inventoried and their quality will be assessed and upgraded in terms of: i) accuracy, ii) extent of documentation, and, iii) availability of seed/plants, so that the service builds on validated genetic stocks that meet high-quality data standards.

GCP will allocate USD 2m to support the GRSS in Phase II.

### ***The Molecular Breeding Platform***

The key to successful adoption of molecular breeding techniques in the private sector has been having platforms or pipelines which integrate the field and laboratory processes and harvest, and having an integrative data management system, analysing the data collected at every step to guide crop improvement for better cultivars. Drawing lessons on this success, the MT approved this pipeline approach in the first proposed public Molecular Breeding Platform open to both public and private breeding projects. The platform will alleviate the constraints to adoption of molecular breeding technologies by providing access to tools (SP4), services and training (SP5) aimed at priming and maintaining molecular breeding pipelines. It is expected that this will have a significant impact on the speed and effectiveness of breeding programmes focused on food security and livelihoods in the developing world.

A workshop was held in Montpellier, France, on March 5–7 2009 to discuss the MBP concept and design. The overall objective of the workshop was to provide a forum to learn about the latest achievements and strategies in molecular breeding from a panel of world experts, and provide an opportunity for the platform user community to exchange views with colleagues from other projects, and with the scientists who will develop the different elements of the platform. The outputs of this workshop<sup>15</sup> were a significant input in drafting the final version of our proposal, *A Molecular Breeding Platform*.

The proposal was submitted to the Bill & Melinda Gates Foundation in April 2009. The overall budget for the Molecular Breeding Platform is about US\$ 21m spread over five years through multilateral funding from various funding agencies and in-kind contribution from different institutes

---

<sup>15</sup> <http://www.generationcp.org/latestnews.php?i=1451>



participating in the project. The DFID and EC financial support will be drawn from their current contribution to GCP and accounts for USD 6.5m, while the Foundation will support the proposal at USD 12m. Participating institutes will provide the remaining resources through in-kind contribution.

### Managing our research strategy

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

The current management structure<sup>16</sup> is oriented along Subprogrammes, thereby tending to lean more towards prioritising activities within Subprogrammes, and less so across Subprogrammes. While this structure stimulates and supports excellence in scientific research by providing the possibility of selecting the highest-quality projects within each Subprogramme, it is challenging to support any integrated and harmonised approach across the different Subprogrammes with end-products of the whole Programme in mind.

Therefore, there is an increasing need to introduce a second dimension in our management matrix that will run across the Subprogramme dimension. This dimension must ensure that once our end-products at Programme level and their corresponding impact indicators have been identified, there is a management function that will ensure that activities and resources across Subprogrammes will deliver those end-products.

#### *Product Delivery Leader and Product Delivery Coordinators*

The 'product/crop'-specific complementary management function above has been 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 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 monitor 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.

PDCs will champion their target trait-crop, therefore they need to have a very good understanding of 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. All seven PDCs were identified at the end of 2008, and they are listed in Box 5 below. The seven PDCs were formally contracted starting January 1<sup>st</sup> 2009 to assume this management responsibility for approximately 10 percent of their time. The nature of this commitment might evolve as a function of the nature and the progress of each particular Challenge Initiative.

The PDL position is new, and we hope to have it filled by mid-2009. The PDL will lead the design and implementation of all GCP activities related to product delivery. S/he will ensure the effective and sustainable marketing of products, including packaging, promotion, and dissemination to users. Major responsibilities for this position include:

- Interacting with the Management Team to ensure the link between research and product delivery across the Subprogrammes

<sup>16</sup> GCP's current management structure at [http://www.generationcp.org/pdg/?page\\_id=9#212](http://www.generationcp.org/pdg/?page_id=9#212)

### Box 5. Product Delivery Coordinators

No	Product Delivery Coordinator, home institute	Challenge Initiative
<i>Cereals</i>		
1	Nouroollah 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, 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

- Designing and implementing a business plan for the GCP product delivery platforms
- Mentoring PDCs, and articulating their perspectives to the Management Team
- Coordinating and monitoring product delivery for major initiatives, including the CIs
- Overseeing the distribution of genomic resources and liaison with Programme researchers, clients and customers.

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 (Figure 2).

The management of the platforms is in the hands of the Subprogramme Leaders. The GRSS platform is the responsibility of SP1 Leader, while the Molecular Breeding Platform is jointly the responsibility of the SP4 Leader and the SP5 Leader. The management of the genomic resources will be led by the Product Delivery Leader.

Graham McLaren, the SP4 Leader, is the overall coordinator of the proposed Molecular Breeding Platform. Should the proposal be approved, he will ensure the compilation of the reports and be the GCP contact person for the Bill & Melinda Gates Foundation. He is responsible for four of the six platform objectives related to platform management, analytical tools

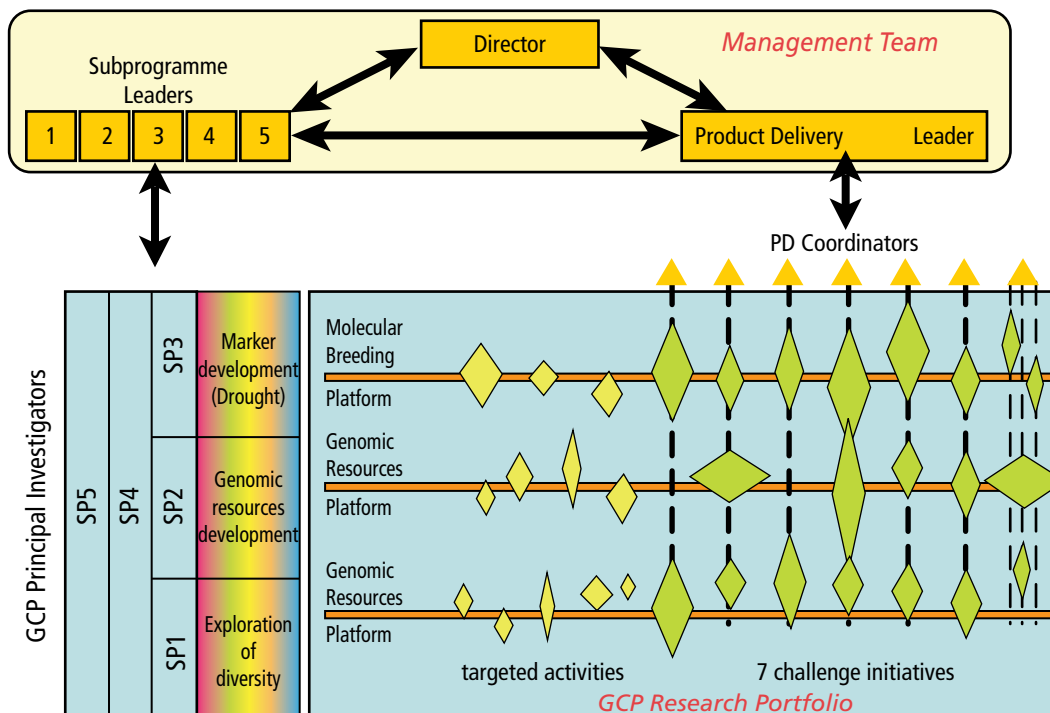
development and information management. The SP5 Leader is responsible for the two objectives aiming to provide services and support to platform users, while the SP 3 Leader will ensure the link between the leaders of the 10 user cases and the scientists in charge of tool development and support service. As already indicated above, the Product Delivery Leader will ensure the development and implementation of the platform business plan.

## Product management and delivery

Most, if not all, GCP activities aim at generating usable products – in both the short and long term – in the form of knowledge, as well as materials and tools for plant breeders.

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 marker-assisted selection experiments in SP3, using analytical tools developed by SP4 in partnership with breeders in national programmes supported by SP5.

**Figure 2. GCP's research management**



GCP products can be classified into eight 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
- vii. learning materials, and,
- viii. biological and technical information on using genetic resources.

## Data release and quality

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

In this regard, a number of concrete steps have been taken, as illustrated by an ongoing project on quality control for the GCP reference set (Project 1, Output 1, in the SP1 logframe). In this project, a subsample of the reference set generated in SP1 for the different crops will be re-genotyped by an external genotyping facility. 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 data from GCP-funded research available as international public goods for public access at no cost. We do this through the online GCP Central Data Registry.<sup>17</sup>

## Product management

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. We now have a product catalogue that 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 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 create, use, and disseminate research products. Product management has also stimulated collaboration between Subprogrammes, which – in turn – has considerably improved the use of the products that they deliver. 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 regarding the identification and validation of 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 as an integral part of research projects to strengthen partner expertise and ensure the effective transfer of products and technologies to national programmes and breeders. The revision and implementation of our delivery strategy will be one of the major responsibilities of the Product Delivery Leader.

## Financial indicators

Original predictions for 2009 were quite positive and apart from a reduction announced by the EC, we are expecting support from our major funders at about the same level as in previous years. We recently received the 2009/2010 notification from DFID, and we are very pleased to report that this contribution will remain at GBP 2.5m. The World Bank also confirmed their support for 2009 at the level of USD 2.0m. As anticipated from the three-year workplan developed in 2008, the EC will progressively reduce its contribution to the GCP: EUR 4.1 million in 2008, 3.5 million in 2009 and finally to 3.2 million in 2010. However, from the explanation accompanying these budget notifications,

<sup>17</sup> <http://gcpcr.grinfo.net/>

we understand that the adjustments are not related to the performance of the Programme *per se*. Rather, the reductions are driven by external factors.

Despite this EC reduction, overall financial figures appear quite positive for the coming years. With the current figures, projected income for 2009 stands at USD 22m, which includes a conservative reduction of USD 1.0m before an eventual loss of 25 percent on the DFID contribution due to an unfavourable exchange rate. In terms of new funding, we are optimistic about a proposal submitted to the Bill & Melinda Gates Foundation to support a Molecular Breeding Platform. The overall budget for the Molecular Breeding Platform is about US\$ 21m spread over five years through multilateral funding from different funding agencies and in-kind contribution from different institutes involved on the project. The DFID and EC financial support will be drawn from their current contribution to GCP and accounts for USD 6.5m, while the Foundation will support the proposal at USD 12m, with USD 2.5m for 2009. Participating institutes will provide the remaining resources through in-kind contribution. There is also a good probability that the Cooperative Research Centre (CRC) of Australia may support the platform at a level of US\$ 1.5m spread over five years and discussions are ongoing with the Syngenta Foundation for Sustainable Agriculture (SFSA) to jointly support a project on molecular breeding for sorghum in Africa. If this MB proposal is approved for funding, it will represent a supplementary amount of about USD 600K from SFSA over the next three years. As we reported in the previous MTP, GCP should be in a good position to achieve its current objectives with an annual budget of about USD 15m per year, and we anticipate that we will indeed attain this income over the coming years. Discussions are already underway with the Bill & Melinda Gates Foundation for a proposed Phase II of the Tropical Legumes I project.

However, two uncertainties remain, namely: i) exchange rate trends – more than half of our income is in currencies other than the US dollar, and, ii) how the shift of the CG system to megaprogrammes will affect the funding strategy of GCP's funders.

## Collaboration and partnerships

GCP was created to ensure upstream–downstream links in crop research. Therefore, to fulfil its mission, GCP has forged and nurtured R&D partnerships in research, breeding and delivery. Annex A provides a complete list of GCP partners in 2009, while the full breadth of GCP's collaborations is evidenced in the Output Descriptions in the SP Project Narratives.

Right from its inception, GCP was premised on 'flesh-and-blood' partnerships in the sense that operating as a geographically distributed network, virtually each and every GCP project was collaborative, involving several partners within and beyond the GCP Consortium. This trend has not changed. GCP partners are very diverse, traversing upstream discovery research to applied research and delivery. Currently numbering about 190 and drawn from more than 60 countries, GCP partners are from advanced research institutes, academia, CGIAR Centres, regional networks, national research programmes, the private sector and civil society.

The changes we are making in our research strategy also carry implications in our collaborations and partnerships, in terms of balancing between maintaining the momentum and motivation of the community we have nurtured through the years, while also keeping an eye on focus, priorities and strategic initiatives and alliances (details in *Trends*, in the subsection *Challenges*).

Further below, we elaborate that as we continue to implement our strategy – increasingly shifting focus from discovery to applied science as had been originally envisioned – there is naturally a corresponding shift to greater collaboration with partners at the delivery end of the spectrum, with breeders increasingly at the fore, working more closely with upstream scientists.

As reported in the previous MTP, the EPMR panel observed in its March 2008 report that this diverse yet collective GCP community is one of the Programme's most crucial assets. To quote the report:

*"Perhaps the most important value of GCP thus far, is the opportunities it has provided for people of diverse backgrounds to think collectively about solutions to complex problems, and, in the process, to learn from one another."*

Therefore, 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 regional platforms to link national researchers working on the same crop and in the same region. These platforms are premised a novel type of partnership closely linked to the validation phase in GCP research. For instance, the proposed Molecular Breeding Platform will rally together a community of diverse public sector breeders and users of platform outputs, working alongside private sector partners. We anticipate that the MB platform will open pathways to new partners in and for breeding in the

developing world who are currently not directly supported by GCP, as well as new engagements with the private sector. Among the new partners from the platform, particularly for Project 4, are the following: AAFC–SPARC will be involved in development and deployment of breeding tools for pedigree management and sample tracking, while Agropolis–INRA (France) and UoQ and CSIRO in Australia will be involved in research into molecular breeding analysis tools.

The seven CIs will also see existing (as well as new) partners working more closely together in whole new ways, with the Programme and end-product vision in mind. By devolving the Programme vision to project level, this means that PIs involved in CI projects have a clear vision of the entire pipeline from discovery to delivery through the collective workplans at CI level. With this vision comes a sense of what their own research product means at the scope, and in the context, of the Programme (and not just at project or SP level). By definition and design, we expect the CIs to create closer and more interactive and complementary partnerships between national programmes, CGIAR Centres and advanced research institutes.

In addition, GCP is increasing interactions with the private sector. In working with the private sector, we adopt 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 side-by-side with breeders in Africa to improve sorghum.

We continue to seek and cultivate partnerships with small- and medium-scale enterprises (SMEs) and NGOs, using our Annual Research Meeting (ARM) as a regional entry point. Starting with Africa in 2007, we invite SME representatives in the region to present their perspectives 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 3<sup>rd</sup> call in 2008 for competitive research ushered in new partners into our network, particularly in Asia. These included the Agharkar Research Institute (India) and the Bureau of Rice Research and Development (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.

## Alignment with CGIAR Systemwide Priorities

GCP's fundamental efforts to develop new knowledge and products support the United Nations Millennium Development Goal (MDG) of *halving, by 2015, the number of hungry people and those living on less than a dollar a day*. When these efforts result in superior crop varieties, they offer potential for poor farm households to improve their food and nutritional security and income. They also offer the prospect of affordable food for poor consumers.

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

GCP has several means of establishing and maintaining its focus, relevance and applicability. All GCP activities fulfil one – or more – of the CGIAR System Priorities for 2005–2015. The characterisation of crop diversity is at the heart of GCP's work, fulfilling Priority 1A: *Promoting conservation and characterisation of staple crops*. However, the most important for GCP is Priority Area 2: *Producing more and better food at lower cost through genetic improvement*. This

Priority Area easily describes GCP's own overall objective. GCP activities that fulfil other System Priorities nevertheless contribute to the overarching goal of Priority Area 2. These activities fulfil the following CG priorities:

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

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

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

## Achievements in 2008

- 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 cDNA libraries for sweet potatoes, pearl millet, common beans, chickpeas and pigeonpeas, providing the first access to genic contents 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 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
- In collaboration with the West African Centre for Crop Improvement (WACCI) at the University of Ghana, 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; 2nd call) 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 MAB over conventional breeding approaches in terms of speed and cost

## Implications for future work

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

- SP1 will finalise the development and delivery of its diverse products, and foster their use to access the most relevant diversity. Fundamental work will focus on securing the germplasm as genetic stocks. Reference representative samples will all be finalised and made available, associated with characterisation data of validated quality and fully documented interpretations of diversity patterns. This foundation will be augmented with current segregating progenies which provide analytical resolution and accelerate global genetic gain
- SP2 will focus exclusively on the identification and validation of genes/QTLs for drought tolerance so that in addition to having a better understanding of drought regulatory pathways, generated information is directly translated to crop improvement. Instead of having SP2-focused projects, research activities of the Subprogramme will be embedded, together with others SPs, in the Challenge Initiatives.
- In 2008 SP3 projects identified a wide range of markers for disease resistance in multiple crops that will be used in breeding programmes. Markers for aluminium toxicity in sorghum, and salinity and phosphorus deficiency in rice, have been characterised and will be tested in African and Asian target environments. Finally, segregating genotypes of major cereals and tropical legumes were evaluated under drought conditions and molecular breeding for drought tolerance will be a major future activity.
- SP4 activities will be aligned with the main objectives of GCP Phase II by providing support for utilisation of genetic resources and crop improvement, especially through the Challenge Initiatives. Work will be carried out in four themes: Informatics Infrastructure, Data Curation and Quality, User Support and Methodology Development. Much of SP4 work will contribute to the Molecular Breeding Platform, but support will be provided to maintain and deploy tools and methodology developed during Phase I.
- The second phase of SP5's work to build capacity, both in terms of human resource development and infrastructure enhancement, will focus on a smaller number of target beneficiaries with the expectation of increasing the chances of impact. The main criteria for the selection of partners will be their engagement in either one of the seven Challenge Initiatives, the Tropical Legumes I project and/or the Molecular Breeding Platform.

## Slower than expected progress

### Subprogramme 1 (Project 1 in the MTP)

The first results of the genotyping validation exercise show some examples of mis-scoring (allele size, binning, scoring of artefactual bands/peaks) and some examples of apparently unrelated results (through to mislabelling of markers).

Therefore the validation of the reference set structure and representativeness will represent a significant amount of work, including some cross-tests between the outsourced lab and the labs which initially produced the data. This exercise will take more time than initially thought, and will include more data analysis.

Besides the uncertainty of some data, which may delay the availability of genetic stocks for accurately representing the diversity of the crops, the interactions between the GCP MT and the CGIAR scientists in charge of germplasm conservation and distribution reveal that there are complex institutional discussions needed to have this activity recognised and possibly embedded in the mandate. Experimenting on the basis of case studies (proof of concept) is needed in order to forge the collective approach to a sustainable genetic resource support service.

Both points above are being addressed by the formalisation of a new project called the 'Genetic Resource Support Service' which takes into account both biological and institutional components and also represents an output for SP4 and SP5 as a support service within the GCP's Molecular Breeding Platform.

The project on allele mining in large collections was based on the availability of molecular diversity (in this case SSR) data for rice from an earlier project. This latter project is meeting considerable data quality issues, to the point that the lab in charge has re-done the production of many, which, however, does not appear to have solved all problems. A new project layout is being negotiated with the PI and the earlier project and output targets have been deleted.

The development and characterisation of interspecific progenies has met some practical difficulty, including delays in seed exchange due to international regulations. The completion of the respective projects on barley and on rice has thus been postponed to 2010.

### Subprogramme 2 (Project 2 in the MTP)

Whilst on the whole, research activities under SP2 are on track, it should be mentioned that slower than expected progress was observed in one particular SP2 project, mainly as a result

of some technical problems in phenotyping and managing database information. In addition, another project suffered a delayed start because of uncertainty of NARS partners, and consequently the end-date for that project is now projected to end one year later than originally planned.

### **Subprogramme 3 (Project 3 in the MTP)**

Although SP3 activities as reported in this MTP align with, on the whole, the workplan as projected in the previous MTP, it is also true to say that several sources of delay have been observed.

The first source of delay is general to the Programme level and relates to project management. Indeed, progress was slower than expected in five SP3 outputs due to a delayed start compared to the projected start-dates as presented in the previous MTP. Late project start-dates are generally the result of delayed contract finalisation, leading to delayed funding.

Most SP3 projects contain a field trial component to test and validate allelic values under target environments. Those trials need to be conducted under specific conditions related to the trait that is being evaluated. With drought tolerance improvement as our target trait, it is anticipated that unexpected rains or inadequate irrigations to control the level of stress might compromise the success of the experiments. This was the case for two Outputs in 2009, and delays were caused by problems with planting or adverse weather conditions.

The last source of delays arose from problems in timely germplasm exchange due to delays in import permit issuance or unexpected customs issues upon the arrival of the material in the targeted country.

### **Subprogramme 4 (Project 4 in the MTP)**

The development of trait ontologies for selected crops has been slow due to time taken to develop the informatics tools to manage the ontologies and the time to bring the teams of crop specialists together. This is continuing into 2010 and probably beyond with no-cost extensions. Capture of outstanding data to the central registry is slow due to PI reluctance to deposit 'unfinished' data and to the slow adoption of the templates. Work will continue in 2010. The development of the phenotyping data wizard has been slow due to a lack of testers from the GCP community to provide real data and test the wizard. Application development and integration for the Informatics Platform has been delayed by a shortage of programming staff and this work will continue into 2010.

The data quality and quality management tasks have been slow due to researcher over-commitment but these will be carried out in 2009 and 2010. The extension of iMAS tools to NARS partners was delayed by inability to find suitable dates to host training courses. These will be carried out in 2009. Research on design and analysis of studies for marker-trait associations was delayed due to researcher over-commitment, but will be completed in 2009.

The integration and further development of GreenPhyl and GOST has been slow due to a shortage of programming staff and the move of a post-doctoral fellow from IRRI to Bioversity, but this will be largely complete in 2009 with some work (mostly publishing) continuing to 2010. The project on *Breeding for drought tolerance for the Mekong Region* was slow to start due to slow contract agreement and output targets will shift upwards by one year.

### **Subprogramme 5 (Project 5 in the MTP)**

SP5 activities have, essentially, progressed as planned. A few Outputs have been suspended, pending re-evaluation in the light of the new structure of GCP's research portfolio scheduled for the second phase (explained in *Changes from Previous MTP* section).

However, some slowness has been revealed in the implementation of Delivery Plans by the third round of competitive projects approved in 2008. This has a two-fold explanation: firstly, the role of SP5 in this activity was put on hold because of a newly created staff position for product delivery. The person taking up this position will be responsible for this activity in the future. Secondly, the signing of contracts happened later than initially expected, in November 2008.

The execution of genotyping services through the GSS has also been slower, (though not delayed in meeting its targets), because of the decision to open the call and align the announcement of the awards in collaboration with the Crop Diversity Trust and the Global Initiative for Plant Breeding Capacity Building. In addition, the decision was made to use the current set of awards as a trial for new service providers in light of the launch of the Molecular Breeding Platform.



# Highlights of the 2009–2010 project portfolio

## 2010 selected highlights

- Initiation of a first phase of a genetic resource support service for one cereal (sorghum) and one legume (chickpea)
- Large-scale association analysis in rice conducted for drought-related traits
- MAGIC progenies advanced for sorghum and rice
- Gains derived from introgression of related species assessed in rice and barley, both in terms of breeding value and genetic information
- Large scale SNPs identified and SNP genotyping platforms in selected legume crops
- Genetic maps developed and molecular markers associated with drought tolerance and selected biotic stresses identified in selected legume crops
- Candidate genes associated with drought tolerance identified in rice and wheat
- Efforts initiated towards cloning, characterisation and validation of Al-tolerance gene(s) in rice and maize
- Efforts initiated towards cloning, characterisation and validation of P-efficiency gene(s) in sorghum and maize
- Efforts initiated in training African sorghum NARS programmes on molecular breeding
- Implementation of the new CI project for yield improvement in cassava: Development and validation of new markers for resistance to biotic stresses, start of new drought tolerance efforts centred on MARS
- Implementation of the new CI projects for drought tolerance in rice (Africa) and wheat (China and India): Use of molecular markers to introgress pre-identified drought tolerance QTLs into adapted varieties (rice and wheat), start of MARS project for drought tolerance in rice
- Implementation of the new CI project in comparative genomics for the transfer of alleles for aluminum tolerance and phosphorus uptake efficiency across a number of cereal crops important to Africa (rice, sorghum and maize)
- Start of Phase II of the Tropical Legumes 1 (TL1) project, with increased emphasis on the application of markers for variety improvement in beans, chickpeas, cowpeas and groundnuts
- Establishment of the Molecular Breeding Portal will be a key output driving the use of the MBP
- GCP Crop Ontologies will fill important gaps in the standards for biological science
- Mixed model methodology for QTL detection and association analysis and decision support tools for MARS breeding will increase the effectiveness and efficiency of breeding for quantitative traits
- Freely available tools for the analysis of Next Generation Sequence data will facilitate the development of genomics and genetic resources for less studied crops
- Integration of data sources from CIMMYT, Bioversity and Agropolis–CIRAD into the GCP Informatics Platform will increase the applicability of analysis tools and provide access to a wider variety of GCP data
- Three new graduate students from developing countries registered in their academic programmes towards a degree in modern plant breeding
- A learning module on research and product delivery made available
- An award given to a selected group of African legume researchers to enhance their knowledge and expertise for phenotyping and genotyping, with the aim of boosting breeding programmes in their home institutions
- New crop Communities of Practice promoted as a means to encourage and sustain the use of molecular markers for breeding in developing countries
- A number of breeding and support services offered to user cases of the Molecular Breeding Platform

## Subprogramme 1: Crop genetic diversity (Project 1 in the MTP)

### 2009 highlights

Germplasm maintained in the collections has to be mobilised in breeding activities. Representative samples give access to the whole species diversity. They have to be made available as high quality genetic stocks, requiring additional management

efforts, already started in 2008. These have to be characterised for diverse features as well as for targeted drought-related traits, in order to simplify both trait understanding of and access to valuable donors. More and more they will be sub-sampled in order to be evaluated together with elite materials preferred by farmers as well as diverse pre-breeding materials. They will thus best contribute to future hybridisation schemes. Access to genotyping capacities has become

generalised. Emphasis will be reinforced on the development and characterisation of populations of diverse genetic breadth, from intercrosses among cultivars to interspecific combinations, which reconcile genetic gain and knowledge production for sustaining future breeding.

## 2010 highlights

By 2010, changes related to the Programme's strong focus on product delivery and breeding will be settled, enhancing osmosis between SP1 and the other Subprogrammes.

The distribution of the products from GCP's first phase will be operational through a formalised support service. The quality of the data and composition of the reference sample will have been validated for all crops. A steering committee will start to work on setting the priorities for the GRSS. The service will be run for sorghum and chickpea by ICRISAT and service provision will be contracted for other priority crops. The first two cases will be used as a proof of concept. Coordination will be established with SINGER and proper communication will be implemented.

The current wave of drought-related phenotyping will yield a first generation of data for four cereals and four legumes. This type of experiment is very difficult and the analysis of the data will raise questions. Having experiences which are diverse in species and environments will provide a challenge and an opportunity. Some coordination will be exercised in order to extract both a better understanding of the array of plant behaviours as means for adaptation and an array of potential donors for bringing complementary favourable traits into breeding materials. The case of rice will enable a first broad-scale association analysis.

A new category of field experiments will be implemented, consisting of comparative phenotyping of mixed materials, referred to as targeted elite nurseries. These include part of the reference samples found to display a broad array of drought-related phenotypes as well as locally preferred materials and pre-bred materials. These experiments aim at selecting the most promising and complementary materials in very specific conditions in order to enrich the genetic base of hybridisation schemes. The principles for their constitution will be a matter of concentration among crop-specialised communities. Four multiple parent intercrossing schemes will progress during the year, two in rice and sorghum which started in 2008 and two in cowpea and chickpea which will start in 2010. The experiences on sorghum and rice will be analysed and will serve to guide those in the two legumes.

Among various activities focused on the introgression from crop relatives, those in rice and barley will come to

completion. It will be possible to assess the value of this type of approach in two cases of diploid crop, both in terms of genetic gain potential and production of genetic information. This will inspire parallel work going on in more complex crops such as wheat and groundnut.

## Subprogramme 2: Genomics towards gene discovery (Project 2 in the MTP)

### 2009 highlights

In 2009, SP2 has delivered significant genomic resources for crop species important in sub-Saharan Africa and Asia. Hundreds to thousands of new markers have been developed in tropical legume species to generate dense genetic maps and identify the markers associated with drought tolerance and selected biotic stresses. Several hundred SNPs in four legumes and First Illumina-GoldenGate assays have been developed in cowpea and chickpea. Commissioned projects are delivering genetic and genomic resources amenable to molecular breeding for some less-studied species (such as sweet potato and pearl millet). A critical and integrated gene discovery approach has been amplified in rice and initiated in wheat. In 2009, some commissioned projects on developing SNP resources in chickpea, optimising the SNP genotyping platform in cowpea, as well as SNP mapping in tropical legumes and cloning of Al-tolerance in rice will be initiated. Efforts to develop a pipeline for analysing new sequencing technology data, in collaboration with SP4 is in progress.

### 2010 highlights

With the first phase of the TLI project, together with three commissioned projects in legumes which started in 2009, due for completion in 2010, significant genomic resources such as ESTs, SSRs and large scale SNPs will be delivered. In the case of chickpea and cowpea, an SNP genotyping platform should be made available and put to use. Moderated genetic maps and the first set of molecular markers associated with drought tolerance-related traits and selected biotic stresses should also be made available in 2010. Large-scale sequence data, ESTs and DArT markers should be available in pearl millet, pigeonpea and sweet potatoes. Gene discovery projects being undertaken in rice and wheat should provide some ideas about candidate genes associated with drought tolerance in these cereals. One commissioned project on the development and evaluation of drought-adapted sorghum germplasm has initiated in 2009 and should provide the first data on drought-adapted germplasm evaluation in 2010.

Four commissioned projects under CI7 will start in 2009 and 2010. These projects should deliver genomic information related to cloning of Al-tolerance and P-efficiency gene(s) in

three cereal species. Another commissioned project under the sorghum CI (CI15), set to begin in 2010, will provide some crosses. It is expected that SP2, in collaboration with SP4, will also provide the pipeline to analyse the next generation of sequence data. Besides the capacity-building link with SP5, several projects within SP2 already collaborate closely with projects within other GCP Subprogrammes, and an even stronger integration of activities is foreseen in 2010 and beyond. For instance, collaboration with SP4 will be strengthened in genome analysis and gene expression studies, while work on validation of identified perfect markers, genes/QTLs and improved germplasm will strengthen ties between SP2 and SP3.

### **Subprogramme 3: Trait capture for crop improvement (Project 3 in the MTP)**

#### **2009 highlights**

In 2009, SP3 saw the first implementation of marker-assisted recurrent selection (MARS) projects. The first two Outputs using this approach in 2009 are Outputs 24 (*Yield improvement of sorghum in Africa*) and 25 (*Drought tolerant maize for Asia*). Also launched in 2009 were GCP's Challenge Initiatives (CIs), with new CI Outputs being introduced in the 2010–2012 MTP for cassava, rice, wheat and comparative genomics, with many of them focusing on the MARS approach. New markers were used for the genotyping of breeding populations for resistance to biotic stresses in potato and cassava, and large-scale marker-assisted backcrossing (MABC) of drought tolerance QTLs took place for wheat in China and rice in India. In addition, previous gene candidate work led to the practical application of markers to transfer the phosphorus uptake gene (*Pup1*) across rice cultivars in Asia and the aluminum tolerance locus (*Alt*) in sorghum from Brazil to Africa.

#### **2010 highlights**

As GCP enters its second phase, the importance of SP3 activities that validate and apply the products of previous research done in SPs 1 and 2 to the benefit of breeding programmes continues to grow. This is reflected by the relatively large number of Outputs (28) compared to the other Subprogrammes.

The implementation of marker-assisted recurrent selection (MARS) projects that began in 2009 mark a focus area set to continue, with many of the new Challenge Initiative (CI) projects incorporating MARS in their approaches.

This shift towards applications closer to breeding can also be seen in the implementation of Phase II of the Tropical Legumes I (TLI) initiative. Activity 5 of the various TLI projects focuses on the breeding application of marker discoveries – an area

that is increasing in importance in Phase II of TLI. This also includes the implementation of MARS approaches across the TLI crops.

The emphasis on drought and abiotic stress tolerance is continuing, with all new CI Outputs either focusing entirely on those areas, or at least including projects targeting them. These include rice drought tolerance for Africa, wheat drought tolerance for China and India, cassava yield improvement for Africa, and comparative genomics for aluminum tolerance and phosphorus uptake.

Efforts currently underway to build simulation models for the testing of various marker selection strategies will be very beneficial to an optimum implementation of the drought tolerance and MARS projects outlined above.

Subprogramme 3 is collaborating closely with the efforts being undertaken to establish a Molecular Breeding Platform (MBP). The previously-initiated effort to establish a phenotyping platform feeds directly into the Phenotyping Services area of the MBP and will be critical to ensure that high-quality field data are generated to support the growing number of drought tolerance projects. SP3 is also closely linked with the Genotyping Support Services of the MBP through its shared interest in consolidating efforts to both identify optimum contract genotyping service suppliers and advise the potential users of the platform on the best approach to conduct their molecular breeding experiments.

Research products to be delivered in 2010 will include validated markers, new approaches or methodologies, and improved germplasm. Validated markers will target resistance to aluminum tolerance in sorghum, improvement of phosphate uptake in rice, resistance to various biotic stresses in maize, wheat and sweet potatoes, and QTLs for drought tolerance in rice. New methodologies will help improve both the efficiency of marker-assisted breeding and the accuracy of drought phenotyping. New germplasm resources available to breeders or farmers include new potato germplasm for Southern Africa, drought-tolerant wheat for China, and beans resistant to various biotic and abiotic stresses for Central America.

Collaboration with other GCP Subprogrammes will continue, with examples including the evaluation with SP1 of reference sets in target environments, the identification and validation with SP2 of genes/markers in target germplasm, the collaboration with SP4 and SP5 on the establishment of the Molecular Breeding Platform, and the training of MARS breeders and scientists on new molecular breeding techniques in close partnership with SP5.

## Subprogramme 4: Bioinformatics and crop information systems (Project 4 in the MTP)

### 2009 highlights

Project 4 has moved gradually from building the initial technical infrastructure for GCP to a Subprogramme aimed at supporting users by creating tools and methodologies applying the infrastructure. The Greenphyl database and Orthologous Search Tool (GOST) have been expanded and enhanced by adding new genome data and developing a new web interface to provide a fast and user-friendly comparative genomics analysis tool. In the biometrics arena, research on the reconstruction of genealogies based on haplotypes related to geographic patterns leads to more efficient analysis of genotypic data and research on the design and analysis of marker-trait association studies improves the efficiency of the exploration of QTLs. Direct support to GCP scientists has also been expanded; the helpdesk for all bioinformatics and biometrics questions has been developed further. It acts as a broker between GCP scientists and bioinformatics expertise and products. The infrastructure of the GCP information platform, distributed web services, the underlying models, ontologies and tools has been enhanced. Activities to increase the value of GCP data, defined by quality, accessibility and usability, have continued.

### 2010 highlights

The reorganisation and rationalisation of Project 4 activities allows them to align better with the revised objectives of the GCP in Phase II.

User support becomes the key theme with the establishment of the Molecular Breeding Portal as a key output driving the use of the MBP. Training and support for data curation, and statistical design and analysis of GCP research and MBP breeding projects will be important.

Work on the crop ontologies will have a large impact in the global arena as the GCP works to fill important gaps in the standards developed by the global community. These ontologies allow the integration and comparison of data across studies and species, allowing comparative biology to attain its promise.

The new research area of methodology to support new molecular breeding techniques has tremendous potential impact in speeding up the harnessing of genetic variability for quantitative traits such as drought tolerance in target GCP crops. This research involves new mixed model methodology

for QTL detection and BLUP estimation of breeding values, new algorithms for tracing identity by descent of markers and genomic segments, and new modules for genetic simulation of breeding strategies.

The development of a pipeline of freely available tools for the analysis of Next Generation Sequence data will be an important step in facilitating the development of genomics and genetic resources for functional genomics and breeding of less studied crops which are nevertheless important for food security in developing countries.

Activities to adopt and adapt data management and breeding logistics tools and also make them available to users of the MBP will have a big impact on the efficiency of molecular breeding, and will make the data collected during breeding available to assist with future breeding decisions.

Deployment of the GCP Informatics Platform for several GCP data sources makes these readily accessible to the GCP community and will demonstrate the value of such networking technology. A series of query interfaces and graphical tools will illustrate the opportunities that the technology represents for integrating analysis and visualisation tools. Its application to the MBP breeding platform will revolutionise breeding logistics and workflow management in the public sector.

## Subprogramme 5: Capacity-building and enabling delivery (Project 5 in the MTP)

### 2009 highlights

In 2009 GCP entered its second phase (2009–2013). This had important consequences in our research portfolio, which in the coming years will focus more on the Challenge Initiatives. For SP5, the transition conveys a sense of urgency because of the role the SP plays in facilitating impact after the life of the Programme. Development of human resources, implementation of computer, field and basic laboratory infrastructure and promotion of research through crop networks are the three main paths followed by SP5 in 2009 which will continue from 2010 to 2013. The Delivery Plan kit is undergoing a period of enhancement and validation, and its implementation will remain the basis for identification of capacity needs. Most SP5 projects will be planned around and embedded within the technical projects of the CIs, and, in line with the enabling delivery notion of the Subprogramme, SP5 will house the services of the Molecular Breeding Platform.

## 2010 highlights

By 2010, changes resulting from the evolution of the Programme's second phase will already be settled. For SP5, a major effect of these changes will be the increased attention to partners in a selected group of countries – namely those targeted by the Challenge Initiatives (CIs), the Tropical Legumes (TLI) project and those of the Molecular Breeding Platform's (MBP's) user cases. This sharpened targeting approach denotes an important effort to avoid spreading too thinly – a lingering risk of capacity building initiatives in general.

By means of the Pioneer–GCP graduate fellow and the PhD candidates who will conduct their studies at the West African Center for Crop Improvement, SP5 will strive for human resource development as the basis for a meaningful effort to enhance capacity. These students will be selected to contribute to one of the major research initiatives of our portfolio so as to increase the critical mass of qualified professionals working in these crops and regions. Training will be offered *à la Carte* to a number of collaborators, including technicians, in the TLI to strengthen skills and expertise in phenotyping, genotyping and data analysis – all major areas of the research workplan.

Training will be complemented by enhancement of infrastructure, mostly for field experiments but also for basic genotyping. This is a continuing effort of the Subprogramme which has already made a difference through equipping our partners to engage meaningfully in research at their home institutions.

Two Communities of Practice (CoP) in GCP have proven successful, and the plan is to build on this concept. CoP researchers strive towards common goals, share knowledge and practices, support efforts and solve problems together. Pre-existing CoP projects (eg, cassava) will continue, and new ones will be promoted through the CIs and the MBP. This is so because of the belief that for most of our research, CoP might be the best assurance for sustained impact of our work. SP5 funding of CoP in the coming years might provide the needed incentive to keep these informal networks alive after GCP's exit.

The new Delivery Plan Kit will be validated in 2010 and the associated learning module will be completed and made fully available. This is an important output of SP5 that helps to identify not only products and users of GCP research, but also capacity needs to apply results and intellectual property issues to be solved in order to ensure our outputs comply with our calling to deliver global public goods.

In the same vein of delivery, and building on three years' experience of the Genotyping Support Service, SP5 will pilot the implementation of a suite of services (Breeding and Support) in the Molecular Breeding Platform (MBP). These services will deliver tangible outputs (such as training materials, to give an example) and will provide guidance to users. As such, it is hoped that the MBP will inspire the needed confidence in an increasing number of users to undertake the application of molecular markers as a means of advancing breeding in developing countries.



# Project 1 – Subprogramme 1: Crop genetic diversity

## Project narrative

### Project overview and rationale

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

A massive campaign of molecular characterisation of broad germplasm has enabled the generation of representative samples, and a subset of analyses is being repeated within a complementary independent exercise in order to validate the global structure of the diversity and to provide as a reference for the future. Seed is being purified for generating genetic stocks.

SP1 also undertakes activities that contribute data while consolidating capacity within GCP and providing access to external facilities. An effort to explore a new marker system is being completed and translated into an access through the genotyping support service managed by SP5, thus closing the corresponding SP1 theme. Emphasis is placed on the development and optimisation of phenotyping capacities in relation to drought. Altogether, this integration of capacities should enable a biological understanding of diversity and of the genetic and functional architecture of adaptation.

The comparison between genotypic and phenotypic diversity is being performed with a view to identify favourable genetic factors through association studies. In light of the strong focus on breeding, these studies concentrate on elite, pre-screened or pre-bred materials rather than on panels of diverse landraces. This fulfils the recurrent need to assemble germplasm with the potential for providing high contribution towards breeding programmes before undertaking new hybridisations. The corresponding theme has been renamed accordingly and numbered last in the Subprogramme because it collects materials and data from all the other themes.

As a complement to exploitation of the representative reference samples, SP1 also orchestrates various exploratory approaches building on new types of population and new analytical angles that enable the production of genetic information and/or the contribution of pre-adapted germplasm for breeders. This type of development is focused on the crops selected for the Challenge Initiatives set to commence in GCP's second phase.

### Impact pathways

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

- Theme 1: Creation of an improved understanding of the structure of the diversity for the major world food crops
- Theme 2: Establishment and implementation of a scientific and organisational framework to describe tolerance to drought
- Theme 3: Development of novel populational approaches for relating genotypes to phenotypes
- Theme 4: Assembly of global elite materials as reservoirs for enhancing mobilisation of genetic diversity

Each theme conducts particular contributions to the overall impact of the Programme, as described below.

#### ***Theme 1: Creation of an improved understanding of the structure of the diversity for the major world food crops Output 1 to Output 3***

Access to genetic diversity available in large crop germplasm collections requires identification of representative samples of a smaller size to make them suitable for different surveys: screening of traits, evaluation of phenotypic diversity, evaluation of combining ability, assessment of molecular diversity, etc. Moreover, integrating diverse types of characterisation in the same materials makes it possible to assess correlations among traits and investigate gene effects such as epistasis and pleiotropy. Passport data enable selection based on eco-geographic information; molecular markers offer means to further refine assessment of relatedness and to reduce sample size. Use of standardised methods yields data that can be compared across materials, laboratories and time, providing a durable momentum to enrich global understanding and representativeness.

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

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

In order to realise this potential, the various partners involved must share views and interests. To this end, a joint SP5–SP1 workshop took place in November 2008. Participants included scientists involved in GCP projects, who presented their work, as well as germplasm managers/curators and plant breeders from various horizons. This was done in consultation with players that have a coordination and animation role in the field of germplasm management and use, such as the System-wide Genetic Resources Programme (SGRP) of the CGIAR, the Global Crop Diversity Trust and the Global Partnership Initiative for Plant Breeding Capacity Building (GIPB). This set the stage for designing a cohesive key germplasm distribution system and for specifying the role that GCP could play in this scheme. A specific project, aimed at launching a genetic resource support service, was initiated.

## ***Theme 2: Establishment and implementation of a scientific and organisational framework to describe tolerance to drought***

### ***Output 4 to Output 7***

Accurate and high-throughput characterisation of materials is crucial to efficient germplasm exploitation, be it by genotyping with diverse markers or by evaluating materials for their behaviour when confronted to drought-related stresses. Within GCP, both fields converge when the two types of data are compared for association studies. Past lines of efforts (Themes 2 and 3 in previous years) were identified with the principal goal of serving the GCP community and helping it fulfil its obligation to mobilise the most efficient capacities within the GCP Consortium and beyond. In the meantime it became apparent that this collective platform of proven capacities could serve a broader community. A global concept of a molecular breeding platform is being developed, with the proposed platform to include a genetic resource support service, a genotyping support service (already running and managed by SP5) and a phenotyping support service (to be refined). This platform would be accessible to all structured breeding programmes worldwide, thus hopefully multiplying the efficiency of the breeding community. The concept is currently being proposed to donors for potential implementation in 2010.

Recent effort on DArTs has expanded the number of crops which benefit from this efficient and cost-effective marker system. Early efforts on allele resequencing have provided the basis for a community of practice with gene specialists primarily from outside the CGIAR, who look at orthologous genes across species, together with crop specialists within the CGIAR centres, who look at diverse genes for their specific crops. The progress made in SP2 on the generation of genomic resources on many crops has provided the template for efficiently surveying diversity at selected candidate genes identified. Consequently, the corresponding theme (Theme 2 in the 2009–2011 MTP) has been deleted in this MTP. The phenotyping capacity has been consolidated in the EMBRAPA network. However, its use is being opposed by phytosanitary constraints associated with intercontinental germplasm movement. GCP, with all the expertise located in the CGIAR Centres, is in a perfect position to anticipate and address such constraints. The organisational component of phenotyping is being transferred to SP5.

Current phenotyping experiments are embracing a broad genetic base. Whilst this represents a challenge in terms of management and data analysis, it is very valuable in order to apprehend the whole array of behaviours. It is hoped that the main means explored by plants for adaptation to drought will thus be characterised.



By construction, association studies are possible and productive when balanced materials have been carefully genotyped and extensively phenotyped. This is happening in maize in research extended to 2009. The next crops are likely to be rice and sorghum, followed by legumes. An effort on aluminium tolerance which successfully led to the identification of a major gene in sorghum is being extended in two directions and two crops: firstly, the characterisation of a complete association panel in sorghum and maize will give access to a broader range of alleles and is likely to highlight comparable and complementary mechanisms in the two crops; secondly, the characterisation of the materials for aluminium tolerance and drought tolerance will address the relation between both traits.

***Theme 3: Development of novel populational approaches for relating genotypes to phenotypes***

***Output 8 to Output 15***

This theme used to be the most upstream for its generic content, aimed at keeping germplasm research active beyond the release of reference samples and to ensure continuous input from germplasm collections. The main output expected in the past (Output 1.3 in 2009–2011 MTP, *Methodology developed for resampling genetic diversity in large germplasm collections*) has been temporarily suspended due to specific difficulties, but it is hoped that this can be reinitiated in the near future. The current clear focus of the programme lays emphasis on populations which allow rigorous analyses powerful enough to point at novel sources of allele diversity in genes involved in target traits at the same time as bearing genetic gain and approaching the standards acceptable for breeders to use in hybridisation.

A particular case is that of the materials derived from intercrossing among diverse selected parents, such as the so-called MAGIC design which generally mobilises eight parents, which is currently under development for two cereals and two legumes. Other cases can build around reference elite parents, such as the nested association mapping populations (one elite parent being crossed to 20 diverse counterparts) are in the course of development for rice, and the Backcross NAM, which includes one generation of backcrossing to the recurrent parent, is planned for sorghum.

Another category is based on the production of specific new populations bearing higher allele richness through wide interspecific crosses. This activity relates to pre-breeding, which has long been the core of the CGIAR mandate. As a flagship for this type of analytically rich improvement approach, rice chromosome segment substitution lines developed at CIAT, with the participation of Agropolis-IRD and EMBRAPA, have started to be widely distributed among

rice specialists and breeders worldwide. Similar materials exist in barley. More complex cases are also being explored in groundnut and in hexaploid wheat.

***Theme 4: Assembly of global elite materials as reservoirs for enhancing mobilisation of genetic diversity***

***Output 16 to Output 18***

Breeding programmes regularly need to integrate new materials in their hybridisation scheme. Typically this will imply characterisation steps in environmental conditions which are close to the target environments and in accordance with local standards, be they local farmer-preferred varieties, trait donors or international standards. Such materials will also encompass adapted diverse sub-samples of the reference sets promoted by the GCP, pre-bred materials such as recombinant chromosome segment substitution lines or other types of recombinant inbred lines.

This theme represents a compromise between the option of typical association studies in a panel of diverse landraces with limited structure, as theoretically recommended, and the demand of breeders to focus on materials which would not deter the breeding value of subsequent generations. It makes particular sense when the target is adaptation to drought, whose evaluation requires homogenisation of many other features such as phenology. Essentially, this theme acts as a bridge between SP1 and SP3, posing challenging methodological questions worth addressing in GCP. This situation is currently being explored with Output 6 in this current MTP for rice, where the materials comprise both landraces and breeding materials (although this Output is classified under theme 2), and will also be explored with wheat in India and China through Output 16, and with groundnut in Africa under Output 17. Output 18 represents a first step in the same direction for cassava.

**Changes from previous MTP**

The MTP for 2009–2011 described 16 Outputs distributed across five themes. The current 2010–2012 MTP for has 18 outputs and four themes. Former theme 2, which focused on genotyping, was terminated together with its two Outputs, which were both completed in 2009. The activity of phenotyping was earlier distributed between one specialised theme (former theme 3) and one general theme aimed at association studies (former theme 4). This emphasis on association studies confronting phenotypic and genotypic features has been reduced, as it turned out to be particularly challenging. Instead, it appears that phenotyping to serve breeding must be more targeted to improved materials that the breeder would be happy to use. In order to accommodate this evolution, former theme 4 was suppressed while a new theme was created around the comparative phenotyping

of various sorts of materials of interest to the breeder. This newly created theme appears as theme 4 in the current MTP, Coming at the bottom of the list of themes because it builds upon results of the three preceding themes. Therefore, some Outputs have been moved between themes and the order has, where appropriate, been modified.

The MTP for 2009–2011 described 16 Outputs, of which the following 3 will have been completed by the end of 2009 and were therefore omitted from this 2010–2012 MTP:

5. Output 1.4. *DArTs developed as a genome-wide molecular characterisation technology for crops with little sequence information* (the end-date of 2010, as presented in the previous MTP, was an error).
6. Output 1.5. *Database developed on allelic diversity at candidate genes across species (ADOC)*. Whilst output targets were given for up to 2010 for this Output in the previous MTP, the constitution of a database for 'Allelic diversity on orthologous candidate genes' has since been limited to the initial project which was commissioned on this topic with this title. At this time, it now appears more likely that the analysis of candidate gene diversity will be directed by crop-specific dynamics rather than through a systematic comparative approach in the future. Consequently, the output target for 2010 has been deleted.
7. Output 1.13. *Linkage disequilibrium and patterns of selection in the genome of sorghum used for mapping useful genes*.

In addition, three other outputs from the previous MTP were suspended for diverse reasons:

8. Output 1.2. *Seed of reference germplasm readily available for all crops*: the first results of the genotyping validation exercise show some examples of mis-scoring (allele size, binning, scoring of artefactual bands/peaks) and some examples of apparently unrelated results (possibly due to the mislabelling of markers). Therefore the validation of the reference set structure and representativeness will represent a significant amount of work, including some cross-tests between the outsourced lab and the labs which initially produced the data. This exercise will take more time than initially thought, and will include more data analysis, thus possibly delaying the availability of genetic stocks for accurately representing the diversity of the crops. Moreover, the interactions between the GCP Management Team and the CGIAR scientists in responsible for germplasm conservation and distribution reveal that complex institutional discussions are needed in order for this activity to be recognised and possibly embedded in mandates. Experimenting on the basis of case studies (proof of concept) is needed in order to forge the collective approach to a sustainable Genetic Resource Support Service. These points are being addressed in the new Output 2, leading to the deletion of the earlier Output 1.2.

9. Output 1.3. *Methodology developed for resampling genetic diversity in large germplasm collections*: This output was based on the availability of molecular diversity (in this case SSR) data for rice from an earlier activity. This latter activity is meeting considerable data quality issues, to the point that the lab in charge has re-done the production of many, which, however, does not appear to have solved all problems. Therefore the 'mining' activity has been stuck for several years. Yet it is central to the GCP's entire rationale. A new proposal layout is currently being negotiated with the PI and the earlier output and output targets have been deleted.
10. Output 1.6. *Database established on field-proven drought-tolerant and drought-susceptible genotypes*: The activity of collecting information on contrasting genotypes for drought tolerance is not an appropriate topic for mobilising a PI and a proposal; it has therefore been deleted as a specific output. It is probable that this process will take place spontaneously within theme 4 of the current MTP.

The remaining Outputs of the previous MTP will continue.

The MTP for 2010–2012 describes 18 Outputs, of which the following Outputs are new:

1. Output 2. *Genetic resource support service established*
2. Output 3. *Adjust/complement the current cassava reference set with new materials from Southern, Eastern and Central Africa*
3. Output 9. *Populations for multiple allelic segregation developed in cowpea and chickpea through multiple parent intercrossing (MAGIC)*
4. Output 11. *Populations for multiple allelic segregation developed through nested backcross1-derived lines in sorghum*
5. Output 15. *Base of current crop diversity in groundnut broadened using chromosome segments from ancestral species*
6. Output 16. *Selection of future parents through phenotypic comparisons for heat- and drought-adaptive traits within wheat germplasm for India and China*
7. Output 17. *Promising groundnut germplasm described and compared*
8. Output 18. *Selection of future parents through comparative genotyping within cassava breeding and reference germplasm*

## Output descriptions and partnerships

### Overview

In this MTP, SP1 has 18 Outputs distributed among four themes. In this MTP, Theme 1 shifts from a phase of decentralised production of genotyping data among a broad range of partners, usually more than one partner per crop, to

a phase of centralised assessment of data quality, validation of reference sample representativeness and publication of certified characterisation data. This involves some outsourcing to an external independent laboratory and some centralised comparison between initial data and new data. Similarly, SP1 is advancing towards the constitution of a Genetic Resource Support Service which requires careful contracting with diverse partners and establishment of a steering committee representing actors and users.

Theme 2 accommodates activities which result in the accumulation of phenotypic information on the reference samples, as well as constructing a collective competence for drought-related field characterisation, to be optimised and mobilised within a support service focused on phenotyping, homologous to the one focused on genotyping. In both cases the implementation is to be managed by SP5, within a platform managed by SP4.

Theme 3 rests on a network of partners working on specific crops on the basis of their specific expertise required to conduct base-broadening programmes. Yet some approaches are shared and will benefit from, and induce, methodological coordination among actors.

Theme 4 guides SP1 activities towards active breeding programmes and represents an active interface between germplasm specialists, pre-breeders and breeders, in a continuous approach between SP1 and SP3.

### **Output descriptions**

For each Output below, the Lead Institute (LI), PI, type of project and funding mechanism are all indicated.

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

*Output 1: Genotyping data validated for the reference samples and the reference markers for all GCP crops*

- Commissioned: G4007.01
- StraP
- 2008–2010
- LI/PI: Agropolis–CIRAD/J-F Rami
- Linked to P4-O4, P4-O5 and P5-O21

The aim is to select and verify those data which will remain the reference for the future. Initially meant to assess data quality in various data batches coming from diverse partner laboratories, this Output was modified to become a verification of data for the reference samples using the best markers, which are easy to use and have a representative resolution power for describing germplasm structure. It involves collection of DNA and subcontracting to a service laboratory. The first results of the genotyping validation exercise show some examples of

mis-scoring (allele size, binning, scoring of artefactual bands/peaks) and some examples of apparently unrelated results (possibly through the mislabelling of markers). Therefore the validation of the reference set structure and representativeness will represent a significant amount of work and will take more time than initially thought, but will include more data analysis. The output has been extended until 2010.

*Partners:* BI, CIAT, CIMMYT, CIP, ICARDA, ICRISAT, IITA, IRRI

#### *Output 2: Genetic resource support service established*

- Commissioned: Project No. TBD
- StraP
- 2009–2011
- PI: GCP/Agropolis–CIRAD/JC Glaszmann
- Linked to P4-O12 and P5-O19

Seed management appears to have been very diverse in the various CGIAR Centres. Departure from rigorous seed management which is necessary for founding genetic stocks is being assessed. The interactions between the GCP MT and the CGIAR scientists in charge of germplasm conservation and distribution reveal that there are complex institutional discussions needed to have this activity recognised and possibly embedded in the mandate. Experimenting on the basis of case studies (proof of concept) is required in order to forge the collective approach to a sustainable genetic resource support service. This has been formalised in a new Output which takes into account both biological and institutional components

*Partners:* BI, CIAT, CIMMYT, CIP, ICARDA, ICRISAT, IITA, IRRI

#### *Output 3: Adjust/complement the current cassava reference set with new materials from Southern, Eastern and Central Africa*

- Commissioned: Project No. TBD
- CI1
- 2009–2013
- LI(PI): IITA/M Ferguson

A large set of materials has been analysed by several partners in the first phase of GCP, leading to a first reference set. Yet there appears to be considerable under-representation of materials from South-East-Central (SEC) Africa. In the meantime, a large analysis has been performed on SEC African materials with other markers. It is proposed to use existing data on SEC Africa in order to select a representative sample which will be analysed with reference SSRs together with the reference set: a total of 384 genotypes x 18 SSRs. This will provide complete 'square' information for finalising the selection of a balanced reference set by adding some 50 genotypes from SEC Africa. Another target is to facilitate germplasm movement in Africa by developing and applying a protocol for cleaning CBSD infected material; if quarantine constraints allow, the reference set will thus be distributed to Tanzania, Ghana and Nigeria.

*Partners:* N/A

**Theme 2: Establishment and implementation of a scientific and organisational framework to describe tolerance to drought**

*Output 4: Drought-related phenotyping of specific populations with high quality molecular information implemented and Phenotyping Support Service consolidated*

- Commissioned: G4008.02
  - StraP
  - 2008–2011
  - LI/PI: ICRISAT/HD Upadhyaya
- Commissioned: Project No. TBD
  - CI5
  - 2009–2012
  - LI/PI: IER/N Tene
- Commissioned: Project No. G4008.03
  - StraP
  - 2008–2010
  - LI/PI: CIMMYT/S Dreisigacker
- Commissioned: Project No. G4008.05
  - StraP
  - 2008–2011
  - LI/PI: IRRI/J Cairns
- Commissioned: Project No. G4008.33
  - StraP
  - 2008–2010
  - LI/PI: KARI/J Gethi
- Linked to P3-O7

This is a group of activities which consist of phenotyping the GCP reference germplasm sets. They will provide information about the variation, under well-characterised drought conditions, of phenotypic traits, particularly those associated with drought tolerance. Depending on the crop, specific objectives include high quality seed multiplication, multi-location evaluation and generation of a set of hybrids from the GCP maize reference set, as well as a specific description of some traits based on the expertise of research partners. The current wave of projects covers sorghum, wheat, rice and maize. The inclusion of an activity planned as part of the CI on sorghum has led to the extension of this output by one year until 2012.

*Partners: (multiple PIs and partner teams):* AfricaRice, Agropolis–CIRAD, Agropolis–INRA, BIOTEC, CRR1, ETH–Zürich, ICRISAT, IER, INRA–Morocco, ISRA/CERAAS, IGKV, NPGRC, TNAU, UAS–Dharwad

*Output 5: Favourable genetic factors for drought tolerance in rice identified*

- Commissioned: G4008.05
- StraP
- 2008–2011
- LI/PI: IRRI/J Cairns
- Linked to P3-O7

Phenotyping data will be analysed in conjunction with genotyping data that the rice community is currently developing using the Perlegen data. Up to several hundred thousand SNPs are expected; ultrafine association analysis will be possible, requiring innovative analytical approaches.

*Partners:* AfricaRice, Agropolis–CIRAD, IGKV, CRR1, TNAU, BIOTEC

*Output 6: Favourable genetic factors for stress tolerance in four legume species identified*

- Focus: G6007.01–G6007.04
- StraP
- 2007–2010
- LI/PI: GCP/C de Vicente
- Linked to P2-O1, P2-O2, P2-O3, P2-O4, P2-O12, P2-O15, P3-O1, P3-O7, P3-O21

This focus project includes phenotyping of reference sets for drought tolerance and genotyping with the most advanced tools – SNP-based assay as well as DArTs–on groundnuts, cowpeas, chickpeas and common beans. Association analyses will be performed in a concerted manner.

*Partners:* ARI–Naliendele, CRS, INRAN, ISRA, EMBRAPA, UCB, UGA, INERA, IRAD, IITA, UoC–Davis, UEM, ART, CBI, SARI–Ethiopia, ECABREN, SABRN, EIAR, LZARDI, EgU, IIPR

*Output 7: Genetic factors underlying aluminum and drought tolerance in sorghum and maize identified*

- Competitive: G3008.02
- StraP
- 2008–2011
- LI/PI: CU/L Kochian

This research proposed in the third competitive call focuses on the genetic architecture of aluminium tolerance in sorghum and maize. Association panels will be phenotyped, first for aluminium tolerance, then for drought tolerance, with both field testing and high throughput root system imaging. Whole-genome SNP arrays will be developed for sorghum and will be used together with existing maize arrays for characterising the panels. Maize candidate genes will also be monitored by re-sequencing. Association analyses will help characterise genetic factors for drought tolerance in relation to root system structure and the particular role of aluminium tolerance.

*Partners:* USDA–ARS, EMBRAPA, CU, MU

**Theme 3: Development of novel populational approaches for relating genotypes to phenotypes**

**Output 8: Populations for multiple allelic segregation developed in rice and sorghum through multiple parent intercrossing**

- Commissioned: G4008.01
  - StraP
  - 2008–2011
  - LI/PI: IRRRI/H Leung
- Commissioned: G4008.46
  - StraP
  - 2008–2011
  - LI/PI: ICRISAT/T Hash

The overall goal of these projects is to develop populations suitable for localising multiple QTL for multiple traits to regions of 3 cM or less in populations targeted at specific agroecological environments. The Multiparent Advanced Generation Inter-Crosses (MAGIC) scheme theoretically enables this resolution to be reached. The current projects focuses on rice and sorghum. In each case several populations will be developed, counting at least 1,000 inbred lines from each population. The process includes crude phenotyping and fingerprinting in order to ensure quality and to monitor progress of each breeding cycle. Recurrent selfing until 2011 will generate lines which can then be phenotyped and genotyped accurately.

*Partners: (multiple PIs and partner teams):* IRRRI, NIAB, ICRISAT

**Output 9: Populations for multiple allelic segregation developed in cowpea and chickpea through multiple parent intercrossing (MAGIC)**

- Focus: Project No. TBD
  - Strap
  - 2010–2012
  - LI/PI: UC/J Ehlers
- Focus: Project No. TBD
  - Strap
  - 2010–2012
  - LI/PI: ICRISAT/P Gaur
- Linked to P2-O2

The overall goal of these projects is to develop populations suitable for localising multiple QTL for multiple traits to regions of 3 cM or less in populations targeted at specific agroecological environments. The Multiparent Advanced Generation Inter-Crosses (MAGIC) scheme theoretically enables this resolution to be reached. The current activities focus on cowpea and chickpea. In each case several populations will be developed, counting approximately 1,000 inbred lines from each population. The process includes crude phenotyping and fingerprinting in order to ensure quality and to monitor progress of each breeding cycle. Recurrent selfing until 2012 will generate lines which can then be phenotyped and genotyped accurately.

*Partners:* Multiple PIs and partner teams (TBD)

**Output 10: Populations for multiple allelic segregation developed through nested intercrossing in rice**

- Commissioned: G4008.45
- StraP
- 2008–2011
- LI (PI): Agropolis–IRD/CIAT (M Lorieux)

The project proposes to develop a nested association mapping population (NAM) in rice, following strategies developed in maize and sorghum. It will provide much higher allelic diversity of the important QTLs than conventional mapping approaches do, enable fine mapping of QTLs (ie, localise them with high precision on the rice genome), and provide genetic materials (advanced lines) for direct introduction in breeding schemes. It will focus on African germplasm but also be of value for Latin America and the Caribbean, which share similar agro-ecosystems with Africa.

*Partner:* AfricaRice

**Output 11: Populations for multiple allelic segregation developed through nested backcross1-derived lines in sorghum**

- Commissioned: Project No. TBD
- CI5
- 2009–2013
- LI/PI: IER/Agropolis–CIRAD/M Vaksman
- Linked to P2-O22

The Nested Association Mapping design has been elaborated for combing the advantages of high recombinational resolution, thanks to a large number of lines having a common parent, and high allelic diversity, as a result of the use of a broad range of diverse parents. A variation to it is the Backcross NAM using a recurrent parent that is already locally-adapted elite material, so that the BC1RILs are closer to the local ideotype and effectively contribute well-performing material. The latter has been practiced successfully for several years at QDPI. Building populations using several recurrent parents (RP) adapted to the target regions in combination with both local specific donor parents (SDP) and a set of diverse common donor parents (CDP) results in a set of connected progenies expected to have highest value in terms of breeding and of mapping genome regions bearing favorable factors in the right genomic background.

*Partners:* IER, ICRISAT, QDPI, HUJ

**Output 12: Base broadened of current crop diversity in rice using interspecific bridges with African rice**

- Competitive: G3007.01
- StraP
- 2008–2010
- LI/PI: Agropolis–IRD/A Ghesquière

This project aims to overcome an important obstacle to rice breeding: the interspecific sterility barrier separating the two cultivated rice species, *O sativa* and *O glaberrima*. New allelic diversity is expected to be incorporated in Asian

rice germplasm from African germplasm, with emphasis on drought resistance and better water-use efficiency. However, because of a late start to the project, almost all Output targets have been redistributed over three years, up to 2010.

*Partners:* AfricaRice, PhilRice, IER, Fedearroz, INERA, UoA, CIAT, PAU

*Output 13: New alleles introgressed from wide crosses using crop wild relatives in barley*

- Competitive: G3007.02
- StraP
- 2008–2010
- LI/PI: SCRI/R Waugh

This project aims at resolving the potential of wild barley to contribute to improving drought tolerance in cultivated barley. It builds on the availability of 140 lines composed of an advanced elite background containing chromosome segments from a wild barley accession from the Fertile Crescent. Recombinant Segment Substitution Lines will be used for intensive genotyping and phenotyping. Because of a late start of the project, almost all Output targets have been redistributed over three years up to 2010.

*Partners:* ICARDA, OSU, INIA–Chile, UdT, UoC–Riverside

*Output 14: New wheat germplasm generated with broadened AB genome diversity*

- Competitive: G3008.01
- StraP
- 2008–2011
- LI/PI: ARI/SC Misra
- Linked to P3-O28

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

*Partners:* CIMMYT, UoS, UAS–Dharwad, PARC

*Output 15: Base of current crop diversity in groundnut broadened using chromosome segments from ancestral species*

- Focus: Project No. TBD
- StraP
- 2010–2012
- LI/PI: ISRA/O N'Doye

This activity consists in developing chromosome segment substitution lines in groundnut between a synthetic interspecific amphidiploid already used in a previous GCP activity and an elite variety widely used in West Africa. Current

materials derived from two generations of backcrossing will be further advanced using a panel of SSR markers covering the genome in order to develop materials with introgressions spanning the whole genome by little segments. These will then be evaluated in comparison with the recurrent parent for a panel of traits including resistance to important diseases and tolerance to drought, in connection with Output 17.

*Partners:* ISRA, Agropolis–CIRAD, ICRISAT, EMBRAPA, UCB

**Theme 4: Assembly of global elite materials as reservoirs for enhancing mobilisation of genetic diversity**

*Output 16: Selection of future parents through phenotypic comparisons for heat- and drought-adaptive traits within wheat germplasm for India and China*

- Commissioned: Project No. TBD
- 2009–2013
- CI6
- LI/PI: TBD
- Linked to P3-O28

This activity will consist in gathering an 'elite subset' composed of heat and drought-tolerant germplasm with good adaptation characteristics, and some doubled haploid lines of selected mapping populations. The selection of these materials involves CIMMYT breeders and physiologists derived from efforts for physiological inbred breeding. Some synthetic-derived lines will be also included. Most of these materials are of 'spring wheat' type and will be best adapted to the Indian breeding programme. Careful thinking is required for addressing the needs of the Chinese wheat breeding programme, which is more focused on winter wheat. The potential use of materials from the reference samples for spring and winter wheat will be explored.

*Partners:* TBD

*Output 17: Promising groundnut germplasm described and compared*

- Focus: G6007.01
- StraP
- 2010–2011
- LI/PI: ISRA/O N'Doye
- Linked to P3-O21

Phase 1 of Tropical Legumes I project led to characterisation of the reference sample in relation to drought, production and characterisation of diverse recombinant inbred populations and production of introgression materials using wild progenitors. Collaboration with TLII, which is heavily involved in breeding in African countries, gives access to a range of other materials and to 'participatory varietal selection' set-ups. This activity will manage comparative phenotyping of such materials of diverse origin with the view to selecting the best complementary parents for subsequent breeding, possibly through marker-assisted recurrent selection.

*Partners:* TBD

*Output 18: Selection of future parents through comparative genotyping within cassava breeding and reference germplasm*

- Commissioned: Project No. TBD
- CI1
- 2009–2010
- LI(PI): IITA/M Ferguson
- Linked to P3-O26

This activity consists in comparing breeding materials to diverse representative materials in order to analyse the structure of the genetic resources available for breeding and to rationalise hybridisation in this highly complex crop where standard genetic analyses cannot be performed due to heterozygosity and difficulty to make diverse and large progenies. Existing arrays bearing 1536 SNPs discovered on ESTs from some 12 genotypes and already used with diverse germplasm will be further used to characterise over 600 genotypes sampled among breeding materials.

*Partners: N/A*

### **International public goods**

SP1 is delivering sets of germplasm with associated documentation that are a condensed representation of germplasm diversity for major food crops worldwide. These consist of germplasm reference samples with validated data on reference markers, accessible as a global public good in a robust form. The GCP partners contribute germplasm, markers, laboratories and capacity, which, altogether, made the programme an extremely comprehensive initiative equipped to yield reference germplasm and reference markers of international value. The second phase will enable development and delivery of numerous materials derived from massive recombination (MAGIC, NAM lines) and introgression from exotic germplasm into elite varieties (BC-NAM, CSS lines) which are likely to have a global value for breeding.

### **Elaboration of partner roles**

Within SP1's Theme 1, partnerships for analysing structure of the diversity, extracting representative reference samples and organising their distribution involve most- and principally – CGIAR Centres, in association with other Consortium

members from the North and the South, including Cornell University, Agropolis (–CIRAD and –INRA) and EMBRAPA. Agropolis–CIRAD acts as a facilitator for assessment of data quality. The formalisation of the genetic resource support service first involves ICRISAT and Bioversity, in their respective capacities as SINGER manager and host of the System-wide Genetic Resource Programme. This theme is expected to lead to a concerted mobilisation of CGIAR Centres for proactive distribution of reference germplasm samples, in order to foster interaction with breeders as well as plant specialists in ARIs.

Theme 2 focuses on drought-related phenotyping for eight crops, mobilises CGIAR Centres as well as numerous NARS involved in breeding for the respective crops. It contributes to the development of a community led by the CGIAR Centres, and to the consolidation of capacity and facilities for NARS.

Theme 3 features CGIAR-centered activities by IRRI, ICRISAT and CIAT, such as the development of recombinant populations from diverse representative materials, as well as ad hoc networks of partners with specific expertise on the creation and use of broad-based hybrid materials. This is often the result of a competitive process, usually led by a developed country partner or a strong developing country partner, and including the respective CGIAR centre and other developing country collaborators. This creates effective crop communities bringing together diverse partners. These communities include: SCRI, ICARDA, OSU, INIA–Chile, Universidad de Talca (Chile), UoC–Riverside for barley; Agharkar Research Institute, CIMMYT, University of Sydney, University of Agricultural Sciences–Dharwad, Pakistani Agricultural Research Council for wheat; Agropolis–IRD, PhilRice, IER, Fedearroz, INERA, University of Arizona, CIAT, AfricaRice, Punjab Agricultural University for rice; and ISRA, Agropolis–CIRAD, ICRISAT, EMBRAPA and UCB for groundnut.

Theme 4 actually represents the initial step of a breeding cycle and consequently features SP3-type partnerships, involving well-resourced partners in the South, such as ICAR and CAAS for wheat, as well as partners in Africa.

## Project 1 logframe – SP1: Crop genetic diversity

Notes:

1. Each Output is followed by:
  - a) the type of research activity/funding contributing to the Output (commissioned, competitive, focus, or discretionary) and GCP project number
  - b) Identification of Output as a StraP (Strategic project) or CI (Challenge Initiative) project
  - c) start and end year, and
  - d) the lead institute (LI) and Principal Investigator(s) (PI[s]) responsible for the Output (and its Output targets).
2. Some Outputs are managed internally within GCP, in some cases involving coordination of a number of external institutes. In most such cases, the entry under 'PI' is denoted as 'Various'.

Intended users	Outcome	Impact		
<b>Theme 1: Creation of an improved understanding of the structure of the diversity for the major world food crops</b>				
<b>Output 1</b>	<b>Genotyping data validated for the reference samples and the reference markers for all GCP crops</b> <ul style="list-style-type: none"> <li>• Commissioned: G4007.01</li> <li>• StraP</li> <li>• 2008–2010</li> <li>• LI/PI: Agropolis–CIRAD/J-F Rami</li> <li>• Linked to P4-04, P4-05 and P5-021</li> </ul>	Plant breeders and germplasm specialists worldwide	Users have opportunities to explore genetic diversity in breeding and in further characterisation for phenotypic and molecular traits	Better access to genetic diversity for breeding, resulting in more efficient crop improvement programmes
<i>Target 2010: Other kinds of knowledge</i>	Validated description of the reference samples structure and representativeness for all GCP crops			
<b>Output 2</b>	<b>Genetic resource support service established</b> <ul style="list-style-type: none"> <li>• Commissioned: Project No. TBD</li> <li>• 2009–2011</li> <li>• StraP</li> <li>• PI: GCP and Agropolis–CIRAD/JC Glaszmann</li> <li>• Linked to P4-012 and P5-019</li> </ul>	Plant breeders and germplasm specialists worldwide	For each crop, users have access to reference materials which will serve to represent wider collections and to compile information from diverse origins	Better access to genetic diversity for breeding, resulting in more efficient crop improvement programmes
<i>Target 2010: Practices</i>	Service established for all GCP priority crops			
<i>Target 2011: Practices</i>	Facilities implemented in SINGER for handling sets of materials and genotyping/phenotyping data			
<b>Output 3</b>	<b>Adjust/complement the current cassava reference set with new materials from Southern, Eastern and Central Africa</b> <ul style="list-style-type: none"> <li>• Commissioned: Project No. TBD</li> <li>• C11</li> <li>• 2009–2013</li> <li>• LI(PI): IITA/M Ferguson</li> </ul>	Cassava breeders and germplasm specialists worldwide	Users have access to reference materials which will serve to represent wider collections and to compile information from diverse origins	Better access to genetic diversity for breeding, resulting in more efficient crop improvement programmes
<i>Target 2010: Other kinds of knowledge</i>	A unified description of SSR diversity among 384 accessions including representatives from Southern, Eastern and Central Africa			
<i>Target 2011: Capacity</i>	A method for cleaning CBSD contaminated germplasm			
<i>Target 2012: Capacity</i>	Representative germplasm from Southern, Eastern and Central Africa placed in vitro and made available for distribution			
<b>Theme 2: Establishment and implementation of a scientific and organisational framework to describe tolerance to drought</b>				
<b>Output 4</b>	<b>Drought-related phenotyping of specific populations with high quality molecular information (rice, sorghum, wheat and maize)</b> <ul style="list-style-type: none"> <li>• Commissioned: G4008.02</li> <li>• StraP</li> <li>• 2008–2011</li> <li>• LI/PI: ICRISAT/HD Upadhyaya</li> </ul>	GCP scientists; pearl millet, sorghum and other cereal geneticists and breeders	Users have access to the best drought tolerance screening facilities within GCP; more targets are available for MAS for improving drought tolerance in cereals	Increased efficiency in analysing the genetic control of tolerance to drought



Output	title, type and target(s)	Intended users	Outcome	Impact
	<ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>CI5</li> <li>2009–2012</li> <li>LI/PI: IER/N Tene</li> <li>Commissioned: G4008.03</li> <li>StraP</li> <li>2008–2010</li> <li>LI/PI: CIMMYT/S Dreisigacker</li> <li>Commissioned: G4008.05</li> <li>StraP</li> <li>2008–2011</li> <li>LI/PI: IRRJ/J Cairns</li> <li>Commissioned: G4008.33</li> <li>StraP</li> <li>2008–2010</li> <li>LI/PI: KARI/J Gethi</li> <li>Linked to P3-07</li> </ul>			
<i>Target 2010: Other kinds of knowledge</i>	Further phenotyping conducted after collective prioritisation			
<i>Target 2011: Other kinds of knowledge</i>	Further phenotyping conducted after collective prioritisation; data used for conducting association studies			
<i>Target 2012: Other kinds of knowledge</i>	Final phenotyping conducted for sorghum in Mali; key traits refined for implementing selection among recombinant progenies			
<b>Output 5</b>	<b>Favourable genetic factors for drought tolerance in rice identified</b> <ul style="list-style-type: none"> <li>Commissioned: G4008.05</li> <li>StraP</li> <li>2008–2011</li> <li>LI/PI: IRRJ/J Cairns</li> <li>Linked to P3-07</li> </ul>	Geneticists and breeders for rice and other cereals	Users have more targets available for MAS for improving drought tolerance in cereals	Increased efficiency in crop research and improvement
<i>Target 2010: Other kinds of knowledge</i>	Integrated phenotyping repeated and identification of favourable alleles/haplotypes in rice carried out using whole-genome SNPs among 500 rice accessions			
<i>Target 2011: Other kinds of knowledge</i>	Fine data analysis and further favourable alleles detected			
<b>Output 6</b>	<b>Favourable genetic factors for stress tolerance in four legume species identified</b> <ul style="list-style-type: none"> <li>Focus: G6007.01–G6007.04</li> <li>StraP</li> <li>2007–2010</li> <li>LI/PI: GCP/C de Vicente</li> <li>Linked to P2-01, P2-02, P2-03, P2-04, P2-012, P2-015, P3-01, P3-07, P3-021</li> </ul>	Legume scientists worldwide	Users have more targets available for MAS for improving stress tolerance in legumes	Increased efficiency in crop research and improvement
<i>Output target 2010</i>	Identification of favourable donors of complementary drought tolerance traits in target legumes			
<b>Output 7</b>	<b>Genetic factors underlying aluminum and drought tolerance in sorghum and maize identified</b> <ul style="list-style-type: none"> <li>Competitive: G3008.02</li> <li>StraP</li> <li>2008–2011</li> <li>LI/PI: CU/L Kochian</li> </ul>	Sorghum geneticists and breeders	Users have clearer options for association studies in sorghum	Increased efficiency in crop research and improvement

Output	title, type and target(s)	Intended users	Outcome	Impact
<i>Target 2010: Other kinds of knowledge</i>	Association panels of sorghum and maize genotyped with whole-genome SNPs, including candidate genes in maize; whole-root systems digitally characterised for both association panels			
<i>Target 2011: Other kinds of knowledge</i>	Genetic architecture of aluminium tolerance determined in maize; panels of sorghum and maize phenotyped for drought tolerance and comparative genetic architecture of drought/aluminum tolerance described			
<b>Output 8</b>	<b>Populations for multiple allelic segregation developed in rice and sorghum through multiple parent intercrossing</b> <ul style="list-style-type: none"> <li>• Commissioned: G4008.01</li> <li>• StraP</li> <li>• 2008–2011</li> <li>• LI/PI: IRRI/H Leung</li> <li>• Commissioned: G4008.46</li> <li>• StraP</li> <li>• 2008–2011</li> <li>• LI/PI: ICRISAT/T Hash</li> </ul>	Rice and sorghum geneticists and breeders	Users have increased opportunities for mapping favourable genes and alleles in cereals	Increased efficiency in crop research and improvement
<i>Target 2010: Materials</i>	Further intercrossing and advancement of selfing generations based on 1,000 S1 families for each of two sorghum populations for Asia and two rice populations			
<i>Target 2011: Materials</i>	Further advancement of selfing generations carried out; materials used for phenotyping and genotyping for association analyses			
<b>Theme 3: Development of novel populational approaches for relating genotypes to phenotypes</b>				
<b>Output 9</b>	<b>Populations for multiple allelic segregation developed in cowpea and chickpea through multiple parent intercrossing (MAGIC)</b> <ul style="list-style-type: none"> <li>• Focus: Project No. TBD</li> <li>• Strap</li> <li>• 2010–2012</li> <li>• LI/PI: UC/J Ehlers</li> <li>• Focus: Project No. TBD</li> <li>• Strap</li> <li>• 2010–2012</li> <li>• LI/PI: ICRISAT/P Gaur</li> <li>• Linked to P2-02</li> </ul>	Cowpea and chickpea geneticists and breeders	Users have increased opportunities for mapping favourable genes and alleles in cowpea and chickpea	Increased efficiency in crop research and improvement
<i>Target 2010: Materials</i>	Second intercrossing and advancement of selfing generations carried out			
<i>Target 2011: Materials</i>	Further advancement of selfing generations carried out; materials used for phenotyping and genotyping for association analyses			
<i>Target 2012: Other kinds of knowledge</i>	Further phenotyping and genotyping and association analyses performed			
<b>Output 10</b>	<b>Populations for multiple allelic segregation developed through nested intercrossing in rice</b> <ul style="list-style-type: none"> <li>• Commissioned: G4008.45</li> <li>• StraP</li> <li>• 2008–2011</li> <li>• LI (PI): Agropolis–IRD/CIAT (M Lorieux)</li> </ul>	Rice geneticists and breeders	Users have increased and improved power and resolution for mapping favourable genes and alleles in rice	Increased efficiency in crop research and improvement
<i>Target 2010: Materials</i>	Nested intercrossing and first selfing generation performed and selfing generations advanced through single seed descent for 4,000 lines			
<i>Target 2011: Materials</i>	Seed stocks of 4,000 lines increased for distribution; a specific database established			

Output	title, type and target(s)	Intended users	Outcome	Impact
<b>Output 11</b>	<b>Populations for multiple allelic segregation developed through nested backcross1-derived lines in sorghum</b> <ul style="list-style-type: none"> <li>• Commissioned: Project No. TBD</li> <li>• CI5</li> <li>• 2009–2013</li> <li>• LI/(PI): IER/Agropolis–CIRAD (M Vaksman)</li> <li>• Linked to P2-022</li> </ul>	Sorghum geneticists and breeders	Users have clearer options for association studies in sorghum	Increased efficiency in crop research and improvement
<i>Target 2010: Materials</i>	Recurrent parents converted to ms3 male sterility and first generation hybrids and backcrosses produced for three recurrent parents in Mali			
<i>Target 2011: Materials</i>	Selfing generations advanced through single seed descent for 6,000 lines			
<i>Target 2012: Materials</i>	Further selfing of 6,000 lines and release for phenotyping and genotyping			
<b>Output 12</b>	<b>Base broadened of current crop diversity in rice using interspecific bridges with African rice</b> <ul style="list-style-type: none"> <li>• Competitive: G3007.01</li> <li>• StraP</li> <li>• 2008–2010</li> <li>• LI/PI: Agropolis–IRD/A Ghesquière</li> </ul>	Rice germplasm specialists and breeders	Novel rice germplasm tailored for genetic analysis of trait variation and innovative breeding available to users	Increased efficiency in crop research and improvement
<i>Target 2010: Materials</i>	Favourable alien chromosome segments from African cultivated rice identified, and a range of interspecific materials establishing a bridge between Asian and African rices produced			
<b>Output 13</b>	<b>New alleles introgressed from wide crosses using crop wild relatives in barley</b> <ul style="list-style-type: none"> <li>• Competitive: G3007.02</li> <li>• StraP</li> <li>• 2008–2010</li> <li>• LI/PI: SCRI/R Waugh</li> </ul>	Barley germplasm specialists and breeders	Users have access to novel barley germplasm tailored for genetic analysis of trait variation and innovative breeding	Increased efficiency in crop research and improvement
<i>Target 2010: Materials</i>	Favourable introgressions from wild barley into cultivated materials identified based on two cropping seasons			
<b>Output 14</b>	<b>New wheat germplasm generated with broadened AB genome diversity</b> <ul style="list-style-type: none"> <li>• Competitive: G3008.01</li> <li>• StraP</li> <li>• 2008–2011</li> <li>• LI/PI: ARI/SC Misra</li> <li>• Linked to P3-028</li> </ul>	Wheat germplasm specialists and breeders	Users have access to novel synthetic wheat germplasm tailored for genetic analysis of trait variation and innovative breeding	Increased efficiency in crop research and improvement
<i>Target 2010: Materials</i>	A range of 400 emmer-based synthetic back-cross lines developed			
<i>Target 2011: Materials</i>	Around 50 drought-/heat- tolerant emmer-based synthetic derivatives identified; a broad range of derivatives genotyped with SSR and DArT markers			
<b>Output 15</b>	<b>Base of current crop diversity in groundnut broadened using chromosome segments from ancestral species</b> <ul style="list-style-type: none"> <li>• Focus: Project No. TBD</li> <li>• StraP</li> <li>• 2010–2012</li> <li>• LI/PI: ISRA/O N'Doye</li> </ul>	Groundnut germplasm specialists and breeders	Novel groundnut germplasm tailored for genetic analysis of trait variation and innovative breeding available to users	Increased efficiency in crop research and improvement
<i>Target 2010: Materials</i>	Advanced backcross introgression materials derived from synthetic amphidiploid towards chromosome segment substitution lines			
<i>Target 2011: Materials</i>	Chromosome segment substitution lines produced and favourable alien chromosome segments from ancestral wild <i>Arachis</i> identified			

Output	title, type and target(s)	Intended users	Outcome	Impact
<b>Theme 4: Assembly of global elite materials as reservoirs for enhancing mobilisation of genetic diversity</b>				
<b>Output 16</b>	<b>Selection of future parents through phenotypic comparisons for heat- and drought-adaptive traits within wheat germplasm for India and China</b> <ul style="list-style-type: none"> <li>• Commissioned: Project No. TBD</li> <li>• 2009–2013</li> <li>• C16</li> <li>• LI/PI: TBD</li> <li>• Linked to P3-028</li> </ul>	Wheat geneticists and breeders in India and China	Users have access to broad diversity in improved background to be used for hybridisation in wheat breeding	Increased efficiency in wheat improvement
<i>Target 2010: Materials</i>	Core elite nurseries representing contrasting reference germplasm, sources of traits and segregating populations identified and distributed amongst a panel of partners in diverse environments in India and China			
<i>Target 2011: Other kinds of knowledge</i>	Core elite nurseries characterised for drought-adaptive physiological and agronomic traits in four locations in India and one and two locations for spring wheat and winter wheat (respectively) in China			
<i>Target 2012: Other kinds of knowledge</i>	Phenotypic data analysed for refining target traits, identifying complementary donors and validating QTLs			
<b>Output 17</b>	<b>Promising groundnut germplasm described and compared</b> <ul style="list-style-type: none"> <li>• Focus: G6007.01</li> <li>• StraP</li> <li>• 2010–2011</li> <li>• LI/PI: ISRA/O N'doye</li> <li>• Linked to P3-021</li> </ul>	Groundnut germplasm specialists and breeders	Users gain access to promising germplasm of composite origin confronted through coordinated phenotyping	Increased efficiency in crop research and improvement
<i>Target 2010: Materials</i>	Promising targeted germplasm assembled from reference set, base-broadening, participatory varietal selection, etc., and evaluated in representative environments			
<i>Target 2011: Materials</i>	Contrasting sources of valuable features identified and re-hybridised			
<b>Output 18</b>	<b>Selection of future parents through comparative genotyping within cassava breeding and reference germplasm</b> <ul style="list-style-type: none"> <li>• Commissioned: Project No. TBD</li> <li>• C11</li> <li>• 2009–2010</li> <li>• LI(PI): IITA/M Ferguson</li> <li>• Linked to P3-026</li> </ul>	Cassava breeders in Africa	Users have an improved rationale for hybridisation among cassava germplasm	Increased efficiency in cassava breeding
<i>Target 2010: Other kinds of knowledge</i>	Over 600 selected breeding materials genotyped using existing Illumina 1536 array			

# Project 2 – Subprogramme 2: Genomics towards gene discovery

## Project narrative

### Project overview and rationale

Adaptation to environmental stresses in crop plants is often controlled by complex genetic systems that are subjected to influence by genotype by environment interactions. To combine the right complements of genes/alleles effectively in a breeding programme, sufficient understanding is needed of the genetic mechanisms underlying the adaptive processes, especially for traits like drought tolerance. Therefore, the main objective of this Subprogramme is to provide a scientific and collaborative environment so that interdisciplinary and integrated approaches can be used for gene discovery to dissect the genetic mechanisms underlying adaptive processes for drought. Comparative approaches are applied to leverage genetic knowledge on multiple plant species to investigate and validate gene functions important to stress tolerance. Specifically, SP2 aims to: (i) develop cross-cutting research platforms for efficient application of genomic tools and knowledge to decipher genetic control of complex traits, and (ii) identify genes to alleviate target problems in the most efficient manner by pooling resources and expertise. To realise the full potential of these approaches requires capacity-building in the use of the new tools and creation of a pipeline to translate results into practice.

While the focus will be more on drought tolerance traits in the coming years, comparative genomics will be used to clone homologues of both AI-tolerance and P-efficiency genes (already cloned in sorghum and rice, respectively, in GCP's Phase I) in cereal species, namely sorghum, maize and rice.

### Impact pathways

One of the bottlenecks in the development of stress tolerance in crops is inadequate understanding of the genetic basis of stress tolerance. The complexity of the stress response requires a multi-pronged approach to reveal the underlying mechanisms. By grouping different activities into four Themes, this Subprogramme uses or develops genomic tools and technologies and evaluates multidisciplinary approaches to better understand gene function and interaction to improve knowledge of gene system across crops.

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

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

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

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

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

#### *Output 1 to Output 5*

Until recently, the tropical legume crops (groundnuts, cowpeas, common beans and chickpeas), which represent very important crop commodities in Sub Saharan Africa (SSA), South Asia (SA) and Latin America (LA), have been untouched by the genomic revolution and are often considered the 'orphan legume crops'. Significant progress is being made under Outputs 1 to 4 towards developing genomic resources such as molecular markers, ESTs, genetic and physical maps, markers associated with drought and selected biotic stresses in these legume crops. These results will have significant implications on molecular breeding of so called orphan legume crops that will lead to the development of improved varieties of these legume crops with enhanced tolerance to drought and biotic stresses. Beneficiaries of the results will include not only the breeding communities of these legume crops in targeted environments, but also the legume genetics/ breeding/genomics communities across the world.

In its first five years, GCP played a catalytic role by supporting the assembly and the production of mutant collections of several crops. Output 5 in this MTP deals with the utilisation of a rice mutant collection with the candidate genes to identify 'gain-of-function' mutants with improved drought tolerance and water-use efficiency phenotype in rice. The production and use of new genetic resources and development of tools will expand the research community's means of understanding gene function relevant to stress tolerance not only in rice but also in other cereals worldwide.

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

***Output 6 to Output 10***

Under Output 6, Orthologous gene markers are being developed across four tropical legume crops that provide a permanent genomic resource base for each species and enable construction of genetic maps and marker-aided selection applications at various stages of genetic analyses and breeding. These activities will help to determine the relationship of the ancestral genome segments in these legumes, and facilitate genomics-enabled legume breeding in SSA, SA and LA.

For Outputs 7, 8, 9 and 10, research teams are aiming to generate genome-wide genetic resources in previously neglected crop species such as cassava, pearl millet, sweet potato and pigeonpea. These genomic resources include the development of SSRs, ESTs, SNPs, DArT markers and genetic maps (and physical maps in cassava) in these species. A key point of emphasis amongst these activities is that the genomic resources be anchored in well-used mapping or breeding populations. These efforts are expected to increase the genetic knowledge base of important crops that have thus far suffered under-investment. Outputs from these projects will promote mapping and genetic dissection of a suite of traits, particularly drought tolerance, and will eventually enable the respective communities to undertake molecular breeding activities for developing improved crop cultivars for drought tolerance in the targeted regions of SSA, SA and LA.

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

***Output 11 to Output 17***

For Outputs 11, 12 and 13, research focuses on the employment of the chip technology by using agronomically-relevant experimental conditions and genetic materials, in such a way that the genetic knowledge generated from these experiments is relevant to researchers and breeders. The adoption of genome-wide approaches should be fruitful in suggesting new genes or regulatory mechanisms for validation. Transcript profiling projects on rice and wheat, together with a next generation sequencing technology project on sorghum, are expected to provide candidate genes and promising markers for molecular breeding for a complex trait like drought tolerance with the aim of eventually developing drought-tolerant varieties of wheat, rice and sorghum for Asia and Africa.

Outputs 14, 15, 16 and 17 deal with the cloning of Al-tolerance and P-efficiency genes in three cereal species. Indeed, in Phase I of GCP, Al-tolerance and P-efficiency genes have already been

cloned in sorghum and rice, respectively, with comparative biology approaches now being used to clone these genes in other cereal species. The outcome of these activities will lead to enhanced knowledge of the tolerance genes to counter soil problems in three cereal species which can then be used to identify similar genes in other cereals or legumes. Furthermore, gene-based diagnostic markers would facilitate molecular breeding in the cereal species for developing the varieties with enhanced tolerance to Al and higher P-efficiency in targeted environments of SSA, LA and SA.

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

***Output 18 to Output 22***

The projects under Output 18 and 19 deal with the validation of the roles of the *Pup1* gene and pSARK-IPT gene in rice, using over-expression and reverse genetics approaches. The outcome of these activities will lead to: (i) enhanced knowledge on cross-talking between P-deficiency and drought stress at the molecular and physiological level, and (ii) the testing of the role of pSARK-IPT gene in rice for drought tolerance, and the subsequent identification of key determinant genes. In addition, both pyramided QTL lines for P-efficiency and drought tolerance, as well as knock-out mutant lines for pSARK-IPT genes are expected to be generated. Rice genomics, breeding and genetics communities worldwide, as well as crop physiologists in general will greatly benefit from the research of these outputs.

As 'stay-green' and 'root-traits' have been identified as major targeted traits for drought tolerance in sorghum and chickpea, Outputs 20 and 21 place emphasis on the validation of the QTLs associated with 'stay-green' in sorghum and 'root-traits' in chickpea in the germplasm of targeted countries. The outcomes of these projects will provide validated QTLs for drought tolerance in sorghum and chickpea to users for introgressing into drought-sensitive lines for the improvement of sorghum and chickpea in SSA and SA. The sorghum and chickpea researchers will be the main beneficiaries of these projects.

Research carried out under Output 22 forms part of the Sorghum Challenge Initiative that deals with the development of backcross populations and their phenotyping for key measures of both productivity and response to water limitation, as well as focusing on the development of an economical universal genotyping platform and its application to the genotyping of developed populations, together with development and application of supporting analytical tools. Expected results of this research include the development of a large number of improved lines that exceed the

productivity of cultivated germplasm and approach the quality of local standards in each of the target ecological zones that are immediately suitable for advanced testing as germplasm or even cultivars. These genotypes will also be well suited to intercrossing with one another to achieve further improvements in elite genetic backgrounds in targeted environments of Africa.

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

A potential factor that may impede the dissemination of knowledge and new tools is intellectual property (IP) protection for information and genetic resources where there is a strong commercial interest. Although GCP research policies demand complete open access to the results and resources generated by GCP-funded projects, there are still some issues relating to pre-existing IP rights that may sometimes deter full access and sharing. Such issues should be addressed by the appropriate governmental authorities to enable the rapid and smooth flow of materials.

### Changes from previous MTP

When preparing the current 2010–2012 MTP, some errors were noticed in the start- or end-dates in the last 2009–2011 MTP. These errors are listed below and have been corrected in this 2010–2012 MTP:

1. Focus projects (2009–2011 MTP Outputs 2.1 to 2.4 and 2.6): The start-date should have been indicated as 2007 in all cases
2. Commissioned projects: The end-date should have been indicated as 2009 for Output 2.5, and as 2010 for Output 2.10
3. Round II Competitive projects: For Output 2.14, the duration should have been indicated as 2007–2009.
4. Round III Competitive projects (2009–2011 MTP Outputs 2.12, 2.15 and 2.16): The duration should have been indicated as 2008–2011 for all cases

These errors have been addressed in this 2010–2012 MTP, with the necessary adjustments for a true representation of project dates, as projected at this time of writing the 2010–2012 MTP, having been carried out.

Two of the 18 Outputs listed in the 2009–2011 MTP (Output 2.14 and Output 2.5) were supposed to be completed by end of 2009. Of these two Outputs, Output 2.14 *Drought-adaptive mechanisms in bread and durum wheat determined through large-scale phenotyping methodologies* is expected to be completed as scheduled, and has therefore not been included in this 2010–2012.

However, due to some technical problems relating to phenotyping and managing database information, progress has been slower than expected in Output 2.5 (Output 5 in current MTP) *Validation of drought-response/resistance pathways genes by phenotypic analysis of mutants*. Consequently, the output target scheduled for 2009 in Output 2.5 of the previous MTP has been shifted to 2010 in this 2010–2012 MTP.

Similarly, Output 2.18 of the previous MTP (Output 21 in the current MTP), was expected to initiate at the beginning of 2009. However, this project suffered a delayed start because of uncertainty of NARS partners. Consequently, Output targets as presented in the previous MTP have shifted by one year, with the project now expected to end in 2012. The title of this Output has also been amended.

Output 2.17 of the previous MTP (Output 20 in this 2010–2012 MTP), following on from the introduction of new partners to the project, was amended from a two-year project to a three-year project, with the project now due to end in 2011. The Output targets in this MTP have been adjusted accordingly.

In anticipation of Phase II of the Focus Tropical Legume I project for 2010–2013, adjustments have been made in the Output targets for the following Outputs:

1. Output 2.1 (Output 1 in 2010–2012 MTP). *Bean genetic and genomic resources developed*: The projected end-date is now 2013, and Output targets have therefore been added for up to and including 2012 in this MTP
2. Output 2.2 (Output 2 in 2010–2012 MTP). *Chickpea genetic and genomic resources developed*: One commissioned project, forming an integral element of the Chickpea Challenge Initiative (CI2), has been added to this Output in 2009. The projected end-date for the whole Output is 2013, and Output targets have therefore been added for up to 2012 in this MTP.
3. Output 2.3 (Output 3 in 2010–2012 MTP): *Cowpea genetic and genomic resources developed*: One commissioned project, an integral element of the Cowpea Challenge Initiative (CI3), has been added to this Output in 2009. The projected end-date for the whole Output is 2013, and Output targets have therefore been added for up to 2012 in this MTP.

4. Output 2.4 (Output 4 in 2010–2012 MTP). *Groundnut genetic and genomic resources developed*: One commissioned project was added to this Output as a natural support to the activities already underway in the Focus project G4006.01. The projected end-date for the whole Output is 2013, and Output targets have therefore been added for up to and including 2012.
5. Output 2.6 (Output 6 in 2010–2012 MTP). *Cross-species resources developed for comparative biology in tropical crop legumes*: In order to help increase delivery speed and achieve the Output targets of Output 2.6 as outlined in the previous MTP, a new commissioned project, which will begin in mid-2009, was added to this Output. Consequently, it is projected that Output targets scheduled for 2011 in the previous MTP will in fact be achieved by 2010 for this Output. Output targets for 2011 have therefore been removed from this current MTP.

As GCP has entered its second phase, SP2 activities, wherever possible, have been embedded in different Challenge Initiatives (CIs). For instance, two new projects as a part of Chickpea and Cowpea CIs have initiated in 2009 and these have been integrated with Output 2 and Output 3, respectively. In addition, four Outputs, forming part of the Comparative Genomics CI (CI7) and one Output, forming part of the Sorghum CI (CI5) have been included in the new 2010–2012 MTP.

The current MTP describes 22 Outputs for 2010–2012, of which the following five are new:

1. Output 14. *Cloning characterisation and validation of aluminum tolerance gene(s) in rice*
2. Output 15. *Cloning characterisation and validation of aluminum tolerance gene(s) in maize*
3. Output 16. *Cloning, characterisation and validation of P-efficiency gene(s) in sorghum*
4. Output 17. *Cloning, characterisation and validation of P-efficiency gene(s) in maize*
5. Output 22. *Development of drought tolerant sorghum for Africa by a Backcross-NAM approach-genotyping component*

In GCP's Phase II, SP2 activities as indicated in the previous 2009–2011 MTP will continue to focus on drought tolerance and cloning, validation and characterisation of Al-tolerance and P-efficiency genes (already cloned in sorghum and rice respectively in the first phase of GCP) in three cereal crops, namely rice, maize and sorghum. All SP2 research activities will place emphasis on validation of cloned/candidate genes and diagnostic markers for transferring SP2 products to SP3.

## Output descriptions and partnerships

### Overview

In this MTP, Subprogramme 2 has a total of 22 Outputs. The SP uses or develops genomic tools and technologies and evaluates multidisciplinary approaches to better understand gene function and interaction to improve knowledge of gene systems across crops. The Subprogramme believes in maximising the use of genomic and genetic resources available in the research community, and develops, where required, specialised genetic stocks or genomic tools to elevate the level of genetic research in different crops. Comparative biology approaches are applied to leverage genetic knowledge from multiple species to investigate and validate gene functions important for stress tolerance. While achieving its goals, SP2 forms multidisciplinary teams in GCP's targeted environments with the aim of incorporating SP2 products into breeding programmes.

Theme 1 of SP2 deals with the assembly and development of genetic and genomic resources. Under this theme, to develop the genomic resources, including markers associated with abiotic and biotic stress resistance in tropical legumes, the SP is working with CGIAR centres. For utilising the rice mutant resources, the SP is working with CG centre and ARIs. For developing genome infrastructure under themes 2 in less studied species such as cassava, pearl millet, pigeonpea and sweet potato, while mapping populations are being developed by CG centres, genomic resources are being developed by ARIs and private companies together with CG centres and NARS partners. Under theme 3, which deals with identification and cloning of genes, transcript profiling of rice, wheat and sorghum is being done by ARIs in collaboration with CG and NARS partners. Theme 4 acts as an interface between SP2 and SP3, dealing with the validation of candidate genes/QTLs – an activity which is currently being led mainly by CG Centres, together with NARS partners.

### Output descriptions

For each Output below, the Lead Institute (LI), PI, type of project and funding mechanism are all indicated.

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

##### *Output 1: Bean genetic and genomic resources developed*

- Focus: G6007.03
- StraP
- 2007–2010 (Phase II: 2010–2013)
- LI/PI: CIAT/M Blair
- Linked to P1-O6

Genomic resources including ESTs, SSR, SNP and COS markers are being developed for identifying markers associated with drought tolerance and BCMV/bruchid resistance with a final



goal of developing improved bean varieties with enhanced pest and disease resistance, and tolerance to drought in Africa. Although this project was scheduled to be completed in 2011 (extended from the originally-planned end-date of 2010, for reasons explained under Output description 2.1 in the previous MTP), Phase II of this project is expected for 2010–2013. Consequently, Output targets have been added for 2012.

*Partners:* ART, CBI, ECABREN, EIAR, PU, RIKEN, SABRN, UoC–Davis

#### *Output 2: Chickpea genetic and genomic resources developed*

- Focus: G6007.04
  - StraP
  - 2007–2011 (Phase II: 2010–2013)
  - LI/PI: ICRISAT/R Varshney
- Commissioned: Project No. TBD
  - CI2
  - 2009–2010
  - LI/PI: UoC-Davis/D Cook
- Linked to P1-O6, P1-O9, P3-O4, P4-O9 and P4-O12

A larger number of molecular markers (DArT and SSR) are being generated to prepare a high-density reference map of chickpea. These genomic resources will be used to identify molecular markers for drought tolerance and insect (*Helicoverpa*) resistance in chickpea to develop drought-tolerant and insect-resistant chickpea varieties in Asia and Africa. As per the previous MTP, this project was scheduled to be completed in 2011 (extended from the originally-planned end-date of 2010, for reasons explained under Output description in the previous MTP). However, Phase II of this project is expected for 2010–2013. As a result, Output targets have been added for 2012.

*Partners:* ICRISAT, EIAR, LZARDI, DArT P/L, IIPR, NIPGR, UoF

#### *Output 3: Cowpea genetic and genomic resources developed*

- Focus: G6007.02
  - StraP
  - 2007–2011 (Phase II: 2010–2013)
  - LI/PI: UoC–Riverside/J Ehlers
- Commissioned: Project No. TBD
  - CI3
  - 2009–2010
  - LI/PI: UoC–Riverside/J Ehlers
- Linked to P1-O6

Genomic resources including cDNA libraries, BAC libraries, EST sequences and BAC-end sequences are being generated to develop SNP markers and place BAC contigs onto the genetic map. These resources will be used to identify markers for drought tolerance and resistance to biotic stress (flower thrips, root nematode). As Phase II of this project is expected for 2010–2013, Output targets have been added for 2012.

*Partners:* IITA, INERA, IRAD, ISRA, UoC–Davis

#### *Output 4: Groundnut genetic and genomic resources developed*

- Focus: G6007.01
  - StraP
  - 2007–2011 (Phase II: 2010–2013)
  - LI/PI: ICRISAT/V Vadez
- Commissioned: G4008.06
  - StraP
  - 2008–2010
  - LI/PI: UGA/S Knapp
- Linked to P1-O6 and P4-O12

Molecular markers (SSR and SNP) are being developed in large numbers from genomic and cDNA libraries to develop a genetic map for *Arachis*. In addition to identifying the markers for drought tolerance and foliar disease resistance, a linked genetic and physical map will be developed for the AA genome. Because of a late start and some IP and technical issues relating to sharing the BAC library with project partners, and in anticipation of Phase II (2010–2013), the project is now expected to end in 2013, with Output targets have been added for 2012 accordingly.

*Partners:* EMBRAPA, Dart P/L, IAC, CRS, INRAN, ISRA, ARI–Naliende

#### *Output 5: Validation of drought-response/resistance pathways genes by phenotypic analysis of mutants*

- Commissioned: G4007.02
- StraP
- 2007–2010
- LI/PI: VBI, VPI/A Pereira

After identification of mutant lines for drought response phenotypes, sib-lines will be characterised by physiological parameters (transpiration rate, stomatal conductance, root and water-use efficiency) using field screen and high-throughput phenotyping techniques. Subsequently, drought-resistant/sensitive phenotypes will be identified for several candidate gene mutants in rice/*Arabidopsis*, and datasets developed. Because of some technical issues, plant phenotypes and integration of all data obtained in a gene interaction network has not yet been completed. Therefore, the Output target for 2009 as indicated in the previous MTP has been extended to 2010 in this current MTP.

*Partners:* IRRI, HZAU

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

##### *Output 6: Cross-species resources developed for comparative biology in tropical crop legumes*

- Focus: G6007.05
  - StraP
  - 2007–2010
  - LI/PI: UoC–Davis/DCook

- Commissioned: Project No. TBD
  - StraP
  - 2009–2010
  - LI/PI :UoC–Davis/D Cook
- Linked to P4-O8

In order to develop cross-species markers for legume species, gene-based orthologous markers are being developed and mapped onto the genetic maps of bean, cowpea, chickpea and groundnut. This will help determine the relationships of the ancestral genome segments in these legumes and facilitate genomics-enabled legume breeding in Africa and Asia. In order help to increase delivery speed and meet the necessary targets, a new commissioned project (expanding 2009–2010) has been added to this Output. As a result of this additional commissioned project, it is projected that Output targets scheduled for 2011 in the previous MTP will in fact be achieved by 2010. Output targets for 2011 have therefore been removed from this current MTP.

*Partners:* UGA, UCB, UoC–Riverside, ICRISAT, CIAT, IITA

*Output 7: Genetic and physical mapping resources produced for drought breeding in cassava*

- Competitive: G3007.03
- StraP
- 2008–2010
- LI/PI: University of Maryland/P Rabinowicz

This Output plans to develop genome-wide BAC fingerprint contigs and the minimum tilling path to sequence several thousand BAC clones and develop a genome-wide SNP map that will be used to identify markers for drought tolerance. Because of a late start due to the PI changing institutes and the late signing of the contract, all Output targets were rescheduled by one year in the 2009–2011 MTP. It is anticipated that the planned Output target will be by completed by 2010.

*Partners:* UoP, UoW

*Output 8: Genomic resources and mapping populations for sweet potato developed to enable trait/gene identification*

- Commissioned: G4008.09
- StraP
- 2008–2010
- LI/PI: CIP/R Schafleitner

In order to develop genomic and genetic resources in under-resourced sweet potato, cDNA libraries, ESTs, EST-based markers and DArT arrays are being developed. In addition, a virus-free diploid mapping population is being generated *in vitro*. Developing a medium-density reference map based on these resources will be very useful for enabling trait mapping in the crop. Because sweet potato is not a GCP target crop (reflecting the EPMR recommendations), only limited funds have been allocated to this work. It is expected that the

Output target for 2010 as presented in the 2009–2011 MTP will be completed on schedule.

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

*Output 9: Genomic resources and mapping populations developed and assembled for pearl millet to enable trait/gene identification*

- Commissioned: G4008.07
- StraP
- 2008–2010
- LI/PI: ICRISAT/T Hash

To enrich the genomic resources in pearl millet, a large number of ESTs are being developed for developing and integrating gene-based markers into existing pearl millet genetic maps. This will enable the pearl millet community to identify markers for terminal drought tolerance and grain and stover yield potential in Africa and Asia. Because pearl millet is not a GCP target crop (reflecting the EPMR recommendations), again, only limited funds have been allocated to this work. The Output target for 2010 as presented in the 2009–2011 MTP is still scheduled to be completed on time.

*Partners:* ICRISAT, AICPMIP, CAZRI, RAU, ILRI

*Output 10: Genomic resources (ESTs, markers and maps) developed for pigeonpea to enable trait/gene identification*

- Commissioned: G4008.47
- StraP
- 2008–2010
- LI/PI: NCGR/G May
- Linked to P4-O12

In order to establish linkage between the TLI and TLII projects, development of genomic resources has been planned in pigeonpea since it is an important target crop in TLII. Next generation sequencing technologies and a high-throughput SNP genotyping platform are being established, in addition to SSR markers, to develop a linkage map of pigeonpea to enable trait mapping. As per progress made so far under this Output, the 2010 Output target as presented in the previous MTP should be completed on schedule.

*Partners:* NCGR, NRCPB, ICRISAT, PDKV

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

*Output 11: Causal relationship between whole-genome expression patterns and stress tolerance determined in rice via analysis of near-isogenic lines*

- Commissioned: G4008.08
- StraP
- 2008–2010
- LI/PI: NIAS/S Kikuchi

In continuation of earlier work, this Output plans to develop and characterise NILs for drought tolerance. Use of a high-density microarray with the field-grown NILs will determine expression patterns for genes involved in drought tolerance. Subsequently, candidate chromosomal regions with expression signatures will be aligned with drought QTLs. Because additional research activities were commissioned in 2008 within this Output, based on results from previous research and taking into account the feasibility of achieving objectives, Output targets were adjusted accordingly in the last MTP (2009–2011). It is anticipated that the 2010 Output target as presented in the previous MTP will be completed on time.

*Partners:* IRRI

*Output 12: Discovery and development of alleles contributing to sorghum drought tolerance*

- Competitive: G3008.05
- StraP
- 2008–2011
- LI/PI: University of Georgia/A Paterson
- Linked to P1-O7 and P4-O10

This Output deals with exploitation of the stay-green QTLs in applied sorghum improvement. The Output plans to generate all pairwise combinations of QTL introgression heterozygotes, as well as the double heterozygotes, to measure their epistatic interactions. Furthermore, high-throughput genome sequencing (Solexa 1GB) of 10 genotypes involved in target populations (MAGIC, RIL and stay-green NILs) will provide the large number of SNPs for application of high-throughput genotyping approaches to MAGIC populations that will be key to both discovery research and product development. The start-date of this three-year project was presented inaccurately in the previous MTP, an error which has been corrected in this MTP. The project began mid-2008, and is expected to end mid-2011.

*Partners:* ICRISAT, SARI, MAU, NRCS, ARC

*Output 13: Examining natural variation in the transcriptional regulation of drought responses in wheat*

- Commissioned: G7009.01
- CI6
- 2009–2011
- LI/ PI: ACPFG/P Langridge

Within this Output, candidate genes/transcription factors that are known to increase drought tolerance when showing modified expression will be identified. Subsequently, new alleles will be identified at each of the candidate genes that show expression levels correlated to drought tolerance. Efforts will be made to introgress the new alleles into cultivated germplasm to develop drought-tolerant wheat varieties in Asia and Africa.

*Partners:* ACPFG, ICS–CAAS, CIMMYT

*Output 14: Cloning characterisation and validation of aluminum tolerance gene(s) in rice*

- Commissioned: Project No. TBD
- CI7
- 2010–2013
- LI/PI: Cornell University and USDA–ARS/S McCouch and L Kochian

This new Output has been added in the context of GCP's new Challenge Initiative on Comparative genomics to improve cereal yields in high-aluminium and low-phosphorous soils (CI7). This Output will be utilising information on cloned sorghum Al tolerance genes to identify rice homologues that are candidate tolerance genes. Computational analysis of the MATE family in rice has identified 5 MATE genes that are co-localised with a previously identified Al tolerance QTL. Consequently, these candidate Al tolerance genes will be tested using T-DNA rice knockout lines. If these homologues are not functional in rice, complementary approaches will be undertaken. Eventually, the Output aims to fine-scale mapping and clone a novel major rice Al tolerance QTL, and also develop diagnostic markers to implement in rice breeding.

*Partners:* IRRI, ICABIOGRAD

*Output 15: Cloning characterisation and validation of aluminum tolerance gene(s) in maize*

- Commissioned: Project No. TBD
- CI7
- 2010–2013
- LI/PI: EMBRAPA/C Guimaraes
- Linked to P1-O7

In this new Output, efforts will be made, based on information on cloned sorghum Al tolerance genes, to identify candidate Al tolerance genes in maize. The Output deals with QTL and Expressed QTL mapping for Al-tolerance candidate genes and their validation, as well as the development of gene/allele-specific markers for aluminum tolerance for use in breeding programme in Africa and Brazil.

*Partners:* USDA–ARS, Cornell University, MU, KARI

*Output 16: Cloning, characterisation and validation of P-efficiency gene(s) in sorghum*

- Commissioned: Project No. TBD
- CI7
- 2010–2013
- LI/PI: EMBRAPA/J Magalhaes
- Linked to P3-O13

This new Output will use the genomic information available on *Pup1* locus in rice and complete sequence of the sorghum genome to establish a framework based on comparative genomics to identify sorghum *Pup1* homologues and validate their role as *bona fide* P-efficiency genes. This Output will be

using both association genetics as well as linkage mapping approaches to identify and validate P-efficiency genes that will eventually be deployed in molecular breeding programmes targeting marginal soil areas in Niger and Kenya.

*Partners:* USDA-ARS, CU, INRAN, MU, KARI

*Output 17: Cloning, characterisation and validation of P-efficiency gene(s) in maize*

- Commissioned: Project No. TBD
- CI7
- 2010–2013
- LI/PI: USDA-ARS/CU/L Kochian

This new Output aims to identify, characterise and validate gene(s) associated with maize P-efficiency. Bioinformatics will be used to identify homologues of the rice *Pup1* gene in maize, and both association genetics and linkage mapping approaches will be used to identify QTLs and clone the gene(s) for P-efficiency. Subsequently, EMBRAPA's elite inbred lines panel and the maize association panel will be used to validate candidate genes and identify diagnostic markers for P-efficiency in maize.

*Partners:* EMBRAPA, IRRI, MU, KARI

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

*Output 18: Drought from a different perspective: Improved tolerance through phosphorus acquisition*

- Competitive: G3008.04
- StraP
- 2008–2011
- LI/PI: IRRI/S Heuer
- Linked to P3-O14

This output is based on an earlier output where the team demonstrated that maintenance of higher root growth rates of rice lines carrying P uptake QTL (*Pup1*) under P-deficiency and *Pup1* locus was considered a prime target in improving P-deficiency and drought tolerance in rice. This output plans to identify the gene(s) and understand the underlying physiological mechanisms; development of allele-specific markers for MAS and the development of the QTL pyramided lines will take place. The start-date of this three-year project was presented inaccurately in the previous MTP, an error which has been corrected in this MTP. The project began mid-2008, and is expected to end mid-2011.

*Partners:* UoPd/MPIMPP, JIRCAS, ICABIOGRAD, ZU

*Output 19: Delayed senescence and drought tolerance in rice*

- Competitive: G3008.03
- StraP
- 2008–2011
- LI/PI: UoC-Davis/ E Blumwald

This Output is based on the hypothesis (proved in tobacco) that drought-induced plant senescence is due to a type of cell death programme naturally activated during drought. Based on the success of over expression of the IPT gene (mediating the synthesis of cytokinins) under the control of SARK promoter in tobacco, the team plans to test the efficacy of stress-induced cytokinin synthesis in conferring drought tolerance in upland and lowland rice varieties. If successful, the researchers will identify genes with significant roles in conferring drought tolerance in rice and generate drought tolerant and water-use-efficient rice plants in different genetic backgrounds. The start-date of this three-year project was presented inaccurately in the previous MTP, an error which has been corrected in this MTP. The project began mid-2008, and is expected to end mid-2011.

*Partner:* IRRI

*Output 20: Validation of QTLs associated with drought tolerance traits in chickpea*

- Commissioned: G7009.02
- CI2
- 2009–2011
- LI/PI: ICRISAT/PM Gaur

Identification and validation of QTLs for drought traits eg. root traits, d13C and harvest index have been planned within this output. Candidate drought QTLs will eventually be used for marker-assisted breeding for drought tolerance so that improved chickpea cultivars with drought tolerance can be developed for Africa and Asia. The end-date of this project was presented as 2010 in the previous MTP as at the time of writing last year, this project was intended as a 2-year project. However, following on from the subsequent inclusion of some additional partners, this project's duration was amended to 3 years and therefore the end-date has now been amended to 2011 in this MTP, with the Output targets having been adjusted accordingly.

*Partners:* DZARC, UAS-Bangalore, RARS-Nandyal, ARS-Durgapura, RAKCA-Sehore

*Output 21: Development and evaluation of drought-adapted sorghum germplasm for Africa and Australia*

- Commissioned: G7009.04
- CI5
- 2009–2012
- LI/PI: DPI&F/D Jordan and A Borrell

This Output plans to evaluate the stay-green drought resistance mechanism in plant architectures and genetic backgrounds appropriate to Mali. The Output aims to develop sorghum germplasm populations enriched for stay-green genes that also carry genes for adaptation to cropping environments in Mali. In parallel, training activities will be carried out for African sorghum researchers in drought

physiology and selection for drought adaptation in sorghum. Due to uncertainty of NARS partners, this project suffered a delayed start, and is now expected to end in 2012. The Output title has also been adjusted in this current MTP.

*Partners:* IER, Agropolis–CIRAD

*Output 22: Development of drought-tolerant sorghum for Africa by a Backcross-Nam approach genotyping component*

- Commissioned: Project No. TBD
- CI5
- 2010–2013
- LI/PI: UGA/Cornell University/A Paterson/S Kresovich, respectively
- Linked to P1-O11 and P5-O4

This new Output, to be initiated in 2010 under GCP's new Challenge Initiative on sorghum, represents the genotyping component of an integrated programme for the development of improved germplasm that balances local agronomic and grain quality preferences with the incorporation of well characterised drought adaptations and exploration for cryptic valuable alleles. This Output plans to develop 180 BC<sub>1</sub>F<sub>4</sub> populations, carry out phenotyping of key measures of productivity, assess response to water limitation, develop an economical universal genotyping platform and address its application to genotype 100 segregants per population (18,000 total). The development and application of supporting analytical tools will also be undertaken.

*Partners:* ICRISAT, Agropolis–CIRAD and others (TBD)

### International public goods

The overall research portfolio of this Subprogramme focuses on drought-tolerance traits as well as genes and agronomic characters that improve crop resilience in difficult environments (eg, P-deficiency, Al-toxicity in soil, etc.). The Outputs are primarily resources, knowledge and technologies that are international public goods consistent with the goals of the CGIAR System Priorities 2a and 2b. The key resources and tools produced are specialised genetic stocks (eg, mutants and advanced backcross lines), gene expression data, cloned genes for specific trait improvement (tolerance to drought and soil problems) and desirable gene combinations in elite genetic backgrounds (prebreeding materials).

### Elaboration of partner roles

Subprogramme 2 is working with a wide range of partner on 22 Outputs. As the SP2 activities deal with the development of genomic tools and technologies and the evaluation of multidisciplinary approaches to better understand gene

function and interaction, all with the aim of increasing knowledge of gene systems across crops, ARIs play a very important role. However, the SP also makes its best effort to ensure the active participation of CG centres and developing country institutes.

Theme 1 of this SP deals with the assembly and development of genetic and genomic resources. In this area, SP2 is working with several ARIs, such as UoC–Davis, UoC–Riverside, UGA, UoF and RIKEN; CG centres, including ICRISAT, CIAT, IITA, developing country institutes such as EMBRAPA, IIPR, EIAR, LZARDI, ECABREN, SABRN, Egerton Uni, ISRA and private company/service provider DARt Pty Ltd. Together, these partners are working to develop genomic resources in legumes, with VBI and IRRI for utilising the rice mutant resources.

For the development of genome infrastructure in less studied species such as cassava, pearl millet, pigeonpea and sweet potato under theme 2, mapping populations are being developed at CG centres ICRISAT, CIP and IITA; genomic resources are being developed by ARIs/private companies such as UoC–Davis, UGA, UoM, NCGR and DARt Pty Ltd together with the above-mentioned CG Centres and NARS partners such as UoW, NAARI, NRCPB, PDKV, etc.

Under theme 3, the SP is working with ARIs like NIAS, ACPFG and UGA in collaboration with CG centres (IRRI, CIMMYT and ICRISAT) and partners in developing countries such as ICS–CAAS, SARI, NRCS and ARC. Similarly, ARIs (ie, Cornell University and USDA–ARS) are leading the projects on cloning of Al-tolerance and P-efficiency genes in cereal species in close collaboration with CG centre IRRI and developing country partners such as EMBRAPA, Moi University, ICABIOGRAD, INRAN and more.

Theme 4, which deals with the validation of candidate genes/QTLs, is mainly driven by CG Centres such as IRRI and ICRISAT together with NARS partners such as DZARC, UAS–Bangalore, ICABIOGRAAD and Zhejiang University in collaboration with ARIs such as the University of Potsdam, JIRCAS and Agropolis–CIRAD.

## Project 2 logframe – SP2: Genomics towards gene discovery

Notes:

1. Each Output is followed by:
  - a) the type of research activity/funding contributing to the Output (commissioned, competitive, focus, or discretionary) and GCP project number
  - b) Identification of Output as a StraP (Strategic project) or CI (Challenge Initiative) project
  - c) start and end year, and
  - d) the lead institute (LI) and Principal Investigator(s) (PI[s]) responsible for the Output (and its Output targets).
2. Some Outputs are managed internally within GCP, in some cases involving coordination of a number of external institutes. In most such cases, the entry under 'PI' is denoted as 'Various'.

Output	title, type and target(s)	Intended users	Outcome	Impact
<b>Theme 1: Assembly of genomics and germplasm resources through consolidating and developing specialised genetic stocks</b>				
<b>Output 1</b>	<b>Bean genetic and genomic resources developed</b> <ul style="list-style-type: none"> <li>• Focus: G6007.03</li> <li>• StraP</li> <li>• 2007–2010 (Phase II: 2010–2013)</li> <li>• LI/PI: CIAT/M Blair</li> <li>• Linked to P1-06</li> </ul>	Bean breeders in Africa and South America; legume genetics/genomics community worldwide	New markers for drought tolerance deployed to the bean research and breeding communities	Improved efficiency in developing adaptive bean varieties for the resource-poor
<i>Target 2010: Materials</i>	200 new SSR, COS or SNP markers developed or mapped from EST, BAC and cross-legume sequences			
<i>Target 2011: Materials</i>	At least five new markers developed for selection of BCMV and/or bruchid resistance			
<i>Target 2012: Materials</i>	Molecular markers for BCMV, bruchid resistance and drought tolerance validated			
<b>Output 2</b>	<b>Chickpea genetic and genomic resources developed</b> <ul style="list-style-type: none"> <li>• Focus: G6007.04</li> <li>• StraP</li> <li>• 2007–2011 (Phase II: 2010–2013)</li> <li>• LI/PI: ICRISAT/R Varshney</li> <li>• Commissioned: Project No. TBD</li> <li>• CI2</li> <li>• 2009–2010</li> <li>• LI/PI: UoC-Davis/D Cook</li> <li>• Linked to P1-06, P1-09, P3-04, P4-09 and P4-012</li> </ul>	Chickpea breeders in Asia and Africa; legume genetics/genomics community worldwide	New markers for drought tolerance are used in the chickpea research and breeding communities	Improved efficiency in developing adaptive chickpea varieties for the resource-poor
<i>Target 2010: Materials</i>	At least 500 SNPs assembled and a reference map with at least 1,000 marker loci developed			
<i>Target 2011: Materials</i>	At least five molecular markers associated with drought-related component traits identified			
<i>Target 2012: Materials</i>	Molecular markers for drought tolerance and <i>Helicoverpa</i> resistance validated			
<b>Output 3</b>	<b>Cowpea genetic and genomic resources developed</b> <ul style="list-style-type: none"> <li>• Focus: Project: G6007.02</li> <li>• StraP</li> <li>• 2007–2011 (Phase II: 2010–2013)</li> <li>• LI/PI: UoC-Riverside/J Ehlers</li> <li>• Commissioned: Project No. TBD</li> <li>• CI3</li> <li>• 2009–2010</li> <li>• LI/PI: UoC-Riverside/J Ehlers</li> <li>• Linked to P1-06</li> </ul>	Cowpea breeders in Africa; legume genetics/genomics community worldwide	Users have access to permanent genomic resources (including ESTs), a physical map, a source of SNPs, gene knowledge, the foundation of a high-density SNP map and a high-throughput marker system	Improved efficiency in developing adaptive cowpea varieties
<i>Target 2010: Materials</i>	At least 10,000 BAC end sequences and BAC contigs placed onto the genetic map; 1,000 SNP markers on map; SNP genotyping platform validated			

Output	title, type and target(s)	Intended users	Outcome	Impact
Target 2011: Materials	Consensus map with at least 2000 SNP markers developed based on 10 RIL population; ATL/genes for Aphid resistance and drought tolerance identified			
Target 2012: Materials	Molecular markers for drought tolerance and <i>Helicoverpa</i> resistance validated			
<b>Output 4</b>	<b>Groundnut genetic and genomic resources developed</b> <ul style="list-style-type: none"> <li>• Focus: G6007.01</li> <li>• StraP</li> <li>• 2007–2011 (Phase II: 2010–2013)</li> <li>• LI/PI : ICRISAT/V Vadez</li> <li>• Commissioned: G4008.06</li> <li>• StraP</li> <li>• 2008–2010</li> <li>• LI/PI :UGA/S Knapp</li> <li>• Linked to P1-06 and P4-012</li> </ul>	Groundnut breeders in Africa, Asia and South America; legume genetics/genomics community worldwide	New markers being used by the groundnut research and breeding communities	Improved efficiency in developing adaptive groundnut varieties for the resource-poor
Target 2010: Materials	Genomic resources (ESTs, SNPs) and one linked physical and genetic map developed for AA diploid genome			
Target 2011: Materials	QTLs for rust, rosette, leaf spots, and drought-related traits identified			
Target 2012: Materials	Molecular markers associated with rust, rosette, leaf spots, and drought-related traits identified			
<b>Output 5</b>	<b>Validation of drought-response/resistance pathways genes by phenotypic analysis of mutants</b> <ul style="list-style-type: none"> <li>• Commissioned: G4007.02</li> <li>• StraP</li> <li>• 2007–2010</li> <li>• LI/PI: VBI, Virginia Polytechnic Institute and State University/A Pereira</li> </ul>	Cereal crop genetics/genomics and breeding community worldwide	Existing mutant resources leveraged to generate supporting evidence for selecting high-confidence candidate genes for cross-species comparative studies	High-confidence drought responsive candidate genes used in cereal genetics and breeding
Target 2010: Materials	Drought resistant/sensitive phenotypes identified for 100 candidate gene mutants in rice/ <i>Arabidopsis</i> at vegetative and reproductive stages of drought stress			
<b>Theme 2: Development of comparative maps within and across species and framework genetic markers for target crops</b>				
<b>Output 6</b>	<b>Cross-species resources developed for comparative biology in tropical crop legumes</b> <ul style="list-style-type: none"> <li>• Focus: G6007.05</li> <li>• StraP</li> <li>• 2007–2010</li> <li>• LI/PI:UoC–Davis/DCook</li> <li>• Commissioned: TBD</li> <li>• StraP</li> <li>• 2009–2010</li> <li>• LI/PI :UoC–Davis/D Cook</li> <li>• Linked to P4-08</li> </ul>	Legume genomics/genetics and breeding community worldwide	Knowledge of genomic information and agronomic traits across legume species leveraged, leading to increased use of molecular-genetic markers for legume improvement	General principles established for genomics-enabled breeding in tropical legumes; development of improved legume varieties based on MAS
Target 2010: Materials	Integration of at least 300 orthologous markers into genetic maps for four legume crops (beans, cowpeas, chickpeas and groundnuts)			
<b>Output 7</b>	<b>Genetic and physical mapping resources produced for drought breeding in cassava</b> <ul style="list-style-type: none"> <li>• Competitive: G3007.03</li> <li>• StraP</li> <li>• 2008–2010</li> <li>• LI/PI: University of Maryland/P Rabinowicz</li> </ul>	Cassava genomics/genetics and breeding community worldwide	Expanded cassava genomic resources offering opportunities for improvement of multiple traits in cassava	Cassava cultivars improved for multiple traits through molecular breeding

Output	title, type and target(s)	Intended users	Outcome	Impact
<i>Target 2010: Materials</i>	1,000 SNP markers identified on a genome-wide scale; a genetic linkage map with 500 SNP markers constructed and SNP markers associated with at least five selected QTLs for drought tolerance identified			
<b>Output 8</b>	<b>Genomic resources and mapping populations for sweet potato developed to enable trait/gene identification</b> <ul style="list-style-type: none"> <li>• Commissioned: G4008.09</li> <li>• StraP</li> <li>• 2008–2010</li> <li>• LI/PI: CIP/R Schafleitner</li> </ul>	Sweet potato genomics/genetics and breeding community worldwide	Increased knowledge-base in under-resourced crops, opening up opportunities for genetic manipulation of various traits eg, drought tolerance and improving the crop	Improved sweet potato cultivars developed with enhanced drought tolerance
<i>Target 2010: Materials</i>	Sequence resource and DArT arrays developed and a medium-density reference map created			
<b>Output 9</b>	<b>Genomic resources and mapping populations developed and assembled for pearl millet to enable trait/gene identification</b> <ul style="list-style-type: none"> <li>• Commissioned: G4008.07</li> <li>• StraP</li> <li>• 2008–2010</li> <li>• LI/PI: ICRISAT/T Hash</li> </ul>	Pearl millet genetics and breeding community and general cereal genetics/genomics community worldwide	Increased knowledge-base available to users on under-resourced crops, opening up opportunities for genetic manipulation of various traits eg, drought tolerance and improving the crop	Improved pearl millet cultivars with enhanced drought tolerance developed
<i>Target 2010: Materials</i>	Linkage map with at least 150 new markers developed and putative QTLs for terminal drought tolerance and grain and stover yield potential identified			
<b>Output 10</b>	<b>Genomic resources (ESTs, markers and maps) developed for pigeonpea to enable trait/gene identification</b> <ul style="list-style-type: none"> <li>• Commissioned: G4008.47</li> <li>• StraP</li> <li>• 2008–2010</li> <li>• LI/PI: NCGR/G May</li> <li>• Linked to P4-012</li> </ul>	Pigeonpea genetics and breeding community; general legume genetics/genomics community worldwide	Increased knowledge-base in under-resourced crops, opening up opportunities for genetic manipulation of various traits eg, drought tolerance and improving the crop	Improved pigeonpea cultivars developed using molecular breeding strategies
<i>Target 2010: Materials</i>	At least 1000 genic SNPs identified and linkage map of pigeonpea with at least 200 markers generated			
<b>Theme 3: Assignment of genes and pathways to phenotypes through the convergence evidence of genome variation, expression patterns and phenotypic data</b>				
<b>Output 11</b>	<b>Causal relationship between whole-genome expression patterns and stress tolerance determined in rice via analysis of near-isogenic lines</b> <ul style="list-style-type: none"> <li>• Commissioned: G4008.08</li> <li>• StraP</li> <li>• 2008–2010</li> <li>• LI/PI : NIAS/S Kikuchi</li> </ul>	Rice genomics/genetics and breeding community worldwide	Gene expression polymorphisms serve to bridge the genotype-phenotype gap; providing users with a generalised method to assign gene functions to phenotypes in crop studies to improve drought tolerance in the crop	Increased knowledge about drought tolerance at gene level will aid rice improvement for drought tolerance
<i>Target 2010: Materials</i>	At least 10 regions of chromosomes with expression signatures identified in the genomes of two drought tolerant NILs; 10 candidate genes made available with supporting evidence from expression pattern and QTL alignment			
<b>Output 12</b>	<b>Discovery and development of alleles contributing to sorghum drought tolerance</b> <ul style="list-style-type: none"> <li>• Competitive: G3008.05</li> <li>• StraP</li> <li>• 2008–2011</li> <li>• LI/PI: UoG/A Paterson</li> <li>• Linked to P1-07 and P4-010</li> </ul>	Sorghum genomics/genetics and breeding community worldwide	Large set of SNPs for high-throughput genotyping, and improved germplasm that combines enhanced drought tolerance with additional traits required for local adaptation in Western and Central Africa, Eastern and Southern Africa and South Asia	Enhanced genomic resources and genetic knowledge about drought tolerance at allele level will aid sorghum improvement for drought tolerance



Output	title, type and target(s)	Intended users	Outcome	Impact
Target 2010: Materials	Sequencing of 10 parental genotypes of different populations completed using Solexa 1G sequencing; a large set of SNPs identified, with the intention of being useful for deterministic breeding in MAGIC populations as well as developing high-throughput genotyping platform in sorghum			
Target 2011: Materials	Genetic maps of two RIL populations segregating for stay-green as well as host plant resistance to Striga and charcoal rot saturated with more molecular markers and identification of allele-specific markers			
<b>Output 13</b>	<b>Examining natural variation in the transcriptional regulation of drought responses in wheat</b> <ul style="list-style-type: none"> <li>Commissioned: G7009.01</li> <li>CI6</li> <li>2009–2011</li> <li>LI/PI: ACPFG/P Langridge</li> </ul>	Wheat genomics/genetics and breeding community worldwide	Regulatory proteins isolated and evaluated to screen for natural variation in expression of regulatory genes shown to moderate the drought tolerance response in wheat	Increased knowledge about genomics for aiding wheat improvement through molecular breeding
Target 2010: Materials	Isolation of at least five genes that are known to increase drought tolerance when showing modified expression			
Target 2011: Materials	Two new alleles identified at each of the five target genes that show expression levels correlated to drought tolerance; diagnostic markers developed for each of the new alleles			
<b>Output 14</b>	<b>Cloning characterisation and validation of aluminum tolerance gene(s) in rice</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>CI7</li> <li>2010–2013</li> <li>LI/PI: Cornell University and USDA–ARS/S McCouch and L Kochian</li> </ul>	Rice genomics/genetics and breeding communities worldwide	Cloned, characterised and validated aluminium tolerance gene(s) in rice to deploy in breeding	Diagnostic markers and increased knowledge about tolerance for aluminium in rice
Target 2010: Materials	Five mutants with knockouts in the major putative <i>Alt<sub>sb</sub></i> homologues with information on tolerance level identified			
Target 2011: Materials	5 top candidate genes validated through complementation in respective knockout mutants, and, if successful, a major rice Al tolerance gene identified; a population of ~4000 RILs made available for fine mapping			
Target 2012: Materials	Recombinants in the QTL region identified and target QTL fine-mapped; NILs available for additional cycles of fine-mapping if needed			
<b>Output 15</b>	<b>Cloning characterisation and validation of aluminum tolerance gene(s) in maize</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>CI7</li> <li>2010–2013</li> <li>LI/PI: EMBRAPA/C Guimaraes</li> <li>Linked to P1-07</li> </ul>	Maize genomics/genetics and breeding communities worldwide	Cloned, characterised and validated aluminium tolerance gene(s) in maize to deploy in breeding	Diagnostic marker and increased knowledge about aluminium tolerance in maize
Target 2010: Materials	Sequence annotation in the maize QTL region containing putative <i>Alt<sub>38</sub></i> homologues improved and SNPs identified in the candidate sequences			
Target 2011: Materials	SNPs significantly associated with aluminum tolerance identified and cis/trans regulatory factors affecting ZmMATE1 expression profile analysed			
Target 2012: Materials	120 RILs characterised for organic acid exudation and for aluminum content in root tips; candidate genes expressed QTLs and QTLs mapped			

Output	title, type and target(s)	Intended users	Outcome	Impact
<b>Output 16</b>	<b>Cloning, characterisation and validation of P-efficiency gene(s) in sorghum</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>CI7</li> <li>2010–2013</li> <li>LI/PI: EMBRAPA/J Magalhaes</li> <li>Linked to P3-013</li> </ul>	Sorghum genomics/ genetics and breeding communities worldwide	Cloned, characterised and validated P-efficiency gene(s) in sorghum deployed in breeding	Diagnostic markers made available and increased knowledge about P-efficiency in sorghum
<i>Target 2010: Materials</i>	Homologues in sorghum <i>Pup1</i> identified			
<i>Target 2011: Materials</i>	SNPs within candidate genes for <i>Pup1</i> reported; 200 lines characterised for P-acquisition (30-45 days)			
<i>Target 2012: Materials</i>	200 lines characterised for P acquisition (maturity) and for grain yield and grain P content; one or more candidate genes for <i>Pup1</i> tested			
<b>Output 17</b>	<b>Cloning, characterisation and validation of P-efficiency gene(s) in maize</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>CI7</li> <li>2010–2013</li> <li>LI/PI: USDA–ARS/Cornell University/L Kochian</li> </ul>	Maize genomics/ genetics and breeding communities worldwide	Validated QTLs for drought tolerance available to users for introgressing into drought-sensitive lines for chickpea improvement	Diagnostic markers and increased knowledge about P-efficiency in maize
<i>Target 2010: Materials</i>	Maize elite panel defined for field evaluation; at least 100 maize lines characterised for P-efficiency traits in the field and <i>Pup-1</i> homologues identified in maize			
<i>Target 2011: Materials</i>	SNPs identified within the candidate genes; 120 maize elite topcrosses characterised for P-efficiency and genetic map constructed for tropical maize cross contrasting for P-efficiency (L3 x L22)			
<i>Target 2012: Materials</i>	Markers for <i>Pup1</i> candidate genes developed and genetics and gene action of maize root morphology traits determined			
<b>Theme 4: Validation of genes and pathways through evaluation of under- or over-expression constructs or variants (induced or natural) of the target genes</b>				
<b>Output 18</b>	<b>Drought from a different perspective: Improved tolerance through phosphorus acquisition</b> <ul style="list-style-type: none"> <li>Competitive: G3008.04</li> <li>StraP</li> <li>2008–2011</li> <li>LI/PI: IRRI/S Heuer</li> <li>Linked to P3-014</li> </ul>	Rice genomics, breeding and genetics communities worldwide; crop physiologists and agronomists in general	Function of <i>Pup1</i> candidate genes understood and novel regulatory genes for tolerance to P-deficiency and drought identified and validated; rice breeding lines developed by MAS with pyramided QTLs for drought and P-deficiency tolerance	Increased knowledge about cross-talking between P-deficiency and drought stress at molecular and physiological/ phenological level; development of pyramided QTL lines will help rice improvement for drought tolerance and P-deficiency
<i>Target 2010: Materials</i>	<i>Pup1</i> haplotypes determined in IRRI breeding lines and GCP representative set; root growth parameters and characteristics of <i>Pup1</i> NILs evaluated under combined P stress and drought stress			
<i>Target 2011: Materials</i>	Transcription factor (TF) differentially expressed under P-deficiency and drought stress in contrasting <i>Pup1</i> NILs identified and validated; nutrient x water interaction established; and at least two F3 pyramiding populations developed by MAS and screened under P-deficiency and drought stress			
<i>Target 2011: Materials</i>	Introgression of stay-green QTLs initiated on sorghum in Africa			

Output	title, type and target(s)	Intended users	Outcome	Impact
<b>Output 19</b>	<b>Delayed senescence and drought tolerance in rice</b> <ul style="list-style-type: none"> <li>Competitive: G3008.03</li> <li>StratP</li> <li>2008–2011</li> <li>LI/PI: UoC–Davis/ E Blumwald</li> </ul>	Rice genomics, breeding and genetics community worldwide; crop physiologists in general	Function of pSARK-IPT gene tested in rice for drought tolerance and additional determinant key genes identified for identification of knock-out mutant lines	Testing of pSARK-IPT gene in rice for drought tolerance and subsequently identification of key determinant genes and their knock-out mutant lines will help breeding of commercial rice varieties for drought tolerance
<i>Target 2010: Materials</i>	At least 10 lines (showing overexpression) phenotyped under green house and field conditions for drought and at least 5 lines selected and used for microarray analysis to identify the key genes playing significant roles during the adaptation to drought			
<i>Target 2011: Materials</i>	Ten determinant candidate genes selected and lines for upland as well as lowland rice generated for overexpression of the selected determinant genes; knock-out mutants for determinant genes identified and tested in field conditions			
<b>Output 20</b>	<b>Validation of QTLs associated with drought tolerance traits in chickpea</b> <ul style="list-style-type: none"> <li>Commissioned: G7009.02</li> <li>CI2</li> <li>2009–2011</li> <li>LI/PI: ICRISAT/PM Gaur</li> </ul>	Chickpea breeding and genetics communities in Asia	Validated QTLs for drought tolerance made available to users for introgressing into drought-sensitive lines for chickpea improvement	Chickpea with improved drought tolerance made available in Asia and Africa
<i>Target 2010: Materials</i>	At least 3 QTLs for drought-related traits identified			
<i>Target 2011: Materials</i>	At least two QTLs for drought traits validated in different genetic backgrounds			
<b>Output 21</b>	<b>Development and evaluation of drought-adapted sorghum germplasm for Africa and Australia</b> <ul style="list-style-type: none"> <li>Commissioned: G7009.04</li> <li>CI5</li> <li>2009–2012</li> <li>LI/PI: DPI&amp;F/ D Jordan/A Borrell</li> </ul>	Sorghum breeders in Africa and sorghum genetics communities worldwide	Stay-green QTLs available to users for introgression into African sorghum lines for enhanced drought tolerance	Sorghum lines with drought tolerance made available in Africa; African breeders trained
<i>Target 2010: Materials</i>	Stay-green QTL donor (Australian) and recipient African lines identified and crosses initiated			
<i>Target 2011: Materials</i>	Increased understanding of the association between plant height and stay-green, generating knowledge critical for the adoption of stay-green in Africa; introgression of stay green QTLs initiated on sorghum in Africa			
<i>Target 2012: Capacity</i>	Two African Scientists trained in Australia in sorghum crop improvement			
<b>Output 22</b>	<b>Development of drought-tolerant sorghum for Africa by a Backcross-Nam approach genotyping component</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>CI5</li> <li>2010–2013</li> <li>LI/PI: UGA/Cornell University/A Paterson/S Kresovich, respectively</li> <li>Linked to P1-011 and P5-04</li> </ul>	Sorghum genomics/ genetics and breeding communities worldwide	Drought tolerant sorghum germplasm for breeding	Improved sorghum germplasm for drought tolerance
<i>Target 2010: Materials</i>	Stay-green QTL donor (Australian) and recipient African lines identified and crosses initiated			
<i>Target 2011: Materials</i>	Increased understanding of the association between plant height and stay-green, generating knowledge critical for the adoption of stay-green in Africa; introgression of stay green QTLs initiated on sorghum in Africa			
<i>Target 2012: Materials</i>	Economical universal genotyping platform developed and applied to genotype segregants per population			



# Project 3 – SP3: Trait capture for crop improvement

## Project narrative

### Project overview and rationale

SP3 aims to create product-driven teams that 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 and bioinformatics to accelerate genetic progress in simple traits such as resistance to biotic stresses. More importantly, though, 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. Firstly, it seeks to validate candidate genes and markers in target environments and adapted germplasm. Secondly, it aims to develop better means of optimising MAB, such as decision-support tools and protocols, and MAB simulation models and software. Its MAB projects span from introgression of a few target genes to marker-assisted recurrent selection that stack favourable alleles at multiple genomic regions. SP3's third objective is to expand and support phenotyping. Drought tolerance phenotyping remains difficult because of limited capacity, inadequate protocols and problems in the design of controlled stress experiments. Consequently, particular attention is being given to establishing high-quality phenotyping networks, as well as defining robust protocols.

SP3 activities are aligned with GCP's renewed strategy and refocused research priorities, with active collaboration with other Subprogrammes. With SP5, SP3 has played a major role in developing communities of practices, helping to reinvigorate and also stimulate collaboration and exchange of germplasm, information and skills. Collaborative activities also include evaluating reference sets with SP1, identifying and validating genes and markers with SP2, and developing decision-support tools with SP4.

### Impact pathways

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

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

### *Theme 1: Characterisation of segregating populations and identification of genomic regions for plant breeding* *Output 1 and Output 2*

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

Output 1. (*Tailoring superior alleles for abiotic stress genes for deployment into breeding programmes: association analysis of  $Alt_{SB}$ , a major aluminium tolerance gene in sorghum*) is very representative of Theme 1. The PI of this project and his team have been able to identify an apparently improved version of  $Alt_{SB}$  in the framework of an SP2 Competitive project. Through the present project, they are now applying association mapping to undertake a comprehensive scan for even better versions of this gene for deployment to sorghum breeding programmes. Using cutting-edge genomics and statistical genetics approaches, this research is really bridging the gap between basic research on Al tolerance and applied breeding

programmes to develop efficient and effective tools that plant breeders can use to improve acid soil tolerance. To ensure continuity in the delivery chain and application in breeding, this project is linked with a commissioned project in Theme 3 (Output 13. *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)*). This Output is led by a sorghum breeder with the objective of validating  $Alt_{SB}$  alleles in West Africa (Niger and Mali) by transferring the gene into local backgrounds for cultivation in local acid soil conditions. Clearly, this example, with a gene discovery phase in SP2, a refinement phase in SP3's Theme 1, and a validation/application phase in SP3's Theme 3, is a typical example of GCP's impact pathway from upstream research to application in breeding.

The number of Outputs under this Theme has decreased under the present MTP because of the greater shift to marker applications closer to breeding under Phase II of GCP. This was made possible by the large number of SP2 and SP3 Theme 1 projects that have led to successful applications.

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

***Output 3 to Output 10***

In addition to the discovery of novel markers and the development of pre-breeding germplasm, there is also a need to develop and/or test new methodologies and tools to improve the efficiency of molecular breeding. This is the objective of activities under Theme 2. The new methodologies essentially cover two areas: the refinement and modelling of marker-assisted breeding strategies and the development of innovative phenotyping protocols.

As an output of the research conducted in SP3 and SP4 to improve the development of molecular breeding systems, MAB simulation models and corresponding software are now being developed. Output 3 (*Breeding for drought tolerance with known gene information*) is a great example of this approach. It helps optimise applied efforts to introgress and pyramid previously identified QTLs into adapted germplasm (such as Output 11 *Integrating marker-assisted selection into the conventional breeding procedure for improvement of wheat in the drought-prone areas of Northern China*). MAS-monitoring software will be developed in collaboration with SP4, and made available to the entire molecular breeding community. The new breeding methodologies developed in Theme 2 also involve applying to African crops marker-assisted recurrent selection methodology (MARS), an

innovative approach developed by the private sector that we implemented for the first time for sorghum and maize in 2009 and that will be greatly expanded across multiple crops starting with our new Challenge Initiative Outputs planned for 2010.

Another component of Theme 2 is drought phenotyping. The objectives of the ongoing activities, conducted under both competitive and commissioned projects, are to develop better descriptions of the testing environments and to access innovative traits, either for large-scale or precision phenotyping. A strategic network of GCP evaluation sites is being established for all GCP target crops. The geographic coordinates of these locations permit access to soil/climatic databases that provide information about the respective environment. These locations are being clustered according to their environmental characteristics, to estimate their representativeness and to help monitor germplasm exchange. A subset of locations has been identified to become a phenotyping platform for large, high-quality drought phenotyping of GCP crops. These locations will be part of the Phenotyping Services that will be provided under the Molecular Breeding Platform that is being built by GCP and that will serve our NARS partners particularly well. Since the aim is to develop new methodologies and innovative support tools, activities under Theme 2 are generally led by CGIAR Centres or ARIs but the applications will benefit the NARS directly.

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

***Output 11 to Output 18***

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

Product management activities create the conditions for a global and rationalised selection/management of validation projects. Projects in Theme 3 are all based on the concept of validation and value-adding of existing GCP products. They are all commissioned and defined on the basis of scientific quality (evaluated from reports, on-site visits and expert opinion), risk factors, alignment to the GCP Strategic Framework, competitive advantage for users (breeders, farmers), synergy with other projects and products and

feasibility and expectations for adoption. These projects that aim to transfer QTLs/genes identified by SP1, SP2 or SP3 in well adapted/adopted germplasm, involve breeders. As far as possible, they are led by NARS (eg, CAAS, China; INRA, Morocco; EMBRAPA, Brazil, for Outputs 11, 12, and 13 respectively). Most of the genes/QTLs to be transferred involve drought or other abiotic stresses. Evaluation and impact assessments of the transferred genes/QTLs are done locally (eg. Northern China, Morocco, Niger and Mali, and Indonesia for Outputs 11, 12, 13 and 14 respectively). All the validation projects will take advantage of the phenotyping platform developed through Theme 2 for better monitoring of testing conditions and management of germplasm exchange.

Research on the *Alt<sub>SB</sub>* and *Pup1* genes, which is expanded in the new CI Outputs 16, 17 and 18, aims to validate products that have been generated under SP2. Consequently, these are good examples of upstream products generated by another GCP Subprogramme, identified as having a large potential impact, and consequently validated for further use and dissemination. Importantly, in all these cases, there is also significant support from SP5 for training and enhancing the capacity of the NARS involved in the validation projects in Niger, Mali and Indonesia. This ensures not only the delivery of germplasm, but also the transfer of MAB technologies.

#### **Theme 4: Application of molecular markers in breeding programmes**

##### **Output 19 to Output 28**

This theme not only targets the application of markers developed by GCP (or by others) in breeding programmes via the most efficient approaches, but also implements the new MARS methodology to directly identify favourable alleles in breeding populations and recombine them to generate superior varieties. It represents the last step in the product delivery pathway. GCP is mainly focusing on the use of MAB for drought and other abiotic stresses. Due to the complexity of these traits, the use of markers in breeding programmes often still involves disease-resistance traits but the focus is increasingly placed on drought and abiotic stresses. For instance the two new CI Outputs included under this Theme in the current MTP both focus on drought tolerance (rice and wheat, Outputs 27 and 28).

Efforts to fine-map four genes that reliably affect yield under both artificially imposed and natural drought (Output 20) are drawing on a large body of information from several other projects. The objective is to transfer these outputs to breeding, after analysing the physiological basis of tolerance and confirming their effects in farmers' environments in India and Southern China, in collaboration with relevant NARS.

#### **Changes from previous MTP**

The 2009–2011 MTP described 28 Outputs. Of these, seven will be completed by the end of 2009:

1. Output 3.1. *Enhancing groundnut (Arachis hypogaea L.) genetic diversity and speeding its utilisation in breeding for improving drought tolerance*
2. Output 3.2. *Association mapping of downy mildew resistance in elite maize inbred lines in Thailand*
3. Output 3.5. *Field evaluation of wheat-barley introgression lines under different water regimes*
4. Output 3.6. *Seed smoke treatment to favour germination under water stressed conditions*
5. Output 3.18. *Validation of Saltol, a major salinity-tolerance gene in rice*
6. Output 3.20. *Integration of genomic tools with conventional screening for developing NERICA rice cultivars for West Africa*
7. Output 3.24. *Marker-assisted selection for resistance to Striga gesnerioides in cowpea*

Output titles were modified for Outputs 3.4 (Output 2 in current MTP), 3.7 (Output 3 in current MTP), 3.17 (Output 13 in current MTP) and 3.28 (Output 25 in current MTP).

The GCP project number was corrected for former Output 3.7 (3 in current MTP). It is now G4008.14 instead of G4007.06 that had been entered by mistake in the 2009–2011 MTP.

Progress was slower than expected in ten Outputs for different reasons:

- a) For five of them, the reason was a delayed start, often due to delayed contract finalisation and resulting delayed funding. This affected the following Outputs:
  1. Output 2 (3.4 in previous MTP). *Developing potato cultivars adapted to Southern African countries*
  2. Output 3 (3.7 in previous MTP). *Breeding for drought tolerance with known gene information*
  3. Output 11 (3.15 in previous MTP). *Integrating marker-assisted selection into the conventional breeding procedure for improvement of wheat in the drought-prone areas of Northern China*
  4. Output 19 (3.21 in previous MTP). *Marker-assisted selection for sweet potato virus disease (SPVD) resistance in sweet potato germplasm and breeding populations*
  5. Output 22 (3.25 in previous MTP). *Marker-assisted selection for resistance to streak virus in maize*
- b) For two of them, delays were caused by problems with planting or weather which caused some of the field seasons to be delayed. This affected the following Outputs:
  1. Output 4 (3.8 in previous MTP). *Linking genetic diversity with phenotype for drought tolerance traits through molecular and physiological characterisation of a diverse reference collection of chickpea*

2. Output 20 (3.22 in previous MTP). *Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-assisted breeding*

c) The following three Outputs were delayed for case-specific reasons:

1. Output 1 (3.3 in previous MTP) *Tailoring superior alleles for abiotic stress genes for deployment in breeding programmes—association analysis of  $Alt_{SB}$ , a major aluminium tolerance gene in sorghum* suffered from delays in germplasm exchange due to customs problems.
2. Output 12 (3.16 in previous MTP) *Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco* got an optional third year extension in agreement with the original agreement.
3. Output 14 (3.19 in previous MTP) *Application and validation of the major QTL Phosphate Uptake 1 (Pup1)* suffered from a combination of funding and hiring delays.

The following two Outputs will be extended beyond the proposed end-dates indicated in the previous MTP:

1. Output 6 (3.10 in previous MTP). *Development of a GCP phenotyping network*
2. Output 21 (3.23 in previous MTP). *Local germplasm enhanced via molecular breeding for target traits in tropical legumes (groundnuts, beans, cowpeas and chickpeas)*

For the following four Outputs, it had been indicated by mistake in the 2009-2011 MTP that the projects would commence in 2009, but these in fact started in 2008. The correction is being made in this MTP:

1. Output 8 (3.12 in previous MTP). *Targeting drought-avoidance root traits to enhance rice productivity under water-limited environments*
2. Output 9 (3.13 in previous MTP). *Basal root architecture and drought tolerance in common bean*
3. Output 10 (3.14 in previous MTP). *Breeder-friendly high-throughput phenotyping tools to select for adaptive traits in drought environments*
4. Output 25 (3.28 in previous MTP). *Drought tolerant maize for Asia*

Twenty-one of the 28 Outputs presented in the current MTP build upon those described for the Subprogramme in the 2009–2011 MTP.

All seven new Outputs are part of the new GCP Challenge Initiative projects to be started in early 2010 and to continue

until 2013 for a four-year period. Four of those are in Theme 3 and three are in Theme 4:

### Theme 3

1. Output 15. *Improvement and deployment of markers for biotic stress traits in cassava*
2. Output 16. *Validation of candidate Pup1 gene(s) in rice and MABC for Pup1 in rice (including pyramiding  $Alt_{SB}/Al$  tolerance and Pup1 in rice*
3. Output 17. *MABC for Pup1/P efficiency and  $Alt_{SB}/Al$  tolerance in sorghum (including pyramiding  $Alt_{SB}$  and Pup1/P efficiency in sorghum*
4. Output 18. *MABC for Pup1/P efficiency and  $Alt_{SB}$  in maize*

### Theme 4

5. Output 26. *QTL mapping and implementation of marker-assisted recurrent selection (MARS) for improvement of drought tolerance in cassava*
6. Output 27. *Molecular breeding for drought tolerance in rice in Africa*
7. Output 28. *Molecular breeding for drought tolerance in wheat for China and India*

## Output descriptions and partnerships

### Overview

In this MTP, SP3 has 28 Outputs grouped into four themes. 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 activities in this Subprogramme require coordinated input from scientists of different disciplines, eco-regions and types of institution.

For SP3's discovery activities, partners are principally NARS institutes with relatively extensive facilities and expertise, although African partners with less extensive facilities also play a role here. In some cases, the research is based on a South–South collaboration.

Coordination among ARIs, CGIAR centres and national programmes is critical for the activities focusing on phenotyping in different conditions, and very often the expertise developed in one country serves as the basis for the development of phenotyping facilities with other partners. For instance the SP3 activities of the tropical legumes initiative link research across continents and contribute to reinforcing the phenotyping capacities and expertise of the African and Asian partners involved in this work.



SP3's product validation activities mainly involve institutions from the South but there is often a strong mentorship from researchers in Universities or CG Centres. However, a large amount of projects are led by a national partner, thereby ensuring validation of markers in the adapted/ adopted background and the transfer of the associated MAS technologies, especially through the molecular breeding communities of practices developed in collaboration with SP5.

All partners listed under the Output descriptions below have a collaborative role in the research; the lead institute with principal responsibility, together with his/her home institution, type of project and funding mechanism are all also indicated.

### **Output descriptions**

For each Output below, the Lead Institute (LI), PI, type of project and funding mechanism are all indicated.

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

*Output 1: Tailoring superior alleles for abiotic stress genes for deployment in breeding programmes: association analysis of  $Alt_{SB}$ , a major aluminium tolerance gene in sorghum*

- Competitive: G3007.04
- StraP
- 2007–2010
- LI/PI: EMBRAPA/J Magalhaes
- Linked to P1-O6

$Alt_{SB}$  alleles are being surveyed across diverse sorghum germplasm to identify superior  $Alt_{SB}$  haplotypes by association mapping. Haplotype-specific markers will be developed and used for introgression into African landraces.

*Partners:* USDA–ARS, CU, KSU

*Output 2: Developing potato cultivars adapted to Southern African countries*

- Commissioned: G4008.15
- StraP
- 2008–2010
- LI/PI: INIA–Uruguay/F Vilaro

Virus-free planting material (minitubers) from South American NARS and CIP will be sent to Malawi and Mozambique and selected locally, based on adaptation to local growing conditions (dormancy-maturity), consumer preferences and necessary resistance or tolerance (mainly virus and late blight). DArT markers will be used to characterise germplasm and PCR-based tools applied to identify and characterise genotypes for resistance to various pests/diseases.

*Partners:* INIA–Chile, INTA–Argentina, EMBRAPA, IIAM, DARS, CIP

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

*Output 3: Breeding for drought tolerance with known gene information*

- Commissioned: G4008.14
- StraP
- 2008–2010
- LI/PI: CIMMYT–CAAS/J Wang
- Linked to P4-O7

Simulation tools are being developed and applied by CAAS and CIMMYT to facilitate effective implementation of QTLs in MAS for polygenic traits, such as drought tolerance. Activities will link with ongoing projects using MAS (for instance Outputs 8 and 14 of Subprogramme 3).

*Partners:* CSIRO, UoQ, Agropolis–INRA, IRRI, ICRISAT

*Output 4: Linking genetic diversity with phenotype for drought tolerance traits through molecular and physiological characterisation of a diverse reference collection of chickpea*

- Commissioned: G4008.12
- StraP
- 2008–2010
- LI/PI: ICRISAT/L Krishnamurthy
- Linked to P2-O2

A reference set of chickpea (300 accessions) identified as an output of the SP1 chickpea genotyping activity (Output 1.1 in the previous MTP) is being phenotyped for carbon isotope discrimination and other drought tolerance related traits and genotyped with DArT markers.

*Partners:* JIRCAS, UAS–Bangalore

*Output 5: Improving drought tolerance phenotyping in cowpea*

- Commissioned: G4008.13
- StraP
- 2008–2010
- LI/PI: UC–Riverside/J Ehlers

Cowpea varieties are compared for grain yield and drought tolerance-related physiological traits (including thermal imaging) in several environments in West Africa and USA. This will provide baseline drought tolerance information for analysing GxE interactions and refine phenotyping protocols.

*Partners:* TAMU, ISRA, INERA, IITA

*Output 6: Development of a GCP phenotyping network (complementary to Output 7 of Subprogramme 3)*

- Commissioned: G4007.25
- StraP
- 2007–2012
- LI/Pis: GCP and Consultants (A Blum, G Edmeades, J O'Toole)
- Linked to P4-O4, P5-O12 and to Activity 3.2.5 of the Molecular Breeding Platform

A strategic network of field phenotyping sites for target GCP crops is being established. This phenotyping network will be very important to develop the infrastructure to generate good and reliable field data, a critical element to several SP3 outputs dealing with MAB. At least five field locations will become centres of excellence in phenotyping for drought tolerance, while other locations will be supported to increase phenotyping capacity. This Output is an extension of Output 3.10 of the 2009–2011 MTP.

*Output 7: Environmental assessment for phenotyping network*

- Commissioned: G4008.34
- StraP
- 2009–2010
- LI/PI: CIAT/G Hyman
- Linked to P1-O4, P1-O5, P1-O6 and P5-O12

Sites are selected on the basis of environmental data (assessed using geographic information systems software, spatial overlay, and distance and proximity tools) and modelling tools.

*Partners:* KUL, EMBRAPA, Waen Associates

*Output 8: Targeting drought-avoidance root traits to enhance rice productivity under water-limited environments*

- Competitive: G3008.06
- StraP
- 2008–2011
- LI/PI: IRRI/R Serraj
- Linked to P4-O4

Screening tools and protocols will be developed and refined for high-throughput phenotyping of dehydration-avoidance traits in rice.

*Partners:* AfricaRice, AU, BF, CSU, NaU, TNAU, UoMi,

*Output 9: Basal root architecture and drought tolerance in common bean*

- Competitive: G3008.07
- StraP
- 2008–2011
- LI/PI: PSU/J Lynch
- Linked to P4-O4

Basal root whorl number and basal root growth angle measurement protocols will be developed in bean and QTLs identified for these two traits.

*Partners:* CIAT, SABRN, IIAM

*Output 10: Breeder-friendly high-throughput phenotyping tools to select for adaptive traits in drought environments*

- Competitive: G3008.08
- StraP
- 2008–2011
- LI/PI: ICARDA/F Ogonnaya
- Linked to P4-O4

Field-based, low-cost and high throughput phenotyping protocols will be developed for crop water status and canopy size and functionality in wheat. The impact of selecting for those traits will be estimated in several drought-prone mega-environments.

*Partners:* CSIRO, CIMMYT, INRA–Morocco, EIAR

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

*Output 11: Integrating marker-assisted selection into the conventional breeding procedure for improvement of wheat in the drought-prone areas of Northern China*

- Commissioned: G4007.06
- StraP
- 2007–2010
- LI/PI: CAAS/R Jing

Major drought-tolerance QTLs identified previously are being introduced into cultivars largely cultivated in the main regions of Northern China (Hebei, Henan, Shanxi, Shanxi and Ningxia Provinces) and will be phenotyped in those same regions.

*Partners:* NU, NWSUAF, SAAS, LAAS, HAAS

*Output 12: Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco*

- Commissioned: G4007.05
- StraP
- 2007-2010
- LI/PI: INRA–Morocco/AA Fouad

Contrasting bread and durum wheat genotypes are to be characterised at both molecular and phenotypic levels. Markers will be developed and used to screen for biotic stresses. Markers will also be developed for abiotic stresses, mainly drought.

*Partners:* ICARDA, UdB, CU, UoMi, EMBRAPA, INRAN, ICRISAT

*Output 13: Assessment of the breeding value of superior haplotypes for Alt<sub>SB</sub>, a major Al tolerance gene in sorghum: linking upstream genomics to acid soil breeding in Niger and Mali (ALTFIELD)*

- Commissioned: G4008.10
- StraP
- 2008–2010
- LI/PI: EMBRAPA/R Schaffert
- Linked to P2-O16

Elite Alt<sub>SB</sub> haplotypes identified by association analysis within the ALTSORGHUM competitive project (Output 3.3. in the 2009–2011 MTP) will be validated on acid soils in West Africa. Technologies for evaluating and developing sorghum germplasm and cultivars with enhanced tolerance to Al toxicity will be transferred to NARS in Niger and Mali.

*Partners:* INRAN, ICRISAT, CU

*Output 14: Application and validation of the major QTL Phosphate Uptake 1 (Pup1)*

- Commissioned: G4008.41
- StraP
- 2008–2010
- LI/PI: IRRI/S Heuer
- Linked to P2-O17, P2-O18

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

*Partners:* JIRCAS, ICABIOGRAD

*Output 15: Improvement and deployment of markers for biotic stress traits in cassava*

- Commissioned: Project No. TBD
- CI1
- 2010–2013
- LI/PI: CIAT/E Okogbenin
- Linked to P4-O1, P5-O8 and P5-14

This Output is part of the new GCP Challenge Initiative programme for cassava. The goal is to identify new molecular markers linked to established and new sources of tolerance to major cassava biotic stresses such as cassava mosaic disease (CMD), cassava brown streak disease (CBSD) and cassava green mite (CGM), and to implement those markers broadly across cassava breeding programmes.

*Partners:* ARI–Naliendele, CRI, IITA, NRCRI, SARI

*Output 16: Validation of candidate Pup1 gene(s) in rice and MABC for Pup1 in rice (including pyramiding  $Alt_{SB}/AI$  tolerance and Pup1 in rice)*

- Commissioned: Project No. TBD
- CI7
- 2010–2013
- LI/PIs: IRRI/S Heuer (*Pup1*); A Ismail (*AI* tolerance)
- Linked to P4-O1

This Output is part of the new GCP Challenge Initiative programme for the use of comparative genomics to improve cereal yields in problem soils (CI7). It builds on the work done in a previous SP2 project (Output 2.16, 2009–2011 MTP) in which Phosphate uptake 1 (*Pup1*) was identified as a major QTL for tolerance to phosphorus deficiency. This links to a similar SP2 Output aimed at identifying a candidate gene for *Pup1* and will focus on the validation of this candidate gene and its backcrossing into adapted rice germplasm. This gene will also later be combined with another candidate gene for a  $Alt_{SB}/AI$  rice homologue.

*Partners:* JIRCAS, ICABIOGRAD, EMBRAPA, CU, USDA–ARS

*Output 17: MABC for Pup1/P efficiency and  $Alt_{SB}/AI$  tolerance in sorghum (including pyramiding  $Alt_{SB}$  and Pup1/P efficiency in sorghum)*

- Commissioned: Project No. TBD
- CI7
- 2010–2013
- LI/PI: INRAN/S Souley
- Linked to P4-O1

This Output is part of the new GCP Challenge Initiative programme for the use of comparative genomics to improve cereals yield in problem soils (CI7). It builds on the work done with the *Pup1* gene in rice (see Output 16 above) to identify a candidate gene homologue for *Pup1* in sorghum and recombine it with the  $Alt_{SB}$  gene that had previously been identified in sorghum (see Output 13).

*Partners:* KARI, EMBRAPA, CU, USDA–ARS

*Output 18: MABC for Pup1/P efficiency and  $Alt_{SB}$  in maize*

- Commissioned: Project No. TBD
- CI7
- 2010–2013
- LI/PI: MU/KARI/S Gudu
- Linked to P4-O1

This Output is part of the new GCP Challenge Initiative on the use of comparative genomics to improve cereal yields in problem soils (CI7). It builds on the work done as part of the cloning of the *Pup1/P* candidate gene in rice (see Output 16, Project 3, above) and the  $Alt_{SB}$  candidate gene in sorghum (see Output 13, Project 3, above) to identify potential candidate gene homologues for those genes in maize and combine them in adapted maize germplasm for improved performance under poor soil conditions. Due to the time needed for preparatory work for the Subprogramme 2-led activities of this project, no significant Output targets are foreseen for 2010, with most of the results expected to emerge in 2011.

*Partners:* EMBRAPA, JIRCAS, IRRI, CU, USDA–ARS, CIMMYT

**Theme 4: Application of molecular markers in breeding programmes**

*Output 19: Marker-assisted selection for sweet potato virus disease (SPVD) resistance in sweet potato germplasm and breeding populations*

- Commissioned: G4007.07
- StraP
- 2007–2010
- LI/PI: CIP/W Grüneberg

Markers for resistance to SPVD will be developed and used to screen orange-fleshed sweet potatoes (OFSP) breeding populations (with high provitamin A content) and CIP germplasm.

*Partners:* NAARI

*Output 20: Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-assisted breeding*

- Competitive: G3007.05
- StraP
- 2007–2010
- LI/PI: IRRI/A Kumar

Quantitative trait loci (QTLs) with large effects on yield under stress, detected in a population derived from parents differing greatly in yield under drought (Vandana and Way Rarem) are being fine-mapped. Their impact on yield will be confirmed in India and China, and they will be introgressed into elite varieties via marker-assisted selection. The resulting lines will be disseminated via the INGER network.

*Partners:* TNAU, CRURRS, UAS, YAAS, UoAI

*Output 21: Local germplasm enhanced via molecular breeding for target traits in tropical legumes (groundnuts, beans, cowpeas and chickpeas)*

- Focus: G6007.01–G6007.04 (inclusive)
- StraP
- 2007–2010 (Phase II: 2010–2013)
- LIs/PIs:
  - ICRISAT/V Vadez
  - ICRISAT/GCP (R Varshney)
  - CIAT/M Blair
  - UoC–Riverside/J Ehlers
- Linked to P1-O6, P1-O17, P4-O1, P5-O10 and P5-O13

Backcross populations incorporating farmer/market preferences and disease resistance are being developed in the context of research funded by the Bill & Melinda Gates Foundation, that aims to increase yields in farmers' fields and increase incomes through the development and cultivation of improved local varieties. This research is now being extended into a Phase II that will be funded through 2013 and that will have a bigger focus on marker applications to enhance breeding. Marker-assisted recurrent selection (MARS) projects are being implemented as part of this enhanced MAB effort.

*Partners:* ARI–Naliendele, CRS, INRAN, ISRA, EMBRAPA, UCB, UGA, INERA, IRAD, IITA, UoC–Davis, UEM, ART, CBI, SARI–Ethiopia, ECABREN, SABRN, EIAR, LZARDI, EgU, IIPR

*Output 22: Marker-assisted selection for resistance to streak virus in maize*

- Commissioned: G4008.19
- StraP
- 2008–2010
- LI/PI: UKZN/M Laing

MABC technology is being used to rapidly introgress maize streak virus (MSV) resistance from CIMMYT sources into Mozambican maize germplasm. A local genotyping capacity is also being established at UKZN to support this effort.

*Partners:* IIAM

*Output 23: Dry bean improvement and marker-assisted selection for diseases and abiotic stresses in Central America and the Caribbean*

- Commissioned: G4008.11
- StraP
- 2008–2010
- PI/LI: INIFAP/JA Acosta-Gallegos
- Linked to P4-O1

Drought nurseries will be established for opaque black and small red seed classes by grouping the most drought-tolerant accessions from Mexico, Nicaragua, Cuba and Haiti. The nurseries will be screened for bean golden yellow mosaic virus (BGYMV) and root-rot resistance. Segregating populations will be developed in Mexico and at CIAT with the best accessions, and selected for BGYMV and root-rot resistance using MAS. The best lines will be distributed in Mexico, Nicaragua, Cuba and Haiti.

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

*Output 24: Yield improvement of sorghum in Africa through marker-assisted recurrent selection (MARS) and a public–private partnership*

- Commissioned: G4008.48
- StraP
- 2009–2013
- LI/PI: Agropolis–CIRAD/J-F Rami
- Linked to P4-O1, P5-O4 and P5-O8

An ARI (Agropolis–CIRAD), a private company (Syngenta) and an African NARS institution (IER, Mali) will work together to develop drought-tolerant sorghum germplasm through MARS, an approach already successfully applied to maize by the private partner.

*Partners:* IER, Syngenta

*Output 25: Drought tolerant maize for Asia*

- Commissioned: G4008.56
- StraP
- 2008–2013
- LI/PI: CIMMYT/B Vivek
- Linked to P4-O1

CIMMYT and NARS in Asia (China, India, Indonesia, Pakistan, Philippines, Nepal, Thailand and Vietnam), with the support of the private sector, will develop drought-tolerant lines and hybrids through MARS.

*Partners:* YAAS, DMR, MRP, ICERI, MMRI, DAT, NMRI, BIOSEED, Syngenta, IFSSA, Monsanto, Pioneer

*Output 26: QTL mapping and implementation of marker-assisted recurrent selection (MARS) for improvement of drought tolerance in cassava*

- Commissioned: Project No.TBD
- CI1
- 2010–2013
- LI/PI: CIAT/E Okogbenin
- Linked to P1-O18, P2-O7, P4-O1 and P5-O14

This Output is part of the new GCP Challenge Initiative for cassava. The goal is to complete previous work aimed at identifying major QTLs responsible for drought tolerance in South American cassava populations and to start the implementation of marker-assisted recurrent selection (MARS) for improvement of drought tolerance in West African cassava cultivars.

*Partners:* CRI, CU, EMBRAPA, IITA, NRCRI, SARI

*Output 27: Molecular breeding for drought tolerance in rice in Africa*

- Commissioned: Project No. TBD
- CI4
- 2010–2013
- LI/PI: AfricaRice/MN Ndjiondjop
- Linked to P4-O1 and P5-O12

This Output is part of the new GCP Challenge Initiative programme for drought tolerant rice in Africa (CI4). The goal is to implement molecular marker techniques to validate and transfer a number of previously identified drought-tolerant QTL loci into rice varieties adapted to Africa, as well as to start marker-assisted recurrent selection (MARS) projects to recombine and accumulate drought tolerant loci within African breeding germplasm.

*Partners:* IRRRI, CIAT, Agropolis–CIRAD, INERA, IER, UES, Agropolis–IRD, NRCRI

*Output 28: Molecular breeding for drought tolerance in wheat for China and India*

- Commissioned: Project No. TBD
- CI6
- 2010–2013
- LI/PI: IARI/V Prabhu (for India); CAAS/R Jing (for China)
- Linked to P1-O14, P1-O16, P4-O1

This Output is part of the new GCP Challenge Initiative for drought-tolerant wheat in India and China (CI6). The goal is to transfer previously-identified drought tolerant QTLs to Indian and Chinese wheat breeding lines to validate those QTLs in those backgrounds and pyramid the successful ones to develop new Indian and Chinese cultivars with improved drought tolerance.

*Partners:* HAAS, ICAR, PAU, NRCPB

## International public goods

SP3 is delivering marker technologies that are available as international public goods to generate germplasm with enhanced tolerance to drought, salinity or acid soils. Germplasm with resistance to pests and diseases has also been delivered. The new approaches developed by SP3 to improve molecular breeding efficiency (low-cost, high-throughput markers, new marker-assisted recurrent selection (MARS) methodologies tailored to specific crops, modelling for better monitoring of MAB strategies, innovative phenotyping protocols, etc.) are also international public goods, as well as the products generated from these approaches, technologies and protocols (eg, virus-resistant cassava and sweet potato, rice resistant to bacterial blight and new drought-tolerant varieties of rice, wheat, sorghum and cassava). Finally, the development of a phenotyping platform, comprising experimental stations with adequate facilities and expertise, also constitutes a public good, available for germplasm evaluation and marker validation.

## Elaboration of partners roles

Under SP3's Theme 1, partnerships for implementing these projects are mainly developing country institutions with relatively developed facilities and expertise such as EMBRAPA (Brazil) and INIA–Uruguay. EMBRAPA is performing the survey of *Alt<sub>SB</sub>* alleles for Output 1 and working with the national programmes in Africa to access their germplasm. INIA–Uruguay is managing the effort to test South American potato germplasm in Malawi and Mozambique; national programmes in South America along with CIP are providing the germplasm and these line are evaluated locally by the Southern African NARS.

Activities under Theme 2 mainly involve ARIs (eg, Aberdeen University, Charles Sturt University, CSIRO, INRA, JIRCAS, Katholieke Universiteit Leuven, Nagoya University, Pennsylvania State University, Texas A&M University, University of California–Riverside, University of Missouri) and CGIAR Centres (CIAT, CIMMYT, ICARDA, ICRISAT, IITA, IRRRI, AfricaRice). It is these institutes that lead the development of new protocols for phenotyping in their laboratories, but this is still done in close collaboration with several developing country partners, especially for testing under field conditions (eg, EMBRAPA, INERA, ISRA, TNAU and the University of Bangalore). The MAB modelling activity is actually being led by a developing country institute (CAAS), in collaboration with several ARIs and CGIAR Centres.

In Theme 3, validation activities mainly involve developing country institutes (EMBRAPA in Brazil; CAAS, HAAS, LAAS, Ningxia University, NWSUAF and SAAS in China; ICABIOGRAD in Indonesia; INRA in Morocco; and INRAN in Niger) even if they may be led by CGIAR Centres. These institutes are the ones who perform most of the marker introgression work and the testing of the resulting lines under their field conditions. Output 11 (Integrating marker-assisted selection into the conventional breeding procedure for improvement of wheat in the drought-prone areas of Northern China) is being led and implemented solely by national programmes from various parts of China. Output 12 (*Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco*) is being led primarily by developing country partners (INRA–Morocco) with contributions from a number of ARIs and CGIAR Centres.

In Theme 4, most activities are led by CGIAR Centres (CIP, IRRI, ICRISAT/CIAT, CIMMYT, CIAT and AfricaRice for Outputs 19, 20, 21, 25, 26 and 27, respectively) but all involve close collaboration with, or are led by, developing country institutes (eg, INIFAP is the Lead Institute for Output 23, with IARI and CAAS leading Output 28). These NARS-led activities include the establishment of a network of field locations for testing both the progenies involved in the marker-assisted breeding programmes but also the local development of breeding populations targeted specifically to their areas.

The vision of Themes 3 and 4 is that most of the projects will be performed primarily by developing country programmes in the future and will focus on germplasm and traits relevant to their specific areas.

### Project 3 logframe – SP3: Trait capture for crop improvement

Notes:

1. Each Output is followed by:
  - a) the type of research activity/funding contributing to the Output (commissioned, competitive, focus, or discretionary) and GCP project number
  - b) Identification of Output as a StraP (Strategic project) or CI (Challenge Initiative) project
  - c) start and end year, and
  - d) the lead institute (LI) and Principal Investigator(s) (PI[s]) responsible for the Output (and its Output targets).
2. Some Outputs are managed internally within GCP, in some cases involving coordination of a number of external institutes. In most such cases, the entry under 'PI' is denoted as 'Various'.

Output	title, type and target(s)	Intended users	Outcome	Impact
<b>Theme 1: Characterisation of segregating populations and identification of genomic regions for plant breeding</b>				
Output 1	<b>Tailoring superior alleles for abiotic stress genes for deployment in breeding programmes: association analysis of <i>Alt<sub>sg</sub></i>, a major aluminium tolerance gene in sorghum</b> <ul style="list-style-type: none"> <li>• Competitive: G3007.04</li> <li>• StraP</li> <li>• 2007–2010</li> <li>• LI/PI: EMBRAPA/J Magalhaes</li> <li>• Linked to P1-06</li> </ul>	Sorghum breeders and breeding programmes in Niger and other countries facing soil acidity problems	Superior <i>Alt<sub>sg</sub></i> haplotypes identified by association mapping, and pre-breeding near-isogenic lines (NILs) carrying different <i>Alt<sub>sg</sub></i> haplotypes used in breeding programmes	Improvement of breeding efficiency in sorghum under acid soil conditions
Target 2010: Materials	A set of <i>Alt<sub>sg</sub></i> haplotype-specific markers identified and easy-to-use SNP genotyping assays developed			
Output 2	<b>Developing potato cultivars adapted to Southern African countries</b> <ul style="list-style-type: none"> <li>• Commissioned: G4008.15</li> <li>• StraP</li> <li>• 2008–2010</li> <li>• LI/PI: INIA–Uruguay/F Vilario</li> </ul>	Potato breeders and breeding programmes in the Southern Cone of Latin America, Mozambique and Malawi	New breeding tools as DNA-based markers used in NARS in Latin America and Africa to select for key resistance traits, advanced germplasm disseminated to less-developed countries, and capacity-building and expertise of breeding programmes improved	New and more sustainable varieties deployed to resource-poor farmers in Latin America and Africa
Target 2010: Materials	Elite germplasm phenotyped for drought tolerance and markers developed for priority resistance traits (eg, late blight, potato tuber moth, <i>Diabrotica</i> , bacterial wilt, potato leaf-roll virus)			

Output	title, type and target(s)	Intended users	Outcome	Impact
<b>Theme 2: Development and evaluation of novel breeding or molecular technologies to better serve modern plant breeding</b>				
<b>Output 3</b>	<b>Breeding for drought tolerance with known gene information</b> <ul style="list-style-type: none"> <li>Commissioned: G4008.14</li> <li>StraP</li> <li>2008–2010</li> <li>LI/PI: CIMMYT–CAAS/J Wang</li> <li>Linked to P4-07</li> </ul>	MAS programmes in Asia and Africa	MAS models and software used in several breeding programmes in Asia and Africa	More efficient MAS strategies and protocols available for breeding programmes in Asia and Africa
<i>Target 2010: Practices</i>	Feasible and cost-efficient MAS strategies for pyramiding multiple favourable alleles in wheat breeding, strategies in using MARS proposed			
<b>Output 4</b>	<b>Linking genetic diversity with phenotype for drought tolerance traits through molecular and physiological characterisation of a diverse reference collection of chickpea</b> <ul style="list-style-type: none"> <li>Commissioned: G4008.12</li> <li>StraP</li> <li>2008–2010</li> <li>LI/PI: ICRISAT/L Krishnamurthy</li> <li>Linked to P2-02</li> </ul>	Chickpea breeding programmes in India	QTLs used for chickpea marker-assisted breeding in India	More efficient MAS strategies and protocols available for breeding programmes in Asia and Africa
<i>Target 2010: Materials</i>	QTLs identified for at least three drought tolerance traits in chickpea			
<b>Output 5</b>	<b>Improving drought tolerance phenotyping in cowpea</b> <ul style="list-style-type: none"> <li>Commissioned: G4008.13</li> <li>StraP</li> <li>2008–2010</li> <li>LI/PI: UC–Riverside/J Ehlers</li> </ul>	Cowpea breeding programmes in West Africa	Innovative phenotyping tools and protocols developed; phenotyping capacity and expertise for cowpea strengthened; drought-tolerant germplasm and efficient tools for drought tolerance screening identified in cowpea	Large-scale phenotyping facilitated for cowpea in Africa
<i>Target 2010: Materials</i>	Genotype by environment interaction analysed for drought-tolerance related traits			
<b>Output 6</b>	<b>Development of a GCP phenotyping network (complementary to Output 7 of Subprogramme 3)</b> <ul style="list-style-type: none"> <li>Commissioned: G4007.25</li> <li>StraP</li> <li>2007–2012</li> <li>LI/PIs: GCP and Consultants (A Blum, G Edmeades, J O'Toole)</li> <li>Linked to P4-04, P5-012 and to Activity 3.2.5 of the Molecular Breeding Platform</li> </ul>	GCP projects and breeders of target crops in Africa, Asia and Latin America	At least 5 hubs used for high-quality and high-throughput drought phenotyping	Efficiency of drought phenotyping and germplasm deployment improved in GCP projects
<i>Target 2010: Capacity</i>	Phenotyping and screening protocols finalised; at least five phenotyping sites for proficiency in drought tolerance screening updated			
<i>Target 2011: Capacity</i>	At least five phenotyping sites for proficiency in drought tolerance screening updated			
<i>Target 2012: Capacity</i>	At least five phenotyping sites for proficiency in drought tolerance screening updated			
<b>Output 7</b>	<b>Environmental assessment for phenotyping network</b> <ul style="list-style-type: none"> <li>Commissioned: G4008.34</li> <li>StraP</li> <li>2009–2010</li> <li>LI/PI: CIAT/G Hyman</li> <li>Linked to P1-04, P1-05, P1-06 and P5-012</li> </ul>	Phenotypers and plant breeders of GCP target crops	At least 10 'hubs' used for high-quality and high-throughput drought phenotyping	Efficiency of drought phenotyping and germplasm deployment improved in GCP projects
<i>Target 2010: Practices</i>	Database of environmental and climate data, homologue maps, and drought stress indicators (soil–water balance modelling) made available for GCP phenotyping locations			

Output	title, type and target(s)	Intended users	Outcome	Impact
<b>Output 8</b>	<b>Targeting drought-avoidance root traits to enhance rice productivity under water-limited environments</b> <ul style="list-style-type: none"> <li>Competitive: G3008.06</li> <li>StraP</li> <li>2008–2011</li> <li>LI/PI: IRRI/R Serraj</li> <li>Linked to P4-04</li> </ul>	Lowland rice phenotypers and breeders in India and Africa	Screening tools and high-throughput phenotyping protocols for drought-avoidance in lowland rice	A high-throughput phenotyping platform available for lowland rice
<i>Target 2010: Capacity</i>	A collection of 300 accessions as well as NILs with and without major QTLs for yield under drought phenotyped for root morphology and water uptake, and under field conditions, for validation			
<i>Target 2011: Materials</i>	New donors of dehydration-avoidance root traits identified; QTLs controlling root phenotypic plasticity validated; NILs with putative root QTLs evaluated; at least 10 advanced breeding lines with improved dehydration avoidance evaluated by NARS			
<b>Output 9</b>	<b>Basal root architecture and drought tolerance in common bean</b> <ul style="list-style-type: none"> <li>Competitive: G3008.07</li> <li>StraP</li> <li>2008–2011</li> <li>LI/PI: PSU/J Lynch</li> <li>Linked to P4-04</li> </ul>	Common bean phenotypers and breeders in Latin America and Southern Africa	New phenotyping traits and protocols and markers available for tolerance to drought and low phosphorus availability in bean	Breeding efficiency improved for tolerance to drought and low phosphorus availability in bean
<i>Target 2010: Practices</i>	100 RILs from the cross DOR364xG19833 evaluated for basal root whorl number and basal root growth angle and QTLs identified			
<i>Target 2011: Materials</i>	150 RILs genotyped in key genomic regions for basal root whorl number and basal root growth angle; six segregating populations used for marker-assisted selection; four QTLs for basal root growth angle validated in backcross or recurrent selection populations			
<b>Output 10</b>	<b>Breeder-friendly high-throughput phenotyping tools to select for adaptive traits in drought environments</b> <ul style="list-style-type: none"> <li>Competitive: G3008.08</li> <li>StraP</li> <li>2008–2011</li> <li>LI/PI: ICARDA/F Ogbonnaya</li> <li>Linked to P4-04</li> </ul>	Wheat breeders in drought-prone areas	Robust, field-based and non-invasive drought phenotyping tools and protocols available in wheat	Breeding efficiency improved for drought tolerance in wheat
<i>Target 2010: Practices</i>	Relative value of drought-adaptive traits evaluated in the eight phenotyping locations			
<i>Target 2011: Materials</i>	Development and validation of algorithms for season-long phenotypic signature describing growth and water use. Assessment of the relative impact of putative key traits on drought adaptation in different mega-environments, and characterisation of ICARDA's elite drought germplasm to identify adaptive traits behind enhanced performance under drought			
<b>Theme 3: Markers/alleles validation in adapted germplasm under target environments</b>				
<b>Output 11</b>	<b>Integrating marker-assisted selection into the conventional breeding procedure for improvement of wheat in the drought-prone areas of Northern China</b> <ul style="list-style-type: none"> <li>Commissioned: G4007.06</li> <li>StraP</li> <li>2007–2010</li> <li>LI/PI: CAAS/R Jing</li> </ul>	Wheat breeders from Northern China (Ningxia, Shanxi, Henan and Hebei Provinces)	Drought-tolerant wheat germplasm disseminated and used in Northern China breeding programmes	Wheat breeding efficiency improved in several provinces of Northern China
<i>Target 2010: Materials</i>	At least 50 lines carrying drought tolerance QTLs selected			



Output	title, type and target(s)	Intended users	Outcome	Impact
<b>Output 12</b>	<b>Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco</b> <ul style="list-style-type: none"> <li>Commissioned: G4007.05</li> <li>StraP</li> <li>2007–2010</li> <li>LI/PI: INRA-Morocco/AA Fouad</li> </ul>	Plant breeders, wheat and barley breeding programmes and, ultimately, small-scale farmers in resource-poor cropping systems of North Africa	Novel genes and alleles conferring tolerance to stresses and improving end-use quality mined from the germplasm collections and used through MAS in breeding	More efficient MAS strategies available for wheat and barley improvement programmes under drought-prone environments
<i>Target 2010: Materials</i>	New markers generated for many traits of importance to wheat and barley production in Morocco			
<b>Output 13</b>	<b>Assessment of the breeding value of superior haplotypes for <i>Alt<sub>SB</sub></i>, a major Al tolerance gene in sorghum: linking upstream genomics to acid soil breeding in Niger and Mali (ALTFIELD)</b> <ul style="list-style-type: none"> <li>Commissioned: G4008.10</li> <li>StraP</li> <li>2008–2010</li> <li>LI/PI: EMBRAPA/R Schaffert</li> <li>Linked to P2-016</li> </ul>	Sorghum breeding programmes facing soil acidity constraints	Local germplasm carrying <i>Alt<sub>SB</sub></i> evaluated on acid soils, and available to West African scientists and breeders	Al toxicity genes/markers available for MAS in sorghum, and improved sorghum germplasm for acid soil conditions
<i>Target 2010: Materials</i>	<i>Alt<sub>SB</sub></i> transferred in sorghum African landraces			
<b>Output 14</b>	<b>Application and validation of the major QTL Phosphate Uptake 1 (<i>Pup1</i>)</b> <ul style="list-style-type: none"> <li>Commissioned: G4008.41</li> <li>StraP</li> <li>2008–2010</li> <li>LI/PI: IRRI/S Heuer</li> <li>Linked to P2-017, P2-018</li> </ul>	Asian rice breeding programmes facing phosphorus deficiency problems	<i>Pup1</i> , a major phosphorus -efficiency tolerance gene in rice validated in acid soil conditions by an Asian NARS (Indonesia), and available to breeders	Yield of rice varieties increased under phosphorus-deficient and acid soil conditions
<i>Target 2010: Materials</i>	Seeds of the best <i>Pup1</i> lines disseminated for field screening in Laos and India within ongoing IRRI activities and made available to NARS partners within the GCP 'Rice in Asia' platform for further testing			
<b>Output 15</b>	<b>Improvement and deployment of markers for biotic stress traits in cassava</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>C11</li> <li>2010–2013</li> <li>LI/PI: CIAT/E Okogbenin</li> <li>Linked to P4-01, P5-08 and P5-14</li> </ul>	Cassava breeders in Africa	Molecular markers closely linked to important cassava biotic traits can be broadly deployed in cassava breeding programmes	Improved cassava varieties with improved productivity under disease and insect pressure
<i>Target 2010: Practices</i>	New sources of tolerance to CMD, CBSD and/or CGM stresses identified; relevant populations identified or initiated for trait mapping of existing or new biotic stress tolerance sources			
<i>Target 2011: Materials</i>	Phenotypic evaluation of populations segregating for tolerance to CMD, CBSD or CGM; identification of new molecular markers linked to significant tolerance loci			
<i>Target 2012: Materials</i>	Validation of new disease tolerance loci identified; plans in place to implement MAS to introgress new tolerance loci into breeding programmes			
<b>Output 16</b>	<b>Validation of candidate <i>Pup1</i> gene(s) in rice and MABC for <i>Pup1</i> in rice (including pyramiding <i>Alt<sub>SB</sub></i>/Al tolerance and <i>Pup1</i> in rice)</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>C17</li> <li>2010–2013</li> <li>LI/PIs: IRRI/S Heuer (<i>Pup1</i>); A Ismail (Al tolerance)</li> <li>Linked to P4-01</li> </ul>	Rice breeders in Asia	New loci for tolerance to phosphorus and aluminum deficiencies available for rice breeding programmes	Improvement of rice performance under poor soil conditions (phosphorus and aluminum deficiencies in acid soils)
<i>Target 2010: Materials</i>	At least three <i>Pup1</i> introgression lines of mega varieties developed and validated in greenhouse and under field irrigated sites			

Output	title, type and target(s)	Intended users	Outcome	Impact
Target 2011: Materials	Major QTLs associated with Al toxicity tolerance identified			
Target 2012: Materials	Al-tolerance QTLs identified in parallel projects validated in Indonesian varieties			
<b>Output 17</b>	<b>MABC for <i>Pup1/P</i> efficiency and <i>Alt<sub>SB</sub></i>/Al tolerance in sorghum (including pyramiding <i>Alt<sub>SB</sub></i> and <i>Pup1/P</i> efficiency in sorghum)</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>C17</li> <li>2010–2013</li> <li>LI/PI: INRAN/S Souley</li> <li>Linked to P4-01</li> </ul>	Sorghum breeders	New loci for tolerance to phosphorus and aluminum deficiencies available for sorghum breeding programmes	Improvement of sorghum performance under poor soil conditions (phosphorus and aluminum deficiencies in acid soils)
Target 2010: Materials	Minimum of one validated marker for <i>Alt<sub>SB</sub></i>			
Target 2011: Materials	Minimum of two validated markers for <i>Pup1</i>			
Target 2012: Materials	Minimum of two target materials introgressed with <i>Alt<sub>SB</sub></i> for both Niger and Kenya			
<b>Output 18</b>	<b>MABC for <i>Pup1/P</i> efficiency and <i>Alt<sub>SB</sub></i> in maize</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>C17</li> <li>2010–2013</li> <li>LI/PI: MU/KARI/S Gudu</li> <li>Linked to P4-01</li> </ul>	Maize breeders in Africa	New loci for tolerance to phosphorus and aluminum deficiencies available for maize breeding programmes	Improvement of maize performance under poor soil conditions (phosphorus and aluminium deficiencies in acid soils)
Target 2010: Unassigned	None			
Target 2011: Materials	At least one pair of markers flanking the <i>Alt<sub>SB</sub></i> homologues or Al tolerance QTLs polymorphic between donor and receptor lines from Brazil, Kenya and Zambia			
Target 2012: Materials	At least one pair of markers flanking the <i>Pup1</i> homologues or P efficiency QTLs polymorphic between donor and receptor lines from Brazil, Kenya and Zambia			
<b>Theme 4: Application of molecular markers in breeding programmes</b>				
<b>Output 19</b>	<b>Marker-assisted selection for sweet potato virus disease (SPVD) resistance in sweet potato germplasm and breeding populations</b> <ul style="list-style-type: none"> <li>Commissioned: G4007.07</li> <li>StraP</li> <li>2007–2010</li> <li>LI/PI: CIP/W Grüneberg</li> </ul>	Plant breeders, breeding programmes and, ultimately, small-scale farmers in resource-poor cropping systems	Improved drought-tolerant and virus-resistant sweet potato lines available to users	Improved sweet potato germplasm for Africa
Target 2010: Materials	At least 700 sweet potato lines screened for the frequency of the SPVD resistant allele			
<b>Output 20</b>	<b>Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-assisted breeding</b> <ul style="list-style-type: none"> <li>Competitive: G3007.05</li> <li>StraP</li> <li>2007–2010</li> <li>LI/PI: IRRI/A Kumar</li> </ul>	Plant breeders in India and China	Large-effect QTLs for yield under drought stress available for drought tolerance MAB in rice in India and China	Rice germplasm with improved drought tolerance disseminated in Asia; improved capacity to map and deploy drought yield QTLs developed in Asian NARS
Target 2010: Materials	At least 20 high yielding and drought-tolerant lines identified among RILs and NILs disseminated via the INGER network			

Output	title, type and target(s)	Intended users	Outcome	Impact
<b>Output 21</b>	<b>Local germplasm enhanced via molecular breeding for target traits in tropical legumes (groundnuts, beans, cowpeas and chickpeas)</b> <ul style="list-style-type: none"> <li>• Focus: G6007.01–G6007.04 (inclusive)</li> <li>• StraP</li> <li>• 2007–2010 (Phase II: 2010–2013)</li> <li>• LIs/PIs: <ul style="list-style-type: none"> <li>• ICRISAT/V Vadez</li> <li>• ICRISAT/GCP (R Varshney)</li> <li>• CIAT/M Blair</li> <li>• UoC–Riverside/J Ehlers</li> </ul> </li> <li>• Linked to P1-06, P1-017, P4-01, P5-010 and P5-013</li> </ul>	Breeding programmes and, ultimately, small-scale farmers in resource-poor cropping systems	New germplasm and improved breeding programmes for tropical legumes in Africa	Germplasm available for drought-prone areas, increased yields in farmers' fields and increased incomes due to improved local varieties
<i>Target 2010: Materials</i>	Diversified breeding populations developed with resistance to diseases and tolerance to drought and heat			
<i>Target 2011: Practices</i>	Marker-assisted recurrent selection projects implemented for selection and recombination of drought-tolerant loci in targeted populations			
<i>Target 2012: Practices</i>	Marker-assisted recurrent selection projects implemented for selection and recombination of drought-tolerant loci in targeted populations			
<b>Output 22</b>	<b>Marker-assisted selection for resistance to streak virus in maize</b> <ul style="list-style-type: none"> <li>• Commissioned: G4008.19</li> <li>• StraP</li> <li>• 2008–2010</li> <li>• LI/PI: UKZN/M Laing</li> </ul>	Maize breeding programmes and, ultimately, small-scale farmers in resource-poor cropping systems in Southeast Africa	MAS for maize streak virus developed in Southeast Africa; hybrids and OPVs with streak virus resistance disseminated in Mozambique	New maize germplasm (with improved resistance to streak virus) for Southeast Africa
<i>Target 2010: Materials</i>	OPVs and hybrids with resistance to streak virus resistance developed using streak virus resistance markers deployed by UKZN			
<b>Output 23</b>	<b>Dry bean improvement and marker-assisted selection for diseases and abiotic stresses in Central America and the Caribbean</b> <ul style="list-style-type: none"> <li>• Commissioned: G4008.11</li> <li>• StraP</li> <li>• 2008–2010</li> <li>• PI/LI: INIFAP/JA Acosta-Gallegos</li> <li>• Linked to P4-01</li> </ul>			
<i>Target 2010: Materials</i>	20 best advanced lines distributed in partner countries			
<b>Output 24</b>	<b>Yield improvement of sorghum in Africa through marker-assisted recurrent selection (MARS) and a public-private partnership</b> <ul style="list-style-type: none"> <li>• Commissioned: G4008.48</li> <li>• StraP</li> <li>• 2009–2013</li> <li>• LI/PI: Agropolis–CIRAD/J-F Rami</li> <li>• Linked to P4-01, P5-04 and P5-08</li> </ul>	Sorghum breeding programmes in West Africa	Improved sorghum genotypes developed for marginal environments in Sahelian West African countries, and MARS protocols adapted to drought-prone environments	Sorghum yields enhanced in West Africa through a marker-assisted breeding approach developed by the private sector in the North and applied in the South
<i>Target 2010: Practices</i>	400 F <sub>3</sub> individual of each population genotyped with 150 SSR markers and 400 F <sub>4</sub> families of each population phenotyped in 4 different locations in Mali			
<i>Target 2011: Materials</i>	QTLs involved in target traits and environments detected, F <sub>4</sub> families genotyped for flanking markers of selected QTLs and improved lines from the material selected by MARS phenotyped in different locations			
<i>Target 2012: Materials</i>	A set of improved genotypes cumulating favourable alleles at selected QTLs chosen for successive cycles of recurrent selection			

Output	title, type and target(s)	Intended users	Outcome	Impact
<b>Output 25</b>	<b>Drought tolerant maize for Asia</b> <ul style="list-style-type: none"> <li>Commissioned: G4008.56</li> <li>StratP</li> <li>2008–2013</li> <li>LI/PI: CIMMYT/B Vivek</li> <li>Linked to P4-01</li> </ul>	Maize breeding programmes in China, India, Indonesia, Pakistan, Philippines, Nepal, Thailand and Vietnam	Drought-tolerant lines and hybrids identified and available to farmers	Maize yields enhanced in Asia through a marker-assisted breeding approach
<i>Target 2010: Practices</i>	Top-crosses of BC <sub>1</sub> F <sub>2</sub> and BC <sub>2</sub> F <sub>2</sub> phenotyped and genotyped			
<i>Target 2011: Materials</i>	Double haploids extracted from BC <sub>1</sub> C <sub>2</sub> and BC <sub>2</sub> C <sub>2</sub>			
<i>Target 2012: Materials</i>	4*200 doubled haploids of 4 MARS-improved populations between two DT CIMMYT line and 4 Asian adapted elite maize inbreds			
<b>Output 26</b>	<b>QTL mapping and implementation of marker-assisted recurrent selection (MARS) for improvement of drought tolerance in cassava</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>CI1</li> <li>2010–2013</li> <li>LI/PI: CIAT/E Okogbenin</li> <li>Linked to P1-018, P2-07, P4-01 and P5-014</li> </ul>	Cassava breeders in Africa	Main loci involved in drought tolerance identified and pyramided in cassava varieties	Improved cassava varieties with improved productivity under drought conditions
<i>Target 2010: Practices</i>	Drought evaluation of segregating drought-targeted population in South America; development of breeding populations suitable for MARS approach to drought tolerance in West Africa			
<i>Target 2011: Materials</i>	Identification of main drought tolerance QTLs in South American population; genotyping and drought evaluation of West African MARS populations			
<i>Target 2012: Materials</i>	Identification of main drought and yield QTLs to recombine in West African cassava breeding populations; start of QTL pyramiding process			
<b>Output 27</b>	<b>Molecular breeding for drought tolerance in rice in Africa</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>CI4</li> <li>2010–2013</li> <li>LI/PI: AfricaRice/MN Ndjiondjop</li> <li>Linked to P4-01 and P5-012</li> </ul>	Rice breeders in Africa	New drought-tolerant QTLs identified and recombined for implementation in African rice breeding programmes	New African rice varieties with improved performance under drought conditions
<i>Target 2012: Materials</i>	Three F <sub>3</sub> biparental breeding populations adapted to the target country and improved for drought tolerance and biotic stresses such as RYMV resistance			
<b>Output 28</b>	<b>Molecular breeding for drought tolerance in wheat for China and India</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>CI6</li> <li>2010–2013</li> <li>LI/PI: IARI/V Prabhu (for India); CAAS/R Jing (for China)</li> <li>Linked to P1-014, P1-016, P4-01</li> </ul>	Wheat breeders in India and China	New drought-tolerant QTLs transferred, validated and used for breeding in Indian and Chinese germplasm	New wheat varieties for India and China with improved performance under drought conditions
<i>Target 2010: Materials</i>	Confirmation of presence of drought tolerance QTL in crosses with adapted background			
<i>Target 2011: Materials</i>	Potentially drought-tolerant F <sub>4</sub> lines prepared for yield testing			
<i>Target 2012: Materials</i>	20-30 recombinant substitution lines evaluated for drought tolerance			

# Project 4 – SP4: Bioinformatics and crop information systems

## Project narrative

### Project overview and rationale

Bioinformatics and information systems are the heart and arteries of any research network and particularly so for the GCP which is dispersed over many disciplines and locations. Project 4 (GCP SP 4) has developed infrastructure to network diverse databases and supported tools and standards for the integration and analysis of data from different sources and disciplines. In addition it has established procedures and infrastructure for storage and publication of quality data for reuse as global public goods.

With the shift in emphasis and focus of GCP in phase II, SP4 has made conformable adjustments. Emphasis in this MTP is on user support, both for the molecular breeding platform and for the Challenge Initiatives. The previous themes for SP4 are somewhat out of step with the directions of GCP in Phase II. This has resulted in strained classification of some Outputs in the previous MTP. For example, research into phylogenomics is classified in Infrastructure, and development of the Informatics Platform into Quality Improvement. For 2010 onwards, Project 4 Outputs will be organised four Themes covering i) user support; ii) data curation and quality; iii) methodology development; and, vi) infrastructure.

User support to GCP scientists and MBP users will be a priority. Work continues on defining standards and procedures for quality data management and an important contribution is the development of crop ontologies which will contribute to the international effort in biological standards.

With the new emphasis on molecular breeding, methodology development will focus on breeding questions using statistics, quantitative genetics, simulation and modeling to develop new analysis methods for molecular breeding. Similarly, further development of informatics infrastructure will concentrate on networking breeding information and delivering new and improved applications for breeding logistics and decision support.

### Impact pathways

Project 4 achieves its main impact through service to activities in other projects of the GCP and to external users of the platforms: namely GSS, GRSS and MBP. The project will work

towards delivering 13 outputs during this MTP period, and these are organised into four themes which have different impact targets.

Theme 1: User Support – Ensure that all GCP scientists have access to advice and tools to facilitate data management, analysis and publication

Theme 2: Data Curation and Quality – Provide access to fully documented GCP data of certified quality for GCP partners and other interested researchers

Theme 3: Methodology Development – Bioinformatics research required to provide the methodology and informatics tools needed for GCP and MBP activities

Theme 4: Informatics Infrastructure – Provide standards, guidelines and facilities for data integration and sharing among GCP and MBP partners

***Theme 1: User support – Ensure that all GCP scientists have access to advice and tools to facilitate data management, analysis and publication***

#### ***Output 1 to Output 3***

Output 1 is concerned with establishing and managing the Molecular Breeding Portal which will be the key entry point for breeders wishing to use the platform services and applications to undertake molecular breeding. A key objective of Output 2 is the curation of historical breeding information into the breeding databases so that logistical and analysis tools have a basis from which to develop lists and fieldbooks for the next steps in the breeding cycle and to undertake analysis for breeding decisions. Output 3 concentrates on the appropriate design and analysis of GCP research and MBP breeding projects. This will have impact on quality of data and precision of conclusions.

All outputs in this theme will affect the efficiency and effectiveness of GCP research and molecular breeding. Immediate users of these outputs will be researchers and breeders focusing on development agriculture, and their use of these tools, methodologies and knowledge will speed up the development of new technologies and cultivars for adoption by farmers in the developing world.

***Theme 2: Data curation and quality – Provide access to fully documented GCP data of certified quality for GCP partners and other interested researchers***

***Output 4 to Output 6***

Output 4 continues the work of standards development for data quality and integration. The development of crop ontologies through this activity will provide important standards for the global community to annotate data in a way that makes it comparable across studies and even across crops – a critical step in realising the potential for comparative biology to overcome constraints in less studied crops by transferring knowledge from better studied ones. Some of the less studied crops are nevertheless critical for food security in developing countries.

Output 5 deals with the curation and quality assurance of GCP data and its publication as global public goods for secondary use. Output 6 aims to improve the quality of genotyping data from GCP commissioned laboratories. This will impact the speed and efficiency of breeding efforts as well as improve our understanding of the structure and potential of genetic resource collections.

This focus on standards and quality of data will have impact on future research by speeding it up, increasing the usefulness of conclusions and avoiding duplication, which in turn will lead to the faster release of improved technologies and cultivars for farmers.

***Theme 3: Methodology development – Bioinformatics research required to provide the methodology and informatics tools needed for GCP and MBP activities***

***Output 7 to Output 10***

Output 7 comprises a major effort to develop new methodologies for analysis of molecular breeding data. These methodologies are needed for new molecular-assisted breeding techniques such as marker-assisted recurrent selection (MARS) and genome-wide marker-assisted selection (GWMAS) which promise to exploit quantitative genetic variation within breeding populations. This will impact the speed and efficiency of breeding new cultivars with improved quantitative traits such as yield potential and drought tolerance.

Output 8 brings together the Outputs of two successful activities from previous years: GOST, a web-based, fast and user-friendly comparative genomics programme, and 'Dayhoff', an online resource to document stress-response genes comparatively across plant species. Building on their success, it was decided to create a new activity that would aim at combining these tools and expanding the underlying database, to increase the quality and functionality of products.

The next Output in this theme is concerned with methodology for breeding for drought tolerance in rainfed lowland rice. This involves identifying traits related to drought tolerance, developing screening methods and location of QTL as well as characterisation of drought stress environments using GIS and crop models.

Output 10 will have an impact on the effectiveness and speed of research into overcoming the constraints of less studied crops. Next generation sequencing can quickly lead to the genomic resources required to support functional genomics and breeding in these crops, but is constrained by a lack of publicly available analysis tools. This output will provide those tools.

All these outputs lead to new or improved methodologies which will be used by biologists and breeders to improve the focus and efficiency of their research towards new methodologies and cultivars for adoption by farmers.

***Theme 4: Informatics infrastructure – Provide facilities for data integration and sharing among GCP and MBP partners***  
***Output 11 to Output 13***

Output 11 will enable and improve the efficiency of molecular breeding by providing a suite of data management and logistic tools to support breeding. One of the major constraints to the adoption of molecular breeding is the need for better logistical support and information management. This output aims to make existing tools available to users of the MBP.

Output 12 continues the development of platform infrastructure to support GCP research through integrated data sources and analysis tools which will enhance the quality and focus of GCP research. This includes a wide range of facilities split across different outputs during Phase I of GCP – namely web services, high performance computing, tools for functional genomics and query and visualisation interfaces for data integrated across diverse data sources and disciplines.

The final output in this theme will bring the same integration and workbench technology to the MBP to support integration of data from different sources to improve breeding decisions and provide a customisable workflow system which will improve the speed and efficiency of molecular breeding to deliver new cultivars to farmers in developing countries.

The focus of Theme 4 is on facilities and infrastructure for data integration. This is a crucial element in modern biological research and crop improvement. Having integrated data sources and analysis tools able to provide insights through analysis across data sources and data types will increase the effectiveness and efficiency of agricultural research for development.

## Changes from previous MTP

This MTP represents a major reorganisation of activities in Project 4. This was necessary due to the maturity of several activity streams and well as to support the orientation of the GCP in Phase II following the EPMP. Project themes for *User support*, *Data curation and quality*, and *Informatics infrastructure* have been refined and re-ordered from the previous MTP and a new theme, *Methodology development*, has been added.

*User support*, theme 1 in this MTP, has been strengthened and expanded to cover MBP activities. Output 1 is a new output covering management and support for the MBP. Output 2 is also new and covers support for curation of breeding data for users of the MBP. Output 3 continues and expands the statistical support service of Output 4.11 of the 2009–2011 MTP to cover support for breeding projects using the MBP.

Theme 2, *Data curation and quality*, focuses on the development and publication of standards and best practices for data management. Output 4 amalgamates ontology development activities, the development of the Central Registry and the development of the phenotyping template (Outputs 4.1, 4.3 and 4.4 respectively of the 2009–2011 MTP). Output 5 continues and expands the work of Output 4.10 of the 2009–2011 MTP, by supporting the further development of the Informatics Helpdesk and its integration into the MBP portal to support molecular breeding. It also includes support for management of breeding databases and applications. Output 6 carries over a scaled-down version of Output 4.8 from the 2009–2011 MTP. This Output failed to start in 2008 due to staffing constraints and an over-ambitious programme so the new version represents a pilot case study with one laboratory to test the effectiveness of the approach to implementing quality management procedures.

The new theme, *Methodology development* comprises four outputs. Output 7 is new and supports the development of statistical and informatics methodology to support molecular breeding. Output 8 is inherited from Output 4.12 of the 2009–2011 MTP. It reorients support for Subprogramme 2 research towards the development of tools for analysis of Next Generation Sequencing data. Output 9 is the same as Output 4.17 in the 2009–2011 MTP with output targets delayed by one year due to the slow start of the project resulting from contract delays with a new GCP partner.

The fourth and final theme, *Informatics infrastructure*, has three outputs. Output 11 will support the adoption, adaptation and deployment of existing applications to support molecular breeding. It will continue and expand the work of Output 4.13 from the 2009–2011 MTP but will

concentrate initially on logistics tools. Output 12 continues the GCP Informatics Platform development combining the activities of Outputs 4.1 (domain model part), 4.2, 4.5, 4.6 and 4.9 from the 2009–2011 MTP. Output 13 is a new output to develop new infrastructure to support molecular breeding using technology from the GCP Informatics Platform (Output 12).

Looking at the evolution of the 2009–2011 MTP to 2010–2012 we now have the following Output changes:

1. Output 4.1 *Domain model maintenance* continues in Output 12
2. Output 4.1 *Ontology development* continues in Output 4
3. Output 4.2 continues in Output 12
4. Output 4.3 continues in Output 4
5. Output 4.4 continues in Output 4
6. Output 4.5 continues in Output 12
7. Output 4.6 continues in Output 12
8. Output 4.7 is completed
9. Output 4.8 is scaled down and becomes Output 6
10. Output 4.9 continues in Output 12
11. Output 4.10 continues in Output 5
12. Output 4.11 continues in Output 3
13. Output 4.12 changes emphasis and continues in Output 8
14. Output 4.13 is completed with products supported in Output 11
15. Output 4.14 is completed
16. Output 4.15 is completed
17. Output 4.16 will be completed in 2010 as Output 8
18. Output 4.17 becomes Output 9 with a delayed timeframe due to late start.

## Output descriptions and partnerships

### Overview

In this MTP, SP4 has 13 Outputs. The partnerships in SP4 are presented by Output, corresponding to the MTP logframe. All partners listed have a collaborative role in the research of the respective Output, and the lead institute (LI) with principal responsibility (ie, where the PI is located) is indicated, as well as the type of project and the funding mechanism.

Typically, bioinformatics tools and methods are developed in ARIs and CGIAR centres, and made available to partners by ARIs, CGIAR centres and developing country institutes. SP4 largely operates through central 'nodes' or 'hubs' but the impact goes beyond the institute hosting the node and is of relevance and benefit to developing country programme collaborators and associates. It should be noted that as SP4 increasingly shifts focus from infrastructure development to infrastructure release and use, developing country institute participation in SP4 activities is expected to increase. Several

tools will be tested by a diverse set of NARS partners involved in breeding activities in GCP target environments, and feedback will be taken into account to improve the tools and identify new needs.

### **Output descriptions**

For each Output below, the Lead Institute (LI), PI, type of project and funding mechanism are all indicated.

#### **Theme 1: User support – Ensuring that all GCP scientists have access to advice and tools to facilitate data management, analysis and publication**

*Output 1: A portal for the Molecular Breeding Platform established and managed*

- Commissioned: Project No. TBD
- StraP
- 2009–2013
- LI/PI: GCP/G McLaren
- Linked to P3-O15 to P3-O18, P3-O21, P3-O23 to P3-O28, P5-O1, P5-O16 and P5-O20

The Molecular Breeding Portal will provide access to all the tools and services of the Molecular Breeding Platform. It will be a web-based portal where users can select and download tools and instructions, as well as order material and procure laboratory services. There will be a helpdesk facilitating the use of the portal and updating of the interface, as well as providing access to the different elements of the platform for users who cannot efficiently use the web-based interface (eg. via CD and other non-internet-based media). The portal and Helpdesk will provide a focal point and collaborative environment for the development of breeding communities of practice. This Output links to MABC projects for cassava, rice, sorghum and maize and MARS projects for legumes, sorghum, maize, cassava, rice and wheat in Project 3 and to MBP activities for training and support for communities of practice in Project 5.

*Output 2: Quality, integration and access for GCP and MPB data ensured*

- Commissioned: Project No. TBD
- StraP
- 2009–2013
- LI/PI: GCP/G McLaren
- Linked to P5-O1, P5-O16 and P5-O20

This Output provides support and training to researchers responsible for managing MBP data. It will provide training materials and consultation through a helpdesk attached to the MBP Portal. This Output ensures the standards and best practices developed through SP4 Output 4 can be put into practice in all MBP projects. It will provide advice and assistance with curating historical breeding data into breeding databases so that the breeding data management applications have primary data as input to the breeding workflows. This

project links to the training and expert support activities of Project 5 and to all GCP and MBP projects for support in data management and curation.

*Partners: IRRI, CIMMYT, AAFCS-SPARC*

*Output 3: Statistical support provided for the design and data analysis of GCP and MBP projects*

- Commissioned: G4006.35
- StraP
- 2006–2013
- LI/PI: WUR/M Malossetti
- Linked to P5-O1 and P5-O20

The statistical service for design and analysis of GCP and GSS experiments established under Output 4.11 of the previous MTP is continued and expanded to cover MBP. It provides training and consultation on design, analysis and interpretation of GCP and GSS research experiments and ensures that proposals include the best statistical practices. For breeders it will provide support on statistics, bioinformatics, quantitative genetics and molecular biology and it will ensure that the methodology developed for design and analysis of breeding trials is rapidly available to the users. This project links to training and expert services for the MBP in Project 5 and to all GCP and MBP projects requiring statistical services.

*Partners: Agropolis-CIRAD, CIMMYT*

#### **Theme 2: Data curation and quality – Provide access to fully documented GCP data of certified quality for GCP partners and other interested researchers.**

*Output 4: Data standards and best practices for capture and publication of quality GCP and MBP data developed and used*

- Commissioned: G4009.03
- StraP
- 2009–2012
- LI/PI: Bioversity-France/E Arnaud
- Linked to P1-O1, P1-O4, P3-O6 and P3-O8 to P3-O10

This output continues the work of Outputs 4.2, 4.3 and 4.4 of the 2009–2011 MTP in defining data standards, crop ontologies, best practices for data management and templates for data input. These standards, best practices and tools ensure GCP and MPB data will have appropriate quality and annotation to be of value for secondary use. This Output also continues the management and development of the Central Registry of GCP datasets which ensures the preservation, publication and re-use of this data as global public goods. This project has explicit links to the Project 1 activities on standards and quality assurance for data on the reference collections, but also links to Project 3 for use of crop ontologies in the Phenotyping Network and development of the ontologies through the phenotyping projects.

*Partners: CIMMYT, IRRI, CIP, ICRISAT, WUR*



*Output 5: Informatics and data management support to GCP and MBP scientists*

- Commissioned: Project No. TBD
- StraP
- 2009–2013
- LI/PI: GCP/G McLaren
- Linked to P5-O1, P5-O16 and P5-O20

This output continues the work of Output 4.10 in the previous MTP but extends its scope to include a service for the MBP. It will maintain and update the SP4 Informatics Helpdesk and Bioinformatics Portal and ensure these are accessible from the MBP portal also. It will extend support to data managers on the installation and maintenance of breeding databases and applications. Requests for support will be acted upon within 48 hours, indicating which tool to use or which expert to consult. Links to activities in Project 5 on training, support for communities of practice and expert services for the MBP. Links to all GCP and MBP projects requiring support for information systems.

*Partners:* WUR, IRRI, CIMMYT, AAFC–SPARC

*Output 6: Quality management procedures in GCP research laboratories promoted*

- Commissioned: G4008.32
- StraP
- Timeframe: Ongoing; extension decided on an annual basis
- LI/PI: CIMMYT/G Davenport
- Linked to P5-O21

This output picks up the work of Output 4.8 in the previous MTP which did not get started until 2009 due to unavailability of specialist staff to undertake the technical work. A scaled-down pilot project is being undertaken to determine the success of the approach and its impact on quality of GCP Genotyping work. It aims to consult with the BecA Laboratory to implement formal Quality Management Procedures and to provide a workshop for a wider group on these procedures. Links to the Genotyping Support Service activity of Project 5.

*Partners:* FERA and BecA

***Theme 3: Methodology Development–Bioinformatics research required to provide the methodology and informatics tools needed for GCP and MBP activities***

*Output 7: A toolbox of analysis and decision support applications to support molecular breeding developed*

- Commissioned: Project No. TBD
- StraP
- 2009–2013
- LI/PI: GCP/G McLaren
- Linked to P3-O3, P5-O1 and P5-O20

This Output will develop statistical and quantitative genetic methods for the analysis of molecular breeding data and develop methodology for tracing marker alleles through breeding populations and predicting progeny genotypes

so that crossing schemes can be developed to increase the frequency of beneficial alleles. It will also enhance genetic simulation tools and make them accessible to breeding projects for analysis of strategic and tactical options. Links to activities on Project 3 using simulation tools for breeding decisions and to activities in Project 5 supporting training and expert advice for the MBP.

*Partners:* WUR, CIMMYT, Agropolis–INRA, UoQ, CSIRO, CAAS

*Output 8: Large-scale phylogenomic analyses tools developed for gene function prediction for GCP crops*

- Commissioned: G4008.21
- StraP
- 2008–2010
- LI/PI: BI/M Rouard
- Linked to P2-O6

As part of the 2008–2010 MTP Output 4.6, a rapid and user-friendly web-based comparative genomics programme, GreenPhyl Orthologous Search Tool (GOST) was implemented, allowing biologists to perform online phylogenomic analysis. In parallel, as 2008–2010 MTP Output 4.19, an online resource called Dayhoff was developed to document stress-responsive genes comparatively across plant species. Since both products have been very well received by the plant genomic community, a new activity has been designed to combine these tools and expand the underlying database, so as to increase the quality and functionality of the products. The Output is an extension of Output 4.16 in the 2009–2011 MTP, allowing completion of that work which has been slower than expected due to staffing delays. Links to activities in Project 3 developing cross-species genomics resources.

*Partners:* Agropolis–CIRAD, IRRI

*Output 9: Breeding drought tolerance for rainfed lowland rice in the Mekong region*

- Competitive: G3008.09
- StraP
- 2009–2012
- LI/PI: BRRD/B Jongdee

This project will develop strategies and protocols for selection of drought-tolerant genotypes. It will start by using diverse populations to identify germplasm adapted to aerobic and anaerobic conditions which also have tolerance to vegetative stage and flowering stage drought. It will identify traits related to drought tolerance as well as screening methods and QTL for those traits, and it will use GIS and crop modelling to characterise drought-prone environments. Finally, drought-tolerant cultivars with appropriate grain and eating quality will be selected using farmer participatory selection.

*Partners:* BIOTEC, UoQ, NAFRI, CARDI

*Output 10: Methodology, tools and support available for analysis and interpretation of Next Generation Sequencing data*

- Commissioned: G4009.04
- StraP
- 2009–2010
- LI/PI: ICRISAT/RK Varshney
- Linked to P2-O2 and P2-O12

Next generation sequencing methods have the capacity to accelerate acquisition of genomic resources. NGS methods however generate a deluge of data; the shorter read lengths require considerable bioinformatics effort in assembly. The choices of methods available to dealing with this kind of data are many and depend on the technology used as well as the biological application. Since the sequencing itself is being carried out at NCGR and uses the NCGRs computational pipeline, bioinformatics efforts at ICRISAT are related to putting together an open access, open-source alternative to the NCGR proprietary pipeline. Links to activities in Project 2 developing genomic resources for chickpea and undertaking allele discovery in sorghum.

*Partners:* NCGR, TSL, IRRI

***Theme 4: Informatics Infrastructure–Provide facilities for data integration and sharing among GCP partners***

*Output 11: Existing tools for data management and logistics of molecular breeding available to MBP users*

- Commissioned: Project No. TBD
- StraP
- 2009–2013
- LI/PI: GCP/G McLaren
- Linked to P5-O1, P5-O16 and P5-O20

This output will adopt and adapt existing applications for data management and logistics of molecular breeding and make them available to users of the MBP. These tools include applications for pedigree information management, field data management and laboratory information management. The first element provides tools to facilitate sample and pedigree tracking for lists of germplasm to be evaluated in nurseries, trials or laboratory assays. The second provides applications which facilitate the production of electronic fieldbooks for germplasm screening, characterisation and evaluation. The third element ensures the quality and compatibility of genotyping data so that it can be integrated with pedigree information and phenotype data in a breeding database. Links to activities in Project 5 providing training, supporting communities and providing expert advice for users of the MBP.

*Partners:* IRRI, CIMMYT, ICRISAT, AAFCS-SPARC

*Output 12: Integrated GCP Informatics Platform created*

- Commissioned: G4006.16
- StraP
- 2006–2013
- LI/PI: IRRI/M Senger
- Linked to P1-O2, P2-O2, P2-O4 and P2-O10

Based on a formal domain model, a three-layer architecture has been defined and implemented in the GCP Informatics Platform to facilitate the integration of diverse data sources and analysis tools to provide an informatics workbench to support biological research. This Platform has been implemented in two main environments: Koios for web-based applications and Genomedium for client-based applications. This Output develops these further and improves functionality for the analysis of genetic diversity, functional genomics and crop improvement. This is a continuation of the 2009–2011 MTP Outputs 4.1, 4.2, 4.5 and 4.6. This Output has explicit links to activity in Project 1 publishing data for genetic resources, activities in Project 2 developing genetic and genomic resources for chickpea, groundnut and pigeonpea as well as to all projects publishing data in public databases connected to the platform.

*Partners:* IRRI, Agropolis–CIRAD, CIMMYT, ICRISAT, CIP, BI

*Output 13: Information network and configurable workflow system for molecular breeding developed and deployed*

- Commissioned: Project No. TBD
- StraP
- 2009–2013
- LI/PI: GCP/G McLaren
- Linked to P5-O1, P5-O16 and P5-O20

This Output will use the technology developed for the GCP Informatics Platform (Output 12) to implement a network of breeding information resources so that local breeding information from any breeding project can be integrated with public information and analysed to provide better predictions for breeding decisions. This output will also use the platform technology to develop a web-based, configurable workflow system for data management, logistics and analysis of breeding information. This system will gradually replace the existing tools supported through Output 11. This Output links to activities in Project 5 providing training, supporting communities and providing expert advice to users of the MBP.

*Partners:* IRRI, CIMMYT, ICRISAT, AAFCS-SPARC

## International public goods

SP4 is primarily concerned with producing international public goods and making them available worldwide. All software developed in SP4 is, in principle, made available under licenses approved by the Open Source Initiative (OSI), preferably the GNU General Public License (GPL) or GNU Lesser General Public License (LGPL). All web services created in SP4, both for databases and analytical facilities, are freely available to any interested user. Documentation and training materials are freely available and, where possible, released under open content licenses to ensure their availability for re-use and improvement.

## Elaboration of partner roles

Under the theme of *User support*, partners have the skills and experience to train and support GCP researchers in biometrics, bioinformatics and data management. Researchers at WUR in the Netherlands and at Agropolis–CIRAD in France are key partners in supplying support for statistics and data quality, and the research informatics teams at IRRI, CIMMYT, ICRISAT, Bioversity International and CIP provide specialist support for analysis of particular data types and for the maintenance and use of particular informatics applications.

Under theme 2, *Data curation and quality*, the development of data standards requires a large network of crop specialists coordinated by Bioversity International and CIMMYT. These specialists, based in many CGIAR centers and ARIs, work in teams to develop crop ontologies. Partners at IRRI, CIMMYT and AAFC–SPARC in Canada have skills in installing and maintaining breeding applications, and researchers from Central Science Laboratories, UK, are specialists in quality management procedures.

For methodology development, our partners are world experts in statistical methodology (WUR, CIMMYT), quantitative genetics (Agropolis–INRA, CAAS), genetic simulation and eco-physiological modelling (UoQ and CSIRO), phylogenomics (Bioversity International), bioinformatics (ICRISAT) and breeding methodology (BRRD). These experts are conducting research into new methodologies and GCP has focused these diverse efforts towards providing tools to improve genetic resource use and crop improvement.

SP4's Informatics infrastructure work is being developed by partners with skills and experience in software engineering and database development at IRRI, CIMMYT, Bioversity International, Agropolis–CIRAD, ICRISAT, CIP, AAFC-SPARC, CSIRO and UoQ.

## Project 4 logframe – SP4: Bioinformatics and crop information systems

Notes:

1. Each Output is followed by:

- a) the type of research activity/funding contributing to the Output (commissioned, competitive, focus, or discretionary) and GCP project number
- b) Identification of Output as a StraP (Strategic project) or CI (Challenge Initiative) project

- c) start and end year, and
  - d) the lead institute (LI) and Principal Investigator(s) (PI[s]) responsible for the Output (and its Output targets).
2. Some Outputs are managed internally within GCP, in some cases involving coordination of a number of external institutes. In most such cases, the entry under 'PI' is denoted as 'Various'.

Output	title, type and target(s)	Intended Users	Outcome	Impact
<b>Theme 1: User Support–Ensuring that all GCP scientists have access to advice and tools to facilitate data management analysis and publication</b>				
<b>Output 1</b>	<b>A portal for the Molecular Breeding Platform established and managed</b> <ul style="list-style-type: none"> <li>• Commissioned: Project No. TBD</li> <li>• StraP</li> <li>• 2009–2013</li> <li>• LI/PI: GCP/G McLaren</li> <li>• Linked to P3-015 to P3-018, P3-021, P3-023 to P3-028, P5-01, P5-016 and P5-020</li> </ul>	Plant breeders using molecular breeding techniques	Plant breeders gain access to public crop information and configurable informatics applications to conduct successful molecular breeding projects	New cultivars are developed sooner and more efficiently and used by farmers to improve food security and increase livelihoods in developing countries
<i>Target 2010: Capacity</i>	MBP, including Steering Committee, business plan, manager and communications strategy established; MBP developed, deployed and managed			
<i>Target 2011: Capacity</i>	MBP managed under direction of Steering Committee and in consultation with users; portal updated according to user requirements			
<i>Target 2012: Capacity</i>	MBP managed under direction of Programme Steering Committee and in consultation with users; portal updated according to user requirements			

Output	title, type and target(s)	Intended users	Outcome	Impact
<b>Output 2</b>	<b>Quality, integration and access for GCP and MPB data ensured</b> <ul style="list-style-type: none"> <li>• Commissioned: Project No. TBD</li> <li>• StraP</li> <li>• 2009–2013</li> <li>• LI/PI: GCP/G McLaren</li> <li>• Linked to P5-01, P5-016 and P5-020</li> </ul>	Data managers supporting GCP research projects or molecular breeding projects using the MBP	Research and crop improvement data managed with appropriate quality standards and annotated in sufficient detail to be integrated with data from other research and breeding projects to facilitate meta analysis and data mining for better research and breeding decisions	Research and breeding improved and accelerated in their delivery of technologies and improved cultivars used by farmers to improve food security and livelihoods
<i>Target 2010: Capacity</i>	Methodology for management and curation of breeding data developed and deployed on the MBP portal; MBP user case projects able to curate current and historical data into breeding databases; best practices, standard operating procedures and templates developed for each priority crop in the MBP			
<i>Target 2011: Capacity</i>	Crop databases identified/established for GCP target crops with data managers able to include public MBP breeding data			
<i>Target 2012: Capacity</i>	Methodology for integration and access to GCP and MBP data maintained and updated; tools for collaborative use among MBP communities of practice available on the MBP portal			
<b>Output 3</b>	<b>Statistical support provided for the design and data analysis of GCP and MBP projects</b> <ul style="list-style-type: none"> <li>• Commissioned: G4006.35</li> <li>• StraP</li> <li>• 2006–2013</li> <li>• LI/PI: WUR/M Malossetti</li> <li>• Linked to P5-01 and P5-020</li> </ul>	Germplasm specialists and plant breeders within GCP; NARS collaborators reached through GSS	More efficiency in data handling and analysis for scientists involved in GCP and GSS activities	Increased efficiency in crop research and improvement
<i>Target 2010: Capacity</i>	Proactive support provided to GCP, MPB and NARS scientists for design and analysis of research and breeding projects; statistical methodology developed, tested and packaged for training and support through P5020			
<i>Target 2011: Capacity</i>	Proactive support provided to GCP, MPB and NARS scientists for design and analysis of research and breeding projects; statistical methodology developed, tested and packaged for training and support through P5020			
<i>Target 2012: Capacity</i>	Proactive support provided to GCP, MPB and NARS scientists for design and analysis of research and breeding projects; statistical methodology developed, tested and packaged for training and support through P5020			
<b>Theme 2: Data Curation and Quality - Provide access to fully documented GCP data of certified quality for GCP partners and other interested researchers.</b>				
<b>Output 4</b>	<b>Data standards and best practices for capture and publication of quality GCP and MBP data developed and used</b> <ul style="list-style-type: none"> <li>• Commissioned: G4009.03</li> <li>• StraP</li> <li>• 2009–2012</li> <li>• LI/PI: BI–France/E Arnaud</li> <li>• Linked to P1-01, P1-04, P3-06 and P3-08 to P3-010</li> </ul>	Bioinformatics and biodiversity scientists worldwide	High quality, fully annotated GCP and MBP data made accessible to scientists and breeders worldwide	Better access to quality, integrated research data for crop researchers and improvement of programmes speeds up and increases the efficiency of research and breeding
<i>Target 2010: Practices</i>	Methodology for crop ontology development produced and validated and a community of practice based on crop experts created; Central Registry upgraded, enabling a readily secondary use of quality data sets; quality of data sets linked to the reference sets improved and documented; assurance that data sets produced in GCP projects are uploaded to Central Registry using enhanced templates			

<b>Output</b>	<b>title, type and target(s)</b>	<b>Intended users</b>	<b>Outcome</b>	<b>Impact</b>
<i>Target 2011: Practices</i>	Validated agronomic trait ontologies produced for GCP priority crops; management of metadata for GCP datasets in the CR improved; a workflow for managing GCP data files including reporting on data-quality and secondary use defined; Crop Registry integrated into the GCP project WMS; assurance that the data sets produced in GCP projects are uploaded to the Central Registry using enhanced templates			
<i>Target 2012: Practices</i>	Agronomic trait ontologies for the GCP priority crops refined; assurance that data sets produced in GCP projects are uploaded to the Central Registry using enhanced templates			
<b>Output 5</b>	<b>Informatics and data management support to GCP and MBP scientists</b> <ul style="list-style-type: none"> <li>• Commissioned: Project No. TBD</li> <li>• StraP</li> <li>• 2009–2013</li> <li>• LI/PI: GCP/G McLaren</li> <li>• Linked to P5-01, P5-016 and P5-020</li> </ul>	Bioinformatics and biodiversity scientists worldwide	User bioinformatics capabilities enhanced through better access to GCP Subprogramme 4 products and expertise	Increased efficiency in GCP crop research and improvement
<i>Target 2010: Capacity</i>	Helpdesk, website and bioinformatics portal maintained and integrated into the MBP; quality of collected data sets checked with support from the help desk; SP1 backlog data and phenotyping data loaded in the Central Registry; data managers from MBP user case projects familiar with installation and management of breeding databases and logistical applications			
<i>Target 2011: Capacity</i>	Helpdesk, website and bioinformatics portal maintained within the MBP portal; methodology and tools for installation and management of breeding databases and applications updated and enhanced			
<i>Target 2012: Capacity</i>	Data managers for new and old users of the MBP supported in the installation and management of breeding databases, applications and their integration into the breeding information network			
<b>Output 6</b>	<b>Quality management procedures in GCP research laboratories promoted</b> <ul style="list-style-type: none"> <li>• Commissioned: G4008.32</li> <li>• StraP</li> <li>• Timeframe: Ongoing; extension decided on an annual basis</li> <li>• LI/PI: CIMMYT/G Davenport</li> <li>• Linked to P5-021</li> </ul>	Laboratory staff commissioned by GCP to undertake genotyping analysis	Quality of GCP data production better assured and managed at source	More reliable data and thus better crop research leading to improved technologies and cultivars used by farmers
<i>Target 2010: Practices</i>	Existing practices for one selected laboratory reviewed; workshop and consultancy organised to develop and build capacity in quality management			
<i>Target 2011: Practices</i>	TBD depending on the success and impact of the pilot case			
<b>Theme 3: Methodology Development – Bioinformatics research required to provide the methodology and informatics tools needed for GCP and MBP activities</b>				
<b>Output 7</b>	<b>A toolbox of analysis and decision support applications to support molecular breeding developed</b> <ul style="list-style-type: none"> <li>• Commissioned: Project No. TBD</li> <li>• StraP</li> <li>• 2009–2013</li> <li>• LI/PI: GCP/G McLaren</li> <li>• Linked to P3-03, P5-01 and P5-020</li> </ul>	Plant breeders using molecular breeding techniques	Plant breeders have access to analysis and decision support methodology to conduct successful molecular breeding projects	New cultivars are available and used by farmers to improve food security and increase livelihoods in developing countries
<i>Target 2010: Other kinds of knowledge</i>	Methodology for basic experimental design and analysis for molecular breeding published; methodology and decision support tools for tracing parental origin of markers in biparental recombinant populations for molecular breeding developed; prototype simulation module for MARS breeding developed			

Output	title, type and target(s)	Intended users	Outcome	Impact
<i>Target 2011: Other kinds of knowledge</i>	Methodology for mixed model framework for QTL, GxE and QTLxE analysis for molecular breeding developed, tested and published; methodology and decision support tools for tracing parental origin of markers in multi-parental recombinant populations for molecular breeding developed; simulation platform enhanced with facilities for modeling epistatic networks			
<i>Target 2012: Other kinds of knowledge</i>	Methodology for meta analysis of QTL experiments and breeding data developed, tested and published; implementation of new methods to optimise allele assembly in breeding populations; simulation using integrated eco-physiological models and genetic models available; mature simulation module for MARS breeding released.			
<b>Output 8</b>	<b>Large-scale phylogenomic analyses tools developed for gene function prediction for GCP crops</b> <ul style="list-style-type: none"> <li>• Commissioned: G4008.21</li> <li>• StraP</li> <li>• 2008–2010</li> <li>• LI/PI: BI/M Rouard</li> <li>• Linked to P2-06</li> </ul>	Bioinformaticians within GCP and worldwide	Users are better able to predict gene function	Increased efficiency in crop research and improvement
<i>Target 2010: Other kinds of knowledge</i>	Integration of multiple full genomes of other plants into GreenPhyl; nhancement of the clustering methodology and phylogenetic analysis; GHOST application enhanced to accept nucleic acid sequences, multiple sequences and use the HPC for computations; enhanced web access and web interface; Community of practice for plant family curation established with Web 2.0 curation tools; GCP functional genomics data cross-referenced to gene families in GreenPhyl			
<b>Output 9</b>	<b>Breeding drought tolerance for rainfed lowland rice in the Mekong region</b> <ul style="list-style-type: none"> <li>• Competitive: G3008.09</li> <li>• StraP</li> <li>• 2009–2012</li> <li>• LI/PI: BRRD/B Jongdee</li> </ul>	Farmers in the Mekong Region, breeders in Thailand, Laos and Cambodia, scientists working on rainfed lowland rice	Improved methodology and genomic regions identified for drought screening in rainfed lowland rice	Improved drought tolerant cultivars to be used by farmers in the Mekong region
<i>Target 2010: Materials</i>	Two populations selected for aerobic and anaerobic conditions, different soil properties and for drought tolerance in pot experiments and rainout shelters; GIS characterisation of drought environments for Savannakhet Province			
<i>Target 2011: Materials</i>	Selected drought-tolerant lines screened under different conditions for drought at vegetative and flowering stage in multi-location trials; identification of drought-related traits and genome regions affecting those traits; GIS characterisation of drought environments for Ubon, Kampong Cham, Vientiane and Champassak Provinces			
<i>Target 2012: Other kinds of knowledge</i>	Effective field screening for drought tolerance demonstrated and adapted, drought-tolerant lines available and used in farmer participatory variety selection for grain and eating quality; GIS characterisation of drought environments for Khon Kaen and Takeo provinces and the rest of Laos			
<b>Output 10</b>	<b>Methodology, tools and support available for analysis and interpretation of Next Generation Sequencing data</b> <ul style="list-style-type: none"> <li>• Commissioned: G4009.04</li> <li>• StraP</li> <li>• 2009–2010</li> <li>• LI/PI: ICRISAT/RK Varshney</li> <li>• Linked to P2-02 and P2-012</li> </ul>	Crop geneticists and genomics specialists, especially those working with NGS technology	Users better able to analyse NGS data	Increased efficiency in crop research and improvement

Output	title, type and target(s)	Intended users	Outcome	Impact
<i>Target 2010: Other kinds of knowledge</i>	Open-source software tools that could be used for NGS data analysis identified, tested and made available; data analysis support for the SP2 projects generating NGS data provided; NGS results across legume species using a relational database analysis pipeline including assembly viewing tools integrated and visualised; database and pipeline made publicly available			
<b>Theme 4: Informatics Infrastructure – Provide facilities for data integration and sharing among GCP partners</b>				
<b>Output 11</b>	<b>Existing tools for data management and logistics of molecular breeding available to MBP users</b> <ul style="list-style-type: none"> <li>• Commissioned: Project No. TBD</li> <li>• StraP</li> <li>• 2009–2013</li> <li>• LI/PI: GCP/G McLaren</li> <li>• Linked to P5-01, P5-016 and P5-020</li> </ul>	Plant breeders using molecular breeding technique	Plant breeders granted access to data management and breeding logistics tools to conduct successful molecular breeding projects	New cultivars are developed faster and more efficiently and used by farmers to improve food security and increase livelihoods in developing countries
<i>Target 2010: Capacity</i>	Tools facilitating management of germplasm lists, pedigrees, intellectual property and other passport data identified and supported; tools for management of phenotypic characterisation and evaluation identified and supported; tools for management of genotypic characterisation identified and supported			
<i>Target 2011: Capacity</i>	Tools facilitating management of germplasm lists, pedigrees, intellectual property and other passport data upgraded according to user needs; tools for management of phenotypic characterisation and evaluation upgraded according to user needs; tools for management of genotypic characterisation upgraded according to user needs			
<i>Target 2012: Capacity</i>	Enhanced tools facilitating management of germplasm lists, pedigrees, intellectual property and other passport data supported and analysed to support web deployment; enhanced tools for management of phenotypic characterisation and evaluation supported and analysed to support web deployment; enhanced tools for management of genotypic characterisation supported and analysed to support web deployment			
<b>Output 12</b>	<b>Integrated GCP Informatics Platform created</b> <ul style="list-style-type: none"> <li>• Commissioned: G4006.16</li> <li>• StraP</li> <li>• 2006–2013</li> <li>• LI/PI: IRRRI/M Senger</li> <li>• Linked to P1-02, P2-02, P2-04 and P2-010</li> </ul>	GCP software developers, informatics staff and database managers	Better integration of software and web services for use in germplasm conservation and crop improvement; GCP scientists have improved access to integrated tools and databases	More efficient bioinformatics research for crop improvement programmes
<i>Target 2010: Other kinds of knowledge</i>	Enhanced GenDiversity Workbench supporting SNP data and linked to the Haplophyle pipeline; an ontology browser developed and GCP ontologies integrated into the platform; Zeus query interface developed for germplasm, genotype and pedigree data; two data sources added to the platform (Ontology and Central Registry); platform linked to structure analysis and R statistical language on the HPC-enhanced domain model and GCP Development toolkit			
<i>Target 2011: Other kinds of knowledge</i>	Three data sources added to the platform (SINGER, ICRIS and GDPC); Taverna, SoapLab2, and R statistical package mediated workflows defined and implemented; Zeus query interface developed for cross-study genotype and phenotype data; scalability of Koios query engine for multiple data sources and users ensured; Domain Model and GCP Development Toolkit enhanced			
<i>Target 2012: Other kinds of knowledge</i>	Data source, query development and application integration to be decided based on user needs; enhanced Domain model and GCP Development toolkit			

Output	title, type and target(s)	Intended users	Outcome	Impact
<b>Output 13</b>	<b>Information network and configurable workflow system for molecular breeding developed and deployed</b> <ul style="list-style-type: none"> <li>• Commissioned: Project No. TBD</li> <li>• StraP</li> <li>• 2009–2013</li> <li>• LI/PI: GCP/G McLaren</li> <li>• Linked to P5-01, P5-016 and P5-020</li> </ul>	GCP software developers, informatics staff and database managers	Better integration of software and web services for use in germplasm conservation and crop improvement; GCP scientists have improved access to integrated tools and databases	More efficient bioinformatics research for crop improvement programmes
<i>Target 2010: Other kinds of knowledge</i>	GCP Informatics Platform technology reviewed to support the MBP; prototype molecular breeding decision support tools released for planning crosses and selecting lines in MAB projects; design specifications, technology choices and prototype web-based workflow system linking to existing tools for molecular breeding released			
<i>Target 2011: Other kinds of knowledge</i>	GCP Informatics Platform technology adapted and adopted to support the MBP; mature molecular breeding decision support tools released for planning crosses and selecting lines in MAB projects; enhanced data exchange between existing tools in the workflow system available through web services			
<i>Target 2012: Other kinds of knowledge</i>	Fully web-based workflow system with logistic and analysis tools released; information in public crop information databases integrated with local information through the platform network for analysis and decision support in molecular breeding			



# Project 5 – SP5: Capacity-building and enabling delivery

## Project narrative

### Project overview and rationale

Whilst GCP's transition to its second phase does not represent any major track change in terms of content, it does mark, following on from the recommendations of the EPMR in 2007–2008 and other reviews, a development towards concentrating efforts to guarantee impact at the end of the Programme. Since its inception, SP5 (Capacity-building and enabling delivery) has focused on the delivery pathway from research to its application so as to secure the chances that GCP outputs reach the anticipated users of our work. In this sense, SP5 activities are already aligned with the new phase, and the evolution at Programme level will simply help reinforce both past and current efforts in this Subprogramme.

SP5 contributes directly and indirectly to several CGIAR System Priorities, especially Priorities 2a and 2b, producing more and better food at lower cost through genetic improvements. Equally, in conducting activities in direct support of all GCP Subprogrammes (1–4), SP5 contributes to Priorities 1a and 1b.

SP5 fulfils its role by building technical capacity for the efficient implementation of GCP research, and by facilitating the flow of GCP products through the research–delivery continuum. It also engages in socio-economic studies to identify GCP research priorities (by crop, region and trait) to support decision-making and resource allocation. Essentially, SP5 adds value to the activities of the other Subprogrammes.

New emphasis in the coming years will be given to the establishment of Communities of Practice and the enhanced offer of support through a suite of services for breeding.

### Impact pathways

SP5 paves the way for the impact of GCP as a whole, by enhancing the readiness of partners to participate in ongoing and future research and by supporting the uptake of GCP products among partners and by a wider audience. Communities of Practice aid delivery and promote sustainability, as do the enhanced offer of breeding and support services. Socio-economic studies assist with decision-making and resource allocation.

SP5's work is organised into five themes:

- Theme 1: Creation of a platform of training resources and a cadre of trained scientists to apply advanced technologies and add value to GCP products
- Theme 2: Cultivation of research and learning opportunities for GCP collaborators and NARS scientists to further the GCP mission and progress
- Theme 3: Construction of systems for ensuring product delivery
- Theme 4: Development and implementation of support services
- Theme 5: *Ex ante* impact analysis and impact assessment

Each SP5 Theme makes particular contributions to the overall impact of the Programme, as described below.

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

#### *Output 1 to Output 3*

Activities in Theme 1 will benefit the wide scientific community of researchers and institutions working with GCP, in particular those in developing countries in target regions, or whose work impacts farmers in those regions.

Training activities and some learning materials will be organised and designed to provide full understanding, and therefore enable full benefit of, the support services offered by the Molecular Breeding Platform (MBP), referred to in Outputs 19 and 20 in Theme 4. In the beginning, while the operation of the MBP is being established, participants in these training activities will be selected from among the user case communities. Later, when a wider audience is targeted, lessons learned will streamline training and procedures to take full advantage of the MBP and its resources. Researchers outside of the MBP scope, but engaged with GCP through other projects may also be invited. Both training workshops and learning materials will be organised in close collaboration with Project 4, when content deals with data analysis, management and curation.

Sets of learning materials will be completed and, consequently, comprehensive and updated information on topics related to GCP research will be provided to an expanded pool of scientists. Thus, close collaborators will remain scientifically

capable. These materials can form the basis of a number of training tasks, not funded by GCP, but rather in which these GCP collaborators become trainers of other colleagues, causing a significant spillover effect in their home institutions and countries. The materials can also be used for undergraduate or postgraduate classroom teaching, particularly for locations where up-to-date material is difficult to obtain. Altogether, learning materials help create a growing community of competent intermediaries for research and development based on GCP products.

SP5 and the GCP Communications unit will continue disseminating learning materials that have been produced so far. This will be achieved through the GCP website, and, importantly, through links with related outreach organisations, such as the Global Initiative for Plant Breeding Capacity Building (GIPB) and also via CD-ROM upon request of researchers who do not have easy access to the Internet. Feedback will be sought via one-to-one electronic communication or through an online form to elicit suggestions for improvement or translation.

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

#### ***Output 4 to Output 8***

This Theme supports GCP developing country partner research and collaboration, with a three-pronged approach covering teams, individuals and institutions. Specific activities include the Capacity-building *à la Carte* Programme, the Pioneer–GCP fellowship, travel grants, the professorship at ACCI and the plant breeding PhD programme at WACCI. Developing country researchers engaged in GCP projects are the frontline beneficiaries of this Theme's Outputs since their role and active participation are critical ingredients for product delivery. The overall goal is to increase the use of GCP-generated products, by engaging users directly involved in GCP research.

Next year the Capacity-building *à la Carte* programme will specifically target the partners of the Tropical Legumes I project in an effort to guarantee the end of the project's first phase with a core community of highly skilled legume researchers. These champions will be ready to play a major role in the project's second phase, which will emphasize the application of markers in their own breeding programmes. This will help realise the product delivery goals of GCP's Strategic Framework and ensure that genetic and genomic resources plus pre-breeding materials, generated by SP1, SP2 and SP3 through TLI, will flow through the research–delivery pipeline.

Individual training in SP5 will be the focus of both the Pioneer–GCP fellowship and the PhD programme at WACCI. Application to these calls will be promoted among the teams of the Challenge Initiatives and the Tropical Legumes project. These opportunities are not only unique for the students to progress professionally, but also serve to benefit others within their home institutions, countries and regions. If the students' degree research is embedded in one of these high-impact GCP projects, they will become, upon graduation, leaders of modern breeding in their institutions and will also become the best guarantee of GCP success in the long term.

Support to the professorship in molecular breeding at the ACCI will help build a cadre of skilled plant breeders in Africa, resulting in reliable breeding programmes and better crop varieties for target farmers.

### ***Theme 3: Construction of systems for ensuring product delivery***

#### ***Output 9 to Output 17***

Theme 3 is anchored in the GCP Delivery Strategy and focuses on capacity-building to meet project goals and ensure product uptake by targeted user groups. The learning materials to prepare Delivery Plans (Output 9) will help researchers understand the process and mechanisms by which their innovations reach farmers. Based on this, GCP research will be more driven by the needs of the end-user, with the anticipated impact of all GCP products being delivered to users, and each intermediate user developing additional products to improve farmer livelihoods. Building capacity of productive links is another mechanism for encouraging delivery. Examples of this are Outputs 10, 11 and 12, which seek to build and strengthen infrastructure in partner institutions so that researchers in developing country programmes are enabled to carry out research in modern breeding, whether field- or laboratory-based, resulting in a higher chance of adoption of GCP products.

The community of practice (CoP) is a mechanism that provides training opportunities for individuals, team-to-team technical backstopping and links between breeders in different countries within a framework, facilitating the exchange of germplasm, information and know-how. This is conducive to both research and delivery, and is successfully ongoing in cassava in Africa, and rice in Asia (the Mekong region). Output 16 will promote these stories of success to other crops and regions, particularly in Africa, through the user cases of the Molecular Breeding Platform and in selected Challenge Initiatives. CoPs will help GCP build on dependable partners and refine capacity-building to better address their needs.

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

#### ***Theme 4: Development and implementation of support services***

##### ***Output 18 to Output 22***

In its second phase, GCP significantly commits to building public access platforms for useful tools and technologies, enhancing human capacity and strengthening institutions. This commitment is now partly realised through the launching of the Molecular Breeding Platform, which in addition to developing new information and data analyses tools (carried out by Project 4), offers a suite of Breeding Services (Output 19, incorporating the following elements: Genetic Resources Supply Service, in collaboration with Project 1, and Marker and Trait Services), and Support Services (Output 20, which includes: Business Plan Development, Data Management, Data Curation, Design and data analysis, Phenotyping Sites and Protocols, Genotyping Support Service and IP Helpdesk). These Services will provide learning materials, and one-to-one remote support and advice to assist researchers in their own working environments.

While in the medium term the services of the MBP will be offered on a cost-recovery basis, the GSS (Output 21) will continue to reach national research programmes and offer the service for free for first-time users to promote the application of molecular markers to assess the potential value of germplasm and breeding materials for relevant agronomic traits.

The toolbox of available molecular markers for MAS in GCP target crops will continue to be updated and made publicly available to all at no cost via the Internet. The toolbox offers information, normally dispersed in restricted literature, in an easy-to-find format.

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

##### ***Output 23***

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

The primary user of this information will be GCP's Management Team. However, in keeping with GCP's spirit of capacity-building, the information will be publicly available for the benefit of other researchers and research managers in science and technology programmes for development. Output 23 subjects GCP's selected target countries and partners to a second-phase evaluation that makes provision for the likely capacity of local institutions and farmers to realise the projected potential for GCP impact.

#### **Changes from previous MTP**

Of the 27 Outputs in the 2009–2011 MTP, seven will have been completed by the end of 2009:

1. Output 5.3. *Training materials for phenotyping developed*
2. Output 5.7. *GCP Fellowship Programme*
3. Output 5.17. *A Project Development Guide (PDG) design and implemented*
4. Output 5.20. *Interactive Resource Center established and maintained*
5. Output 5.24. *Targeting and impact analysis of GCP technologies*
6. Output 5.25. *Ex ante impact analysis of marker-assisted selection technologies supported by GCP*
7. Output 5.26. *Getting the focus right: food crops and smallholder constraints*

Four Outputs were suspended. This was the consequence of the implementation of changes in the new GCP research structure for the second phase, which led to a new way of thinking in terms of how capacity building would be realised and also in terms of its content:

1. Output 5.2 *Online course on intellectual property, freedom-to-operate, and genetic resources policies, including the International Treaty on Plant Genetic Resources for Food and Agriculture*. The instructional materials are available on the internet. Also, a course was run in the past. A re-assessment of needs will be conducted with partners in the new projects and action will be taken accordingly.
2. Output 5.13 *Comprehensive support provided to competitive projects to define delivery and capacity-building plans*. This Output dealt with the implementation of delivery plans and the identification of needs to fulfill them. The relevance of the Output continues, and consequently so will the request for delivery plans. However, this will be done on a case-by-case basis, within each of the Challenge Initiatives.
3. Output 5.16 *Establishment of and support to crop and regional platforms*. This Output has been replaced by Output 16 in this MTP as a result of the emphasis on the establishment of Communities of Practice that GCP wants to give within the Challenge Initiative projects as well as the user case communities of the Molecular Breeding Platform.

4. Output 5.19. GCP product distribution. Also this Output loses its relevance in the context of the general offer of the Molecular Breeding Platform, and in particular with the services. These services are now presented in Outputs 19 and 20 of this MTP.

The remaining Outputs will continue, representing activities extending beyond one year or repeated annually such as the Travel Grants.

The title of Output 5.14 (Output 13 in this MTP) has been amended to *Enhanced capacity to improve cowpea productivity for marginal environments in Mozambique*.

In this MTP, SP5 presents 23 Outputs for 2010–2012, of which 8 are new. These are:

1. Output 1 *Training activities to support full access to the Molecular Breeding Platform (MBP) organised and coordinated*
2. Output 5 *Pioneer—GCP Graduate Fellowship*
3. Output 11 *Capacity building mechanisms and product pipelines established for GCP Challenge Initiatives*
4. Output 12 *Establishing a phenotyping network for rice drought breeding in West Africa*
5. Output 15 *The rice community of practices: strengthening rice breeding programmes in the Mekong region building capacity for genotyping and phenotyping for biotic and abiotic stresses*
6. Output 16 *Crop molecular breeding communities of practice for user communities of the Molecular Breeding Platform set up and supported*
7. Output 19 *Facilitated access to germplasm, markers and trait services to boost modern breeding*
8. Output 20 *Comprehensive expert support provided for matters related to modern breeding*

## Output descriptions and partnerships

### Overview

In this MTP, SP5 has 23 Outputs distributed among five Themes. SP5 deals with building capacity, creating links, offering public knowledge platforms, providing services, supporting collaborators, disseminating knowledge and much more. All SP5 activities are collaborative, involving Consortium member institutions as well as partners outside the Consortium. This GCP partnership philosophy is very pronounced in SP5, which, by definition, begins by building internal partnerships with the other GCP Subprogrammes. All SP5 Outputs rely on the complementary participation of a variety of external collaborators. Partners are presented by Output in the Output descriptions section of the SP5 narrative.

Because of its nature, most of SP5 partners are from developing country national institutions, ie. working in the national agricultural research system or academia. Developing country partners (such as recipients of a Capacity Building *à la Carte* or a Genotyping Support Service award, or winners of a fellowship or travel grant opportunity, for example) are more and more carefully selected from the target countries of GCP projects. A particular type of partnership is that of the Communities of Practice, a type of network that GCP intends to emphasise through SP5 in the coming years.

Advance Research Institutes (ARIs) and CGIAR Centers are also commissioned to conduct SP5 activities, with examples including the development of learning materials and the organisation of training courses. CGIAR Centers are the main partners who carry out activities in socio-economic studies. Another important group amongst the array of SP5 partners are the numerous service providers to whom genotyping requests are being outsourced. Service providers are expected to increase in the future once the Molecular Breeding Platform becomes operational.

### Output descriptions

The next section has SP5 partners, with the lead institute (LI), PI, funding mechanism and type of project also indicated.

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

*Output 1: Training activities to support full access to the Molecular Breeding Platform (MBP) organised and coordinated*

- Commissioned: Project No. TBD
- StraP
- 2009–2013
- LI/PI: GCP/PI TBD
- Linked to P4-O2

The established Molecular Breeding Platform will involve a number of structures and procedures to facilitate access to and full benefit from the offer of applications and services. This Output will coordinate human resource development through training courses and workshops responding to users demands so that know-how is appropriate to take advantage of the Platform. It replaces a previous Output for training courses and its designed is based on the evolving needs of the Programme. It links closely with other Outputs based on the MBP in this project as well as in Subprogramme 4.

*Partners:* TBD

*Output 2: Training materials for modern plant breeding developed*

- Commissioned: G4005.53.03
- StraP
- 2009–2011
- LI/PI: CU/T Fulton

This project was intended to develop learning materials for modern breeding, covering MAS in different breeding schemes and use of single-trait as well as quantitative trait genotyping. Later, it was decided to extend its content to also include basic notions and links with conventional breeding – an aspect usually forgotten by modern technologies when they are practised only at the academic level.

*Partners:* N/A

*Output 3: Learning materials completed and disseminated*

- Commissioned: G4008.44
- StraP
- 2009–2013
- LI/PI: GCP/C de Vicente

This Output deals with the refinement of the quality of learning materials, packaging them in appropriate formats for wide distribution and use, and disseminating them as widely as possible within the GCP partner community and beyond.

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

*Output 4: Capacity-building à la Carte programme*

- Commissioned: Project No. TBD
- StraP
- 2007–2013
- LI/PI: TBD
- Linked to P2-O21, P3-O5 and P3-O24

This Output aims to fill gaps in human resources to enable selected developing country partners collaborating closely with GCP to update their skills, expertise and education in order to become both better collaborators in GCP projects, and in the long term, the pillars on which GCP research is sustained. Support is provided for personnel training and technical backstopping. To guarantee higher relevance and impact, this Output will concentrate on the crop Objectives of the Tropical Legumes I project, and as such links with related Outputs in Subprogrammes 1, 2 and 3. New Output targets for the following years will be defined in agreement with proposals for the Challenge Initiative currently under development.

*Partners:* ART, ARI, CRS, CBI, EIAR, INERA, IRAD, INRAN, ISRA, LZARDI, SARI

*Output 5: Pioneer–GCP Graduate Fellowship*

- Commissioned: Project No. TBD
- StraP
- 2010–2013
- LI/PI: TBD

The Pioneer–GCP Graduate Fellowship supports graduate studies in plant breeding and genetics. The programme targets top performers who will advance plant science, with emphasis on international agriculture. It is financially supported by Pioneer and implemented by GCP's Subprogramme 5. A candidate will be selected in 2009 to begin studies in 2010. Selection will be made, as far as possible, to match GCP's second phase priorities in terms of countries, crops, traits and projects.

*Partner:* TBD

*Output 6: GCP Travel Grant Programme*

- Commissioned: TBD
- StraP
- 2005–2013
- LI/PI: GCP/C de Vicente

Travel grants cover mainly participation in the GCP Annual Research Meeting, as a very good opportunity to expose developing country partners to the wide range of research being conducted in GCP, while at the same time building linkages between the upstream and the downstream communities. Other travel opportunities may be offered for selected meetings and conferences related to GCP research content.

*Partners:* Various (TBD)

*Output 7: Academic position in molecular breeding established and supported*

- Commissioned: G4006.36
- StraP
- 2008–2013
- LI/PI: UKZN/M Laing

The University of Kwazulu–Natal hired a professor to build capacity among sub-Saharan Africa scientists in molecular biology applied to food security and genetic diversity. The professor will teach a module on advanced technologies, genomics and molecular markers to students at the African Centre for Crop Improvement (ACCI), and will mentor students to incorporate molecular breeding components into their research proposals. This Output was commissioned as a project in 2006. However, its start was delayed because of difficulties to recruit an appropriate candidate. Recruitment reopened and the successful candidate was appointed in November 2008. As a consequence, an addendum was prepared to shift the dates of the project by two years.

*Partners:* RF, AGRA

*Output 8: PhD in Plant Breeding Training at the West Africa Centre for Crop Improvement, University of Ghana*

- Commissioned: G4008.37
- StraP
- 2008–2013
- LI/PI: UoG/EY Danquah
- Linked to P3-O15 and P3-O24

A new generation of plant breeders with knowledge in both traditional field-based selection methods and laboratory-based tools is needed to develop and provide the necessary high-yielding varieties to farmers, especially in Africa. The University of Ghana, through the West Africa Centre for Crop Improvement (WACCI), is dedicated to the training of plant breeders with skills in genetic improvement of the staple crops of the West and Central Africa subregion. Four PhD candidates (2 started in 2009 and the other 2 will do so in 2010) will undertake two years of coursework, and three years of field research at their local research institutions. Candidates are selected to contribute to the Challenge Initiative projects.

*Partners:* AGRA, CU, CRI, IER

**Theme 3: Construction of systems for ensuring product delivery**

*Output 9: Delivery Plan remote learning modules*

- Commissioned: G4008.50
- StraP
- 2008–2010
- LI/PI: INCAE/L Pratt

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

*Partner:* CU

*Output 10: Capacity-building mechanisms and product pipelines established for tropical legume improvement in Africa*

- Focus: G6007.06
- StraP
- 2007–2010 (Phase II: 2010–2013)
- LI/PI: GCP/C de Vicente
- Linked to P3-O21

This Output relates to the capacity-building objective of the focus project for legume improvement in Africa (TLI). It serves two main purposes: (i) training activities and workshops to upgrade scientific knowledge of NARS partners to work optimally in the project; and (ii) upgrading field, computer and

laboratory infrastructure for project partners. It complements human resource capacity offered by Output 4. It links with Outputs related to TLI and described in Subprogrammes 1, 2 and 3 supporting the research undertaken by developing country partners.

*Partners:* ART, ARI, CRS, CBI, EIAR, INERA, IRAD, INRAN, ISRA, LZARDI, SARI

*Output 11: Capacity building mechanisms and product pipelines established for GCP Challenge Initiatives*

- Commissioned: TBD
- CI
- 2009–2013
- LI/PI: TBD
- Linked to P1, P2 and P3

This Output relates to the capacity-building objectives of the new Challenge Initiatives whose proposals are currently under development. The plan is to fulfill infrastructure needs of developing country partners (eg. the upgrading of field, computer and laboratory equipment) enabling them to fully participate in the research activities in which they will be involved with GCP. This Output will be closely linked to the technical Outputs of the CI(s), either embedded in each project or as a separate project of its own, combining capacity building plans for the entire CI.

*Partner:* TBD

*Output 12: Implementation of a phenotyping network for rice drought breeding in West Africa*

- Commissioned: TBD
- CI
- 2009–2013
- LI/PI: AfricaRice/F Koichi
- Linked to P3-O6, P3-O7 and P3-O27

This Output will establish a network for drought phenotyping, enhancing varietal improvement for rainfed lowland, with the capacity to evaluate breeding lines or accessions in Burkina Faso, Mali and Nigeria. The capacity in the areas of proper environmental characterisation and drought phenotyping will also be enhanced within these three countries' national programmes. The network can act as a model and facilitate up-scaling of research results to non-project countries. It will be linked to Outputs related to rice breeding activities in the rice CI.

*Partners:* IER, UES, INERA, Agropolis–CIRAD

*Output 13: Enhanced capacity to improve cowpea productivity for marginal environments in Mozambique*

- Commissioned: G4008.43
- StraP
- 2008–2010
- LI/PI: UEM/R Chiulele
- Linked to P3-O21

This Output builds capacity in drought tolerance screening, offers training in analysing data for GxE interaction, provides baseline information on drought tolerance for cowpea varieties, and assesses the importance of GxE interactions for grain yield under drought in Mozambique. The national partner in Mozambique is linked with a mentor at UC–Riverside, to provide guidance in the design and implementation of a MAS-based programme. In addition to NARS strengthening, new breeding populations for the application of MAS and marker-assisted recurrent selection (MARS) will be produced. It is linked to Outputs related to Objective 2 of the focus project TLI (Subprogrammes 2 and 3).

*Partner:* UoC–Riverside

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

- Commissioned: G4008.26
- StraP
- 2008–2011
- LI/PI: NRCRI/E Okogbenin
- Linked to P3-O26 and P3-O15

This project builds on successful collaboration with cassava teams in Africa (linked through IITA and CIAT). It builds a CoP through breeder-to-breeder training in traditional and new methods of breeding, germplasm exchange and web-based information-sharing to achieve set breeding goals and address common problems. It facilitates the integration of MAS with field-based breeding by implementing effective breeding strategies for disease and pest resistance in Nigeria, Ghana, Uganda and Tanzania. It strengthens the capacity of developing country breeders through formal (MSc) and informal (exchange visits and workshops) training and builds linkages with users to ensure rapid uptake of technologies. This Output very much complements cassava CI Outputs in other GCP projects.

*Partners:* ARI, CIAT, CRI, IITA, NARO

*Output 15: The rice community of practices: strengthening rice breeding programmes in the Mekong region building capacity for genotyping and phenotyping for biotic and abiotic stresses*

- Commissioned: Project No. TBD
- StraP
- 2009–2012
- LI/PI: BIOTEC/PI TBD

This project builds on a successful collaboration between Thai rice researchers and their counterparts in Cambodia, Laos and Myanmar. In its second phase, it aims to train six students (MSc or Ph.D) while developing new improved varieties. Partner institutes will be conducting trials for the developed lines under the GCP project including lines (submergence, drought tolerance and good cooking quality) from Thailand

that may be useful in the neighbouring countries. As the students finish their research, the newly developed varieties will also be evaluated in the trials to assess the impact on farmers.

*Partners:* ARC, CARDI, DAR

*Output 16: Crop molecular breeding communities of practice for user communities of the Molecular Breeding Platform set up and supported*

- Commissioned: Project No. TBD
- StraP
- 2009–2013
- LI/PI: TBD
- Linked to P1, P2, P3, P4-O4 and P4-O5

This project is an essential component for the success of the Molecular Breeding Platform (MBP). It aims to establish crop networks and work with their communities connecting crop researchers, mainly breeders, involved in the user cases and willing to share a free flow of experiences and information on modern breeding methods and best field practices. It will link with Outputs of the MBP, especially those of this GCP project that relate to services.

*Partners:* Various (TBD)

*Output 17: Validation of GCP products*

- Commissioned: Project No. TBD
- StraP
- 2009–2013
- LI/PI: TBD

As GCP enters into its second phase products are becoming available. However, for research results to translate into products that can be passed to the intended users (usually, either other partners in the GCP community or downstream links with partners in developing countries), the results need to first be validated. Validation involves guaranteeing the quality (essentially performance and suitability) of the products and packaging them appropriately. After validation, awareness is needed through wide dissemination to potential users.

*Partner:* TBD

**Theme 4: Development and implementation of support services**

*Output 18: Toolbox of available molecular markers useful for marker assisted selection in GCP crops*

- Commissioned: G4008.35
- StraP
- 2008–2013
- PI: V van Damme (consultant)

This Output develops a toolbox providing free and easy access to information on all publicly available molecular markers ready for use for MAS in 19 food security crops. It compiles information on internet resources, public databases

and scientific papers, plus information gathered through communication with molecular crop breeding experts. Results, available via the internet, will be promoted as a global public good and its use disseminated. An update will be made in the first year, and the project will end with this. However, the potential suitability of/need for repeated updates will be evaluated at later stages, and as the project's duration has been expanded to cover this possibility.

Partners: N/A

*Output 19: Facilitated access to germplasm, markers and trait services to boost modern breeding*

- Commissioned: Project No. TBD
- StraP
- 2009–2013
- LI/PI: GCP/PI TBD
- Linked to P1-O2

This Output refers to the Breeding Services module of the Molecular Breeding Platform. These services are considered critical to the success of molecular breeding. They will provide access to and exchange of specific well characterised germplasm and information, assistance with contracting service laboratories to conduct marker work or to evaluate and quantify specific traits. Strong links will exist with all other Outputs in the MBP, both within SP5 and with SP4, as well as with the Output referring to the Genetic Resource Supply Service in SP1 and the projects of the user case communities.

Partners: Agropolis–CIRAD

*Output 20: Comprehensive expert support provided for matters related to modern breeding*

- Commissioned: Project No. TBD
- StraP
- 2009–2013
- LI/PI: GCP/TBD
- Linked to P4-O3, P4-O5 and P4-O7

This Output refers to the Support Services module of the Molecular Breeding Platform. These services will provide support to breeders to address technical and logistical bottlenecks. The main objective is to provide backstopping and training in a broad set of complementary disciplines to support the other components. Part of this Output will be closely linked with those in Project 4 related to Information Systems, as well as those in this project that will support capacity building (human resource development and communities of practice).

Partners: WUR, Others (TBD)

*Output 21: Genotyping Support Service*

- Commissioned: G4007.21
- StraP
- 2006–2013
- LI/PI: GCP/H Gómez-Paniagua
- Linked to P1-O1

The GSS facilitates access to modern breeding technologies for developing world agricultural research and development organisations. It offers world-class, cost-efficient genotyping services, including support and training in analysis for proper interpretation of genotypic and phenotypic data. The GSS subcontracts genotyping work, and assists undertaking the intricacies of the legal issues and administrative procedures. Whilst this Output is one of the Services of Output 20 of this MTP, it is however individualised because it was launched long before the MBP initiative and has an independent identity.

Partners: BecA, DArT, ICRISAT, IRR, others (TBD)

*Output 22: Development and implementation of a GCP Workflow and Repository System*

- Commissioned: Project No. TBD
- StraP
- 2009–2010
- LI/PI: Cropster GmbH/N Niederhauser

This Output deals with the development of a project information and document management tool through a central online system. It extends an existing internet-based GCP system (Output 5.23 in the MTP 2009–2011). In terms of this MTP, components will be enhanced based on the validation period in which they have already been put to use. The tool facilitates interactions between project collaborators and the GCP Management Team and Project Office. It facilitates collaborative work, provides traceability for project review processes, integrates different GCP activities in one location and promotes inter-Subprogramme information exchange.

Partners: N/A

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

*Output 23: A strategic assessment of the capacity to develop and adopt GCP technologies*

- Commissioned: G4008.24
- StraP
- 2008–2010
- LI/PI: IFPRI/S Wood

Prior GCP studies identified priority crops and farming systems for GCP efforts, assuming that broadly-targeted GCP technologies will be successfully adapted by local breeding



efforts and will then be adopted by local smallholders. Since these are both strong assumptions, GCP's initial target/focus areas will be subjected to a second-phase evaluation on the likely capacity of local institutions and farmers. This may be described as an assessment of the feasibility of achieving desired outcomes in high-priority (most attractive) focus areas.

*Partners:* CIAT, GCP

### **International public goods**

All generated SP5 products—such as learning materials, Delivery Plan Kit, resource platforms and impact studies—are intended to benefit the wider scientific community. They are always made available, without restriction, to the widest possible audience. SP5 also offers capacity-building opportunities, which strengthen institutions and individuals in target countries. While the activities benefit a selected group of collaborators in the first instance, they can truly be considered public goods in the sense that the spill-over arising from GCP's open policy on the availability of capacity-building materials is expected to influence a wider community of researchers in the countries and regions from which the collaborators are drawn, supporting the collective effort to solve the needs of resource-poor farmers. The same applies to the services that are either free (initially all those offered through the Molecular Breeding Platform) or provided at cost-recovery basis as a means to self-sustain them.

### **Elaboration of partner roles**

Within SP5's Theme 1, partnerships for developing learning materials are mainly with ARIs as the developers. For example, Cornell University will complete reference materials for modern breeding, including basic concepts of conventional breeding. Courses are arranged in collaboration with competent partners, usually in CGIAR Centres, ARIs and other dependable educational institutions.

Activities within Theme 2 rely on partnerships with ARIs, CGIAR Centres and developing country institutions, including Academia in the South. Capacity-building *à la Carte* awards go to research teams in the South engaged in ongoing GCP projects (Tropical Legumes I in 2010). Other partnerships

established by SP5 include Pioneer, to offer a joint degree fellowship, ACCI at the University of Kwazulu–Natal (South Africa) and WACCI at the University of Ghana, both for training PhD students from the region.

In Theme 3, INCAE, a business school in Costa Rica, and Cornell University develop the learning materials on product delivery and the improved version of the Delivery Plan Kit. A special partnership in this Theme is the project Improving tropical legume productivity for marginal environments in sub-Saharan Africa (TLI), in which SP5 collaborates with upstream as well as downstream partners, overseeing the development of capacity-building (both infrastructure and training). Similar examples are expected to emerge soon from the Challenge Initiatives. SP5 continues to support the establishment of communities of practice. A cassava Community of Practice (CoP) in Africa connects IITA, CIAT, and developing country breeding programmes in Ghana, Nigeria, Tanzania and Uganda, while promoting links with international initiatives. The Rice in the Mekong CoP links BIOTEC (Thailand) with the rice breeding programmes of Cambodia, Lao and Myanmar. The establishment of new CoP will be promoted, especially in Africa, through the Molecular Breeding Platform and the Challenge Initiatives, as mechanisms for streamlining delivery and ensuring sustainability of GCP research.

Partnerships in Theme 4 will mostly mimic those of the Genotyping Support Service. User cases of the Molecular Breeding Platform will combine CGIAR Centres, ARIs and breeding programmes in the South. They will collaborate with SP5 to request services, or benefit from the training courses and learning materials. The Services themselves (markers, traits, etc) will be outsourced to cost-competitive laboratory service providers.

Theme 5 deals with an area that complements GCP research, and so it brings in new partners and new ways of doing business with experts from IFPRI and CIAT for the evaluation of the capacity of local institutions and delivery pathways to farmers to realise the projected potential for GCP impact.

## Project 5 logframe – SP5: Capacity-building and enabling delivery

Notes:

1. Each Output is followed by:
  - a) the type of research activity/funding contributing to the Output (commissioned, competitive, focus, or discretionary) and GCP project number
  - b) Identification of Output as a StraP (Strategic project) or CI (Challenge Initiative) project
  - c) start and end year, and
  - d) the lead institute (LI) and Principal Investigator(s) (PI[s]) responsible for the Output (and its Output targets).
2. Some Outputs are managed internally within GCP, in some cases involving coordination of a number of external institutes. In most such cases, the entry under 'PI' is denoted as 'Various'.

Output	title, type and target(s)	Intended Users	Outcome	Impact
<b>Theme 1: Creation of a platform of training resources and a cadre of trained scientists to apply advanced technologies and add value to GCP products</b>				
<b>Output 1</b>	<b>Training activities to support full access to the Molecular Breeding Platform (MBP) organised and coordinated</b> <ul style="list-style-type: none"> <li>• Commissioned: Project No. TBD</li> <li>• StraP</li> <li>• 2009–2013</li> <li>• LI/PI: GCP/PI TBD</li> <li>• Linked to P4-02</li> </ul>	The user case communities of the MBP	All partners involved in the user case communities understand the offer of the Platform and are able to use the different their breeding programmes	The user case communities become fully effective in the application of molecular markers and molecular breeding schemes towards the production of better crops varieties for poor farmers
<i>Target 2010: Capacity</i>	A training strategy and programme developed to promote molecular breeding and the use of the molecular breeding platform (MBP)			
<i>Target 2011: Capacity</i>	TBD once the MBP is operational and the training strategy is developed			
<i>Target 2012: Capacity</i>	TBD once the MBP is operational and the training strategy is developed			
<b>Output 2</b>	<b>Training materials for modern plant breeding developed</b> <ul style="list-style-type: none"> <li>• Commissioned: G4005.53.03</li> <li>• StraP</li> <li>• 2009–2011</li> <li>• LI/PI: CU/T Fulton</li> </ul>	GCP researchers and collaborators, particularly crop geneticists and breeders	GCP researchers' and collaborators' capabilities enhanced in the application of modern plant breeding techniques	NARS scientists in target countries better able to collaborate with GCP and conduct their own research to improve crop varieties for farmers
<i>Target 2010: Practices</i>	Course materials completed and made available online and on CD-ROM			
<i>Target 2011: Practices</i>	Course materials more widely disseminated			
<b>Output 3</b>	<b>Learning materials completed and disseminated</b> <ul style="list-style-type: none"> <li>• Commissioned: G4008.44</li> <li>• StraP</li> <li>• 2009–2013</li> <li>• LI/PI: GCP/C de Vicente</li> </ul>	GCP researchers and collaborators, particularly crop geneticists and breeders	GCP researchers' and collaborators' capabilities enhanced in a number of subjects related to effective breeding in the 21st century	NARS scientists in target countries better able to collaborate with GCP and conduct their own research to improve crop varieties for farmers
<i>Target 2010: Capacity</i>	All completed training materials disseminated and their use monitored			
<i>Target 2011: Capacity</i>	All completed training materials disseminated and their use monitored			
<i>Target 2012: Capacity</i>	All completed training materials disseminated and their use monitored			

Output	title, type and target(s)	Intended Users	Outcome	Impact
<b>Theme 2: Cultivation of research and learning opportunities for GCP collaborators and NARS scientists to further the GCP mission and progress</b>				
<b>Output 4</b>	<b>Capacity-building à la Carte Programme</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>StraP</li> <li>2007–2013</li> <li>LI/PI: TBD</li> <li>Linked to P2-021, P3-05 and P3-024</li> </ul>	NARS partners in the crop. Objectives of the Tropical Legumes I project	More and better prepared developing country partners engaged in field, laboratory and data analysis project activities	GCP research for modern crop improvement sustained by an increasing number of developing country researchers
<i>Target 2010: Capacity</i>	At least four grants provided to collaborating GCP researchers and their institutions for comprehensive capacity-building			
<i>Target 2011: Capacity</i>	TBD, based on Challenge Initiative proposals in progress			
<i>Target 2012: Capacity</i>	TBD, based on Challenge Initiative proposals in progress			
<b>Output 5</b>	<b>Pioneer–GCP Graduate Fellowship</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>StraP</li> <li>2010–2013</li> <li>LI/PI: TBD</li> </ul>	GCP collaborators seeking to pursue graduate studies and with a desire to remain in, or return to, their country of origin and contribute to agricultural development	More and better prepared developing country partners engaged in modern crop improvement	Increased human capacity for plant breeding in the developing world
<i>Target 2010: Capacity</i>	The selected candidate begins academic course requirements towards a graduate degree in modern plant breeding			
<i>Target 2011: Capacity</i>	The graduate student continues his/her advanced training			
<i>Target 2012: Capacity</i>	The graduate student continues his/her advanced training			
<b>Output 6</b>	<b>GCP Travel Grant Programme</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>StraP</li> <li>2005–2013</li> <li>LI/PI: GCP/C de Vicente</li> </ul>	GCP collaborators, particularly those from developing countries engaged in ongoing GCP projects	Supportive relationships built between GCP scientists and collaborators; capacity of collaborators to participate in GCP research in their home institutions boosted	Increased collaborative and independent research activities and outputs in target countries towards improved crop varieties for farmers
<i>Target 2010: Other kinds of knowledge</i>	At least 10 travel grants awarded			
<i>Target 2011: Other kinds of knowledge</i>	At least 10 travel grants awarded			
<i>Target 2012: Other kinds of knowledge</i>	At least 10 travel grants awarded			
<b>Output 7</b>	<b>Academic position in molecular breeding established and supported</b> <ul style="list-style-type: none"> <li>Commissioned: G4006.36</li> <li>StraP</li> <li>2008–2013</li> <li>LI/PI: UKZM/M Laing</li> </ul>	PhD candidates in selected African countries and breeding programmes	A selected group of African plant breeders well-trained in modern plant breeding	Increased human capacity in national plant breeding programmes in Africa
<i>Target 2010: Capacity</i>	10 PhD candidates acquainted with topics on advanced technologies, genomics and molecular markers for breeding			
<i>Target 2011: Capacity</i>	10 PhD candidates acquainted with topics on advanced technologies, genomics and molecular markers for breeding			
<i>Target 2012: Capacity</i>	10 PhD candidates acquainted with topics on advanced technologies, genomics and molecular markers for breeding			

Output	title, type and target(s)	Intended Users	Outcome	Impact
<b>Output 8</b>	<b>PhD in Plant Breeding Training at the West Africa Centre for Crop Improvement, University of Ghana</b> <ul style="list-style-type: none"> <li>Commissioned: G4008.37</li> <li>StraP</li> <li>2008–2013</li> <li>LI/PI: UoG/EY Danquah</li> <li>Linked to P3-015 and P3-024</li> </ul>	PhD candidates in selected African countries and breeding programmes	A selected group of African plant breeders well-trained in modern plant breeding	Increased human capacity in national plant breeding programmes in Africa
<i>Target 2010: Capacity</i>	Two PhD candidates continue their academic requirements towards a graduate degree in modern plant breeding; Two PhD candidates registered and begin their academic requirements towards a graduate degree in modern plant breeding			
<i>Target 2011: Capacity</i>	Four PhD candidates continue their advanced training			
<i>Target 2012: Capacity</i>	Four PhD candidates continue their advanced training			
<b>Theme 3: Construction of systems for ensuring product delivery</b>				
<b>Output 9</b>	<b>Delivery Plan remote learning modules</b> <ul style="list-style-type: none"> <li>Commissioned: G4008.50</li> <li>StraP</li> <li>2008–2010</li> <li>LI/PI: INCAE/L Pratt</li> </ul>	Project investigators of GCP grants, their collaborators and developing country researchers	Two-way flow of communication activated from users to producers, and user capacity needs identified and fulfilled	Clear delivery pathways between upstream and downstream research actors. Greater likelihood of adoption of GCP products
<i>Target 2010: Practices</i>	Learning modules and Delivery Plan tool validated and disseminated			
<i>Target 2011: Practices</i>	Use of the Delivery Plan online tool promoted and monitored			
<i>Target 2012: Practices</i>	Use of the Delivery Plan online tool promoted and monitored			
<b>Output 10</b>	<b>Capacity-building mechanisms and product pipelines established for tropical legume improvement in Africa</b> <ul style="list-style-type: none"> <li>Focus: G6007.06</li> <li>StraP</li> <li>2007–2010 (Phase II: 2010–2013)</li> <li>LI/PI: GCP/C de Vicente</li> <li>Linked to P3-021</li> </ul>	African legume researchers and plant breeders in selected countries and programme	African researchers are enabled to apply modern plant breeding techniques and applications, through specialised training and updating of infrastructure in their institutions	Improved groundnut, bean, cowpea and chickpea varieties delivered to resource-poor farmers
<i>Target 2010: Capacity</i>	Field and laboratory infrastructure improved in at least five African countries; implementation plan of research results in African partner institutions devised			
<i>Target 2011: Capacity</i>	TBD, based on the Tropical Legumes I proposal for the second phase			
<i>Target 2012: Capacity</i>	TBD, based on the Tropical Legume I proposal for the second phase			
<b>Output 11</b>	<b>Capacity building mechanisms and product pipelines established for GCP Challenge Initiatives</b> <ul style="list-style-type: none"> <li>Commissioned: TBD</li> <li>CI</li> <li>2009–2013</li> <li>LI/PI: TBD</li> <li>Linked to P1, P2 and P3</li> </ul>	Developing country partners from target countries of the seven GCP Challenge Initiatives	Developing country researchers are enabled to use modern plant breeding techniques and applications, through updating of infrastructure in their institutions	Improved rice, wheat, sorghum, cassava, cowpea and chickpea varieties delivered to resource-poor farmers
<i>Target 2010: Capacity</i>	Capacity needs of developing country partners identified and a plan developed to fulfill them in the CI project proposals approved			
<i>Target 2011: Capacity</i>	Implementation of capacities as proposed and approved in the CI projects			
<i>Target 2012: Capacity</i>	Further implementation of capacities, evaluation and adjustments made to enhance adequacy and use			

Output	title, type and target(s)	Intended Users	Outcome	Impact
<b>Output 12</b>	<b>Implementation of a phenotyping network for rice drought breeding in West Africa</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>CI</li> <li>2009–2013</li> <li>LI/PI: AfricaRice/F Koichi</li> <li>Linked to P3-06, P3-07 and P3-027</li> </ul>	GCP rice partners from Burkina Faso, Mali and Nigeria	Capacity built within the national programmes to conduct reliable drought screening	Enhanced opportunity to develop rice varieties with better performance than existing ones in rainfed lowland contributing to increased rice production in West Africa
<i>Target 2010: Other kinds of knowledge</i>	<ul style="list-style-type: none"> <li>Database on environmental characteristics of rainfed lowlands in Burkina Faso, Mali and Nigeria available</li> <li>Maps on drought profiles of rainfed lowland rice produced</li> <li>Site characterisation, equipment and personnel available for drought screening at three sites in Burkina Faso, Mali and Nigeria documented</li> </ul>			
<i>Target 2011: Capacity</i>	TBD, based on the rice CI proposal in progress			
<i>Target 2012: Capacity</i>	TBD, based on the rice CI proposal in progress			
<b>Output 13</b>	<b>Enhanced capacity to improve cowpea productivity for marginal environments in Mozambique</b> <ul style="list-style-type: none"> <li>Commissioned: G4008.43</li> <li>StraP</li> <li>2008–2010</li> <li>LI/PI: UEM/R Chiulele</li> <li>Linked to P3-021</li> </ul>	Cowpea breeders in Mozambique	Mozambican researchers are enabled to apply modern plant breeding techniques and applications, through specialised training and research	Improved cowpea varieties delivered to resource-poor farmers in Mozambique
<i>Target 2010: Materials</i>	Drought-tolerant reference varieties identified; efficient tools for drought tolerance screening in use by the Mozambican partner; genetic populations suitable for MARS and varietal development for Mozambique			
<b>Output 14</b>	<b>A cassava breeding community of practice in Africa for accelerated production and dissemination of farmer-preferred cassava varieties resistant to pests and diseases</b> <ul style="list-style-type: none"> <li>Commissioned: G4008.26</li> <li>StraP</li> <li>2008–2011</li> <li>LI/PI: NRCRI/E Okogbenin</li> <li>Linked to P3-026 and P3-015</li> </ul>	Cassava breeders in Ghana, Nigeria, Tanzania and Uganda	Shared germplasm, information and training made available through the CoP to cassava breeders, and primary, secondary and tertiary users	A new generation of developing country breeders trained in cassava field-based and MAS breeding working effectively to develop better varieties to respond to farmers' needs
<i>Target 2010: Capacity</i>	A community of cassava breeders validating markers and molecular breeding schemes for resistance to CMD, CBSD, and CGM in farmer-preferred germplasm established in participating developing country institutions; four MSc graduates trained in participating countries			
<i>Target 2011: Materials</i>	A community of cassava breeders selecting at least 10 genotypes following MAS and conventional breeding approaches in their respective country; best five genotypes selected by farmers in participatory variety testing (PVT) trials for large-scale dissemination			
<i>Target 2012: Capacity</i>	TBD, based on continuation within the cassava CI proposal currently in progress			
<b>Output 15</b>	<b>The rice community of practices: strengthening rice breeding programmes in the Mekong region building capacity for genotyping and phenotyping for biotic and abiotic stresses</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>StraP</li> <li>2009–2012</li> <li>LI/PI: BIOTEC/PI TBD</li> </ul>	Rice breeders in Cambodia, Laos, Myanmar and Thailand	Increased critical mass of well-trained researchers working in rice in the Mekong region	A new generation of developing country breeders trained in rice field-based and marker-assisted selection working effectively to develop better varieties to respond to farmer's needs in the Mekong region
<i>Target 2010: Capacity</i>	TBD based on final project proposal (currently in progress)			

Output	title, type and target(s)	Intended Users	Outcome	Impact
Target 2011: Capacity	TBD based on final project proposal (currently in progress)			
Target 2012: Capacity	TBD based on final project proposal (currently in progress)			
<b>Output 16</b>	<b>Crop molecular breeding communities of practice for user communities of the Molecular Breeding Platform set up and supported</b> <ul style="list-style-type: none"> <li>• Commissioned: Project No. TBD</li> <li>• StraP</li> <li>• 2009–2013</li> <li>• LI/PI: TBD</li> <li>• Linked to P1, P2, P3, P4-04 and P4-05</li> </ul>	Crop communities encompassing the user cases of the MBP	Crop communities effectively sustaining the use of molecular breeding approaches in selected countries	Increased number of improved cultivars produced for food security and development
Target 2010: Practices	A plan developed to build communities of practice based on selected user teams of the MBP			
Target 2011: Practices	Communities of Practice for crop molecular breeding established for at least four of GCP's target crops			
Target 2012: Practices	Continued support to activities in four crop Communities of Practice for molecular breeding			
<b>Output 17</b>	<b>Validation of GCP products</b> <ul style="list-style-type: none"> <li>• Commissioned: Project No. TBD</li> <li>• StraP</li> <li>• 2009–2013</li> <li>• LI/PI: TBD</li> </ul>	GCP community and other stakeholders, eg. germplasm curators and managers, crop breeders and crop geneticists	Good quality germplasm and markers facilitate breeding progress	Increased efficiency and effectiveness in crop improvement for development
Target 2010: Unassigned	TBD, based on GCP research progress and products available			
Target 2011: Unassigned	TBD, based on GCP research progress and products available			
Target 2012: Unassigned	TBD, based on GCP research progress and products available			
<b>Theme 4: Development and implementation of support services</b>				
<b>Output 18</b>	<b>Toolbox of available molecular markers useful for marker assisted selection in GCP crops</b> <ul style="list-style-type: none"> <li>• Commissioned: G4008.35</li> <li>• StraP</li> <li>• 2008–2013</li> <li>• PI: V van Damme (consultant)</li> </ul>	Crop breeders wishing to integrate molecular markers in the selection processes	Facilitated use of molecular markers and technologies for crop breeding in developing countries	Enhanced progress in crop variety development
Target 2010: Practices	Database updated and use monitored			
Target 2011: Practices	Database updated and use monitored			
Target 2012: Practices	Database updated and use monitored			
<b>Output 19</b>	<b>Facilitated access to germplasm, markers and trait services to boost modern breeding</b> <ul style="list-style-type: none"> <li>• Commissioned: Project No. TBD</li> <li>• StraP</li> <li>• 2009–2013</li> <li>• LI/PI: GCP/PI TBD</li> <li>• Linked to P1-02</li> </ul>	Crop breeders wishing to upgrade the efficiency of their breeding programmes	Facilitated access to resources and assistance to advance crop breeding in developing countries	Enhanced progress in crop variety development
Target 2010: Practices	Assessment of user requirements and a plan developed for the Genetic Resource Supply Service; the Marker and Trait Services to become operational			

Output	title, type and target(s)	Intended Users	Outcome	Impact
<i>Target 2011: Practices</i>	Pilot implementation of the Genetic Resource Supply Service; main characteristics of selected genotyping service providers available. Catalogue of providers available for major phenotypic traits			
<i>Target 2012: Practices</i>	The Genetic Resource Supply Service implemented with selected partners for at least all GCP priority crops; at least six marker service provided; at least three trait evaluation or metabolite screening services provided			
<b>Output 20</b>	<b>Comprehensive expert support provided for matters related to modern breeding</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>StraP</li> <li>2009–2013</li> <li>LI/PI: GCP/TBD</li> <li>Linked to P4-03, P4-05 and P4-07</li> </ul>	Crop breeders wishing to upgrade the efficiency of their breeding programmes	Enhanced capacity for the adoption of all necessary elements to succeed in the implementation of modern breeding approaches	Increased progress in crop variety development
<i>Target 2010: Practices</i>	A plan to operate the Support Services (Business Plan Development, Information Management, Data Curation, Design and Analysis, Phenotyping sites and Screening Protocols, Genotyping Support Service and IP Helpdesk) of the MBP available			
<i>Target 2011: Practices</i>	Expert assistance provided to at least 10 users through combining all helpdesks and support services of the MBP; Work flow templates for main breeding schemes made available; sets of training materials developed for information management, data curation and design and analysis; selected phenotyping reference sites characterised; panel of reliable IP experts identified and operating structure of the helpdesk put in place			
<i>Target 2012: Practices</i>	Expert assistance provided to at least 10 users through combining all helpdesks and support services of the MBP and reported in Annual Reports; at least one training course organised for each of the following components: Information Management, Data Curation and Design and Analysis; list of secondary traits and associated protocols related to drought tolerance available; complete repository of IP resources available			
<b>Output 21</b>	<b>Genotyping Support Service</b> <ul style="list-style-type: none"> <li>Commissioned: G4007.21</li> <li>StraP</li> <li>2006–2013</li> <li>LI/PI: GCP/H Gómez-Paniagua</li> <li>Linked to P1-01</li> </ul>	Developing country breeders who lack access to molecular marker labs and those whose genotyping needs outstrip their capacity	Developing country breeders have access to rapid and efficient genotyping of relevant germplasm	Advanced crop improvement in developing countries due to the application of modern marker technologies
<i>Target 2010: Practices</i>	At least 10 genotyping services provided to National Programmes of Agriculture of selected countries, in agreement with Programme priorities and user needs/feedback			
<i>Target 2011: Practices</i>	At least 10 genotyping services provided to National Programmes of Agriculture of selected countries, in agreement with Programme priorities and user needs/feedback			
<i>Target 2012: Practices</i>	At least 10 genotyping services provided to National Programmes of Agriculture of selected countries, in agreement with Programme priorities and user needs/feedback			
<b>Output 22</b>	<b>Development and implementation of a GCP Workflow and Repository System</b> <ul style="list-style-type: none"> <li>Commissioned: Project No. TBD</li> <li>StraP</li> <li>2009–2010</li> <li>LI/PI: Cropster GmbH/N Niederhauser</li> </ul>	GCP community	Users are provided with facilitated procedures to store, manage and exchange project-related information	Enhanced Programme efficiency and transparency
<i>Target 2010: Practices</i>	Development of web-based modules finalised with enhancements required after validation; sustainability tested			

Output	title, type and target(s)	Intended Users	Outcome	Impact
<b>Theme 5: Ex-ante impact analysis and impact assessment</b>				
<b>Output 23</b>	<b>A strategic assessment of the capacity to develop and adopt GCP technologies</b> <ul style="list-style-type: none"> <li>• Commissioned: G4008.24</li> <li>• StraP</li> <li>• 2008–2010</li> <li>• LI/PI: IFPRI/S Wood</li> </ul>	GCP Management Team; wider scientific and development community; other decision-makers	Detailed information about impact factors of GCP research in target regions, crops and traits	Better informed decisions regarding research and development interventions as they refer to regions, crops and traits contributing to reduce poverty and hunger
<i>Target 2010: Other kinds of knowledge</i>	At least three validated country-specific case studies of the application of the revised GCP strategic priority-setting approach; maps, tabulations and interpretations of applying the validated method across all GCP focus regions, farming systems and crops			
<i>Target 2011: Other kinds of knowledge</i>	Completed			



# Annexes

## Annex A: GCP Consortium members and partners – 2009

### 1. Consortium members<sup>1</sup>

#### *Full members*

1. Africa Rice Center (AfricaRice)
2. African Centre for Gene Technologies (ACGT), South Africa (incorporating CSIR, UoP and UotW)
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 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. Agharkar Research Institute, Pune, Maharashtra, India
2. Agricultural Biotechnology Research Institute of Iran (ABRII)
3. Agricultural Research in Tanzania (ART), Tanzania
4. Agricultural Research Institute (ARI), Naliendele Research Station, Tanzania
5. All India Co-ordinated Millet Improvement Project (AICMIP)
6. Bangladesh Rice Research Institute (BRRI)
7. Barwale Foundation, India
8. Bidhan Chandra Krishi Viswavidyalaya (BCKV), India
9. Biosciences Eastern and Central Africa (BecA), Kenya
10. Bureau of Rice Research and Development (BRRD), Rice Department, Thailand
11. Cambodia Agricultural Research and Development Institute (CARDI), Cambodia
12. Central Arid Zone Research Institute (CAZRI), India
13. Central Rainfed Upland Rice Research Station (CRURRS), India
14. Central Rice Research Institute (CRRRI), India
15. Centre d'étude régional pour l'amélioration de l'adaptation à la sécheresse (CERAAS), Senegal
16. Chinese Academy of Agricultural Sciences (CAAS)\*
17. Chitedze Research Station, Malawi
18. Coconut Research Institute of Sri Lanka (CRISL), Sri Lanka
19. Crop Breeding Institute (CBI), Department of Research for Development, Zimbabwe
20. Crop Research Institute (CRI)—Council for Scientific and Industrial Research, Ghana
21. Debre Zeit Agricultural Research Centre (DZARC), Ethiopia
22. Department of Agricultural Research (DAR), Myanmar
23. Department of Agriculture, Thailand
24. Department of Agriculture Research Services (DARS), Malawi
25. Directorate of Maize Research (DMR), India
26. Dr Panjabrao Deshmukh Krishi Vidyapeeth (PDKV; Dr Panjabrao Deshmukh Agricultural University), India
27. Egerton University, Kenya
28. Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA), Brazil\*
29. Escuela Superior Politécnica del Litoral—Centro de Investigaciones Biotecnológicas del Ecuador (ESPOL–CIBE)
30. Ethiopian Institute of Agricultural Research (EIAR)
31. Federación Nacional de Arroceros (Fedearroz), Colombia

<sup>1</sup> In the partner lists from subheading No 2 onwards, Consortium members are also included, and denoted by an asterisk\*, and provisional members by ♣

32. Promoción e Investigación de Productos Andinos (PROINPA), Bolivia
33. Hebei Academy of Agricultural Sciences, Institute of Dry Farming (HAAS), China
34. Huazhong Agricultural University (HZAU), China
35. Indian Agricultural Research Institute (IARI), India
36. Indian Council of Agricultural Research (ICAR)\*
37. Indian Institute of Pulses Research (IIPR)
38. Indira Gandhi Krishi Vidyalaya (IGKV), India
39. Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD), Indonesia
40. Indonesian Cereals Research Institute (ICERI), Indonesia
41. Institut d'économie rurale (IER), Mali
42. Institut de l'environnement et recherches agricoles (INERA), Burkina Faso
43. Institut de recherche agricole pour le développement (IRAD), Cameroon
44. Institut national de la recherche agronomique (INRA–Morocco)♣
45. Institut national de la recherche agronomique du Niger (INRAN)
46. Institut sénégalais de recherches agricoles (ISRA), Senegal
47. Instituto Centroamericano de Administración de Empresas (INCAE), Costa Rica
48. Instituto de Investigação Agrária de Moçambique (IIAM; Institute for Agricultural Research), Mozambique
49. Instituto de Investigaciones Agropecuarias (INIA), Chile
50. Instituto Nacional de Ciencias Agrícolas (INCA), Cuba
51. Instituto Nacional de Investigación Agropecuaria (INIA), Uruguay
52. Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias (INIFAP), Mexico
53. Instituto Nacional de Tecnología Agropecuaria (INTA), Argentina
54. Instituto Nacional de Tecnología Agropecuaria (INTA), Nicaragua
55. Instituto Agronomico de Campinas, Brazil
56. Jimma University College of Agriculture & Veterinary Medicine, Ethiopia
57. Kasetsart University, Thailand
58. Kenya Agricultural Research Institute (KARI), Kenya
59. Lake Zone Agricultural Research and Development Institute (LZARDI), Tanzania
60. Luoyang Academy of Agricultural Sciences (LAAS), China
61. Mahidol University—Institute of Molecular Biology and Genetics, Thailand
62. Marathwada Agricultural University (MAU), India
63. Melkassa Agricultural Research Center (MARC), Ethiopia
64. Moi University, Kenya
65. MRP University of Science and Technology (MRP), India
66. Muhammad Saleem Shaheen Yusafwala Maize and Millets Research, Pakistan
67. Namulonge Agricultural and Animal Research Institute (NAARI), Uganda
68. National Agricultural and Forestry Research Institute (NAFRI), Laos
69. National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand♣
70. National Crop Resources Research Institute (NaCRRRI), Uganda
71. National Institute for Plant Genome Research (NIPGR), India
72. National Key Lab of Crop Genetics and Germplasm Enhancement, China
73. National Maize Research Institute (NMRI), Vietnam
74. National Plant Genetic Resources Centre (NPGRC), Tanzania
75. National Research Centre on Plant Biotechnology (NRCPB), India
76. National Research Centre on Sorghum (NRCS), India
77. National Root and Tuber Crop Research Institute (NRCRI), Nigeria
78. Ningxia University, China
79. Northwest Sci-tech University of Agriculture and Forestry (NWSUAF), China
80. Organisation for the Rehabilitation of the Environment (ORE), Haiti
81. Pakistani Agricultural Research Council (PARC), National Agricultural Research Center, Pakistan
82. Philippine Rice Research Institute (PhilRice)
83. Plant Genetic Resources Research Institute—Council for Scientific and Industrial Research, Ghana
84. Punjab Agricultural University (PAU), India
85. Rajasthan Agricultural University (RAU), Beechwal, India
86. RAK College of Agriculture—Sehore, Madhya Pradesh, India
87. Regional Agricultural Research Station—Nandyal (RARS—Nandyal), Andhra Pradesh, India
88. Research Center for Biotechnology, Bogor Agricultural University (RCB—IPB), Indonesia
89. Savannah Agricultural Research Institute (SARI), Ghana
90. Shanxi Academy of Agricultural Sciences (SAAS), China
91. South Agricultural Research Institute (SARI), Ethiopia
92. Southern Africa Bean Network (SABRN), Zambia
93. Tamil Nadu Agricultural University (TNAU), India
94. Universidad Nacional Agraria La Molina (UNALM), Peru
95. Universidade Católica de Brasília (UCB), Brazil
96. Universidad de Talca, Chile
97. Universidade de São Paulo (USP), Brazil
98. Universidade Eduardo Mondlane, Mozambique
99. Universiti Kebangsaan Malaysia (UKM), Malaysia

100. University of Agricultural Sciences (UAS) Bangalore, India
101. University of Agricultural Sciences (UAS), Dharwad, India
102. University of Dhaka, Bangladesh
103. University of Ebonyi State, Nigeria
104. University of Ghana–West African Centre for Crop Improvement (WACCI), Ghana
105. University of KwaZulu–Natal (UKZN), South Africa
106. University of Pretoria, South Africa\*
107. University of The Philippines Los Baños–Crop Science Cluster
108. University of the Witwatersrand, South Africa\*
109. Yunnan Academy of Agricultural Sciences (YAAS), China
110. Zhejiang University, China

### 3. Developed country partners

1. Agriculture and Agri-Food Canada (AAFC), Semiarid Prairie Agricultural Research Centre (SPARC), Canada
2. Agropolis, France (incorporating CIRAD, IRD and INRA)\*
3. Australian Centre for Plant Functional Genomics Pty Ltd (ACPGF)
4. Centre de coopération internationale en recherche agronomique pour le développement (CIRAD), France\*
5. Centro Internacional de Altos Estudios Agronómicos Mediterráneos–Instituto Agronómico Mediterráneo de Zaragoza (CIAEAM–IAMZ), Spain
6. Charles Sturt University, Australia
7. Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia
8. Cornell University, USA\*
9. Department of Primary Industries & Fisheries (DPI&F), Australia
10. Eidgenössische Technische Hochschule (ETH), (Swiss Federal Institute of Technology), Zürich, Switzerland
11. Food and Environment Research Agency (Fera), UK (Previously known as the Central Science Laboratory)
12. Hebrew University of Jerusalem, Israel
13. Institut de recherche pour le développement (IRD), France\*
14. Institut national de la recherche agronomique (INRA), France\*
15. Institute for Genomic Diversity (IGD), Cornell University\*, USA
16. Institute for Plant Genetics and Crop Plant Research (IPK), Germany
17. Institute for Plant Genetic Resources (IPGR), Bulgaria
18. Japan International Research Center for Agricultural Sciences (JIRCAS), Japan
19. Kansas State University, USA
20. Katholieke Universiteit Leuven (KUL), Belgium
21. Max Planck Institute for Molecular Plant Physiology (MPIMPP), Germany
22. Nagoya University, Japan

23. National Institute of Agrobiological Sciences (NIAS), Japan\*
24. National Institute of Agricultural Biology (NIAB), UK
25. Oregon State University (OSU), USA
26. Pennsylvania State University, USA
27. Plant Breeding Institute–University of Sydney, Australia
28. Queensland Department of Primary Industries (QDPI), Australia
29. Scottish Crop Research Institute (SCRI), UK
30. Texas A&M University, USA
31. United States Department of Agriculture–Agricultural Research Service (USDA–ARS)
32. Università di Bologna, Italy
33. University of Aberdeen, UK
34. University of Alberta, Canada
35. University of Arizona, USA
36. University of California, Davis, USA
37. University of California, Riverside, USA
38. University of Frankfurt, Germany
39. University of Georgia (UGA), USA
40. University of Maryland, USA
41. University of Missouri, USA
42. University of Potsdam, Germany
43. University of Queensland (UQ), Australia
44. Virginia Polytechnic Institute and State University (VPI), USA
45. Wageningen University and Research Centre (WUR), The Netherlands\*

### 4. Funders

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

### 5. CGIAR Centres and Programmes

1. Africa Rice Center (AfricaRice)\*
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. Challenge Program on Climate Change Agriculture and Food Security (CCAFS)
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**

1. BIOSEED–India, Thailand, Philippines and Vietnam
2. IFSSA, India
3. Monsanto
4. Pioneer
5. Syngenta
6. Waen Associates, UK

## **7. Service providers**

1. Cropster GmbH
2. Diversity Arrays Technology Pty Ltd (DArT P/L), Australia
3. J Craig Venter Institute, USA
4. National Centre for Genome Resources (NCGR), USA

## **8. Other partners**

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

## Annex B: Progress report on implementation of external review recommendations

**Name of CP:** Generation Challenge Programme (GCP)

**Dates of External Evaluation Report presentation and discussion:**

- *Science Council:* 31 March 2008, Nairobi, Kenya
- *Executive Council:* 14 May 2008, Ottawa, Canada
- *CGIAR Annual General Meeting:* Maputo, Mozambique, December 2008

NB: Cells that have been greyed out indicate that milestone(s) have been achieved

Recommendations as listed in the External Review report	Response accepted or not accepted	Implementation	Progress achieved	Target date of completion	
		Milestones		MTP 2009–2011	MTP 2010–2012
1. The review panel recommends that GCP establish simple Programme-level success criteria to provide GCP Management Team the means to focus, measure and monitor GCP programme effectiveness.	Accepted	<ul style="list-style-type: none"> <li>• Establish Programme-level impact indicators</li> <li>• Develop a Programme logframe to better monitor Programme achievements</li> </ul>	Pending: no progress to report at the time of submitting this MTP	End 2009	
2. The review panel recommends that GCP management establish and apply a prioritisation process to identify the highest impact opportunities that GCP (Programme-level) can actually achieve and deliver to appropriate impact channels during its remaining six years.	Accepted	<ul style="list-style-type: none"> <li>• Focus on a few platforms that are easily accessible</li> <li>• Prioritise a few challenge initiatives to focus the research of the Programme</li> <li>• Milestones identified for recommendations 1 and 3 are also relevant to a certain extent to this recommendation</li> </ul>	<ul style="list-style-type: none"> <li>• Proposals under development for Genetic, Genomic and Molecular Breeding platforms</li> </ul>	June 2009	Achieved (See <i>Trends</i> , in Overview section)
3. The review panel recommends that GCP deploy the majority (at least 50 percent) of its resources in pursuit of the seven highest impact Programme-level trait-in-crop products that it can achieve over the next five years.	Accepted	<ul style="list-style-type: none"> <li>• Seven challenge initiatives identified and resources allocated accordingly</li> </ul>	<ul style="list-style-type: none"> <li>• The seven initiatives identified for refinement in 2009, and and implementation in 2010</li> </ul>	June 2009	Achieved (see i) <i>Trends</i> , and, ii) <i>Challenge Initiatives</i> , both in <i>Evolution of the GCP strategy and research trends</i> in Overview section)
4. The review panel recommends that GCP management in consultation with the curators of the source collections establish the protocols by which each GCP reference set will be maintained and distributed; and the means by which the current genotypic data and passport (catalogued) information on these reference sets will be maintained and augmented by current and future (non-GCP) discovery efforts that employ these collections.	Accepted	<ul style="list-style-type: none"> <li>• Protocols established for maintaining and distributing GCP's products after 2013</li> <li>• A Genetic Resource Support Service that should ensure quality, timely distribution and easy access to GCP breeding germplasm, with specific attention to the reference sets, through standardised procedures</li> </ul>	<ul style="list-style-type: none"> <li>• Workshop in late 2008 to sensitise germplasm curators and breeders on research steps leading to the reference sets</li> <li>• Recruitment of a Product Delivery expert approved by the new Executive Board and under way</li> <li>• GRSS to be established (see <i>Genetic Resource Support Service</i> in Overview section)</li> </ul>	End 2011	In progress
5. The Review Panel recommends that GCP management revisit the skills training aspect of SP5 and focus skills training on the specific needs of the case studies and highest priority trait improvement projects.	Accepted	<ul style="list-style-type: none"> <li>• Greater participation by NARS in research through enhanced capacity</li> <li>• Increased adoption of research results and more support to the 'Capacity-building <i>à la Carte</i> Programme', with a special focus on the seven new Challenge Initiatives</li> </ul>	<ul style="list-style-type: none"> <li>• A substantial number of validation projects are increasingly being led by NARS partners.</li> <li>• By 2008, nine NARS applied research teams benefiting from tailored capacity building</li> </ul>	June 2009	To be achieved through CI partnerships (see Project 5, Outputs 5, 11, 16, 19 and 20)

Recommendations as listed in the External Review report	Response accepted or not accepted	Implementation		Target date of completion	
		Milestones	Progress achieved	MTP 2009–2011	MTP 2010–2012
6. The review panel recommends that during setup of the Executive Board, a strong emphasis is placed on creating sufficient capacity and expertise for the Board to fulfill its duties, especially in: <ul style="list-style-type: none"> <li>• setting strategic direction for GCP; and,</li> <li>• overseeing GCP finances and managing risks, also those relating to the host centre.</li> </ul>	Accepted	<ul style="list-style-type: none"> <li>• Executive Board established with relevant expertise</li> </ul>	<ul style="list-style-type: none"> <li>• Seven-member Executive Board<sup>1</sup> created as per PSC resolution<sup>2</sup>, spanning the following professional fields: science, finance and corporate governance.</li> <li>• 1<sup>st</sup> EB meeting in July 2008</li> <li>• Board to seek or co-opt special expertise as necessary</li> </ul>	June 2008	
7. The review panel recommends that an attempt is made to further simplify and clarify GCP governance by adapting the Consortium Agreement to the de facto status quo, and to clearly define the role and responsibilities of additional GCP governance bodies (the PSC, the PAC, the Stakeholder Committee).	Accepted	<ul style="list-style-type: none"> <li>• Revise PSC status (organisation and <i>modus operandi</i>).</li> <li>• Consortium Agreement<sup>3</sup> (CA) revised to reflect, among others, the transfer of some responsibilities from the PSC to the new Executive Board</li> </ul>	Partially achieved, and in progress (see <i>GCP governance in Overview</i> section). <ul style="list-style-type: none"> <li>• PSC Task Force to redefine PSC's new role established in December 2007 and report presented in December 2008 PSC meeting</li> <li>• Unanimity clause for CA amendment modified to three quarters</li> <li>• Revised Consortium Agreement – also redefining PSC's role – drafted and to be signed in the 3rd quarter of 2009</li> <li>• Liaison established with GFAR to revamp and redefine SHC role</li> </ul>	March 2009	Delayed to September 2009.
8. The review panel recommends that GCP upgrade all Subprogramme Leader positions to fulltime positions for the next three years. Since SP3 and SP5 Leaders already have fulltime positions, this implies to move the leadership of SP1, SP2 and SP4 from halftime to fulltime positions (in order to provide the necessary management capacity for Programme-level management and the fulfillment of management duties in their respective SPs; and to avoid split responsibilities between the GCP and the SP Leaders' home institutions).	Accepted, but to be implemented only when current half-time SP Leaders, of their own volition, leave the MT	<ul style="list-style-type: none"> <li>• The three halftime SPL positions converted to fulltime positions</li> </ul>	Partially achieved <ul style="list-style-type: none"> <li>• SP4 Leader position converted to fulltime in September 2008</li> </ul>	Subject to current halftime SPLs (1 & 2) turnover, leaving of their own volition	
9. The review panel recommends GCP management adopt an end-product orientation for GCP activities, ie, the integration, alignment and prioritisation of product-oriented projects across Subprogrammes in line with high-priority programme-level product objectives. To support this, the Review Panel recommends that GCP management acquire or develop a product project portfolio management system to help it plan, monitor and manage its best opportunities (achievable high-priority Programme-level objectives).	Accepted	<ul style="list-style-type: none"> <li>• Product Development Coordinators identified for each of the Challenge Initiatives</li> <li>• Programme-level impact indicators defined</li> <li>• Two-dimension management matrix with a product-/crop-specific axis</li> <li>• Milestones here linked to those in Recommendation 3 above</li> </ul>	Partially achieved: (linked to progress on Recommendation 3 above) <ul style="list-style-type: none"> <li>• Workflow system established to streamline portfolio management</li> <li>• Specific objectives drawn up for the seven trait-crop CIs, and associated activities</li> <li>• 5-year CI workplans drafted with milestones and outputs. See <i>Managing our research strategy and Evolution of the GCP strategy and research trends in Overview</i></li> <li>• Programme-level impact indicators pending (linked to Recommendation 1)</li> </ul>	March 2009	CI workplans in progress for implementation in 2010

<sup>1</sup> Details on Executive Board at <http://www.generationcp.org/whoware.php?da=08124404>

<sup>2</sup> PSC resolution at [http://www.generationcp.org/UserFiles/File/final-resolution\\_executive-board-15Dec07\\_final.pdf](http://www.generationcp.org/UserFiles/File/final-resolution_executive-board-15Dec07_final.pdf)

<sup>3</sup> Consortium Agreement at [http://www.generationcp.org/UserFiles/File/Consortium\\_agreement\\_signed.pdf](http://www.generationcp.org/UserFiles/File/Consortium_agreement_signed.pdf)

## Annex C: Financing plan

**Table 1: Allocation of project costs by Priority Area and Priorities, 2010**  
(in \$ millions)

Project	Priority Area 1	Priority Area 2		Total
	1A	2A	2B	
Subprogramme 1: Crop Genetic Diversity	1.438	0.863	0.574	2.875
Subprogramme 2: Genomics towards gene discovery		0.645	2.578	3.223
Subprogramme 3: Trait capture for crop improvement		0.878	2.635	3.513
Subprogramme 4: Bioinformatics and crop information systems	1.085	1.266	1.266	3.617
Subprogramme 5: Capacity-building and enabling delivery	0.873	0.524	2.093	3.490
<b>Total</b>	<b>3.396</b>	<b>4.176</b>	<b>9.146</b>	<b>16.718</b>

**Table 2: Allocation of project costs to CGIAR Priorities, 2008–2012**  
(in \$ millions)

Projects Priorities	Actual 2008	Estimated 2009	Proposal 2010	Plan 1 2011	Plan 2012
Subprogramme 1: Crop genetic diversity					
1A	1.548	1.962	1.438	1.167	1.002
2A	0.929	1.177	0.863	0.700	0.601
2B	0.618	0.785	0.574	0.467	0.400
<b>Total project</b>	<b>3.095</b>	<b>3.924</b>	<b>2.875</b>	<b>2.334</b>	<b>2.003</b>
Subprogramme 2: Genomics towards gene discovery					
1A	0.000	0.000	0.000	0.000	0.000
2A	1.133	0.915	0.645	0.428	0.391
2B	4.532	3.660	2.578	1.711	1.562
<b>Total project</b>	<b>5.665</b>	<b>4.575</b>	<b>3.223</b>	<b>2.139</b>	<b>1.953</b>
Subprogramme 3: Trait capture for crop improvement					
2A	0.829	1.278	0.878	0.788	0.577
2B	2.488	3.833	2.635	2.363	1.729
<b>Total project</b>	<b>3.317</b>	<b>5.111</b>	<b>3.513</b>	<b>3.151</b>	<b>2.306</b>
Subprogramme 4: Bioinformatics and crop information systems					
1A	0.651	1.670	1.085	0.868	0.758
2A	0.759	1.949	1.266	1.013	0.884
2B	0.759	1.949	1.266	1.012	0.884
<b>Total project</b>	<b>2.169</b>	<b>5.568</b>	<b>3.617</b>	<b>2.893</b>	<b>2.526</b>
Subprogramme 5: Capacity-building and enabling delivery					
1A	0.834	0.961	0.873	0.631	0.530
2A	0.501	0.577	0.524	0.378	0.318
2B	2.002	2.306	2.093	1.514	1.272
5A	0.000	0.000	0.000	0.000	0.000
<b>Total</b>	<b>17.583</b>	<b>23.022</b>	<b>16.718</b>	<b>13.040</b>	<b>10.908</b>
<b>Total project</b>	<b>3.337</b>	<b>3.844</b>	<b>3.490</b>	<b>2.523</b>	<b>2.120</b>

**Table 3: Summary of project costs, 2008–2012**

(in \$ millions)

Project	Actual 2008	Estimated 2009	Proposal 2010	Plan 1 2011	Plan 2 2012
Subprogramme 1: Crop genetic diversity	3.095	3.924	2.875	2.334	2.003
Subprogramme 2: Genomics towards gene discovery	5.665	4.575	3.223	2.139	1.953
Subprogramme 3: Trait capture for crop improvement	3.317	5.111	3.513	3.151	2.306
Subprogramme 4: Bioinformatics and crop information systems	2.169	5.568	3.617	2.893	2.526
Subprogramme 5: Capacity-building and enabling delivery	3.337	3.844	3.490	2.523	2.120
<b>Total</b>	<b>17.583</b>	<b>23.022</b>	<b>16.718</b>	<b>13.040</b>	<b>10.908</b>

**Table 4: Summary of priority costs, 2008–2012**

(in \$ millions)

Priorities	Actual 2008	Estimated 2009	Proposal 2010	Plan 1 2011	Plan 2 2012
1A	3.033	4.593	3.396	2.666	2.290
2A	4.151	5.896	4.176	3.307	2.771
2B	10.399	12.533	9.146	7.067	5.847
5A					
<b>Total</b>	<b>17.583</b>	<b>23.022</b>	<b>16.718</b>	<b>13.040</b>	<b>10.908</b>

**Table 5: Investments by undertaking, activity and sector, 2008–2012**

(in \$ millions)

	Actual 2008	Estimated 2009	Proposal 2010	Plan 1 2011	Plan 2012
Increasing productivity	11.781	15.425	11.201	8.737	7.309
Germplasm enhancement & breeding	11.781	15.425	11.201	8.737	7.309
Production systems development & management	0.000	0.000	0.000	0.000	0.000
Cropping systems	0.000	0.000	0.000	0.000	0.000
Livestock systems	0.000	0.000	0.000	0.000	0.000
Tree systems	0.000	0.000	0.000	0.000	0.000
Fish systems	0.000	0.000	0.000	0.000	0.000
Protecting the environment	0.000	0.000	0.000	0.000	0.000
Saving biodiversity	2.637	3.453	2.508	1.956	1.636
Improving policies	0.352	0.460	0.334	0.261	0.218
Strengthening NARS	2.813	3.684	2.675	2.086	1.745
Training and professional development	1.125	1.474	1.070	0.834	0.698
Documentation, publications, info. dissemination	0.422	0.553	0.401	0.313	0.262
Organisation & management counselling	0.563	0.737	0.535	0.417	0.349
Networks	0.703	0.920	0.669	0.522	0.436
<b>Total</b>	<b>17.583</b>	<b>23.022</b>	<b>16.718</b>	<b>13.040</b>	<b>10.908</b>



**Table 6: Project investments by developing region, 2008–2012**

(in \$ millions)

Project	Region	Actual 2008	Estimated 2009	Proposal 2010	Plan 1 2011	Plan 2 2012
Subprogramme 1: Crop genetic diversity	Asia	1.395	1.766	1.295	1.052	0.902
	CWANA	0.200	0.256	0.186	0.151	0.130
	LAC	0.500	0.634	0.465	0.377	0.324
	SSA	1.000	1.268	0.929	0.754	0.647
	<b>Total project</b>	<b>3.095</b>	<b>3.924</b>	<b>2.875</b>	<b>2.334</b>	<b>2.003</b>
Subprogramme 2: Genomics towards gene discovery	Asia	2.677	2.162	1.523	1.011	0.923
	CWANA	0.312	0.252	0.177	0.118	0.107
	LAC	0.446	0.360	0.254	0.168	0.154
	SSA	2.230	1.801	1.269	0.842	0.769
	<b>Total project</b>	<b>5.665</b>	<b>4.575</b>	<b>3.223</b>	<b>2.139</b>	<b>1.953</b>
Subprogramme 3: Trait capture for crop improvement	Asia	1.261	1.942	1.335	1.197	0.876
	CWANA	0.265	0.409	0.281	0.253	0.184
	LAC	0.398	0.613	0.422	0.378	0.277
	SSA	1.393	2.147	1.475	1.323	0.969
	<b>Total project</b>	<b>3.317</b>	<b>5.111</b>	<b>3.513</b>	<b>3.151</b>	<b>2.306</b>
Subprogram 4: Bioinformatics and crop information systems	Asia	0.977	2.508	1.630	1.303	1.138
	CWANA	0.140	0.360	0.233	0.187	0.164
	LAC	0.351	0.900	0.585	0.468	0.408
	SSA	0.701	1.800	1.169	0.935	0.816
	<b>Total project</b>	<b>2.169</b>	<b>5.568</b>	<b>3.617</b>	<b>2.893</b>	<b>2.526</b>
Subprogramme 5: Capacity-building and enabling delivery	Asia	1.586	1.825	1.655	1.197	1.005
	CWANA	0.292	0.337	0.306	0.221	0.186
	LAC	0.363	0.419	0.382	0.276	0.232
	SSA	1.096	1.263	1.147	0.829	0.697
	<b>Total project</b>	<b>3.337</b>	<b>3.844</b>	<b>3.490</b>	<b>2.523</b>	<b>2.120</b>
<b>Total</b>	<b>17.583</b>	<b>23.022</b>	<b>16.718</b>	<b>13.040</b>	<b>10.908</b>	

**Table 7: Summary of investments by developing region, 2008–2012**

(in \$ millions)

Region	Actual 2008	Estimated 2009	Proposal 2010	Plan 1 2011	Plan 2 2012
SSA	6.420	8.279	5.989	4.683	3.898
Asia	7.896	10.203	7.438	5.760	4.844
LAC	2.058	2.926	2.108	1.667	1.395
CWANA	1.209	1.614	1.183	0.930	0.771
<b>Total</b>	<b>17.583</b>	<b>23.022</b>	<b>16.718</b>	<b>13.040</b>	<b>10.908</b>

**Table 8: Expenditure by object, 2008–2012**

(in \$ millions)

Object of expenditure	Actual 2008	Estimated 2009	Proposal 2010	Plan 1 2011	Plan 2 2012
Personnel	0.486	0.770	0.780	0.790	0.790
Supplies and services	1.352	2.175	1.945	1.286	0.780
Collaboration/ Partnerships	15.667	19.927	13.843	10.864	9.288
Operational Travel	0.078	0.150	0.150	0.100	0.050
Depreciation	0.000	0.000	0.000	0.000	0.000
<b>Total</b>	<b>17.583</b>	<b>23.022</b>	<b>16.718</b>	<b>13.040</b>	<b>10.908</b>

**Table 9a: Member and non-member unrestricted grants, 2008–2010**

(in \$ millions NC = National currency)

Unrestricted grants	Type NC	Actual 2008 (US\$)	Actual 2008 (NC)	Estimated 2009 (US\$)	Estimated 2009 (NC)	Proposal 2010 (US\$)	Proposal 2010 (NC)
Sweden	SEK	0.061	0.500	0.090	1.000	0.090	1.000
Switzerland	CHF	0.436	0.450	0.294	0.450	0.294	0.450
United Kingdom	GBP	3.284	2.000	3.317	3.000	3.085	2.500
World Bank	USD	2.000	2.000	2.000	2.000	2.000	2.000
<b>Subtotal</b>		<b>5.781</b>		<b>5.701</b>		<b>5.469</b>	
<b>Non-member</b>							
Pioneer	USD	0.000	0.000	0.025	0.025	0.025	0.025
<b>Subtotal</b>		<b>0.000</b>		<b>0.025</b>		<b>0.025</b>	
<b>Total unrestricted</b>		<b>5.781</b>		<b>5.726</b>		<b>5.494</b>	

**Table 9b: Member and non-member unrestricted and restricted grants, 2008–2010**

(in \$millions)

Member/Non-member	Actual 2008	Estimated 2009	Proposal 2010
<b>Unrestricted grants</b>			
<b>Member</b>			
Sweden	0.061	0.090	0.090
Switzerland	0.436	0.294	0.294
United Kingdom	3.284	3.317	3.085
World Bank	2.000	2.000	2.000
<b>Subtotal</b>	<b>5.781</b>	<b>5.701</b>	<b>5.469</b>
<b>Non-member</b>			
Pioneer	0.000	0.025	0.025
<b>Subtotal</b>	<b>0.000</b>	<b>0.025</b>	<b>0.025</b>
<b>Total unrestricted</b>	<b>5.781</b>	<b>5.726</b>	<b>5.494</b>
<b>Restricted grants</b>			
<b>Member</b>			
European Commission	11.091	5.342	3.371
<b>Subtotal</b>	<b>11.091</b>	<b>5.342</b>	<b>3.371</b>
<b>Non-member</b>			
Bill and Melinda Gates Foundation	3.077	5.028	2.562
<b>Subtotal</b>	<b>3.077</b>	<b>5.028</b>	<b>2.562</b>
<b>Total restricted</b>	<b>14.168</b>	<b>10.370</b>	<b>5.933</b>
<b>Total grants</b>	<b>19.949</b>	<b>16.096</b>	<b>11.427</b>
<b>Summary and statement of activities</b>			
<b>Total grants</b>	<b>19.949</b>	<b>16.096</b>	<b>11.427</b>
<b>Center income</b>	<b>0.188</b>	<b>0.080</b>	<b>0.060</b>
<b>Revenue</b>	<b>20.137</b>	<b>16.176</b>	<b>11.487</b>
<b>Total investment</b>	<b>17.583</b>	<b>23.022</b>	<b>16.718</b>
<b>Surplus (Deficit)</b>	<b>2.554</b>	<b>-6.846</b>	<b>-5.231</b>

**Table 10: Allocation of member, non-member grants and other sources to projects, 2008–2010**  
(in \$ millions)

Project	Member		Actual 2008	Estimated 2009	Proposal 2010
Subprogramme 1: Crop Genetic Diversity	Member	European Commission	2.321	1.397	0.626
	Non-member	Bill and Melinda Gates Foundation	0.485	0.403	0.101
	Unrestricted + other sources		0.289	2.124	2.148
	<b>Project total</b>		<b>3.095</b>	<b>3.924</b>	<b>2.875</b>
Subprogramme 2: Genomics towards gene discovery	Member	European Commission	2.374	0.941	0.626
	Non-member	Bill and Melinda Gates Foundation	1.751	1.461	0.365
	Unrestricted + other sources		1.540	2.173	2.232
	<b>Project total</b>		<b>5.665</b>	<b>4.575</b>	<b>3.223</b>
Subprogramme 3: Trait capture for crop improvement	Member	European Commission	1.596	1.442	1.148
	Non-member	Bill and Melinda Gates Foundation	0.485	0.403	0.101
	Unrestricted + other sources		1.236	3.266	2.264
	<b>Project total</b>		<b>3.317</b>	<b>5.111</b>	<b>3.513</b>
Subprogramme 4: Bioinformatics and crop information systems	Member	European Commission	2.031	0.609	0.313
	Non-member	Bill and Melinda Gates Foundation	0.000	1.438	0.941
	Unrestricted + other sources		0.138	3.521	2.363
	<b>Project total</b>		<b>2.169</b>	<b>5.568</b>	<b>3.617</b>
Subprogramme 5: Capacity-building and enabling delivery	Member	European Commission	2.769	0.953	0.658
	Non-member	Bill and Melinda Gates Foundation	0.356	1.323	1.054
	Unrestricted + other sources		0.212	1.568	1.778
	<b>Project total</b>		<b>3.337</b>	<b>3.844</b>	<b>3.490</b>
		<b>Total restricted</b>	<b>14.168</b>	<b>10.370</b>	<b>5.933</b>
		<b>Total unrestricted + other sources</b>	<b>3.415</b>	<b>12.652</b>	<b>10.785</b>
		<b>Total</b>	<b>17.583</b>	<b>23.022</b>	<b>16.718</b>

**Table 11: Internationally- and nationally-recruited staff, 2008–2012**  
(in \$millions)

	Actual 2008	Estimated 2009	Proposal 2010	Plan 1 2011	Plan 2 2012
NRS	5	5	5	5	5
IRS	6	6	6	6	6
<b>Total</b>	<b>11</b>	<b>11</b>	<b>11</b>	<b>11</b>	<b>11</b>

**Table 12: Currency structure of expenditure, 2008–2010**  
(in millions of units and percent)

Currency	Actual 2008			Estimated 2009			Proposal 2010		
	Amount	\$ Value	% Share	Amount	\$ Value	% Share	Amount	\$ Value	% Share
MXN	3.239	0.290	2	3.350	0.240	1	3.500	0.269	2
USD	17.293	17.293	98	22.782	22.782	99	0.000	16.449	98
<b>Total</b>		<b>17.583</b>	<b>100 %</b>		<b>23.022</b>	<b>100 %</b>		<b>16.718</b>	<b>100%</b>

**Table 13: Statement of Financial Position (SFP), 2008–2010**  
(in \$ millions)

Assets, liabilities and net assets	2008	2009	2010
<b>Current assets</b>			
Cash and Cash Equivalents	0.000	0.000	0.000
Investments	3.000	3.000	0.000
Accounts Receivable			
– Donor	6.031	0.000	0.000
– Employees	0.000	0.000	0.000
– Other CGIAR Centers	3.817	2.697	0.466
– Others	0.000	0.000	0.000
– Inventories	0.000	0.000	0.000
– Pre-paid expenses	0.000	0.000	0.000
<b>Total current assets</b>	<b>12.848</b>	<b>5.697</b>	<b>0.466</b>
<b>Non-current assets</b>			
Net Property, Plan and Equipment	0.000	0.000	0.000
Investments	0.000	0.000	0.000
Other assets	0.000	0.000	0.000
<b>Total non-current assets</b>	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>
<b>Total assets</b>	<b>12.848</b>	<b>5.697</b>	<b>0.466</b>
<b>Current liabilities</b>			
Overdraft/Short-term borrowings	0.000	0.000	0.000
Accounts payable			
– Donor	0.305	0.000	0.000
– Employees	0.000	0.000	0.000
– Other CGIAR Centers	0.000	0.000	0.000
– Others	0.000	0.000	0.000
Accruals and provisions	0.000	0.000	0.000
<b>Total current liabilities</b>	<b>0.305</b>	<b>0.000</b>	<b>0.000</b>
<b>Non-current liabilities</b>			
Accounts payable			
– Employees	0.000	0.000	0.000
– Deferred grant revenue	0.000	0.000	0.000
– Others	0.000	0.000	0.000
<b>Total non-current liabilities</b>	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>
<b>Total liabilities</b>	<b>0.305</b>	<b>0.000</b>	<b>0.000</b>
<b>Net assets</b>			
Unrestricted			
– Fixed assets	0.000	0.000	0.000
– Unrestricted net assets excluding fixed assets	3.000	3.000	0.466
<b>Total unrestricted net assets</b>	<b>3.000</b>	<b>3.000</b>	<b>0.466</b>
Restricted	9.543	2.697	0.000
<b>Total net assets</b>	<b>12.543</b>	<b>5.697</b>	<b>0.466</b>
<b>Total liabilities and net assets</b>	<b>12.848</b>	<b>5.697</b>	<b>0.466</b>

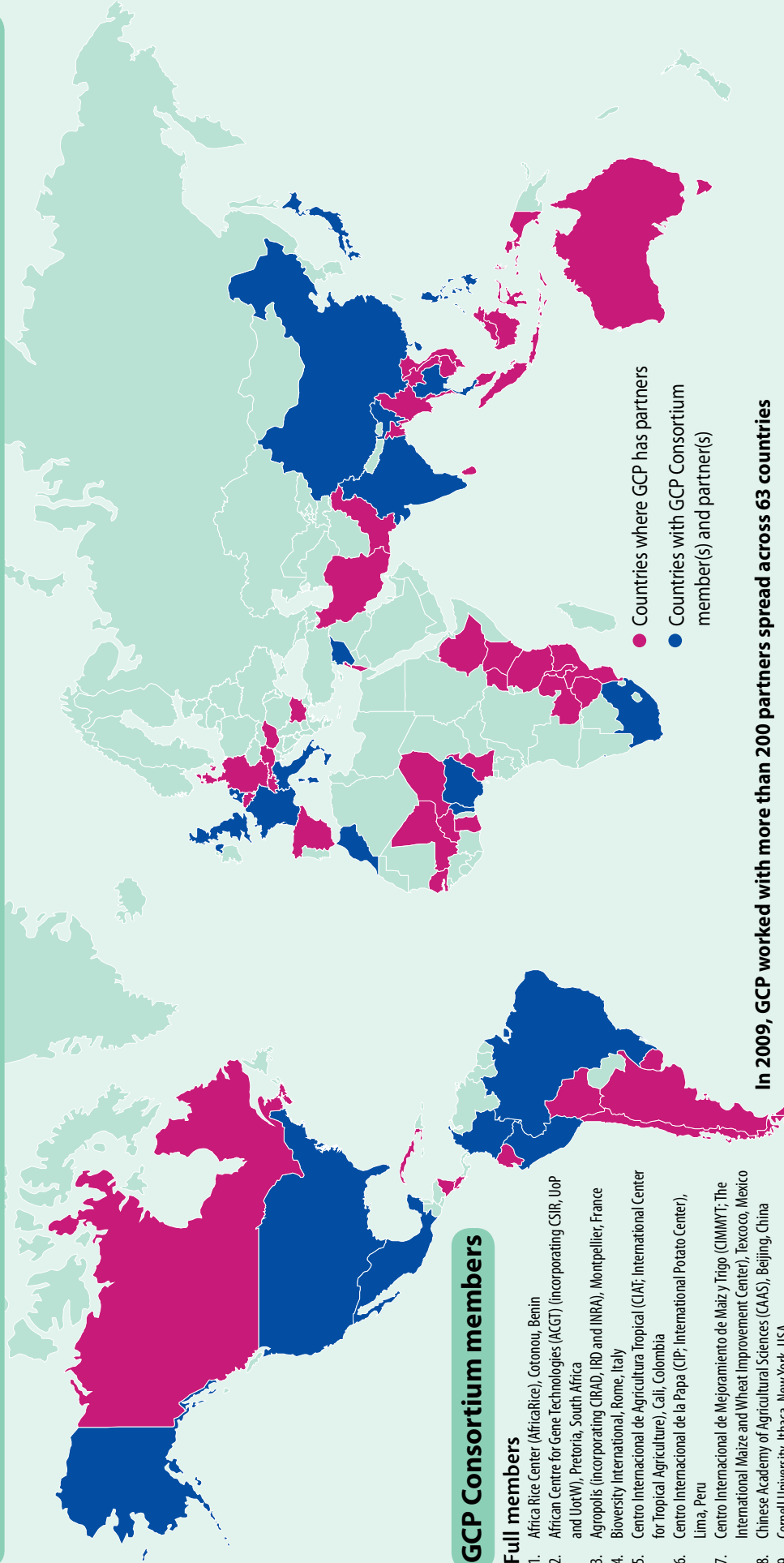
**Table 14: Statement of activities (SOA), 2008–2010**

(in \$millions)

		Unrestricted	Restricted		2008	Total	
			Temporary	Challenge Programs		2009	2010
Revenue and gains	Grant revenue	5.781	0.000	14.168	19.949	16.096	11.427
	Other revenue and gains	0.188	0.000	0.000	0.188	0.080	0.060
	Total revenue and gains	5.969	0.000	14.168	20.137	16.176	11.487
Expenses and losses	Programme-related expenses	1.499	0.000	14.168	15.667	19.927	13.843
	Management and general expenses	1.916	0.000	0.000	1.916	3.095	2.875
	Other losses expenses	0.000	0.000	0.000	0.000	0.000	0.000
	Sub-total expenses and losses	3.415	0.000	14.168	17.583	23.022	16.718
	Indirect cost recovery	0.000	0.000	0.000	0.000	0.000	0.000
	Total expenses and losses	3.415	0.000	14.168	17.583	23.022	16.718
	Net operating surplus/(Deficit)	2.554	0.000	0.000	2.554	-6.846	-5.231
	Extraordinary Items	0.000	0.000	0.000	0.000	0.000	0.000
	NET SURPLUS/(DEFICIT)	2.554	0.000	0.000	2.554	-6.846	-5.231
Object of expenditure	Personnel	0.486	0.000	0.000	0.486	0.770	0.780
	Supplies and services	1.352	0.000	0.000	1.352	2.175	1.945
	Collaboration/Partnerships	15.667	0.000	0.000	15.667	19.927	13.843
	Operational travel	0.078	0.000	0.000	0.078	0.150	0.150
	Depreciation	0.000	0.000	0.000	0.000	0.000	0.000
	<b>Total</b>	<b>17.583</b>	<b>0.000</b>	<b>0.000</b>	<b>17.583</b>	<b>23.022</b>	<b>16.718</b>



# Where in the world is GCP? The GCP network in 2009



## GCP Consortium members

- Full members**
1. Africa Rice Center (AfricaRice), Cotonou, Benin
  2. African Centre for Gene Technologies (ACGT) (incorporating CSIR, UoP and UotW), Pretoria, South Africa
  3. Agropolis (incorporating CIRAD, IRD and INRA), Montpellier, France
  4. Bioregional International, Rome, Italy
  5. Centro Internacional de Agricultura Tropical (CIAT; International Center for Tropical Agriculture), Cali, Colombia
  6. Centro Internacional de la Papa (CIP; International Potato Center), Lima, Peru
  7. Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT; The International Maize and Wheat Improvement Center), Texcoco, Mexico
  8. Chinese Academy of Agricultural Sciences (CAAS), Beijing, China
  9. Cornell University, Ithaca, New York, USA
  10. Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA; Brazilian Agricultural Research Corporation), Brasília, Brazil
  11. Indian Council of Agricultural Research (ICAR), New Delhi, India
  12. International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo, Syria
  13. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India
  14. International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria
  15. International Rice Research Institute (IRRI), Los Baños, The Philippines
  16. John Innes Centre (JIC), Norwich, UK
  17. National Institute of Agrobiological Sciences (NIAS), Tsukuba, Japan
  18. Wageningen University and Research Centre (WUR), Wageningen, The Netherlands

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

## In 2009, GCP worked with more than 200 partners spread across 63 countries

### Developing country partners

- |   |  |                           |
|---|--|---------------------------|
| <b>Central and West Asia and North Africa</b> | <b>Latin America and the Caribbean</b> | <b>Sub-Saharan Africa</b> |
| 1. Iran                                       | 6. Argentina                           | 25. Benin                 |
| 2. Morocco                                    | 7. Bolivia                             | 26. Burkina Faso          |
| 3. Syrian Arab Republic                       | 8. Chile                               | 27. Cameroon              |
|   | 9. Colombia                            | 28. Ethiopia              |
|   | 10. Costa Rica                         | 29. Ghana                 |
| <b>Eastern Europe</b>                         | 11. Cuba                               | 30. Kenya                 |
| 4. Bulgaria                                   | 12. Ecuador                            | 31. Malawi                |
| 5. Hungary                                    | 13. Haiti                              | 32. Mali                  |
|   | 14. Nicaragua                          | 33. Mozambique            |
|   | 15. Peru                               | 34. Niger                 |
|   | 16. Uruguay                            | 35. Nigeria               |
|   |  | 36. Senegal               |
|   |  | 37. Tanzania              |
|   |  | 38. Uganda                |
|   |  | 39. Zambia                |
|   |  | 40. Zimbabwe              |

### Newly industrialised country partners

- |  |                                 |
|--|---------------------------------|
| <b>Latin America and the Caribbean</b> | <b>South and Southeast Asia</b> |
| 41. Brazil                             | 43. China                       |
| 42. Mexico                             | 44. India                       |
|  | 45. Malaysia                    |
|  | 46. Thailand                    |
|  | 47. The Philippines             |
|  | <b>Sub-Saharan Africa</b>       |
|  | 48. South Africa                |

### Developed country partners

- |                     |                      |
|---------------------|----------------------|
| <b>Asia</b>         | <b>North America</b> |
| 49. Israel          | 61. Canada           |
| 50. Japan           | 62. USA              |
| <b>Europe</b>       | <b>Oceania</b>       |
| 51. Austria         | 63. Australia        |
| 52. Belgium         |                      |
| 53. Denmark         |                      |
| 54. France          |                      |
| 55. Germany         |                      |
| 56. Italy           |                      |
| 57. Spain           |                      |
| 58. Switzerland     |                      |
| 59. The Netherlands |                      |
| 60. United Kingdom  |                      |

● Countries where GCP Consortium member(s) and partner(s)

● Countries where GCP has partners

## GCP Annual Research Meeting participants, September 2009, Bamako, Mali.

"Perhaps the most important value of GCP thus far, is the opportunities it has provided for people of diverse backgrounds to think collectively about solutions to complex problems, and, in the process, to learn from one another." —*Excerpt from the report of the First External Programme and Management Review, March 2008.*



Hosted by CIMMYT

(Centro Internacional de Mejoramiento de Maíz y Trigo;  
the International Maize and Wheat Improvement Center)

Mailing address:

Apdo Postal 6-641  
06600 México, DF, México

Physical address:

Km 45 Carretera México-Veracruz  
El Batán, Texcoco, México, CP 56130

Tel: +52 55 5804 2004 | Fax: +52 55 5804 7558

Email: [generationcp@cgiar.org](mailto:generationcp@cgiar.org) or [info@generationcp.org](mailto:info@generationcp.org)  
[www.generationcp.org](http://www.generationcp.org)