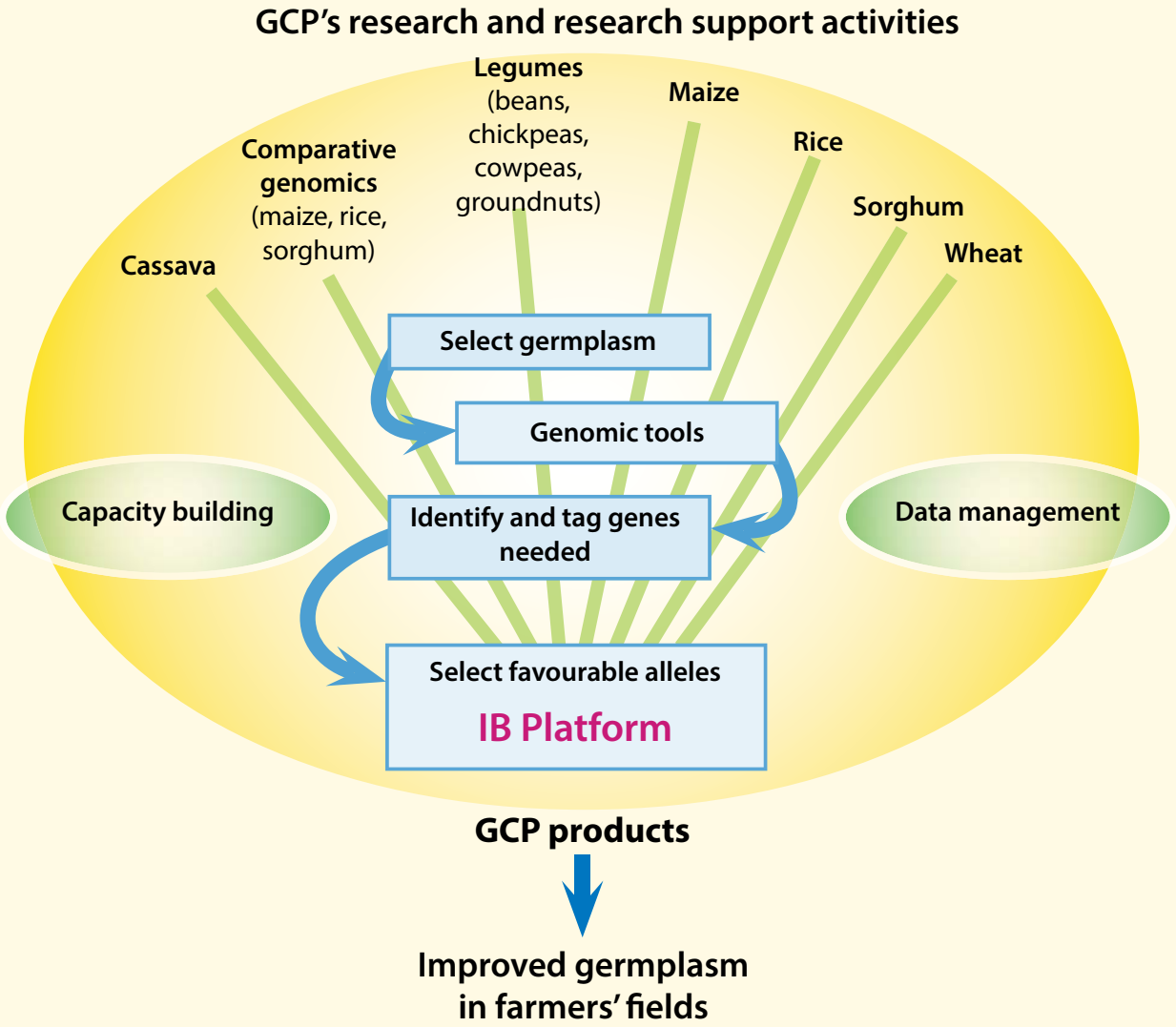
2011 Project Briefs

Generation Challenge Programme

Partnerships in modern crop breeding for food security

Our activities and structure

In Phase II, GCP (2009–2014), GCP primarily focuses on seven Research Initiatives (RI) organised by crop and crop clusters (see diagram) as well as a service component – the Integrated Breeding Platform (IBP): a web-based one-stop shop for information, analytical tools and related services to design and carry out integrated breeding projects. The RIs are trait- and country-specific. As selected user cases of IBP, the RIs aim to demonstrate that modern and integrated breeding approaches can have a significant impact on crop productivity in developing countries.



Generation Challenge Programme

Partnerships in modern crop breeding for food security

2011 Project Briefs

February 2013

The Project Briefs are extracted from the original proposals.

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Contents

Acronyms and abbreviations

AAFC	Agriculture and Agri-Food Canada
ABRII	Agriculture Biotechnology Research Institute of Iran
ACCI–UKZN	African Centre for Crop Improvement, University of KwaZulu–Natal, South Africa
ACGT	African Centre for Gene Technologies, South Africa
ACGT–UoP	African Centre for Gene Technologies–University of Pretoria, South Africa
ACGT–UoW	African Centre for Gene Technologies–University of the Witswatersrand, South Africa
ACGT–CSIR	African Centre for Gene Technologies– Council for Scientific and Industrial Research, South Africa
ACPFG	Australian Centre for Plant Functional Genomics, Pty Ltd
AfricaRice	Africa Rice Center
AGI	Agricultural Genetics Institute, Vietnam
AGRA/PASS	Alliance for a Green Revolution in Africa/Program for African Seed Systems
Agropolis–CIRAD	Centre de coopération internationale en recherche agronomique pour le développement, France
Agropolis–INRA	Institut national de la recherche agronomique, France
Agropolis–IRD	Institut de recherche pour le développement, France
AICPMIP	All-India Coordinated Pearl Millet Improvement Project
Al	aluminium
Alt1	marker diagnostic for aluminium tolerance
Alt^{SB}	marker diagnostic for aluminium tolerance
ARC	Africa Rice Center
ARI(s)	advanced research institute(s)
ARI–HAS	Agricultural Research Institute of the Hungarian Academy of Sciences, Hungary
ARI–ICAR	Agharkar Research Institute, Pune, Maharashtra–Indian Council of Agricultural Research
ARI–Naliendele	Agricultural Research Institute, Naliendele, Tanzania
ARI–SRI	Agricultural Research Institute, Sugarcane Research Institute, Kibaha, Tanzania
ARS	Agricultural Research Station, Durgapura, Rajasthan, India
BAU	Birsa Agricultural University, Ranchi, India
BC^1, BC^2,etc	backcross 1, backcross 2, etc
BC^{1}F^4	4_{th} filial generation progenies derived from backcross 1
BCKV	Bidhan Chandra Krishi Viswavidyalaya, India
BCNAM	backcross nested association mapping
BecA	Biosciences Eastern and Central Africa
BF	Barwale Foundation, India
BI	Bioversity International
BIOTEC	National Center for Genetic Engineering and Biotechnology, Thailand
Bioversity	Bioversity International
BMGF	Bill & Melinda Gates Foundation
BRAC	Bangladesh Rehabilitation Assistance Committee
BRRD	Bureau of Rice Research and Development, Rice Department, Thailand
BRRI	Bangladesh Rice Research Institute
CAAS	Chinese Academy of Agricultural Sciences
CAAS–MST	Chinese Academy of Agricultural Sciences, Ministry of Science & Technology
CAP	Coordinated Agricultural Project (USDA project)
CARDI	Cambodian Agricultural Research and Development Institute
CAS–IP	Central Advisory Service – Intellectual Property
CAZRI	Central Arid Zone Research Institute, India
CB	capacity building
CBI–DR&SS	Crop Breeding Institute, Department of Research and Specialist Services, Zimbabwe
CBS	Centre de biotechnologie de Sfax, Tunisia
CBSD	cassava brown-streak disease
CERAAS	Centre d'étude régional pour l'amélioration de l'adaptation à la sécheresse, Senegal
CG	*abbreviation for* 'CGIAR'
CGIAR	Consultative Group on International Agricultural Research
CI	Challenge Initiative
CIAT	Centro Internacional de Agricultura Tropical (International Center for Tropical Agriculture)
CIBE–ESPOL	Centro de Investigaciones Biotecnológicas del Ecuador, Escuela Superior Politécnica del Litoral, Ecuador
CIMMYT	Centro Internacional de Mejoramiento de Maíz y Trigo (the International Maize and Wheat Improvement Center)
CIMS–INCAE	Centro de Inteligencia sobre Mercados Sostenibles, INCAE Business School, Costa Rica
CINVESTAV	Centro de Investigación y de Estudios Avanzados, Mexico
CIP	Centro Internacional de la Papa (International Potato Center)
CIRAD	see Agropolis–CIRAD
CMD	cassava mosaic disease
CNPMF	Centro Nacional de Pesquisa de Mandioca e Fruticultura (National Center for Research on Cassava and Fruit Crops, EMBRAPA, Brazil)
CO	crop ontology
CoP(s)	community(ies) of practice
CORAF/WECARD	Conseil Ouest et Centre africain pour la recherche et le développement agricoles/West and Central African Council for Agricultural Research and Development
CP	Challenge Programme of the CGIAR
CPATSA	Centro de Pesquisa Agropecuária do Trópico Semi-Árido, EMBRAPA, Brazil
CRI–CSIR	Crops Research Institute, Council for Scientific and Industrial Research, Ghana
CRISL	Coconut Research Institute, Sri Lanka
CRP(s)	CGIAR Research Programme(s)
CRRI	Central Rice Research Institute, India
CRS	Chitedze Research Station, Malawi
CRURRS	Central Rainfed Upland Rice Research Station, India
CSIRO	Commonwealth Scientific and Industrial Research Organisation, Australia
CSU	Charles Sturt University, Australia
CU	Cornell University, USA
CWS	configurable workflow system
DAR	Department of Agricultural Research, Myanmar
DAR4D	Department of Agricultural Research for Development, Zimbabwe
DArT	diversity arrays technology
	diversity arrays technology
DarT P/L	Diversity Arrays Technology Pty, Ltd
DARTS	Department of Agricultural Research and Technical Services, Malawi
DBT–GoI	Department of Biotechnology, Government of India
DDPSC	The Donald Danforth Plant Science Center
DLM	DNA LandMarks Inc, Canada
DNA	deoxyribonucleic acid
DPI&F	Department of Primary Industries and Fisheries, Australia
DPKit	Delivery Plan kit
DPSPP–EKC	Department of Plant Sciences and Plant Physiology, Eszterházy Károly College, Eger, Hungary
DR&SS	Department of Research and Specialist Services, Zimbabwe
DRR	Directorate of Rice Research, India
DZARC	Debre Zeit Agricultural Research Centre, Ethiopia
EAST	Embu Agricultural Staff Training (EAST) College, Kenya
EB	(GCP) Executive Board
EC	European Commission
ECABREN	Eastern and Central Africa Bean Research Network
ECOWAS	Economic community of West African States
EgU	Egerton University, Kenya
EIAR	Ethiopian Institute of Agricultural Research
ELS	early leaf spot

EMBRAPA	Empresa Brasileira de Pesquisa Agropecuária (Brazilian Agricultural Research Corporation)
EMBRAPA Labex–USDA	EMBRAPA's 'virtual' laboratory in USA at USDA
EST	expressed sequence tag
ETH	Eidgenössische Technische Hochschule, (Swiss Federal Institute of Technology), Zürich, Switzerland
F^1, F^2, etc	1st filial generation, 2nd filial generation, etc
FCRI	Field Crop Research Institute, Vietnam
Fe	iron
Fedearroz	Federación Nacional de Arroceros, Colombia
FERA	Food and Environment Research Agency, UK (previously known as the Central Science Laboratory)
G×E	genotype by environment interaction
GBP	British pound
GCP	Generation Challenge Programme of the CGIAR
GIS	geographic information system(s)
GSS	Genotyping Support Service
HAAS	Hebei Academy of Agricultural Sciences, China
HAU	Huazhong Agricultural University, China
HI	harvest index
HU	Haramaya University, Ethiopia
IARI	Indian Agricultural Research Institute
IARI–ICAR	Indian Agricultural Research Institute–Indian Council of Agricultural Research
IBP	Integrated Breeding Platform
ICABIOGRAD	Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development
ICAR	Indian Council of Agricultural Research
ICARDA	International Center for Agricultural Research in the Dry Areas
ICERI	Indonesian Cereals Research Institute
ICGGC	International Chickpea Genetics and Genomics Consortium
ICIS	International Crop Information System
ICPMB3	3_{rd} International Conference on Plant Molecular Breeding, September 2010, Beijing, China
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
ICS–CAAS	Institute of Crop Science, Chinese Academy of Agricultural Sciences
ICT	information and communication technology
IDF–HAAS	Institute of Dry Farming, Hebei Academy of Agricultural Sciences, China
IER	Institut d'économie rurale, Mali
IFPRI	International Food Policy Research Institute
IGD–CU	Institute for Genomic Diversity, Cornell University, USA
IGKV	Indira Gandhi Krishi Vishwavidyalaya (Indira Gandhi Agricultural University), India
IIAM	Instituto de Investigação Agrária de Moçambique (Institute for Agricultural Research, Mozambique)
IICRD–KU	Inseechandrastitya Institute for Crop Research and Development, Kasetsart University, Thailand
IIPR	Indian Institute of Pulses Research
IITA	International Institute of Tropical Agriculture
ILRI	International Livestock Research Institute
INERA	Institut de l'environnement et de recherches agricoles, Burkina Faso
INIA–Chile	Instituto de Investigaciónes Agropecuarias, Chile
INIA–Uruguay	Instituto Nacional de Investigación Agropecuaria, Uruguay
INIFAP	Instituto Nacional de Investigaciónes Forestales y Agropecuarias, Mexico
INRA–Morocco	Institut national de la recherche agronomique, Morocco
INRAN	Institut national de la recherche agronomique du Niger
INTA–Argentina	Instituto Nacional de Tecnología Agropecuaria, Argentina
INTA–Nicaragua	Instituto Nicaragüense de Tecnología Agropecuaria, Nicaragua
IP	intellectual property
IPAC	Intellectual Property Advisory Committee (of the GCP EB)
IPB–UPLB	Institute of Plant Breeding, University of the Philippines Los Baños
IPGR	Institute for Plant Genetic Resources, Bulgaria
IPK	Institute for Plant Genetics and Crop Plant Research, Germany
iPlant	iPlant Collaborative
IRAD	Institut de la recherche agronomique pour le développement, Cameroon
IRD	see Agropolis–IRD
IRIS	International Rice Information System
IRRI	International Rice Research Institute
ISMU	integrated SNP mining and utilisation
ISRA	Institut sénégalais de recherches agricoles, Senegal
ISRs	intron spanning regions
IT	information technology
JCVI	J Craig Venter Institute, USA
JIRCAS	Japan International Research Center for Agricultural Sciences
JNKVV	Jawaharlal Nehru Krishi Vishwa Vidyalaya, India
JUCAVM	Jimma University College of Agriculture & Veterinary Medicine, Ethiopia
KAgRI	KATRIN Agricultural Research Institute, Tanzania
KARI	Kenya Agricultural Research Institute
KASPar®	KBioscience's PCR SNP genotyping system
KATRIN	Kilombero Agricultural Training and Research Institute, Tanzania
KBi	KBioscience, UK
KSL	Krishidhan Seeds Ltd, India
KUL	Katholieke Universiteit Leuven, Belgium
LAAS	Luoyang Academy of Agricultural Sciences, China
LI	lead institute
LIMS	Laboratory Information Management System
LZARDI	Lake Zone Agricultural Research and Development Institute, Tanzania
MAB	marker-assisted breeding
MABC	marker-assisted backcrossing
MAGIC	multiparent advanced generation inter-cross
MahU	Mahidol University, Thailand
MakU	Makerere University, Uganda
MARS	marker-assisted recurrent selection
MAS	marker-assisted selection
MATE	multidrug and toxic compound extrusion
MAU	Marathwada Agricultural University, India
MBP	Molecular Breeding Platform *(now renamed IBP)*
MoU	Memorandum of Understanding
MPIMPP	Max Planck Institute for Molecular Plant Physiology, Germany
MSc	Master of Science
MST	Ministry of Science & Technology, China
MSV	maize streak virus
MT	(GCP) Management Team
MTP	*depending on context,* Medium-Term Plan *or* minimum tiling path
MU	Moi University, Kenya
NaCRRI	National Crop Resources Research Institute, Uganda
NAFRI	National Agricultural and Forestry Research Institute, Laos
NagU	Nagoya University, Japan
NAM	nested association mapping
NARS	national agricultural research system(s)
NCAR	National Center for Atmospheric Research, USA
NCE	no-cost extension
NCGR	National Center for Genome Resources, USA
NCRI	National Cereals Research Institute, Nigeria
NCSRC–KU	National Corn and Sorghum Research Center, Kasetsart University, Thailand
NCSU	North Carolina State University, USA
NDUAT	Narendra Deva University of Agriculture and Technology, India
NGS	next-generation sequencing
NIAB	National Institute of Agricultural Botany, UK
NIAS	National Institute of Agrobiological Sciences, Japan
NIL(s)	near-isogenic line(s)
NIPGR	National Institute for Plant Genome Research, India

NMRI	National Maize Research Institute, Vietnam
NPGRC	National Plant Genetic Resources Centre, Tanzania
NRCPB	National Research Centre on Plant Biotechnology, India
NRCRI	National Root Crops Research Institute, Nigeria
NRCS	National Research Centre on Sorghum, India
NRTP–ARI	National Root and Tuber Programme, Agricultural Research Institute, Naliendele Research Station, Tanzania
NSF	National Science Foundation, USA
NSFCRC	Nakhon Sawan Field Crops Research Center, Thailand
NU	Ningxia University, China
NWSUAF	Northwest Sci-tech University of Agriculture and Forestry, China
OSU	Oregon State University, USA
P	phosphorus
PAC	(GCP) Programme Advisory Committee (defunct)
PAU	Punjab Agricultural University, India
PBI–UoS	Plant Breeding Institute, University of Sydney, Australia
PCR	polymerase chain reaction
PD	Product Delivery (Leader)
PDA–GPS	personal digital assistant–Global Positioning System
PDC	Product Delivery Coordinator
PDKV	Dr Panjabrao Deshmukh Krishi Vidyapeeth (Dr Panjabrao Deshmukh Agricultural University), India
PDL	Product Delivery Leader
PGRRI	Plant Genetic Resources Research Institute, Council for Scientific and Industrial Research, Ghana
PHI	Pioneer Hi-Bred International, Inc
PhilRice	Philippine Rice Research Institute
PI	Principal Investigator
PROINPA	Promoción e Investigación de Productos Andinos, Bolivia
PSC	(GCP) Programme Steering Committee (defunct)
PSU	Pennsylvania State University, USA
Pup1	marker diagnostic for phosphorus uptake
QTL	quantitative trait locus
QTL×E	QTL by environment interaction
R&D	research and development
R4D	research for development
RAD	restriction site associated DNA sequencing
RAKCA	RAK College of Agriculture–Sehore, Madhya Pradesh, India
RAP	Review and Advisory Panel
RARS	Regional Agricultural Research Station, Nandyal, India
RAU	Rajasthan Agricultural University, India
RCSL(s)	recombinant segment substitution line(s)
RGDU–BIOTEC	Rice Gene Discovery Unit, National Center for Genetic Engineering and Biotechnology, Thailand
RI(s)	(GCP) Research Initiative(s)
RIKEN	Rikagaku Kenkyūsho (Institute of Physical and Chemical Research), Japan
RIL(s)	recombinant inbred line(s)
RRDI	Rice Research and Development Institute, Sri Lanka
RYMV	rice yellow mottle virus
SAAS	Shanxi Academy of Agricultural Sciences, China
SABRN	Southern Africa Bean Research Network
Saltol	marker diagnostic for salt tolerance
SARI–CSIR	Savanna Agricultural Research Institute, Council for Scientific and Industrial Research, Ghana
SARI–Ethiopia	South Agricultural Research Institute, Ethiopia
SCRI	Scottish Crop Research Institute, UK
SEC	southern, eastern and central (Africa)
SGRP	(CGIAR) System-wide Genetic Resources Programme
SHW	synthetic hexaploid wheat
Sida	Swedish International Development Cooperation Agency
SiMAC	Scientific and Management Advisory Committee (of the IBP)
SINGER	(CGIAR) Systemwide Information Network for Genetic Resources
SME(s)	Small- and medium-scale enterprise(s)
SMTA	standard material transfer agreement
SNP	single nucleotide polymorphism
SP	(GCP) Subprogramme
SP1, SP2, etc	Subprogramme 1, Subprogramme 2, etc
SP2L	SP2 Leader
SPARC	Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food (AAFC), Canada
SPL	Subprogramme Leader
SPVD	sweet potato virus disease
SSA	sub-Saharan Africa
SSR	simple sequence repeat
SUA	Sokoine University of Agriculture, Tanzania
TAMU	Texas A&M University, USA
TL	Theme Leader
TLI	Tropical Legumes I Project
TLII	Tropical Legumes II Project
TLM	Tropical Legumes I annual meeting (GCP)
TNAU	Tamil Nadu Agricultural University, India
TPE	target of population environments
TUSs	tentative unique sequences
UAS–B	University of Agricultural Sciences, Bangalore, India
UAS–D	University of Agricultural Sciences, Dharwad, India
UCB	Universidade Católica de Brasilia, Brazil
UC–D	University of California, Davis, USA
UC–R	University of California, Riverside, USA
UdB	Università di Bologna, Italy
UdR	Universidad de la Republica, Uruguay
UEM	Universidade Eduardo Mondlane, Mozambique
UFS	University of Free State, South Africa
UG	University of Ghana
UGA	University of Georgia, USA
UK	United Kingdom
UKM	Universiti Kebangsaan, Malaysia
UKZN	University of KwaZulu–Natal, South Africa
UNALM	Universidad Nacional Agraria La Molina, Peru
UNIBO	Università di Bologna, Italy
UoA	University of Arizona, USA
UoAb	University of Aberdeen, Scotland
UoAl	University of Alberta, Canada
UoD	University of Dhaka, Bangladesh
UoI	University of Ibadan, Nigeria
UoM	University of Maryland, USA
UoMi	University of Missouri, USA
UoN	University of Nairobi, Kenya
UoP	University of Pretoria, South Africa
UoPd	University of Potsdam, Germany
UoW	University of the Witwatersrand, South Africa
UoZ	University of Zambia
UPLB	University of The Philippines Los Baños
UQ	University of Queensland, Australia
USA	United States of America
USAID	United States Agency for International Development
USD	United States dollar
USDA–ARS	United States Department of Agriculture–Agricultural Research Service
UTM	Université de Tunis El Manar, Tunisia
VBI	Virginia Bioinformatics Institute, VPI
VPI	Virginia Polytechnic Institute and State University, USA
WA	Waen Associates, UK
WACCI	West Africa Centre for Crop Improvement, University of Ghana
WB	The World Bank
WMS	(GCP) Workflow Management System
WUE	water-use efficiency
WUR	Wageningen University and Research Centre, The Netherlands
XAAS	Xuzhou Academy of Agricultural Sciences, China
YAAS	Yunnan Academy of Agricultural Sciences, China
ZmMATE	MATE gene of maize (Zea mays)
Zn	zinc
ZU	Zhejiang University, China
$\Delta_{13}C$	carbon isotope discrimination
$_0C$	degrees Celsius

2011 Project Briefs
I. Research Initiatives

1. Cassava

1. Project No G3007.03: Genetic and physical mapping resources produced for drought breeding in cassava

- *Duration: Aug 2007–Feb 2010*
- *Total budget: USD 758,058*

Principal Investigator and lead institute
Pablo Rabinowicz, The Institute of Genome Sciences, School ofMedicine, University of Maryland, Baltimore MD, USA

Collaborating institutes and scientists

- African Center for Gene Technologies [ACGT], University of Pretoria, Pretoria, South Africa – Jane Morris
- ACGT, Department of Genetics, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa – Alexander Myburg
- ACGT, School of Molecular and Cell Biology, University of the Witwatersrand, Johannesburg, South Africa – Chris Rey
- UCD, Davis, CA, USA – Ming-Cheng Luo

Cassava is one of the most important crops in unfavorable environments in developing countries, where poverty is common and severe. Because of its high productivity, even in extreme conditions, cassava constitutes a source of food and income for poor farmers in Africa, Asia and Latin America. Although cassava is fairly resistant to water stress, the molecular basis for this tolerance is poorly understood. Several traits have been associated with its drought tolerance, such as regulation of stomata activity, changing leaf expansion rates due to decrease in cell proliferation, and modifications of photosynthetic pathways to maintain high photosynthetic activity. Improving cassava's tolerance to drought is important to help increasing yields in the semi-arid Sub Saharan African regions where cassava as an essential crop. Cassava's natural stress tolerance can be substantially improved by breeding, especially by marker-assisted selection of key physiological traits associated with drought tolerance. In recognition of the importance of cassava improvement for dry areas in the developing world, the Generation Challenge Program (GCP) awarded a grant to study drought tolerance traits and develop molecular markers to improve cassava breeding for drought tolerance. This proposal builds on that project by offering to develop single nucleotide polymorphism (SNP) markers throughout the genome to identify favourable alleles related to drought tolerance in these mapping populations. In order to achieve this goal, a physical map of the cassava genome will be generated that will allow the development of SNP markers uniformly distributed around the genome. In this way we will be able to identify quantitative trait loci (QTL) associated with drought tolerance in a high-throughput manner. These markers will be useful for marker-assisted selection of favourable traits.

2. Project No G7009.09/G7010.01.03: Implement MARS projects for drought tolerance

- *Duration:*
  - *G7009.09: Dec 2009–Feb 2010*
  - *G7010.01.03: Mar 2010–Oct 2014*
- *Budget by year:*
  - *Total budget (G7009.09): USD 2,124*
  - *Total budget (G7010.01.03): USD 515,604*

Principal Investigator and lead institute
Emmanuel Okogbenin, National Root Crops Research Institute (NRCRI), Umudike, Nigeria.

Collaborating institutes and scientists

- CRI–CSIR – Elizabeth Parkes
- SARI–CSIR (Joseph Adjebeng)
- Cornell University, Ithaca, NY USA – Tim Setter

Although cassava produces more energy per unit area compared to other crops under marginal conditions of limited annual rain fall (<500mm) or a long dry season (5-6 months), yield potential under drought varies widely in the gene pool. Previous work revealed certain varieties from Africa are tolerant to drought. The afore-mentioned drought tolerant germplasm is the basis of an innovative molecular breeding scheme based on marker assisted recurrent selection (MARS) that seeks to deploy drought tolerance hybrids more widely in cassava gene pools of the major cassava growing agro-ecologies of West Africa.

The scheme employs a two-pronged approach: first, a drought tolerant genotype identified using phenotypic information will be used in crosses with a commonly

grown elite lines and the progeny used for QTL mapping. Secondly, marker-assisted breeding through MARS will be employed to improve the efficiency of producing elite germplasm with exceptional performance under drought by identifying useful allele (QTL) combinations and pyramiding (and fixing) multiple sources of genes for drought tolerance into a set of new progenitors. Genotypic information will be generated by a high throughput SNP marker genotyping platform based on SNP marker resources currently being developed.

Partners in the project are two African NARs programs of Ghana, and Nigeria, Cornell University and an advanced genotyping facility to be identified. Indicators of success of the project include identification of molecular markers for selection of high yield and drought tolerance in breeding schemes. Other indicators are production of new cassava varieties that a) rank high in yield and perform better under drought than any currently available lines, b) are high ranking under non-drought conditions, and c) will serve as improved progenitors for future breeding of drought tolerance in cassava.

3. Project No G7009.10/G7010.01.02 Improving and deploying markers for biotic traits

- *Duration:*
  - *G7009.10: Dec 2009–Feb 2010*
  - *G7010.01.02: Mar 2010–Feb 2014*
- *Total budget*
  - *G7009.10: USD 17,936*
  - *G7010.01.02: USD 394,356*

Principal Investigator and lead institute
Chiedozie Egesi, National Root Crops Research Institute (NRCRI) Umudike, Nigeria
Co-PI: Dr Emmanuel Okogbenin, National Root Crops Research Institute (NRCRI) Umudike, Nigeria

Collaborating institutes and scientists

- CRI–CSIR – Elizabeth Parkes
- NRTP–ARI – Geoffrey Mkamilo

The genetics of cassava is the least understood of major staple crops in the world. This is largely due in part to its heterozygous nature which makes it difficult to develop appropriate stocks for classical genetic studies. The first genetic map of cassava was published in 1997 using first generation of markers including RFLPs, AFLPs, RAPDs and isozymes. This map was further developed by anchoring SSR markers, which are randomly distributed on the map. The map has been utilized in QTL mapping studies in cassava for various traits including resistance to pests and diseases, yield, morphological and quality traits. While QTLs have been detected for several traits, majority of the markers have yet to be applied in breeding programs due to poor association with traits in MAS schemes. Only markers associated with the CMD2 gene and CGM have so far been deployed in breeding programs. Results of MAS conducted so far for CMD2 gene was 68% efficient, while validation studies for markers linked to the CGM resistance was good in East Africa, but response to the CGM for the markers in West Africa was relatively moderate or tolerant to the pest. The lack of strongly linked markers to economic traits of importance necessitated the need for development of over 800 SSR markers for further mapping of the genomic regions controlling traits of interest. While success has been made in improving map saturation, recent efforts indicate that efficient fine mapping has not been successfully attained using SSR markers. To improve MAS for CMD2 gene, SCAR markers (at 4 cM to the gene) were developed which is now routinely used in breeding programmes. However, the need to accelerate the application of more markers in breeding programmes, means that more efficient marker systems are necessary to efficiently tag genes for MAS schemes. Current initiatives to develop SNPs for cassava in a GCP funded project and another by the BMGF provides a new vista and array of immense opportunities to identify markers closely linked to new sources of CMD resistance and other biotic constraints. This proposal therefore seeks to develop new mapping populations for QTL mapping for new sources of CMD resistance, and validation studies of the detected QTLs using available SNP markers developed from other GCP and BMGF projects.

4. Project No G7010.01.01: Improvement and evaluation of the existing cassava reference set for Africa (Development of a genetic resources base for drought and biotic stress improvement in cassava)

- *Duration: Apr 2010–Mar 2013*
- *Total budget: USD 302,788*

Principal Investigator and lead institute
Morag Ferguson, IITA

Collaborating institutes and scientists:

- CIAT – Hernan Ceballos
- NRCRI – Emmanuel Okogbenin
- NRTP–ARI – Geoffrey Mkamilo
- CRI–CSIR – Elizabeth Parkes

Progress has been made in defining the southern, eastern and central (SEC) Africa reference set. A strategy has been developed and 40 genotypes from Madagascar, Rwanda, Uganda and Tanzania have been identified from the 1401 varieties originally genotyped under the previous project. This constitutes largely farmer-preferred varieties and varieties with specific traits of interest. Plans are in place to acquire leaf material of these samples at BecA for DNA extraction and subsequent SNP genotyping through the use of cryo shippers.

5. Project No G7010.01.04: Phenotyping cassava for drought tolerance to identify QTLs

- *Duration: Apr 2010–Mar 2012*
- *Total budget: USD 128,620*

Principal Investigator and lead institute:
Alfredo Alves, EMBRAPA Cassava and Tropical Fruits (CNPMF)

Collaborating institutes and scientists:

- CIAT – Hernán Ceballos
- Cornell University – Tim Setter

Given cassava's long breeding cycle and duration to harvest maturity, there is a strong incentive to use molecular markers and enhanced phenotyping methods that will assist the breeding process. This project will use a mapping population representing diversity in cassava drought tolerance that was developed in our previous GCP project (*G3005.03-Identifying the Physiological and Genetic Traits that make Cassava one of the most Drought Tolerant Crops*). This population will be phenotyped for drought tolerance in Brazil and Colombia, and QTLs will be identified. This information will be valuable in future marker assisted breeding of cassava.

Capacity-building activities:

Community of practice project

6. Project No G4008.26/G7010.01.05: A cassava breeding community of practice in Africa for accelerated production and dissemination of farmer-preferred cassava varieties resistant to pests and diseases

G4008.26

- *Duration: Jan 2008–Dec 2010*
- *Total budget: USD 647,750*

Principal Investigator and lead institute
Emmanuel Okogbenin, National Root Crops Research Institute (NRCRI), Nigeria

Collaborating institutes and scientists

- NRCRI – Chiedozie Egesi
- CRI – Elizabeth Okai
- NaCRRI – Yona Baguma
- NaCRRI – Anthony Pariyo
- IITA – G Melaku

Cassava has become a major staple and food security crop in Africa. However, there is an urgent need for improved varieties to stop the rapid spread of pest and diseases, especially the cassava brown streak disease (CBSD) and the cassava mosaic disease (CMD), two resurgent crop diseases that have already caused low-grade famine in parts of Africa. Although National Agricultural Research Systems (NARs) are best suited to breed cassava for local needs, NARs in the past limited their activities mainly to testing and selection of improved germplasm, but more recently NARs breeders have begun formal cassava breeding. Several donor funded projects, including a Generation Challenge Program (GCP) competitive grant to CIAT, Brazil, and 3 African countries – Ghana, Nigeria, and Uganda, and a Rockefeller foundation grant to Tanzania, IITA, and CIAT, are now conducting field-based, Marker Assisted Selection (MAS), and participatory cassava breeding. There is a need to build synergies between these 4 NARS breeding programs, IITA, and CIAT through exchange of experience and improved germplasm to ensure rapid production of improved varieties and delivery to farmers. A community of practice (CoP) has been set up involving cassava breeders in the 4 target countries that will permit a free-flow of experiences and information on breeding methods, best field practices, and improved varieties amongst the 4 countries. A primary activity of the CoP will be integration of MAS with field-based breeding and pre-breeding strategies. The project will also provide training in MAS as well as field-based and participatory plant breeding for current and a new generation of breeders. MAS is a specialized form of cassava breeding complementary to traditional field-based breeding. The CoP will therefore create and maintain close links with International Institute Tropical Agriculture (IITA) and CIAT, and NARs breeding programs via sharing of germplasm/information and training that are outcomes of this project. MAS activities of the CoP will be further supported through collaborative activities with the Genotyping Support Service (GSS), and any other advanced laboratories and research centers having existing relationships

with current members of the CoP. In addition, linkages will be built with primary, secondary, and tertiary users of improved cassava varieties to ensure prompt uptake of improved varieties. Lastly, the CoP will be proactive in developing linkages with existing cassava breeding networks, International breeding programs, and related GCP projects, including the genotyping support services (GSS), to bring the best expertise and experiences to bear on the breeding goals.

G7010.01.05

- *Duration: Jan 2011–Dec 2013*
- *Total budget: USD 753,480*

Principal Investigator and lead institute
Emmanuel Okogbenin, National Root Crops Research Institute (NRCRI), Nigeria

Collaborating institutes and scientists

- National Root and Tuber Crop Improvement Institute (NRCRI), Umudike, Nigeria – Chiedozie Egesi
- Crop Research Institute (CRI), Kumasi, Ghana – Elizabeth Parkes
- National Crops Resources Research Institute (NaCRRI), Namulonge, Uganda – Yona Baguma
- National Root and Tuber Program, ARI-Naliendele, Tanzania – Geoffrey Mkamilo
- International Institute for Tropical Agriculture, Ibadan, Nigeria – G. Melaku
- International Center for Tropical Agriculture (CIAT), Cali, Colombia – H. Ceballos
- DDPSC, St. Louis, Missourri, USA – M. Fregene
- Cornell University, Ithaca, New York, USA – Tim Setter

Cassava is staple food for over 200 million people in sub-Saharan Africa. Significant improvements have been made through breeding to develop improved varieties which meet the needs and requirements of farmers and other end-users. , Through previous GCP funded projects, markers associated with CMD resistance have been identified and have been used to deploy useful germplasm from the primary center of diversity in the Neo tropics. In order to consolidate on gains made so far the cassava breeding community of practice project was initiated by the SP5 sub-programme of the GCP to facilitate rapid uptake of MAS breeding in Africa. The CoP primarily aims to facilitate the routine application of MAS in breeding programs and to develop relevant schemes that effectively integrates MAS with field – based strategies. Other goals of the GCP include the strengthening of capacity of NARs in modern breeding, development of an efficient network that integrates breeding among NARs breeder and the establishment of web-based database for information sharing including germplasm exchange. Under the CoP, different breeding populations are being developed, and through genotyping activities initiated by NARs in collaboration with CIAT and the GSS. Excellent genotypes developed through MAS have been identified and are currently being evaluated in four countries (Nigeria, Ghana, Tanzania, and Uganda). The member states in the CoP are target countries in the second phase of the GCP which is mainly focused on improving yield in drought prone environment. NARs are very strategic in the development of products to farmers. The success of this will depend on the capacity or ability of NARs to rapidly take up products from the GCP cassava CI initiatives. Principally, use of more efficient marker systems e.g. SNPs, access to high throughput genotyping platforms and use of efficient breeding schemes such as marker assisted recurrent selection (MARS) require that effective training component is put in place to sustain rapid gains from the CI in Africa. . This project therefore seeks to undertake capacity building activities which will give the needed impetus required for NARS to rapidly deploy new tools or technologies from present cassava CI projects in routine molecular breeding of improved varieties for the benefit of poor resource farmers whose livelihood depends on cassava. The proposal would also seek to use these markers to develop useful genetic stocks, breeding populations and elite gene pools in aid of cassava improvement in Africa.

2. Legumes

Beans

7. Project No G3008.07: Basal root architecture and drought tolerance in common bean

- *Duration: Nov 2008–Oct 2011*
- *Total budget: USD 900,000*

Principal Investigator and lead institute
JP Lynch, PSU

Collaborating institutes and scientists

- CIAT – SE Beebe, MW Blair, I Rao
- PSU – K Brown
- SABRN, Malawi – R Chirwa
- IIAM – C Jochua, M Miguel
-

Root traits have critical importance for drought tolerance, but have not yet been widely employed in crop breeding programmes. A major reason for this is that root systems are a complex aggregation of poorly understood individual traits that are hard to evaluate in the field. This project will offer bean breeders two new root traits with potential to improve drought tolerance. These traits vary substantially among genotypes and are known to play important roles in rooting depth, which is the most important determinant of drought tolerance in bean. Before these traits can be deployed in bean breeding, we must confirm their value under drought conditions, and because bean producers in developing countries often confront low soil fertility as well as drought, we must be confident that selection for these root traits will not have negative consequences for plant performance in low fertility soil. A major objective of this project is to rigorously determine the utility of these traits for plants under water stress and combined water/phosphorus stress. A second objective is to survey bean germplasm for variation in these traits, to aid breeders in identifying sources and parents. A third objective is to characterise the genetic control of these traits, and to develop molecular markers, which would be especially useful since root traits are difficult to evaluate in the field. These products will be powerful new tools for bean breeders and will also have relevance to the breeding of other crops. Our research team has a long history of successful collaboration, combining the group at Penn State that discovered these traits, bean genetics expertise at CIAT, and bean breeders and researchers in Mozambique where drought and low soil fertility are severe problems. We look forward to this opportunity to develop new tools for the selection of drought tolerant crops.

8. Project No G4008.11: Dry bean improvement and marker assisted selection for diseases and abiotic stresses in Central America and the Caribbean

- *Duration: Jan 2008–Dec 2010; NCE: Jul 2011*
- *Total budget: USD 382,590*

Principal Investigator and lead institute
Jorge A Acosta-Gallegos, INIFAP Mexico

Collaborating institutes and scientists

- CIAT – Steve Beebe; Matthew Blair
- INCA – Humberto Rios Labrada; Orlando Chaveco
- INIFAP – Ernesto Lopez Salinas; Raul Rodriguez Guerra; Victor Montero
- INTA – Aurelio del Llano; Julio Molina

Diseases, drought and low soil fertility are the most important constraints to dry bean production in Latin America and the Caribbean. The development of bean cultivars with resistance to these stresses represents a cost-effective and sustainable means to address these constraints. Bean golden yellow mosaic virus (BGYMV) transmitted by the sweetpotato whitefly is an endemic disease threat to production in the region and tends to explode with vector populations that increase during drought years. Root-rot resistance is another important trait that needs to be tackled along with drought, low soil fertility and BGYMV resistance. Two nurseries, in the opaque black and small red seed classes will be formed and established for the main bean growing areas in Cuba, Nicaragua, Mexico and possibly Haiti in 2008. Nurseries will include best lines identified among the partners to conform a drought nursery. In these nurseries disease reaction and productivity will be recorded along with climatic parameters. Segregating populations will be developed at Mexico and CIAT with best local parents from the partners and sources of BGYMV and root-rot resistance genes possessing molecular markers to assist in the selection. In this project we will make use of prior knowledge in the development of bean cultivars better able to resist BGYMV and root-rot to cope with drought and low soil fertility stress. One aim is to explore the available genetic diversity for tolerance to water stress, adaptation to low soil fertility, as well as for BGYMV and root rot resistance. This project will be one of the first to apply molecular breeding on a large scale to common bean improvement for the region and will focus on tolerance to drought stress and diseases that occur under drought and low soil fertility conditions.

9. Project No G6010.03: Improve common bean productivity for marginal environments in sub-Saharan Africa

- *Duration: May 2010–May 2014*
- *Total budget: USD 1,449,227*

Principal Investigator and lead institute
Steve Beebe/Bodo Raatz wef Novemeber 2011, (CIAT)

Collaborating institutes and scientists

- CIAT – Idupulapati Rao,
- DR&SS/CBI, Zimbabwe – Godwill S Makunde
- CU –
- UC–D –
- SABRN/CIAT – Rowland M Chirwa
- ECABREN/University of Nairobi (Kenya) – Paul M Kimani
- DARS (Malawi) –
- SARI (Ethiopia) – Asrat Asfaw Amele

Phase II of this project will continue to focus on drought as the primary constraint to crop production throughout Eastern and Southern Africa where drought events are associated with cyclical weather patterns such as the El Niño phenomenon, which can cause severe losses to the maize–bean systems of Southern and Eastern Africa, with climate models predicting that such events are set to worsen. Drought is the primary yield constraint to bean production throughout the region, affecting over 70 percent of the bean production area.

The project will exploit the genetic tools and breeding populations created in Phase I for the marker-assisted selection of drought-tolerant germplasm in common beans. In Phase I, it was found that the diversity of response to drought is due primarily to variation in rooting depth and resulting access to soil, earliness (drought escape), and seed filling capacity. Drought tolerance has been identified within each genepool through the screening of the reference collection in Phase I and the evaluation of CIAT breeding lines. Drought tolerance was found to be at a higher level in the Mesoamerican small-seeded types than the large-seeded Andean types that are preferred for marketability in Eastern and Southern Africa. However, some recently developed DAB and SAB (Drought Andean Bean) series advanced lines as well as some red kidney types from the SEQ, DRK and RAA series have some level of tolerance. One important source of drought tolerance has been germplasm derived from the Durango race, although this race is not yet widely grown or used in breeding programmes. To address this, in Phase I populations were developed using Durango and Mesoamerican sources for improvement of Andean classes of common bean, especially based on advanced backcrosses with SER lines and inter-genepool populations with SEA lines. In Phase II, these populations will form the basis for marker-assisted breeding (MAB). The advantage of the new populations is that they incorporate new genetic resources into the African common bean genepool with a potential major leap in productivity over current varieties.

Utilisation of specific traits in drought tolerance breeding, through marker-assisted selection under Phase II, will be based on the selection of QTL identified in Phase I as well as on MARS breeding using elite x elite crosses and identification of QTL in advanced backcross populations. It is expected that marker-assisted breeding will be more efficient than field screening under drought conditions, and that molecular breeding will be especially useful for transferring the deep rooting trait that is difficult to phenotype. Enhanced carbohydrate mobilisation, highly correlated with yield under drought stress, is also expected to be transferred. Molecular breeding for drought tolerance is now possible based on the SSR marker set and SNP assay from Phase I, as well as the better understanding of physiological traits and root architecture gathered through physiology activities in the first.

In terms of germplasm development, Phase II will focus on two molecular breeding approaches to transfer and enhance drought tolerance in the Andean genepool and then will use more narrow crosses for pyramiding. The first approach will be marker-assisted backcrossing of QTL for drought tolerance from the Mesoamerican genepool into the Andean genepool using the baseline of QTL mapping and advanced-backcross populations developed in Phase I. The second approach will be MARS breeding within the Andean genepool using farmer- and market-preferred varieties and the Durango sources of drought tolerance.

The principal linkages of this project are with other bean breeding activities, such as those in the Tropical Legumes II project and in the CGIAR HarvestPlus Challenge Programme. Germplasm flows between the TLI and TLII projects as advanced lines are selected or identified is promising. Drought tolerance has been pyramided with nutritional quality in some crosses linking the TLI project to HarvestPlus activities. Marker development is linked with projects at the University of California–Davis (UC–Davis), USA, funded by GCP and National Science Foundation, and Phase II will benefit from sequencing by USDA-funded projects at North Dakota State University (NDSU) and Purdue University,

USA. This project will also benefit from linkages with other universities and institutions in the United States (Cornell University, Pennsylvania State University), Spain (Programa Iberoamericano de Ciencia y Tecnología para el Desarrollo) and Japan (RIKEN) as well as linkages to the GCP-funded project on low phosphorus tolerance (Mozambique). The Eastern and Central Africa Bean Research Network (ECABREN) and Southern Africa Bean Research Network (SABRN) within the Pan Africa Bean Research Alliance (PABRA) link with TLI and TLII and are funded by the Canadian International Development Agency and the Kirkhouse Trust (UK).

Chickpeas

10. Project No G4008.12: Linking genetic diversity with phenotype for drought tolerance traits through molecular and physiological characterisation of a diverse reference collection of chickpea

- *Duration: Jan 2008–Dec 2009; NCE: Sep 2011*
- *Total budget: USD 156,215*

Principal Investigator and lead institute
Lakshmanan Krishnamurthy, ICRISAT

Collaborating institutes and scientists

- ICRISAT – Rajeev Varshney, Lekha Pazhamala, Hari Upadhyaya, Subhash Chandra, David Hoisington, L Krishnamurthy
- JIRCAS – Satoshi Tobita, Osamu Ito
- UAS – MS Sheshshayee

Chickpea is the third most important grain legume crop, and drought is one of the major constraints limiting the productivity. This research project is to enhance the productivity of chickpea under drought environments, and comprise three key research components, that is, i) characterising the target drought environments, ii) phenotyping the transpiration efficiency (TE), specific leaf area (SLA) and chlorophyll content (SPAD) by noble idea and sophisticated devices to improve the drought tolerance, and iii) identifying robust molecular markers for marker assisted breeding selection. The component i) is important as the drought environments is not uniform among the arid or semi-arid regions. The target drought environments need to be characterised so that logistic understanding could be obtained on the plant mechanisms and traits to cope with the target drought environments. It will also help us to apply the drought tolerant mechanisms and traits when it is applied to other drought environments to improve the productivity. The component ii) is important as TE, SLA and SPAD are directly contribute to the crop growth under drought environments, viz., TE for improving photosynthetic products per unit water, SLA for maintaining proper chlorophyll concentration for photosynthesis, and SPAD for maintaining the capability of photosynthesis. Since drought stress is a very complex stress, several of these mechanisms and traits need to be brought under a single elite genetic background. To achieve it effectively in terms of the time as well as cost, the component iii) is important because introgressing complex multi-gene regulated physiological mechanisms and traits can be better achieved based on the robust molecular markers linked with QTL conditioning these traits.

The objective of this project is to improve the drought tolerance of chickpea via marker assisted selection for critical characteristics to improve the drought tolerance under proper drought environment characterisation, and to provide training opportunities to share new knowledge and skills for NARS scientists.

11. Project No G4011.08: Harnessing the potential of multiparent advanced generation intercross (MAGIC) populations for gene discovery and breeding applications in chickpeas

- *Duration: Jan 2008–Dec 2009; NCE: Sep 2011*
- *Total budget: USD 156,215*

Principal Investigator and lead institute
Pooran M Gaur and Rajeev K Varshney, ICRISAT

Collaborating institutes and scientists

- Mahendar Thudi and Aravind Kumar Jukanti – ICRISAT, India
- Paul Kimurto- Egerton University, Kenya
- Asnake Fikre, Ethiopian Institute of Agricultural Research (EIAR), Ethiopia

Chickpea (Cicer arietinum L.) is the world's third largest grown food legume and the developing countries account for over 95% of its production and consumption. The crop productivity in developing countries, due to exposure of the crop to several abiotic and biotic stresses, is less than 1 ton per hectare. Although molecular breeding has a great potential to improve the yield, narrow genetic diversity present in the elite germplasm collection is a serious bottleneck in this context. This proposal plans to harness the genetic diversity present in the elite germplasm collection in a systematic manner.

The proposal is built on the progress made in the Objective 4 of TLI Phase I and complements the ongoing efforts of TLI Phase II on development of the

multi-parent advanced generation inter-cross (MAGIC) population. Although some efforts were initiated to develop MAGIC populations by deploying eight well performing genotypes in Kenya, Ethiopia and India (no genotyping or phenotyping was planned in TLI Phase II), severe cuts made in the planned budget of Objective 4 of Phase II and recent implementation of full cost recovery system at ICRISAT are the serious constraints that are affecting development of MAGIC population in chickpea. Therefore this proposal will ensure smooth achievement of development of MAGIC population milestone. More importantly, this proposal plans to undertake genotyping of at least 1000 MAGIC lines with at least 1500 SNP markers using KASPar assays through Marker Services of Integrated Breeding Platform (IBP) of GCP. Based on SNP and haplotype data, the MAGIC lines will be classified into different groups. Subsequently, a set of 200- 500 lines possessing non-redundant set of haplotypes will be identified and used for extensive phenotyping for drought tolerance related traits in Kenya, Ethiopia and India. Genotyping data and phenotyping data collected on the set of MAGIC lines will be analyzed for establishing marker-trait association via genome wide association study (GWAS) for drought tolerance that will be helpful for molecular breeding. In addition, the well characterized set of MAGIC lines at both molecular as well as phenotypic level will be an ideal resource for deploying in chickpea breeding programmes. In summary, the SNP genotyping and phenotyping of MAGIC population and GWAS for drought tolerance are entirely new components of this proposal that are not present in TLI Phase II.

12. Project No G6010.04: Improve chickpea productivity for marginal environments in sub-Saharan Africa and South Asia

- *Duration: May 2010–May 2014*
- *Total budget: USD 1,400,000*

Principal Investigator and lead institute
Rajeev Varshney, ICRISAT

Collaborating institutes and scientists

- ICRISAT – NVPR Ganga Rao, Pooran Gaur, Lakshmanan Krishnamurthy, Trushar Shah, Hari C Sharma, Mahendar Thudi, Siva K. Chamarthi, Nalini Mallikarjuna
- EIAR (Ethiopia) – Asnake Fikre
- Egerton University (Kenya) – Paul K Kimurto
- UCD (USA) – Douglas Cook
- NCGR (USA)
- NIPGR

Terminal drought is considered the major constraint to chickpea production. Root traits, particularly rooting depth density and root depth, have been shown to improve drought tolerance under receding soil moisture conditions by improving water availability to the plant through more efficient extraction of available soil moisture.Thus, opportunities exist for enhancing drought tolerance of chickpea by improving these root characteristics. There is also a need to identify genotypes that are more water use efficient and able to achieve high harvest index under scarce water conditions, and to eventually pyramid all of these traits together. For these two traits (water-use efficiency and harvest index), the project is limited to assessing the range of variations and heritabilities of these traits and to identify the suitable parents to develop the populations needed to map these traits in the future.

The project will develop breeding populations with superior genotypes for drought tolerance based on Phase I phenotyping of the GCP reference collection, which will provide new pre-breeding lines for TLII. Furthermore, multi-parent advanced generation intercross (MAGIC) populations will be created from identified superior lines by TLII. A subset of these MAGIC lines will be phenotyped for drought-related traits that will lead to the identification of superior lines with accumulation of favorable alleles for drought tolerance. The project will coordinate the development of a SNP genotyping platform and will integrate SNPs to the genetic maps. Mapping of SNPs with already mapped and DArT markers will facilitate identification of diagnostic markers associated with drought tolerance and accelerate molecular breeding in coordination with the IBP project. Because of the limited number of markers in target QTL regions, it is difficult to introgress these QTL in elite genotypes. To overcome this problem, the project will build a partial physical map for selected drought tolerance QTL regions. Integrated genetic and physical maps will support enhanced genetics studies and will provide more diagnostic markers for the QTLs to be monitored in MABC activities. A 'hot spot' harboring many root trait QTLs was identified in Phase I, contributing up to 30% phenotypic variation. This region also harbors some QTL for carbon-isotope discrimination and yield. In Phase I phenotypic data were collected for drought-related traits such as root traits, water-use efficiency, harvest index (HI) and more, and CID data are available from another GCP project, meaning that another important component of drought tolerance–transpiration efficiency (TE) - will be used for phenotyping the reference. Detailed analysis of different sets of phenotypic data should facilitate breeders to adopt precise selection criteria to breed for drought tolerant chickpea.

In Phase I, MABC and MARS breeding were initiated for the improvement of drought tolerance. Phase II of the project will enhance MABC and MARS through NARS partners with at least one cross in each country (Kenya, Ethiopia and India). ICRISAT will back up MABC activities in these countries with additional crosses. NARS partners will complete two rounds of MABC; therefore MABC lines should be available at the end of Phase II at each NARS institution. Moreover, MABC lines developed during Phase I and available in the first year of Phase II (2010), will be deployed for multi-location phenotyping in Ethiopia, Kenya and India, in collaboration with TLII. Most suitable lines with enhanced drought tolerance will be promoted in TLII. Based on TLII demand during the Annual 2009 meeting in Mali, a new sub-activity will genotype TLII breeding populations with markers for root traits and *Fusarium* wilt (linked with Government of India's sponsored project on molecular breeding of chickpea for biotic stresses) so that the TLII team can save time and costs on developing the desired breeding populations.

The project will place heavy emphasis on capacity building for NARS, by supporting at least one PhD and two Master students from the three collaborating NARS (Kenya, Ethiopia and India). Data management and storage activities will enable results from the project (e.g. marker sequence / genotypic/ mapping data, phenotypic data, MABC data and MARS data) to be readily disseminated, which will be of benefit to the wider chickpea community.

13. Project No G7009.02: Mapping and validation of QTLs associated with drought tolerance traits in chickpea

- *Duration: Jan 2009–Dec 2011; NCE: June 2012*
- *Total budget: USD 220,880*

Principal Investigator and lead institute
Pooran M Gaur, ICRISAT

Collaborating institutes and scientists

- ICRISAT – Rajeev Varshney, L Krishnamurthy, Vincent Vadez, Shailesh Tripathi
- UAS–B – KP Viswanatha, MS Sheshashaye
- RARS–N – Veera Jayalakshmi
- ARS–D – SJ Singh
- RAKCA–ICAR – Md Yasin
- DZARC

Chickpea (*Cicer arietinum* L.) is globally the third most important food legume mainly grown and consumed in the developing countries. During 2006, chickpea was grown on 10.7 m ha across 51 countries with over 95% of the production and consumption in the developing countries. Chickpea is rich in protein, minerals and vitamins and plays an important role in nutrition of millions of poor, particularly in South Asia and sub-Saharan Africa. Being a leguminous crop, chickpea contributes to improving and maintaining soil fertility and productivity of cropping system when grown in rotation with cereals.

The average global productivity of chickpea continues to be low (~800 kg ha-1), whereas the potential yield is reported to be over 5 t ha-1. Over 90% of chickpea crop is grown rainfed on residual soil moisture stored during the previous rainy season and the crop often experiences drought at the critical stage of pod filling and seed development. Thus drought is the most serious constraint to chickpea production and together with heat stresses accounts for over 40% yield losses annually.

The grain yield under drought environments is the product of Transpiration (T), Transpiration Efficiency (TE) and Harvest index (HI). The root system that can extract water from deeper soils can increase T and contributes to improving the total biomass productivity and also the HI. A measure of carbon isotope discrimination (δ13C) gives a good estimation of TE as these are positively correlated.

This project builds on Tropical Legume I project, where efforts are being made to map QTLs for root traits. In this project, we propose to map and validate QTLs affecting all three components, T, TE and HI, of the grain yield under drought environments. The root traits will be used for T, carbon discrimination factor for TE and biological and grain yield for HI.

14. Project No G7009.06: Development of an SNP platform for molecular breeding in elite material of chickpea

- *Duration: Nov 2009–Oct 2010; NCE: Oct 2011*
- *Total budget: USD 66,538*

Principal Investigator and lead institute
Douglas Cook, UC–D

Collaborating institutes and scientists

- NCGR – Greg May
- ICRISAT – Rajeev Varshney

Recent efforts under Tropical Legume 1 (TL1) and allied projects have yielded a significant increase in molecular marker resources for chickpea. Nevertheless, there remains a pressing need to identify polymorphisms

that discriminate cultivated accessions, especially the elite germplasm that will form the foundation of phase 2 of TL1 (eg, MARS parents and the focus of current breeding and QTL analyses). The objective of this proposal is to use Next Generation sequencing for deep re-sequencing of cDNA libraries from a select set of elite accessions. This project benefits from earlier efforts funded by the Generation Challenge Programme (SPL-2 discretionary grant) in which the transcriptome of chickpea was sequenced by means of 454 technology. Here we propose to use deep re-sequencing with Solexa technology to develop sequence alignments to these 454 transcript sequences, thereby discovering sequence polymorphisms (SNPs). A subset of 1536 SNPs will be selected to produce an Illumina Golden Gate assay, to ascertain allelic variation in a wider set of breeding and pre-breeding materials.

Cowpeas

15. Project No G4008.13: Improving drought tolerance phenotyping in cowpea

- *Duration: Jan 2008–Dec 2010; NCE: Mar 2011*
- *Total: USD 450,836*

Principal Investigator and lead institute
Jeff Ehlers, UCR

Collaborating institutes and scientists

- IITA – Ousmane Boukar, Satoru Muranaka
- INERA–Burkina Faso – Issa Drabo
- ISRA – Ndiaga Cissé
- TAMU – William Payne

This proposal seeks to (1) provide baseline drought tolerance information for early and medium cycle cowpea varieties and assess the importance of genotype x environment interactions for grain yield under drought across a range of environments; (2) study the relationship between grain yield under drought and various traits, and select applicable methodologies for practical and efficient indirect measures of drought tolerance, such as thermal imaging, that are relevant to the major cowpea production zones in Africa; and (3) determine the relationship between drought tolerance and shoot and root traits, and select potential drought tolerant genotypes with beneficial root characteristics which contribute higher productivity under drought conditions.

Thirty early maturing and thirty medium maturing cowpea varieties will be compared for grain yield under terminal drought conditions using late plantings at two sites during the main growing season in West Africa and in four controlled irrigation and rain-free environments in West Africa and California. This will provide baseline drought tolerance information that will allow identification of drought tolerant and susceptible 'checks' for future drought studies and provide an estimate of genotype x environment interaction for grain yield under drought, including the degree of correlation between the results of off-season controlled environment screening and results from main-season African growing environments. Information about the importance of genotype x environment interactions will guide future investigators on whether to breed for specific regions separately, or whether region-based and/or off-season drought-screening nurseries can be employed effectively to breed for improved drought tolerance. Identification of efficient indirect selection methods like thermal imaging allows screening of a large number of germplasm lines to help ensure capture of traits that exist in the cowpea germplasm pool, and may also help reveal important component characteristics contributing to grain yield under drought. Thermal imaging is a potentially powerful method for drought tolerance screening that has not be comprehensively evaluated for its ability to discriminate drought tolerant and susceptible cowpea genotypes and this proposal seeks to establish its usefulness in cowpea.

16. Project No G6010.02/G7010.07.01: Improve cowpea productivity for marginal environments in sub-Saharan Africa

- *Duration:*
  - *G6010.02: Aug 2007–Feb 2010*
  - *G7010.07.01: Jun 2010–May 2014*

- *Total budget*
  - *G6010.02: USD 2,027,880*
  - *G7010.01.02: USD 700,000*

Principal Investigator and lead institute
Jeff Ehlers, UC–Riverside (USA)

Collaborating institutes and scientists

- University of California–Riverside (USA) – Phillip A Roberts, Shizhong Xu, Timothy Close
- IITA (TLI & TLII) – Melaku A Gedil, Boukar Ousmane, Satoru Muranaka
- ISRA (Senegal) – Ndiaga Cisse
- INERA (Burkina Faso) – Issa Drabo
- UEM (Mozambique) – Rogerio Chiulele

G6010.02

In TLI Phase I the genomic resources needed to implement modern breeding of cowpea were developed, and in Phase II the proposal is to fully engage these resources by implementing MARS breeding on a pilot

scale in three African NARS. Thus, this project will test the effectiveness and practicality of MARS breeding for delivery of improved cowpea varieties in this region, and guide the way for potential wider-scale adoption by NARS throughout SSA for cowpea as well as providing general experience for MARS breeding of other crops in the region. This effort will interact closely with the IBP, particularly in improving information management capability, decision-making tools for MARS breeding and experimental design for precision phenotyping. In addition to MARS breeding, genome-wide marker-assisted backcrossing (GWMABC) will be used to breed improved versions of locally adapted varieties. In Phase I, QTL for resistance to flower thrips, root-knot nematode, ashy stem blight (*Macrophomina*), *Striga* and components of drought tolerance were identified. Phase II of this objective will rapidly introgress these traits into locally adapted varieties. Using this approach, only two, as opposed to the usual six backcrosses, are required to recover the improved version of the local variety, thereby cutting varietal development time in half. MAGIC populations are a valuable community resource for genetic analysis and dissection of traits and should be developed for all economic crop species. Presently, no MAGIC population is being developed for cowpea. Genotypic fingerprints of 640 cowpea accessions, and phenotypic performance evaluatoins conducted under Phase I will be used to help select a genetically diverse set of parents for the MAGIC population to be developed in Phase II.

The TLI cowpea project will be linked to other research efforts focused on genetic improvement of cowpea. These programmes include the GCP project *Improving drought phenotyping in cowpea*, headed by University of California–Riverside (UC–Riverside), USA, and involving partnerships with Texas A&M University, USA, the International Institute of Tropical Agriculture (IITA), Institut sénégalais de recherches agricoles (ISRA), Senegal, and Institut de l'environnement et de recherches agricoles (INERA), Burkina Faso. The second phase will apply the improved drought phenotyping protocols developed under this project to phenotype elite x elite cowpea progenies being evaluated as part of MARS breeding. During TLI Phase I, seed from the TLII project of 50 farmer-preferred varieties were received and genotyped with the 1536 SNP marker platform, providing an information foundation for its crossing programme and for further joint research activities. In Phase II, a key aim of this project is to train NARS breeders in modern breeding. The work of this project will also be closely linked with the USAID-funded Dry Grain Pulses Collaborative Research Support Program (Pulse CRSP), a project on genetic improvement of cowpea and improvement of the cowpea seed system headed by UC–Riverside in partnerships with three 'non-TLII' countries (Senegal, Burkina Faso and Angola). Outputs of the project in Phase I, such as the high-throughput genotyping platform and consensus genetic map, have already been utilised in the CRSP project, and future outputs will be similarly utilised. Genetic materials and information were exchanged with a Kirkhouse Trust-funded project targeting marker-assisted breeding of cowpea for resistance to the parasitic weed *Striga gesneriodes* in several West African countries and this linkage will continue in Phase II. A link with the GCP Integrated Breeding Platform as a user case study has been created, and interaction with this project has taken place, specifically through the implementation of ICIS, as well as through the development of the MARS breeding strategy. The IBP is seen as a critical resource with which to form strong linkages in order to facilitate the development of optimised marker-assisted breeding approaches for NARS in SSA.

G7010.07.01

New plant breeding strategies have emerged from the genomics revolution that expedite delivery of improved crop varieties. These strategies emphasize selection of desirable segments across the genome and rely on the availability of high-density genetic maps and high-throughput genotyping systems. The 'genomic' selection strategies, such as marker-assisted recurrent selection (MARS), have been widely adopted by major breeding companies for improvement of maize and soybean, but their adoption in public breeding, especially in the National Agricultural Research Systems (NARS) of Sub-Saharan Africa (SSA), has lagged behind due in large measure to the necessary upfront investment in genomic tool development for each crop and lack of awareness and expertise by conventional breeders. These technologies also generate larger amounts of data, and types of data that are unfamiliar to most plant breeders. To quickly and successfully make use of the data of modern breeding, plant breeders require information management tools that are more sophisticated than those traditionally used, yet at the same time are easy to use. In Phase I of the Tropical Legumes I (TL-I) project the genomic resources needed to implement modern breeding of cowpea were developed. This Cowpea Challenge Initiative (CCI) will fully engage these resources by contributing to and complimenting the MARS breeding efforts proposed under the TL-I Phase II project. This includes a major contribution to SNP genotyping and genotype data production, decision support tool development and optimization, and

implementing breeding program data management systems in three African NARS and at the International Institute of Tropical Agriculture (IITA). As a designated 'User Case' of the Integrated Breeding Platform (IBP), this effort will interact closely with the IBP, particularly in the areas of improving information management capability, decision-making tools for MARS breeding, and experimental design for precision phenotyping.

Groundnuts

17. Project No G4008.06: Single Nucleotide Polymorphism discovery, validation, and mapping in groundnut

- *Duration: Jan 2008–Dec 2008; NCE: Jun 2011*
- *Total budget: USD 152,543*

Principal Investigator and lead institute
Peggy Ozias Akins, wef October 2010; Steven J Knapp, UGA

Collaborating institutes and scientists

- ICRISAT – David Hoisington, Rupakula Aruna, Rajeev Varshney
- NCGR – Gregory May and Andrew Farmer
- USDA–ARS – Corley Holbrook, Peggy Ozias-Akins

DNA marker resources are currently inadequate for routine genomic and molecular breeding applications in cultivated groundnut (*Arachis hypogaea* L.; 2n = 4x = 40). The proposed research focuses on significantly enhancing the infrastructure for translational genomics and molecular breeding research in groundnut by testing the efficacy of massively parallel DNA sequencing and highly parallel single nucleotide polymorphism (SNP) genotyping strategies for SNP discovery, validation, and mapping. We are specifically proposing to: (i) develop protocols for reduced representation allele sequencing (RRS) in groundnut; (ii) enhance DNA sequence resources for groundnut using a combination of Sanger and Solexa sequencing; (iii) identify 2,000 or more common SNPs in elite lines and cultivars; (iv) develop a 1,536-SNP Illumina GoldenGate SNP genotyping array; and (v) complete the validation and genetic mapping of 1,536 SNPs in two elite recombinant inbred line (RIL) populations using an Illumina GoldenGate SNP genotyping array. The proposed research will dramatically increase DNA sequence resources and the supply of mapped DNA markers in groundnut, should enable the identification and assembly of 20 linkage groups using elite mapping populations, particularly when coupled with genetic mapping of SSR markers, and should identify additional SNPs for genotyping assay development, validation, and mapping.

18. Project No G6010.01: Improve groundnut productivity for marginal environments in sub-Saharan Africa

- *Duration: May 2010–May 2014*
- *Total budget: USD 1,718,691*

Principal Investigator and lead institute
Vincent Vadez, ICRISAT

Collaborating institutes and scientists

- ARI–Naliendele (Tanzania) – Omari Kalanje Mponda
- CIAT – Idupulapati Rao
- CIRAD – Jean-Francoise Rami
- DARS (Malawi) – Albert MZ Chamango
- CERAAS – Ndoye Ousmane
- ICRISAT – Emmanuel S. Monyo, Bonny Ntare, Trushar Shah,Hamidou Falalu, Nalini Mallikarjuna
- ISRA (Senegal) – Issa Faye
- Agropolis–CIRAD (France),
- UGA (USA) – Andrew H Paterson
- UCB (Brazil)- David Bertiolli;
- EMBRAPA Genetic Resources and Biotechnology (Brazil) - Soraya CML Leal Bertiolli

The limited level of groundnut genetic polymorphism restricts the use of modern breeding. Nevertheless, large phenotypic differences exist for traits such as disease resistance and drought tolerance – traits that are very much needed to enhance groundnut productivity for resource-poor farmers in SSA). The project will develop the first products of molecular breeding by building on the sources of disease resistance and drought tolerance, as well as on the breeding materials identified and advanced in Phase I. SNP markers will be generated to eventually support the use of marker-assisted recurrent selection (MARS) approaches and adequate breeding populations combining sources of tolerance, and high phenotypic and genotypic contrast will also be developed. Given that absolute resistance to foliar diseases, especially to early leaf spot (ELS), is unavailable in the cultivated germplasm, additional diversity will be sought in allo-tetraploid groundnut synthetics, developed from wild diploid groundnut, where higher levels of disease resistance are expected, as found for nematode resistance All these research activities also offer rich training ground for scientists and technicians from SSA country programmes.

Links to other projects include the TLII project; other links have also been forged with a number of Brazilian-funded projects, and with a GCP-funded capacity-building project which targets TLI NARS scientists and technicians. Aflatoxin contamination has been tested in seed lots from the drought trials carried out in Niger, a

naturally infested site with *A. flavus*. This adds value to the TLI work, provides materials with superior tolerance to aflatoxin contamination, and opens opportunities for collaboration since aflatoxin seriously affects health and excludes SSA groundnut from export. The Indian government is funding the improvement of groundnut for drought tolerance (NAIP) and a project on drought tolerance with DREB1A to produce transgenic groundnut (DBT). In addition, a recently completed initiative, through a USAID grant to ICRISAT in collaboration with the University of Florida, USA, examines water conservation traits.

Cross-cutting activities

19. Project No G6010.05: TLI Phase II Cross-cutting crop activities (drought phenotyping, data management and capacity building)

- *Duration: May 2010–May 2014*
- *Total budget: USD 1,872,337*

Drought Phenotyping Activity Leader and lead institute
Vincent Vadez, ICRISAT

Collaborating institutes and scientists

- ICRISAT
- CIAT
- IITA
- ISRA (Senegal)
- NCSU (USA) – Thomas R Sinclair
- CERAAS (Senegal)

Data Management Activity Leader and lead institute
Trushar Shah, ICRISAT

Collaborating institutes and scientists

- CIAT
- IITA
- ICRISAT

Capacity Building Activity Leader and lead institute
Ndeye Ndack Diop, GCP

Collaborating institutes and scientists
NARS involved in the four crop specific TLI Phase II projects

- TLII partner institutions
- University of Kwazulu–Natal in South Africa through the African Center for Crop Improvement (ACCI)
- University of Ghana through the West African Centre for Crop Improvement (WACCI)

This project combines three activities in support of the specific crop activities of the TLI Phase II Project (G6010.01, G6010.02, G6010.03, G6010.04): crop comparative drought phenotyping; data management; and project management. The rationale for combining such activities is that they each cut across the four crop-specific projects and provide support towards effective implementation of their respective Activities.

The first activity focuses on identifying critical traits to refine selection indices for drought for TLI crops. Crop adaptation to water limitation relates to essential or basic processes at the plant or organ level that determine how plants use water to maximise return (yield). These traits relate essentially to three domains: water conservation, higher or better use of soil water, and success of reproduction or remobilisation. Whether these traits relate to yield across environments is difficult to assess experimentally, as these effects are crop- and weather- or location-specific. In addition, how such traits 'translate' into a breeding phenotype is unclear. So, to further improve the breeding efficiency for yield of legume crops in water-limited environments, better guidance is needed on critical traits and related phenotypes. Three tasks are proposed: predict by modelling the effect of critical traits on crop yield across years and environments; assess the available variability for those critical traits demonstrating a high probability of conferring a substantial yield advantage in representative situations; and relate such traits to phenotypes that can be easily measured by breeders. The main output is a better-equipped 'toolbox' for breeders.

This fully fits with the perspective of using MARS in large-scale breeding programmes; so new cohorts of breeders will need to generate much finer phenotyping data than in the past, combining both yield and traits, to better understand the basic plant or organ level processes conferring drought adaptation.

A thorough, rigorous, multi-location cross-species comparison will be made of key adaptation traits to water limitation, including yield and yield components. 'Process-based' traits (eg, depth of rooting), and 'breeder-traits' (eg, grain size or staygreen) will be assessed and their relationships to yield tested. The relationship between 'process-based' and 'breeder-traits' will be analysed to develop a breeder toolkit of what to measure, and for what aspects. This evaluation will be done on highly contrasting genotypes from a yield-based selection under managed drought conditions, including widely-used varieties and parental lines of mapping populations.

A modelling component will predict the effect of each selected 'process-based' trait on yield across a range of environment–weather combinations, and guide breeding decisions traits showing a high probability of yield increase. Modelling will be further integrated into breeding decisions by connecting the yield prediction of a given trait to a phenotype. Modelling may directly add tools to the MARS approach used in the crop specific projects. It will also greatly enrich the phenotyping network of the Integrated Breeding Platform. Existing crop simulation models for grain legumes will be adapted to the four TLI legumes.

Activity 2 will deal with curation and management of data from TLI's Phase I and Phase II projects. TLI Phase II projects are built on multiple individual objectives and activities, generating large volumes of diverse data from phenotyping experiments across generations of crop breeding, genotyping platforms, sequencing and re-sequencing studies, etc. The second phase of the project will continue to generate more data over the next four years. Although data management is implicit in each of the current and proposed TLI projects, coordinating curation and publication through common ontologies, standards and semantics and integrating across data repositories will add considerable value by facilitating comparisons across species and subsequent data mining activities.

In this project, diverse data will be managed and catalogued. A coordination centre will be established in close collaboration with the IBP. A list of all existing and projected datasets will be compiled. This list will be used to fully gauge the project (identification of public database to be used, knowledge management tools to be developed, etc). A detailed strategy and action plan will be developed, for implementation. This strategy will be aligned to the IBP project and the action plan will include the tools and technologies developed in the IBP. The strategy will also bear in mind that the data consumers will to a large extent include breeders in the TLII project. In cases where TLI researchers have uploaded data into public databases, such data must be tagged for retrieval and cross-database comparison. In other cases, assistance will be provided in the publication of curated data to the appropriate public databases, with such data also registered in the GCP Central Registry with the necessary metadata.

The third activity will deal with the infrastructural support for partner institutions in sub-Saharan Africa and with project management. The grouping of infrastructure support and capacity building in a single activity draws from experience in TLI Phase I, in which this approach proved to be useful in terms of planning, execution, cost-effective administration, and monitoring and evaluation. Amalgamating these activities under this project will ensure that sub-Saharan Africa NARS researchers receive the support required to enable them fully participate in the project and conduct quality research at their home institutions. This activity will facilitate the building of bridges across all TLI NARS partners on the one hand, and with TLI-related GCP projects on the other hand, and will also serve as the mechanism to engage NARS in the management of the project. It will do so in close collaboration with the crop specific projects that will be in charge of human resource development, the second prong of capacity building in this project. Installation of local infrastructure (mainly informatics and field equipment) is needed to conduct reliable phenotyping as an essential step towards molecular breeding, and implementation will follow a thorough process of identification of needs (equipment and infrastructure) among partners of the crop specific projects.

This third Activity will also be in charge of the launch, planning and end-of-project workshops; the development of delivery plans for each of the five related projects to map out how project outputs will be used by SSA partners; and the assurance of transfer of Outputs to TLII.

Capacity-building activities:

Capacity-building projects: training components for TLI scientists and students

20. Project No G4009.07.01: Capacity-building à la carte 2009 – TLI students for analysis of drought tolerance in common bean

- *Duration: Oct 2009–Oct 2010; NCE: May 2013*
- *Total Budget USD 100,000*

Principal Investigator and lead institute
Matthew Blair/Steve Beebe, CIAT

Collaborating institutes and scientists

- *SARI–Ethiopia – Fitsum Alemayehu*
- *DR&SS – Godwill Makunde*
- *SABRN/UoZ – Lizzie Kalolokesya*

The project will provide for 1) training for a PhD candidate from Ethiopia (ECABREN region) to engage in marker assisted recurrent selection of common bean for drought tolerance and 2) training at CIAT for current students (SABRN region) in projects that are

complementary to the TL1 – bean objective. The candidate identified for Ethiopia is from SARI and is conducting breeding for the southern region of Ethiopia, while the training opportunities are for researchers representing DAR4D (Zimbabwe) and SABRN (Malawi) or EIAR (Ethiopia). The research conducted will support detailed physiological evaluation of the common bean genotypes for drought tolerance and marker assisted selection for common bacterial blight or arcelin-based bruchid resistances which are part of the TL1 project.

21. Project No G4009.07.02: Capacity-building à la carte 2009 – Capacity-building in modern cowpea breeding

- *Duration: Oct 2009–Oct 2010; NCE: May 2013*
- *Total budget: USD 49,800*

Principal Investigator and lead institute
Jeffrey D Ehlers, UoC–Riverside

Collaborating institutes and scientists

- UoC–Riverside – Philip A Roberts, Timothy J Close
- ISRA – Ndiaga Cisse
- UEM – Rogerio Chiulele

High-throughput genotyping platforms enable new strategies for crop improvement, including more efficient approaches to marker-assisted backcrossing that involve simultaneous selection for flanking markers associated with the target trait(s) and for 'backbone' markers throughout the genome associated with the recurrent parent genetic background. Few if any African plant breeders are trained in the application of this powerful new resource for crop improvement. This Capacity Building Proposal targets training of two African PhD students (from Senegal and Mozambique) in this area, utilising the new high-throughput SNP genotyping platform we developed for cowpea under TI-1 Phase I. The students will employ modern breeding tools and a marker-assisted backcrossing strategy to conduct both foreground and background selection to develop an improved version of a preferred local cultivar for each country. QTLs associated with drought tolerance, including the delayed drought-induced senescence trait and drought tolerance candidate genes identified by this and earlier projects will be targeted for introgression, along with markers for resistance to biotic stresses such as diseases caused by *Macrophomina phaseolina*, which devastates cowpea and other crops when drought is present.

22. Project No G4009.07.03: Capacity-building à la carte 2009 – Marker-assisted back crossing (MABC) for drought tolerance in chickpea students for analysis of drought tolerance in chickpea (TLI- Kenyan student)

- *Duration: Dec 2009–Dec 2010; NCE: May 2013*
- *Total budget: USD 100,320*

Principal Investigator and lead institute
Rajeev K Varshney, ICRISAT

Collaborating institutes and scientists

- EgU – Paul Kimurto, Richard Mulwa
- ICRISAT – Pooran Gaur, Mahendar Thudi

The project will provide a studentship, for a PhD candidate from Egerton University (EU), Kenya for marker assisted introgression of drought tolerance related root trait QTLs into elite Kenyan cultivar of chickpea. Root trait QTLs (a hot spot region) have been identified in the Phase I of TLI. In Phase II, Egerton University Kenya, a collaborative partner, is supposed to take the lead on MABC for introgressing the root trait QTL in the farmers preferred cultivar of Kenya. As a part of TLI, there is a plan to train one PhD student at EU-Kenya and this student has already been identified. This student will undertake the research activities of Activity 5 of TLI- Phase II in Kenya. It is also important to note that this student would be working in close collaboration of ICRISAT and Egerton Uni and would keep on travelling to these places. For instance, majority of crossing and phenotyping work will be carried out at Egerton Uni while genotyping work will be carried out either at ICRISAT or by Molecular Breeding Platform of GCP. Expected costs on genotyping, making crosses and phenotyping etc. has been planned under TLI Phase II proposal. This project will take care of studentship of the student as well as living expenses in Kenya and ICRISAT, India.

23. Project No G4009.07.04: Ensuring 'good' and relevant phenotypic data to feed molecular breeders: The need for long-term training of scientists of NARS partners to TLI Objective 1

- *Duration: Dec 2009–Dec 2010; NCE: May 2013*
- *Total budget: USD 50,032*

Principal Investigator and lead institute
Vincent Vadez, ICRISAT

Collaborating institutes and scientists

- ICRISAT – SN Nigam, Bonny Ntare, Emmanuel Monyo

Intended trainees:

- *Nouhoun Belko, Senegal*
- *Omar, Niger*
- *Philippo Mashamba, Tanzania*
- *Collins Chitawo, Malawi*

The Tropical Legume I project is targeting disease resistance and drought tolerance as the major traits limiting crop production of 4 legumes (groundnut, bean, cowpea, chickpea) in sub-saharian Africa. Skills to phenotype these traits and use the information in a marker-assisted approach are the key to the future success of breeding in sub-Saharan Africa. For that, there is an urgent need to train a critical mass of plant breeders and technicians to the techniques and protocols that they will need to master in order to usefully assess germplasm and breeding materials and undertake breeding in their locations. In 2008, a training course has been organized at ICRISAT to train a range of scientists and technicians in drought phenotyping. Although very successful, the course did not offer the long term training that is also required to gain full confidence in the skills acquired. In addition, the training was limited to drought phenotyping and had no breeding and disease phenotyping components. Here, we propose a longer term, truly "a la carte" training, where scientists/technicians would receive training over extended stays at ICRISAT's location, and covering all aspects needed for breeding in TLI. The experiments of TLI taking place at ICRISAT would be the learning ground, and those at NARS location would be where trainees would implement the skills acquired, with a close follow up by PI trainers. The objective of the capacity building is to train one scientist or technician, depending on need, at each of the national programs involved in the Objective 1 (groundnut), although we will also be looking for overlap with objective 2 (cowpea). For the latter reason, the training will be designed to cater specific needs of partners. The training targets are for: (i) Breeding, (ii) drought phenotyping (iii) disease phenotyping (iv) marker use. We want to focus on young scientists already working with the national program, and through that developing strong linkage CG-NARS.

24. Project No G7010.06.01: Accelerating development of genomic resources and strengthening NARS partner capacities for enhancing adoption of molecular breeding for drought tolerance in chickpea

- *Duration: Jun 2010–Jun 2014*
- *Total Budget USD 700,000*

Principal Investigator and lead institute
Rajeev K Varshney, ICRISAT

Collaborating institutes and scientists:

- ICRISAT – Mahendar Thudi, C Siva Kumar and Pooran Gaur
- Egerton University, Kenya – Paul Kimurto
- Ethiopian Institute of Agricultural Research (EIAR), Ethiopia – Asnake Fikre

Marker assisted backcrossing (MABC) and marker assisted recurrent selection (MARS)- two most important molecular breeding approaches are gaining importance in the recent past. These are extensively being employed for more precise selection and introgression of desired traits into elite cultivars in variety of crop plants. Chickpea is most important food legume in the arid and semi-arid regions especially in Sub-Saharan Africa (SSA) and South Asia (SA). Drought is one of major constraints to chickpea production. Significant genomic tools like SSRs (simple sequence repeats), SNPs (single nucleotide polymorphisms) and DArT (Diversity Array Technologies) arrays and a hot spot containing QTLs for several drought related traits has been identified in Phase I of Tropical Legumes –I (TL-I). For efficient molecular breeding especially for MABC, while markers closely linked with QTLs are desirable, cost effective marker (e.g. SNP) genotyping platform are critical for successful implementation of MARS and background selection of MABC. Some efforts are being made to help NARS partners such as Egerton University and EIAR to undertake molecular breeding activities for developing superior genotypes with enhanced drought tolerance. The current Chickpea Challenge Initiative (CCI) will capitalize the resources developed in TL-I Phase I and supplement the above mentioned activities planned in Phase II of TL-I through strong linkages with Integrated Breeding Platform (IBP).

3. Maize

25. Project No G4008.33: Drought tolerance phenotyping of the GCP maize inbred line reference set

- *Duration: Jan 2008–Feb 2011; NCE: Feb 2012*
- *Total budget: USD 257,301*

Principal Investigator and lead institute
James Gethi, KARI

Collaborating institutes and scientists

- CIMMYT – M Warburton, M Zaharieva, S Taba, M Vargas, JL Araus, C Sanchez
- ETH – P Stamp, A Hund, R Messmer
- Agropolis–INRA – F Tardieu, C Welcker

Under GCP Subprogramme 1, several projects have assessed the genetic structure of crop germplasm collections held by the CG centers and their partners, including maize in which a collection of 987 inbred lines, provided by CAAS, CIMMYT and IITA was characterised by CIMMYT and CAAS with 47 SSR markers. As a product of this study, a subset of 240 reference lines has been chosen to represent a majority of the neutral genetic diversity of the whole collection. The objective of the present project is to characterize the phenotypic variation associated with the reference set, particularly for drought tolerance related traits. The expected output is to ensure a better access to new genes and alleles involved in drought tolerance.

In winter 2007-2008, the reference set will be sown at the Tlaltizapan experimental station (Mexico) under irrigated conditions to ensure seed multiplication of the 240 lines, and identify and discard those that are un-adapted to the local, subtropical growing conditions. Phenological traits will be scored during this growing cycle to improve further phenotyping design by grouping similar individuals (for example by earliness and plant height). At Tlaltizapan, single hybrids will be generated by crossing the lines having produced ears and grain with a tester with high general combining ability and good adaptation to African conditions (ie, CML 312). Inbred lines and hybrids will be phenotyped at Tlaltizapan and Kiboko (Kenya) using different secondary traits. In addition, variation in growth of main axile and lateral roots under controlled conditions will be assessed at ETH Zűrich using a non-invasive imaging technique, and variation in leaf elongation rate under vegetative drought conditions will be examined at INRA Montpelllier. During the seed multiplication step carried out at CIMMYT, leaf tissue will be collected for DNA extraction. Leaf tissue will be collected from two separate plants presuming that at least one of them will produce grain. This plant will be retained as founder for generating a stock of seeds available for further research activities. Its DNA will be made available to GCP for genotyping the 240 lines (using the 20 most discriminant SSR markers from the 47 used for genotyping the composite set). This will permit a validation of the original genotyping of the reference set. Any lines missing marker data for the 47 SSR markers will be genotyped at CIMMYT to allow a complete data set. The remaining DNA will be made available for further research activities, including high density genotyping using SNP markers in future projects planned by CIMMYT and others.

This project will permit i) a validation of the previous genotyping of the composite set and of the identification of the reference set, ii) a high quality seed multiplication and creation of hybrids, iii) a multi-years and multi-locations phenotyping of the reference set and of the hybrids generated from this set, and iv) a phenotyping of root morphology and leaf elongation rate under drought controlled conditions.

A NARS from Eastern Africa, KARI (Kenyan Agricultural Research Institute) will be PI of the project and play a major role from the very beginning of the phenotyping process. Parts of the drought areas in Kenya (and particularly the Kiboko region) are representative of many areas in Eastern and Southern Africa (ESA).

26. Project No G4008.56: Drought tolerant maize for Asia

- *Duration: Nov 2008–Oct 2013*
- *Total budget: USD 1,500,000*

Principal Investigator and lead institute
Bindiganavile S Vivek, CIMMYT

Collaborating institutes and scientists

- ICERI – M Azrai
- Institute of Plant Breeding, UPLB – Eureka Teresa Ocampo
- Krishidhan Seeds, India – IS Singh
- NMRI – Dang Ngoc Ha
- NSFCRC – Pichet Grudloyma
- YAAS – Fan Xingming

Maize area in South and South-East Asia has been expanding by 2.2% annually from 16.5 (2001) to 18.0 (2006) million hectares. Over 80% of the maize is grown under rainfed conditions and prone to drought. Addressing the problem of drought has been estimated to provide the highest technical returns to rainfed maize R&D investments in Asia. Based on substantial breeding progress made for drought tolerance in maize in other regions (Central America and eastern and southern Africa), this project proposes to apply marker-assisted selection within pedigree breeding or backcrosses made between drought tolerant source inbreds and a minimum of four elite Asian adapted inbreds, and more through execution of additional self-funded and donor-funded MARS projects by public and private partners. Inbred lines will be extracted from improved populations, using either selfing or doubled haploids, and new drought tolerant Asia-adapted hybrids tested. GCP support will result in a minimum of four Asian adapted drought tolerant inbreds and hybrids, molecular marker information associated with drought tolerance, and NARS and private sector scientists with experience in integrating MARS in applied breeding programmes. The project intends to integrate self-funded public and private sector partners for a larger number of MARS breeding projects (for drought tolerance and other traits) and wider capacity building. This project is expected to become the impetus for significant levels of drought tolerance being introduced into highly relevant Asian maize germplasm with resulting impact in diverse environments and by diverse suppliers, and for a molecular community of practice being established among the Asian maize breeding community.

4. Rice

27. Project No G3007.05: Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-aided breeding

- *Duration: Aug 2007–Jul 2009; NCE: Dec 2011*
- *Total budget: USD 598,590*

Principal Investigator and lead institute
Arvind Kumar, IRRI

Collaborating institutes and scientists

- CRRI – ON Singh, P Swain
- CRURRS – NP Mandal
- NDUAT – JL Dwivedi
- UAS–Bangalore – S Hittalmani, Venkatesh Gandhi
- TNAU – R Chandrababu, A Senthil, S Robin
- BAU – BN Singh, RL Mahato
- JNKV – P Perraju
- BF – HE Shashidhar, Abhinav Jain
- YAAS – D Tao
- UoAlb – Dean Spaner
- IRRI – R Anitha, R Serraj, D Mackill
- IGKV – SB Verulkar

Rice production losses due to drought are a risk on more than 20 million ha, and primarily affect the poorest communities. Drought risk depresses productivity even in favorable years because risk of crop failure drives farmers to limit investment in fertilizer.

Varieties with improved tolerance could reduce risk and help alleviate poverty, but progress in their development has been slow because few rice breeding programmes screen directly for grain yield under drought stress, assuming that the trait is too complex for conventional breeding approaches. However, research by IRRI and collaborators has shown that, when stress is carefully imposed in the field, large differences in the yield of tolerant and susceptible varieties can be reliably detected. Recent experiments also show that much of the difference between tolerant and susceptible cultivars appears to result from the effects of a small number of genes. Several such genes have been identified at IRRI, but they must be precisely "tagged" by DNA markers to be used in developing improved varieties. The proposed project will tag (or fine-map) four genes that have been shown to reliably affect yield under both artificially imposed and natural drought. The physiological basis for their effects on tolerance will be studied, and their effects in farmers' environments in India and southern China will be confirmed. Many such genes probably exist in rice genebanks, but have not been identified because conventional mapping requires that large populations derived from crosses between tolerant and susceptible parents be subjected to expensive DNA analysis. However, only genes with large effects on stress tolerance are likely to be useful in breeding; these can be detected by "quick and dirty" methods that involve DNA testing of only the most tolerant and susceptible progeny of a cross. This approach, known as selective genotyping, will be optimised for rice drought gene detection. Lines developed by introducing genes that improve drought tolerance into elite varieties will be disseminated in collaboration with NARES partners.

28. Project No G3008.03: Delayed senescence and drought tolerance in rice

- *Duration: Nov 2008–Oct 2011; NCE: Oct 2012*
- *Total budget: USD 851,896*

Principal Investigator and lead institute
Eduardo Blumwald, UoC–Davis, USA

Collaborating institutes and scientists

- *IRRI – Abdelgabi M Ismail, Rachid Serraj*

Drought is the major constraint to rice production in the drought-prone rainfed environments, and enhanced drought tolerance and crop water productivity are major targets for improving and sustaining food security in these areas. We hypothesised that drought-induced plant senescence is due to a type of cell death programme naturally activated during drought. Down-regulating such programme could therefore enable plants to acquire vigorous acclimation responses to stress, resulting in enhanced drought tolerance with reduced yield losses. We generated plants overexpressing an IPT gene (mediating the synthesis of cytokinins) under the control of SARK, an inducible maturation- and stress-dependent promoter, and demonstrated that the suppression of drought-induced leaf senescence results in significantly enhanced drought-tolerance of the plants. These plants maintained relatively high relative water content, retained photosynthetic activity and survived longer periods without irrigation, Moreover, the plants overexpressing PSARK-IPT were able to grow under restrictive water supply with a lower yield penalty compared to controls and displayed minimal yield losses when watered with only 30% of the amount of water used under control conditions.

Based on all previous results, in this proposal we will test the efficacy of stressinduced cytokinin synthesis in conferring drought tolerance in upland and lowland rice varieties overexpressing IPT. The general objective is to identify genes with significant roles in conferring drought tolerance in rice, and the generation of drought-tolerant and water useefficient rice plants in different genetic backgrounds. We will use forward-, reverse-genetics and TILLING to assess and confirm the roles of the identified genes in drought tolerance. The development of drought-tolerant rice varieties able to grow and produce higher biomass and yield under restricted water regimes would considerably minimise drought-related losses and increase food production in water-limited rainfed rice lands.

29. Project No G3008.06: Targeting drought-avoidance root traits to enhance rice productivity under water-limited environments

- *Duration: Nov 2008–Oct 2011; NCE: Oct 2012*
- *Total budget: USD 900,000*

Principal Investigator and lead institute
Rachid Serraj, IRRI

Collaborating institutes and scientists

- IRRI – K McNally, A Kumar, N Kobayashi
- AfricaRice – S Mande (Co-PI); T Hiroshi (collaborator)
- SUA – A Kijoji
- TNAU – R Chandra Babu
- BF – HE Shashidhar
- UoAb – A Price
- ChSU – LJ Wade
- UoMi – RE Sharp and HT Nguyen
- NagU – A Yamauchi
- Drought Breeding Network, India

Water shortage is the overarching environmental constraint for the sustainable productivity of rice in rainfed cropping systems, where yields remain low and unstable. Despite various efforts deployed over past decades, the identification and characterisation of drought-resistance traits, which can be transferred into cultivars with high-yielding genetic backgrounds, have been generally unsuccessful. In most agricultural situations, the focus on tolerance traits and plant survival mechanisms has little relevance to increasing/stabilising crop yield. Thus, increasing both crop yields and water-use efficiency requires the optimisation of the physiological processes involved in the most critical stages of plant responses to soil dehydration. The focus of this project will be on dehydration avoidance and the plant's ability to maintain its water status under conditions of soil water deficits, through increased water uptake by the roots. Our research team combining expertise in drought-stress physiology, plant breeding, and molecular genetics will target the understanding and improvement of drought-avoidance root traits to enhance rice productivity under water-limited environments. We will first address the need for highthroughput precision phenotyping protocols for drought-avoidance traits and detailed site environmental characterisation systems. We will develop and refine innovative screening tools and protocols for dehydration avoidance and root traits, and compare the various methods and screening techniques. We will screen large numbers of rice germplasm accessions, cultivars, and breeding lines for drought-avoidance traits. We will also assess the value of these droughtavoidance traits and their relationships with grain yield in the major rainfed lowland target environments. The ultimate targets will be to assist with molecular breeding for drought resistance and to enhance the capacity of NARES researchers in the use of improved tools and methods for the genetic enhancement of drought resistance in rice.

30. Project No G3008.09: Breeding drought tolerance for rainfed lowland rice in the Mekong region

- *Duration: Nov 2008–Oct 2011; NCE: Sep 2012*
- *Total budget: USD 847,600*

Principal Investigator lead institute
Boonrat Jongdee, BRRD

Collaborating institutes and scientists

- *UoQ – Shu Fukai*
- *NAFRI – Phoumi Inthapanya*
- *CARDI – Ouk Makara*

The rainfed lowland rice ecosystem is the major food production system in the Mekong region, covering Northeast Thailand, Laos and Cambodia. Drought is considered to be the main constraint for rice production, and development of drought resistant varieties will stabilise yield in the region.

Over the last 10 years, NARS and BIOTEC of Thailand, CARDI of Cambodia, NAFRI of Laos, and the University of Queensland have had collaborative programmes on drought tolerance improvement, supported by the Rockefeller Foundation and the Australian Center for International Agriculture Research. Field screening for drought tolerance was conducted, more than 20 populations from crosses between parents with drought tolerance and popular varieties have been developed, a few secondary traits such as leaf water potential, have been identified as potentially useful, and QTLs and

their linked markers for drought tolerance have been identified and developed. We have adopted a concept that widely acceptable varieties require drought tolerance and high yield potential. However, research is required to improve strategies for selecting for yield potential, to test the identified drought tolerant traits and the genotypes in different drought environments, and to identify drought-prone areas that are suitable for these genotypes.

The objective of this proposed project is to develop strategies and protocol for selection of drought tolerant genotypes by using diverse populations which have been developed by us. This study will be conducted in Thailand, Laos and Cambodia. A strong advantage of our work is that the populations have been developed from popular varieties and donors which have been identified for drought tolerance under field condition. The outcome of this work, in addition to developing strategies for selecting drought tolerance, will be release of drought tolerant genotypes as commercial varieties, identification of traits corresponding to adaptation to aerobic condition, confirmation of putative secondary traits and identification of their genomic regions, and GIS maps that identify drought prone areas.

31. Project No G4006.01: Developing strategies for allele mining within large collections

- *Duration: Jan 2006–Jul 2008; NCE: Aug 2011*
- *Total budget: USD 200,000*

Principal Investigator and lead institute
NR Sackville Hamilton, IRRI

Collaborating institutes and scientists

- EMBRAPA
- ICARDA – M Baum
- ICRISAT – H Upadhyaya
- IRRI

GCP SP1 has undertaken new steps towards rationalising the utilisation of germplasm collections. It has assembled a large percentage of the diversity of crop genepools into progressively refined subsets as composite, core and reference collections. These will enable improved understanding of the structure of genetic diversity and its ecogeographic distribution, and discovery of new functional genes and the range of alleles of each gene included in the composite collections.

However, they represent only a small percentage of the larger collections: in the case of rice, the composite collection contains only around 2% of the germplasm held in the genebank at IRRI, and probably less than 0.5% of global holdings in all rice genebanks. Many distinctive alleles, haplotypes and genotypes have not been captured in the composite collections. The next big challenge is to explore this additional diversity.

This project seeks to establish a strategy for efficiently exploring diversity held within the large collections outside the composite collections. The strategy constitutes true "allele mining": "tunnelling" through the collections, sampling and testing accessions as we go, and using the results to determine where to tunnel next.

SP1 results to date will be analysed to identify genetic gaps and boundaries in the composite collection, and to establish relationships between the rich new molecular data and the sparse passport and phenotypic data previously available. Objective functions will be developed to predict which additional accessions are most likely to lie in specified locations of the hyperspace of molecular data. Those accessions will be fingerprinted to test the predictions and thence to refine the objective functions. The efficiency of the approach will be analysed. The output will be a generic strategy for discovering novel diversity without systematically fingerprinting every accession and more efficiently than using random subsets.

32. Project No G4008.45: A nested association mapping (NAM): Laying the bases for highly efficient QTL characterisation population of rice

- *Duration: Aug 2008–Jul 2010; NCE: May 2012*
- *Total budget: USD 226,000*

Principal Investigator and lead institute
Mathias Lorieux, Agropolis–IRD/CIAT

Collaborating institutes and scientists

- ARC – Marie-Noelle Ndjiondjop

Crop improvement is a crucial area of research and development for food stability at the world level. Virtually all crop species have reached a yield plateau, due to various and distinct reasons. In order to generate a real breakthrough in crop yields, technologies able to boost crop breeding efficiency are urgently needed. Modern breeding strategies often fail to include precise genetic information. Marker-Aided Selection (MAS) strategies have proven to be more efficient than conventional selection in several cases, but still suffers of (1) lack of precision in the localisation of the genes of agronomical importance (the so-called QTLs, for Quantitative Trait Loci) and

(2) are often limited to the alleles available in the crossing scheme used for QTL detection, i.e., the genetic information obtained from a particular cross between two genotypes (or lines) will not be useful when working with other genotypes. The area of research called Genomics (i.e., the massive and parallel analysis of the thousands of DNA sequences that constitute the genetic code of an organism) has made considerable progress in the last few years. Currently, we have access to the complete genome information for several crops, and rice is the most advanced of them in this sense. However, there is a strong need to bridge the gap between Genomics and Crop Improvement. Rice, as one of the most important cereals for human nutrition, must be considered a priority. In Africa, rice is getting increasing importance as a staple food. It constitutes a major source of calories for the urban and rural poor, with a fast growing demand. At the same time, the germplasm (i.e., cultivated varieties) grown in Africa suffers of low genetic diversity and needs to be enriched in order to develop new varieties, more adaptable to the inherent or new environmental constraints (e.g., drought stress, pests and diseases, low inputs). We propose to develop a new genetic resource, called a Nested Association Mapping population, that would (1) help in linking the genomic tools available for rice, (2) give access to a much higher allelic diversity at the important QTLs than "conventional" mapping approaches do, (3) allow fine mapping of QTLs (i.e., localise them with high precision on the rice genome), thus increasing significantly the efficiency of MAS strategies, and (4) provide interesting and promising genetic materials (advanced lines) for direct introduction in breeding schemes.

33. Project No G4010.04: Enhancing capacity for use of advance genotyping for fine-mapping and pyramiding of major salt tolerant QTLs through MABC for the development of durable saline tolerant rice varieties

- *Duration: Jul 2010–Jun 2011; NCE: November 2011*
- *Total budget: USD 22,086*

Principal Investigator and lead institute
Zeba I. Seraj, University of Dhaka

Collaborating institutes and scientists

- Bangladesh Rice Research Institute (BRRI) – Sazzadur Rahman (Ph.D. student, University of Dhaka)
- International Rice Research Institute (IRRI) – Abdelbagi M. Ismail, Michael J. Thomson

In Bangladesh, about 1 million hectares of cultivatable land in the coastal areas are affected by salinity. Due to the high sensitivity of modern rice varieties, resource-poor farmers of these areas can grow only one crop in the monsoon when salinity is lower. Therefore, the development of salt tolerant rice lines with wider adaptability is the only sustainable and cost effective way to improve the livelihood of marginal farmers of these areas and sustain total production of the country. In order to strengthen the capacity in rice breeding by use of molecular genetics and genomics to gear-up the rice variety development process in Bangladesh, a previous GCP SP3commissioned project has made substantial progress in the use of marker-assisted backcrossing for introgression of *Saltol* into Bangladeshi mega rice varieties. Another GCP SP5 a la carte project gave good support for the continuation of the GCP activity by establishing a marker laboratory at BRRI. In addition to *Saltol* introgression, preliminary mapping of additional QTLs from a rice landrace, Boilam was also done at IRRI and Dhaka University with funding from another SP5 capacity building fellowships to Dhaka University. The notable progress made in these projects however remains incomplete, where one MABC BC^3F^2 product, Saltol-BR11 will be tested in Farmers field this year, while the Saltol-BR28 BC^3 crossing is currently being done. This current capacity building support grant therefore aims to support hands on training for the use of advance genotyping in fine-mapping of previously identified QTLs from Boilam for pyramiding and complete characterization of *Saltol* introgression into BRRI dhan28 for the development of more durable saline tolerant rice varieties.

34. Project No G4011.04: Dissemination and community of practice for newly developed drought-tolerant QTLs pyramided breeding lines

- *Duration: Jul 2011–Jun 2014*
- *Total budget: USD 179,292*

Principal Investigator and lead institute
Arvind Kumar, IRRI

Collaborating institutes and scientists

- CRRI – ON Singh
- CRURRS – NP Mandal
- DRR–ICAR – T Ram
- NDUAT – J.L. Dwivedi

Drought is the most severe stress that reduces yield in drought prone rainfed environment. Development of drought tolerant high yielding varieties with the ability to better sustain yield losses under drought

has been initiated as high priority program by several institutes. Marker assisted backcrossing (MAB) and marker assisted recurrent selection (MARS) have been proposed as the strategies that could hasten the development of drought tolerant varieties. Efficient testing under target population of environment and identification of adaptable lines through community of practices has been suggested to lead to better dissemination of developed product. At IRRI, successful marker assisted introgression of major quantitative trait loci (QTLs) for grain yield under drought in Vandana and IR64 background was achieved. Yield under drought of Vandana, a prominent drought tolerant cultivar for upland ecosystem improved by 0.5 t ha-1 through introgression of DTY12.1 whereas introgressed IR64 lines with two to three QTLs showed yield advantage of 1.0-1.5 tha-1 under drought with no adverse effect on yield under control and quality traits. Mapping populations for MARS has been developed to improvegrain yield under control, grain yield under drought and disease resistance. The present proposal shall target dissemination of Vandana and IR64 introgressed lines through community of practices and follow MARS to improve grain yield under control, grain yield under drought and disease resistance.

35. Project No G4011.06: Field phenotyping for drought resistance of the MARS population developed under the GCP Rice RI

- *Duration: Nov 2011–Oct 2012*
- *Total budget: USD 179,292*

Principal Investigator and lead institute
Cécile Grenier, Agropolis–CIRAD/CIAT

Collaborating institutes and scientists

- *ARC – M Ndjiondjop*

The activities described in this project aim at reinforcing the GCP Rice Challenge Initiative "Improving rice productivity in lowland systems of Burkina Faso, Mali and Nigeria" leaded by Africa Rice. The goal of the GCP-Rice CI is to establish the integration of the information on drought profiles with novel phenotyping methodologies in a marker-assisted recurrent selection (MARS) scheme to develop better-adapted germplasm for each major target environment. The focus will be on the rainfed lowland ecosystems of Sudanean and Guinean savannah areas in Burkina Faso, Mali and Nigeria. The MARS populations developed under the GCP-Rice CI will be phenotyped under controlled drought conditions, mimicking the drought profiles of the target environments, and under well-characterized field conditions. The QTLs involved in conferring drought tolerance or in increasing yield potential in the target environment will be mapped within each cross, and the QTL × environment interactions will be elucidated. Recurrent recombination of specific individuals of the population carrying the favorable allele of the detected QTLs will lead to the creation of adapted lines bearing the favorable QTLs/alleles for drought tolerance and for other important traits.

CIAT's participation in the GCP-Rice CI was sought to contribute in two major activities 1: phenotyping MARS population for drought tolerance, and 2: building up the capacity of and relationship between players within and around the project.

The 1-year project that will be taking place in CIAT-Colombia will aim at consolidating the regional phenotyping done in Africa, but also to train on phenotyping technology used by rice breeders in Latin America. As part of a much broader scope, we will contribute to the building of a proof concept that the application of MARS in rice, with a focus on drought as target trait, can contribute to increased yield and change the way breeders are tackling crop improvement for drought tolerance.

36. Project No G4011.07: Rice multiparent advanced generation intercrosses (MAGIC) – Phase II

- *Duration: Nov 2011–Oct 2013*
- *Total budget: USD 753,772*

Principal Investigator and lead institute
Hei Leung, IRRI

Germplasm populations produced through multi-parent advanced generation inter-crosses (MAGIC) can be used directly as source materials for the development of breeding lines and varieties adapted to different environments. We have developed two MAGIC populations under the GCP project G4008.01. These two populations include intercrossing eight elite lines as founders from the Asia indica pool (indica MAGIC) and the japonica group (japonica MAGIC). The founder lines include modern varieties known to exhibit tolerance of a range of biotic and abiotic stresses, high yield potential, and good grain quality. Here, we propose a second phase of the MAGIC project to disseminate, genetically characterize, and field-evaluate prebreeding lines through a network consisting of three countries in Southeast Asia and one country in Africa. We will examine the transmission pattern of tolerance of abiotic stresses (drought,

submergence, Fe toxicity, and salinity), resistance to biotic stresses (blast and bacterial blight, rice yellow mottle virus), wide adaptation to different environments, high yield potential, and good grain quality.

The project will be implemented through four specific objectives:

1. Advancing multiple MAGIC populations
2. Genotyping and phenotyping to tag essential QTLs for breeding
3. Evaluation and varietal selection through a breeding network
4. Data curation and analysis, and deployment of MAGIC lines

We will achieve the following outputs:

- Providing solutions to a range of production constraints (particularly stress tolerance) in the target countries through the use of advanced MAGIC lines.
- An assessment and understanding of the potential of enhanced recombination in generating novel diversity.
- Broadening of germplasm adaptation in multiple environments.
- Novel traits precisely tagged by molecular markers, which can be deployed in selection.
- An integrated genotype and phenotype data set from multiple environments, providing a resource to enable breeding selection.

This project will produce a dynamic genetic resource that will be used by geneticists, molecular biologists, and breeders working in diverse ecologies. In Asia, we will work in the Philippines, Vietnam, and Cambodia, and with the community of practice organized by the Generation Challenge Program (GCP) in Thailand. For Africa, we will concentrate on Tanzania. All MAGIC populations are potentially valuable for Asia, while japonica MAGIC and global MAGIC populations could have high potential for diverse ecologies in Africa.

37. Project No G7010.04.01: Improving rice productivity in lowland ecosystems of Burkina Faso, Mali and Nigeria through marker-assisted recurrent selection for drought tolerance and yield potential

- *Duration: May 2010–Apr 2014*
- *Total budget: USD 3,270,000*

Principal Investigator and lead institute:
Marie-Noëlle Ndjiondjop, AfricaRice

Collaborating institutes and scientists

- Institut de l'environnement et des recherches agricoles (INERA), Burkina Faso – Drissa Hema
- Institut d'économie rurale (IER), Mali – Fousseyni Cisse
- National Cereals Reserch Institute (NCRI), Nigeria – Alhassan Maji
- International Rice Research Institute (IRRI), Philippine – Rachid Serraj
- Institut de recherche pour le développement (IRD), France – Alain Ghesquiere
- Centre de coopération internationale en recherche agronomique pour le développement (CIRAD) – France: Michael Dingkuhn

Work packages (WPs) of Project G7010.04.01:

- WP 1: Characterisation of the IV-TPE, establishment of drought evaluation sites and description of ideotypes fitting major sub-classes of TPE
- WP 2: Phenotyping for yield potential and drought tolerance
- WP 3: Developing improved lines combining favourable QTL alleles for drought adaptation and productivity for target environments in Burkina Faso, Mali and Nigeria
- WP 4: Rice drought molecular biology and breeding community of practice for West Africa
- WP 5: Project and information management

Details of these work packages can be seen in the Projects table at the beginning of this publication

World paddy production is reached a new record level of 666 million tonnes in 2008. However, in Africa, rice production has not increased at the same rate and has not been able to keep pace with increasing demand. Only 54% of the Sub-Saharan Africa rice consumption is supplied locally. In 2009, rice imports in Africa were forecast to approach 9.3 million tonnes. Among the various abiotic and biotic factors reducing rice yield in West Africa, drought is considered the most important. Rice yield is affected by drought in rain-fed lowland ecosystems in around 80% of the total rice area in Mali, 67% in Burkina Faso and 48% in Nigeria, as a result of erratic rainfall and poor water control. Three drought-related risks can be distinguished in rain-fed lowlands: (1) early drought, especially in direct-seeded, poorly managed systems; (2) mid-season drought spells alternating with flooding; and (3) terminal drought. Rice breeders have developed improved varieties for rain-fed lowland ecosystems, but the complex nature of rain-fed lowlands makes it difficult to delineate clearly the target domains of these varieties. Developing drought-tolerant cultivars that have a high yield potential in normal years and provide a good yield

under drought and other major stresses for each target environment will help sustain rice production in the large rain-fed lowland ecosystem across Africa.

The project will focus on the rain-fed lowland ecosystems of Sudanean and Guinean savannah areas in Burkina Faso, Mali and Nigeria. Within 4 years, it will establish (i) the drought profiles of the target population of environments (TPE) in inland valley lowlands; (ii) the identification of traits of interest for targeted environments, using novel phenotyping methodologies enabling an efficient separation of genetic (G) and environmental (E) effects; and (iii) the integration of the information on drought profiles with novel phenotyping methodologies in a marker-assisted recurrent selection (MARS) scheme to develop better adapted germplasm for each major target environment.

The MARS approach consists of concentrating breeding investments in a few crosses of high potential, and fully exploiting this potential. Quantitative trait loci (QTL) for target traits are detected within the population from each cross and are then 'pyramided' by crossing lines within the population using marker information at each generation. The approach is widely used by private companies to improve breeding efficiency for quantitative traits. The MARS populations developed under this project will be phenotyped under controlled drought conditions, mimicking the drought profiles of the target environments, and under well-characterised field conditions. The QTLs involved in conferring drought tolerance or in increasing yield potential in the target environment will be mapped within each cross, and the QTL × environment interactions will be elucidated. Recurrent recombination of specific individuals of the population carrying the favourble allele of the detected QTLs will lead to the creation of adapted lines bearing the favourable QTLs/alleles for drought tolerance and for other important traits.

The combined results of TPE characterisation and the adapted lines developed will facilitate the up-scaling of research results to non-project countries, will increase the adoption rate of the improved varieties and, finally, increase the contribution of rain-fed lowland rice in the total rice production of Sub-Saharan Africa.

The project will introduce a new approach – MARS – into NARS and AfricaRice breeding programs through building capacity for modern plant breeding and establishing the systematic use of molecular tools in breeding for quantitative traits. This 4-years project will aim to build a proof concept that the application of MARS in rice, with a focus on drought as target trait, can contribute to increased yield and to change the way breeders involved in this project work. Consequently, the project should put in place a flow of long-term capacity-building with the objective of establishing a modern breeding program for complex traits such as drought in West Africa.

Capacity-building activities:

Community of practice

38. Project No G4009.09: The Community of Practices strengthening rice breeding programme using genotyping building strategy and improving phenotyping capacity for biotic and abiotic stresses in the Mekong region

- *Duration: Nov 2009–Oct 2012*
- *Total budget: USD 210,630*

Principal Investigator amd lead institute

Jonaliza Lanceras-Siangliw, BIOTEC

Collaborating institutes and scientists

- BIOTEC – Theerayut Toojinda
- NAFRI – Monthathip Chanphengsay
- CARDI – Ouk Makara
- DAR – Toe Aung

Line conversion of popular rice varieties in Laos, Cambodia, Myanmar and Thailand, through the recently concluded project "The Community of Practice: Concept applied to rice production in the Mekong Region: Quick conversion of popular rice varieties with emphasis on drought, salinity and grain quality improvement" proved that working as a community of rice breeders in the region can hasten the development and release of varieties that may answer existing problems affecting rice production in the area. It was also proven that what is useful to one group can be also be beneficial to other groups.

Rainfed lowland areas in Mekong region share common problems in rice production. Drought, soil acidity and salinity or nutrient deficiency are encountered in this region. Diseases and insect pests such as blast, bacterial leaf blight, brown planthopper, white back plant hopper, gal midge and a lot more are also common in the region as well as strains/races of pathogen and insect biotypes. MAS was introduced to partner institutes and lines that had been developed in the previous project are now ready for more intensive trait validation and field trials. In this proposal, new traits will be added to the improved varieties to be managed by students from each institute through

marker-assisted breeding. Proper validation of traits introgressed through efficient phenotyping will strengthen MAS and breeding programmes thus, submergence screening facilities will be established in Laos, Cambodia and Myanmar as well as facilities for bacterial leaf blight, blast and brown planthopper phenotyping.

The objectives of this proposal are to implement research by adding new traits particularly on abiotic and biotic stresses through MAS to the improved varieties from the previous project and to promote phenotyping capacity on abiotic and biotic stresses in order to assess germplasm and developed improved varieties for accurate validation of traits in rice breeding programmes of DAR, NAFRI and CARDI.

39. Project No g4010.04/G4010.01.01: Identification of novel QTLs for salinity tolerance and pyramiding of salinity and submergence tolerance QTLs to develop improved rice varieties

- *Duration: Mar 2010–Mar 2013*
- *Total budget: USD 75,000*

Principal investigator and lead institute
Armin Bhuiya, PhD Student from Bangladesh Rice Research Institute

Collaborating institutes and scientists

- Bangladesh Agricultural University – M Wazuddin
- International Rice Research Institute, Philippines – Abdelbagi M Ismail

Crop production is highly dependent upon favorable interaction of genotype and environment during its entire growth period. Various biotic and abiotic stresses greatly affect rice productivity. Salinity is one of the most common abiotic stresses in rice growing areas of the world, and over 54 million hectares of land in Asia alone are affected by salinity; out of which, 9.5 million hectares of saline soils can be amended and effectively used for rice production given that tolerant varieties become available (Gregorio et al., 2002). Use of salt tolerant varieties is considered the most economic and effective way of increasing crop production in saline soils, and is considered the most important entry point for soil reclamation (Ismail et al., 2007).

Salinity of soil and water is caused by the presence of soluble salts. These are originating from the inundation of coastal tidal saline water and/or from dissolving rocks and concentration by evaporation of saline water. Salt stress adversely affects plant growth and products quality. The salt suppresses plant growth even at lower concentration and can cause detrimental effects to plants including plant death. Na+ and Cl- are usually the most prevalent ions in saline soils and water, account for most of the deleterious effect to plants through either ion toxicity, osmotic stress and/or disruption of nutritional homeostasis. Tolerance of salinity in rice involves numerous physiological traits that are mostly independent, and development of rice varieties with higher levels of tolerance entails pyramiding of these, using either physiological or molecular approaches (Ismail et al., 2007).

Beside salinity, transient submergence caused by either flash floods or tidal movements is also a major problem during the wet season. Combining tolerance of both salinity and salt stress are therefore, considered prerequisites for the development of varieties that can broadly be adapted to these areas, which are also characterized by high levels of poverty due to limited livelihood options.

40. Project No G7010.04.01/G4009.02.01: Study of Burkina Faso rice landraces diversity and breeding for resistance to Rice Yellow MottleVirus (RYMV)

- *Duration: Mar 2009–Feb 2011; NCE: Jun 2011*
- *Total budget: USD 36,000*

Principal investigator and lead institute
Honore Kam, PhD student from INERA, Burkina Faso

Collaborating institutes and scientists

- Cooperation International en Recherche Agronomique pour le Developpement (CIRAD), France – Nour AHMADI
- Institut de Recherche pour le Developpement (IRD), France) – Alain Ghesquiere, Laurence Albar, Mathias Lorieux,
- Africa Rice Centre (AfricaRice) – Marie Noelle Ndjiondjop
- Institut National de l'Environnement et de la Recherche Agricole (INERA), Burkina Faso – Oumar Traore
- University of Kwazulu Natal (UKZN), South Africa – Mark D. Laing

Rice is the staple food in many countries of Africa and constitutes a major part of the diet in many others. A series of abiotic and biotic stresses continue to limit rice productivity. Rice yellow mottle virus (RYMV) is one of the most important rice pathogens in most rice-growing countries of Africa and Madagascar, but not elsewhere. Two types of natural resistance to RYMV have been reported in rice: a partial-resistance in *Oryza sativa* cultivar Azucena and a high-resistance on cultivars Gigante and Tog5681, which represent *Oryza sativa* and *O. glaberrima*, repectively. The high and partial resistances are controlled by a single recessive gene (*rymv*) and several genes, respectively. IRD in collaboration with The Africa Rice Center (WARDA) developed a fine genetic map and the cloning of the high level of resistance and the SNP gene markers tight are used to facilitate the screening of germplasm for their resistance to RYMV. Recently, however, the partial resistance in Azucena has been completely broken down, and high level of resistance in both Gigante and Tog5681 has been overcome by several resistant-breaking-isolates from five countries of the west and central African Sudano-savannah zone. Therefore, there is an urgent need for searching other rice genotypes with high and durable resistance to RYMV in Africa. This project seeks to: (i) genotype 350 accessions collected recently in Burkina Faso with 20-30 SSR diversity markers used by The Generation Challenge Programme, and (ii) conduct extensive search for durable RYMV resistance among traditional rice accessions from Burkina Faso.

5. Sorghum

41. Project No G3008.05: Discovery and development of alleles contributing to sorghum drought tolerance

- *Duration: Nov 2008–Oct 2011; NCE: Dec 2012*
- *Total budget: USD 756,225*

Principal Investigator and lead institute
Andrew H Paterson, UGA

Collaborating institutes and scientists

- SARI–CSIR – IDK Atokple
- ICRISAT – C Thomas Hash
- MAU – SP Mehtre
- DSR–ICAR – R Madhusudhana

Sorghum is the most drought-tolerant dual-purpose (grain + straw) cereal crop of the semi-arid tropics and subtropics, where development challenges are the greatest and market failure is most acute. As such, it is both a priority for further improvement and a botanical model from which we might glean information about drought tolerance that might be leveraged in improvement of many other cereals by comparative approaches. Sorghum has recently become only the second cereal (after rice), to have its genome fully sequenced, opening new doors to its improvement and enhancing its value for comparative biology.

In a partnership joining African and Asian sorghum improvement researchers with genomic scientists experienced in crop breeding and germplasm enhancement, we will engage the sorghum sequence in a balanced approach to durably increase rates of sorghum improvement. Toward a pathway joining discovery research of increasing scope and sensitivity with application to the needs of resource-poor farmers living in drought-prone environments, early study of a few genes already known to have qualitative effects on drought tolerance will set the stage for identifying a growing pipeline of additional genes/alleles with more subtle effects, engaging several previously GCP-funded resources. Key to both discovery research and product development/delivery will be our focus on breeding populations in which drought tolerance will be combined with other traits that address production constraints in West and Central Africa, Eastern and Southern Africa, and South Asia. By applying sorghum's fully-sequenced genome to study of these field-proven genetic resources, we will elucidate genotype x environment interactions that render drought tolerance a difficult trait to work with. Improved knowledge of sorghum presents a singularly-promising opportunity to leverage comparative genomics approaches to benefit improvement of many other cereals. NARS scientists are full research partners, and will also benefit from training visits to UGA and/or ICRISAT.

42. Project No G4008.02: Phenotyping sorghum reference set for drought tolerance

- *Duration: Jan 2008–Dec 2010; NCE: May 2012*
- *Total budget: USD 473,650*

Principal Investigator and lead institute
HD Upadhyaya, ICRISAT

Collaborating institutes and scientists

- ICRISAT – V Vadez, CT Hash, L Krishnamurthy, F Rattunde, E Weltzien-Rattunde, MA Mgonja, SL Dwivedi, B Clerget
- UAS–Dharwad – PM Salimath
- KARI – CK Karari
- NPGRC – W Ntundu
- IER – M Diourte
- ISRA/CERAAS – N Cissé

Drought is one of the most important yields reducing abiotic constraint worldwide. It is proposed to evaluate sorghum reference germplasm set (about 360 of the 384 reference set accessions), selected based on the genotyping information of composite collection (41 SSR loci data on 3372 accessions), for post-flowering drought tolerance. In the first year, the reference set will be characterised for morpho-agronomic traits to classify accessions into distinct flowering and plant height groups at ICRISAT locations in India, Mali, and Kenya. In the second year, these subgroups will be evaluated for post-flowering drought tolerant traits at three ICRISAT locations (as above). In addition, they will also be evaluated at ICRISAT Patancheru, India for seed micronutrients (Zn and Fe) under varying water regimes (stressed vs unstressed conditions) to identify seed micronutrient dense lines. In third year, selected reference set accessions and stay-green QTL introgression lines will be evaluated for water uptake under stressed conditions in PVC tubes (2.0-m long and 25-cm diameter), and for the proportion of water used prior/after anthesis. In the same year, the most promising post-flowering drought tolerant reference set accessions and stay-green QTL introgression lines will be multilocationally evaluated for post-flowering drought tolerance at ICRISAT and NARS locations in India and Africa. In addition to evaluating for post-flowering drought tolerance traits, additional data will be collected on grain/stover yield and component traits to identify lines that are better able to maintain

normal growth/yield processes under stress. It is proposed to evaluate this select group of materials in the fourth year (subject to GCP provides funds) at NARS locations to generate additional data on the performance of post-flowering drought tolerant lines. At the completion of project, we will have a better understanding of post-flowering drought tolerance in sorghum, the traits associated with post-flowering drought tolerance, and a range of post-flowering drought tolerant sorghum lines for use in crop improvement programmes.

43. Project No G4008.46: Sorghum MAGIC: Multiparent advanced generation inter-cross development for gene discovery and allele validation

- *Duration: Aug 2008–Jul 2010; NCE: Feb 2011*
- *Total budget: USD 92,286*

Principal Investigator and lead institute
Tom Hash, ICRISAT

Collaborating institutes and scientists

- NIAB – Ian Mackay
- ICRISAT – Mary A Mgonja, H Fred W Rattunde, S Senthilvel, SP Deshpande
- DSR–ICAR – R Madhusudhana

MAGIC is an experimental method to increase the precision with which genetic markers are linked to quantitative trait loci (locations in the genome that have a quantifiable effect on measured traits). MAGIC involves two extensions to traditional methods of searching for marker-trait correlations among segregating progeny of crosses between two parents. First, the mapping population is established by intercrossing multiple founder lines. A MAGIC population is therefore more genetically diverse than a conventional bi-parental mapping population and more QTLs can be detected. Second, the MAGIC population can be cycled through several extra generations of forced intermating. Each extra generation mills the genetic contribution from the founder lines finer. QTLs are therefore located with greater accuracy and flanking markers for QTLs detected are potentially of greater value for use in plant breeding and genetic research.

We will establish several MAGIC-like populations for sorghum, each having 8-16 founder lines, and each targeting a specific tropical agro-ecology where sorghum is an important component of current crop-livestock production systems.

There is an increasing amount of fundamental work in the genomics and molecular genetics of sorghum and the aligned genome sequence for elite sorghum inbred BTx623 is now available. Further, BTx623 is being used as the common parent in a set of nested sorghum RIL populations that are being developed in the USA as a tool for allele mining and association mapping of QTLs for many sorghum traits of economic importance, and has been used as the genetic background for development of a sorghum TILLING population. For outputs of this upstream research to be applied to development of improved crop varieties, our knowledge of the DNA sequence and population structure of the primary genepool of this crop must be linked to the traits of importance to farmers. MAGIC populations provide a means to this end.

We will establish initial cycle intermated bulks of two sorghum MAGIC populations, targeting South Asian rainy season and postrainy season sorghum production environments, respectively. We will then initiate development of 1000 inbred lines from each of these. We will also intermate population bulks of these two MAGIC populations, following the initial cycle of crosses to create a given population, in preparation for generation of second-cycle lines for finer mapping. We will validate the structure and pedigree of these two MAGIC populations targeting South Asia with a small number of SSR markers (one per chromosome arm) drawn from the GCP programme.

We will also introduce sets of proposed founder parents for two additional sorghum MAGIC populations [one each targeting sorghum production environments in Western and Central Africa (WCA) and Eastern and Southern Africa (ESA)] for which all of the proposed founder parents are not currently available at ICRISAT–Patancheru. Following introduction in 2008 of the founder parents of these latter two MAGIC populations, through the Post-Entry Quarantine Isolation Area facility at ICRISAT–Patancheru, cycles of crossing to generate the initial cycle intermated bulks of these two populations will be undertaken in 2009.

Founder parents of all four sorghum MAGIC populations will be fingerprinted with SSR-anchored DArT markers to assess the level of marker variation within each MAGIC population, and the distribution of this variation across the genome, to help us plan the future genotyping of finished inbred line sets from the initial and more advanced generation cycles of these populations.

44. Project No G4008.48: Improve sorghum productivity in semi-arid environments of Mali through integrated MARS

- *Duration: Aug 2008–Jul 2013; NCE: Oct 014*
- *Total budget: USD 678,600*

Prinicpal investigator and lead institute
Jean-Francois Rami, Agropolis–CIRAD

Collaborating institutes and scientists

- Syngenta – Denis Lespinasse, Michel Ragot
- IER – Niaba Témé, Sidy Bekaye Coulibaly
- Agropolis–CIRAD/IER – Michel Vaksmann

Sorghum is, together with pearl millet, one the most important cereals in West Africa. It is the second most important crop in Africa after maize. However its yield is low and has not really progressed during the past 20 years. The sorghum production in West Africa is principally based on traditional, low harvest index cultivars and the breeding efforts of the past 40 years showed limited impact.

The present project propose to associate recent approaches on sorghum breeding that have been developed at IER and methodologies for marker assisted recurrent selection (MARS) that have proven to provide significant improvement of breeding efficiency for complex traits, especially in the case of maize.

Two populations dedicated to two different environments of sorghum crop in Mali will be developed from the cross of local well characterised advanced breeding cultivars exhibiting complementary traits for the target environment. A multilocal evaluation of the progenies as F4 families, together with genotyping will provide accurate QTL detection for as many traits that have to be considered for breeding. This QTL information will be used in several consecutive cycles of recurrent selection aiming at monitoring recombinations and pyramiding favorable alleles for selected QTLs. All along the recurrent process material will be released for evaluation and selfing to develop new varieties.

This project will illustrate through a private-public partnership the value of the MARS approach for sorghum breeding in Mali.

45. Project No G7009.04: Development and evaluation of drought-adapted sorghum germplasm for Africa and Australia

- *Duration: Jul 2009–Jun 2012*
- *Total budget: USD 215,785*

Principal Investigator and lead institute
David Jordan and Andrew Borrell, DPI&F

Collaborating institutes and scientists

- IER – Sidi Bekaye Coulibaly, Niaba Teme, Mamoutou Kouressy
- Agropolis–CIRAD, Mali – Michel Vaksmann

The aim of this project is to improve drought adaptation and productivity in Malian sorghum by integrating three complementary activities:

1. Evaluating the stay-green drought resistance mechanism in plant architectures and genetic backgrounds appropriate to Mali. Stay-green enhances grain yield under post-flowering water stress in the Queensland Primary Industries and Fisheries (QPIF) breeding programme in Australia.
2. Developing sorghum germplasm populations enriched for stay-green genes that also carry genes for adaptation to cropping environments in Mali. The source of the stay-green trait would be an elite line from the QPIF sorghum breeding programme that may carry other useful genes for productive and defensive traits.
3. Carrying out training activities for African sorghum researchers in drought physiology and selection for drought adaptation in sorghum. This would involve detailed training for one or two of our African partner scientists in Australia as part of the project, and sorghum drought breeding/physiology workshops in Africa.

If successful, the project would deliver knowledge of the likely impact of deploying the stay-green trait in Mali, germplasm adapted to Mali containing the trait, and enhanced capacity within Malian sorghum research teams to use this knowledge and germplasm to develop superior varieties with local adaptation. If the results of the project are sufficiently valuable, then the approach would be expanded to other sorghum programmes targeting regions of Africa where post-flowering drought is a major constraint to productivity (eg, Ethiopia and Sudan).

46. Project No G7010.05.01: Enhancing sorghum grain yield and quality for the Sudano-Sahelian zone of West Africa using the back-cross nested associated mapping (BCNAM) approach

- *Duration: Jan 2010–Jun 2014*
- *Total budget: USD 1,672,138*

Principal Investigator and lead institute

Niaba Témé, IER
Michel Vaksmann, Agropolis–CIRAD
Eva Weltzien, ICRISAT

Collaborating institutes and scientists

- IER – Abdoulaye Diallo, Mamoutou Kouressy, Korotimi Théra
- ICRISAT–Patancheru – C. Tom Hash, Trushar Shah, Fred Rattunde, Ibrahima Sissoko
- CIRAD – Jean-François Rami

Sorghum improvement in Africa deals with a wide range of harsh and highly variable environments. The local varieties are specifically adapted to the biotic and abiotic constraints and have an excellent grain quality but with low yield potentials. Sorghum breeding programs in West Africa must work with a considerable number of traits, and address the specific adaptation requirements for specific and variable agro-ecologies. This project will enhance the capacity of national and international breeding programs while using sorghum germplasm diversity and advanced molecular tools.

This project will result in the development of modified backcross populations that will be of long-term value in relating sorghum traits to their corresponding genes. The planned population structure will facilitate the QTL mapping of range of traits conditioning productivity, adaptation, and preferred grain quality traits.

Forty to fifty populations of 100 lines each will be developed from back-crosses carried out with 3 recurrent parents which represent the target ideotypes to be improved. The donor parents include 10 common donors and 20 specific donors representing the diversity of the improved and local varieties.

The capacity of National breeding programs will be strengthened by creating a regional data management unit within the IER (Mali), which will support scientists in the effective application and use of molecular data for improved effectiveness of sorghum breeding activities.

The project is divided into 2 subprojects, IER and ICRISAT each will lead one. Each subproject has 4 components: Population development, Phenotyping, data management and Capacity building. A fifth component, genotyping, will be common to both subprojects (ICRISAT and IER). The genotyping component will be financed directly by the GCP and its methods will be specified later.

6. Wheat

47. Project No G3008.01: Generating new wheat germplasm with enhanced drought/ heat tolerance using AB genomes genetic diversity

- *Duration: Nov 2008–Oct 2011; NCE: Oct 2012*
- *Total budget: USD 779,820*

Principal Investigator and lead institute
SC Misra, ARI–India

Collaborating institutes and scientists

- ARI–India – S Tetali
- CIMMYT – M Zaharieva, S Dreisigacker, J Crossa and T Payne
- PBI–UoS – R Trethowan and P Sharp
- UAS–Dharwad – RR Hanchinal, A Shreenivas Desai, IK Kalappanavar, KK Math, B Nirmal Yenagi

The recent evidence of climatic change (reflected by rises in global temperature and unpredictable rainfall) and the increase in wheat prices have considerably questioned the optimistic food supply scenarios of the past decade. Increasing cereal production in developing countries by enhancing crop resilience under high temperatures and irregular rainfall or water supply is now a tremendous challenge. To address this challenge we propose combining the use of new sources of novel genetic diversity and of molecular markers to create new wheat germplasm as a potential source of drought and heat tolerance.

Emmer wheat will constitute the reservoir of new diversity and drought/heat tolerance traits. Highly diverse accessions will be crossed to *Aegilops tauschii* accessions to create synthetic hexaploid wheats (SHW) that will be re-crossed to elite bread wheats to produce a large set of synthetic back-crossed lines (SBL). In addition, some emmer x hexaploid bread wheat crosses will be made to recombine the A and B genomes.

Molecular markers will be used to analyse diversity within a large collection of emmer wheats and to develop a reference set of diverse individuals to be crossed to *Aegilops tauschii* accessions. Markers will help to estimate the genetic diversity within families or populations originating from different regions.

Germplasm generated by this project will be further extensively used by CIMMYT, Agharkar Institute, Dharwad University, Pakistan Agricultural Research Council and Sydney University breeding programmes to improve drought/heat tolerance and will be made available to the entire wheat breeding community. Inter and intra family variation for drought tolerance traits in synthetic back-crossed lines and their association with genomic regions are expected to provide important information for further marker-assisted breeding activities.

48. Project No G3008.08: Breeder-friendly high-throughput phenotyping tools to select for adaptive traits in drought environments

- *Duration: Nov 2008–Oct 2011; NCE: Jun 2013*
- *Total budget: USD 897,073*

Principal Investigator and lead institute
Francis Ogbonnaya, ICARDA

Collaborating institutes and scientists

- CSIRO –M Fernanda Dreccer
- ICARDA – Osman Abdalla, Mohammed Karrou
- CSIRO –Tony Condon
- CIMMYT – Matthew Reynolds, D Bonnett
- INRA–CRRA, Morocco – Hassan Ouabbou
- ICARDA–INRA Cooperative Research Program, Morocco – Sripada M Udupa
- INRA–CRRA, EIAR – Solomon Gelacha

Drought continues to be a major limiting factor to wheat crop production worldwide, with often devastating consequences especially in developing countries. This project proposes to facilitate plant breeding for drought adaptation by developing a package of high-throughput non-invasive techniques to detect genetic variation for single and combined or complex (water use) drought adaptive traits under field conditions. We will also assess the value of different plant characteristics (transpiration efficiency, early vigour, storage of sugars in the stem, flowering date, tillering and stay green) on performance under different types of drought. Finally, we will investigate the traits or trait combinations behind ICARDA's elite drought adapted material. We believe this new knowledge will help focus breeding programmes in the partner regions, particularly Central and West Asia and North Africa (CWANA). All project lines will be genotyped using markers from the GCP genetic diversity kit and markers related to agronomic and drought adaptive characteristics. The project will be executed by a multidisciplinary team operating from cornerstone centres for wheat breeding located in contrasting drought environments (from summer to winter rainfall), working in contrasting wheat gene pools, and with a wide range of relevant expertise (from genetics to remote sensing). A workshop targeted at mainly

breeding programmes in the CWANA region as well as Generation Challenge Programme (GCP) members will be held to demonstrate the breeder-friendly tools, the value of several drought adaptive traits per region and the physiological and genetic knowledge on ICARDA's elite lines.

49. Project No G4008.03: Precision phenotyping of the GCP spring wheat reference sample for drought

- *Duration: Jan 2008–Dec 2010; NCE: Mar 2011*
- *Total budget: USD 153,600*

Principal Investigator and lead institute
Susanne Dreisigacker, CIMMYT

Collaborating institutes and scientists

- CIMMYT – Matthew Reynolds, Yann Manes, Karim Ammar, Tom Payne, Hans-Joachim Braun, Jose Crossa, M. Warburton, M. Zaharieva
- INRA–M – Rachid Dahan, Nsarellah Nasrolhaq, Hassan Quabbou
- CIMMYT–Iran in collaboration with the Dryland Agricultural Research Institute (DARI) – M.R. Jalal Kamali
- SPII

Global genetic resources provide a fundamental source for further crop improvement. The GCP subprogram 1 aims to characterize the diversity of crop germplasm collections held by the CGIAR and its partners. This characterization includes an assessment of the genetic structure of the collections as well as the phenotypic variation associated with that structure. The ultimate goal is to provide access to sources of genetic diversity that may supply genes and alleles involved in key agricultural traits, especially stress tolerance. During the last three years, 3000 wheat accessions provided by major germplasm banks were characterized by CIMMYT and collaborators with 50 SSR markers for the development of reference samples including accessions maximizing neutral genetic diversity. In the first year of this project we will build up a seed stock for three developed international reference samples in wheat: the spring bread wheat, winter wheat and durum wheat reference samples. Seed will be stored in the CIMMYT wheat germplasm bank and made available for distribution. A drought specific spring bread wheat reference sample will be defined and characterized in multi-location trails for relevant agronomic traits, as well as physiological traits related to the main drivers of yield under drought. The same reference sample will be genotyped with high density DArT markers. This will allow associating the observed trait variation with the genotypic information in order to uncover QTL related to drought tolerance.

50. Project No G7009.01: Natural variation in the transcriptional regulation of drought responses in wheat

- *Duration: Jan 2009–Dec 2011*
- *Total budget: USD 820,100*

Principal Investigator and lead institute
Peter Langridge, ACPFG

Collaborating institutes and scientists

- ACPFG – Sergiy Lopato, Serik Eliby
- ICS/CAAS – Jizeng Jia, Xiuying Kong, Guangyao Zhao, Lifeng Gao
- CIMMYT – Matthew Reynolds

Drought stress can affect plants in many ways and plants have evolved complex response pathways that involve the activation or silencing of many genes and many interactions between regulatory proteins or compounds. Despite this complexity, our knowledge of the regulatory pathways is developing rapidly. Key to the drought response is the activity of transcription factors and associated proteins that lead to the activation of multiple pathways. Many of the regulatory sequences that these transcription factors bind to have been described and additional components, such as phosphorylation of the transcription factors are also known. When the expression level of the genes encoding these regulatory proteins is altered, for example in mutants or in transgenic plants, enhanced, or reduced, drought tolerance can be seen in the plants. This project will build on a well-established programme to isolate and evaluate these regulatory proteins to screen for natural variation in expression of regulatory genes shown to moderate the drought tolerance response in wheat. Several genes are already available for screening and more will be identified over the life of this project. A wheat germplasm collection assembled to encompass a wide section of variation in cultivated, land race and wild wheat will form the base for the screen. Tissues collected from field grown plants under both well-watered and drought stress conditions will provide the RNA for evaluation. The screen will give preliminary correlation of expression with drought tolerance. These results will be confirmed using introgression lines and other genetic populations. Where expression correlation is validated the germplasm plus diagnostic marker will be made available to breeders for introgression.

51. Project No G7010.02.01 Breeding and selection strategies to combine and validate quantitative trait loci for water-use efficiency and heat tolerance of wheat in China

- *Duration: Apr 2010–Mar 2014*
- *Total budget: USD 1,563,840*

Principal Investigator and lead institute
Ruilian Jing, NFCRI & ICS–CAAS

Collaborating institutes and scientists

- CAAS – Zhonghu He, Xinmin Chen, Xinguo Mao, Ang Li, Xiaoping Chang,
- HAAS–IDF – Xiumin Chen, Kejiang Li, Wenchen Qiao
- SAAS – Meirong Sun, Xiurong Li, Yongfeng Chai, Junling Zhang,
- XAAS–INBT – Zhenlu Wu, Zheru Fan, Yueqiang Zhang**,** Jianfeng Li
- CIMMYT – Matthew Reynolds
- PBI–UoS – Richard Trethowan

Good phenotypic data underpins genotyping and much of the breeding process. This project aims to assemble and integrate into breeding programs genetic diversity for WUE and heat tolerance from key sets of genetic resources (including drought-adapted cultivars, advance lines, elite landraces, products of inter-specific hybridization, from China, India, CIMMYT, ICARDA, Australia etc.). These materials will be shared with all partners so that analysis of trait and QTL by environment interaction and assessment of genetic gains associated with each trait can be evaluated in target breeding environments. Characterization of target experimental sites will be essential to interpret data, while training in standardized phenotyping protocols -of measuring drought and heat adaptive traits- will facilitate precise characterization in all environments as well as build human resource capacity.

QTLs have been identified for stress adaptation in a range of different wheat mapping populations. Many of the parents of these populations are adapted cultivars with good agronomic type. The challenge now is to combine these QTLs in a breeding program using marker assisted recurrent selection (MARS) and backcrossing. We propose combining existing QTLs for performance under moisture stress in elite Chinese backgrounds using a combination of empirical selection for yield, marker selection for genomic regions and selection for relevant physiological traits. The QTLs will be combined using MARS and backcrossing strategies. Validation of the QTLs will be conducted concurrently under managed stress in China and India as part of objective 1. The expectation is that the frequency of favorable alleles for tolerance to moisture stress will be improved.

52. Project No G7010.02.02: Molecular breeding and selection strategies to combine and validate quantitative trait loci for water-use efficiency and heat tolerance of wheat in India

- *Duration: Jul 2010–Jun 2014*
- *Total budget: USD 1,614,198*

Principal Investigator and lead institute
Vinod Prabhu, IARI–ICAR

Collaborating institutes and scientists

- IARI–ICAR – GP Singh
- ARI–ICAR – SC Misra
- JNKVV – PC Mishra
- NRCPB – NK Singh, TR Sharma
- PAU – VS Sohu, Parveen Chunneja, GS Mavi
- Collaborators : PBI–UoS, CIMMYT, ACPFG, ICAR

Precise phenotypic data underpins genotyping and much of the breeding process. This project aims to assemble and integrate into breeding programs genetic diversity for WUE and heat tolerance from key sets of genetic resources (including drought-adapted cultivars, advanced lines, landraces, products of inter-specific hybridization and mapping population parents from China, India, CIMMYT, ICARDA, Australia etc.). Many of these materials will be multiplied and provided by CIMMYT. The lines will be shared among the project partners so that analysis of trait and QTL by environment interaction and assessment of genetic gains associated with each trait can be evaluated in target breeding environments. Characterization of target experimental sites will be essential to interpret data, while training in standardized phenotyping protocols for measuring heat and drought adaptive traits and high throughput genotyping will facilitate precise characterization, in all environments, of traits and genotypic variation as well as build human resource capacity.

QTLs have been identified for stress adaptation in a range of different wheat mapping populations. Many of the parents of these populations are adapted cultivars with good agronomic type. The challenge now is to combine these QTLs in a breeding program using marker assisted recurrent selection (MARS) and backcrossing. We propose combining existing QTLs for performance under moisture stress in elite Indian backgrounds using a combination of empirical selection for yield, marker selection for genomic regions and selection for relevant physiological traits. The QTLs will be combined using MARS and backcrossing strategies. Validation of the QTLs will be conducted concurrently under managed stress in India as part of objective 1. The expectation is that the frequency of favorable alleles for tolerance to moisture stress will be improved.

7. Comparative genomics

53. Project No G3008.02: Improving grain yield on acid soils by the identification of genetic factors underlying drought and aluminium tolerance in maize and sorghum

- Duration: Nov 2008–Oct 2011
- Total budget: USD 857,366

Principal Investigator and Lead institute
Leon Kochian, CU/USDA–ARS

Collaborating Institutes and Scientists

- Embrapa Maize and Sorghum – Jurandir Vieira Magalhães, Claudia Guimaraes, Robert Schaffert, Reinaldo Gomide, Vera Alves, Flavio Tardin, Lauro Guimarães, Sidney Parentoni
- IGD–CU – Stephen Kresovich, Sharon Mitchell and Martha Hamblin
- MU – Sam Gudu
- Robert W Holley Center for Agriculture and Health, USDA–ARS – Owen Hoekenga, Jiping Liu, and Lyza Maron

Two of the most important limitations to crop production in sub-Saharan Africa are drought and acid soils. It is estimated that nearly 50% of the soils in this region suffer from insufficient water, while agriculture on nearly a quarter of the lands of sub-Saharan Africa are constrained by aluminium (Al) toxicity on acid soils. Because the primary symptom of Al toxicity is root growth inhibition and damage, resulting in compromised water and nutrient uptake, Al toxicity is a significant however poorly understood component of drought stress in Africa and other developing regions of the world. We already have assembled an effective research consortium that in ongoing GCP projects has identified a major sorghum Al tolerance gene which is now being exploited to improve sorghum Al tolerance in Africa. We also have recently identified several very promising candidate maize Al tolerance genes and QTLs that are poised to enter into a molecular breeding pipeline for assessing/validating their breeding values, and ultimately for generating maize genotypes with superior performance on acid soils. In this proposal, we will build upon this progress to generate maize and sorghum breeding lines with enhanced acid soil tolerance. Using our capability to phenotype maize and sorghum genotypes for drought tolerance in the field and a newly developed platform for high-throughput root imaging analysis, we also will begin to focus on the molecular and genetic determinants of maize and sorghum drought tolerance. This will involve the generation of new genetic resources in sorghum and maize, taking advantage of recent advances in sequencing and association genetics to develop a SNP genotyping array in sorghum and a maize breeding association panel. In particular the sorghum platform should become an useful community resource not only for drought and Al tolerance, but also for many other agronomically important traits. Finally, we will continue our field testing of improved sorghum and maize lines on acid soils in Kenya, and expand that programme to begin assessing the interplay between drought and Al tolerance on soils in Africa.

54. Project No G3008.04: Drought from a different perspective: Improved tolerance through Phosphorous acquisition

- *Duration: Nov 2008–Oct 2011; NCE: Oct 2012*
- *Total budget: USD 900,000*

Principal Investigator and lead institute
Sigrid Heuer, IRRI

Collaborating institutes and scientists

- IRRI – Stephan Haefele, Arvind Kumar, Abdelbagi Ismail
- UoPs and MPI of Molecular Plant Physiology, Germany – Bernd Mueller-Roeber, Slobodan Ruzicic
- JIRCAS – Matthias Wissuwa
- ICABIOGGRAD – Masdiar Bustamam, J Prasetiyono

Partner (without budget)
ZU – Ping Wu

Almost 50% of rice soils are currently deficient in phosphorous (P), yet resource-poor farmers in upland and drought-prone rainfed lowland environments typically apply little fertilizer. P deficiency therefore often coincides with drought and frequently aggravates its negative effects. Efforts to improve tolerance of either stress have typically been carried out separately without addressing nutrient x drought interactions. We have shown repeatedly that rice lines with the major P uptake QTL *Pup1* maintain higher root growth rates under P deficiency than lines lacking *Pup1*.We thus hypothesised that this effect would enhance drought tolerance. First results from pot experiments confirmed this hypothesis. Lines containing *Pup1* had 5-fold higher yield when P deficiency was combined with drought compared with 3-fold higher yield under P deficiency alone. The *Pup1* locus therefore represents a prime target in improving P deficiency and drought tolerance in rice. Previous analyses of tolerance mechanisms and genes associated with P uptake suggest that *Pup1* confers tolerance via a novel gene of unknown function. One objective of this project is to identify this

gene and to understand the underlying physiological mechanisms. An immediate product of these activities will be the development of allele-specific markers for marker-assisted selection (MAS). Understanding how *Pup1* exerts its positive effect will furthermore aid in identifying complementary genes and tolerance mechanisms that should be combined with *Pup1* to further improve dual tolerance of P deficiency and drought. For that purpose, we will evaluate the effect of four additional QTLs known to be associated with root growth, and tolerance of drought and P deficiency, respectively. QTLs that best complement *Pup1* will be pyramided through MAS using markers developed within the project. By this approach, it will be possible to develop tolerant varieties while preserving all important traits (eg. disease resistances, grain quality) of locally adapted varieties.

55. Project No G4008.10: Assessment of the breeding value of superior haplotypes for AltSB, a major Al tolerance gene in sorghum: linking upstream genomics to acid soil breeding in Niger and Mali (ALTFIELD)

- *Duration: Jan 2008–Dec 2010; NCE: Dec 2011*
- *Total budget: USD 205,200*

Principal Investigator and lead institute
Robert Schaffert, Embrapa Maize and Sorghum

Collaborating institutes and scientists

- INRAN – Maman Nouri, Soumana Souley, Magagi Abdou, Adam Kiari, Fatouma Beidari, Issoufou Kapran
- ICRISAT – Bettina Haussmann, Eva Weltzien Rattunde, Fred Rattunde
- EMBRAPA Maize and Sorghum – Jurandir Magalhães, FC Santos, J Herbert M Viana

Aluminium (*Al*) toxicity is a major agricultural constraint on acid soils, which comprise over 50% of the world's potentially arable lands, particularly jeopardising food security in the poorest regions of the globe. We have recently cloned a major sorghum Al tolerance gene, *Alt^{SB}*, which is a membrane transporter that confers Al tolerance via Al-induced citrate release into the rhizosphere. We have also gathered evidences that a thorough scan into the sorghum genetic diversity can be used to identify improved versions of *Alt^{SB}* that may yield significant agronomic advantages upon crop cultivation on acid soils. Thus, a research project was then designed and funded in the last competitive call from the Generation Challenge Programme to apply association genetics to identify superior haplotypes of *Alt^{SB}*, generate pre-breeding near-isogenic lines carrying these haplotypes, develop haplotype-specific markers and identify new Al tolerance genes in sorghum (ALTSORGHUM project). The concept note presented here aims at establishing the connection between the outputs of the ALTSORGHUM project and sorghum breeding programmes from Niger and Mali, ensuring that products will be properly validated in the specifically developed phenotyping sites and effectively used to attain higher and more stable yields in farmer's field on acid, Al toxic African soils.

56. Project No G7009.07: Cloning, characterisation and validation of AltSB/Al tolerance in rice

- *Duration: Oct 2009–Mar 2012*
- *Total budget: USD 250,000*

Principal Investigator and lead institute
Leon Kochian/Susan McCouch, CU and USDA–ARS

Collaborating institutes and scientists

- IRRI – Abdelbagi M Ismail
- ICABIOGRD – Sugiono Moeljopawiro

A primary limitation to crop production on acid soils, which make up as much as 50% of the world's arable lands, is aluminium (Al) toxicity. On acid soils Al toxicity results in rapid damage and growth inhibition of root systems, which leads to significant yield reductions due to inhibited uptake of water and nutrients. Rice is the most Al tolerant cereal, yet Al toxicity is still a major limitation to rice production in both rainfed lowlands and uplands. In this proposal we will take advantage of our recently cloned sorghum Al tolerance gene that is a member of the MATE family of organic solute transporters, to identify rice homologs that are candidate tolerance genes. In rice, we have conducted a computational analysis of the MATE family and have identified 5 MATE genes that are co-localised with previously identified Al tolerance QTL. Here we will test them as candidate Al tolerance genes using T-DNA rice knockout lines. If these homologs are not functional in rice, complementary approaches are already in place. We are poised to fine-scale map and clone a novel major rice Al tolerance QTL. Furthermore, by the fall of 2009, we will have completed whole genome association mapping of rice Al tolerance, which will also identify novel rice genomic regions harboring Al tolerance loci. These will be a resource for the rapid cloning of novel rice *Al* tolerance genes.

57. Project No G7010.03.01: Cloning, characterisation and validation of PUP1/P efficiency in maize

- *Duration: Apr 2010–Mar 2014*
- *Total budget: USD 755,617*

Principal Investigator and lead institute:
Leon Kochian, USDA–ARS/Cornell University

Collaborating institutes and scientists:

- USDA–ARS/Cornell – Lyza Maron, Miguel Pineros, Jiping Liu, Randy Clark, Ed Buckler
- EMBRAPA Maize and Sorghum – Claudia Guimarães, Sidney Parentonia, Jurandir Magalhães, Vera Alves, Maria Jose Vasconselos, Sylvia Sousa, Roberto Noda
- JIRCAS – Mathias Wissuwa;
- IRRI – Abdel Ismail, Sigrid Heuer
- Moi University/KARI – Sam Gudu

A multidisciplinary team involving USDA, Embrapa, JIRCAS, IRRI and MOI University will work on the successful implementation of the identification and characterization of genes associated with maize P efficiency (tolerance to low P). Bioinformatics will be used to identify homologues of the rice *Pup-1* gene in maize and a set of markers for these genes will be developed. An Embrapa inbred line panel that was developed for breeding for P efficiency be phenotyped in the field for P efficiency (grain yield under contrasting P conditions and in the greenhouse/lab for root architecture traits; also the Buckler association panel will be phenotyped for P efficiency and root architecture traits in the green house/lab at USDA-Cornell. A linkage map will be developed using SSR, STS and SNP markers in 150 RILSs from the cross of a highly P efficient tropical maize line (L3) with a P inefficient line (L22). Top crosses of these RILs which were developed from a cross of L3xL22 with a P inefficient tester line (L53), will be field phenotyped in Kenya and Brazil on high P (25 ppm P) and low P (<6ppm P) soils.QTLs for P acquisition, internal P efficiency and root architecture traits will be mapped in this cross, as well the *Pup-1* homologues, in order to verify the co-segregation of *Pup-1* homologues with QTLs for different P-efficiency traits. Inheritance studies for root morphology traits will be conducted using seven different generations of the cross LS x L22 (P1, P2, F1, F2, BC1-L3, BC1-L22, BC2-L3 and BC-L22). Association analysis using Embrapa's elite inbred lines panel and the Buckler maize association panel will be carried out to validate candidate genes, and also characterization of near isogenic lines developed from BC2F2 (L3xL22) xL22xL22) for P efficiency.

58. Project No. G7010.03.02: Cloning, characterisation and validation of AltSB/Al tolerance in maize

- *Duration: Apr 2010–Mar 2012*
- *Total budget: USD 250,000*

Principal Investigator and lead institute:
Claudia Guimarães, Embrapa Maize and Sorghum

Collaborating institutes and scientists:

- Embrapa Maize and Sorghum – Jurandir Magalhães, Sidney Parentoni, Lauro Guimarães, Andrea Carneiro, Newton Carneiro, Robert Schaffert, Sylvia Sousa, Vera Alves
- Robert W. Holley Center for Agriculture and Health, USDA-ARS/Cornell University – Leon Kochian, Lyza Maron, Jiping Liu, Miguel Pineros, Ed Buckler
- Moi University – Sam Gudu

Over 50% of the world's potentially arable lands consist of acid soils, where aluminum (Al) toxicity is the primary factor limiting maize yield, one of the world's most important food crop. This problem is particularly important for low input agricultural systems, which includes a large portion of the farmers in Sub-Saharan Africa and as well as small farm holders in other developing country areas. Al tolerance is a quantitatively inherited trait in maize, a crop that displays considerable variation for this trait, as well a highly complex genome organization. Taking advantage of the Al tolerance gene cloned in sorghum (*Alt^{SB}*) and findings from our recent research in maize, where two major Al tolerance QTLs were co-localized with *Alt^{SB}* homologues (*ZmMATE* genes), we will characterize and validate functional *ZmMATE* genes or QTLs conferring superior Al tolerance in maize. This strategy will be based on our genetic resources already available as near isogenic lines for both QTLs, segregating populations and crosses between Brazilian sources of Al tolerance and Kenyan adapted germplasm. This structured germplasm, as well as newly developed crosses, will be subjected to molecular, physiological and field evaluations in order to accomplish the functional validation of candidate genes or QTLs for improving Al tolerance in different tropical maize germplasm. Our Challenge Initiative will involve Embrapa, USDA/Cornell University, Moi University and KARI, a research group with a long history of successful partnership on maize and sorghum Al tolerance. The research findings from this project will both greatly increase our understanding of the molecular and genetic basis for cereal Al tolerance, and more importantly, will provide the basic materials for molecular breeding programs focusing on improving maize production and stability on acid soils in Africa and other developing countries.

59. Project No G7010.03.03: Establishing a molecular breeding program based on the aluminum tolerance gene, AltSB, and the P efficiency QTL, Pup-1, for increasing sorghum production in Sub-Saharan Africa

- *Duration: Apr 2010–Mar 2014*
- *Total budget: USD 545,492*

Principal Investigator and lead institute
Eva Weltzien, ICRISAT–Mali

Collaborating institutes and scientists:

- Moi University/KARI, Kenya – Sam Gudu, Dickson
- Embrapa Maize and Sorghum, Brazil – Robert Schaffert, Jurandir Magalhaes, Alvaro V. Resende, João H. Viana, Claudia T. Guimarães, Sylvia M. Souza and Vera Alves
- Cornell University (Institute for Genomic Diversity), USA – Theresa Fulton, Sharon Mitchel
- USDA-ARS Robert Holley Center for Agriculture and Health, USA – Leon Kochian
- ICRISAT – Fred Rattunde, Bettina I.G. Haussmann
- INRAN Niger – Soumana Souley

In Africa, a combination of soil constraints and a lack of adapted crop cultivars are clearly two of the most important factors responsible for low grain yield. Low productivity is a serious problem in many parts of Africa where sorghum is a staple food supporting millions of the rural poor. Within the SorghumPup1 project in this Comparative Genomics Challenge Initiative we will attempt to validate homologs of the major rice P uptake QTL, *Pup1*, functioining as P deficiency tolerance genes in sorghum, and investigate a similar role for the major Al tolerance gene, Alt_{SB}. If successful, we will develop molecular markers for *Pup1* validated homologs for marker assisted selection for P deficiency tolerance in sorghum. We are also developing and validating gene-specific markers for Alt_{SB} within other competitive GCP projects. The project described here implements a molecular breeding program targeting Mali, Niger and Kenya using random mating ms3 populations (RMPs) for the eventual development of improved varieties and breeding materials with Al tolerance and improved performance under low P stress. These two target traits largely underlie adaptation to acid soil and low phosphorus conditions. Also included is a capacity building component to be held at Moi University for training scientists from Mali, Niger, and Kenya and nearby countries to establish the necessary skills for sustainable molecular breeding activities. This project will build upon the progress achieved in the GCP commissioned project, "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). The results will be validated in Kenya, Mali and Niger as well as in Embrapa Maize and Sorghum (Embrapa MS) using S_1 and S_2 selected progenies from RMPs in phenotyping sites specifically developed for this purpose. The ultimate goal is to develop the capacity and necessary tools in African institutions for stacking desirable genes in the development of elite multiple trait cultivars and to develop breeding materials that show superior performance in soils where Al toxicity and low P availability can cause serious reductions in productivity.

60. Project No G7010.03.04: Developing rice with dual tolerance of phosphorus deficiency and aluminum toxicity: marker-assisted pyramiding of Pup1 with novel tolerance QTLs

- *Duration: Apr 2010–Mar 2014*
- *Total budget: USD 512,590*

Principal Investigator and lead institute:
Sigrid Heuer, IRRI

Collaborating institutes and scientists

- JIRCAS – Matthias Wissuwa
- ICABIOGRAD – Masdiar Bustamam
- IRRI – Abdelbagi Ismail

Phosphorus (P) deficiency is a widespread problem, especially in rain-fed environments, where it is often accompanied by other stresses such as drought, low pH, and Al and Fe toxicity. The application of P fertilizer can improve productivity on such problem soils; however, resource poor farmers generally lack the necessary resources. We have identified a major QTL (*Pup1*) for tolerance of P deficiency and are in the process of cloning the underlying gene. The development of *Pup1* varieties by marker-assisted backcrossing (MABC) is well advanced and *Pup1* versions of three upland and two irrigated varieties will be available in 2010. These breeding lines and the *Pup1* marker information (SNP, SSR, and STS) will be distributed to IRRI NARES partners in Asia and Africa. Assistance to these partners in the implementation of screening protocols and marker technology for the development of local *Pup1* varieties will be provided. Likewise, information on the *Pup1* candidate genes and their function generated within a parallel GCP project (G3008.04) will be made available for the cloning of *Pup1* in sorghum, maize, and other crops.

To further improve yield in rainfed environments, it will be necessary to combine *Pup1* with tolerance of other stresses, most importantly drought and Al toxicity. Two drought QTLs available at IRRI are at an advanced stage of validation and molecular marker development.

One of the main objectives of this project is therefore to apply the genetic information and marker technology available for *Pup1* and the drought QTLs for the development of rice varieties with dual tolerance of both stresses. For the development of rice with tolerance of Al toxicity, an existing mapping population derived from a cross with a highly Al-tolerant Indonesian upland variety will be advanced. Molecular markers for the fine-mapped QTL will be used to combine tolerance of the three targeted abiotic stresses by QTL pyramiding into relevant varieties. The MABC-derived breeding lines developed within this project will be widely distributed to NARS in Asia and Africa using established linkages and partnerships, and existing distribution channels.

61. Project No G7010.03.05: Marker-assisted backcrossing for improving phosphorous-use efficiency and tolerance to aluminium toxicity via Pup-1 and AltSB genes in maize

- *Duration: Apr 2010–Mar 2014*
- *Total budget: USD 410,080*

Principal Investigator and lead institute:
Samuel Gudu, Moi University/KARI, Kenya

Collaborating institutes and scientists

- Embrapa Maize and Sorghum – Claudia Guimaraes, Sidney Parentoni, Jurandir Magalhaes, Vera Alves, Sylvia Sousa, Lauro Guimaraes
- JIRCAS – Mathias Wissuwa
- IRRI – Abdel Ismail, Sigrid Heuer
- USDA-ARS/Cornell – Leon Kochian, Lyza Maron, Miguel Pineros, Jiping Liu, Ed Buckler
- KARI Kitale – Dickson Ligeyo

Phosphorus deficiency and aluminum toxicity are two of the most important constraints responsible for low maize productivity on acid soils worldwide, and particularly in Africa where because of resource limitations low input agriculture is the norm. In this project we will use molecular breeding approaches as well as conventional breeding to speed up development of maize varieties adapted to the acid soils of Africa. The sources of tolerance to Al toxicity to be used include: two major Al tolerance QTLs mapped in maize RIL populations derived from Cateto that appear to be homologues of the sorghum Al tolerance gene (*Alt^{SB}*) as well as highly tolerant inbred lines from Kenya (203B, CON 5 and K4) we have identified, that as of yet we have not characterized for Al tolerance genes/QTLs. For P efficiency, in the related project led by Dr. Kochian, we will use the *Pup-1* locus associated with rice P efficiency and the candidate *Pup-1* genes identified by our IRRI/JIRCAS collaborators, to identify homologues in maize and validate their function as P efficiency genes/QTLs, using genetic and genomic-based approaches. As we expect that markers flanking the maize homologues of *Pup-1* will be available in the beginning of the project, our approach will start with the phenotypic selection based on field data in Kenya using crosses of Kenyan germplasm with a major Brazilian source of P efficiency, L3. Then, the markers developed in the other Challenge Initiative proposals will be screened in the crosses and lines from Kenya and Brazil for further validation. MABC is proposed to introgress *Alt^{SB}* homologues into locally adapted lines from Kenya and Brazil. In addition, synthetics and single cross hybrids pyramiding Al tolerance and P efficiency will be generated and evaluated in Kenyan acid soils, which are expected to exhibit superior agronomic performance on these acid soils. The research proposed here is well connected to the other two CI maize proposals, and should result in significant improvements in maize yields on acid soils in Kenya and other African countries, as well as in Brazil.

62. Project No G7010.03.06: Improving phosphorus efficiency in sorghum by the identification and validation of sorghum homologues for Pup1, a major QTL underlying phosphorus uptake in rice, and identification of other P efficiency QTLs

- *Duration: Apr 2010–Mar 2014*
- *Total budget: USD 804,931*

Principal Investigator and lead institute:
Jurandir Magalhães, Embrapa Maize and Sorghum

Collaborating institutes and scientists:

- Embrapa Maize and Sorghum (Brazil) – Robert Schaffert, Claudia Guimarães, Vera Alves, Maria Jose Vasconcelos, Sylvia Morais de Souza, Alvaro Vilela Resende, João Herbert Moreira Viana
- USDA-ARS Robert W. Holley Center for Agriculture and Health (USA) – Leon Kochian, Jiping Liu, Randy Clark
- Cornell University (Institute for Genomic Diversity) – Steve Kresovich, Martha Hamblin, Sharon Mitchell, Theresa Fulton
- INRAN (Niger) – Soumana Souley
- Moi University (Kenya) – Sam Gudu
- ICRISAT – Eva Weltzien and Fred Rattunde
- JIRCAS – Matthias Wissuwa
- IRRI – Sigrid Heuer

Low productivity due to soil constraints and a lack of properly adapted crop cultivars is a serious problem in many parts of Africa, where sorghum is a staple food

supporting millions of the rural poor. *Pup1* is a major QTL located on rice chromosome 12 that underlies phosphorus efficiency and has the potential to increase P acquisition efficiency in other cereals. Research findings from a long term collaboration between IRRI and JIRCAS has resulted in the fine mapping of the *Pup1* locus to a ~150 Kb region on chr 12, and 2-4 high quality *Pup1* candidate genes have been identified. Taking advantage of the complete sequence of the sorghum genome, we will establish a framework based on comparative genomics to identify sorghum *Pup1* homologs and will validate their role as *bona fide* genes underlying tolerance to P deficiency. This research will be based primarily on association analysis to identify statistically significant associations between allelic variation for *Pup1* candidate genes and P efficiency assessed both in the field and under controlled conditions in the laboratory and greenhouse. Positive associations will be validated by bi-parental mapping and analysis of near-isogenic lines. The Al tolerance gene, Alt_{SB}, is an Al-induced root citrate efflux transporter and citrate can mobilize P that is fixed in the soil clay fraction and increase its availability for root P uptake. Therefore, we will use the same approach to study a possible synergistic role of Alt_{SB} in increasing P uptake into sorghum roots. The genetic framework that will be developed for this research will also be useful for identifying other novel QTL related to P efficiency, which can then be deployed into a molecular breeding platform (see sorghum marker assisted breeding project based on Alt_{SB}/*Pup1* in this Challenge Initiative - SorghumMB) should functional *Pup1* homologs not be found in sorghum. Thus, this project sets the foundation for a molecular breeding program targeting marginal soil areas in southern Mali, Niger and Kenya and other areas of Sub-Saharan Africa to improve food security and farmer's income.

II. Thematic projects

Theme 1 – Comparative and applied genomics

63. Project No G4008.07 Genomic reources and mapping populations developed and assembled for pearl millet to enable trait/ gene identification

- *Duration: Jan 2008–Dec 2009 (final report submitted in 2011)*
- *Total budget: USD 296,429*

Principal Investigator and lead institute
C Tom Hash, ICRISAT

Collaborating institutes and scientists

- ICRISAT – FR Bidinger, V Vadez, RK Varshney, T Nepolean and S Senthilvel
- AICPMIP–ICAR – IS Khairwal
- Central Arid Zone Research Institute (CAZRI) – OP Yadav
- Rajasthan Agricultural University, Agricultural Research Station Beechwal (SKRAU) – PC Gupta
- ILRI – Michael Blümmel/International Livestock Research Institute

Pearl millet (*Pennisetum glaucum*) is a dual-purpose grain and fodder crop that is an essential component of dryland crop-livestock production systems of sub-Saharan Africa (e.g., Nigeria, Niger, Burkina Faso, Mali, Senegal, Sudan, and Chad) and South Asia (e.g., India) in areas that are too hot, too dry, and/or have soils that are too acid or too infertile for reliable production of maize, sorghum or any other cereal crop. The crop is also increasingly used as the mulch component of sustainable minimum tillage crop production systems in the humid tropics (e.g., Brazil) , where its acid soil tolerance, deep root system, and high vegetative growth rates under high temperature conditions often make it the best option for retrieving soil nutrients from depth, smothering weeds, and producing a mulch that protecting the soil surface from erosion by rain drop impact or surface water movement. There are limited genomic tools available for this orphan crop despite pearl millet being the 6th most important cereal crop globally and being likely to be, along with sorghum, an important source of genes and alleles that will enable plant breeders to engineer other crops (e.g., rice, wheat and maize) to better tolerate higher temperatures and increased frequencies of drought stress that are predicted to arise from on-going global warming.

This project proposes to strengthen genomic resources for pearl millet, developing cDNA libraries from the parents (841B-P3 and 863B-P2) of a well-characterized pearl millet drought tolerance mapping population, identifying EST sequence polymorphisms between the parents of this population, and mapping these polymorphisms using the 150 RIL progenies of this population. The augmented linkage map of this population, combined with information on the positions in the completed sorghum and rice genome sequences of homologues of the pearl millet ESTs from which these newly mapped markers are derived, be used to refine the rice-pearl millet comparative map and develop at sorghum-pearl millet comparative map. We will then use the additional markers mapping to pearl millet linkage group 2 to better define the position of a major drought tolerance QTL from 863B, using available segmental substitution lines (developed in a DBT-supported project) for this genomic region in the genetic background of elite seed parent maintainer line 841B (using funding from a BBSRC project that will start in April 2008).

In addition, we will use STS and SSR markers to skeleton linkage map two new conventional biparental pearl millet mapping populations of random inbred lines, and conduct initial testcross hybrid evaluations of these populations for terminal drought stress tolerance (measured in terms of grain and stover yield maintenance under stress conditions) and grain and stover nutritional value (measured in terms of digestibility and metabolizable energy content). Finally, we will advance eight additional pearl millet RIL populations to F7 inbred lines that will be ready for map saturation with DArT markers in a future project, which would permit development of a high density consensus linkage map for pearl millet.

Theme 2 – Integrated crop breeding

64. Project No G4007.07: Marker-assisted selection for sweet potato virus disease (SPVD) resistance in sweet potato germplasm and breeding populations

- *Duration: Aug 2007–Jul 2009; NCE: Jun 2011*
- *Total budget: USD 379,800*

Principal Investigator and lead institute
Wolfgang Grüneberg, CIP

Collaborating institutes and scientists

- CIP – Marc Ghislain, Roland Schafleitner, CIP,
- NARI – Robert Mwanga

Sweetpotato is an important food crop and due to extreme high pro-vitamin A content orange fleshed sweetpotatoes (OFSP) can alleviate vitamin A deficiency in many regions of the world. However, sweetpotato virus disease (SPVD) is often causing serious yield losses, especially in high virus pressure zones within Sub-Saharan Africa, where OFSPs are often not sufficient SPVD virus tolerant. The disease occurs after infection of two viruses: the sweetpotato feathery mottle virus (SPFMV) and the sweetpotato clorotic stunt virus (SPCSV). The SPCSV is the more problematic component of SPVD, because yield losses due to SPFMV - without SPCSV infection – are low and SPFMV resistance of sweetpotato breaks after the plant is infected by SPCSV. There was no SPCSV resistance known until recently in the CIP germplasm one SPCSV resistant clone was found (termed "Resitan"). This resistance is a new option to foster OFSP production, but marker assisted selection (MAS) should be applied. It is nearly certain that this new resistance to SPVD is recessive and inherited by one or two genes. This will be confirmed in the first step of this project by developing the required populations (Resistan x Resitan and OFSP parents x Resistan). Marker associated with the recessive allele(s) conferring SPVD resistance are an ideal tool to identify clones in breeding populations and germplasm, which carry the recessive allele(s) with high frequency. It should be noted, that sweetpotato is hexaploid and highly heterozygous and this makes resistance breeding for a recessive inherited characteristic without MAS very slow. In the second step markers for SPVD will be developed, by using backcross populations, AFLP, and SSR or SNP markers. In a third step OFSP breeding populations and the CIP germplasm will be screened with the marker system to increase the use of parental material segregating for the phenotype "SPVD Resistance".

65. Project No G4008.05: Connecting performance under drought with genotypes through phenotype associations

- *Duration: Jan 2008–Dec 2010; NCE: Jun 2012*
- *Total budget: USD 467,676*

Principal Investigator and lead institute
Arvind Kumar, IRRI

Collaborating institutes and scientists

- IRRI – Ken McNally, Arvind Kumar, Rachid Serraj, Hei Leung
- CIRAD – Michael Dingkuhn, Delphine Luquet, Brigitte Courtois
- WARDA – Mande Semon
- Indira Ghandi Krishi Viswavidyalaya – RL Pandey, S Verulkar, Prabha Dongre
- Central Rice Research Institute, Cuttack, Orissa, India – Padmi Swain
- Tamil Nadu Agricultural University – S. Robin, M. Raveendran
- BIOTEC – T. Theerayut

Water stress is frequently the main limitation of rice productivity and yield stability in rainfed systems. Most "mega-varieties" that are grown over vast areas of South and Southeast Asia are highly susceptible to water deficits. Yet, within the primary rice gene pool resides a large amount of genetic diversity for abiotic stress tolerance (Ali et al 2006). Indeed, drought-tolerant landraces are in the parentage of many of the megavarieties. Rapid advances in molecular biology provide great potential to harness this genetic diversity within rice but, to fully exploit this information, by relating allelic variation to agronomic performance, an in-depth phenonomics initiative is necessary. By developing a standardized, high-throughput, precise phenotyping strategy, employed across a range of drought environments, valuable data sets on performance under field drought stress on a large reference set of accessions will be generated. This information can be combined with data obtained from new high-throughput SNP platforms in association studies linking field performance to DNA sequence variation (McNally et al 2006). This project will build on individual partners' phenotyping capabilities to develop a large-scale phenotyping program incorporating standardized protocols, environmental characterization, and new analytical tools for rapid phenotypic analysis. Successful application for breeding programs must target developmental stages during which yield is sensitive to drought. The greatest yield losses occur when drought stress occurs at the

same time as irreversible reproductive processes (Cruz and O'Toole 1984, Boyer and Westgate 2004). This project will focus on reproductive-stage stress, with specific emphasis on grain yield and key physiological traits related to grain yield decline caused by stress.

66. Project No G4008.15: Developing potato cultivars adapted to Southern Africa countries

- *Duration: Jan 2008–Dec 2009; NCE: Nov 2011*
- *Total budget: USD 209,868*

Principal Investigator and lead institute
F. Vilaró, INIA Uruguay

Collaborating institutes and scientists

- INIA Chile – J. Kalazich
- INTA Balcarce – M. Huarte
- EMBRAPA – Arione Pereira
- IIAM Mozambique – Carolino Martinho
- DARTS Malawi – Obed J. Mwenye
- CIP Malawi – Paul Demo
- CIP Perú – Stef de Han

Potato is one of the highest value crops and provides high nutritious food in a very short growing period. Many developing countries including non Andean South American and in Southern Africa, grow long day adapted Tuberosum potatoes, almost year round. Breeding programs in the northern hemisphere have developed varieties from this same Group, with high commercial quality. However, most of these varieties are mainly adapted to temperate climate and lack resistance to diseases and pests making potato highly dependent on external inputs. They also require well established seed programs and are mainly adapted just to one crop per year. Adequate planting material is usually expensive and difficult to obtain in appropriate condition for most developing countries. Short day germplasm and landrace varieties from the Andes, have valuable traits but adapt poorly to long days and or high temperature. Genetic resistance sources for various diseases have been incorporated in advanced potato germplasm from participant non Andean South American countries. These countries cover a wide region of environments, from southern temperate Chile to subtropical Brazil, possessing germplasm with a wide range of adaptation. In this region, with the exception of the most southern area, potatoes are grown on a two crop per year regime. Several varieties significantly improved on quality aspects have been released and are being grown in and out of the region. This project will evaluate advanced germplasm from this region, along with CIP improved germplasm on Southern Africa (Malawi and Mozambique). Microarray DaRt technology analysis will be employed to analyze population structure of germplam from participating programs. Secondarily, easy to use molecular markers will be validated and applied in Latin America helping to characterize degree and stability of disease resistance. GIS site characterization will be employed to determine potential variety deployment in given locations. It is anticipated that promising germplasm sources and very valuable genotypes adapted to various growing constraints, could be identified and multiplied for releasing new cultivars. This would promote a more sustainable crop for helping resource poor farmers in these countries.

Theme 3 – Crop information systems

Project sfor this theme are listed below under Integrated breeding system

Theme 4 – Capacity building

67. Project No G4006.36: Capacity-building and research project

- *Duration: Jan 2007–Dec 2011*
- *Total budget: USD 500,312*

Principal Investigator and lead institute
Mark Laing, ACCI/UKZN

Collaborating institutes and scientists

- ACCI/UKZN – Jedidah W Danson
- 10 countries in east and southern Africa

We are working in 14 countries in East and Southern Africa, with National Agricultural Research programmes, together with AfricaRice, CIAT, IITA, CIMMYT, ICRISAT and BECA

In this Project, the University will conduct capacity building and research Activities in sub-Saharan Africa in the disciplines of plant breeding and molecular biology. These Activities shall be conducted with the ultimate aim of enhancing food security and plant genetic diversity for the benefit of resource-poor people within sub-Saharan Africa.

The University shall serve as Lead institute on this project. Its principal investigator shall be Mark Laing (or a mutually agreed upon substitute for Dr. Laing) of the African Center for Crop Improvement (ACCI) on the University's Pietermaritzburg campus. The principal investigator shall have primary responsibility for ensuring that the University complies with this Agreement.

One of the major capacity building Activities that the University will carry out in this Project is aimed at producing highly-trained Ph.D. scientists from sub-Saharan Africa. In order to accomplish this goal, among other things, the University will use the Grant to recruit and employ a full-time professor of molecular biology, who will teach and mentor Ph.D. students in the discipline of plant breeding and conduct research on food security crops. The University shall direct the Professor to carry out the Activities, and shall be responsible for producing the outputs and products, set forth in this Appendix I.

The University will also identify a "molecular toolbox" – an inventory of molecular tools available for important crops and traits in Africa, and identification of tools that would be particularly useful if developed), to be made broadly available in sub-Saharan Africa. The University will also collaborate with a number of institutes and scientists, including Generation Challenge Programme Consortium Members, Rockefeller Foundation, Bill and Melinda Gates Foundation; University of Illinois, Urbana-Champagne, University of Cape Town, University of the Witwatersrand, RIKEN, Japan; and the University of Kansas. As the lead institution for this project, the University shall have overall responsibility for contracting with, and coordinating the activities of, those other institutes and scientists. The University will also provide support to the implementation of SP5 activities in the region as requested (e.g. assessment of existing and needed capacity at selected NARS institutions, support to training events in the region).

68. Project No G4008.37: PhD in plant breeding training at the West Africa Centre for Crop Improvement

- *Duration: Mar 2008–Feb 2014*
- *Total budget: USD 667,054*

Principal Investigator and lead institute
EricY Danquah, UoGh

Collaborating institutes and scientists

- UoGh – S Kwame Offei
- CU – Vern Gracen

It has long been recognised that capacities in plant breeding, including both conventional and modern technologies, in most developing countries are neither sufficient nor properly integrated to fully capture the benefits of the plant genetic resources that are conserved. Today, sub-Saharan Africa remains the only region that may not meet the millennium development goal of eradicating extreme poverty and hunger by 2015. New high-yielding varieties of staple crops with tolerance to biotic and abiotic stresses can help provide food security for increasing populations in the sub-Saharan Africa. A critical mass of a new generation of plant breeders with knowledge in both traditional field based selection methods and emerging laboratory based tools and techniques is needed to develop and provide the necessary high yielding varieties to farmers.

The University of Ghana has received a project support grant of $5.78 from the Alliance for a Green Revolution in Africa to establish a West Africa Centre for Crop Improvement (WACCI). WACCI, a collaboration between

the University of Ghana and Cornell University, started operating in the University of Ghana in June 2007 as an autonomous institution in the College of Agriculture and Consumer Sciences. WACCI is dedicated to the training of plant breeders with skills in genetic improvement of the staple crops of the west and central Africa sub-region. Plant breeding is an integrative science that combines the knowledge, information and expertise from a range of disciplines to produce scientists with the capacity to undertake research for germplasm enhancement and development of improved cultivars of the staple crops. The first cohort of eight students enrolled in February 2008. They will undertake two years of course work in the University of Ghana and three years of field research in their local research institutions. WACCI intends to increase its enrollment to ten students a year and to accommodate two additional students in 2009 and 2010 who would be sponsored by Generation Challenge.

69. Project No G4009.08: Plant Breeding: concepts & methods – a Learning Module

- *Duration: Nov 2009–Jun 2011*
- *Total budget: USD 25,058*

Principal Investigator and lead institute
Theresa Fulton, Cornell University

Collaborating institute and scientist

- CropGen International – Robert Koebner

A number of new training materials have recently been developed by the GCP, training courses held, and software and bioinformatics tools developed, all directed towards facilitating the use of molecular markers and genomic information by plant breeders. However, all these materials have been based on the assumption that a working knowledge of core plant breeding concepts is already firmly in place. Without this, any positive improvement in plant breeding practice, with or without molecular markers, is unlikely, and much of the effort in exposing trainees to "molecular breeding" will have been wasted. Furthermore, the growing cadre of scientists trained in molecular biology, genetic diversity and other related fields, all too often lack any appreciation or knowledge of basic plant breeding techniques, thereby limiting the potential for fruitful interaction and collaboration between disciplines.

The proposed learning module aims to fill this gap, via the development of a resource covering basic plant breeding concepts and techniques. It seeks, in much the same way as previous SP5 modules have done, to complement, rather than to replace more conventional learning materials; and to supply the content in a way which will be readily accessible for institutions which lack the resources to support comprehensive and up-to-date printed literature. The module will be useful either as a teaching tool or as a self-learning tutorial.

Theme 5 – Product delivery

70. Project No G4007.01: Genotyping validation of the GCP reference sets

- *Duration: Jan 2007–Dec 2008; NCE: Oct 2011*
- *Total budget: USD 379,280*

Principal Investigator and lead institute
Jean-Francois Rami, Agropolis–CIRAD

Collaborating institutes and scientists

- Validation labs subcontracted by Agropolis–CIRAD
- ICRISAT – HD Upadhyaya, T Hash
- IRRI – K McNally
- CIP – M Ghislain, W Gruneberg
- CIMMYT – M Zaharieva, S Dreisigacker
- CIAT – M Fregene, M Blair
- ICARDA – M Baum
- Bioversity – N Roux
- Agropolis–CIRAD – L Baudouin
- IITA – R Asiedu
- UoC–Riverside – J Ehlers

The scientific community involved in the SP1 sub-programme of the Generation Challenge Programme is about to deliver one of the biggest efforts of characterisation of genetic diversity on 21 crop species. This characterisation was based on the utilisation of microsatellite markers, which constitute a powerful marker system for such a purpose. However, this work was by nature composite, involving different species and different partners using different technologies. For each crop, one of the main products of this exercise is a reference set of representative germplasm to serve as a material for international coordination in the future. The present project proposes to assess the different microsatellite datasets produced in SP1 by having a subsample of germplasm accessions re-genotyped by an external genotyping facility (service provider). This subsample will be the reference set, so that the new data will also serve to validate and certify the genotypic information attached to the reference set. This genotyping validation project will be connected to the management of the genetic material constituting the reference sets. As an output, stabilised materials specifically handled as genetic stocks by gene bank curators and associated to validated genetic diversity data will be available.

71. Project No G4010.02: Potential Benefits of Marker-Assisted Selection Technologies on Wheat, Sorghum, Cassava, and Rice, and of the Molecular Breeding Platform

- *Duration: May 2010–Dec 2011; NCE: Jun 2012*
- *Total budget: USD 157,602*

Principal Investigator and lead institute
George W Norton, Virginia Polytechnic Institute (VPI)

Collaborating institutes and scientists

- IFPRI – Stan Wood

This project will assess the potential benefits versus risks of failure of ongoing Challenge Initiative projects on wheat (India, China), sorghum (Mali, Ethiopia), cassava (Nigeria, Ghana, Tanzania), rice (Benin, Mali, Burkina Faso, Nigeria). Assessment of their relative benefits in several dimensions will be completed, including their economic value if successful, their risks of failure, and their potential for alleviating malnutrition. This assessment will assist the Management Team of the Generation Challenge Program in prioritizing research resources. It may also provide information that can be presented to donors in support of the program. The project will assess the potential benefits of Molecular Breeding Platform services, activities, and applications for selected Challenge Initiative (CI) user cases. This assessment will provide the Management Team and donor with a prediction of the economic value of the IBP for the years ahead. It will indicate its value for specific cases, with and without the IBP.

72. Project No G4011.02: Seed increase for interspecific chromosome segment substiution lines (CSSSLs) of rice at CIAT

- *Duration: Apr 2011–Sep 2011*
- *Total budget: USD 11,500*

Principal Investigator and lead institute
M Lorieux, Agropolis–IRD/CIAT

Operational cost for multiplying an interspecific population of 60 lines in "normal conditions" is around 500 US$. In order to multiply the available populations (*O. sativa* x *O. glaberrima*, *O. sativa* x *O. rufipogon*, *O. sativa* x *O. meridionalis*), we'd also need a full time technician for about 6 months (around 9 k US$).
This activity is part of the project entitled "Exploring Natural genetic variation: developing genomic resources and introgression lines for four AA genome rice relatives"

III. Service Component – Integrated Breeding Platform

Integrated Breeding Platform portal and helpdesk

G8009: Integrated Breeding Platform

- *Duration: Jul 2009–Jul 2014*
- *Total: USD 20,979,939*

Principal Investigator and lead institute
Graham McLaren, GCP

Collaborating institutes and scientists

- GCP – Graham McLaren, Larry Butler, Xavier Delannay, Ndeye Ndack Diop, Antonia Okono, Chunlin He, Arllet Portugal, Delphine Fleury
- AAFC – Fran Clarke, Shawn Yates
- CIMMYT – Jose Crossa, Hector Sanchez
- ICRISAT – Trushar Shah
- WUR – Fred van Eeuwijk, Marcos Malosetti
- CSIRO – Scott Chapman
- Agropolis–INRA – Alain Charcosset, Laurence Moreau
- UoQ – Mark Dieters
- CIMMYT/CAAS – Jiankang Wang
- IRRI – Guoyou Ye, C. Liang
- Agropolis–CIRAD – JC Glaszmann
- Bioversity – E Arnaud
- SGRP – D Williams
- CU – Theresa Fulton, T Setter
- CIAT – G Hyman
- KUL – S Geerts

The revolutions in molecular biology and information technology offer tremendous opportunities for enhancing the effectiveness and efficiency of breeding programmes. Molecular characterisation, accurate phenotyping, information systems and data analysis tools must be integrated with breeding workflows generating pedigree, phenotypic genotypic and adaptation data, relevant to better prediction of the performance of different genotypes in target environments. The goals of this integration of technologies are: 1) to create gene-to-phenotype trait knowledge for breeding objectives, and 2) to use that knowledge in product development and deployment (Cooper et al 2006). Marker-assisted breeding (MAB), the transfer of a few genomic regions or several quantitative trait loci (QTL) involved in target traits by following molecular markers, has been successfully deployed in the private sector (Crosbie et al 2006), but it is not generally used in the public sector and hardly ever in developing countries. Reasons for this include shortage of well-trained personnel, inadequate access to high-throughput genotyping, inappropriate phenotyping infrastructure, unaffordable information systems and analysis tools, and the logistical difficulty of integrating new approaches with traditional breeding methodologies, including problems of scale when scaling up from small to large breeding programmes.

Purpose:
Provide access to modern breeding technologies, breeding material and related information in a centralised and functional manner to improve plant breeding efficiency – and therefore crop productivity – in developing countries.

Aim:
Develop and deploy a sustainable web-based Molecular Breeding Platform (MBP) as a one-stop-shop for information, analytical tools and related services to design and efficiently conduct molecular-assisted breeding experiments.

Such a platform will enable breeding programmes in the public and private sector to accelerate variety development for developing countries using marker technologies for various breeding purposes, such as major gene or transgene introgression, gene pyramiding and complex marker-assisted recurrent selection (MARS), and in the near future, genome-wide marker-assisted selection (GWMAS). The platform will also deliver support services to guide and train breeders from national agricultural research systems in accessing and using marker technologies. Critical for the adoption of modern breeding technologies in developing countries will be supporting communities of practice on molecular breeding for the most important food security crops, developing local infrastructure to improve plant phenotyping, and appropriate and targeted capacity building. Through these efforts, the platform will be part of a global strategy on food security and poverty alleviation.

For details of each activity, please see the Projects table at the beginning of this publication

Component 1: Integrated Breeding Platform portal and helpdesk

This component is designed to provide access to all the tools and services of the Molecular Breeding Platform. It will have 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 media). The portal and Helpdesk will provide a focal point and collaboration environment for the development of breeding communities of practice.

73. Project No G8009.01 Objective 1.1: Establish and manage the Integrated Breeding Platform (IBP)

Principal Investigator and lead institute
Graham McLaren, GCP

This objective includes the following elements in its workplan:

- Platform management
- Integrated breeding portal
- Helpdesk
- Molecular breeding communities of practice

Integrated breeding information system

Component 2: Integrated breeding information system

The information system will be an open-source, public, modular crop information system which can be deployed individually or as a node of a network to support breeding projects and provide access to shared databases to facilitate identification of donor lines from partners. A model-driven architecture will be used to extend the middleware layer of the GCP Informatics Platform that can interface with different database back ends and applications, either directly or via web services, provided they conform to the data source or data consumer specifications of the middleware and model. The architecture is independent of the database engine and various ones will be supported depending on user requirements. Modules will need to be assembled and parameterised to suit individual breeding projects. The Information System comprises three modules: (i) logistics and data management, (ii) analysis and decision support and, (iii) information network and workflow system.

This component includes the following objectives:

74. Project No G8009.02 Objective 2.1: Make existing tools for data management and breeding logistics available to molecular breeding projects through the MBP

Principal Investigator and lead institute
Arllet Portugal, GCP

This objective includes the following elements in its workplan:

- Pedigree Information Management
- Field Data Management
- Laborotory Information Management

75. Project No G8009.03/G8009.04 – Objective 2.2: Develop and deploy an integrated breeding (IB) configurable workflow system

Principal Investigator and lead institute
Graham McLaren, GCP

This objective includes the following elements in its workplan:

- Statistical and genetic analysis
- Methodology and tools for Molecular Breeding
- Modelling and simulation tools
- Visualisation and decision support
- Information network and public crop information
- Public crop information
- Configurable workflow system

Component 3: Integrated breeding services

The service component of the platform will build on products already being developed and deployed through ongoing GCP activities and other mechanisms. The first module provides services to conduct molecular breeding projects. The second module deals with training and capacity-building, aiming to provide support and improve capacity of NARS breeders to deliver improved germplasm through marker approaches. Developing the capacity of NARS partners to understand and use modern breeding technologies is essential for the adoption of the Molecular Breeding Platform.

This component includes the following objectives:

76. Project No G8009.05 Objective 3.1: Provide access to critical molecular breeding services

Principal Investigator and lead institute
X Delannay, GCP

These services provide access to specific germplasm, and assist with contracting a service laboratory to conduct the marker work or to quantify specific traits, such as metabolite profiles or grain quality parameters.

- Genetic Resource Support Service
- Marker service
- Trait and metabolite service

77. Project No G8009.06 Objective 3.2: Provide assistance with a range of molecular breeding support

Principal Investigator and lead institute
Graham McLaren, GCP

These services provide support to breeders to address technical and logistical bottlenecks. Expert assistance is essential for the proper use and uptake of new technologies. The main objective of this component of the platform is to provide backstopping and training in a broad set of complementary disciplines, to support the other services. Services that will be available on a full-cost recovery basis include:

- Business plan development
- Information management
- Data curation
- Design and analysis
- Phenotyping sites and screening protocols
- Genotyping Support Service
- IP and policy

Projects reported under Theme 3 – Crop information systems

78. Project No G4008.32: Quality Management procedures in GCP research laboratories promoted

- *Duration: Jul 2008–Jun 2009; NCE: Jul 2011*
- *Total budget: USD 192,000*

Principal Investigator and lead institute
J Smith, FERA; G Davenport (up to August 2010), CIMMYT

Many software tools, databases and web resources that could help support GCP projects are not available to GCP research due to poor documentation, user friendliness or is too complex all but the most experience statistician to use. For example, good data quality in laboratories is an important requirement for GCP projects, however poor documentation and the lack of a good example case is stopping some laboratories to implement these measures. Well defined trait ontology is required by the GCP in order for the results from different groups and even species to be compared. At the moment GCP datasets do not use such a ontology. Sequenced genomes are good resources to aid in the development of molecular markers for breeding, however the use of bioinformatics tools to analysis these sequence are usually outside the knowledge of the average plant breeder. Selection indices and simulation tools are also useful in deciding crosses and selection in breeding programs, but they usually require an experienced statistician to use them. Finally, tools such as ICIS can be used in breeding program, however there is not sufficient documentation or a suitable example case for breeders to implement these tools in their breeding program.

79. Project No G4009.03/G4010.06/G4011.01/ G4011.10: Enhancement and implementation of the Crop Ontology for data integration and data interoperability, and expanding its use within communities of practice and to partners to integrate datasets for GCP priority crops through the IBP

- *Duration: Jan 2009–Dec 2012*
- *Budget by project:*
  - *G4009.03: USD 303,775*
  - *G4010.06: USD 67,200*
  - *G4011.01: USD 153,102*
  - *G4011.10: USD 200,000*
  - *7Total budget: 724,077*

G4009.03/G4010.06

Principal Investigator and lead institute
Elizabeth Arnaud, Bioversity

Collaborating institutes and scientists

- Bioversity – Stephanie Channeliere, Milko Skofic
- CIMMYT – Rosemary Shrestha; Guy Davenport (up to August 2010)
- CIP – Simon Reinhardt
- IRRI – Mauleon Ramil, Jeffrey Detras
- IITA – Peter Kulakow with the Cassava breeders' group:
- NCRI – Emmanuel Okogbenin and
- CIAT – Hernan Ceballos

Major external (self-funded) collaborators:
Plant Ontology Consortium – Pankaj Jaiswal
NERC Environmental Bioinformatics Centre, University of Manchester – Norman Morrison

Within the scope of work undertaken in 2008 and 2009, this project will continue the incremental validation and refinement of the GCP Crop Ontology (CO). This work will be coordinated and implemented by Bioversity International (Bioversity). The collaborating partner, CIMMYT, will coordinate the CO community and the implementation of the CO in crop-specific databases such as IMIS, IRIS and IWIS. Another collaborating partner, IRRI, will coordinate implementation of the GCP Crop Ontology-based Terminizer. Priority crops for the GCP and Bioversity, such as cassava and coconut will be included in the CO. Data curation for important crops such as maize, rice and wheat within the CO will allow researchers and end users to query keywords related to traits, plant structure, growth stages and molecular functions, and to access associated GCP phenotyping and genotyping datasets such as germplasm, crop physiology, geographic information, genes and quantitative trait loci (QTL). The CO will be integrated

into the data-entry user interface or data templates wizard as pick lists to facilitate data annotation. In addition, the GCP CO will be integrated with the Plant Ontology (PO) and Gramene Trait Ontology (TO), as well as the Environment Ontology (EO) to develop a common, internationally shared crop trait and anatomy ontology. External collaborators such as AGROVOC, Thai Rice Ontology, the SGN genomic network and Maize GDB will work with the CO team.

G4011.01

Principal Investigator and Lead institute
Elizabeth Arnaud, Bioversity International

Collaborating institutes and scientists

- Bioversity – Adriana Alercia, Stephanie Channeliere, Kenny Murguia (Bioversity International, Linux expert, consultant, Hannes Gaisberger, Luca Matteis, Milko Skofic, Imke Thormann
- IITA – Peter Kulakow and Bakare Moshood Agba
- IRRI – Mauleon Ramil, Chengzhi Liang
- Consultant – Martin Senger
- ICRISAT – Trushar Shah
- CIMMYT – Rosemary Shrestha

External (self-funded) collaborator:
Plant Ontology Consortium – Pankaj Jaiswal and Laurel Cooper

The Generation Challenge Programme (GCP) understood from its inception the importance of controlled vocabularies and ontologies for the annotation of data, to provide a mechanism for the rigorous retrieval of data from databases. Within the International Agricultural Research Centres of the Consultative Group on International Agricultural Research (CGIAR) and GCP, the volume of agriculture-related information is steadily increasing and is stored in several databases and distributed worldwide. In order to make data accessible in and/or across the databases, GCP initiated the development of a Crop Ontology (CO) in 2008 for chickpea, maize, *Musa*, potato, rice and wheat, and in 2010 for cassava. Initial sources of ontology terms include crop databases and Bioversity descriptors. The GCP Crop Ontology is a public good; it can be used online to search for specific terms and is fully downloadable at the Ontology Look-up Service (OLS): http://koios.generationcp.org/ontology-lookup/.

G4011.10

In order to make data accessible in and/or across the crop databases, in 2008 GCP initiated the development of a Crop Ontology (CO) facilitating powerful manipulations of the data itself through ontology-driven approaches. Trait Dictionaries were produced in 2010 and 2011 following an agreed template for chickpea, cassava, common beans, groundnut, cowpea, sorghum and this work will continue for barley, pigeon pea, soybean, sweet potatoes and yam. The Trait Dictionaries are used by the Integrated Breeding (IB) Fieldbooks and provide detailed lists of important breeding traits that must be included in the Crop Ontology.

This project continues the validation and refinement of the GCP Crop Ontology (CO) for all crops currently included, with the integration of information from the Crop Trait dictionaries, particularly on methods and scales to enable the mapping of ontology IDs onto measured, stored or published variables.

This will be achieved through two main project objectives, namely to: (1) Publish online fully documented lists of the most used GCP breeding traits that facilitate the creation of trait templates in the Integrated Breeding (IB) Fieldbook; and (2) Support the integration of genetic and phenotypic data from sources of information important to GCP through the cross-referencing of the respective ontologies, building an international agreed list of traits.

The project will follow the steps defined with the GCP management team, which are to: (i) identify within the Crop Ontology, the GCP most frequently used breeding traits for the priority crops as selected by the Crop Community of Practice and a team of committed curators for barley, cassava, chickpea, common beans, cowpea, groundnut, *Musa*, pigeon pea, sorghum, soybean, sweet potatoes and yam; (ii) translate the GCP short lists of breeding traits into Chinese, English, French, Portuguese and Spanish; (iii) publish the Trait Dictionaries online making them available through the Crop Ontology curation tool, adding necessary filters to select the most used GCP breeding Traits and facilitate the integration of harmonized trait lists into the IB Fieldbooks; (iv) support the upload of all necessary information on the breeding traits included in the short lists, particularly protocols, scales (units) and quality standards; (v) enable online multilingual access of these GCP breeding traits in Chinese, English, French, Portuguese and Spanish; and (vi) collaborate with the teams maintaining information systems important to GCP in order to cross-reference the terms used for data annotation and then support their integration with the Integrated Breeding Platform (IBP).

The project team collaborates with the Climate Change, Agriculture and Food Security CCAFS Global Repository for evaluation sites where evaluation data files are uploaded by partners adding metadata that contains the name of the variable measured. To avoid duplication of work for the scientists in entering the trait names, category and definition, and to avoid misspelling of trait names, the repository will be dynamically linked to the Crop Ontology to obtain trait names and access to the additional information. A first case study was done for rice and the model should be extended to all crops on Agtrials after the development of selected case studies.

80. Project No G4009.04/G4010.05/G4011.05: Development of Integrated SNP Mining and Utilization (ISMU) pipeline based on next generation sequencing (NGS) and high-throughput (HTP) genotyping technologies for facilitating molecular breeding

- *Duration: Sep 2010–Oct 2013*
- *Budget by project:*
  - *G4009.04: USD 85,000*
  - *G4010.05: USD 81,920*
  - *G4011.05: USD 138,000*
  - *Total budget: USD 304,920*

Principal Investigator lead institute
Rajeev Varshney and Trushar Shah, ICRISAT

Collaborating institutes and scientists

- SCRI – David Marshall and Iain Milne
- ICRISAT – Abhishek Rathore
- Uni Queensland, Australia – Dave Edwards (without any budget)
- NCGR, USA – Greg May and Andrew Farmer (without any budget)

G4010.05

Next generation sequencing (NGS) methods are becoming increasingly popular and routine technologies that accelerate the acquisition of genomic resources, through the generation of large volumes of sequence information within a short time period. SP2 projects using 454 FLX and Solexa sequencing technologies are beginning to generate EST and SNP marker resources in pigeonpea and chickpea (especially in the TLI project) that will help overcome a serious bottleneck in the development of these crops – namely shortage of markers and absence of genetic maps.

The efforts in the last project have focused on handling the deluge of data from NGS technologies through an analysis pipeline for the identification of SNPs. These efforts have so far included the evaluation of available open source NGS data assembly, polymorphism detection and visualization software and their benchmarking. The experimental validation of a subset of the predicted SNPs has also been carried out. The next steps after the SNPs have been predicted require the integration of tools for assay design (Illumina GoldenGate Assay), genotype calling and visualization and analysis of the SNP genotyping and haplotype data (graphical genotyping). Several projects as use cases in the Integrated Breeding Platform, in crops like chickpea, sorghum, rice, maize, etc. have a plan to develop GoldenGate assays based on informative SNPs and use them in the respective breeding programmes. Therefore information on haplotype, PIC values as well as selection of parents with superior alleles would be generated. In summary, the proposal has a plan to develop, eventually, an integrated pipeline, based on existing pipeline developed so far, that can be used to predict SNPs based on NGS data at higher precision, select a subset of most informative SNPs for developing the genotyping platform (e.g. GoldenGate assay), identify the set of appropriate parental lines for using them in marker-assisted backcrossing (MABC) or marker-assisted recurrent selection (MARS) programme, identify the polymorphic SNP markers for use in foreground and background selection of MABC or MARS. Therefore, the planned pipeline (ISMU) should be very useful for breeding community under IBP in addition to enhancing the basic research in crop genetics.

G4011.05

Marker-assisted backcrossing (MABC) is the most commonly used approach for molecular breeding in several crop species. However, this approach has bottlenecks for breeding for complex traits like drought tolerance especially when the trait is controlled by many small effect QTLs and pyramiding of such large number of QTLs through MABC often requires unmanagebale population size. In such cases, recently two modern breeding approaches namely marker-assisted recurrent selection (MARS) and genome wide Selection (GWS) have gained momentum in crop breeding. While MARS deals with accumulation of large number of QTLs, GWS approach accumaltes superior allele throughout the genome based on analysis of genome-wide marker profiling data and

historical phenotyping data on a training population. Majority of times, these approaches involve the use of high-throughput (HTP) marker (mainly SNP) genotyping data or genotyping by sequencing (GBS) data. Analysis of these data as well as decision making process in MARS and GWS at present is not straight-forward and user friendly, though some groups are working to develop respective decision support tools. This proposal is built on the success of Integrated SNP Mining and Utilization (ISMU) pipeline that deals with use of next generation sequencing data for SNP mining and their use for parental selection for MABC and MARS approaches. This proposal plans to identify the most appropriate MARS and GWS modules currently available by organizing an international workshop and integrating those tools in the ISMU pipeline in collaboration with experts in the area of MARS and GWS. Integrated ISMU pipeline, alongwith detailed documentation as well as quick Users Manual will be made available on the website of ICRISAT, GCP and Integrated Breeding Platform (IBP). In addition, the proposal plans to develop an interface for importing the HTP and GBS data into Data Management System (DMS) of IBP and for exporting the data from DMS to the ISMU pipeline for analysis for MARS and GWS approaches.

81. Project No G4011.09: Developent of a Genotyping Data Management System (GDMS)

- *Duration: Dec 2011–Nov 2013*
- *Total budget: USD 166,080*

Principal Investigator lead institute
Trushar Shah, ICRISAT

Collaborating institutes and scientists

- IRRI – Chengzhi Liang, Ramil Mauleon
- CIMMYT – Hector Sanchez
- Hutton – David Marshall
- GCP – Mark Sawkins, Delphine Fleury, Arllet Portugal, Graham McLaren
- Andrew Farmer, NCGR
- ICRISAT – Rajeev Varshney, Mahendar Thudi

The effective management of genotyping data and its link to the corresponding germplasm information and phenotyping data is a critical component of any Integrated Breeding project. There are a number of marker technologies and platforms that are used across the different crops in the mandate of the Generation Challenge Program. As some of these marker technologies develop further the amount of data generated drastically increases.

In this project, we will focus on handling the low to high throughput genotyping data (SSRs, DArTs and SNPs). Currently we will not be directly handling the Ultra High Throughput Genotyping by Sequencing data (GBS) as a part of the scope of this project although we will be monitoring the developments in this area. In addition to the marker, genotyping and fingerprinting information the system will also handle maps and QTL data and will allow for exchange of data with the analytical tools using the Flapjack file formats.

The Genotyping Data Management System (GDMS) will be developed in Java as a browser based system with a MySQL database back end. The system is an adoption and modification of the earlier developed system at ICRISAT known as ICRIS, but will also build upon experience of other systems at IRRI (MOLGENIS for SNPs) and Hutton (Germinate).

Within the IBP project, the activities of this project will be closely linked to the management of phenotyping and germplasm information currently under development at CIMMYT.

82. Project No G8009.04.01/G4006.16: Develop an integrated GCP informatics platform

- *Duration: Jul 2009–Jul 2014*

Activity Leader and lead institute
C Liang, IRRI wef July 2010; previous PI:
Guy Davenport, CIMMYT
(This project succeeds G4006.16, which ended June 2009)

Collaborating institutes and scientists

- CIMMYT
- ICRISAT

See IBP Objective 2.2, subactivity 2.2.2.3 for more details about this project.

2011 Project Index

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II. Thematic projects

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2. Theme 2 – Integrated crop breeding
3. Crop information systems
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III. Service Component – Integrated Breeding Platform

I. Research Initiatives

1. Cassava

	Projects		Principal	Target			Project Dates	
#	Axapta No	Project Title	Investigator	Countries	Target Traits	Partners	Start	End
1.	*G3007.03*	*Genetic and physical mapping resources produced for drought breeding in cassava*	Pablo Rabinowicz, IGS–UMD	Africa, Asia, Latin America	• drought tolerance	ACGT–UP, ACGT–UoW, UCD	August 2007	February 2010; NCE: February 2011
2.	*G7009.09/ G7010.01.03*	*Implement MARS projects for drought* tolerance	Emmanuel Okogbenin, NRCRI	Nigeria, Tanzania, Ghana	• drought tolerance, • biotic traits	CRI–CSIR, CU, SARI– CSIR	December 2009	February 2014
3.	*G7009.10/ G7010.01.02*	*Improving and deploying markers for biotic traits in cassava*	Chiedozie Egesi, NRCRI	Nigeria, Tanzania, Ghana	• drought tolerance, • biotic traits	CRI–CSIR, DDPSC, NRTP/ARI– NRS	March 2010	February 2014
4.	*G7010.01.01*	*Improvement and evaluation of the existing cassava reference set for Africa*	Morag Ferguson, IITA	Africa	• drought tolerance • biotic stress	CIAT, CRI–CSIR, NRCRI, NRTP/ARI–NRS	April 2010	March 2013
5.	*G7010.01.04*	*Phenotyping cassava for drought tolerance to identify QTLs*	Alfredo Alves, EMBRAPA		• drought tolerance	CIAT, CU, IITA, IGS–UMD	April 2010	March 2012
Capacity-building activities: Community of practice project								
6.	*G4008.26/ G7010.01.05*	*A cassava breeding community of practice in Africa: for accelerated production and dissemination of farmer-preferred cassava varieties resistant to pests and diseases (Phase II)*	Emmanuel Okogbenin, NRCRI	Ghana, Nigeria, Tanzania, Uganda	• drought tolerance • pest resistance • disease resistance	ARI–NRS, CIAT, CRI–CSIR, IITA, NaCRRI	January 2008	December 2013

2. Legumes

#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Traits	Partners	Project Dates: Start	Project Dates: End
Beans								
7.	*G3008.07*	*Basal root architecture and drought tolerance in common beans*	JP Lynch, PSU	Global	• drought tolerance • rooting	CIAT, IIAM, SABRN	November 2008	October 2011; NCE: Oct 2012
8.	*G4008.11*	*Dry bean improvement and marker-assisted breeding for diseases and abiotic stresses in Central America and the Caribbean*	Jorge A Acosta-Gallegos, INIFAP	Mexico	• drought tolerance • disease & pest resistance	CIAT, INCA, INTA–N	January 2008	December 2010; NCE: July 2011
9.	*G6010.03*	*Improve common bean productivity for marginal environments in sub-Saharan Africa*	S Beebe, CIAT	Kenya, Ethiopia, Malawi, Zimbabwe	• drought tolerance • disease & pest resistance • productivity	DARTS, CBI–DAR4D, ECABREN, KARI, SABRN, SARI–E	May 2010	May 2014
Chickpeas								
10.	*G4008.12*	*Linking genetic diversity with phenotype for drought-tolerance traits through molecular and physiological characterisation of a diverse reference collection of chickpea*	Lakshmanan Krishnamurthy, ICRISAT	Global	• drought tolerance	JIRCAS, UAS–B	January 2008	December 2009; NCE: September 2011
11.	*G4011.08*	*Harnessing the potential of multiparent advanced generation intercross (MAGIC) populations for gene discovery and breeding applications in chickpeas*	Pooran M Gaur and Rajeev K Varshney, ICRISAT			EgU, EIAR	August 2011	July 2014
12.	*G6010.04*	*Improve chickpea productivity for marginal environments in sub-Saharan Africa and South Asia*	RK Varshney, ICRISAT	Kenya, Ethiopia, India	• drought tolerance • disease & pest resistance • productivity	EgU, EIAR, NCGR, NIPGR, UCD	May 2010	May 2014
13.	*G7009.02*	*Validation of QTLs associated with drought tolerance traits in chickpea*	Pooran M Gaur, ICRISAT	Global	• drought tolerance	ARS–D, DZARC, RAKCA–ICAR, RARS–N, UAS–B	January 2009	December 2011; NCE: June 2012
14.	*G7009.06*	*Development of a SNP platform for molecular breeding in elite chickpea materials*	Douglas Cook, UC–D	Ethiopia, Kenya, India		ICRISAT, NCGR	November 2009	October 2010; NCE: October 2011
Cowpeas								
15.	*G4008.13*	*Improving drought-tolerance phenotyping in cowpeas*	Jeff Ehlers, UCR	Mozambique, Senegal, Burkina Faso	• drought tolerance	IER, IITA, ISRA, TAMU	January 2008	December 2010; NCE: March 2011
16.	*G6010.02/ G7010.07.01*	*Improve cowpea productivity for marginal environments in sub-Saharan Africa (TLI project, Objective 2)*	Jeff Ehlers, UC–R	Mozambique, Senegal, Burkina Faso	• drought tolerance • disease & pest resistance • productivity	IITA, INERA, ISRA, UEM	May 2010	May 2014

#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Traits	Partners	Project Dates: Start	Project Dates: End
Groundnuts								
17.	*G4008.06*	*Single nucleotide polymorphism discovery*	Peggy Ozias-Akins, UGA	Global	• multiple traits	ICRISAT	January 2008	December 2008; NCE: December 2011
18.	*G6010.01*	*Improve groundnut productivity for marginal environments in sub-Saharan Africa*	Vincent Vadez, ICRISAT	Tanzania, Senegal, Niger	• drought tolerance • disease & pest resistance • productivity	Agropolis–CIRAD, ARI–Naliendele, CRS, EMBRAPA, ICRISAT, ISRA, UCB, UGA	May 2010	May 2014
Cross-cutting activities								
19.	*G6010.05*	*Cross-cutting crop activities (drought phenotyping, data management and capacity building)* (TLI project, Objective 5)	Drought phenotyping: Vincent Vadez, ICRISAT; Data management: Trushar Shah, ICRISAT; Capacity building: Ndeye Ndack Diop, GCP	Kenya, Ethiopia, Malawi, Zimbabwe, Mozambique, Senegal, Burkina Faso	• drought tolerance • disease & pest resistance • productivity	Agropolis–CIRAD, ARI–NRS, CARS, CIAT, CU, CBI–DAR4D, ECABREN, EgU, EIAR, EMBRAPA, IITA, INERA, ISRA, KARI, NCSU, SABRN, SARI–E, UCB, UCD, UCR, UEM, UGA	May 2010	May 2014

#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates: Start	Project Dates: End
Capacity-building activities:									
Capacity-building projects: training components for TLI scientists and students									
20.	*G4009.07.01*	*Capacity-building à la carte 2009 – TLI students for analysis of drought tolerance in common beans*	Steve Beebe, CIAT	Ethiopia, Zimbabwe	beans	• drought tolerance	SARI–E, UFS	October 2009	October 2010; NCE: May 2013
21.	*G4009.07.02*	*Capacity-building à la carte 2009 – Capacity -building in modern cowpea breeding*	Jeffrey D Ehlers, UCR	Senegal, Mozambique	cowpeas	• drought tolerance	ISRA, UEM	October 2009	October 2010; NCE: May 2013
22.	*G4009.07.03*	*Capacity-building à la carte 2009 – Marker-assisted back crossing (MABC) for drought tolerance in chickpea students for analysis of drought tolerance in chickpea (TLI- Kenyan student)*	Rajeev K Varshney, ICRISAT	Kenya, Ethiopia	chickpeas	• drought tolerance	EgU	December 2009	December 2010; NCE: May 2013
23.	*G4009.07.04*	*Ensuring 'good' and relevant phenotypic data to feed molecular breeders: The need for long-term training of scientists of NARS partners to TLI*	Vincent Vadez, ICRISAT	sub-Saharan Africa	groundnuts	• drought tolerance	ARI–NRS, CARS, ISRA	December 2009	December 2010; NCE: May 2013
24.	*G7010.06.01*	*Accelerating development of genomic resources and strengthening NARS partner capacities for enhancing adoption of molecular breeding for drought tolerance in chickpea*	Rajeev K Varshney, ICRISAT	Kenya, Ethiopia, India	chickpeas	• drought tolerance • disease & pest resistance • productivity	EIAR, EgU, ICGGC (network), IIPR	May 2010	June 2014

3. Maize

#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Traits	Partners	Project Dates: Start	Project Dates: End
25.	*G4008.33*	*Drought-tolerance phenotyping of the GCP maize inbred line reference set*	James Gethi, KARI	Global	• drought tolerance	Agropolis–INRA, CIMMYT, ETH	January 2008	February 2011; NCE: February 2012
26.	*G4008.56*	*AMDROUT: Asian Maize Drought-Tolerance Project*	Bindiganavile S Vivek, CIMMYT	Asia	• drought tolerance	ICERI, KSPL, NMRI, NSFCRC, Syngenta, UPLB, YAAS	November 2008	October 2013

4. Rice

#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Traits	Partners	Project Dates: Start	Project Dates: End
27.	*G3007.05*	*Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-aided breeding*	Arvind Kumar, IRRI	Global	• drought tolerance	BF, BiAU, CRRI, CRURRS, IGKV, JNKVV, NDUAT, TNAU, UoAl, UAS–B, YAAS	August 2007	July 2009; NCE: December 2011
28.	*G3008.03*	*Delayed senescence and drought tolerance in rice*	Eduardo Blumwald, UCD	Global	• drought tolerance	IRRI	November 2008	October 2011; NCE: October 2012
29.	*G3008.06*	*Targeting drought-avoidance root traits to enhance rice productivity under water-limited environments*	K McNally and Amelia Henry, IRRI	Global	• drought tolerance • water use efficiency	ARC, BF, CRRI, CRURRS, CSU, IGKV, NU, NDUAT, TNAU, UoA, UAS–B	November 2008	October 2011; NCE: October 2012
30.	*G3008.09*	*Breeding drought tolerance for rainfed lowland rice in the Mekong region*	Boonrat Jongdee, BRRD	Mekong Delta	• drought tolerance	CARDI, NAFRI, UQ	November 2008	October 2011; NCE: September 2012
31.	*G4006.01*	*Developing strategies for allele mining within large collections*	NR Sackville Hamilton, IRRI	Global		IRRI, EMBRAPA, ICARDA, ICRISAT	Jan 2006	August 2011
32.	*G4008.45*	*A Nested Association Mapping (NAM) population of rice: laying the bases for highly efficient QTL characterisation*	Mathias Lorieux, Agropolis–IRD/CIAT	Global	• drought tolerance	ARC	August 2008	July 2010: NCE: May 2012
33.	*G4010.04*	*Enhancing capacity for use of advance genotyping for fine-mapping and pyramiding of major salt tolerant QTLs through MABC for the development of durable saline tolerant rice varieties*	Zeba I Seraj, DU	Bangladesh	• salt tolerance	BRRI, IRRI	July 2010	June 2011; NCE: November 2011
34.	*G4011.04*	*Dissemination and community of practice for newly developed drought-tolerant QTLs pyramided breeding lines*	Arvind Kumar, IRRI		• drought tolerance	CRRI, CRURRS, DRR–ICAR, NDUAT	July 2011	June 2014

#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Traits	Partners	Project Dates: Start	Project Dates: End
35.	*G4011.06*	*Field phenotyping for drought resistance of the MARS population developed under the GCP Rice RI*	Cécile Grenier, Agropolis–CIRAD/CIAT		• drought tolerance	ARC	November 2011	October 2012
36.	*G4011.07*	*Rice multiparent advanced generation intercrosses (MAGIC) – Phase II*	Hei Leung, IRRI				November 2011	October 2013
37.	*G7010.04.01*	*Improving rice productivity in the lowland ecosystems of Burkina Faso, Mali and Nigeria through marker-assisted recurrent selection (MARS) for drought tolerance and yield potential*	Marie-Noëlle Ndjiondjop, ARC	Burkina Faso, Mali, Nigeria	• drought tolerance • yield	Agropolis–CIRAD, Agropolis–IRD, IER, INERA, IRRI, NCRI	May 2010	April 2014
Work packages (WPs) of Project G7010.04.01								
	WP 1	*Characterisation of the IV-TPE, establishment of drought-evaluation sites and description of ideotypes fitting major sub-classes of TPE to improve rice productivity in the lowland ecosystems of Burkina Faso, Mali and Nigeria*	*Sander Zwart, ARC*	*Burkina Faso, Mali, Nigeria*	• drought tolerance • yield	Agropolis–CIRAD, Agropolis–IRD, IER, INERA, IRRI, NCRI	May 2010	April 2014
	WP 2	*Phenotyping for yield potential and drought tolerance to improve rice productivity in the lowlandecosystmes of Burkina Faso, Mali and Nigeria*	Koichi Futakuchi, ARC	Burkina Faso, Mali, Nigeria	• drought tolerance • yield		May 2010	April 2014
	WP 3	*Developing improved lines combining favourable QTL alleles for drought adaptation and productivity in the lowland ecosystems of Burkina Faso, Mali and Nigeria*	Marie-Noëlle Ndjiondjop, ARC	Burkina Faso, Mali, Nigeria	• drought tolerance • yield		May 2010	April 2014
	WP 4	*Rice drought molecular biology and breeding community of practice for West Africa*	Venuprasad Ramaiah, ARC	Burkina Faso, Mali, Nigeria	• drought tolerance • yield		May 2010	April 2014
	WP 5	*Project and information management*	Ibnou Dieng, ARC	Burkina Faso, Mali, Nigeria	• drought tolerance • yield		May 2010	April 2014

#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Traits	Partners	Project Dates: Start	Project Dates: End
Capacity-building activities: Community of practice								
38.	*G4009.09*	*A Community of Practice for strengthening rice breeding programmes by using genotyping building strategy and improving phenotyping capacity for biotic and abiotic stresses in the Mekong region*	Jonaliza Lanceras-Siangliw, BIOTEC	Cambodia, Laos, Myanmar, Thailand	• drought tolerance • soil acidity • disease resistance	BIOTEC, CARDI, DAR, NAFRI	November 2009	October 2012
39.	*G4010.04/ G4010.01.01*	*Identification of novel QTLs for salinity tolerance and pyramiding with submergence tolerance to develop improved rice varieties for Bangladesh.*	Fellowship – Armin Bhuiya, BRRI	Bangladesh	• salt tolerance • submergence tolerance	BAU, BRRI, IRRI	March 2010	March 2013
40.	*G7010.04.01/ G4009.02.01*	*Study of Burkina Faso rice landraces diversity and breeding for resistance to Rice Yellow Mottle Virus (RYMV)*	Fellowship – Honoré Kam, INERA	Burkina Faso	• disease resistance	Agropolis–CIRAD, Agropolis–IRD, UKZN	March 2009	February 2011; NCE: June 2011

5. Sorghum

#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Traits	Partners	Project Dates: Start	Project Dates: End
41.	*G3008.05*	*Discovery and development of alleles contributing to sorghum drought tolerance*	Andrew H Paterson, UGA	Global	• drought tolerance	DSR–ICAR, ICRISAT, MAU, SARI–CSIR	November 2008	October 2011; NCE: December 2012
42.	G4008.02	Phenotyping sorghum reference set for drought tolerance	HD Upadhyaya, ICRISAT	Global	• drought tolerance	IER, ISRA/CERAAS, KARI, NPGRC, UAS–D	January 2008	December 2010; NCE: May 2012
43.	*G4008.46*	*Sorghum MAGIC: Multiparent advanced generation inter-cross development for gene discovery and allele validation*	C Tom Hash, ICRISAT	Global			August 2008	July 2010; NCE: February 2011
44.	*G4008.48*	*Improve sorghum productivity in semi-arid environments of Mali through integrated MARS*	Jean-François Rami, Agropolis –CIRAD	Mali	• drought tolerance	IER, Syngenta	August 2008	July 2013; NCE: October 2014
45	*G7009.04*	*Development and evaluation of drought -adapted sorghum germplasm for Africa and Australia*	David Jordan and Andrew Borrell, DPI&F/UQ	Africa, Australia	• drought tolerance	Agropolis–CIRAD, IER	July 2009	June 2012
46	*G7010.05.01*	*Enhancing sorghum grain yield and quality for the Sudano-Sahelian zone of West Africa using the backcross nested association mapping (BCNAM) approach*	Niaba Témé – IER; Michel Vaksmann, Agropolis–CIRAD, Eva Weltzien, ICRISAT	Mali	• drought tolerance • yield • quality		January 2010	June 2014

6. Wheat

#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Traits	Partners	Project Dates: Start	Project Dates: End
47.	*G3008.01*	*Generating new wheat germplasm with enhanced drought/heat tolerance using AB genomes genetic diversity*	SC Misra, ARI–ICAR	Global	• drought/heat tolerance	CIMMYT, PBI–UoS, UAS–D	November 2008	October 2011; NCE: October 2012
48.	*G3008.08*	*Breeder-friendly high-throughput phenotyping tools to select for wheat adaptive traits in drought environments*	Francis Ogbonnaya, (ICARDA); Co-PI: M Fernanda Dreccer, CSIRO	Global	• drought	CIMMYT, CAS–INRA, EIAR–KARC	November 2008	October 2011; NCE: June 2013
49.	*G4008.03*	*Precision phenotyping of the GCP spring wheat reference sample for drought*	Susanne Dreisigacker, CIMMYT	Global	various traits	INRA–M, SPII	January 2008	December 2010; NCE: March 2011
50.	*G7009.01*	*Examining natural variation in the transcriptional regulation of drought responses in wheat*	Peter Langridge, ACPFG	Global	• drought tolerance	CIMMYT, ICS–CAAS	January 2009	December 2011
51.	*G7010.02.01*	*Breeding and selection strategies to combine and validate quantitative efficiency and heat tolerance of wheat in China*	Ruilian Jing, NFCRI & ICS–CAAS	China	• drought tolerance • heat tolerance • water-use efficiency	CIMMYT, HAAS–IDF, PBI–UoS, SAAS–ICS, XAAS–INBT	April 2010	March 2014
52.	*G7010.02.02.*	*Molecular breeding and selection strategies to combine and validate quantitative trait loci for improving water-use efficiency and heat tolerance of wheat in India*	K Vinod Prabhu, IARI–ICAR	India	• drought tolerance • heat tolerance • water-use efficiency	ARI–ICAR, CIMMYT, JNKVV, NRCPB, PAU, PBI–UoS	July 2010	June 2014

7. Comparative genomics

#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates: Start	Project Dates: End
53.	*G3008.02*	*Improving grain yield on acid soils by the identification of genetic factors underlying drought and aluminium tolerance in maize and sorghum*	Leon Kochian, CU/USDA–ARS	Global	Maize, Sorghum	• drought tolerance • Al tolerance	EMBRAPA, MU/KARI	November 2008	October 2011
54.	*G3008.04*	*Drought from a different perspective: Improved tolerance through Phosphoros acquisition*	Sigrid Heuer, IRRI	Global	Rice	• drought tolerance • Phosphorous defficiency	ICABIOGRD, JIRCAS, UoP/MPI-MP	November 2008	October 2011; NCE: October 2012
55.	*G4008.10*	*Assessment of the breeding value of superior haplotypes for AltSB, a major Al tolerance gene in sorghum: linking upstream genomics to acid soil breeding in Niger and Mali (ALTFIELD)*	Robert Schaffert, EMBRAPA	Niger, Mali	Sorghum	• Aluminium tolerance	ICRISAT, INRAN	January 2008	December 2010; NCE: December 2011

#	Projects		Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
	Axapta No	Project Title						Start	End
56.	*G7009.07*	*Cloning, characterisation and validation of AltSB/Al tolerance in rice*	Leon Kochian and Susan McCouch, CU/USDA–ARS	Global	Rice	• Aluminium tolerance	ICABIOGRD	October 2009	March 2012
57.	*G7010.03.01*	*Cloning, characterisation and validation of Pup1/P efficiency in maize*	Leon Kochian, CU/USDA–ARS	Global	Maize	• Phosphorous efficiency	EMBRAPA, IRRI, JIRCAS, MU/KARI	April 2010	March 2014
58.	*G7010.03.02*	*Cloning, characterisation and validation of AltSB/Al tolerance in maize*	Claudia Guimãraes, EMBRAPA	Global	Maize	• Al tolerance	CU/USDA–ARS, MU/KARI	April 2010	March 2012
59.	*G7010.03.03*	*Establishing a molecular breeding program based on the aluminum tolerance gene AltSB and the P efficiency QTL, Pup-1, for increasing sorghum production in Sub-Saharan Africa*	Eva Weltzien, ICRISAT	Africa	Sorghum	• Al tolerance • Phosphorous efficiency • Productivity	CU/USDA–ARS, EMBRAPA, INRAN, MU/KARI	April 2010	March 2014
60.	*G7010.03.04*	*Developing rice with dual tolerance of phosphorus deficiency and aluminum toxicity: marker-assisted pyramiding of Pup1 with novel tolerance QTLs*	Sigrid Heuer, IRRI	Asia	Rice	• Phosphorous deficiency • Al tolerance	CU/USDA–ARS, EMBRAPA, ICABIOGRD, JIRCAS	April 2010	March 2014
61.	*G7010.03.05*	*Marker-assisted backcrossing for improving phosphorous-use efficiency and tolerance to aluminium toxicity via Pup-1 and AltSB genes in maize*	Samuel Gudu, MU/KARI	Global	Maize	• Al tolerance • Phosphorous efficiency	CIMMYT, EMBRAPA, IRRI, JIRCAS, USDA–ARS	April 2010	March 2014
62.	*G7010.03.06*	*Improving phosphorus efficiency in sorghum by the identification and validation of sorghum homologs for Pup1, a major QTL underlying phosphorus uptake in rice, and identification of other P efficiency QTLs*	Jurandir Magalhães, EMBRAPA	Global	Sorghum	• Phosphorous efficiency	CU/USDA–ARS, INRAN, MU/KARI	April 2010	March 2014

II. Themes

Theme 1 – Comparative and applied genomics

#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates: Start	Project Dates: End
63.	*G4008.07*	*Genomic resources and mapping populations developed and assembled for pearl millet to enable trait/gene identification*	C Tom Hash, ICRISAT	Africa, Latin America, Asia	pearl millet	• various traits	AICPMIP–ICAR, CAZRI, ILRI, SKRAU	January 2008	December 2009 (final report submitted in 2011)

Theme 2 – Integrated crop breeding

#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates: Start	Project Dates: End
64.	*G4007.07*	*Marker-assisted selection for sweet-potato virus disease (SPVD) resistance in sweet-potato germplasm and breeding populations*	Wolfgang Grüneberg, CIP	various regions	sweet potatoes	• SPVD resistance	CSIRO, NaCRRI	August 2007	July 2010; NCE: June 2011
65.	*G4008.05*	*Connecting performance under drought with genotypes through phenotype associations*	Arvind Kumar, IRRI	Asia	rice	• drought tolerance	Agropolis–CIRAD, ARC, BIOTEC, CRRI, IGKV, TNAU	January 2008	December 2010; NCE: June 2012
66.	*G4008.15*	*Developing potato cultivars adapted to Southern Africa countries*	F Vilaró, INIA–U	Southern Africa countries	potato	• various traits	CIP, DARTS, EMBRAPA, IIAM, INIA–C, INTA–A	January 2008	December 2009 NCE: November 2011

Theme 3 – Crop information systems

Projects for this theme are listed below under Integrated breeding information system

Theme 4 – Capacity building

#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates: Start	Project Dates: End
67.	*G4006.36*	*Capacity-building and research project: Academic position in molecular breeding supported.*	Mark Laing, ACCI–UKZN	Africa	Global	Global		January 2007	December 2011; NCE: March 2012
68.	*G4008.37*	*PhD in plant breeding training at the West Africa Centre for Crop Improvement*	Eric Y Danquah, WACCI–UG	Africa	Global	Global	CU, UG	March 2008	February 2014
69.	*G4009.08*	*Plant Breeding: concepts & methods – a Learning Module*	Theresa Fulton, IGD–CU	Global	Global		CropGen International	November 2009	June 2011

Theme 5: Product delivery

#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates: Start	Project Dates: End
70.	*G4007.01*	*Genotyping validation of the GCP reference sets*	Jean-Francois Rami, Agropolis – CIRAD	Global	Various	Various	BI, CIAT, CIMMYT, CIP, ICARDA, ICRISAT, IITA, IRRI, UCR	January 2007	December 2008; NCE: October 2011
71.	*G4010.02*	*Potential benefits of marker-assisted selection technologies on wheat, sorghum, cassava, and rice, and of the Integrated Breeding Platform*	George W. Norton, VT	Global	Sorghum, Cassava, Rice	Various	IFPRI	May 2010	Dec 2011; NCE: June 2012
72.	*G4011.02*	*Seed increase for interspecific chromosome segment substiution lines (CSSSLs) of rice at CIAT*	M Lorieux, Agropolis– IRD/CIAT		Rice			April 2011	September 2011

III. Service Component – Integrated Breeding Platform

Integrated Breeding Platform portal and helpdesk

#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates: Start	Project Dates: End
	Component 1: Integrated Breeding Platform portal and helpdesk								
73.	**G8009.01 – Objective 1.1: Establish and manage the Integrated Breeding Platform (IBP)** **PI and lead institute: G McLaren, GCP**								
	G8009.01.01	*Activity 1.1.1: Establish and manage the IBP*	Graham McLaren, GCP	Global	Global	Global	AAFC, Agropolis– INRA, BI, CAAS, CIAT, CIMMYT, CSIRO, ICRISAT, IRRI, KUL, UQ, WUR	July 2009	July 2014
	G8009.01.02	*Activity 1.1.2: Develop and deploy the IBP web portal*	Fred Okono, GCP	Global	Global	Global		July 2009	July 2014
	G8009.01.03	*Activity 1.1.3: Establish IBP Helpdesk and coordinate training and communication activities*	Graham McLaren and Ndeye Ndack Diop, GCP	Global	Global	Global	July 2009	July 2014	
	G8009.01.04	*Activity 1.1.4: Establish and support crop molecular breeding communities of practice*	Ndeye Ndack Diop, GCP	Global	Global	Global		July 2009	July 2014

Integrated breeding information system

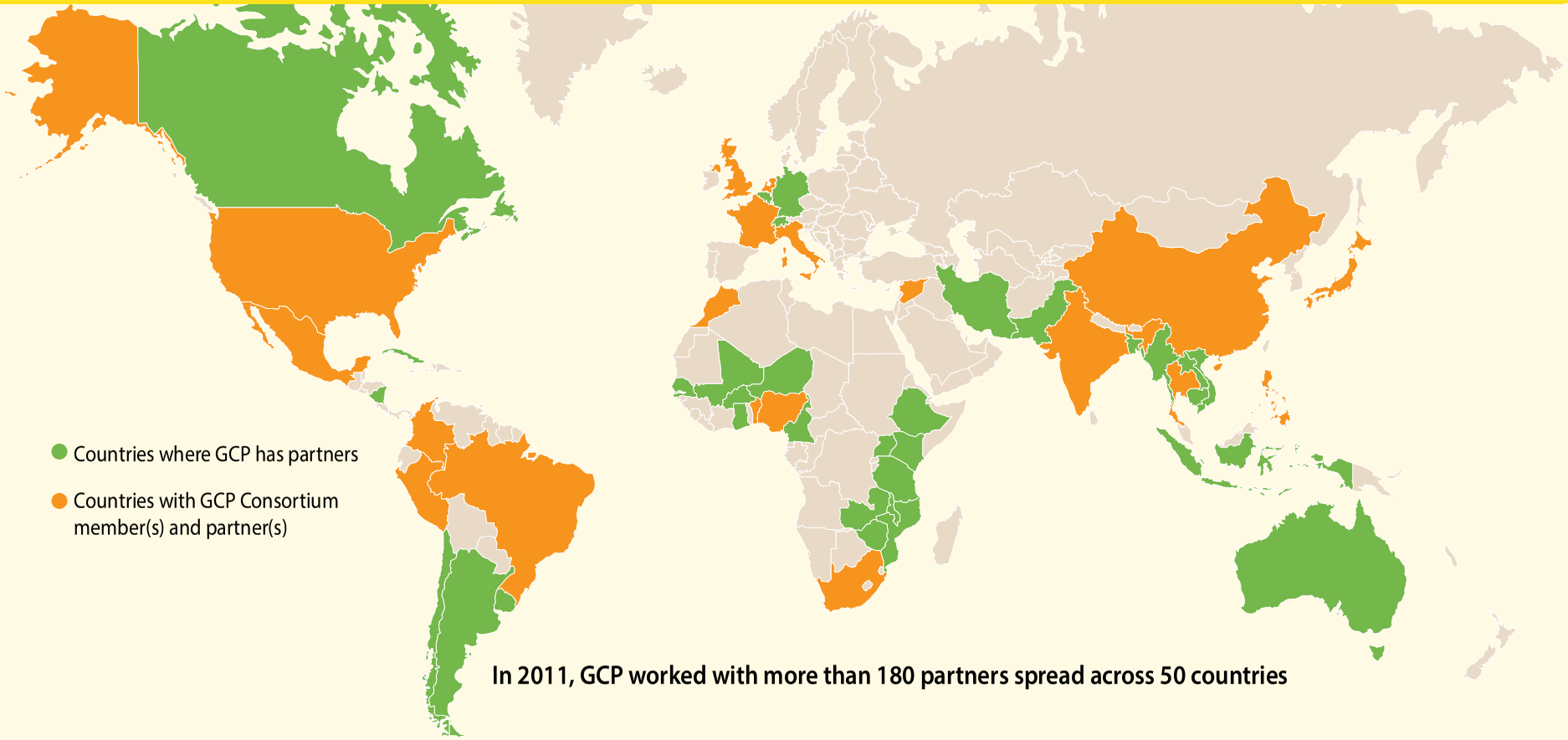
#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates: Start	Project Dates: End
	Component 2: Integrated breeding information system								
74.	***G8009.02 – Objective 2.1: Make existing tools for data management and breeding logistics available to molecular breeding projects through the IBP***								
	PI and lead institute: Arllet Portugal, GCP								
	G8009.02.01	*Activity 2.1.1: Identify, deploy and support tools to facilitate the management of germplasm lists, pedigrees, intellectual property and other passport data*	Shawn Yates and Fran Clarke, AAFC	Global	Global	Global	AAFC, Agropolis–INRA, BI, CAAS, CIAT, CIMMYT, CSIRO, ICRISAT, IRRI, KUL, UQ, WUR	July 2009	July 2014
	G8009.02.02	*Activity 2.1.2: Identify, deploy and support tools to manage phenotypic characterisation and evaluation*	H Sánchez, CIMMYT	Global	Global	Global		July 2009	July 2014
	G8009.02.03	*Activity 2.1.3: Identify, deploy and support tools to manage genotypic characterisation*	Trushar Shah, ICRISAT	Global	Global	Global		July 2009	July 2014
75.	***G8009.03/G8009.04 – Objective 2.2: Develop and deploy an integrated breeding (IB) configurable workflow system***								
	PI and lead institute: Graham McLaren, GCP								
	G8009.03.01	*Activity 2.2.1: Develop and deploy an IB WorkBench Administration & Configuration Application*	Graham McLaren, GCP	Global	Global	Global	AAFC, Agropolis–INRA, Bioversity, CAAS, CCAFS, CIAT, CIMMYT, CSIRO, ICRISAT, IRRI, KU Leuven, UQ, WUR	July 2009	July 2014
		Subactivity 2.2.1.1: Develop an IB Workflow Administration Application	H Sanchez, CIMMYT	Global	Global	Global	July 2009	July 2014	
		Subactivity 2.2.1.2: Develop IB Project Configuration Application	H Sanchez, CIMMYT	Global	Global	Global		July 2009	July 2014
		Subactivity 2.2.1.3: Develop Database back-end for the IB workflow	H Sanchez, CIMMYT	Global	Global	Global		July 2009	July 2014
	G8009.03.02	*Activity 2.2.2: Develop and deploy an IB Management System Application*	*Graham McLaren, GCP*	*Global*	Global	Global	July 2009	July 2014	
		Subactivity 2.2.2.1: Develop Breeding Manager Application	H Sanchez, CIMMYT	Global	Global	Global		July 2009	July 2014
		Subactivity 2.2.2.2: Develop Geneaology Manager Application	G Ye, IRRI	Global	Global	Global		July 2009	July 2014
		Subactivity 2.2.2.3: Develop Query Manager Application	C Liang, IRRI	Global	Global	Global		July 2009	July 2014

#	Projects		Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
	Axapta No	Project Title						Start	End
	G8009.03.03	*Activity 2.2.3: Develop and deploy an IB Field Trial Management System Application*	Graham McLaren, GCP	Global	Global	Global		July 2009	July 2014
		Subactivity: 2.2.3.1 Develop a Trial FieldBook Application Subactivity: 2.2.3.2	H Sanchez, CIMMYT	Global	Global	Global		July 2009	July 2014
		Develop an Environment Characterisation System Application	G McLaren, GCP	Global	Global	Global		July 2009	July 2014
	G8009.03.04	*Activity 2.2.4: Develop and deploy an IB Genotypic Data Management System Application*	G McLaren, GCP	Global	Global	Global		July 2009	July 2014
		Subactivity 2.2.4.1: Develop a Genotypic Data Management Application	Trushar Shah, ICRISAT	Global	Global	Global		July 2009	July 2014
	G8009.03.05	*Activity 2.2.5: Develop and deploy an IB Analytical Pipeline Application*	Activity Leader: Delphine Fleury (ACPFG/GCP)	Global	Global	Global		July 2009	July 2014
		Subactivity 2.2.5.1: Develop a Data Management Application	FA v Eeuwijk (WUR)/G Ye (IRRI)	Global	Global	Global		July 2009	July 2014
		Subactivity 2.2.5.2: Develop a Phenotypic data Analysis Application	FA v Eeuwijk (WUR)/G Ye (IIRI)	Global	Global	Global		July 2009	July 2014
		Subactivity 2.2.5.3: Develop a Molecular Genetic Analysis Application	FA v Eeuwijk (WUR)/G Ye (IIRI)	Global	Global	Global		July 2009	July 2014
		Subactivity 2.2.5.4: Develop a Selection Indices Application	FA v Eeuwijk (WUR)/G Ye (IIRI)	Global	Global	Global		July 2009	July 2014
	G8009.03.06	*Activity 2.2.6 Develop and deploy an IB Decision Support System Application*	Delphine Fleury (ACPFG/GCP)	Global	Global	Global		July 2009	July 2014
		Subactivity 2.2.6.1: Develop Breeding Decision Support Applications	T Shah (ICRISAT)	Global	Global	Global		July 2009	July 2014
		Subactivity 2.2.6.2: Develop MARS Decision Support Application	Alain Charcosset (CIRAD)	Global	Global	Global		July 2009	July 2014
		Subactivity 2.2.6.3: Develop Simulation Application	M Dieters (UoQ)	Global	Global	Global		July 2009	July 2014

#	Projects: Axapta No	Projects: Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates: Start	Project Dates: End
Component 3: Integrated breeding services									
76.	***G8009.05 – Objective 3.1: Provide access to critical molecular breeding services*** **PI and lead institute: X Delannay, GCP**								
	G8009.05.01	*Activity 3.1.1: Genetic Resources Support Service*	Jean Christophe Glaszmann, Agropolis–CIRAD; Larry Butler wef June2011, GCP	Global	Global	Global	AAFC, Agropolis–INRA, BI, CAAS, CCAFS, CIAT, CIMMYT, CSIRO, ICRISAT, IRRI, KU Leuven, UQ, WUR	July 2009	July 2014
	G8009.05.02	*Activity 3.1.2: Marker Services*	Chunlin He, GCP	Global	Global	Global		July 2009	July 2014
	G8009.05.03	*Activity 3.1.3: Trait and metabolite services*	Xavier Delannay, GCP	Global	Global	Global		July 2009	July 2014
77.	***G8009.06 Objective 3.2: Provide assistance with a range of molecular breeding support services*** **PI and lead institute: G McLaren, GCP**								
	G8009.06.01	*Activity 3.2.1: Breeding Plan Development*	Xavier Delannay, GCP	Global	Global	Global	AAFC, Agropolis–INRA, BI, CAAS, CCAFS, CIAT, CIMMYT, CSIRO, ICRISAT, IRRI, KU Leuven, UQ, WUR	July 2009	July 2014
	G8009.06.02	*ACTIVITY 3.2.2: INFORMATION MGT*	Arllet Portugal, GCP	Global	Global	Global		July 2009	July 2014
	G8009.06.03	*Activity 3.2.3: Data curation*	*Arllet Portugal, GCP*	Global	Global	Global		July 2009	July 2014
	G8009.06.04	*Activity 3.2.4: Design & analysis*	Marcos Malosetti, WUR	Global	Global	Global		July 2009	July 2014
	G8009.06.05	*Activity 3.2.5: Phenotyping sites & screening protocols)*	Xavier Delannay, GCP	Global	Global	Global		July 2009	July 2014
	G8009.06.06	*Activity 3.2.6: Genotying Support Service*	Chunlin He, GCP	Global	Global	Global		July 2009	July 2014
	G8009.06.07	*Activity 3.2.7: IP & Policy Helpdesk*	L Butler, GCP	Global				July 2009	July 2014

#	Projects		Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
	Axapta No	Project Title						Start	End
	Projects reported under Theme 3 – Crop information systems								
78.	*G4008.32*	*Quality management procedures in GCP research laboratories promoted*	J Smith, FERA	Global	Global	Global	CIMMYT, FERA	July 2008	June 2009; NCE: July 2011
79.	*G4009.03/ G4010.06/ G4011.01/ G4011.10*	*Enhancement and implementation of the Crop Ontology for data integration and data interoperability, and expanding its use within communities of practice and to partners to integrate datasets for GCP priority crops through the IBP*	Elizabeth Arnaud, Bioversity	Global	Global	Global	CIMMYT, CIP, IRRI, CIAT, IATA, NCRI, Plant Ontology Consortium, NERC Environmental Bioinformatics Centre, University of Manchester	January 2010	December 2012
80.	*G4009.04/* G4010.05/ G4011.05	*Devt of Integrated SNP Mining and Utilization (ISMU) pipeline based on next generation sequencing (NGS) and high-throughput (HTP) genotyping technologies for facilitating molecular breeding*	Rajeev Varshney and Trushar Shah, ICRISAT	Global	Global	Global	ICRISAT, NCGR, SCRI, UoQ	September 2010	October 2013
81.	*G4011.09*	*Developent of a Genotyping Data Management System (GDMS)*	Trushar Shah, ICRISAT				CIMMYT, GCP, Hutton, IRRI, NCGR, SCRI	December 2011	November 2013
83.	G8009.04.01/ G4006.16	*Activity 2.3.1: Establish middleware infrastructure for networking databases and applications*	C Liang, IRRI (This project succeeds G4006.16, which ended December 2009)	Global	Global	Global	CIMMYT, ICRISAT	July 2009	July 2014

Where in the world is GCP? The GCP network in 2011



In 2011, GCP worked with more than 180 partners spread across 50 countries

Developing-country partners

Central and West Asia and North Africa
1. Iran
2. Morocco
3. Syria

Latin America and the Caribbean
4. Argentina
5. Chile
6. Cuba
7. Nicaragua
8. Uruguay

South and Southeast Asia
9. Bangladesh
10. Cambodia
11. Indonesia
12. Laos
13. Myanmar
14. Pakistan
15. Vietnam

Sub-Saharan Africa
16. Burkina Faso
17. Benin
18. Cameroon
19. Ethiopia
20. Ghana
21. Kenya
22. Malawi
23. Mali
24. Mozambique
25. Niger
26. Nigeria
27. Senegal
28. Tanzania
29. Uganda
30. Zimbabwe

Emerging-economy country partners

Latin America and the Caribbean
31. Brazil
32. Colombia
33. Mexico
34. Peru

South and Southeast Asia
35. China
36. India
37. Thailand
38. The Philippines

Sub-Saharan Africa
39. South Africa

Developed-country partners

Asia
40. Japan

Europe
41. Belgium
42. France
43. Germany
44. Italy
45. Netherlands
46. Switzerland
47. United Kingdom

North America
48. Canada
49. USA

Oceania
50. Australia

GCP General Research Meeting participants, September 2011, Hyderabad, India.

Generation Challenge Programme (GCP)
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