



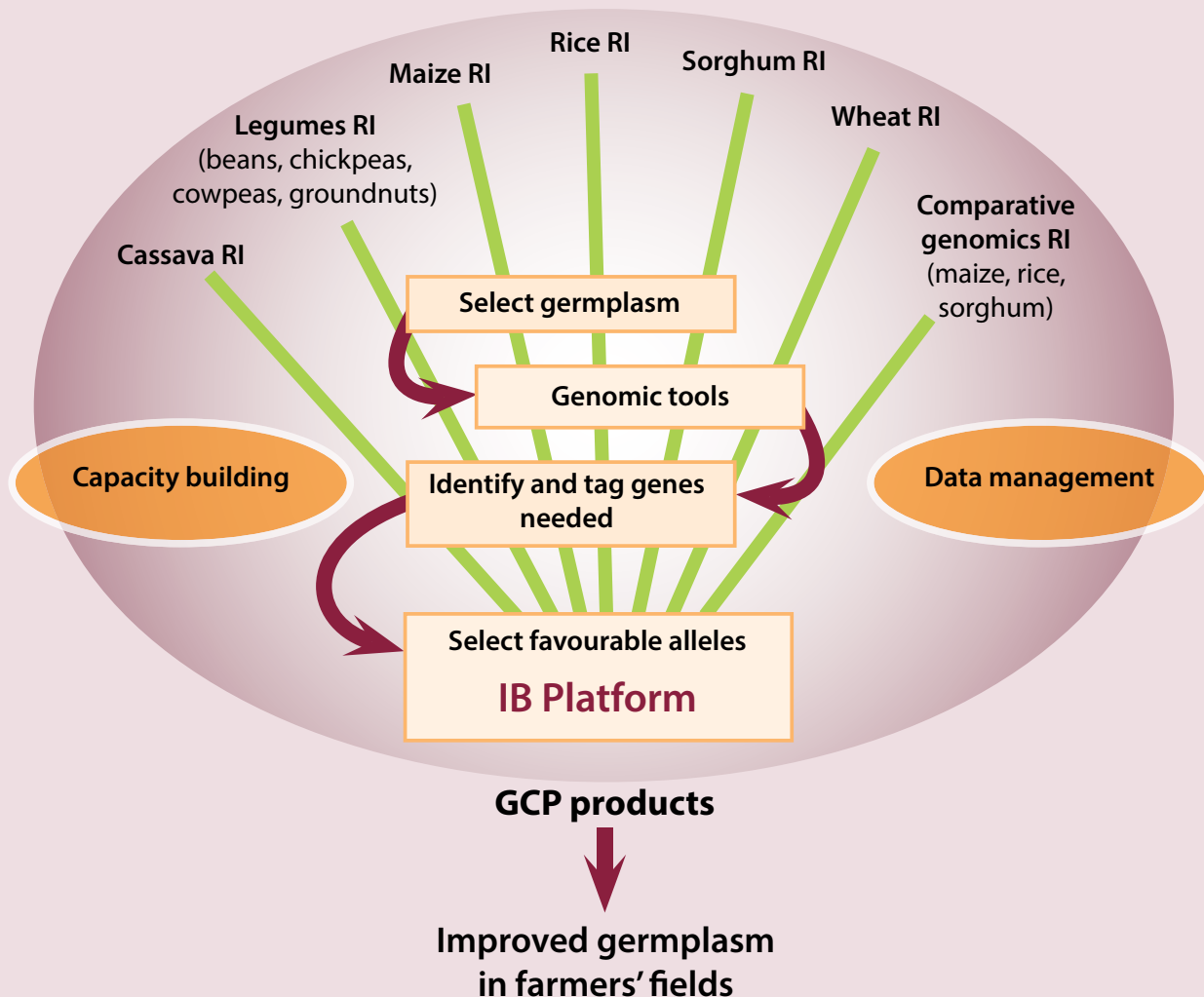
2012

Project Briefs

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.

GCP's research and research support activities





2012 Project Briefs

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Acronyms and abbreviations

AAFC	Agriculture and Agri-Food Canada	CGIAR	Consultative Group on International Agricultural Research
ABRII	Agriculture Biotechnology Research Institute of Iran	CI	Challenge Initiative
ACCI-UKZN	African Centre for Crop Improvement, University of KwaZulu-Natal, South Africa	CIAT	Centro Internacional de Agricultura Tropical (International Center for Tropical Agriculture)
ACGT	African Centre for Gene Technologies, South Africa	CIBE-ESPOL	Centro de Investigaciones Biotecnológicas del Ecuador, Escuela Superior Politécnica del Litoral, Ecuador
ACGT-UoP	African Centre for Gene Technologies–University of Pretoria, South Africa	CIMMYT	Centro Internacional de Mejoramiento de Maíz y Trigo (the International Maize and Wheat Improvement Center)
ACGT-UoW	African Centre for Gene Technologies–University of the Witwatersrand, South Africa	CIMS-INCAE	Centro de Inteligencia sobre Mercados Sostenibles, INCAE Business School, Costa Rica
ACGT-CSIR	African Centre for Gene Technologies– Council for Scientific and Industrial Research, South Africa	CINVESTAV	Centro de Investigación y de Estudios Avanzados, Mexico
ACPFPG	Australian Centre for Plant Functional Genomics, Pty Ltd	CIP	Centro Internacional de la Papa (International Potato Center)
AfricaRice	Africa Rice Center	CIRAD	see Agropolis–CIRAD
AGI	Agricultural Genetics Institute, Vietnam	CMD	cassava mosaic disease
AGRA/PASS	Alliance for a Green Revolution in Africa/Program for African Seed Systems	CNPMF	Centro Nacional de Pesquisa de Mandioca e Fruticultura (National Center for Research on Cassava and Fruit Crops, EMBRAPA, Brazil)
Agropolis–CIRAD	Centre de coopération internationale en recherche agronomique pour le développement, France	CO	crop ontology
Agropolis–INRA	Institut national de la recherche agronomique, France	CoP(s)	community(ies) of practice
Agropolis–IRD	Institut de recherche pour le développement, France	CORAF/WE CARD	Conseil Ouest et Centre africain pour la recherche et le développement agricoles/West and Central African Council for Agricultural Research and Development
AICPMIP	All-India Coordinated Pearl Millet Improvement Project	CP	Challenge Programme of the CGIAR
Al	aluminium	CPATSA	Centro de Pesquisa Agropecuária do Trópico Semi-Árido, EMBRAPA, Brazil
Alt1	marker diagnostic for aluminium tolerance	CRI–CSIR	Crops Research Institute, Council for Scientific and Industrial Research, Ghana
Alt ⁵⁸	marker diagnostic for aluminium tolerance	CRISL	Coconut Research Institute, Sri Lanka
ARC	Africa Rice Center	CRP(s)	CGIAR Research Programme(s)
ARI(s)	advanced research institute(s)	CRRI	Central Rice Research Institute, India
ARI–HAS	Agricultural Research Institute of the Hungarian Academy of Sciences, Hungary	CRS	Chitedze Research Station, Malawi
ARI–ICAR	Agharkar Research Institute, Pune, Maharashtra–Indian Council of Agricultural Research	CRURRS	Central Rainfed Upland Rice Research Station, India
ARI–Naliende	Agricultural Research Institute, Naliende, Tanzania	CSIRO	Commonwealth Scientific and Industrial Research Organisation, Australia
ARI–SRI	Agricultural Research Institute, Sugarcane Research Institute, Kibaha, Tanzania	CSU	Charles Sturt University, Australia
ARS	Agricultural Research Station, Durgapura, Rajasthan, India	CU	Cornell University, USA
BAU	Birsa Agricultural University, Ranchi, India	CWS	configurable workflow system
BC ¹ , BC ² , etc	backcross 1, backcross 2, etc	DAR	Department of Agricultural Research, Myanmar
BC ¹ F ⁴	4 th filial generation progenies derived from backcross 1	DAR4D	Department of Agricultural Research for Development, Zimbabwe
BCKV	Bidhan Chandra Krishi Viswavidyalaya, India	DarT	diversity arrays technology
BCNAM	backcross nested association mapping	DarT P/L	Diversity Arrays Technology Pty, Ltd
Beca	Biosciences Eastern and Central Africa	DARTS	Department of Agricultural Research and Technical Services, Malawi
BF	Barwale Foundation, India	DarT–Gol	Department of Biotechnology, Government of India
BI	Bioversity International	DBT–Gol	Department of Biotechnology, Government of India
BIOTEC	National Center for Genetic Engineering and Biotechnology, Thailand	DDPSC	The Donald Danforth Plant Science Center
Bioversity	Bioversity International	DLM	DNA LandMarks Inc, Canada
BMGF	Bill & Melinda Gates Foundation	DNA	deoxyribonucleic acid
BRAC	Bangladesh Rehabilitation Assistance Committee	DPI&F	Department of Primary Industries and Fisheries, Australia
BRRD	Bureau of Rice Research and Development, Rice Department, Thailand	DPKit	Delivery Plan kit
BRRRI	Bangladesh Rice Research Institute	DPSP–EKC	Department of Plant Sciences and Plant Physiology, Eszterházy Károly College, Eger, Hungary
CAAS	Chinese Academy of Agricultural Sciences	DR&SS	Department of Research and Specialist Services, Zimbabwe
CAAS–MST	Chinese Academy of Agricultural Sciences, Ministry of Science & Technology	DRR	Directorate of Rice Research, India
CAP	Coordinated Agricultural Project (USDA project)	DZARC	Debre Zeit Agricultural Research Centre, Ethiopia
CARDI	Cambodian Agricultural Research and Development Institute	EAST	Embu Agricultural Staff Training (EAST) College, Kenya (GCP) Executive Board
CAS–IP	Central Advisory Service – Intellectual Property	EB	European Commission
CAZRI	Central Arid Zone Research Institute, India	EC	Eastern and Central Africa Bean Research Network
CB	capacity building	ECABREN	Economic community of West African States
CBI–DR&SS	Crop Breeding Institute, Department of Research and Specialist Services, Zimbabwe	ECOWAS	Egerton University, Kenya
CBS	Centre de biotechnologie de Sfax, Tunisia	EgU	Ethiopian Institute of Agricultural Research
CBSD	cassava brown-streak disease	EIAR	early leaf spot
CERAAS	Centre d'étude régional pour l'amélioration de l'adaptation à la sécheresse, Senegal	ELS	
CG	abbreviation for 'CGIAR'		

EMBRAPA	Empresa Brasileira de Pesquisa Agropecuária (Brazilian Agricultural Research Corporation)	IPB–UPLB	Institute of Plant Breeding, University of the Philippines Los Baños
EMBRAPA	EMBRAPA's 'virtual' laboratory in USA at USDA Labex–	IPGR	Institute for Plant Genetic Resources, Bulgaria
EST	expressed sequence tag	IPK	Institute for Plant Genetics and Crop Plant Research, Germany
ETH	Eidgenössische Technische Hochschule, (Swiss Federal Institute of Technology), Zürich, Switzerland	iPlant	iPlant Collaborative
F ₁ , F ₂ , etc	1st filial generation, 2nd filial generation, etc	IRAD	Institut de la recherche agronomique pour le développement, Cameroon
FCRI	Field Crop Research Institute, Vietnam	IRD	see Agropolis–IRD
Fe	iron	IRIS	International Rice Information System
Fedearroz	Federación Nacional de Arroceros, Colombia	IRRI	International Rice Research Institute
FERA	Food and Environment Research Agency, UK (previously known as the Central Science Laboratory)	ISMU	integrated SNP mining and utilisation
G×E	genotype by environment interaction	ISRA	Institut sénégalais de recherches agricoles, Senegal
GBP	British pound	ISRs	intron spanning regions
GCP	Generation Challenge Programme of the CGIAR	IT	information technology
GIS	geographic information system(s)	JCVI	J Craig Venter Institute, USA
GSS	Genotyping Support Service	JIRCAS	Japan International Research Center for Agricultural Sciences
HAAS	Hebei Academy of Agricultural Sciences, China	JNKVV	Jawaharlal Nehru Krishi Vishwa Vidyalaya, India
HAU	Huazhong Agricultural University, China	JUCAVM	Jimma University College of Agriculture & Veterinary Medicine, Ethiopia
HI	harvest index	KAgRI	KATRIN Agricultural Research Institute, Tanzania
HU	Haramaya University, Ethiopia	KARI	Kenya Agricultural Research Institute
IARI	Indian Agricultural Research Institute	KASPar®	KBioscience's PCR SNP genotyping system
IARI–ICAR	Indian Agricultural Research Institute–Indian Council of Agricultural Research	KATRIN	Kilombero Agricultural Training and Research Institute, Tanzania
IBP	Integrated Breeding Platform	KBI	KBioscience, UK
ICABIOGRAD	Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development	KSL	Krishidhan Seeds Ltd, India
ICAR	Indian Council of Agricultural Research	KUL	Katholieke Universiteit Leuven, Belgium
ICARDA	International Center for Agricultural Research in the Dry Areas	LAAS	Luoyang Academy of Agricultural Sciences, China
ICERI	Indonesian Cereals Research Institute	LI	lead institute
ICGGC	International Chickpea Genetics and Genomics Consortium	LIMS	Laboratory Information Management System
ICIS	International Crop Information System	LZARDI	Lake Zone Agricultural Research and Development Institute, Tanzania
ICPMB3	3 _{rd} International Conference on Plant Molecular Breeding, September 2010, Beijing, China	MAB	marker-assisted breeding
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics	MABC	marker-assisted backcrossing
ICS–CAAS	Institute of Crop Science, Chinese Academy of Agricultural Sciences	MAGIC	multiparent advanced generation inter-cross
ICT	information and communication technology	MahU	Mahidol University, Thailand
IDF–HAAS	Institute of Dry Farming, Hebei Academy of Agricultural Sciences, China	MakU	Makerere University, Uganda
IER	Institut d'économie rurale, Mali	MARS	marker-assisted recurrent selection
IFPRI	International Food Policy Research Institute	MAS	marker-assisted selection
IGD–CU	Institute for Genomic Diversity, Cornell University, USA	MATE	multidrug and toxic compound extrusion
IGKV	Indira Gandhi Krishi Vishwavidyalaya (Indira Gandhi Agricultural University), India	MAU	Marathwada Agricultural University, India
IIAM	Instituto de Investigação Agrária de Moçambique (Institute for Agricultural Research, Mozambique)	MBP	Molecular Breeding Platform (<i>now renamed IBP</i>)
IICRD–KU	Inseechandrastitya Institute for Crop Research and Development, Kasetsart University, Thailand	MoU	Memorandum of Understanding
IIPR	Indian Institute of Pulses Research	MPIMPP	Max Planck Institute for Molecular Plant Physiology, Germany
IITA	International Institute of Tropical Agriculture	MSc	Master of Science
ILRI	International Livestock Research Institute	MST	Ministry of Science & Technology, China
INERA	Institut de l'environnement et de recherches agricoles, Burkina Faso	MSV	maize streak virus
INIA–Chile	Instituto de Investigaciones Agropecuarias, Chile	MT	(GCP) Management Team
INIA–Uruguay	Instituto Nacional de Investigación Agropecuaria, Uruguay	MTP	<i>depending on context</i> , Medium-Term Plan or minimum tiling path
INIFAP	Instituto Nacional de Investigaciones Forestales y Agropecuarias, Mexico	MU	Moi University, Kenya
INRA–Morocco	Institut national de la recherche agronomique, Morocco	NaCRRI	National Crop Resources Research Institute, Uganda
INRAN	Institut national de la recherche agronomique du Niger	NAFRI	National Agricultural and Forestry Research Institute, Laos
INTA–Argentina	Instituto Nacional de Tecnología Agropecuaria, Argentina	NagU	Nagoya University, Japan
INTA–Nicaragua	Instituto Nicaragüense de Tecnología Agropecuaria, Nicaragua	NAM	nested association mapping
IP	intellectual property	NARS	national agricultural research system(s)
IPAC	Intellectual Property Advisory Committee (of the GCP EB)	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	SMTA	standard material transfer agreement
NMRI	National Maize Research Institute, Vietnam	SNP	single nucleotide polymorphism
NPGRC	National Plant Genetic Resources Centre, Tanzania	SP	(GCP) Subprogramme
NRCPB	National Research Centre on Plant Biotechnology, India	SP1, SP2, etc	Subprogramme 1, Subprogramme 2, etc
NRCRI	National Root Crops Research Institute, Nigeria	SP2L	SP2 Leader
NRCS	National Research Centre on Sorghum, India	SPARC	Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food (AAFC), Canada
NRTP-ARI	National Root and Tuber Programme, Agricultural Research Institute, Naliende Research Station, Tanzania	SPL	Subprogramme Leader
NSF	National Science Foundation, USA	SPVD	sweet potato virus disease
NSFCRC	Nakhon Sawan Field Crops Research Center, Thailand	SSA	sub-Saharan Africa
NU	Ningxia University, China	SSR	simple sequence repeat
NWSUAF	Northwest Sci-tech University of Agriculture and Forestry, China	SUA	Sokoine University of Agriculture, Tanzania
OSU	Oregon State University, USA	TAMU	Texas A&M University, USA
P	phosphorus	TL	Theme Leader
PAC	(GCP) Programme Advisory Committee (defunct)	TLI	Tropical Legumes I Project
PAU	Punjab Agricultural University, India	TLII	Tropical Legumes II Project
PBI-UoS	Plant Breeding Institute, University of Sydney, Australia	TLM	Tropical Legumes I annual meeting (GCP)
PCR	polymerase chain reaction	TNAU	Tamil Nadu Agricultural University, India
PD	Product Delivery (Leader)	TPE	target of population environments
PDA-GPS	personal digital assistant–Global Positioning System	TUSs	tentative unique sequences
PDC	Product Delivery Coordinator	UAS-B	University of Agricultural Sciences, Bangalore, India
PDKV	Dr Panjabrao Deshmukh Krishi Vidyapeeth (Dr Panjabrao Deshmukh Agricultural University), India	UAS-D	University of Agricultural Sciences, Dharwad, India
PDL	Product Delivery Leader	UCB	Universidade Católica de Brasília, Brazil
PGRRI	Plant Genetic Resources Research Institute, Council for Scientific and Industrial Research, Ghana	UC-D	University of California, Davis, USA
PHI	Pioneer Hi-Bred International, Inc	UC-R	University of California, Riverside, USA
PhilRice	Philippine Rice Research Institute	UdB	Università di Bologna, Italy
PI	Principal Investigator	UdR	Universidad de la Republica, Uruguay
PROINPA	Promoción e Investigación de Productos Andinos, Bolivia	UEM	Universidade Eduardo Mondlane, Mozambique
PSC	(GCP) Programme Steering Committee (defunct)	UFS	University of Free State, South Africa
PSU	Pennsylvania State University, USA	UG	University of Ghana
<i>Pup1</i>	marker diagnostic for phosphorus uptake	UGA	University of Georgia, USA
QTL	quantitative trait locus	UK	United Kingdom
QTL×E	QTL by environment interaction	UKM	Universiti Kebangsaan, Malaysia
R&D	research and development	UKZN	University of KwaZulu–Natal, South Africa
R4D	research for development	UNALM	Universidad Nacional Agraria La Molina, Peru
RAD	restriction site associated DNA sequencing	UNIBO	Università di Bologna, Italy
RAKCA	RAK College of Agriculture–Sehore, Madhya Pradesh, India	UoA	University of Arizona, USA
RAP	Review and Advisory Panel	UoAb	University of Aberdeen, Scotland
RARS	Regional Agricultural Research Station, Nandyal, India	UoAl	University of Alberta, Canada
RAU	Rajasthan Agricultural University, India	UoD	University of Dhaka, Bangladesh
RCSL(s)	recombinant segment substitution line(s)	Uol	University of Ibadan, Nigeria
RGDU-BIOTEC	Rice Gene Discovery Unit, National Center for Genetic Engineering and Biotechnology, Thailand	UoM	University of Maryland, USA
RI(s)	(GCP) Research Initiative(s)	UoMi	University of Missouri, USA
RIKEN	Rikagaku Kenkyūsho (Institute of Physical and Chemical Research), Japan	UoN	University of Nairobi, Kenya
RIL(s)	recombinant inbred line(s)	UoP	University of Pretoria, South Africa
RRDI	Rice Research and Development Institute, Sri Lanka	UoPd	University of Potsdam, Germany
RYMV	rice yellow mottle virus	UoW	University of the Witwatersrand, South Africa
SAAS	Shanxi Academy of Agricultural Sciences, China	UoZ	University of Zambia
SABRN	Southern Africa Bean Research Network	UPLB	University of The Philippines Los Baños
<i>Saltol</i>	marker diagnostic for salt tolerance	UQ	University of Queensland, Australia
SARI-CSIR	Savanna Agricultural Research Institute, Council for Scientific and Industrial Research, Ghana	USA	United States of America
SARI-Ethiopia	South Agricultural Research Institute, Ethiopia	USAID	United States Agency for International Development
SCRI	Scottish Crop Research Institute, UK	USD	United States dollar
SEC	southern, eastern and central (Africa)	USDA-ARS	United States Department of Agriculture–Agricultural Research Service
SGRP	(CGIAR) System-wide Genetic Resources Programme	UTM	Université de Tunis El Manar, Tunisia
SHW	synthetic hexaploid wheat	VBI	Virginia Bioinformatics Institute, VPI
Sida	Swedish International Development Cooperation Agency	VPI	Virginia Polytechnic Institute and State University, USA
SiMAC	Scientific and Management Advisory Committee (of the IBP)	WA	Waen Associates, UK
SINGER	(CGIAR) Systemwide Information Network for Genetic Resources	WACCI	West Africa Centre for Crop Improvement, University of Ghana
SME(s)	Small- and medium-scale enterprise(s)	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 (<i>Zea mays</i>)
		Zn	zinc
		ZU	Zhejiang University, China
		$\Delta_{13}\text{C}$	carbon isotope discrimination
		^0C	degrees Celsius

2012 Project Briefs

I. Research Initiatives

1. Cassava

1. 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–Feb 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 Adjepong)
- 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 aforementioned 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.

2. 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.

3. 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–March 2013; NCE: Mar 2014
- 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.

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

- Duration: Apr 2010–Mar 2012; NCE: Oct 2012
- Total budget: USD 128,620

Principal Investigator and lead institute:

Alfredo Alves, EMBRAPA Cassava and Tropical Fruits (CNPMPF)

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/travel grant

5. 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
- NaCRRRI – Yona Baguma
- NaCRRRI – 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 (NaCRRRI), 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, Missouri, 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.

6. Project No G4012.02.01: Travel grant – GCP 21–II conference

- *Duration: Apr 2010–Mar 2012*
- *Total budget: USD 25,000*

Principal Investigator and lead institute:

Claude M. Fauquet, DDPSC

Collaborating institutes and scientists:

2. Legumes

Beans

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

- Duration: Nov 2008–Oct 2011; NCE: Oct 2012
- 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 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

Bodo Raatz (CIAT)

Collaborating institutes and scientists

- CIAT – Idupulapati Rao,
- DR&SS/CBI, Zimbabwe – Godwill S Makunde
- CU
- UCD
- 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 gene pool 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 gene pool 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 gene pool into the Andean gene pool using the baseline of QTL mapping and advanced-backcross populations developed in Phase I. The second approach will be MARS breeding within the Andean gene pool 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

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

- Duration: Aug 2011–Jul 2014
- 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.

10. 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.

11. 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 ($\delta^{13}C$) 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.

Cowpeas

12. 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
 - G7010.07.01: USD 700,000

Principal Investigator and lead institute

Phil Roberts, 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 evaluations 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 gesnerioides* 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

13. 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 – Ndoeye 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 Bertioli;
- EMBRAPA Genetic Resources and Biotechnology (Brazil) – Soraya CML Leal Bertioli

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

14. 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.

15. Project No G6010.06: Forensic marker service activities

- *Duration: Feb 2012–May 2014*
- *Total budget: USD 500,000*

Principal Investigator and lead institute
Chunlin He, GCP

The Tropical Legumes projects (TLI and TLII) funded by the Bill & Melinda Gates Foundation are focused on improving the productivity and profitability of key tropical legumes in target regions of sub-Saharan Africa and India. TLI is researching the application of molecular tools and approaches for marker-based breeding of the key tropical legume crops and is focused on two main areas: the development of genomic tools in the form of markers and associated linkage information, and the implementation of molecular breeding methodologies such as marker-assisted selection (MAS), marker-assisted backcrossing (MABC) and marker-assisted recurrent selection (MARS). TLI is linked with TLII so that the tools and methodologies developed by TLI are directly applied in TLII as part of the CGIAR and NARS breeding programs, leading to new varieties being made available to the farmers in shorter time than using conventional breeding and selection.

While TLI and TLII are addressing many of the scientific and practical aspects of the integration of molecular approaches in breeding, one area that is not included in the TLI and TLII proposals but that is crucial as molecular tools become more widely used, is the area of forensics (essentially quality assurance/quality control of breeding materials). Therefore, supplementary funding is requested to allow the inclusion of a strong forensics component to the TLII breeding activities that will enable more effective use of molecular markers in the breeding programs and provide higher quality assurance of the materials in the breeding pipeline.

While this proposal is targeting the TLII breeding program, it is proposed to have the forensic services and associated funds managed as a supplemental

fund request to the TLI Phase 2 proposal. As implementing agency of TLI, the Generation Challenge Program (GCP) will facilitate and coordinate access to marker services and will provide training support to TLII breeders on marker applications and on data management for the forensic activities. A project management committee to include TLI and TLII scientists will oversee the supplemental program and determine how the funds should be allocated to best meet the TLII breeding needs. TLII will ensure the proper implementation of the forensic goals within its programs, while the GCP will ensure that the genotyping work is conducted properly and with appropriate technical and logistic support.

Capacity-building activities:

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

16. 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

Bodo Raatz, 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.

17. 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

Phil Roberts wef May 2012 ; previous PI : 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.

18. 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.

19. 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.

20. Project No G4012.02.92: Travel grant – VI ICLGG

- *Duration: Apr 2012–Oct 2012*
- *Total Budget: 25,000*

Principal Investigator and lead institute

Ndeye Ndack Diop, GCP

Collaborating institutes and scientists:

21. 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

22. 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 Zürich using a non-invasive imaging technique, and variation in leaf elongation rate under vegetative drought conditions

will be examined at INRA Montpellier. 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).

23. Project No G4008.56: AMDROUT: Asian Maize Drought Tolerance project

- *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

24. 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: April 2012
- 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.

25. 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 stress-induced 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 use efficient 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.

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

- *Duration:* Nov 2008–Oct 2011; *NCE:* April 2013
- *Total budget:* USD 900,000

Principal Investigator and lead institute

K McNally and Amelia Henry, 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 drought avoidance 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.

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

- *Duration:* Nov 2008–Oct 2011; *NCE:* March 2013
- *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.

28. Project No G4008.45: A Nested Association Mapping (NAM) population of rice: Laying the bases for highly efficient QTL characterisation population of rice

- *Duration: Aug 2008–Jul 2010; NCE: July 2013*
- *Total budget: USD 226,000*

Principal Investigator and lead institute

Mathias Lorieux, Agropolis–IRD/CIAT

Collaborating institutes and scientists

- ARC – Marie-Noelle Ndjondjop

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.

29. 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, IIRRI

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 improve grain 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.

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

- Duration: Nov 2011–Oct 2012; NCE: Oct 2013
- Total budget: USD 179,292

Principal Investigator and lead institute

Cécile Grenier, Agropolis–CIRAD/CIAT

Collaborating institutes and scientists

- ARC – M Ndjondjop

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” led 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.

31. 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 multiparent advanced generation intercrosses (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.

32. 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 end 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 \times environment interactions will be elucidated. Recurrent recombination of specific individuals of the population carrying the favourable 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

33. 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; *NCE:* Jul 2013
- *Total budget:* USD 210,630

Principal Investigator and 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.

34. 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.

5. Sorghum

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

- *Duration: Nov 2008–Oct 2011; NCE: Dec 2013*
- *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.

36. 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 multilocally 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.

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

- *Duration: Aug 2008–Jul 2013; NCE: Oct 2014*
- *Total budget: USD 678,600*

Principal 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 Vaksman

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.

38. Project No G4012.01/G7009.04: Development and evaluation of drought-adapted sorghum germplasm for Africa and Australia

- Duration: Jul 2009–Jun 2014
- 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 Vaksman

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).

39. 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 Vaksman, 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

40. 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 2013
- 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.

41. 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 Ogonnaya, 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.

42. 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.

43. 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

44. 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; NCE: Oct 2012
- 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.

45. 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 Prasetyono

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.

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

- Duration: Oct 2009–Mar 2012; NCE: Mar 2013
- 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.

47. 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 Vasconcelos, 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 RILs 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.

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

- *Duration: Apr 2010–Mar 2012; NCE: Mar 2013*
- *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.

49. 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*, functioning 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 *S₁* and *S₂* 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.

50. 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.

51. 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.

52. 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 Moraes 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 2 – Integrated crop breeding

53. 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 Gandhi 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.

Theme 3 – Crop information systems

Project sfor this theme are listed below under Integrated breeding system

Theme 4 – Capacity building

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

- *Duration: Jan 2007–Dec 2011; NCE: Sep 2012*
- *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-Champaign, 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).

55. 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.

Theme 5 – Product delivery

56. 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.

III. Service Component – Integrated Breeding Platform Project

G8009: Integrated Breeding Platform

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

Project Leader and lead institute

Xavier Delannay, GCP

Collaborating institutes and scientists

- GCP – Graham McLaren, Larry Butler, Xavier Delannay, Ndeye Ndack Diop, Antonia Okono, Chunlin He, Arlet Portugal, Delphine Fleury, Fred Okono, Mark Sawkins
- 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.

G8009.01 Objective 1.1: Establish and manage the Integrated Breeding Platform (IBP)

57. Project No G8009.01.01/Activity 1.1.1: Establish and manage the IBP

Activity Leader and lead institute

Xavier Delannay, GCP

58. Project No G8009.01.02/Activity 1.1.2: Develop and deploy the IBP web portal

Activity Leader and lead institute

Fred Okono, GCP

59. Project No G8009.01.03/Activity 1.1.3: Establish IBP Helpdesk and coordinate training and communication activities

Activity Leader and lead institute

Ndeye Ndack Diop, GCP

60. Project No G8009.01.04/Activity 1.1.4: Establish and support crop molecular breeding communities of practice

Activity Leader and lead institute

Ndeye Ndack Diop, GCP

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.

G8009.02 Objective 2.1: Make existing tools for data management and breeding logistics available to molecular breeding projects through the IBP

Project No 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: COMPLETED IN JULY 2012

Activity Leader and lead institute

Shawn Yates and Fran Clarke, AAFC

Project No G8009.02.02/Activity 2.1.2: Identify, deploy and support tools to manage phenotypic characterisation and evaluation: COMPLETED IN DECEMBER 2012

Activity Leader and lead institute

H Sánchez, CIMMYT

Project No G8009.02.03/Activity 2.1.3: Identify, deploy and support tools to manage genotypic characterization: COLLAPSED INTO ACTIVITY 2.2.4 IN JUNE 2012

Activity Leader and lead institute

Trushar Shah, ICRISAT

G8009.03/G8009.04 – Objective 2.2: Develop and deploy an integrated breeding (IB) configurable workflow system

This objective includes the following activities and subactivities:

61. G8009.03.01/Activity 2.2.1: Develop and deploy an IB WorkBench Administration & Configuration Application

Activity Leader and lead institute

Graham McLaren, GCP

62. Subactivity 2.2.1.1: Develop an IB Workflow Administration Application

Activity Leader and lead institute

Graham McLaren, GCP

63. Subactivity 2.2.1.2: Develop IB Project Configuration Application

Activity Leader and lead institute

Graham McLaren, GCP

- 64. Subactivity 2.2.1.3: Develop Database back-end for the IB workflow**
Activity Leader and lead institute
Graham McLaren, GCP
- 65. G8009.03.02/Activity 2.2.2: Develop and deploy an IB Management System Application**
Activity Leader and lead institute
Graham McLaren, GCP
- 66. Subactivity 2.2.2.1: Develop Breeding Manager Application**
Activity Leader and lead institute
H Sanchez, CIMMYT
- 67. Subactivity 2.2.2.2: Develop Genealogy Manager Application**
Activity Leader and lead institute
William Eusebio, IRRI
- 68. Subactivity 2.2.2.3: Develop Query Manager Application**
Activity Leader and lead institute
Graham McLaren, GCP
- 69. G8009.03.03/Activity 2.2.3: Develop and deploy an IB Field Trial Management System Application**
Activity Leader and lead institute
Graham McLaren, GCP
- 70. Subactivity: 2.2.3.1 Develop a trial FieldBook application**
Activity Leader and lead institute
H Sanchez, CIMMYT
- 71. Subactivity: 2.2.3.2 Develop an environment characterisation system application**
Activity Leader and lead institute
G McLaren, GCP
- 72. G8009.03.04/Activity 2.2.4: Develop and deploy an IB genotypic data management system application**
Activity Leader and lead institute
G McLaren, GCP
- 73. Subactivity 2.2.4.1: Develop a genotypic data management application**
Activity Leader and lead institute
Trushar Shah, ICRISAT
- 74. G8009.03.05/Activity 2.2.5: Develop and deploy an IB analytical pipeline application**
Activity Leader and lead institute
Mark Sawkins, GCP
- 75. Subactivity 2.2.5.1: Develop a data management application**
Activity Leader and lead institute
Mark Sawkins, GCP
- 76. Subactivity 2.2.5.2: Develop a phenotypic data analysis application**
Activity Leader and lead institute
FA v Eeuwijk, WUR/G Ye, IRRI
- 77. Subactivity 2.2.5.3: Develop a molecular genetic analysis application**
Activity Leader and lead institute
FA v Eeuwijk, WUR/G Ye, IRRI
- 78. Subactivity 2.2.5.4: Develop a selection indices application**
Activity Leader and lead institute
J Crossa, CIMMYT/FA v Eeuwijk, WUR
- 79. Subactivity 2.2.5.5: Genstats Breeding View**
Activity Leader and lead institute
J Crossa, CIMMYT/FA v Eeuwijk, WUR
- 80. G8009.03.06/Activity 2.2.6: Develop and deploy an IB decision support system application**
Activity Leader and lead institute
Mark Sawkins, GCP
- 81. Subactivity 2.2.6.1: Develop breeding decision support applications**
Activity Leader and lead institute
T Shah, ICRISAT
- 82. Subactivity 2.2.6.2: Develop MARS decision support application**
Activity Leader and lead institute
Alain Charcosset, CIRAD
- 83. Subactivity 2.2.6.3: Develop simulation application: *TERMINATED DECEMBER 2012***
Activity Leader and lead institute
M Dieters, UoQ

Component 3: 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.

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

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.

84. G8009.05.01/Activity 3.1.1: Genetic Resources Support Service

Activity Leader and lead institute
Larry Butler, GCP

85. G8009.05.02/Activity 3.1.2: Marker services

Activity Leader and lead institute
Chunlin He, GCP

86. G8009.05.03/Activity 3.1.3: Trait and metabolite services

Activity Leader and lead institute
Chunlin He, GCP

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

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:

87. G8009.06.01/Activity 3.2.1: Breeding Plan development

Activity Leader and lead institute
Mark Sawkins, GCP

88. Subactivity 3.2.1.2: PMB (Planning tool for molecular breeding projects – project appraisal and cost-benefit analysis to support decision-making)

Activity Leader and lead institute
Mark Sawkins, GCP and Jiankang Wang, CIMMYT/CAAS

89. G8009.06.02/Activity 3.2.2: Information management

Activity Leader and lead institute
Arlet Portugal, GCP

90. G8009.06.03/Activity 3.2.3: Data curation

Activity Leader and lead institute
Arlet Portugal, GCP

91. G8009.06.04/Activity 3.2.4: Design & analysis

Activity Leader and lead institute
Marcos Malosetti, WUR

92. G8009.06.05/Activity 3.2.5: Phenotyping sites & screening protocols

Activity Leader and lead institute
Xavier Delannay, GCP

93. G8009.06.06/Activity 3.2.6: Genotyping Support Service

Activity Leader and lead institute
Chunlin He, GCP

94. G8009.06.07/Activity 3.2.7: IP & policy helpdesk

Activity Leader and lead institute
L Butler, GCP

Projects reported under Theme 3 – Crop information systems

95. 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
 - Total 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.

96. 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 unmanageable 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 accumulates 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.

97. Project No G4011.09: Development 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, Arlet 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.

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II. Themes

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

I. Research Initiatives

1. Cassava

#	Projects		Principal Investigator	Target Countries	Target Traits	Partners	Project Dates	
	Axapta No	Project Title					Start	End
1.	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
2.	G7009.10/ G7010.01.02	Improving and deploying markers for biotic traits in cassava	Chiedozi Egesi, NRCRI	Nigeria, Tanzania, Ghana	• drought tolerance • biotic traits	CRI–CSIR, DDPSC, NRTP/ARI–NRS	March 2010	February 2014
3	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
4.	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 and travel grant

5.	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
6.	G4012.02.01	Travel grant: GCP21–II conference	Claude M. Fauquet, DDPSC	various	various		February 2012	August 2012

2. Legumes

2. Legumes			Principal Investigator	Target Countries	Target Traits	Partners	Project Dates	
#	Axapta No	Project Title					Start	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.	G6010.03	Improve common bean productivity for marginal environments in sub-Saharan Africa	B Raatz, CIAT	Kenya, Ethiopia, Malawi, Zimbabwe	• drought tolerance • disease & pest resistance • productivity	DARTS, CBI–DAR4D, ECABREN, KARI, SABRN, SARI–E	May 2010	May 2014
Chickpeas								
9.	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
10.	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
11.	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
Cowpeas								
12.	G6010.02/ G7010.07.01	Improve cowpea productivity for marginal environments in sub-Saharan Africa (TLI project, Objective 2)	Phil Roberts, wef May 2012; previous PI: Jeffe Ehlers, UC–R	Mozambique, Senegal, Burkina Faso	• drought tolerance • disease & pest resistance • productivity	IITA, INERA, ISRA, UEM	May 2010	May 2014
Groundnuts								
13.	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								
14.	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
15.	G6010.06	Forensic marker service activities (includes soya bean and pigeonpea)	Chunlin He, GCP	Global	• drought tolerance • Yield and seed quality	Various	February 2012	May 2014

#	Axapta No	Projects	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
		Project Title						Start	End
Capacity-building activities:									
Capacity-building projects: training components for TLI scientists and students									
16.	G4009.07.01	Capacity-building à la carte 2009 – TLI students for analysis of drought tolerance in common beans	Bodo Raatz, CIAT	Ethiopia, Zimbabwe	• beans	• drought tolerance	SARI–E, UFS	October 2009	October 2010; NCE: May 2013
17.	G4009.07.02	Capacity-building à la carte 2009 – Capacity-building in modern cowpea breeding	Phil Roberts wef May 2012; previous PI : Jeffrey D Ehlers, UCR	Senegal, Mozambique	• cowpeas	• drought tolerance	ISRA, UEM	October 2009	October 2010; NCE: May 2013
18.	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
19.	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
20.	G4012.02.02	Travel grant: VI ICLGG	Rajeev K Varshney, ICRISAT		various	various	various		April 2012 October 2012
21.	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

#	Axapta No	Projects	Principal Investigator	Target Countries	Target Traits	Partners	Project Dates	
		Project Title					Start	End
22.	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
23.	G4008.56	AMDR0UT: 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		Principal Investigator	Target Countries	Target Traits	Partners	Project Dates	
	Axapta No	Project Title					Start	End
24.	G3007.05	<i>Detecting and fine-mapping QTLs with major effects on rice yield under drought stress for deployment via marker-aided breeding</i>	Arvind Kumar, IRRI	Global	• drought tolerance	BF, BiAU, CRRI, CRURRS, IGKV, JNKVV, NDUAT, TNAU, UoAI, UAS–B, YAAS	August 2007	July 2009; NCE: April 2012
25.	G3008.03	<i>Delayed senescence and drought tolerance in rice</i>	Eduardo Blumwald, UCD	Global	• drought tolerance	IRRI	November 2008	October 2011; NCE: October 2012
26.	G3008.06	<i>Targeting drought-avoidance root traits to enhance rice productivity under water-limited environments</i>	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: April 2013
27.	G3008.09	<i>Breeding drought tolerance for rainfed lowland rice in the Mekong region</i>	Boonrat Jongdee, BRD	Mekong Delta	• drought tolerance	CARDI, NAFRI, UQ	November 2008	October 2011; NCE: March 2013
28.	G4008.45	<i>A Nested Association Mapping (NAM) population of rice: laying the bases for highly efficient QTL characterisation</i>	Mathias Lorieux, Agropolis –IRD/CIAT	Global	• drought tolerance	ARC	August 2008	July 2010; NCE: July 2013
29.	G4011.04	<i>Dissemination and community of practice for newly developed drought-tolerant QTLs pyramided breeding lines</i>	Arvind Kumar, IRRI		• drought tolerance	CRRI, CRURRS, DRR–ICAR, NDUAT	July 2011	June 2014
30.	G4011.06	<i>Field phenotyping for drought resistance of the MARS population developed under the GCP Rice RI</i>	Cécile Grenier, Agropolis –CIRAD/CIAT		• drought tolerance	ARC	November 2011	October 2012; NCE: October 2013
31.	G4011.07	<i>Rice multiparent advanced generation intercrosses (MAGIC) – Phase II</i>	Hei Leung, IRRI				November 2011	October 2013
32.	G7010.04.01	<i>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</i>	Marie-Noëlle Ndjondjop, ARC	Burkina Faso, Mali, Nigeria	• drought tolerance • yield	Agropolis–CIRAD, Agropolis–IRD, IER, INERA, IRRI, NCRI	May 2010	April 2014

#	Projects		Principal Investigator	Target Countries	Target Traits	Partners	Project Dates	
	Axapta No	Project Title					Start	End
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			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
Capacity-building activities:								
Community of practice								
33.	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; NCE: July 2013
34.	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

5. Sorghum

#	Projects		Principal Investigator	Target Countries	Target Traits	Partners	Project Dates	
	Axapta No	Project Title					Start	End
35.	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
36.	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
37.	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
38.	G4012.01/ G7009.04/	Development and evaluation of drought-adapted sorghum germplasm for Africa and Australia (G4012.01: Phase II)	David Jordan and Andrew Borrell, DPI&F/UQ	Africa, Australia	• drought tolerance	Agropolis–CIRAD, IER	July 2009	June 2014
39.	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 Vaksman, Agropolis–CIRAD, Eva Weltzien, ICRISAT	Mali	• drought tolerance • yield • quality		January 2010	June 2014

6. Wheat

#	Projects		Principal Investigator	Target Countries	Target Traits	Partners	Project Dates	
	Axapta No	Project Title					Start	End
40.	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 2013
41.	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
42.	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	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
43.	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

#	Axapta No	Projects	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
		Project Title						Start	End
44.	G3008.02	<i>Improving grain yield on acid soils by the identification of genetic factors underlying drought and aluminium tolerance in maize and sorghum</i>	Leon Kochian, CU/USDA–ARS	Global	Maize, Sorghum	• drought tolerance • Al tolerance	EMBRAPA, MU/KARI	November 2008	October 2011; NCE: October 2012
45.	G3008.04	<i>Drought from a different perspective: Improved tolerance through Phosphorus acquisition</i>	Sigrid Heuer, IRRI	Global	Rice	• drought tolerance • Phosphorous deficiency	ICABIOGRD, JIRCAS, UoP/MPI-MP	November 2008	October 2011; NCE: October 2012
46.	G7009.07	<i>Cloning, characterisation and validation of AltSB/Al tolerance in rice</i>	Leon Kochian and Susan McCouch, CU/USDA–ARS	Global	Rice	• Aluminium tolerance	ICABIOGRD	October 2009	March 2012; NCE: March 2013
47.	G7010.03.01	<i>Cloning, characterisation and validation of Pup1/P efficiency in maize</i>	Leon Kochian, CU/USDA–ARS	Global	Maize	• Phosphorous efficiency	EMBRAPA, IRRI, JIRCAS, MU/KARI	April 2010	March 2014
48.	G7010.03.02	<i>Cloning, characterisation and validation of AltSB/Al tolerance in maize</i>	Claudia Guimãraes, EMBRAPA	Global	Maize	• Al tolerance	CU/USDA–ARS, MU/KARI	April 2010	March 2012; NCE: March 2013
49.	G7010.03.03	<i>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</i>	Eva Weltzien, ICRISAT	Africa	Sorghum	• Al tolerance • Phosphorous efficiency • Productivity	CU/USDA–ARS, EMBRAPA, INRAN, MU/KARI	April 2010	March 2014
50.	G7010.03.04	<i>Developing rice with dual tolerance of phosphorus deficiency and aluminum toxicity: marker-assisted pyramiding of Pup1 with novel tolerance QTLs</i>	Sigrid Heuer, IRRI	Asia	Rice	• phosphorous deficiency • Al tolerance	CU/USDA–ARS, EMBRAPA, ICABIOGRD, JIRCAS	April 2010	March 2014
51.	G7010.03.05	<i>Marker-assisted backcrossing for improving phosphorous-use efficiency and tolerance to aluminium toxicity via Pup-1 and AltSB genes in maize</i>	Samuel Gudu, MU/KARI	Global	Maize	• Al tolerance • Phosphorous efficiency	CIMMYT, EMBRAPA, IRRI, JIRCAS, USDA–ARS	April 2010	March 2014
52.	G7010.03.06	<i>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</i>	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

NONE

Theme 2 – Integrated crop breeding

#	Axapta No	Projects	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
		Project Title						Start	End
53.	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

Theme 3 – Crop information systems

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

Theme 4 – Capacity building

#	Axapta No	Projects	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
		Project Title						Start	End
54.	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
55.	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

Theme 5 – Product delivery

#	Axapta No	Projects	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
		Project Title						Start	End
56.	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

III. Service Component – Integrated Breeding Platform

Integrated Breeding Platform portal and helpdesk

#	Axapta No	Projects	Principal	Target	Target	Target Traits	Partners	Project Dates	
		Project Title	Investigator	Countries	Crops			Start	End
Component 1: Integrated Breeding Platform portal and helpdesk									
G8009.01 – Objective 1.1: Establish and manage the Integrated Breeding Platform (IBP)									
57.	G8009.01.01	Activity 1.1.1: Establish and manage the IBP	Xavier Delannay, GCP	Global	Global	Global	AAFC, Agropolis –INRA, BI, CAAS, CIAT, CIMMYT, CSIRO, ICRISAT, IRRI, KUL, UQ, WUR	July 2009	July 2014
58.	G8009.01.02	Activity 1.1.2: Develop and deploy the IBP web portal	Fred Okono, GCP	Global	Global	Global		July 2009	July 2014
59.	G8009.01.03	Activity 1.1.3: Establish IBP Helpdesk and coordinate training and communication activities	Ndeye Ndack Diop, GCP	Global	Global	Global		July 2014	July 2009
60.	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

Integrated breeding information system								
#	Axapta No	Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates Start End
Component 2: Integrated breeding information system								
G8009.02 – Objective 2.1: Make existing tools for data management and breeding logistics available to molecular breeding projects through the IBP								
	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

#	Axapta No	Projects	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
		Project Title						Start	End
62.		Subactivity 2.2.1.1: <i>Develop an IB Workflow Administration Application</i>	Graham McLaren, GCP	Global	Global	Global		July 2009	July 2014
63.		Subactivity 2.2.1.2: <i>Develop IB Project Configuration Application</i>	Graham McLaren, GCP	Global	Global	Global		July 2009	July 2014
64.		Subactivity 2.2.1.3: <i>Develop Database back-end for the IB workflow</i>	McLaren, GCP	Global	Global	Global		July 2009	July 2014
65.	G8009.03.02	Activity 2.2.2: <i>Develop and deploy an IB Management System Application</i>	Graham McLaren, GCP	Global	Global	Global		July 2009	July 2014
66.		Subactivity 2.2.2.1: <i>Develop Breeding Manager Application</i>	H Sanchez, CIMMYT	Global	Global	Global		July 2009	July 2014
67.		Subactivity 2.2.2.2: <i>Develop Genealogy Manager Application</i>	William Eusebio, IRRI	Global	Global	Global		July 2009	July 2014
68.		Subactivity 2.2.2.3: <i>Develop Query Manager Application</i>	Graham McLaren, GCP	Global	Global	Global		July 2009	July 2014
69.	G8009.03.03	Activity 2.2.3: <i>Develop and deploy an IB Field Trial Management System Application</i>	Graham McLaren, GCP	Global	Global	Global		July 2009	July 2014
70.		Subactivity: 2.2.3.1 <i>Develop a Trial FieldBook Application</i>	H Sanchez, CIMMYT	Global	Global	Global		July 2009	July 2014
71.		Subactivity: 2.2.3.2 <i>Develop an Environment Characterisation System Application</i>	G McLaren, GCP	Global	Global	Global		July 2009	July 2014
72.	G8009.03.04	Activity 2.2.4: <i>Develop and deploy an IB Genotypic Data Management System Application</i>	G McLaren, GCP	Global	Global	Global		July 2009	July 2014
73.		Subactivity 2.2.4.1: <i>Develop a Genotypic Data Management Application</i>	Trushar Shah, ICRISAT	Global	Global	Global		July 2009	July 2014
74.	G8009.03.05	Activity 2.2.5: <i>Develop and deploy an IB Analytical Pipeline Application</i>	Mark Sawkins, GCP	Global	Global	Global		July 2009	July 2014
75.		Subactivity 2.2.5.1: <i>Develop a Data Management Application</i>	Mark Sawkins, GCP	Global	Global	Global		July 2009	July 2014

#	Axapta No	Projects	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
		Project Title						Start	End
76.		<i>Subactivity 2.2.5.2: Develop a Phenotypic data Analysis Application</i>	FA v Eeuwijk (WUR)/G Ye (IRRI)	Global	Global	Global		July 2009	July 2014
77.		<i>Subactivity 2.2.5.3: Develop a Molecular Genetic Analysis Application</i>	FA v Eeuwijk (WUR)/G Ye (IRRI)	Global	Global	Global		July 2009	July 2014
78.		<i>Subactivity 2.2.5.4: Develop a Selection Indices Application</i>	J Crossa (CIMMYT)/FA v Eeuwijk (WUR)	Global	Global	Global		July 2009	July 2014
79.		<i>Subactivity 2.2.5.5: Develop a Selection Indices Application</i>	J Crossa (CIMMYT)/FA v Eeuwijk (WUR)	Global	Global	Global		July 2009	July 2014
80.	G8009.03.06	<i>Activity 2.2.6 Genstat Breeding View</i>	Mark Sawkins (GCP)	Global	Global	Global		July 2009	July 2014
81.		<i>Subactivity 2.2.6.1: Develop Breeding Decision Support Applications</i>	T Shah (ICRISAT)	Global	Global	Global		July 2009	July 2014
82.		<i>Subactivity 2.2.6.2: Develop MARS Decision Support Application</i>	Alain Charcosset (CIRAD)	Global	Global	Global		July 2009	July 2014
83.		<i>Subactivity 2.2.6.3: Develop Simulation Application</i>	M Dieters (UoQ)	Global	Global	Global		July 2009	Terminated July 2013

Component 3: Integrated breeding services

G8009.05 – Objective 3.1: Provide access to critical molecular breeding services

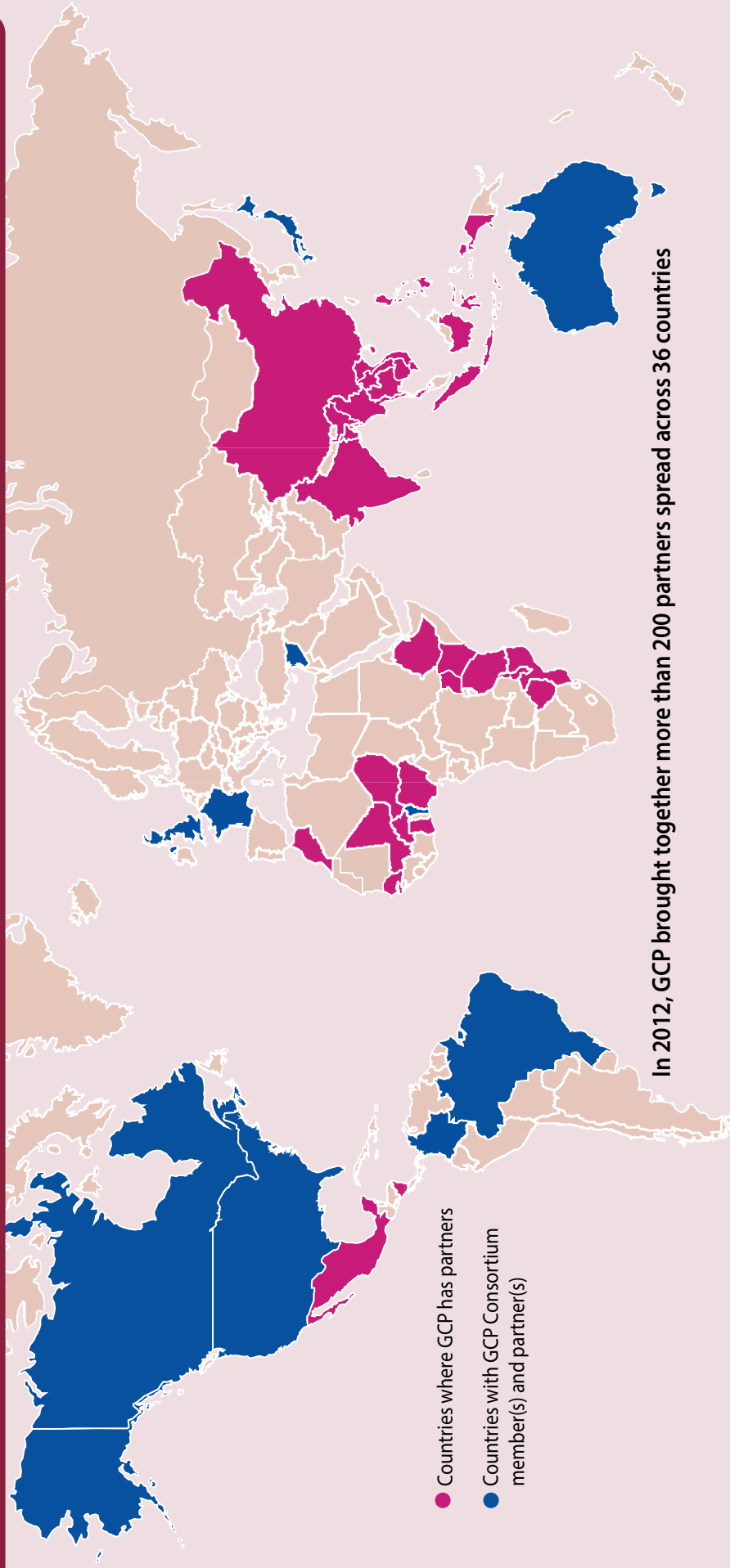
84.	G8009.05.01	<i>Activity 3.1.1: Genetic Resources Support Service</i>	Larry Butler, GCP	Global	Global	Global	AAFC, Agropolis–INRA, BI, CAAS, CCAFS, CIAT, CIMMYT, CSIRO, ICRISAT, IRRI, KU Leuven, UQ, WUR	July 2009	July 2014
85.	G8009.05.02	<i>Activity 3.1.2: Marker Services</i>	Chunlin He, GCP	Global	Global	Global		July 2009	July 2014
86.	G8009.05.03	<i>Activity 3.1.3: Trait and metabolite services</i>	Chunlin He, GCP	Global	Global	Global		July 2009	July 2014

G8009.06 Objective 3.2: Provide assistance with a range of molecular breeding support services

87.	G8009.06.01	<i>Activity 3.2.1: Breeding Plan Development</i>	Mark Sawkins, GCP	Global	Global	Global	AAFC, Agropolis–INRA, BI, CAAS, CCAFS, CIAT, CIMMYT, CSIRO, ICRISAT, IRRI, KU Leuven, UQ, WUR	July 2009	July 2014
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#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
88.		<i>Subactivity 3.2.1.2: PMB (Planning tool for molecular breeding projects – project appraisal and cost-benefit analysis to support decision-making)</i>	Mark Sawkins, GCP and Jiankang Wang, CIMMYT/CAAS	Global	Global	Global		July 2009	July 2014
89.	G8009.06.02	<i>Activity 3.2.2: Information Mgt</i>	Arlet Portugal, GCP	Global	Global	Global		July 2009	July 2014
90.	G8009.06.03	<i>Activity 3.2.3: Data curation</i>	Arlet Portugal, GCP	Global	Global	Global		July 2009	July 2014
91.	G8009.06.04	<i>Activity 3.2.4: Design & analysis</i>	Marcos Malosetti, WUR	Global	Global	Global		July 2009	July 2014
92.	G8009.06.05	<i>Activity 3.2.5: Phenotyping sites & screening protocols)</i>	Xavier Delannay, GCP	Global	Global	Global		July 2009	July 2014
93.	G8009.06.06	<i>Activity 3.2.6: Genotyping Support Service</i>	Chunlin He, GCP	Global	Global	Global		July 2009	July 2014
94.	G8009.06.07	<i>Activity 3.2.7: IP & Policy Helpdesk</i>	L Butler, GCP	Global				July 2009	July 2014
Projects reported under Theme 3 – Crop information systems									
95.	G4009.03/ G4010.06/ G4011.01/ G4011.10	<i>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</i>	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
96.	G4009.04/ G4010.05/ G4011.05	<i>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</i>	Rajeev Varshney and Trushar Shah, ICRISAT	Global	Global	Global	ICRISAT, NCGR, SCRI, UoQ	September 2010	October 2013
97.	G4011.09	<i>Development of a Genotyping Data Management System (GDMS)</i>	Trushar Shah, ICRISAT	Global	Global	Global	IRRI, NCGR, SCRI	December 2011	November 2013

Where in the world is GCP? The GCP network in 2012



In 2012, GCP brought together more than 200 partners spread across 36 countries

Target countries

Africa

1. Burkina Faso
2. Ethiopia
3. Ghana
4. Kenya
5. Malawi
6. Mali
7. Morocco
8. Mozambique
9. Niger
10. Nigeria
11. Senegal
12. Tanzania
13. Uganda
14. Zimbabwe

Asia

15. Bangladesh
16. Cambodia
17. China
18. India
19. Indonesia
20. Laos
21. Myanmar
22. Philippines
23. Thailand
24. Vietnam

Latin America

25. Mexico
26. Nicaragua

Partner countries

1. Australia
2. Benin
3. Brazil
4. Canada
5. Colombia
6. France
7. Japan
8. Syria
9. United Kingdom
10. USA

**3rd Annual Meeting, Integrated Breeding Platform (IBP) 4-8 June 2012
Hosted by the Chinese Academy of Agricultural Sciences (CASS) Beijing, China**



Generation Challenge Programme (GCP)

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(Centro Internacional de Mejoramiento de Maíz y Trigo;
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