



# 2010

## Project Briefs

Generation  Challenge Programme

Partnerships in modern crop breeding for food security

## Research

GCP's research is organised by a two-dimension matrix of seven crop- and crop cluster-based Research Initiatives, and by five Research Themes (see diagram).

### Research Initiatives (RIs)

The RIs are trait-specific, focusing primarily on drought tolerance, alongside other key biotic and abiotic stresses such as pests and diseases, and phosphorous deficiency and aluminium toxicity. They are also region-specific, covering 21 countries in Asia (China, India, Indonesia, Thailand, Philippines, and Vietnam), Latin America (Brazil, Colombia, Mexico, Nicaragua) and sub-Saharan Africa (Burkina Faso, Ethiopia, Ghana, Kenya, Mali, Mozambique, Niger, Nigeria, Senegal, Tanzania, and Uganda).

Capacity-building and crop data management are both fully integrated into the components, and not treated as stand-alone concepts.

### Themes

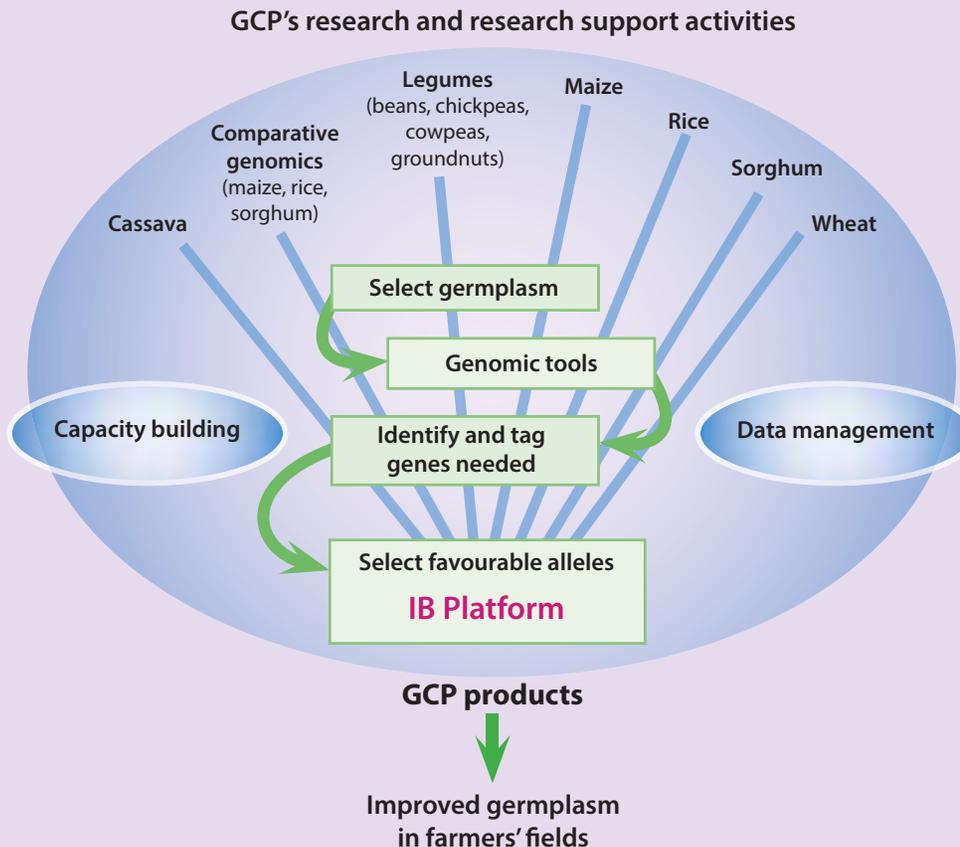
- Theme 1 (Comparative and applied genomics) develops genomics tools and information necessary to enable Theme 2-managed projects
- Theme 2 (Integrated crop breeding) focuses on the integration of molecular breeding in developing-country breeding programmes
- Theme 3 (Crop information systems) develops the analytical and data management tools to support molecular breeding projects
- Theme 4 (Capacity building) helps disseminate the information to the NARS scientists, provides training and infrastructural support to facilitate the work of the other Themes, and establishes a community for sustainable application of integrated breeding
- Theme 5 (Product delivery) has evolved naturally from the increased focus GCP now places on the delivery and, in addition, on management of, project products

## Services

### The Integrated Breeding Platform (IBP)

IBP is envisioned as a sustainable, web-based one-stop shop for information, analytical tools and related services to design and carry out integrated breeding projects. In its formative

years, it supports a pioneer set of 14 'user-cases' – ongoing breeding projects drawn from the RIs above and from outside GCP, covering eight crops and spanning 32 countries in Africa and Asia.





# **2010 Project Briefs**

February 2013

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## The Project Briefs are extracted from the original proposals.

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# Acronyms

AAFC	Agriculture and Agri-Food Canada	CRRI	Central Rice Research Institute, India
ABC	Agricultural Biotechnology Center, Gödöllő, Hungary	CRURRS	Central Rainfed Upland Rice Research Station, India
ABRII	Agricultural Biotechnology Research Institute of Iran	CSIR	Council for Scientific and Industrial Research, Ghana
ACCI	African Centre for Crop Improvement, South Africa	CSIRO	Commonwealth Scientific and Industrial Research Organisation, Australia
ACGT	African Centre for Gene Technologies, South Africa	CU	Cornell University, USA
ACPPFG	Australian Centre for Plant Functional Genomics Pty Ltd	DAR	Department of Agricultural Research, Myanmar
AfricaRice	Africa Rice Center (formerly WARDA)	DARS	Department of Agricultural Research & Technical Services, Malawi
Agropolis–CIRAD	Centre de coopération internationale en recherche agronomique pour le développement, France	DaT P/L	Diversity Arrays Technology Pty Ltd
Agropolis–LGDP	Laboratoire Génome et Développement des Plantes (LGDP)	DPSPP–EKC	Department of Plant Sciences and Plant Physiology, Eszterházy Károly College, Eger, Hungary
Agropolis–INRA	Institut national de la recherche agronomique, France	DOA	Department of Agriculture, Thailand
Agropolis–IRD	Institut de recherche pour le développement, France	DPI&F	Department of Primary Industries and Fisheries, Australia
AICPMIP	All India Coordinated Pearl Millet Improvement Project	DRC	Democratic Republic of Congo
ARI–HAS	Agricultural Research Institute of the Hungarian Academy of Sciences, Hungary	DR&SS	Department of Research & Specialist Services, Zimbabwe
ARI–India	Agharkar Research Institute, India	DWR	Directorate of Wheat Research, India
ARI–Naliende	Agricultural Research Institute–Naliende Research Station, Tanzania	EARO	Ethiopian Agricultural Research Organization
ARTC	Agricultural Research and Technology Corporation, Sudan	EgU	Egerton University, Kenya
ASTI	Agricultural Science & Technology Indicators initiative, IFPRI	EIAR	Ethiopia Institute for Agricultural Research
BAU	Birsra Agricultural University, India	EMBRAPA	Empresa Brasileira de Pesquisa Agropecuária, Brazil
BF	Barwale Foundation	ETH–Zurich	Eidgenössische Technische Hochschule, (Swiss Federal Institute of Technology), Zürich
BINA	Bangladesh Institute of Nuclear Agriculture	Fedearroz	Federación Nacional de Arroceros, Colombia
BIOSS	Biomathematics and Statistics Scotland Research Institution, UK	FERA	The Food and Environment Research Agency
BIOTEC	National Center for Genetic Engineering and Biotechnology, Thailand	FOFIFA–DRA	Foibem–Pirenena Mombra ny Fikarohana Ampiharina Amin'ny Fampandrosoana ny eny Ambanivohitra (National Centre for Applied Research on Rural Development) Département de la recherche agronomique, Madagascar
Bioversity	Bioversity International	GCP	The Generation Challenge Programme
BRRD	Bureau of Rice Research and Development, Rice Department, Thailand	GIS	Geographic Information Systems
BRRRI	Bangladesh Rice Research Institute	HAAS	Institute of Dry Farming, Hebei Academy of Agricultural Sciences, China
CAAS	Chinese Academy of Agricultural Sciences	HZAU	Huazhong Agricultural University, China
CARDI	Cambodia Agricultural Research and Development Institute	IA–Tápiószele	Institute for Agrobotany, Tápiószele, Hungary
CAZRI	Central Arid Zone Research Institute, India	IAMZ	Instituto Agronómico Mediterráneo de Zaragoza
CERAAS	Centre d'Etude Régional pour l'Amélioration de l'Adaptation à la Sécheresse, Senegal	ICABIOGRAD	Indonesian Centre for Agricultural Biotechnology and Genetic Resources and Research Development
CGN–WUR	Centre for Genetic Resources, WUR	ICARDA	International Center for Agricultural Research in the Dry Areas
ChSU	Charles Sturt University, Australia	ICASEPS	Indonesian Center for Agriculture Socio Economic and Policy Studies
CIAT	Centro Internacional de Agricultura Tropical (International Center for Tropical Agriculture)	ICERI	Indonesian Cereals Research Institute
CIMMYT	Centro Internacional de Mejoramiento de Maíz y Trigo (the International Maize and Wheat Improvement Center)	ICL	Imperial College London, UK
CIMS	Centro de Inteligencia sobre Mercados Sostenibles, Costa Rica	ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
CIP	International Potato Center	IER	Institut d'Economie Rurale, Mali
CNG	Centre National de Génotypage, France	IGAU	Indira Gandhi Agricultural University
CRI	Crop Research Institute, Ghana	IGD	Institute for Genomic Diversity, Cornell University, USA
CRIL	(CIMMYT–IRRI) Crop Research Informatics Laboratory	IGKV	Indira Gandhi Krishi Vishwa Vidyalaya (Indira Gandhi Agricultural University), India
		IIAM	Institute of Agricultural Research of Mozambique
		IFPRI	International Food Policy Research Institute

ILRI	International Livestock Research Institute	PDKV	Dr Panjabrao Deshmukh Krishi Vidyapeeth, (Dr Panjabrao Deshmukh Agricultural University) India
IITA	International Institute of Tropical Agriculture	PeU	Peking University, China
INERA–Burkina Faso	Institut de l'Environnement et de Recherches Agricoles, Burkina Faso	PhilRice	Philippine Rice Research Institute
INIA–Chile	Instituto de Investigaciones Agropecuarias, Chile	PROINPA	Promoción e Investigación de Productos Andinos, Bolivia
INIA–Uruguay	Instituto Nacional de Investigación Agropecuaria, Uruguay	PSU	Pennsylvania State University, USA
INIFAP Instituto	Nacional de Investigaciones Forestales, Agrícolas y Pecuarias, Mexico	RAK–CoAg	RAK College of Agriculture, Sehore, Madhya Pradesh, India
INRA–Morocco	Institut National de la Recherche Agronomique, Morocco	RARS–Nandyal	Regional Agricultural Research Station, Nandyal, Andhra Pradesh, India
INRAN	Institut National de Recherches Agronomiques du Niger	RGDU	Rice Gene Discovery Unit, Thailand
INTA	Instituto Nacional de Tecnología Agropecuaria, Nicaragua	SAARI	Serere Agricultural and Animal Production Research Institute, Uganda
IPK	Institute for Plant Genetics and Crop Plant Research, Germany	SAAS	Shanxi Academy of Agricultural Sciences, China
IRRI	International Rice Research Institute	SABRN	Southern Africa Bean Research Network
ISABU	Institut des sciences agronomiques du Burundi	SARI–Ethiopia	South Agricultural Research Institute, Ethiopia
ISAR	Institut des sciences agronomiques du Rwanda	SARI–Ghana	Savannah Agricultural Research Institute, Ghana
ISRA	Institut Sénégalais de Recherches Agricoles	SAU	Sichuan Agricultural University, China
JIC	John Innes Centre, UK	SCRI	Scottish Crop Research Institute, UK
JIRCAS	Japan International Research Center for Agricultural Sciences	SGRP	System-wide Genetic Resource Programme
JNKV	Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur, India	SIRDC	Scientific and Industrial Research and Development Centre, Zimbabwe
KARI	Kenya Agriculture Research Institute	SUA	Sokoine University of Agriculture, Tanzania
KUL	Katholieke Universiteit Leuven, Belgium	TAMU	Texas A&M University, USA
LAAS	Luoyang Academy of Agricultural Sciences, China	TNAU	Tamil Nadu Agricultural University, India
LUMC	Leiden University Medical Center	TSL	The Sainsbury Laboratory, UK
MAU	Marathwada Agricultural University, India	UAS	University of Agricultural Sciences, India
MPI	Max Planck Institute	UBU	Ubon Ratchatani University, Thailand
MU	Moi University, Kenya	UCB	Universidade Católica de Brasília, Brazil
NAARI	Namulonge Agricultural and Animal Production Research Institute, Uganda	UdB	Università di Bologna, Italy
NaCRRI	National Crops Resources Research Institute, Uganda	UdR	Universidad de la República, Uruguay
NagU	Nagoya University, Japan	UdT	Universidad de Talca, Chile
NAFRI	National Agricultural and Forestry Research Institute, Laos	UEM	Universidade Eduardo Mondlane, Mozambique
NARI	National Agricultural Research Institute, Eritrea	UGA	University of Georgia, USA
NARS	National Agricultural Research System	UKZN	University of KwaZulu–Natal, South Africa
NAU	Nanjing Agricultural University, China	UNAM	Universidad Nacional Autónoma de México
NCGR	National Center for Genomics Resources, USA	UoA	University of Arizona, USA
NDUAT	Narendra Dev University of Agriculture and Technology, Faizabad, India	UoAb	University of Aberdeen, UK
NGO	non-governmental organisation	UoAlb	University of Alberta, Canada
NIAB	National Institute of Agricultural Biology, UK	UoC	University of California, USA
NIAS	National Institute of Agrobiological Sciences, Japan	UoC–Davis	University of California–Davis, USA
NMRI	National Maize Research Institute, Vietnam	UoC–Riverside	University of California–Riverside, USA
NPGR	National Plant Genetic Resources Centre, Tanzania	UoD	University of Dhaka, Bangladesh
NRCPB	National Research Centre on Plant Biotechnology	UoGh	University of Ghana
NRCRI	National Root Crops Research Institute, Nigeria	UoH	University of Hohenheim, Germany
NRCS	National Research Centre for Sorghum, India	UoM	University of Maryland, USA
NSFCRC	Nakhon Sawan Fields Crop Research Centre, Thailand	UoMi	University of Missouri, USA
NWSUAF	University of Agriculture and Forestry, China	UoP	University of Perpignan, France
OSU	Oregon State University, USA	UoQ	The University of Queensland, Australia
PAU	Punjab Agricultural University, India	UoZ	The University of Zambia
PBI–UoS	Plant Breeding Institute, University of Sydney, Australia	UPLB	University of the Philippines Los Baños
		USDA–ARS	United States Department of Agriculture–Agricultural Research Service
		VBI	Virginia Bioinformatics Institute, VPI
		VPI	Virginia Polytechnic Institute and State University, USA
		WUR	Wageningen University and Research Centre, The Netherlands
		YAAS	Yunnan Academy of Agricultural Sciences, China
		YU	Yale University, USA
		ZU	Zhejiang University, China

# 2010 Project Briefs

## I. Research Initiatives

### 1. Cassava

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

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

#### **Principal Investigator and lead institute**

Morag Ferguson, IITA

#### **Collaborating institutes and scientists:**

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

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

#### 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 G7009.09/G7010.01.03: Implement MARS projects for drought tolerance

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

#### **Principal Investigator and lead institute**

Emmanuel Okogbenin, National Root Crops Research Institute (NRCRI), Umudike, Nigeria.

#### **Collaborating institutes and scientists**

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

Although cassava produces more energy per unit area compared to other crops under marginal conditions of limited annual rain fall (<500mm) or a long dry season (5-6 months), yield potential under drought varies widely in the gene pool. Previous work revealed certain varieties from Africa are tolerant to drought. The 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.

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

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

#### **Principal Investigator and lead institute:**

Alfredo Alves, EMBRAPA Cassava and Tropical Fruits (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.

### 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 – Chiedozi Egesi
- CRI – Elizabeth Okai
- NaCRRI – Yona Baguma
- NaCRRI – Anthony Pariyo
- IITA – G Melaku

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

#### **G7010.01.05**

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

#### **Principal Investigator and lead institute**

Emmanuel Okogbenin, National Root Crops Research Institute (NRCRI), Nigeria

#### **Collaborating institutes and scientists**

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

## 2. Legumes

### Improving tropical legume productivity for marginal environments in sub-Saharan Africa and South Asia

#### TLI Phase I (May 2007–April 2010)

#### Beans

#### 6. Project No G6007.03: Improve common bean (*Phaseolus vulgaris* L) productivity for marginal environments in sub-Saharan Africa

- Duration: May 2007–Apr 2010
- Total budget: USD 1,867,327

#### Principal Investigator and lead institute

Steve Beebe, wef October 2010; previous PI: Matthew Blair, CIAT

#### Collaborating institutes and scientists

- CIAT – Idupulapati Rao, Manabu Ishitani, Steve Beebe
- University of Nairobi/ECABREN – Paul Kimani
- CIAT/SABRN – Rowland Chirwa
- SARI – Asrat Asfaw Amele
- DR&SS – Godwill Makunde
- RIKEN – Motoaki Seki, Kazuo Shinozaki

Common beans are a major crop for most of the countries of Eastern and Southern Africa and are grown by small-scale farmers because of their high marketability and ready acceptance in the diet. Typical bean yields, however, are only 20 to 30% of the genetic potential of improved varieties due to major production constraints such as drought and several diseases and insects. We will contribute to improved drought tolerance by improving common beans for drought tolerance using genetic knowledge, new germplasm, and improved breeding methods, and we will address disease and insect resistance using molecular marker technology. This approach is justified based on a) the need for drought tolerance in marginal environments of SSA where drought occurrence and severity are on the increase; b) the existence of drought tolerance genes and mechanisms in certain bean accessions and the need to understand these sources better; c) the possibility of combining drought tolerance with disease and insect resistance genes in new varieties through marker-assisted selection; and d) the opportunity to use resistance sources and drought tolerant germplasm developed at CIAT and in Mexico for improving sub-Saharan African germplasm through innovative modern breeding methods.

The traits targeted and the technologies used will address the major limitations of drought-prone marginal environments in five countries of Eastern and Southern Africa (Ethiopia, Kenya, Malawi, Tanzania, and Zimbabwe) in terms of drought as well as the prevalent diseases and insects in these environments.

#### Chickpeas

#### 7. Project No G6007.04: Improve chickpea (*Cicer arietinum* L) productivity for marginal environments in sub-Saharan Africa

- Duration: May 2007–Apr 2010
- Total budget: USD 1,074,125

#### Principal Investigator and lead institute

Rajeev Varshney, GCP/ICRISAT

#### Co-Principal Investigators (Co-PIs):

- ICRISAT-Kenya – Said Silim/ NVPR Ganga Rao, (Leader- Activity 1)
- ICRISAT-India – Rajeev Varshney, (Leader- Activity 2), Hari Sharma, (Leader- Activity 3), Junichi Kashiwagi/ L Krishnamurthy, (Leader- Activity 4), Pooran Gaur, (Leader- Activity 5)

#### Collaborating institutes and scientists

- EIAR, Ethiopia – Million Eshete
- LZARDI, Tanzania – Robert Kileo
- Egerton University, Kenya – Paul Kimurto
- IIPR, India – Massod Ali, Shiv Kumar, Aditya Kumar
- UC–D, USA – Doug Cook
- DArT P/L, Australia – Andrzej Killian
- ICRISAT-India – C Sivakumar, Shailesh Tripathi, Mahendar Thudi

Chickpea (*Cicer arietinum* L.) is an important grain legume in South Asia and sub-Saharan Africa, especially in eastern and southern Africa. It is an excellent source of high quality protein, with a wide range of essential amino acids. Its potential as both a source of human food as well as animal feed, coupled with its ability to fix atmospheric nitrogen, is attracting an increasing number of SSA farmers. Since 1978, the area under chickpea cultivation in SSA has increased 1.2% per year, and continues today at about the same rate. Since major consumer countries such as India are short of supply, there are opportunities for SSA countries to exploit an existing market.

Drought is globally the number one constraint to chickpea production, causing yield losses of around 3.7 million tons (out of a total production of 8.6 million tons). In sub-Saharan Africa and South Asia, drought

stress occurs during the terminal growth stages, as the crop is largely grown rainfed during the post-rainy season on residual soil moisture. With the prediction of continuing water scarcity in the future, terminal drought will continue to be the major constraint to chickpea production in these regions. 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. In addition, there is 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 trait (water use efficiency and harvest index), the scope of the proposal would limit itself to assess the range of variations and heritabilities of these traits and possibly to identify the suitable parents to develop the populations needed to map these traits in the future.

Pod borer (*Helicoverpa armigera* Hubner) is a highly devastating insect pest of chickpea worldwide. It feeds on various plant parts such as leaves, tender shoots, flower buds, and immature seeds. The global yield losses due to this pest are estimated at USD 2 billion annually on chickpea and other high value crops. Farmers who are able spend precious income on chemical control of the pest. In these situations, there are serious concerns of the adverse effects of pesticides on the environment and all living organisms. It has been difficult to breed for *Helicoverpa* resistance in chickpea because sources with a high level of resistance are not available in the cultivated species. Exploitation of wild species appears promising as these have shown higher levels of resistance.

## Cowpeas

### 8. Project No G6007.02: Improve cowpea (*Vigna unguiculata* L) productivity for marginal environments in sub-Saharan Africa

- Duration: May 2007–Apr 2010
- Total budget: USD 1,952,008

#### Principal Investigator and lead institute

Jeff Ehlers, UC–R

#### Co-Principal Investigators (Co-PIs):

- University of California, Riverside – Timothy Close, Philip Roberts

#### Collaborating institutes and scientists

- Institut Senegalais de la Recherches Agricole, Senegal – Ndiaga Cisse
- Institut de l'Environnement et des Recherches Agricole, Burkina Faso – Issa Drabo
- Institut Recherche Agron. pour le Developpement, Cameroon – Ousmane Boukar
- International Institute of Tropical Agriculture, Nigeria – Dong-Jin Kim

Cowpea is the second most important grain legume crop in SSA in terms of total grain production, and the most important in terms of number of cultivators and area sown (see Annex 1). Despite cowpea's importance to millions of farmers and hundreds of millions of consumers (Langyintuo et al. 2003), few investments have been made in improving cowpea (Naylor et al. 2004). As a consequence, this species has lagged behind other grain legume crops in the development of basic genomic resources and tools needed to implement modern breeding approaches that could more quickly alleviate major constraints facing cowpea producers (Kelly et al. 2003; Timko et al. 2006). The proposed work under Objective 2 will rapidly enable the use of some of the modern plant breeding approaches by employing new and efficient molecular marker development methodologies that will densely mark the cowpea genetic map at more than 1000 points in the cowpea genome using single nucleotide polymorphisms, or SNPs. One of the Co-PIs (Close) has used this approach in barley in a National Science Foundation Plant Genome Research project that he heads, and is extending this approach to applied breeding programs in the US through a Department of Agriculture Coordinated Agricultural Project (<http://www.barleycap.org/>) in which he leads SNP marker development. With high-density SNP markers, diverse cowpea germplasm and specially developed genetic populations (recombinant inbred lines, or 'RILs') will be characterized for abiotic and biotic stress resistance/tolerance traits that impact cowpea yields in SSA. The phenotypic data sets and molecular marker information will be combined to identify SNP markers linked to target traits. Selected SNP markers will be converted to easy to use markers such as for agarose gels, and validated for use in African breeding programs. Beyond the proposed project period, the markers and new breeding populations that we will

develop will then be used in MAS by African cowpea breeders to incorporate stress tolerance/pest resistance traits into locally adapted germplasm.

Nearly all cowpea production areas are characterized by very hot temperatures, frequent droughts, and infertile soils with low water-holding capacity (Ehlers and Hall 1997). Presumably cowpea has evolved multiple heat/drought tolerance mechanisms that allow it to cope with these harsh growing conditions. Despite these adaptive mechanisms, cowpea yields are adversely affected by heat and drought and yields could be improved markedly if heat and drought tolerance were increased (Hall et al. 2002; Hall 2004). The proposed studies will evaluate a much larger sample of cowpea germplasm in a much wider range of environments than previous studies of genetic variation of heat (Marfo and Hall 1992; Ehlers and Hall 1996; Hall et al. 1997) and drought (Anyia and Herzog 2004; Dadson et al. 2005) tolerance. Furthermore, while these previous studies assessed either heat or drought tolerance individually, the present proposal targets combined heat/drought tolerance because high temperatures and droughts typically occur together in SSA and it may be more effective to select heat and drought tolerance as one trait complex, as suggested by Mittler (2006).

#### **9. Project No G7009.05: Improving cowpea productivity for marginal environments in sub-Saharan Africa 2009–2010 ‘top-off’**

- Duration: Jul 2009–Jun 2010
- Total budget: USD 50,000

##### **Principal Investigator and lead institute**

Jeff Ehlers, UC–R

##### **Collaborating institutes and scientists**

- University of California, Riverside – Timothy Close, Philip Roberts
- Institut Senegalais de la Recherches Agricole, Senegal – Ndiaga Cisse
- Institut de l’Environnement des Recherches Agricole, Burkina Faso – Issa Drabo
- IITA-Kano, Nigeria – Satoru Muranaka and Ousmane Boukar
- IITA Nairobi – Dong-Jin Kim

We propose to conduct three activities that build on Phase 1 and initiate/complement Phase 2 TL-1 Activities. These include 1) evaluating the cost-effectiveness of two alternative marker platforms for MARS breeding, 2) phenotyping of a RIL set for drought

tolerance that is expected to yield unique drought QTL, and 3) beginning development MAGIC populations for future breeding and genetic analyses. For Activity 1, a comparison of marker platforms, we will conduct a tangible small-scale comparison of cost effectiveness of alternative SNP genotyping platforms, based on the Illumina or KBiosciences platforms, in an actual MARS breeding exercise with two ‘high x high’ MARS populations. This will not only provide platform cost estimates prior to wide adoption of marker-assisted breeding in Phase 2 that is relevant to all GCP crops, but also ‘hands-on’ experience in MARS breeding for NARS partners. Activity 2 seeks to identify unique drought tolerance QTL by phenotyping the RIL population developed from TVu14676/IT845-2246. This population appears to be a good population for drought QTL discovery. Genotyping of this population has already been completed using the 1536 Illumina GoldenGate Assay in Phase 1. For Activity 3, we will develop country specific MAGIC populations for Senegal and Burkina, and one for IITA serving sub-Saharan Africa as a whole. These will be a valuable resource for future breeding and genetic investigation. We believe each NARS partner and IITA should develop MAGIC populations composed of locally-adapted elite genotypes. Phenotyping data from TL1 phase 1 has provided new information for selecting new parental combinations. We will initiate development of MAGIC populations now to help ensure quicker results from the genetic analysis and pre-breeding that follow from this approach during Phase 2.

##### **Groundnuts**

#### **10. Project No G6007.01: Improve groundnut (*Arachis hypogaea* L) productivity for marginal environments in sub-Saharan Africa**

- Duration: May 2007–Apr 2010
- Total budget: USD 3,037, 513

##### **Principal Investigator and lead institute**

Vincent Vadez, ICRISAT-India

##### **Co-Principal Investigators (Co-PIs):**

- University of California, Riverside – Timothy Close, Philip Roberts
- ICRISAT–Mali – Bonny Ntare
- University of Georgia–USA – Andrew Paterson
- Universidade Catholica de Brasilia–Brazil – David Bertoli
- ICRISAT–Malawi – Emmanuel Monyo
- ICRISAT–India – Rajeev Varshney

**Collaborating institutes and scientists**

- EMBRAPA–Brazil – Patricia Guimarães
- CIRAD–France – Jean-Francois Rami
- Chitedze Research Station–Malawi – Tobias Kapewa (now replaced by Albert Chamango)
- ISRA–Senegal – Ousmane Ndoye
- Naliendele Research Station–Tanzania – Omari Mponda
- INRAN–Niger – Adamou Moutari

Groundnut (peanut, *Arachis hypogaea* L.) is an important food and cash crop in sub-Saharan Africa (SSA), cultivated in almost every country across the continent. Africa accounts for almost a quarter of the world production of groundnut, with Nigeria being the third largest producer. In most countries, the crop is grown by smallholder farmers under very low input and rainfed drought-prone conditions. Lack of seed of improved varieties, poor agronomic practices, drought, diseases, and pests are the major factors limiting yield. The potential for increasing farmers' yields through crop improvement, particularly for key biotic and abiotic stresses, is very high, especially if aided by the application of modern science. Rust, late leaf spot, and early leaf spot occur worldwide wherever groundnut is grown. Individually, they can cause 50-60% pod yield loss. However, rust and late-leaf spot often occur together and the pod yield loss can exceed 70%. Besides adversely affecting pod yield and its quality, these foliar diseases also affect haulm (fodder) yield and quality. Whereas the level of resistance available in cultivated groundnut to rust is very high, for early- and late-leaf spot it is low. Cultivars resistant to rust and moderately resistant to late- and early-leaf spot are available, but their acceptability among farmers is low due to some undesirable agronomic traits (low shelling turnover, longer duration, unattractive pod shape) associated with resistance. Of the important biotic constraints specific to SSA, the groundnut rosette disease (GRD) is endemic to the African continent and epidemics occur often throughout SSA, reducing groundnut production and crippling rural food security. GRD epidemics can induce total loss in many fields, with recurring epidemics reported in many SSA countries.

The largest area under groundnut production in SSA lies in the semi-arid tropics, an area characterized by short and erratic rainfall. The crop is grown under rainfed conditions and suffers from both intermittent and terminal drought stress, thus incurring major yield losses. Worldwide, yield losses each year due to drought are estimated to be around US\$500 million (Sharma and Lavanya, 2002). Cultivars that have traits associated with drought tolerance give high yields under water deficit

conditions. Drought-affected crops, however, are often highly susceptible to the fungus *Aspergillus flavus* that produces the highly carcinogenic mycotoxin, aflatoxin. Thus, there is a great need to develop varieties that have the ability to produce with limited available water, and deeper-rooted materials would delay the water deficit-driven aflatoxin contamination of pods at the end of the season.

**Cross-cutting activities****11. Project No G4009.06: Illumina genotyping of SNPs in legume mapping populations and germplasm**

- *Duration: Nov 2009–Oct 2010*
- *Total budget: USD 99,828*

**Principal Investigator and lead institute**

Doug Cook, UC–D

**Collaborating institutes and scientists**

- ICRISAT – Rajeev Varshney
- CIAT – Matthew Blair
- EMBRAPA – David Bertoli

With combined funding from TL1 and the US National Science Foundation, we completed the identification and validation of single nucleotide polymorphisms in a range of legume crop species, including species of interest to the Generation Challenge Program. These species are chickpea, cowpea, common bean and groundnut. In total, 22,827 SNPs were validated and used to design an Illumina GoldenGate genotyping assay to map ~2,400 loci (averaging 600 loci in each species).

The purpose of this Commissioned Research Project Proposal was to extend the SNP discovery activities, which are now complete, to genotyping SNPs in mapping populations and germplasm from each species. Genotyping represented the last major task of TLI Objective 5, and thus this grant allowed us to complete activities that were described and endorsed in the original TL1 proposal to the Bill and Melinda Gates Foundation.

**12. Project No G6007.05: Develop cross-species resources for comparative biology in tropical crop legumes**

- *Duration: May 2007–Apr 2010*
- *Total budget: USD 867,688*

**Principal Investigator and lead institute**

Doug Cook, UC–D

**Collaborating institutes and scientists**

- UCB – David Bertioli
- UGA – Andrew Paterson

Breeding and biotechnology in groundnut, cowpea, common bean, and chickpea suffer from a poorly developed infrastructure for genetic and genomic analysis. The same is true of the more than one dozen legume species that comprise a significant part of the human diet worldwide. The sheer number of these species creates both financial and capacity barriers that preclude their systematic, in-depth analysis. Moreover, even if resources were not limiting, it is not clear that we need to understand each genome in perfect detail in order to address the issue of crop improvement in the developing world. Instead, efforts in the US, Asia, and Europe have aimed to characterize the structure and function of two simple “model” legume genomes, namely *Medicago truncatula* (Cook 1999) and *Lotus japonicus* (Handberg and Stougaard 1992), while similar efforts are underway in the important but notoriously complicated genome of soybean (*Glycine max*). All of these legumes, both crops and models, share a recent common ancestor that existed around 50 million years ago (Doyle and Luckow 2003).

If genes in the common ancestor that controlled desirable traits (such as drought tolerance, protein content, and flowering time) are the same ones operating in today’s crop species, then understanding the genetic basis of such traits in one species will simultaneously elucidate information about the others. Such knowledge could have great impact on breeding and biotechnology of legumes. This prediction motivates a strategy known as “comparative genomics,” where defining ancestral genome segments also identifies the ancestral genes, and thus provides a mechanism to “translate” knowledge gained in the study of one species to related species. The promise of comparative genomics is more than just speculation. We know from extensive studies of symbiotic nitrogen fixation, a trait common among most legumes, that conserved genes with conserved molecular functions reside in conserved genome segments (e.g., Gualtieri et al 2002; Endre et al. 2002; Stracke et al. 2002; Zhu et al. 2006). Work in the Cook laboratory, and others, has led to “comparative genetic maps” that facilitate such translation (e.g., Choi et al 2004a and 2004b). As a consequence, and by way of example, numerous genes have been discovered in the genome of Mendel’s garden pea (*Pisum sativum*) by reference to the models *Medicago* and *Lotus* (reviewed in Riely et al.

2004). Remarkably, evidence also exists for conserved genomic position for the rapidly evolving family of disease resistance genes (NBS-LRR genes) (Zhu et al. 2002; 2005).

**13. Project No G6007.06: Provide training and capacity-building for SSA scientists**

- Duration: May 2007–Apr 2010
- Total budget: USD 851,600

**Principal Investigator and lead institute**

Carmen de Vicente, GCP

**Collaborating institutes and scientists****CGIAR Centers:**

- Centro Internacional de Agricultura Tropical (CIAT; International Center for Tropical Agriculture)
- International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
- Advanced Agricultural Research Institutes:
- University of California, Riverside (UC–R), USA

**National Agricultural Research Systems:**

- Agricultural Research in Tanzania (ART), Tanzania
- Agricultural Research Institute (ARI)-Naliendele Research Station, Tanzania
- Chitedze Research Station, Malawi
- Crop Breeding Institute, Department of Research for Development, Zimbabwe
- Ethiopian Institute of Agricultural Research (EIAR), Ethiopia
- Institut de l’Environnement et de Recherches Agricoles (INERA), Burkina-Faso
- Institut de Recherche Agricole pour le Developpement (IRAD), Cameroon
- Institut National de Recherche Agronomique du Niger (INRAN), Niger
- Institut Sénégalais de Recherche Agricole (ISRA), Senegal
- Lake Zone Agricultural Research and Development Institute (LZARDI), Tanzania
- South Agricultural Research Institute (SARI), Ethiopia
- University of Mozambique

**Other partners:**

- Eastern and Central Africa Bean Research Network (ECABREN)
- Southern Africa Bean Research Network (SABRN)

Objective 6 of this proposal will create a pool of well-trained scientists in SSA who are prepared to apply the research outputs of this project in their

research programs in their home countries. This is a critical output of this project overall and is essential for ensuring the long-term sustainability of the new knowledge and tools developed by this project. This Objective involves 2 Activities: workshops and training in relevant scientific disciplines and skills, and infrastructural support for partner institutions in sub-Saharan Africa.

The rationale for consolidating the capacity building Activities under one Objective in this project as opposed to integrating the training and support Activities in the research Objectives is four-fold. First, because of both the particular capacity building needs of sub-Saharan African national program scientists and the support required for them to be able to participate as partners in this project and carry on research at their home institutions, it is important to centralize the capacity building planning, execution, and assessment to ensure efficient and cost-effective administration of these Activities. Second, by establishing training and capacity building as its own objective, the GCP is better able to facilitate its integration with the GCP's larger program on capacity building and ensuring delivery, and also with the Tropical Legume II project's capacity building program. The Tropical Legume II project, which focuses on large-scale breeding and distribution of seeds, dovetails with the Activities of this project, so it is logical that the capacity building Activities be harmonized between the two projects. Third, some of the traits considered in these projects, in particular those associated with drought tolerance, have similarities and may involve a coordination of common training workshops for scientists working on different crops. Like the critical role it plays in this project, capacity building is a core thrust in the Generation Challenge Program. Fourth, this Objective will build bridges with all NARS involved in the different scientific Objectives. The capacity building and training activities will serve as the mechanism to engage NARS in the management of the project.

### **Improving tropical legume productivity for marginal environments in sub-Saharan Africa and South Asia**

#### ***TLI Phase II (May 2010–April 2014)***

#### **Beans**

#### **14. 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***

Matthew Blair/Steve Beebe wef October 2010, (CIAT)

#### ***Collaborating institutes and scientists***

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

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

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

breeding (MAB). The advantage of the new populations is that they incorporate new genetic resources into the African common bean 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**

### **15. 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
- UC–Davis (USA) – Douglas Cook
- IIPR (India) – Sushil Kumar Chaturvedi
- ICGGC

#### **Service Providers for genomics activities**

- UC–Davis (USA)
- NCGR (USA)
- DArT P/L (Australia)

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.

**16. 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–May 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).

### Cowpeas

#### 17. Project No G6010.02: Improve cowpea productivity for marginal environments in sub-Saharan Africa

- Duration: Aug 2007–Feb 2010
- Total budget: USD 2,027,880

#### Principal Investigator and lead institute

Jeff Ehlers, UC–Riverside (USA)

#### Collaborating institutes and scientists

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

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.

### **18. Project No G7010.07.01: Improving Cowpea Productivity for Marginal Environments in Africa**

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

#### **Principal Investigator and lead institute**

Jeff Ehlers, University of California-Riverside

#### **Collaborating institutes and scientists**

- University of California-Riverside – Timothy Close and Philip Roberts
- ISRA Senegal – Ndiaga Cisse
- INERA Burkina Faso – Issa Drabo
- Eduardo Mondlane University – Rogerio Chiulele
- IITA – Ousmane Boukar, Satoru Muranaka

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**

### **19. 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 Bertiolli;
- EMBRAPA Genetic Resources and Biotechnology (Brazil) - Soraya CML Leal Bertiolli

The limited level of groundnut genetic polymorphism restricts the use of modern breeding. Nevertheless, large phenotypic differences exist for traits such as disease resistance and drought tolerance – traits that are very much needed to enhance groundnut productivity for resource-poor farmers in SSA). The project will develop the first products of molecular breeding by building on the sources of disease resistance and drought tolerance, as well as on the breeding materials identified and advanced in Phase I. SNP markers will be generated to eventually support the use of marker-assisted recurrent selection (MARS) approaches and adequate breeding populations

combining sources of tolerance, and high phenotypic and genotypic contrast will also be developed. Given that absolute resistance to foliar diseases, especially to early leaf spot (ELS), is unavailable in the cultivated germplasm, additional diversity will be sought in allo-tetraploid groundnut synthetics, developed from wild diploid groundnut, where higher levels of disease resistance are expected, as found for nematode resistance. All these research activities also offer rich training ground for scientists and technicians from SSA country programmes.

Links to other projects include the TLII project; other links have also been forged with a number of Brazilian-funded projects, and with a GCP-funded capacity-building project which targets TLI NARS scientists and technicians. Aflatoxin contamination has been tested in seed lots from the drought trials carried out in Niger, a naturally infested site with *A. flavus*. This adds value to the TLI work, provides materials with superior tolerance to aflatoxin contamination, and opens opportunities for collaboration since aflatoxin seriously affects health and excludes SSA groundnut from export. The Indian government is funding the improvement of groundnut for drought tolerance (NAIP) and a project on drought tolerance with DREB1A to produce transgenic groundnut (DBT). In addition, a recently completed initiative, through a USAID grant to ICRISAT in collaboration with the University of Florida, USA, examines water conservation traits.

### **Cross-cutting activities**

#### **20. 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.

### 3. Maize

#### 21. Project No G4008.56: Drought tolerant maize for Asia

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

#### **Principal Investigator and lead institute**

Bindiganavile S Vivek, CIMMYT

#### **Collaborating institutes and scientists**

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

Maize area in South and South-East Asia has been expanding by 2.2% annually from 16.5 (2001) to 18.0 (2006) million hectares. Over 80% of the maize is grown under rainfed conditions and prone to drought. Addressing the problem of drought has been estimated to provide the highest technical returns to rainfed maize R&D investments in Asia. Based on substantial breeding progress made for drought

tolerance in maize in other regions (Central America and eastern and southern Africa), this project proposes to apply marker-assisted selection within pedigree breeding or backcrosses made between drought tolerant source inbreds and a minimum of four elite Asian adapted inbreds, and more through execution of additional self-funded and donor-funded MARS projects by public and private partners. Inbred lines will be extracted from improved populations, using either selfing or doubled haploids, and new drought tolerant Asia-adapted hybrids tested. GCP support will result in a minimum of four Asian adapted drought tolerant inbreds and hybrids, molecular marker information associated with drought tolerance, and NARS and private sector scientists with experience in integrating MARS in applied breeding programmes. The project intends to integrate self-funded public and private sector partners for a larger number of MARS breeding projects (for drought tolerance and other traits) and wider capacity building. This project is expected to become the impetus for significant levels of drought tolerance being introduced into highly relevant Asian maize germplasm with resulting impact in diverse environments and by diverse suppliers, and for a molecular community of practice being established among the Asian maize breeding community.

## 4. Rice

### 22. 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, 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

#### **Projects**

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

World paddy production is reached a new record level of 666 million tonnes in 2008. However, in Africa, rice production has not increased at the same rate and has not been able to keep pace with increasing demand. Only 54% of the Sub-Saharan Africa rice consumption is supplied locally. In 2009, rice imports in Africa were forecast to approach 9.3 million tonnes. Among the various abiotic and biotic factors reducing rice yield in West Africa, drought is considered the most important. Rice yield is affected by drought in rain-fed lowland

ecosystems in around 80% of the total rice area in Mali, 67% in Burkina Faso and 48% in Nigeria, as a result of erratic rainfall and poor water control. Three drought-related risks can be distinguished in rain-fed lowlands: (1) early drought, especially in direct-seeded, poorly managed systems; (2) mid-season drought spells alternating with flooding; and (3) terminal drought. Rice breeders have developed improved varieties for rain-fed lowland ecosystems, but the complex nature of rain-fed lowlands makes it difficult to delineate clearly the target domains of these varieties. Developing drought-tolerant cultivars that have a high yield potential in normal years and provide a good yield under drought and other major stresses for each target environment will help sustain rice production in the large rain-fed lowland ecosystem across Africa. The project will focus on the rain-fed lowland ecosystems of Sudanean and Guinean savannah areas in Burkina Faso, Mali and Nigeria. Within 4 years, it will establish (i) the drought profiles of the target population of environments (TPE) in inland valley lowlands; (ii) the identification of traits of interest for targeted environments, using novel phenotyping methodologies enabling an efficient separation of genetic (G) and environmental (E) effects; and (iii) the integration of the information on drought profiles with novel phenotyping methodologies in a marker-assisted recurrent selection (MARS) scheme to develop better adapted germplasm for each major target environment.

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

## 5. Sorghum

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

- Duration: Aug 2008–Jul 2013
- 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.

### 24. 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

### 25. 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, CAAS

#### **Collaborating institutes and scientists**

- CAAS – Zhonghu He, Xinmin Chen, Xinguo Mao, Ang Li, Xiaoping Chang,
- HAAS – Xiumin Chen, Kejiang Li, Wenchen Qiao
- SAAS – Meirong Sun, Xiurong Li, Yongfeng Chai, Junling Zhang,
- XAAS – 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.

### 26. 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

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

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

#### Principal Investigator and Lead institute

Leon Kochian, CU/USDA–ARS

#### Collaborating Institutes and Scientists

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

Two of the most important limitations to crop production in sub-Saharan Africa are drought and acid soils. It is estimated that nearly 50% of the soils in this region suffer from insufficient water, while agriculture on nearly a quarter of the lands of sub-Saharan Africa are constrained by aluminium (Al) toxicity on acid soils. Because the primary symptom of Al toxicity is root growth inhibition and damage, resulting in compromised water and nutrient uptake, Al toxicity is a significant however poorly understood component of drought stress in Africa and other developing regions of the world. We already have assembled an effective research consortium that in ongoing GCP projects has identified a major sorghum Al tolerance gene which is now being exploited to improve sorghum Al tolerance in Africa. We also have recently identified several very promising candidate maize Al tolerance genes and QTLs that are poised to enter into a molecular breeding pipeline for assessing/validating their breeding values, and ultimately for generating maize genotypes with superior performance on acid soils. In this proposal, we will build upon this progress to generate maize and sorghum breeding lines with enhanced acid soil tolerance. Using our capability to phenotype maize and sorghum genotypes for drought tolerance in the field and a newly developed platform for high-throughput root imaging analysis, we also will begin to focus on the molecular and genetic determinants of maize and sorghum drought tolerance. This will involve the

generation of new genetic resources in sorghum and maize, taking advantage of recent advances in sequencing and association genetics to develop a SNP genotyping array in sorghum and a maize breeding association panel. In particular the sorghum platform should become an useful community resource not only for drought and Al tolerance, but also for many other agronomically important traits. Finally, we will continue our field testing of improved sorghum and maize lines on acid soils in Kenya, and expand that programme to begin assessing the interplay between drought and Al tolerance on soils in Africa.

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

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

#### Principal Investigator and lead institute

Leon Kochian/Susan McCouch, CU and USDA–ARS

#### Collaborating institutes and scientists

- IRRI – Abdelbagi M Ismail
- ICABIOGRAD – 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.

### 29. 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.

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

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

#### **Principal Investigator and lead institute:**

Claudia Guimarães, Embrapa Maize and Sorghum

#### **Collaborating institutes and scientists:**

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

Over 50% of the world's potentially arable lands consist of acid soils, where aluminum (Al) toxicity is the primary factor limiting maize yield, one of the world's most important food crop. This problem is particularly important for low input agricultural systems, which includes a large portion of the farmers in Sub-Saharan Africa and as well as small farm holders in other developing country areas. Al tolerance is a quantitatively inherited trait in maize, a crop that displays considerable variation for this trait, as well a highly complex genome organization. Taking advantage of the Al tolerance gene cloned in sorghum (*Alt<sub>SB</sub>*) and findings from our recent research in maize, where two major Al tolerance QTLs were co-localized with *Alt<sub>SB</sub>* 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.

**31. 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 - (SorghumMB)**

- 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<sub>SB</sub>*. 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<sub>SB</sub>* 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<sub>SB</sub>*, a major Al tolerance gene in sorghum: linking upstream genomics to acid soil breeding in Niger and Mali (ALTFIELD). The results will be validated in Kenya, Mali and Niger as well as in Embrapa Maize and Sorghum (Embrapa MS) using *S<sub>1</sub>* and *S<sub>2</sub>* 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.

**32. 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.

### **33. 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<sub>SB</sub>*) 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<sub>SB</sub>* 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.

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

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

#### **Principal Investigator and lead institute:**

Jurandir Magalhães, Embrapa Maize and Sorghum

#### **Collaborating institutes and scientists:**

- Embrapa Maize and Sorghum (Brazil) – Robert Schaffert, Claudia Guimarães, Vera Alves, Maria Jose Vasconcelos, Sylvia Morais de Souza, Alvaro Vilela Resende, João Herbert Moreira Viana
- USDA-ARS Robert W. Holley Center for Agriculture and Health (USA) – Leon Kochian, Jiping Liu, Randy Clark

- Cornell University (Institute for Genomic Diversity)  
– Steve Kresovich, Martha Hamblin, Sharon Mitchell, Theresa Fulton
- INRAN (Niger) – Soumana Souley
- Moi University (Kenya) – Sam Gudu
- ICRISAT – Eva Weltzien and Fred Rattunde
- JIRCAS – Matthias Wissuwa
- IRRI – Sigrid Heuer

Low productivity due to soil constraints and a lack of properly adapted crop cultivars is a serious problem in many parts of Africa, where sorghum is a staple food supporting millions of the rural poor. *Pup1* is a major QTL located on rice chromosome 12 that underlies phosphorus efficiency and has the potential to increase P acquisition efficiency in other cereals. Research findings from a long term collaboration between IRRI and JIRCAS has resulted in the fine mapping of the *Pup1* locus to a ~150 Kb region on chr 12, and 2-4 high quality *Pup1* candidate genes have been identified. Taking advantage of the complete sequence of the sorghum genome, we will establish a framework based on comparative genomics to identify sorghum *Pup1* homologs and will validate their role as *bona fide* genes underlying tolerance to P deficiency. This research will

be based primarily on association analysis to identify statistically significant associations between allelic variation for *Pup1* candidate genes and P efficiency assessed both in the field and under controlled conditions in the laboratory and greenhouse. Positive associations will be validated by bi-parental mapping and analysis of near-isogenic lines. The Al tolerance gene, *Alt<sub>SB'</sub>*, 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<sub>SB'</sub>* 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<sub>SB'</sub>/Pup1* in this Challenge Initiative - SorghumMB) should functional *Pup1* homologs not be found in sorghum. Thus, this project sets the foundation for a molecular breeding program targeting marginal soil areas in southern Mali, Niger and Kenya and other areas of Sub-Saharan Africa to improve food security and farmer's income.

## II. Thematic projects

### **Theme 1 – Comparative and applied genomics**

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

#### **35. Project No G4007.02 Validation of drought-response/resistance pathway genes by phenotypic analysis of mutants**

- Duration: Aug 2007–Jul 2009; NCE: Jan 2010
- Total budget: USD 200,543

#### **Principal Investigator and lead institute**

Andy Pereira, PBI

#### **Collaborating institutes and scientists**

- IRRI – Hei Leung, Rachid Serraj, Jill Cairns
- HZAU – Lizhong Xiong

Research within the GCP and other ongoing research on abiotic stress biology, has provided researchers a number of candidate genes with a potential role in drought response and resistance. These genes have been identified in a number of crops, in response to a variety of environmental stresses and by data derived from breeding, genetics, physiology and genomics. For most of these candidate genes their exact role has not been determined due to lack of high throughput methods of relating the genes to a drought response/resistance phenotype. The analysis of mutants is one of the most reliable and time-proven ways of correlating the genotype to a phenotype. The international research community has generated significant mutant resources in the two sequenced plants rice and Arabidopsis. Systematic mutant analysis of candidate genes for drought response/resistance in these plants, including field testing at critical drought sensitive stages, will provide supporting evidence, and in some cases the definite answers, of the role of the genes in drought resistance that will be available as a knowledge resource for all plants. This project aims to provide drought response phenotypes for an extensive list of about 500 candidate orthologous genes in the two plants selected for their potential role in drought responses and resistance mechanisms. The comparative analysis

between the dicot and monocot plants would be applicable across a wide number of crop plants. The mutant phenotypes will be evaluated for important physiological components and at vegetative and reproductive drought stages in relevant field or controlled experimental conditions. Results of this project will support the GCP ADOC project analyzing natural variation in a selection of candidate genes, and validate the results of microarray experiments from previous projects, be able to test candidate genes coming from ongoing GCP projects. The results of drought response phenotypes of candidate genes will be curated in a database and made available to all GCP participants and collaborators to aid their research.

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

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

#### **Principal Investigator and lead institute**

Peggy Ozias Akins, wef October 2010; Steven J Knapp, UGA

#### **Collaborating institutes and scientists**

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

DNA marker resources are currently inadequate for routine genomic and molecular breeding applications in cultivated groundnut (*Arachis hypogaea* L.;  $2n = 4x = 40$ ). The proposed research focuses on significantly enhancing the infrastructure for translational genomics and molecular breeding research in groundnut by testing the efficacy of massively parallel DNA sequencing and highly parallel single nucleotide polymorphism (SNP) genotyping strategies for SNP discovery, validation, and mapping. We are specifically proposing to: (i) develop protocols for reduced representation allele sequencing (RRS) in groundnut; (ii) enhance DNA sequence resources for groundnut using a combination of Sanger and Solexa sequencing; (iii) identify 2,000 or more common SNPs in elite lines and cultivars; (iv) develop a 1,536-SNP

Illumina GoldenGate SNP genotyping array; and (v) complete the validation and genetic mapping of 1,536 SNPs in two elite recombinant inbred line (RIL) populations using an Illumina GoldenGate SNP genotyping array. The proposed research will dramatically increase DNA sequence resources and the supply of mapped DNA markers in groundnut, should enable the identification and assembly of 20 linkage groups using elite mapping populations, particularly when coupled with genetic mapping of SSR markers, and should identify additional SNPs for genotyping assay development, validation, and mapping.

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

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

**Principal Investigator and lead institute**

Douglas Cook, UoC–Davis

**Collaborating institutes and scientists**

- NCGR – Greg May
- ICRISAT – Rajeev Varshney

Recent efforts under Tropical Legume 1 (TL1) and allied projects have yielded a significant increase in molecular marker resources for chickpea. Nevertheless, there remains a pressing need to identify polymorphisms that discriminate cultivated accessions, especially the elite germplasm that will form the foundation of phase 2 of TL1 (eg, MARS parents and the focus of current breeding and QTL analyses). The objective of this proposal is to use Next Generation sequencing for deep re-sequencing of cDNA libraries from a select set of elite accessions. This project benefits from earlier efforts funded by the Generation Challenge Programme (SPL-2 discretionary grant) in which the transcriptome of chickpea was sequenced by means of 454 technology. Here we propose to use deep re-sequencing with Solexa technology to develop sequence alignments to these 454 transcript sequences, thereby discovering sequence polymorphisms (SNPs). A subset of 1536 SNPs will be selected to produce an Illumina Golden Gate assay, to ascertain allelic variation in a wider set of breeding and pre-breeding materials.

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

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

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

**Principal Investigator and lead institute**

Pablo Rabinowicz, The Institute of Genome Sciences, School of Medicine, University of Maryland, Baltimore MD, USA

**Collaborating institutes and scientists**

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

Cassava is one of the most important crops in unfavorable environments in developing countries, where poverty is common and severe. Because of its high productivity, even in extreme conditions, cassava constitutes a source of food and income for poor farmers in Africa, Asia and Latin America. Although cassava is fairly resistant to water stress, the molecular basis for this tolerance is poorly understood. Several traits have been associated with its drought tolerance, such as regulation of stomata activity, changing leaf expansion rates due to decrease in cell proliferation, and modifications of photosynthetic pathways to maintain high photosynthetic activity. Improving cassava's tolerance to drought is important to help increasing yields in the semi-arid Sub Saharan African regions where cassava as an essential crop. Cassava's natural stress tolerance can be substantially improved by breeding, especially by marker-assisted selection of key physiological traits associated with drought tolerance. In recognition of the importance of cassava improvement for dry areas in the developing world, the Generation Challenge Program (GCP) awarded a grant to study drought tolerance traits and develop molecular markers to improve cassava breeding

for drought tolerance. This proposal builds on that project by offering to develop single nucleotide polymorphism (SNP) markers throughout the genome to identify favourable alleles related to drought tolerance in these mapping populations. In order to achieve this goal, a physical map of the cassava genome will be generated that will allow the development of SNP markers uniformly distributed around the genome. In this way we will be able to identify quantitative trait loci (QTL) associated with drought tolerance in a high-throughput manner. These markers will be useful for marker-assisted selection of favourable traits.

### **39. Project No G4008.07 Genomic resources and mapping populations developed and assembled for pearl millet to enable trait/gene identification**

- Duration: Jan 2008–Dec 2009; Project under review
- Total budget: USD 296,429

#### **Principal Investigator and lead institute**

C Tom Hash, ICRISAT

#### **Collaborating institutes and scientists**

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

Pearl millet (*Pennisetum glaucum*) is a dual-purpose grain and fodder crop that is an essential component of dryland crop-livestock production systems of sub-Saharan Africa (e.g., Nigeria, Niger, Burkina Faso, Mali, Senegal, Sudan, and Chad) and South Asia (e.g., India) in areas that are too hot, too dry, and/or have soils that are too acid or too infertile for reliable production of maize, sorghum or any other cereal crop. The crop is also increasingly used as the mulch component of sustainable minimum tillage crop production systems in the humid tropics (e.g., Brazil), where its acid soil tolerance, deep root system, and high vegetative growth rates under high temperature conditions often make it the best option for retrieving soil nutrients from depth, smothering weeds, and

producing a mulch that protecting the soil surface from erosion by rain drop impact or surface water movement. There are limited genomic tools available for this orphan crop despite pearl millet being the 6th most important cereal crop globally and being likely to be, along with sorghum, an important source of genes and alleles that will enable plant breeders to engineer other crops (e.g., rice, wheat and maize) to better tolerate higher temperatures and increased frequencies of drought stress that are predicted to arise from on-going global warming.

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

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

#### 40. Project No G4008.09 Genomic resources and mapping populations for sweet potato developed to enable trait/gene identification

- Duration: Jan 2008–Dec 2009; NCE: Jun 2010
- Total budget: USD 299,540

##### **Principal Investigator and lead institute**

Roland Schafleitner, CIP

##### **CIP Working Team Members**

David Tay, Wolfgang Gruneberg, Merideth Bonierbale, Marc Ghislain

##### **Collaborating institutes and scientists**

- IIAM Mozambique – Nurbibi Cossa
- NAARI Uganda – Robert Mwanga
- INIA Uruguay – Francisco Vilaro
- EMBRAPA Brazil – Andre Dusi
- Diversity Arrays Technology (DArT P/L) – Andrzej Kilian

##### **Supporting participants (subcontractors)**

Evrogen, Russia

JCVI, USA

Production of sweet potato, an important staple food in Sub-Saharan Africa, is limited by a number of constraints, such as low adaptability of available varieties and landraces, virus diseases, insect pests and drought. Consequently, yields achieved by resource-poor farmers in SSA are typically low and remain, on average, below 5 tons per hectare. Improved and well adapted sweet potato varieties with increased tolerance to biotic and abiotic stresses can significantly contribute to increasing productivity and will have a large positive impact on food and income security in Sub-Saharan Africa. However, breeding efforts are limited by the crop's genetic complexity and lack of information available about its genetic resources. The development of genetic tools, including populations and markers, and concerted efforts towards understanding the gene pools of sweet potato would improve access to and targeted use of the allelic diversity for breeding improved varieties.

The basic tools needed to mobilize allelic diversity and to monitor introgression of desirable alleles in breeding populations consist of a well-defined Composite Genotype Set and segregating populations for marker development and trait capture. Today, techniques such as DArT that yield a large number of markers for genetic studies and selection should be made

accessible for sweetpotato. A diploid reference map will help to synthesize genetic information already available from independent hexaploid populations, and enable comparative genomics among sweetpotato and other crops.

This project aims at developing genetic and genomic resources for sweetpotato and will stimulate the use of these tools in ongoing breeding programs in CG Centers and NARS.

#### 41. Project No G4008.47 Genomic resources (ESTs, markers and maps) developed for pigeonpea to enable trait/gene identification

- Duration: Aug 2008–Dec 2010
- Total budget: USD 292,200

##### **Principal Investigator and lead institute**

Gregory D May, NCGR

##### **Collaborating institutes and scientists**

- National Centre for Genome Resources (NCGR) – Andrew Farmer
- ICRISAT – Rajeev Varshney, Kulbhushan Saxena
- National Research Centre on Plant Biotechnology (NRCPB) – Nagendra K Singh
- Dr. Panjabrao Deshmukh Krishi Vidyapeeth (PDKV) – Pawan L Kulwal

Legumes are one of the largest and diverse families of higher plants containing more than 20,000 species, and are second only to cereal crops in world-wide agricultural importance. With the exception of soybean, *Medicago* and *Lotus*, legumes have not benefited from the establishment of expanded genomics resources. Pigeonpea (*Cajanus cajan* L.), an important legume crop in Indian subcontinent, ranks sixth in area and production in comparison to other grain legumes such as beans, peas, and chickpeas. It is now widely grown in the Indian subcontinent that accounts for almost 90% of the world's crops. However, the productivity of pigeonpea crop in semi-arid regions is less than 650 kg/ha due to exposure of the crop with several diseases such as fusarium wilt, sterility mosaic and other abiotic stresses. Biotechnological tools especially molecular markers have been proven very useful for improving the breeding efficiency in several major crop species, only about 100 microsatellite or simple sequence repeat (SSR) markers are available for pigeonpea. Furthermore, low level of genetic diversity

in pigeonpea germplasm is another bottleneck to varietal improvement. Because of these two reasons, not a single genetic map has become available for pigeonpea to date. The proposed research will develop genomic resources such as expressed sequence tags (ESTs) and single nucleotide polymorphism (SNP) markers by using 454 FLX and Solexa next generation sequencing technologies. High throughput genotyping assay such as GoldenGate assay (Illumina) will enable the development of a pigeonpea genetic map. Genomic resources, to be developed, in the planned project will be of great use for the pigeonpea community in particular, and the legume community in general.

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

**42. Project No G3007.02 Genomic dissection of tolerance to drought stress in wild barley**

- *Duration: Aug 2007–Jul 2009; NCE: Jul 2010*
- *Total budget: 567,604*

**Principal Investigator and lead institute**

Robbie Waugh, SCRI

**Collaborating institutes and scientists**

- SCRI – Dave Marshall, Joanne Russell, population geneticist
- ICARDA – Michael Baum, Stefania Grando, Maria von Korff Schmising, Salvatore Ceccarelli
- Oregon State University – Patrick M. Hayes
- INIA – Ivan Matus
- Universidad de Talca – Alejandro Del Pozo
- UC–R – Timothy J. Close

Through an existing collaboration we have developed a unique segregating population of 140 barley lines composed of an advanced elite genetic background containing introduced chromosomal segments from a wild barley accession that comes from the Fertile Crescent. The wild species, the donor of the introduced genomic segments, is genetically distant from the cultivated line and is both adapted to, and tolerant of, drought and salt stresses. Using genetic tools that allow us to follow the inheritance of the genomic segments from the donor into the recipient line we have been able to show that in this unique population we have representative segments covering the entire genome of the donor in each of the different lines. In genetical terms we call these lines recombinant

chromosome substitution lines or RCSL's. Evolution by natural selection, domestication and plant breeding has resulted in each of the paired genomic segments from the wild species and elite line having subtly to strikingly different versions of the same genes. This variation will affect the growth and/or performance characteristics of each of the RCSLs compared to each other and to their parents. For example, if the introduced segment contained a version of a gene that conferred resistance to salinity that was absent in the elite line, then we expect all of the individual RCSLs that contain that segment also to become resistant to salinity. The unique feature of RCSLs that is different from standard bi-parental cross populations is that by breaking the donor genome up into many small segments and having these segments in an otherwise identical genetic background, it becomes possible to precisely dissect even complex characteristics into a series of genetically tractable parts. We know that we have been successful in doing this as we have already examined the effects of the introgressed wild species genome segments on a range of phenotypes (Matus et al, 2003). In the interim, we have also developed a technology (we call it an oligo pool assay or OPA) that allows us to very precisely characterise the genomes of each of the RCSLs and identify the genes that are present on the introduced donor segments. In this project we propose to combine the power of our OPA genome characterisation technology with relevant phenotypic trait information on the unique RCSL genetic resource to identify segments of the donor genome that confer increased (or decreased) drought tolerance to the recipient. Although these characteristics are considered to be controlled by many genes, by isolating a small number (sometimes individual) donor genome segments in an identical genetic background, RCSLs effectively fragment the genetic contributions of many loci into individual component loci that can be subsequently analysed in detail by simple genetic analysis. Once we have identified specific target regions of the wild species genome that confer increased drought tolerance, for the most clearcut examples, we will use the model rice genome sequence to provide a putative barley regional gene content and a list of candidate stress tolerance genes. We have successfully used this approach in the past for winter hardiness. We will then pursue the objective of characterising the DNA sequence of a selection of the genes in this region from both parents to develop the tools that will allow us to accurately associate the drought tolerant character with specific genes. We will extend these studies to a broad selection of agro-ecologically

adapted landraces where we will use both the genes identified in the RCSL studies and, in a pilot study, the genes on the OPA, to validate observed, and identify new associations between genes and drought tolerant phenotypes. Finally, we will initiate crosses to mobilise favourable alleles from the landrace germplasm into a common elite genetic background for further testing and validation of their impact on stress tolerance.

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

- Duration: Nov 2008–Oct 2011
- Total budget: USD 756,225

##### ***Principal Investigator and lead institute***

Andrew H Paterson, UGA

##### ***Collaborating institutes and scientists***

- SARI–Ghana – IDK Atokple
- ICRISAT – C Thomas Hash
- MAU – SP Mehtre
- NRCS – Nadoor Seetharama

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.

#### **44. Project No G4008.08: Causal relationship between whole-genome expression patterns and stress tolerance determined in rice via analysis of near-isogenic lines (NILs)**

- Duration: Jan 2008–Dec 2009; NCE: Dec 2010
- Total budget: USD 305,400

##### ***Principal Investigator and lead institute***

Shoshi Kikuchi NIAS, Japan

##### ***Collaborating institutes and scientists***

- IRRI, Philippines – Hei Leung, Venuprasad Ramaiah, Jerome Bernier, Arvind Kumar, Rachid Serraj, Ramil Mauleon and Violeta Bartolome

We propose to make use of two recent advances in gene expression analysis and drought-QTL mapping to test the hypothesis that gene expression patterns in a chromosomal context are causally correlated with manifestation of drought tolerance as detected in near-isogenic lines. We will apply a new comprehensive 44K oligoarray platform to determine the transcriptomes of two pairs of near isogenic lines (NILs) exhibiting large difference in their yield response to drought stress at reproductive stage. Parallel to transcriptome analyses, we will determine the fine-scale genotypes of the NILs to determine whether expression signatures co-segregate with specific regions of the genome. Results from this series of studies will reveal genes or narrow chromosomal regions contributing to drought tolerance. Because the NILs are field-proven genetic stocks that are adapted to the rainfed and upland rice production environment, the results are likely to have high agronomic relevance. Experimental support to a causal relationship between gene expression patterns and QTL is of fundamental and practical interest in understanding the genetic control of a complex trait such as drought tolerance. The proposed project will produce breeding-ready, well-characterized isogenic

lines with specific chromosomal regions tagged for their contribution to drought tolerance. The project will also generate expression/QTL mapping datasets that can be further exploited by data mining. The results will be viewed in Genome Browser that will enable consolidation of multiple sources of information anchored to the rice genome.

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

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

##### ***Principal Investigator and lead institute***

Peter Langridge, ACPFG

##### ***Collaborating institutes and scientists***

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

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

screen will give preliminary correlation of expression with drought tolerance. These results will be confirmed using introgression lines and other genetic populations. Where expression correlation is validated the germplasm plus diagnostic marker will be made available to breeders for introgression.

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

#### **46. Project No G3008.03: Delayed senescence and drought tolerance in rice**

- *Duration: Nov 2008–Oct 2011*
- *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.

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

- Duration: Nov 2008–Oct 2011
- 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.

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

- Duration: Jan 2009–Dec 2011
- 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–Bangalore – KP Viswanatha, MS Sheshashaye
- RARS–Nandyal – Veera Jayalakshmi
- ARS–Durgapura – SJ Singh
- RAKCA – Md Yasin

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<sup>-1</sup>), whereas the potential yield is reported to be over 5 t ha<sup>-1</sup>. 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.

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

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

##### ***Principal Investigator and lead institute***

David Jordan and Andrew Borrell, DPI&F

##### ***Collaborating institutes and scientists***

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

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

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

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

## Theme 2 – Integrated crop breeding

### Objective 1: Crop genetic diversity

#### 50. Project No G3007.01 Base broadened of current crop diversity in rice using interspecific bridges with African rice

- Duration: Aug 2007–Jul 2009; NCE: Dec 2010
- Total budget: USD 669,000

#### Principal Investigator and Lead institute

Alain Ghesquière, LGDP/IRD

#### Collaborating institutes and scientists

- PhilRice – A Alfonso
- IER – F. Cissé
- Fedearroz – M. Diago
- INERA – H. Drissa
- University of Arizona – DW Galbraith
- LGDP/IRD/CIAT – M. Lorieux
- CIAT – C. P. Martinez
- WARDA – M.N. Ndjiondjop
- LGDP/Perpignan University – O. Panaud
- WARDA – M. Semon
- Punjab Agricultural University – J.S. Sidhu
- CIAT – J. Tohme

This project aims to overcome an important obstacle to rice breeding: the interspecific sterility barrier. While many interesting traits have been introgressed into cultivated rice (*Oryza sativa* L.) from African cultivated rice (*O. glaberrima* Steud.) and other rice relatives, this approach is very tedious and time consuming and breeders generally prefer the simplest path of intra-specific crosses since the sterility barrier is not an issue. We propose to combine the power of the latest genetic marker technologies (Single Feature Polymorphisms, Simple Sequence Repeats), gene discovery techniques, and a specially designed crossing scheme to produce interspecific bridges between the two cultivated species of rice. These interspecific bridges basically comprise *O. sativa* lines, carrying large introgressions of the *O. Glaberrima* genome and that are compatible with *O. sativa* in crosses. These would therefore be the materials of choice for large scale introduction of allelic diversity of African rice into Asian cultivated rice germplasm.

Implications and outputs of this project would be substantial with respect to rice breeding: nearly the whole genetic diversity of *O. glaberrima* would become available to breeders for use in classical breeding schemes or, marker-aided selection schemes, whether or not combined with recurrent selection.

If successful, this approach could be applied to other AA-genome rice relatives and even to other crops to obtain a full and quick access to the ancestral allele reservoir that was largely lost during the domestication process.

This project involves nine partners: two ARIs (LGDP-IRD/CNRS/Perpignan University, France and the University of Arizona, USA), two CGIAR Centers (CIAT, Colombia and WARDA, Benin), four NARS – from Africa (IER-Mali, INERA-Burkina Faso), South America (Fedearroz-Colombia) and Asia (PhilRice-Philippines) – and the University of Punjab (India).

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

- Duration: Nov 2008–Oct 2011
- 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.

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

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

### **Principal Investigator and lead institute**

NR Sackville Hamilton, IRRI

### **Collaborating institutes and scientists**

- CIAT – M Lorieux
- ICRISAT – H Upadhyaya
- ICARDA – M Baum

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

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

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

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

## 53. Project No G4008.01: Populations for multiple allelic segregation developed in rice and sorghum through multiple parent intercrossing

- Duration: Jan 2008–Dec 2009; NCE: Dec 2010
- Total budget: USD 113,994

### **Principal Investigator and lead institute**

Hei Leung, IRRI (Project succeeded by G4008.06)

### **Collaborating institutes and scientists**

- IRRI – Ed Redona, R.K. Singh, Glen Gregorio
- NIAB – Ian Mackay (consultant)
- ICRISAT – C Tom Hash

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

There is an increasing amount of fundamental work in the genomics and molecular genetics of these crops. For the outputs of this research to be transferred to new varieties, our knowledge of the DNA of these crops must be linked to the traits of important to farmers. MAGIC populations provide a means to this end.

IRRI proposes to establish MAGIC populations in rice, in parallel to three other MAGIC projects on sorghum, pearl millet and cowpea sponsored by GCP. Specially, we will establish two populations in rice and initiate development of 2000 inbred lines from the populations. One population will be targeted at agro-ecosystem in Africa and one for south and south-east Asia. Each population will have eight founder lines. We shall also intermate each population in preparation for generation of a second cycle of lines for finer mapping. We will monitor with DNA markers to ensure line purity and progress of the mating cycles. Comprehensive genotyping, phenotyping, and QTL mapping work will be considered in next phase of the project after the initial populations are established.

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

- *Duration: Aug 2008–Feb 2011*
- *Total budget: USD 92,286*

***Principal Investigator and lead institute***

Tom Hash, ICRISAT

***Collaborating institutes and scientists***

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

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

are therefore located with greater accuracy and flanking markers for QTLs detected are potentially of greater value for use in plant breeding and genetic research.

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

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

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

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

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

**55. Project No G4008.42: DArTs developed as a genomewide molecular characterization technology for crops with little sequence information**

- Duration: Jan 2008–Dec 2009; NCE: Dec 2010
- Total budget: USD 337,600

**Principal Investigator and lead institute**

JC Glaszmann, Agropolis–CIRAD

**Collaborating institutes and scientists**

- DArT P/L – A Kilian, subcontractor
- ICRISAT – D Hoisington
- IITA, IRD, CIRAD, CRI
- For Potato:
  - INIA Chile – Boris Sagredo
  - USDA – David Spooner
  - CIP – Merideth Bonierbale

This proposal aims at reinforcing the capacity to genotype large numbers of materials with large numbers of markers at a relatively low cost, one of the objectives of SP1 in order to facilitate the use of markers for monitoring genetic diversity. It builds on the successful commissioned project executed in 2005 by the team substantially overlapping with the list of contributors to the current proposal. It includes expanding arrays developed in the previous project for Musa (banana) and coconut, expanding arrays developed by Diversity Arrays Technology Pty Ltd (chickpea, pigeonpea, potato) and developing new arrays for yams, groundnut and pearl millet. For each case, we will genotype with the arrays developed a set of important germplasm in the process of marker discovery. In the case of coconut, groundnut, yam and pearl millet, additional genotyping will be performed to explore the diversity in particular populations of interest. In the case of banana, this project will support high density genetic mapping as a contribution to genome sequencing in ANR and JGI projects. The libraries generated in this project will be available to the GCP; their sequences will be provided when they are available.

**G4008.02/03/05/33: Drought-related phenotyping of specific populations with high-quality molecular information implemented and Phenotyping Support Service consolidated. See below for details:**

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

- Duration: Jan 2008–Dec 2011
- 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–CNRA – 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.

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

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

**Principal Investigator and lead institute**

Susanne Dreisigacker, CIMMYT

**Collaborating institutes and scientists**

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

Global genetic resources provide a fundamental source for further crop improvement. The GCP subprogram 1 aims to characterize the diversity of crop germplasm collections held by the CGIAR and its partners. This characterization includes an assessment of the genetic structure of the collections as well as the phenotypic variation associated with that structure. The ultimate goal is to provide access to sources of genetic diversity that may supply genes and alleles involved in key agricultural traits, especially stress tolerance. During the last three years, 3000 wheat accessions provided by major germplasm banks were characterized by CIMMYT and collaborators with 50 SSR markers for the development of reference samples including accessions maximizing neutral genetic diversity. In the first year of this project we will build up a seed stock for three developed international reference samples in wheat: the spring bread wheat, winter wheat and durum wheat reference samples. Seed will be stored in the CIMMYT wheat germplasm bank and made

available for distribution. A drought specific spring bread wheat reference sample will be defined and characterized in multi-location trails for relevant agronomic traits, as well as physiological traits related to the main drivers of yield under drought. The same reference sample will be genotyped with high density DArT markers. This will allow associating the observed trait variation with the genotypic information in order to uncover QTL related to drought tolerance.

**58. 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, IIRRI

**Collaborating institutes and scientists**

- IIRRI – 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 phenomics 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.

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

- *Duration: Jan 2008–Feb 2011*
- *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).

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

- Duration: Aug 2008–Jul 2010; NCE: Jul 2011
- Total budget: USD 226,000

**Principal Investigator and lead institute**

Mathias Lorieux, Agropolis–IRD/CIAT

**Collaborating institutes and scientists**

- CIAT – César P Martinez, Edgar Torres
- AfricaRice – Marie-Noelle Ndjiondjop

Crop improvement is a crucial area of research and development for food stability at the world level. Virtually all crop species have reached a yield plateau, due to various and distinct reasons. In order to generate a real breakthrough in crop yields, technologies able to boost crop breeding efficiency are urgently needed. Modern breeding strategies often fail to include precise genetic information. Marker-Aided Selection (MAS) strategies have proven to be more efficient than conventional selection in several cases, but still suffers of (1) lack of precision in the localisation of the genes of agronomical importance (the so-called QTLs, for Quantitative Trait Loci) and (2) are often limited to the alleles available in the crossing scheme used for QTL detection, i.e., the genetic information obtained from a particular cross between two genotypes (or lines) will not be useful when working with other genotypes. The area of research called Genomics (i.e., the massive and parallel analysis of the thousands of DNA sequences that constitute the genetic code of an organism) has made considerable progress in the last few years. Currently, we have access to the complete genome information for several crops, and rice is the most advanced of them in this sense. However, there is a strong need to bridge the gap between Genomics and Crop Improvement. Rice, as one of the most important cereals for human nutrition, must be considered a priority. In Africa, rice is getting increasing importance as a staple food. It constitutes a major source of calories for the urban and rural poor, with a fast growing demand. At the same time, the germplasm (i.e., cultivated varieties) grown in Africa suffers of low genetic diversity and needs to be enriched in order to develop new varieties, more adaptable to the inherent or new environmental constraints (e.g., drought stress, pests and diseases, low inputs). We propose to develop a new genetic resource, called a Nested Association Mapping population, that

would (1) help in linking the genomic tools available for rice, (2) give access to a much higher allelic diversity at the important QTLs than “conventional” mapping approaches do, (3) allow fine mapping of QTLs (i.e., localise them with high precision on the rice genome), thus increasing significantly the efficiency of MAS strategies, and (4) provide interesting and promising genetic materials (advanced lines) for direct introduction in breeding schemes.

**Objective 2: Characterisation of segregating populations and identification of genomic regions for plant breeding**

**61. Project No G3007.04: Tailoring superior alleles for abiotic stress genes for deployment into breeding programmes – A case study based on association analysis of AltSB, a major aluminium tolerance gene in sorghum**

- Duration: Aug 2007–Jul 2009; NCE: Dec 2010
- Total budget: USD 603,101

**Principal Investigator and lead institute**

Jurandir Vieira Magalhães, Embrapa Maize and Sorghum

**Collaborating institutes and scientists**

- US Plant, Soil and Nutrition Laboratory (USPSNL), USDA–ARS – Leon Kochian
- Institute for Genomic Diversity (IGD), Cornell University – Stephen Kresovich
- IGD, Cornell University (Kresovich Lab) – Alexandra M Casa
- Embrapa Maize and Sorghum – Claudia Guimaraes, Robert Schaffert, Antonio Marcos Coelho, Vera Alves
- US Plant, Soil and Nutrition Laboratory, USDA-ARS (Kochian Lab) – Owen Hoekenga, Jiping Liu
- Institut National de la Recherche Agronomique du Niger (INRAN) – Issoufou Kapran, Soumana Souley, Maman Nouri, Magagi Abdou, Adam Kiari Fatouma Beidari
- Kansas State University – Jianming Yu

One of the most important factors limiting agriculture in developing countries involves the large areas of acid soils found in these countries. On acid soils, toxic levels of aluminum (Al) ions are released into soil solution, where they damage roots and impair their growth and function. This results in reduced nutrient and water uptake, with concomitant reductions in

crop yield. There is considerable natural variation in Al tolerance both within and between plant species, and we have assembled an interdisciplinary team of scientists to take advantage of this variation to improve crop tolerance to Al toxicity, building upon our recent success in isolating a novel Al tolerance gene in sorghum. Thus, as we have been able to identify at least one apparently improved version of this gene, we will now apply association mapping to undertake a comprehensive scan for even better versions of this gene for deployment into sorghum breeding programs. The research group we have assembled has considerable expertise in the genetics, molecular biology and physiology of aluminum tolerance, and has the necessary genetic resources to ensure the success of this project. Through the use of cutting edge genomics and statistical genetics approaches, this research will bridge the gap between basic research on Al tolerance and applied breeding programs, to develop the tools that plant breeders can use to efficiently and effectively breed for improved acid soil tolerance. The long-term goals of this research are to generate sorghum genotypes expressing improved Al tolerance that ultimately can be distributed to farmers who till acid soils in Africa and other developing regions, thus exploiting a wide range of still hidden genetic variation for Al tolerance. Increasing the Al tolerance of staple crops, such as sorghum, will help increase yields and thus food security worldwide.

**62. Project No G4007.04: Association mapping of downy mildew resistance in elite maize inbred lines in Thailand**

- Duration: Aug 2007–Jul 2009; NCE: Dec 2010
- Total budget: USD 60,464

**Principal Investigator and lead institute**

Chalermphol Phumichai and Julapark Chunwongse, BIOTEC

**Collaborating institutes and scientists**

- Kasetsart University – Sansern Jampatong
- Pichet Grudloyma – Nakhon Sawan Field Crop Research Center

Maize is one of five major crops grown in the uplands of Thailand, which is predominantly used for animal feed, with 80-100% production being sold to commercial poultry and livestock feed mills. It is a highly commercial crop, handled by an extensive network of merchants. Maize sold as animal feed is mainly used domestically, and only a small fraction is exported. Meanwhile, about 5-20% of all maize grown

in Thailand is consumed as food, either as white corn or sweet corn. Downy mildew caused by the fungus *Peronosclerospora sorghi* (Weston & Uppal) C.G. Shaw, is one of the most destructive diseases of maize in Thailand. Genetic resistance is a cost-effective and environmentally safe alternative in controlling the downy mildew disease. The objective of this project is to use the association analysis that is a method relies on linkage disequilibrium to study the relationship between phenotypic variation in maize genome for the dissection of downy mildew resistance and genetic polymorphism (superior alleles). This project will focus on evaluating the loci conferring resistance to downy mildews of maize. We will raise maize inbred lines from public and private sectors and phenotypic evaluation will be conducted by using a spreader-row technique. Haplotypes contributing to a favorable plant phenotype under downy mildew resistance conditions will be identified through association tests. The discovery of superior alleles will permit the development of molecular markers that can facilitate breeding programs.

**63. Project No G4007.23: Field evaluation of wheat–barley introgression lines under different water regimes**

- Duration: Dec 2007–Dec 2010
- Total budget: USD 144,000

**Principal Investigator and lead institute**

Agricultural Research Institute of the Hungarian Academy of Sciences, Hungary – Márta Molnár-Láng

**Collaborating institutes and scientists**

- CIMMYT – Maria Zaharieva
- CAAS – Ruilian Jing
- Eszterházy Károly College, Hungary – Sándor Dulai
- Agricultural Research Institute of the Hungarian Academy of Sciences, Hungary – Éva Darkó

The present project aims to use the wheat/barley addition, substitution and translocation lines developed in Martonvásár to determine how the added barley chromosome (segments) influence various agronomic traits (drought, salt and Al-tolerance) in wheat. It is planned to confirm the results achieved by earlier mapping data or to find new chromosome regions responsible for parameters connected with drought-, salt and Al-tolerance. It is intended to select lines with better drought, salt and Al-tolerance compared to the wheat parent by screening the genetic materials produced from wheat × barley hybrids in Martonvásár.

It is hoped to obtain new results on barley genome mapping which will increase our knowledge on cereal genetics. In this “prebreeding programme” new genetic stocks with valuable agronomic traits can be selected. New valuable translocation lines can be developed from addition lines, carrying useful genes for drought, salt and Al-tolerance.

The wheat × barley derivatives can be used in several international cooperations for analysing the effect of various barley chromosome segments on useful agronomic traits under different environmental conditions. The best lines could be used in wheat breeding programmes, especially in dry areas or on salty soils or on soils with high Al-content.

#### **64. Project No G4008.15: Developing potato cultivars adapted to Southern Africa countries**

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

##### **Principal Investigator and lead institute**

F. Vilaró, INIA Uruguay

##### **Collaborating institutes and scientists**

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

Potato is one of the highest value crops and provides high nutritious food in a very short growing period. Many developing countries including non Andean South American and in Southern Africa, grow long day adapted Tuberosum potatoes, almost year round. Breeding programs in the northern hemisphere have developed varieties from this same Group, with high commercial quality. However, most of these varieties are mainly adapted to temperate climate and lack resistance to diseases and pests making potato highly dependent on external inputs. They also require well established seed programs and are mainly adapted just to one crop per year. Adequate planting material is usually expensive and difficult to obtain in appropriate condition for most developing countries. Short day germplasm and landrace varieties from the Andes, have valuable traits but adapt poorly to long days and or high temperature. Genetic resistance sources for various diseases have been incorporated in advanced

potato germplasm from participant non Andean South American countries. These countries cover a wide region of environments, from southern temperate Chile to subtropical Brazil, possessing germplasm with a wide range of adaptation. In this region, with the exception of the most southern area, potatoes are grown on a two crop per year regime. Several varieties significantly improved on quality aspects have been released and are being grown in and out of the region. This project will evaluate advanced germplasm from this region, along with CIP improved germplasm on Southern Africa (Malawi and Mozambique). Microarray DaRt technology analysis will be employed to analyze population structure of germplasm from participating programs. Secondly, easy to use molecular markers will be validated and applied in Latin America helping to characterize degree and stability of disease resistance. GIS site characterization will be employed to determine potential variety deployment in given locations. It is anticipated that promising germplasm sources and very valuable genotypes adapted to various growing constraints, could be identified and multiplied for releasing new cultivars. This would promote a more sustainable crop for helping resource poor farmers in these countries.

#### **Objective 3: Development and evaluation of novel breeding or molecular technologies to better serve modern plant breeding**

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

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

##### **Principal Investigator and lead institute**

Rachid Serraj, IRRI

##### **Collaborating institutes and scientists**

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

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

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

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

**Principal Investigator and lead institute**

JP Lynch, PSU

**Collaborating institutes and scientists**

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

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

**67. 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 2012*
- *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.

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

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

**Principal Investigator and lead institute**

Lakshmanan Krishnamurthy, ICRISAT

**Collaborating institutes and scientists**

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

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

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

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

- Duration: Jan 2008–Dec 2010
- Total: USD 450,836

#### **Principal Investigator and lead institute**

Jeff Ehlers, UoC–Riverside

#### **Collaborating institutes and scientists**

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

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

Thirty early maturing and thirty medium maturing cowpea varieties will be compared for grain yield under terminal drought conditions using late plantings at two sites during the main growing season in West Africa and in four controlled irrigation and rain-free environments in West Africa and California. This will provide baseline drought tolerance information that will allow identification of drought tolerant and susceptible ‘checks’ for future drought studies and provide an estimate of genotype x environment interaction for grain yield under drought, including the degree of correlation between the results of off-season controlled environment screening and results from main-season African growing environments. Information about the importance of genotype x environment interactions will guide future investigators on whether to breed for specific regions separately, or whether region-based and/or off-season drought-screening nurseries can be employed effectively to breed for improved drought tolerance. Identification of efficient indirect selection methods like thermal imaging allows

screening of a large number of germplasm lines to help ensure capture of traits that exist in the cowpea germplasm pool, and may also help reveal important component characteristics contributing to grain yield under drought. Thermal imaging is a potentially powerful method for drought tolerance screening that has not been comprehensively evaluated for its ability to discriminate drought tolerant and susceptible cowpea genotypes and this proposal seeks to establish its usefulness in cowpea.

### 70. Project No G4008.14: Breeding for drought tolerance with known gene information

- Duration: Jan 2008–Dec 2009; NCE: Jun 2010
- Total: USD 300,000

#### **Principal Investigator and lead institute**

Jiankang Wang, CIMMYT-CAAS

#### **Collaborating institutes and scientists**

- CSIRO and University of Queensland, Australia – Scott Chapman, David Bonnett,
- University of Queensland – Mark Dieters
- CAAS – Ruilian Jing, Xianchun Xia, Huihui Li, Luyan Zhang, Changbin Yin
- GCP – Jean-Marcel Ribaut
- CIMMYT – Gary Atlin, Matthew Reynolds, Yunbi Xu
- INRA – Francois Tardieu, Claude Welcker
- ICRIAT – Dave Hoisington, Shyam Nigam, Vincent Vadez

Despite substantial investment in QTL mapping for many traits important to plant breeders, there are relatively few examples of the effective implementation of QTL in marker-assisted selection (MAS) for polygenic traits, such as drought tolerance. Given that breeders are increasingly able to access genotypic and phenotypic information, the major hurdles are: (i) QTL for such traits typically account for only a relatively small proportion of genotypic variance and simultaneous selection for multiple QTL will be necessary to make useful genetic gain; (ii) Breeders need to retain ‘known’ genes (e.g. of known effects and locations for disease and quality traits) in germplasm that is targeted for improvement in drought adaptation; (iii) Identification of repeatable QTL across genetic backgrounds and growing environments for use in MAS for drought adaptation is still problematic; (iv) Lack of adequate tools and training of breeders to optimize the design of breeding schemes based on the best available genetic and genomic information.

To address these issues, methodology, software training courses and technical backstopping during initial implementation phases are needed to assist breeders to design and validate optimal breeding schemes for their specific profile of goals and constraints. Ideally, outputs from QTL analysis should be fully integrated into this process. Prototypes of the required tools were developed and validated in previous GCP-funded projects, and now need to be integrated with databases of QTL mapping data and known gene information. In particular, software tools need to be able to identify 'robust' breeding schemes that tolerate the presence of 'erroneous' QTL, or at least validate those QTL as you go and have the flexibility to be adjusted based on the outcomes of that validation data. This will enable breeders to develop designed breeding schemes that will greatly improve the efficiency of their breeding efforts both in terms of pace and impact of progress. This will lead to the development of breeding products for resource-poor farmers in the form of higher yielding, better quality, more disease resistant, and more drought tolerant crop varieties.

#### **71. Project No G4008.34: Environmental assessment for the GCP phenotyping network**

- *Duration: Jan 2008–Dec 2009; NCE: Jun 2010*
- *Total: USD 279,403*

##### **Principal Investigator and lead institute**

Glenn Hyman, CIAT

##### **Collaborating institutes and scientists**

- KU Leuven – Dirk Raes, Sam Geerts
- EMBRAPA – Reinaldo Lucio Gomide
- Waen Associates and CIAT – Peter Jones

This project aims to support the selection of sites for drought phenotyping and to support decisions about deployment of GCP genotypes for testing. Initially, information on the climatic and soil conditions of proposed testing sites will be developed using environmental data sets and modeling tools. Environmental conditions of the site and its surrounding neighborhood will be assessed using geographic information systems (GIS) software, spatial overlay, and distance and proximity tools. Climate assessment tools will be used to make a rapid appraisal of climatic conditions at proposed "Field Phenotyping Platform" (FPP) sites (phenotyping hubs) of the GCP. These data will be used at the outset of the project to support the selection of FPP sites by the GCP

management team. Subsequent analysis will support future decisions on how genotypes developed by GCP researchers will be deployed with the aim of optimizing efficiency of testing programs. This work will include site similarity analysis using specialized software for comparing climate and soils of one or more locations. Detailed water budgets will be developed for FPP and "Level 1 Local Phenotyping Platform" (LPP) sites (i.e., locations involved in GCP phenotyping activities for priority crops). All the results and data will be made available to the GCP research community to guide decisions on deployment of genotypes for further phenotyping.

#### **Objective 4: Marker/allele validation in adapted germplasm under target environments**

#### **72. Project No G4007.05: Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco**

- *Duration: Jan 2007–Dec 2009; NCE: Dec 2010*
- *Total: USD 300,000*

##### **Principal Investigator and lead institute**

Abbad Andaloussi Fouad, INRA

##### **Collaborating institutes and scientists**

- INRA – Nsarellah Nasserlehaq, Jlibene Mohammed, Lhaloui Saadia, Labhilili Mustapha, Saidi Seddik
- ICARDA – Sripada M. Udupa
- UNIBO – Roberto Tuberosa
- Cornell University – E. Sorrells
- CIMMYT – Manilal William
- University of Missouri – J. Perry Gustafson

INRA Morocco and the GCP have agreed to develop a cooperative research project, based on a combination of financial resources, to support research activities aiming at harnessing the products of genomic revolution for better utilization of plant genetic resources and improving plant breeding efficiency and effectiveness in INRA research programs. The project proposal aims to enhance the production of wheat and barley in rain-fed farming systems of Morocco, thus offering an effective mode of enhancing the food security and income of local, resource-poor farming families. The proposed project will focus first on bread and durum wheat and barley improvement with emphasis on developing new high- and stable-yielding wheat and barley germplasm with improved quality and tolerance to various stresses. Additionally, the project will exploit new genomics technologies, tools and germplasm developed in other GCP projects.

**73. Project No G4007.06: Integrating marker-assisted selection into the conventional breeding procedure for improvement of wheat (*Triticum aestivum* L.) in the drought-prone areas of Northern China**

- Duration: Aug 2007–Jul 2010
- Total: USD 150,590

**Principal Investigator and lead institute**

Ruilian Jing, Professor, CAAS

**Collaborating institutes and scientists**

- CAAS –Xin-Guo Mao, Xiao-Ping Chang
- Ningxia University (NU) – Xing Xu
- Northwest Scientific University of Agriculture and Forestry (NWSUAF) – Hui-Min Xie
- SAAS – Mei-Rong Sun
- LAAS – Can-Jun Zhang
- HAAS – Xiu-Min Chen

To implement the general objectives of the proposed project, we will develop the following research activities:

1. To hold training courses for molecular marker assisted (MAS) selection techniques and drought tolerance (DT) phenotyping;
2. To integrate MAS tools into conventional breeding program and select stable introgression lines (ILs) carrying target genes/markers;
3. To phenotype and genotype the ILs with the elite Chinese wheat genetic backgrounds in diverse environments and select DT ILs;
4. To exchange the information, technology and methodology associated with the molecular breeding for DT, promote interactions among regions, build the capacity of wheat modern breeding in China and other Asian countries.

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

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

**Principal Investigator and lead institute**

Robert Schaffert, Embrapa Maize and Sorghum

**Collaborating institutes and scientists**

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

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

**Objective 5: Application of molecular markers in breeding programmes**

**75. 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: Mar 2011
- Total budget: USD 598,590

**Principal Investigator and lead institute**

Arvind Kumar, IRRI

**Collaborating institutes and scientists**

- CRRRI – 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.

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

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

**Principal Investigator and lead institute**

Wolfgang Grüneberg, CIP

**Collaborating institutes and scientists**

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

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

step markers for SPVD will be developed, by using backcross populations, AFLP, and SSR or SNP markers. In a third step OFSP breeding populations and the CIP germplasm will be screened with the marker system to increase the use of parental material segregating for the phenotype "SPVD Resistance".

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

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

**Principal Investigator and lead institute**

Jorge A Acosta-Gallegos, INIFAP Mexico

**Collaborating institutes and scientists**

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

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

tolerance to water stress, adaptation to low soil fertility, as well as for BGYMV and root rot resistance. This project will be one of the first to apply molecular breeding on a large scale to common bean improvement for the region and will focus on tolerance to drought stress and diseases that occur under drought and low soil fertility conditions.

**78. Project No G4008.17: Application of marker-assisted selection for Striga resistance in cowpeas**

- Duration: Jan 2008–Dec 2009; NCE: Dec 2010
- Total budget: USD 199,986

**Principal Investigator and lead institute**

Jean Baptiste Tignegre, INERA

**Collaborating institutes and scientists**

- IITA – S Muranaka, Boukar Ousmane
- INERA – Jeremy T. Ouedraogo, Issa Drabo

In West Africa, cowpea is a strategic edible crop due to its high protein and micronutrient contents, and therefore grown in a continuous fashion to alleviate poverty and achieve food security. However, biotic and abiotic constraints limit the production, resulting in severe yield reduction at smallholder farmer level (300-700 kg/ha), even though potential productivity of cowpea reaches 4t/ha under well managed field.

*Striga gesnerioides* (Willd.) is a parasite of cowpea and a major constraint of cowpea production in West and Central Africa. The cowpea infected by *Striga* causing severe chlorosis, wilting, and stunting of susceptible hosts and yield losses is estimated in millions of tons annually.

Conventional breeding efforts have developed some varieties for the *Striga* problems as well as other important agronomic and resistance traits, but it is time-consuming and difficult pyramiding favorable traits. Marker assisted selection (MAS) is a modern and potential tool to fast track the breeding process and increase efficiency of breeding activities. Under GCP project "Marker development and marker-assisted selection for *Striga* resistance in cowpea", MAS methodology for *Striga* resistance is now in the final stage of development. By using the MAS for *Striga* resistance, cowpea breeder can fasten the breeding process and reduce the size of population for field screening.

The cooperative work proposed here, involving the “Institut de l’Environnement et des Recherches Agricoles” (INERA) of Burkina Faso and the International Institute of Tropical Agriculture (IITA), seeks to apply the MAS strategy into cowpea breeding activities for Burkina Faso and Niger to achieve rapid and reliable screening of Striga resistant cowpea lines. The outcome of this work will be well-adapted Striga resistant cowpea varieties available to farmers in Burkina Faso and Niger Rep. It is expected that farmers will achieve higher yields of better quality cowpea that would impact favorably on their general livelihoods.

**79. Project No G4008.19: Incorporation of an MSV-resistance gene in Mozambican maize varieties, mediated by use of MAS**

- *Duration: Jan 2008–Dec 2010*
- *Total budget: USD 240,000*

***Principal Investigator and lead institute***

Mark Laing, University of KZN

***Collaborating institutes and scientists***

- IIAM, Mozambique – David Mariote, Pedro Fato, Calisto Bias
- University of KZN – Tongo Tongoona, John Derera, Greg Watson

Maize streak virus is a serious disease of maize, which is especially severe in Southern Africa. CIMMYT has done a great job of finding an effective resistance gene, and then developing a molecular marker to track it during breeding steps. This is one of the more effective cases of using marker assisted selection. Our goal is to use this MAS technology to rapidly introgress the MSV resistance gene into Mozambican maize germplasm which has been bred for other characteristics. This will include both key inbred lines for hybrid seed production and important open pollinated lines.

### **Theme 3 – Crop information systems**

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

##### **Project No G8009.01.02/Activity 1.1.2: Develop and deploy the Integrated Breeding Portal**

- Duration: Jul 2009–Jul 2014
- Total budget: USD 841,924

##### **Principal Investigator and lead institute**

D González-de-León (up to December 2010), Fred Okono, GCP

##### **Project No G8009.06.02: Activity 3.2.2: Information Mgt**

- Duration: Jul 2009–Jul 2014
- Total budget: USD 349,490

##### **Principal Investigator and lead institute**

A Portugal, GCP

##### **Project No G8009.06.04: Activity 3.2.4: Design & analysis**

(This project succeeds G4006.35, which ended December 2009)

- Duration: Jul 2009–Jul 2014
- Total budget: USD 909,915

##### **Principal Investigator and lead institute**

Marcos Malosetti, WUR

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

##### **80. Project No G4008.31: Upgrading the quality and utility of GCP phenotyping data through the development of a data input template to facilitate the storage of data in crop-specific databases**

- Duration: Feb 2008–Jan 2009; NCE: Jan 2010
- Total budget: USD 72,000

##### **Principal Investigator and lead institute**

Robert Koebner, CropGen International

##### **Collaborating institutes and scientists**

- CropGen International – Paul Brennan
- CRIL/CIMMYT – Guy Davenport (up to August 2010)

The goals of this proposal are to: (1) create a wizard-driven template (“first generation template”) able to store phenotypic observations and all associated data to make them interpretable, whilst assuring compatibility with the GCP domain models and crop information systems such as ICIS; (2) extend to a “second generation template” which is ore crop-specific and prescriptive, via the incorporation of mandatory traits and fields (including drought tolerance indicator traits, experimental designs, environmental indicators etc.) both to facilitate future meta-analyses of the phenotypic data and to improve the homogeneity of experimental protocols across GCP projects; (3) document the use of this template in a user manual; (4) export, as far as possible, the data presently lodged in the GCP Central Registry into the ‘first generation’ template; (5) monitor the use of the templates and the compliance thereof; and (6) explore the possibility of establishing electronic field data capture technology for the GC community, as a tool to improve the accuracy of phenotyping.

##### **81. Project No G4008.32: Quality Management procedures in GCP research laboratories promoted**

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

##### **Principal Investigator and lead institute**

J Smith, FERA; G Davenport (up to August 2010), CIMMYT

Many software tools, databases and web resources that could help support GCP projects are not available to GCP research due to poor documentation, user friendliness or is too complex all but the most experience statistician to use. For example, good data quality in laboratories is an important requirement for GCP projects, however poor documentation and the lack of a good example case is stopping some laboratories to implement these measures. Well defined trait ontology is required by the GCP in order for the results from different groups and even species to be compared. At the moment GCP datasets do not use such a ontology. Sequenced genomes are good resources to aid in the development of molecular markers for breeding, however the use

of bioinformatics tools to analysis these sequence are usually outside the knowledge of the average plant breeder. Selection indices and simulation tools are also useful in deciding crosses and selection in breeding programs, but they usually require an experienced statistician to use them. Finally, tools such as ICIS can be used in breeding program, however there is not sufficient documentation or a suitable example case for breeders to implement these tools in their breeding program.

## **82. Project No G4009.03/G4010.06/G4011.01: Enhancement and implementation of the Crop Ontology for data integration and data interoperability**

- **Duration:** Jan 2009–Dec 2011
- **Budget by project:**
  - G4009.03: USD 303,775
  - G4010.06: USD 67,200
  - G4011.01: USD 153,102
- **Total budget:** 524,077

### **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/>.

**Project No G8009.06.03: Activity 3.2.3: Data curation**

- *Duration: Jul 2009–Jul 2014*
- *Total budget: USD 290,409*

**Principal Investigator and Lead institute**

Arlet Portugal, GCP

**Collaborating institutes and scientists**

Various

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

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

- *Duration: Nov 2008–Oct 2011*
- *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.

**84. Project No G4008.21: Largescale phylogenomic analyses tools developed for gene function prediction for GCP crops**

- *Duration: Jan 2008–Dec 2009; NCE: Feb 2010*
- *Total budget: USD 122,400*

**Principal Investigator lead institute**

Mathieu Rouard, Bioversity International

**Collaborating institutes and scientists**

- Bioversity – Matthieu Conte
- CIRAD – Christophe Périn
- IRRI – Richard Bruskiewich, Ramil Mauleon, Martin Senger

With an increasing amount of data provided by Generation Challenge Programme projects on full or partial genome sequencing, there is an urgent need to transfer the information from model species to

newly sequenced ones. Orthologous and paralogous gene identification is now a major objective for gene function prediction as orthologous sequences are more likely to share the same function than paralogous sequences. The phylogenomic inference approach has been shown to enable the highest accuracy in predicting protein molecular function, avoiding most false homology inference problems and distinguishing between orthologous and paralogous genes. The GCP has already invested some effort in that strategy and has released promising tools for the plant researcher community. This project's aim is to consolidate and further develop those approaches in order to provide new insights into functional genomics.

**85. Project No G4009.04/G4010.05: 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–Aug 2011
- **Budget by project:**
  - G4009.04: USD 85,000
  - G4010.05: USD 81,920
- **Total budget:** USD 166,920

**Principal Investigator lead institute**

Rajeev Varshney and Trushar Shah, ICRIAT

**Collaborating institutes and scientists**

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

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.

**Project No G8009.03: A toolbox of analysis and decision-support applications to support molecular breeding developed (PIs: Graham McLaren/Diego González-de-León, GCP)**

- **Duration:** Jul 2009–Jul 2014

**Project No G8009.03.01: Activity 2.2.1: Develop and deploy statistical and genetic analysis methodology for molecular breeding**

**Activity Leader and lead institute**

Fred van Eeuwijk, WUR

**Collaborating institutes and scientists**

- CIMMYT

**Project No G8009.03.02: Activity 2.2.2: Develop and deploy cross prediction and selection methodology for molecular breeding**

***Activity Leader and lead institute***

Alain Charcosset, Agropolis-INRA

***Collaborating institutes and scientists***

- CIMMYT

**Project No G8009.03.03: Activity 2.2.3: Develop and deploy simulation tools for complex G-E systems**

***Activity Leader and lead institute***

Mark Dieters, UQ

***Collaborating institutes and scientists***

- CAAS
- CIMMYT
- CSIRO

**Objective 4: Informatics infrastructure – Provide facilities for data integration and sharing among GCP partners**

**Project No G8009.04.01: Integrated GCP informatics platform created**

***Activity Leader and lead institute***

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

***Collaborating institutes and scientists***

- CIMMYT
- ICRISAT

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

- *Duration: Jul 2009–Jun 2012*
- *Total budget: USD 409,783*

This objective includes the following elements in its workplan:

- Pedigree Information Management
- Field Data Management
- Laboratory Information Management

***Principal Investigator and lead institute***

Arlet Portugal, GCP

Includes the following:

- G8009.02.01/Activity 2.1.1
- G8009.02.02/Activity 2.1.2
- G8009.02.03/Activity 2.1.3
- G8009.04.03/Activity 2.3.3

For details of each activity, please see the Project Index at the end of this publication.

## Theme 4 – Capacity building

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

#### 86. Project No G4007.20: Managing the Generation Challenge Programme in a Post-International Treaty World: A proposal for a technical training workshop and related materials

- Duration: Aug 2007–Jul 2008; NCE: Oct 2010
- Total budget: USD 34,100

#### Principal Investigator and lead institute

Michael Halewood, Bioversity International

#### Collaborating institutes and scientists

- Bioversity International – Gerald Moore,
- CAS-IP, Bioversity International – Victoria Henson-Apollonio
- Generation Challenge Programme – M Carmen de Vicente
- Empresa Brasileira de Pesquisa Agropecuaria (EMBRAPA) – Maria José Sampaio
- IRRI – Ruairaidh Sackville-Hamilton

The multilateral system of access and benefit sharing (MLS), created by the International Treaty on Plant Genetic Resources for Food and Agriculture (known hereafter as the Treaty), could only become operational after the Governing Body of the Treaty adopted the Standard Material Transfer Agreement in June 2006. In the time since June 2006, there has been considerable evidence that researchers working with plant genetic resources for food and agriculture require assistance in coming to terms with the new 'rules of the game'. In this context, it would be appropriate to hold a workshop to document and reflect upon experiences within the Generation Challenge Program (GCP) concerning the terms and conditions (and related legal instruments) of transfers of materials for use in research and final GCP research products. It would also be useful to raise awareness among research partners in the GCP about the Treaty and the implications of the creation of the MLS, and how to address exchanges of materials that are not covered by the MLS. To make the most out of the documentation and training activities, we propose developing guidelines for best practices for GCP project partners, and finalization of the training materials (and reference materials used) for future

reference by the trainees, and other GCP research partners who could not attend the workshop. Finally, through the workshop, it is anticipated that useful connections will be formed between expert resource people and the GCP research partners, with the result that the latter would contact the former on an as needs basis in the future.

#### 87. Project No G4008.50: Delivery plan remote learning modules

- Duration: Aug 2008–Jul 2009; NCE: Aug 2010
- Total budget: USD 246,620

#### Principal Investigator and lead institute

Lawrence Pratt, CIMIS

#### Collaborating institutes and scientists

CU – Stefan Einarson

GCP has discovered that agricultural research scientists are clear on how their innovations are expected to benefit resource poor farmers. However, they are very unclear of the process and mechanisms by which their innovations actually get to these farmers. The objective of this project is to develop a series of interactive tools to assist scientists involved in GC programmes to develop high quality "Delivery Plans," based on GCP's current DPKits tool. This project will establish a remote learning strategy to guide GCP grantees through the process of internalising the concept of Delivery Plans and its related objectives. A series of interactive training modules will guide grantees through all the steps of delivery plan development. This effort will directly support the development of well-considered, high quality delivery plans at a very great cost reduction when compared to the costs of bringing groups of grantees together for this purpose.

The project team will apply creative pedagogical design, and best practices in distance learning to achieve the goals of this project. The project includes a design phase, production phase, and finally a testing phase to validate its effectiveness.

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

- Duration: Nov 2009–Oct 2010
- Total budget: USD 25,058

#### Principal Investigator and lead institute

Theresa Fulton, Cornell University

**Collaborating institute and scientist**

- CropGen International – Robert Koebner

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

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

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

**Capacity-building à la carte Programme (awards in various years, ongoing in 2010)**

**2010 awards**

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

- Duration: Jul 2010–Jun 2011
- Total budget: USD 22,086

**Principal Investigator and lead institute**

Zeba I. Seraj, University of Dhaka

**Collaborating institutes and scientists**

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

In Bangladesh, about 1 million hectares of cultivatable land in the coastal areas are affected by salinity. Due to the high sensitivity of modern rice varieties, resource-poor farmers of these areas can grow only one crop in the monsoon when salinity is lower. Therefore, the development of salt tolerant rice lines with wider adaptability is the only sustainable and cost effective way to improve the livelihood of marginal farmers of these areas and sustain total production of the country. In order to strengthen the capacity in rice breeding by use of molecular genetics and genomics to gear-up the rice variety development process in Bangladesh, a previous GCP SP3 commissioned project has made substantial progress in the use of marker-assisted backcrossing for introgression of *Salto1* into Bangladeshi mega rice varieties. Another GCP SP5 à la carte project gave good support for the continuation of the GCP activity by establishing a marker laboratory at BRRI. In addition to *Salto1* introgression, preliminary mapping of additional QTLs from a rice landrace, Boilam was also done at IRRI and Dhaka University with funding from another SP5 capacity building fellowships to Dhaka University. The notable progress made in these projects however remains incomplete, where one MABC BC<sub>3</sub>F<sub>2</sub> product, Saltol-BR11 will be tested in Farmers field this year, while the Saltol-BR28 BC<sub>3</sub> crossing is currently being done. This current capacity building support grant therefore aims to support hands on training for the use of advance genotyping in fine-mapping of previously identified QTLs from Boilam for pyramiding and complete characterization of *Salto1* introgression into BRRI dhan28 for the development of more durable saline tolerant rice varieties.

**2009 awards**

**Project No G4009.07: Capacity building à la carte 2009**

- Duration: Oct 2009–Oct 2010

**Principal Investigator and lead institute**

Carmen de Vicente, GCP

**See sub-projects below****90. 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: Oct 2011
- Total Budget USD 100,000

**Principal Investigator and lead institute**

Matthew Blair/Steve Beebe, CIAT

**Collaborating institutes and scientists**

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

The project will provide for 1) training for a PhD candidate from Ethiopia (ECABREN region) to engage in marker assisted recurrent selection of common bean for drought tolerance and 2) training at CIAT for current students (SABRN region) in projects that are complementary to the TL1 – bean objective. The candidate identified for Ethiopia is from SARI and is conducting breeding for the southern region of Ethiopia, while the training opportunities are for researchers representing DAR4D (Zimbabwe) and SABRN (Malawi) or EIAR (Ethiopia). The research conducted will support detailed physiological evaluation of the common bean genotypes for drought tolerance and marker assisted selection for common bacterial blight or arcelin-based bruchid resistances which are part of the TL1 project.

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

- Duration: Oct 2009–Oct 2010; NCE: Oct 2011
- Total budget: USD 49,800

**Principal Investigator and lead institute**

Jeffrey D Ehlers, UoC–Riverside

**Collaborating institutes and scientists**

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

High-throughput genotyping platforms enable new strategies for crop improvement, including more efficient approaches to marker-assisted backcrossing that involve simultaneous selection for flanking markers associated with the target trait(s) and for 'backbone' markers throughout the genome associated with the recurrent parent genetic background. Few

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

**92. 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: Dec 2011
- 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.

**93. 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: Dec 2011
- 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.

**2009 awards**

**Project No G4008.39: Capacity-building à la carte 2008**

- Duration: Apr 2008–Apr 2010

**Principal Investigator and lead institute**

Carmen de Vicente, GCP

**See sub-projects below**

**94. Project No G4008.39.01: Enhancing MAS capacity for salt-stress rice breeding in Bangladesh**

- Duration: Apr 2008–Mar 2009; NCE: Mar 2010
- Total budget: USD 39,926

**Principal Investigator and lead institute**

Vincent Vadez, ICRISAT

**Collaborating institutes and scientists**

- BRRI – MA Salam
- Collaborating institutes and scientists
- BRRI – M Alamgir Hossain, M Rafiqul Islam, M Sazzadur Rahman
- UoD – Zeba I Seraj
- IRRI – Abdelbagi Ismail, Michael Thomson

The application of molecular markers to increase the efficiency of breeding for varietal improvement targeted to problem soils is of vital importance for Bangladesh. Gradually increasing salinity levels in the south of Bangladesh is a major concern, particularly because it affects resource poor farmers living in those areas. About one million hectares of land is affected by different levels of salinity in the coastal areas of Bangladesh. BR11 and BRRI dhan28 are two popular varieties cultivated in Bangladesh for rainfed lowland and irrigated ecosystems, respectively, but those are sensitive to salinity. FL378 is an RIL

having the Saltol QTL for salinity tolerance but is not well adapted to Bangladesh conditions. To introgress Saltol from FL378 into BR11 and BRR1 dhan28, we made backcrosses using BR11 and BRR1 dhan28 with FL378. Marker-assisted backcrossing activities are being pursued through a competitive (Project 2) project which is now coming to an end, and a commissioned GCP project just started with collaboration of IRRI and Dhaka University: population development and salinity screening are done at BRR1 and molecular selection is being performed at Dhaka University. BRR1 has good facilities for population development and phenotyping for salinity tolerance but only partial facilities for molecular analysis and application of MAS. At the same time, BRR1 has experienced scientists trained in molecular marker techniques at IRRI, but due to the lack of adequate facilities they cannot contribute their expertise in the current GCP activities. Strengthening BRR1 molecular research facilities through acquiring the additional equipments that are currently missing (PCR machine, electrophoresis unit with power pack, centrifuge and electronic pipette) will help equip the laboratory of BRR1 to undertake an effective MAB system and deliver the outputs of the ongoing GCP projects more efficiently and, in the long run it will contribute substantially to enhance the capacity of BRR1 to incorporate marker assisted breeding in our current breeding programmes using QTLs of agronomic importance. This current capacity building support grant therefore aims to equip the BRR1 laboratory for DNA marker technology and to support scientific exchanges between BRR1, DU and IRRI for further training and technical backstopping to support and complement the ongoing GCP funded projects.

**95. Project No G4008.39.02: Capacity-building à la carte 2008–Improving capacity for phenotyping for abiotic and biotic stress in Burkina Faso**

- Duration: Apr 2008–Mar 2010
- Total budget: USD 76,383

**Principal investigator and lead institute**

Issa Drabo, INERA–Burkina Faso

**Collaborating institutes and scientists**

- UoC–R – Jeffrey Ehlers, Timothy Close, Philip Roberts
- IITA – Dim-Jong Kim, Satoru Muranaka, Ousmane Boukar

Cowpea is a major grain and fodder crop in Burkina Faso and one of the few crops adapted to the poor soils, low rainfall and high temperatures found in most of the country. Despite its rustiticity, productivity is decreasing due to drought spells and the pressure from pests. With the recent funding of a large GCP project targeting development of improved genomic resources in tropical legumes including cowpea with emphasis on drought tolerance, it is important that capacity exists to properly phenotype germplasm and genetic populations for drought tolerance. Therefore to meet the goals of the TL1 project and better characterise the 500 genotypes for their responses to abiotic stresses (drought and heat) and biotic ones (thrips, nematodes, Fusarium wilt, and bacterial blight), facilities for phenotyping need to be improved. The background of drought research in Burkina Faso is based on multilocation trials and breeding for agronomical traits. Therefore capabilities need to be strengthened. Precise and accurate phenotyping will be needed to take advantage of molecular markers being identified under the TL-1 project. Equipment to precisely link the plants physiological and agronomical responses to water available in the soil is needed.

**96. Project No G4008.39.03: Capacity-building à la carte 2008–Improving capacity for phenotyping for abiotic and biotic stress in Senegal**

- Duration: Apr 2008–Mar 2010
- Total budget: USD 79,232

**Principal Investigator and lead institute**

Ndiaga Cisse, ISRA

**Team members**

- UoC–Riverside – Jeffrey Ehlers, N Ndack Diop, Philip Roberts

Cowpea is a major grain and fodder crop in Burkina Faso and one of the few crops adapted to the poor soils, low rainfall and high temperatures found in most of the country. Despite its rustiticity, productivity is decreasing due to drought spells and the pressure from pests. With the recent funding of a large GCP project targeting development of improved genomic resources in tropical legumes including cowpea with emphasis on drought tolerance, it is important that capacity exists to properly phenotype germplasm and genetic populations for drought tolerance. Therefore to meet the goals of the TL1 project and better characterise the 500 genotypes for their responses to abiotic stresses (drought and heat) and biotic ones (thrips, nematodes,

Fusarium wilt, and bacterial blight), facilities for phenotyping need to be improved. The background of drought research in Burkina Faso is based on multilocation trials and breeding for agronomical traits. Therefore capabilities need to be strengthened. Precise and accurate phenotyping will be needed to take advantage of molecular markers being identified under the TLI project. Equipment to precisely link the plants physiological and agronomical responses to water available in the soil is needed.

### **97. Project No G4008.43: Improve cowpea productivity for marginal environments in Mozambique**

- *Duration: Jul 2008–Jun 2010*
- *Total budget: USD 68,592*

#### **Principal Investigator and lead institute**

Rogério Chiulele, UEM

#### **Collaborating institutes and scientists**

- UoC–Riverside – Jeff Ehlers, Timothy Close, Philip Roberts
- Pennsylvania State University – Jonathan Lynch

This proposal has three objectives, which will contribute to capacity building. The objective 1 will offer opportunity to build capacity in drought tolerance screening through conducting drought trials and interacting with other groups doing the same type of trials. This will also offer training in analysing data for genotype by environment interaction and presentation of results. Apart from the capacity building this objective will provide baseline information on drought tolerance for early and medium cycle cowpea varieties and assess the importance of genotype x environment interactions for grain yield under drought in Mozambique. The objective 2 will provide experience in larger-scale germplasm screening for drought tolerance by assessing the genetic variability for drought tolerance of a set of 300 Mozambican cowpea landrace accessions. The objective 3 will provide experience on how to design and implement an MAS-based programme, in close collaboration with mentors at UoC–Riverside. This objective will also enable to develop breeding populations suitable for application of marker-assisted selection (MAS) and marker-assisted recurrent selection (MARS) using SNP-based markers developed under the associated GCP Tropical Legume 1 (GCP-TL I) project. In Objective 1, thirty early maturing and thirty medium maturing cowpea varieties will be compared for grain yield under

terminal drought conditions using late plantings at two drought-prone sites in Mozambique during the main growing season and in one trial under irrigation during the off-season (dry-season). This will provide baseline drought tolerance information for a wide range of cowpea genotypes in Mozambique and will allow identification of drought tolerant and susceptible 'checks' for future drought studies. By comparing results from identical trials being conducted in West Africa by an associated GCP project "Improving Drought Tolerance Phenotyping in Cowpea" of the SP3, it will be possible to estimate genotype x environment interactions for grain yield under drought across a wide range on conditions, including the degree of correlation between the results of off-season controlled environment screening and results from main-season African growing environments. The effectiveness of a new root screening protocol developed for evaluating drought tolerance and rooting characteristics in common bean (Lynch, 2007) will be evaluated in the Objective 1 trials to determine associations between root ratings and grain yield under drought in cowpea. In Objective 2, 300 landrace accessions from Mozambique will be assessed for tolerance to drought using screening protocols developed for the GCPTL I project and the rapid root screening assay (Lynch, 2007). This will complement assessments of other sets of cowpea germplasm being assessed in the GCP-TL I and ICRISAT Tropical Legume II projects by including unique germplasm not being evaluated in these other projects. In Objective 3, ten breeding populations appropriate for Mozambique and for marker-assisted recurrent selection using SNPbased and SSR markers developed under the GCP-TL I project; targeted training will be conducted in the application of these markers in MAS/MARS through reciprocal two-week visits by UoC–Riverside investigators to EMU and by Mozambique researchers to UoC–Riverside. Overall, the funding will offer opportunities for capacity building on phenotyping for drought tolerance, design and implementation of MAS-based programme. This will also generate useful information on drought tolerance and opportunities for using marker assisted selection in Mozambique.

#### **2007 awards**

### **98. Project No G4007.13.04: Capacity-building à la carte 2007–Characterisation of maize germplasm found in Ghana, using the bulking technique**

- *Duration: Jul 2007–Jul 2009; NCE: Jul 2010*
- *Total budget: USD 72,500*

**Principal Investigator and lead institute**

Allen Oppong, CSIR-CRI, Ghana

**Collaborating institutes and scientists**

- CIMMYT – Yunbi Xu, Claudia Bedoya
- UdR – Jorge Franco
- USDA-ARS – Marilyn Warburton

The Pathology Section of the Crops Research Institute of Ghana, together with our maize breeders and partners, are trying to develop drought tolerant maize with resistance to maize streak virus disease using traits found in local germplasm. We would like to use phenotypic screening to characterise drought resistance in the first stage; however, when drought associated molecular markers become available, we hope to be in a position to use these as well for selection gain in our populations. In the first stage, in addition to selecting diverse, drought resistant germplasm for breeding, we will also use molecular markers linked to MSV resistance in our breeding programme in an MAS programme to speed gain from selection for this trait. Maize germplasm in Ghana is not adequately characterised. We hope to collect, conserve, and fingerprint maize populations from Ghana, in addition to known drought tolerant populations from other breeding programmes in Africa, to ensure that the populations we select for our breeding programme are as diverse as possible. In addition to selecting populations for breeding, we hope to create a core subset, that has been adequately characterised morphologically and genetically, that would be used for selection, hybridisation, association studies, etc in our efforts to develop varieties with the desired traits.

The use of bulk fingerprinting will afford us the opportunity to characterise as much as possible most of our stored seed maize germplasm to the DNA. Inbred lines will be selected from the most diverse populations that also show good drought tolerance. Inbred lines will be selected from these populations, using markers linked to MSV to ensure that all of them will be resistant to this disease. These lines will be used for hybrid production, synthetic maize population production, and association mapping of useful traits in the future.

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\* *Associated GCP Project G3005.14: Characterisation of genetic diversity of maize populations: Documenting global maize migration from the center of origin (PI: Marilyn Warburton)*

**99. Project No G4007.13.05: Capacity-building à la carte 2007 – An integrated proteomics and genomics approach to discover salt tolerance genes\***

- *Duration: Jul 2007–Jul 2009*
- *Total budget: USD 48,970*

**Principal Investigator and lead institute**

Ghasem Hosseini Salekdeh, ABRIL

**Collaborating institutes and scientists**

- IRRI – Abdelbagi M. Ismail
- IPK – Mohammad-Reza Hajirezaei

Proteomics showed to be a powerful approach to discover abiotic stress tolerance genes/proteins. In the past few years we used this approach to study rice response to salinity and drought. However, according to these findings and our works in GCP project 2, we learned that:

1. Many important proteins including transcription factors are masked by high abundant proteins and can not be detected on two dimensional electrophoresis gels.
2. It is important to confirm the function of genes as tolerant ones using relevant approaches like RNAi before applying it in marker assisted breeding (MAB) programme.

To address these two important issues, we are going to isolate nucleus from rice tolerant (FL478) and sensitive (IR29) lines and then extract and study their proteome. These will allow us to study low abundant but very important transcription factors. Then, we will further extend our knowledge by analysing metabolome of similar plant samples and combine the information with proteomics data. We will then examine and verify the contribution of most promising candidate proteins in rice tolerance to salinity by applying RNAi approaches and transient expression of candidate genes.

At the end of project, we expect to contribute in increasing rice tolerance to salinity by developing new molecular markers for MAB programme or generating stable transgenic rice of successful RNAi analysis. To reach these objectives, ABRIL has enough facilities to grow plants and measure different physiological traits. We also have facilities and expertise to perform

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\* *Associated GCP Project G3005.02: Revitalising Marginal Lands: Discovery of Genes for Tolerance of Saline and Phosphorus-Deficient Soils to Enhance and Sustain Productivity (PI: Abdelbagi Ismail)*

2-DE analysis to identify proteins. However, because of lack of Mass Spectrometry (MS) facilities in Iran, we can not identify proteins or analyse enough metabolome in a high-throughput manner. We think that in collaboration with IPK (Germany), we shall be able to both analyse the samples and train ABRII staff to use MS instrument and analyse data. It will also be possible to use IRRI's facilities and expertise to perform RNAi analysis and train ABRII's staff to apply this very important approach.

**100. Project No G4007.13.06: Capacity-building à la carte 2007–Enhancing capacity of ICABIOGRAD in phenotyping and molecular analysis to develop elite rice lines suitable to Indonesian uplands\***

- Duration: Jul 2007–Jul 2009; NCE: Mar 2010
- Total budget: USD 79,709

**Principal Investigator and lead institute**

Masdiar Bustamamm, ICABIOGRAD, Indonesia

**Collaborating institutes and scientists**

- IRRI – Casiana Vera Cruz
- ICABIOGRAD – Kurniawan Rudi Trijatmiko, Wening Enggarini

As a public research institute involved in Asian Rice Biotechnology Network (ARBN) since 1993, ICABIOGRAD had sent several times its best people to be trained at IRRI, mainly to work on blast resistance in rice. But due to minimal support for research in Indonesia, many of them have left to pursue their careers in nations with more advanced research systems. This brain drain situation has limited the capability of the institute to reach its research target and deliver useful product to poor farmers.

In the past two years, ICABIOGRAD has been involved in two GCP projects working on blast resistance (PI, Rebecca Nelson) and P-deficiency tolerance (PI, Abdelbagi Ismail) in rice. Blast is particularly important for upland sub-ecosystem because the environment favours its proliferation. Upland soils in Indonesia are dominated by highly weathered acid soils, whose phosphorus deficiency is usually a major constraint to crop production. Some useful genes and QTLs have been identified and mapped in these projects. The task remains of incorporating the favourable alleles of these genes and QTLs into an elite upland

variety in Indonesia via marker-assisted selection. This task will not be easy to complete through ICABIOGRAD alone due to lack of skills and facilities to do reliable phenotyping and molecular marker analysis. Both phenotypic evaluation and marker-assisted selection of WRxOL5 elite lines for blast resistance and phosphorus deficiency tolerance need to be completed using low-cost marker technology. Training opportunities in advanced research institutes have proven very effective in developing human resources and in reaching targets of research institutes in developing countries. By giving opportunity to get high-quality training for its staff and follow-up research support, ICABIOGRAD will be able to complete the research and delivery of GCP products while encouraging its staff to stay and assist in contributing impact to the society in Indonesia.

**Fellowships and travel grants**

**Fellowships**

**101. 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.

\* Associated GCP Project G3005.08: Targeted discovery of superior disease QTL alleles in the maize and rice genomes (PI: Rebecca Nelson)

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.

**102. Project No G4009.02.01: Study of Burkina Faso rice landraces diversity and breeding for resistance to Rice Yellow Mottle Virus (RYMV)**

- Duration: Mar 2009–Mar 2011
- Total budget: USD 36,000

**Principal investigator and lead institute**

Honore Kam, PhD student from INERA, Burkina Faso

**Collaborating institutes and scientists**

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

Rice is the staple food in many countries of Africa and constitutes a major part of the diet in many others. A series of abiotic and biotic stresses continue to limit

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

**103. Project No 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<sup>+</sup> and Cl<sup>-</sup> 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.

#### Travel grants

##### **104. G4009.02.04: Travel Grant – International Symposium on Genomics of Plant Genetic Resource**

- *Duration: Feb–May 2010*
- *Total budget: USD 15,000*

#### **Principal Investigator and lead institute**

Carmen de Vicente, GCP; Roberto Tuberosa, UNIBO

#### **Collaborating institutes**

CBS, CSIR, EgU, ICAR, ICRISAT, INRA, NRCRI, UTM

The second congress on Genomics of Plant Genetic Resources (GPGR2) held in Bologna, Italy, from April 24 to 27, 2010 and co-organized by Bioversity International, the IPK and the University of Bologna, followed the first edition organized in 2005 in Beijing, China. The objective of GPGR2 has been to critically evaluate how the recent advances in genomics have improved our capacity to harness plant genetic resources for improving crop productivity and nutritional quality. The unifying picture that emerges from over 90 oral and 300 poster presentations is that genomics is becoming increasingly important for selecting superior genotypes. Hereafter, additional details are reported for some of the presentations.

Details of the Congress and all abstracts are available at the Congress website ([www.gpgr2.com](http://www.gpgr2.com)). The June 2011 issue of the journal *Plant Genetic Resources* presents a special volume that collects 53 manuscripts from the invited speakers and the contributed abstracts. GPGR2 was attended by over 400 participants representing 53 countries.

##### **105. G4010.01.02: Travel Grant – ICPBM3 International Training Workshop on Plant Molecular Breeding**

- *Duration: Aug–Sep 2010*
- *Total budget: 25,000*

#### **Principal Investigator and lead institute**

Carmen de Vicente, GCP; Zhikang Li, CAAS–MST

#### **Collaborating institutes**

AGI, BRAC, CBI, CRI–CSIR, FCRI, ICERI, IIAM, INERA, ISRA, KAgRI, RRD

The 12-day workshop was successfully held between August 30th and September 10th, 2010 at the Institute of Crop Sciences of Chinese Academy of Agricultural Sciences. Participation to the ICPMB conference was part of the program, where the delegates could interact and hear the presentations of the most up-to-date molecular sciences from world-renowned scientists of this field. A formal Workshop opening ceremony took place on the August 30th. Dr Dongxin Feng, Deputy Director of the Department of International Cooperation (CAAS), Dr Shumin Wang, Deputy Director of Institute of Crop Sciences (CAAS), Dr Zhikang Li, Chairperson for the International Training Workshop for Plant Molecular Breeding Technique and Dr Graham McLaren,

Subprogramme 4 leader of Generation Challenge Programme, delivered opening speech to welcome the delegates. Twenty delegates from thirteen countries attended this Workshop. Among the twenty delegates, eleven were given financial support to attend the Workshop and ICPMB conference.

#### **Faculty support**

#### **106. Project No G4006.36: Capacity-building and research project**

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

#### **Principal Investigator and lead institute**

Mark Laing, ACCI/UKZN

#### **Collaborating institutes and scientists**

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

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

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

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

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

University shall direct the Professor to carry out the Activities, and shall be responsible for producing the outputs and products, set forth in this Appendix I.

The University will also identify a “molecular toolbox” – an inventory of molecular tools available for important crops and traits in Africa, and identification of tools that would be particularly useful if developed), to be made broadly available in sub-Saharan Africa. The University will also collaborate with a number of institutes and scientists, including Generation Challenge Programme Consortium Members, Rockefeller Foundation, Bill and Melinda Gates Foundation; University of Illinois, Urbana-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).

#### **Objective 3: Constructing systems for ensuring product delivery**

#### **107. Capacity-building mechanisms and product pipelines established for tropical legume improvement in Africa**

*Details in the TLI section of this publication. (Lead institutes: ARI–Naliendele, CRS, CBI–DR&SS, EIAR, INERA, IRAD, ISRA, LZARDI, SARI–Ethiopia, EgU)*

#### **Partners**

ICRISAT, UC–R, CIAT

- G6010.01: Improve groundnut productivity for marginal environments in sub-Saharan Africa (PI: Vincent Vadez, ICRISAT)
- G6010.02: Improve cowpea productivity for marginal environments in sub-Saharan Africa (PI: Jeff Ehlers, UC–R)
- G6010.03: Improve common bean productivity for marginal environments in sub-Saharan Africa (PI: Steve Beebe, wef October 2010/M Blair, CIAT)
- G6010.04: Improve chickpea productivity for marginal environments in sub-Saharan Africa and South Asia (PI: Rajeev K Varshney, ICRISAT)
- G6010.05: Cross-cutting crop activities (drought phenotyping, data management and capacity building) (PI: Carmen de Vicente, GCP [up to October 2010])

**108. 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 (overlaps with Cassava RI)**

**G4008.26**

- Duration: Jan 2008–Dec 2010
- Total budget: USD 651,525

**Principal Investigator and lead institute**

Emmanuel Okogbenin, National Root Crops Research Institute (NRCRI), Nigeria

**Collaborating institutes and scientists**

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

Cassava has become a major staple and food security crop in Africa. However, there is an urgent need for improved varieties to stop the rapid spread of pest and diseases, especially the cassava brown streak disease (CBSD) and the cassava mosaic disease (CMD), two resurgent crop diseases that have already caused low-grade famine in parts of Africa. Although National Agricultural Research Systems (NARS) are best suited to breed cassava for local needs, NARS in the past limited their activities mainly to testing and selection of improved germplasm, but more recently NARS breeders have begun formal cassava breeding. Several donor funded projects, including a Generation Challenge Program (GCP) competitive grant to CIAT, Brazil, and 3 African countries – Ghana, Nigeria, and Uganda, and a Rockefeller foundation grant to Tanzania, IITA, and CIAT, are now conducting field-based, Marker Assisted Selection (MAS), and participatory cassava breeding. There is a need to build synergies between these 4 NARS breeding programs, IITA, and CIAT through exchange of experience and improved germplasm to ensure rapid production of improved varieties and delivery to farmers. A community of practice (CoP) has been set up involving cassava breeders in the 4 target countries that will permit a free-flow of experiences and information on breeding methods, best field practices, and improved varieties amongst the 4 countries. A primary activity of the CoP will be integration of MAS with field-based breeding and pre-breeding strategies. The project

will also provide training in MAS as well as field-based and participatory plant breeding for current and a new generation of breeders. MAS is a specialized form of cassava breeding complementary to traditional field-based breeding. The CoP will therefore create and maintain close links with International Institute Tropical Agriculture (IITA) and CIAT, and NARS breeding programs via sharing of germplasm/information and training that are outcomes of this project. MAS activities of the CoP will be further supported through collaborative activities with the Genotyping Support Service (GSS), and any other advanced laboratories and research centers having existing relationships with current members of the CoP. In addition, linkages will be built with primary, secondary, and tertiary users of improved cassava varieties to ensure prompt uptake of improved varieties. Lastly, the CoP will be proactive in developing linkages with existing cassava breeding networks, International breeding programs, and related GCP projects, including the genotyping support services (GSS), to bring the best expertise and experiences to bear on the breeding goals.

**G7010.01.05**

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

**Principal Investigator and lead institute**

Emmanuel Okogbenin, National Root Crops Research Institute (NRCRI), Nigeria

**Collaborating institutes and scientists**

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

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

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

#### **Principal Investigator and lead institute**

Jonaliza Lanceras-Siangliw, RGDU

#### **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.

#### **Objective 4 : Developing and implementing support services**

##### **110. Project No G4008.35: Toolbox of available molecular markers useful for marker assisted selection in GCP crops**

- Duration: Mar 2008–Mar 2010
- Total budget: USD 41,000

##### **Principal Investigator and lead institute**

Veerle Van Damme, Consultant

##### **Collaborating institutes and scientists**

- GCP (Humberto Gómez Paniagua, M Carmen de Vicente)

Developing countries harbor the majority of the plant genetic resources for food and agriculture. These genetic resources contain numerous genes and alleles possibly useful to overcome most of the challenges of modern agriculture. Genomics has helped in identifying, targeting and deploying useful genes. Molecular markers greatly facilitate the selection of traits that are often difficult and time-consuming to detect based on phenotype. As such, marker assisted selection (MAS) enables speeding up the incorporation of these valuable traits.

Agricultural researchers and plant breeders, in particular in developing countries, face difficulties concerning access to up to date scientific information on useful molecular markers, as the latest discoveries are often scattered in numerous, expensive peer-reviewed journals or in databases of unknown existence to many. If access to information is not a problem, the avalanche of information can be one, as the information offered through digital resources is not always reliable, can be overwhelming and does not provide guidance for its appropriate use.

This project deals with the development of a toolbox providing free and easy access to information of all publicly available molecular markers ready for use for marker assisted selection in 19 food security crops.

The activity will compile information available in internet sources, public databases, papers and that gathered through communications with molecular crop breeding experts. Results will be made available via Internet as a global public good and its features described in a peer-reviewed publication. By sharing the latest advances in molecular plant breeding, the toolbox is an important step into supporting modern agriculture for the benefit of the poor in developing countries.

##### **111. Project No G4010.03: GCP Molecular Marker Toolkit (Extends G4008.35)**

- Duration: Jul 2010–Oct 2010; NCE: Dec 2010
- Total budget: USD 15,750

##### **Principal Investigator and lead institute**

Veerle Van Damme, Consultant

##### **Collaborating institutes and scientists**

- Humberto Gómez Paniagua, M Carmen de Vicente (upto October 2010), GCP

Over the last decade, genomics has become a key factor in biological research worldwide. It has helped in studying germplasm diversity and in targeting, identifying and deploying useful genes. Compared with phenotyping, molecular markers are more precise and cost-effective for screening and selecting breeding material thus speeding up the incorporation of valuable traits. The increase in genomics research has led to a massive amount of publications and databases. With this increase, the search for available user-ready molecular markers cannot only become a real odyssey, as the latest discoveries are often scattered in numerous, expensive peer-reviewed journals or databases, but the information offered through digital resources is not always reliable and does not provide guidance for its appropriate use.

Driven by the demand of agricultural researchers and plant breeders, particularly those in developing countries who face difficulties in accessing up-to-date scientific information on useful molecular markers, GCP designed a rapid-access tool for currently available and validated markers for 19 food security crops, including GCP's 18 mandate crops. The 19 crops covered are: Musa spp., barley, beans, cassava, chickpeas, coconuts, cowpeas, faba beans, groundnuts, lentils, maize, millet, pigeonpeas, potatoes, rice, sorghum, sweet potatoes, wheat and yams. The first version of GCP's Molecular Marker Toolkit (MM Toolkit) is online since July 2009 and

is currently limited to the highly reproducible SSR, STS and SCAR markers. To keep the users abreast of the latest methodologies, the toolkit will be kept updated and extended with marker technologies such as CAPS and MITE. Besides that, more useful QTLs will be included as well. With this extended version of the GCP MM Toolkit plant breeders in the public sector and small private enterprises, particularly in developing countries, will have access to succinct but more complete marker information. In all, this project promotes the adoption of markers for plant improvement and subsequently the increased efficiency in the development of new cultivars.

**112. G8009.06.06/Activity 3.2.6 Genotyping Support Service (excludes 3<sup>rd</sup> call, whose implementation will begin in 2011).**

*(This project succeeds G4007.21, which ended in 2008, and G4009.01, which ended in 2009)*

- Duration: Jul 2009–Jul 2014
- Total budget: USD 800,548

**Principal Investigator and lead institute**

Chunlin He, wef October 2010/Humberto Gómez-Paniagua, GCP

**Genotyping Support Service (GSS):** The GSS was developed to facilitate NARS access to genotyping technologies, and, in turn, to bridge the gap between lab and field research. This service provides financial and technical support for NARS breeders to access cost-efficient genotyping services worldwide, and supports training activities in experimental design and data analysis for molecular breeding projects. The GSS is an ongoing GCP initiative. It will be further refined over the first year of the project, in particular to include MAB experiments in addition to the diversity analysis and MAS experiments facilitated so far. There will be regular updates of protocols and technology every few months, and use of this service should increase in both intensity and diversity as new users come on board.

**113. Project No G4007.22.04: GCP Workflow and Repository System: Phase III**

- Duration: Jun 2009–Jul 2010
- Total budget: USD 100,000

**Principal Investigator and lead institute**

Carmen de Vicente, GCP

**Service provider**

Cropster GmbH

**Phase III**

Details on Phases I and II of this project are available in the 2008 Project briefs ([http://www.generationcp.org/brochure.php#Exec-summaries\\_Project-briefs](http://www.generationcp.org/brochure.php#Exec-summaries_Project-briefs)). Following Cropster's completion of Phase II, GCP identified improvements and additional functionalities and features which it desires to add to the Workflow, hence the necessity for a third phase of the project, which in essence is a contracted service.

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

**114. Project No G4006.13: Targeting and impact analysis of Generation Challenge Programme (GCP) technologies**

- Duration: Nov 2006–Oct 2007; NCE: Mar 2010
- Total budget: USD 149,742

**Principal Investigator and lead institute**

Glenn Hyman, CIAT

**Collaborating institutes and scientists**

- CIAT – Peter Jones, Sam Fujisaka
- IFPRI – Stan Wood
- CIMMYT – John Dixon

The Generation Challenge Programme (GCP) employs cutting edge crop improvement, microbiology and bioinformatics science and technology to improve livelihoods of resource-poor farmers. The programme has identified the need to geographically target GCP products and to assess ex-ante impact of GCP research. This project will work to fill that need by examining GCP research in the context of the distribution and characteristics of farming systems, drought-prone areas and degrees of risk for specific crops, the geographic distribution of the poor, and potential benefits to the poor from agricultural technology.

The project includes four components. First, the spatial distribution of poverty for small areas within GCP priority farming systems will be assessed using a comprehensive poverty database. Second, climatic variability will be modeled at high spatial resolution to determine the severity and type of crop-specific drought. Third, farming systems will be assessed in the context of crop variety adoption and ways that farmer households can escape poverty. Fourth, the

project will conduct an ex-ante impact assessment of the benefits of GCP technologies to the resource-poor. These four components will be synthesised into a comprehensive spatial analysis for geographic targeting and impact assessment of GCP.

**115. Project No G4008.24: From attractiveness to feasibility: A strategic assessment of the capacity to develop and adopt GCP technologies**

- *Duration: Jan 2008–Dec 2009; NCE: Apr 2010*
- *Total budget: USD 261,112*

**Principal Investigator and lead institute**

Stanley Wood, IFPRI

**Collaborating institutes and scientists**

- ASTI – Nienke Beintema
- CIAT – Glenn Hyman, Scientist
- Consultants – Carlos Tovar, Sindi Kasambala
- ICASEPS – Erna Lokollo, Muchjidin Rachmat
- IER – Lamissa Diakite
- INERA–Burkina Faso – Mathieu Ouedraogo
- NRCRI – Godwin Asumugha
- VPI – George Norton

Prior studies have identified focus areas for GCP activities based on their potential contribution to the humanitarian and technical goals of GCP.

These studies, however, identified priority crops and farming systems for GCP efforts *assuming* that broadly-targeted GCP technologies will be successfully adapted by local breeding efforts and will then be adopted by local smallholders. These are both strong assumptions. It is critical, therefore, that GCP’s initial target/focus areas be subjected to a second phase evaluation that makes provision for the likely capacity of local institutions and farmers to realise the projected potential for GCP impact. We can describe this second phase activity as assessing the “feasibility” of achieving desired outcomes in the high-priority (most attractive) focus areas. It is vital to consider attractiveness and feasibility together since in some areas where the potential benefits may be very attractive, the feasibility of achieving them might be quite low; whereas in other cases (e.g., different countries, farming systems, crops, and targeted production constraints) the overall scale of potential benefits may be smaller, but the feasibility of achieving those results might be much higher (and/or may be achieved more quickly). Thus, overall, it is the *combination*, of both attractiveness and feasibility that must be taken into account when fine-tuning the design of a GCP investment portfolio and the targeting of GCP research priorities.

## Theme 5 – Product delivery

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

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

#### Principal Investigator and lead institute

Jean-Francois Rami, Agropolis–CIRAD

#### Collaborating institutes and scientists

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

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

genotypic information attached to the reference set. This genotyping validation project will be connected to the management of the genetic material constituting the reference sets. As an output, stabilised materials specifically handled as genetic stocks by gene bank curators and associated to validated genetic diversity data will be available.

### 117. 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
- 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

#### **G8009: A Molecular Breeding Platform**

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

#### **Principal Investigator and lead institute**

Graham McLaren, GCP

#### **Collaborating institutes and scientists**

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

The revolutions in molecular biology and information technology offer tremendous opportunities for enhancing the effectiveness and efficiency of breeding programmes. Molecular characterisation, accurate phenotyping, information systems and data analysis tools must be integrated with breeding workflows generating pedigree, phenotypic genotypic and adaptation data, relevant to better prediction of the performance of different genotypes in target environments. The goals of this integration of technologies are: 1) to create gene-to-phenotype trait knowledge for breeding objectives, and 2) to use that knowledge in product development and deployment (Cooper et al 2006). Marker-assisted breeding (MAB), the transfer of a few genomic regions or several quantitative trait loci (QTL) involved in target traits by following molecular markers, has been successfully deployed in the private sector (Crosbie et al 2006), but it is not generally used in the public sector and

hardly ever in developing countries. Reasons for this include shortage of well-trained personnel, inadequate access to high-throughput genotyping, inappropriate phenotyping infrastructure, unaffordable information systems and analysis tools, and the logistical difficulty of integrating new approaches with traditional breeding methodologies, including problems of scale when scaling up from small to large breeding programmes.

#### **Purpose:**

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

#### **Aim:**

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

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

***For details of each activity, please see the Project Index at the end of this publication***

### **Component 1: Integrated Breeding Portal & 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.

This component includes the following objective:

#### **118. Project No G8009.01 Objective 1.1: Establish and manage the Molecular Breeding Platform**

This objective includes the following elements in its workplan:

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

### **Component 2: Information system**

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

This component includes the following objectives:

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

This objective includes the following elements in its workplan:

- Pedigree Information Management
- Field Data Management
- Laboratory Information Management

#### **120. Project No G8009.03 Objective 2.2: Develop a suite of analysis, prediction and simulation tools for MAB 2**

This objective includes the following elements in its workplan:

- Statistical and genetic analysis
- Methodology and tools for Molecular Breeding
- Modelling and simulation tools
- Visualisation and decision support

#### **121. Project No G8009.04 Objective 2.3: Develop an information network, decision-support tools and a workflow management system for molecular breeding**

This objective includes the following elements in its workplan:

- Information network and public crop information
- Public crop information
- Configurable workflow system

### **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.

This component includes the following objectives:

**122. 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.

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

**123. Project No G8009.06 Objective 3.2: provide assistance with a range of molecular breeding support**

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

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

# 2010 Project Index

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## I. Research Initiatives

### 1. Cassava

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
1	G7010.01.01	Improvement and evaluation of the existing cassava reference set for Africa	Morag Ferguson, IITA	Africa	Cassava	• drought tolerance • biotic stress	CRI–CSIR, CIAT, NRCRI, NRTP–ARI	April 2010	March 2013
2	G7009.10/ G7010.01.02	Improving and deploying markers for biotic traits	Chiedozi Egesi, NRCRI	Nigeria, Tanzania, Ghana	Cassava	• drought tolerance, • biotic traits	NRTP–ARI, Tanzania; CRI– CSIR Ghana; DDPSC	March 2010	February 2014
3	G7009.09/ G7010.01.03	Implement MARS projects for drought tolerance	Emmanuel Okogbenin, NRCRI	Nigeria, Tanzania, Ghana	Cassava	• drought tolerance, • biotic traits	CRI–Ghana, SARI–Ghana, CU, DDPSC	December 2009	February 2011
4	G7010.01.04	Phenotyping cassava for drought tolerance to identify QTLs	Alfredo Alves, EMBRAPA		Cassava	• drought tolerance	CIAT, CU, Embrapa/CNPMF, Embrapa/CPATSA, IITA–Kenya, TIGR	April 2010	March 2012
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	Emmanuel Okogbenin, NRCRI Uganda	Ghana, Nigeria, Tanzania,	Cassava	• drought tolerance • pest resistance • disease resistance	CRI–CSIR, Ghana, NaCRRI, Uganda, NRCRI, NRTP–ARI Collaborators CIAT, IITA, CU	January 2008	December 2014

### 2. Legumes

Improving tropical legume productivity for marginal environments in sub-Saharan Africa and South Asia  
TLI Phase I (May 2007–April 2010)

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
<b>Beans</b>									
6	G6007.03	Improve common bean productivity for marginal environments in sub-Saharan Africa	S Beebe, CIAT	Kenya, Ethiopia, Malawi, Zimbabwe	beans	• drought tolerance • disease & pest resistance • productivity	CBI–DR&SS, ECABREN/UoN, RIKEN, SABRN, SARI–Ethiopia	May 2007	April 2010

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
<b>Chickpeas</b>									
7	G6007.04	Improve chickpea ( <i>Cicer arietinum</i> L) productivity for marginal environments in sub-Saharan Africa	Rajeev Varshney, GCP/ICRISAT		chickpeas	• drought and disease resistance	DArT P/L, EIAR, EgU, IIPR, LZARDI, UC–D	May 2007	April 2010
<b>Cowpeas</b>									
8	G6007.02	Improve cowpea ( <i>Vigna unguiculata</i> L) productivity for marginal environments in sub-Saharan Africa	Jeff Ehlers, UC–R		cowpeas	• drought and disease resistance	IITA, INERA, IRAD, ISRA	May 2007	April 2010
9	G7009.05	Improving cowpea productivity for marginal environments in sub-Saharan Africa 2009–2010 'top-off'	Jeff Ehlers, UC–R		cowpeas	• drought and disease resistance	IITA, INERA, IRAD, ISRA	July 2009	June 2010
<b>Groundnuts</b>									
10	G6007.01	Improve groundnut ( <i>Arachis hypogaea</i> L) productivity for marginal environments in sub-Saharan Africa	Vincent Vadez, ICRISAT		groundnuts	• drought and disease resistance	Agropolis–CIRAD, ARI–Naliende, CRS, EMBRAPA, INRAN, ISRA, UCB, UGA	May 2007	April 2010
<b>Cross-cutting activities</b>									
11	G4009.06	Illumina genotyping of SNPs in legume mapping populations and germplasm	Doug Cook, UC–D		Beans, chickpeas, cowpeas, groundnuts	• drought and disease resistance	CIAT, EMBRAPA, ICRISAT	November 2009	October 2010
12	G6007.05	Develop cross-species resources for comparative biology in tropical crop legumes	Doug Cook, UC–D		various crops (legumes)	• drought and disease resistance	UCB, UGA	May 2007	April 2010
13	G6007.06	Provide training and capacity-building for SSA scientists	Carmen de Vicente, GCP		various crops (legumes)	• drought and disease resistance	NARS: ARI–Naliende, CBI–DR&SS, CRS, EgU, EIAR, EMBRAPA, IIPR, INERA, INRAN, IRAD, ISRA, LZARDI, SARI–Ethiopia, UCB, UoN CGIAR Centres: ICRISAT, IITA Others: Agropolis–CIRAD, DArT P/L, ECABREN, RIKEN, SABRN, UGA, UC–D	May 2007	April 2010
<b>Improving tropical legume productivity for marginal environments in sub-Saharan Africa and South Asia TLI Phase II (May 2010–May 2014)</b>									
<b>Beans</b>									
14	G6010.03	Improve common bean productivity for marginal environments in sub-Saharan Africa	S Beebe, CIAT	Kenya, Ethiopia, Malawi, Zimbabwe	Common bean	• drought tolerance • disease & pest resistance • productivity	CIAT, CU, DARTS, DR&SS, ECABREN, SABRN, SARI–Ethiopia, UoC–Davis, UoN	May 2010	May 2014

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
<b>Chickpeas</b>									
15	G6010.04	Improve chickpea productivity for marginal environments in sub-Saharan Africa and South Asia	RK Varshney, ICRISAT	Kenya, Ethiopia, India	Chickpea	• drought tolerance • disease & pest resistance • productivity	/CRISAT, EgU, EIAR, IIPR, NCGR (service provider), UoC–Davis	May 2010	May 2014
16	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	Chickpea	• drought tolerance • disease & pest resistance • productivity	/CRISAT, EIAR, EgU, ICGGC, IIPR	May 2010	May 2014
<b>Cowpeas</b>									
17	G6010.02	Improve cowpea productivity for marginal environments in sub-Saharan Africa	Jeff Ehlers, UoC–Riverside	Mozambique, Senegal, Burkina Faso	Cowpea	• drought tolerance • disease & pest resistance • productivity	UC-R, UEM, ISRA, INERA–BF, IITA	May 2010	May 2014
18	G7010.07.01	Improving Cowpea Productivity for Marginal Environments in Africa (2009–2010 'top-off')	Jeff Ehlers, UoC–Riverside	Mozambique, Senegal, Burkina Faso	Cowpea		UC-R, UEM, ISRA, INERA–BF, IITA	June 2010	May 2014
<b>Groundnuts</b>									
19	G6010.01	Improve groundnut productivity for marginal environments in sub-Saharan Africa	Vincent Vadez, ICRISAT	Tanzania, Senegal, Niger	Groundnut	• drought tolerance • disease & pest resistance • productivity	Agropolis–CIRAD, ARI–Naliende, CRS, EMBRAPA, ICRISAT, ISRA, UCB, UGA	May 2010	May 2014
<b>Cross-cutting activities</b>									
20	G6010.05	Cross-cutting crop activities (drought phenotyping, data management and capacity building)	Ndeye Ndack Diop, GCP	Kenya, Ethiopia, Malawi, Zimbabwe, Mozambique, Senegal, Burkina Faso	Groundnut, Cowpea, Common bean, Chickpea	• drought tolerance • disease & pest resistance • productivity	Agropolis–CIRAD, CIAT, CRS, CU, DARS, DAR4D, DR&SS, ECABREN, EIAR, EgU, EMBRAPA, ICRISAT, IER, IIAM, IIPR, IITA, INERA–BF, ISRA, NARI–Naliende, NCSU, SABRN, SARI–Ethiopia, UEM, UGA, UCB, UoC–Davis, UoC–Riverside, UoN	May 2010	May 2014
<b>3. Maize</b>									
#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Start	End
21	G4008.56	Improving drought tolerance in maize for Asia	Bindiganavile S Vivek, CIMMYT	Asia	Maize	• drought tolerance	ICERI, KSL, NMRI, NSFRCR, UPLB, Syngenta, YAAS	November 2008	October 2013

#### 4. Rice

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
22	G7010.04.01	<i>Improving rice productivity in lowland ecosystems of Burkina Faso, Mali and Nigeria through marker-assisted recurrent selection for drought tolerance and yield potential</i>	Marie Noëlle Ndjiondjop, AfricaRice	Burkina Faso, Mali and Nigeria	Rice	• drought tolerance • yield	INERA–BF, IER, IRRI, NCRI, Agropolis–IRD, Agropolis–CIRAD, CIA	May 2010	April 2014

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

#### 5. Sorghum

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
23	G4008.48	<i>Improve sorghum productivity in semi-arid environments of Mali through integrated MARS</i>	Jean-François Rami, Agropolis–CIRAD	Mali	Sorghum	• drought tolerance	IER, Syngenta, CIRAD	August 2008	July 2013
24	G7010.05.01	<i>Enhancing sorghum grain yield and quality for the Sudano-Sahelian zone of West Africa using the backcross nested association mapping (BCNAM) approach</i>	Niaba Témé – IER; Michel Vaksman, Agropolis–CIRAD, Eva Weltzien, ICRISAT	Mali	Sorghum	• drought tolerance • yield • quality	IER, Agropolis–CIRAD, ICRISAT, UGA	January 2010	June 2014

#### 6. Wheat

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
25	G7010.02.01	<i>Breeding and selection strategies to combine and validate quantitative trait loci for water-use efficiency and heat tolerance of wheat in China</i>	Ruilian Jing, CAAS	China	Wheat	• drought tolerance • heat tolerance • water use efficiency	ACPGF, CAAS, CIMMYT, HAAS, PBI–UoS, SAAS, XAAS	April 2010	March 2014
26	G7010.02.02	<i>Molecular breeding and selection strategies to combine and validate quantitative trait loci for improving water-use efficiency and heat tolerance of wheat in India</i>	Vinod Prabhu, IARI –ICAR	India	Wheat	• drought tolerance • heat tolerance • water use efficiency	ACPGF, ARI, CIMMYT, ICAR, JNKVV, NRCPB, PAU, PBI–UoS	July 2010	June 2014

#### 7. Comparative genomics

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
27	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	CU/USDA–ARS, EMBRAPA, MU/KARI	November 2008	October 2011

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
28	G7009.07	<i>Cloning, characterisation and validation of Alt<sub>5B</sub>/Al tolerance in rice</i>	Leon Kochian/ Susan McCouch, USDA-ARS and CU	Global	Rice	• Aluminium tolerance	ICABIOGRAD, USDA-ARS, CU	October 2009	March 2012
29	G7010.03.01	<i>Cloning, characterisation and validation of Pup1/P efficiency in maize</i>	Leon Kochian, CU/USDA-ARS	Global	Maize	• Phosphorous efficiency	CU/USDA-ARS, EMBRAPA, IRRI, JIRCAS, MU/ KARI	April 2010	March 2014
30	G7010.03.02	<i>Cloning, characterisation and validation of Alt<sub>5B</sub>/Al tolerance in maize</i>	Claudia Guimāraes, EMBRAPA	Global	Maize	• Al tolerance	EMBRAPA, CU/USDA-ARS, MU/KARI	April 2010	March 2012
31	G7010.03.03	<i>Establishing a molecular breeding program based on the aluminum tolerance gene Alt<sub>5B</sub> 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	ICRISAT, INRAN, MU/KARI, EMBRAPA, CU/USDA-ARS	April 2010	March 2014
32	G7010.03.04	<i>Improved rice cultivars for Asian problem soils: Pyramiding of major genes/ QTLs for tolerance to phosphorous deficiency and aluminium toxicity</i>	Sigrid Heuer, IRRI	Asia	Rice	• phosphorous deficiency • Al tolerance	IRRI, CU, EMBRAPA, ICABIOGRAD, JIRCAS, USDA-ARS	April 2010	March 2014
33	G7010.03.05	<i>Marker-assisted back-crossing for improving phosphorous-use efficiency and tolerance to aluminium toxicity via Pup-1 and Alt<sub>5B</sub> genes in maize</i>	Samuel Gudu, MU/KARI	Global	Maize	• Al tolerance • Phosphorous efficiency	MU/KARI, CIMMYT, EMBRAPA, IRRI, JIRCAS, USDA-ARS	April 2010	March 2014
34	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 Magalhaes, EMBRAPA	Global	Sorghum	• Phosphorous efficiency	EMBRAPA, INRAN, MU/KARI, CU/USDA-ARS	April 2010	March 2014

## II. Thematic projects

### Theme 1 – Comparative and applied genomics

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
<b>Objective 1: Assembly of genomics and germplasm resources through consolidating and developing specialised genetic stocks</b>									
35	G4007.02	<i>Validation of drought-response/resistance pathway genes by phenotypic analysis of mutants</i>	Andy Pereira, VBI		Rice	• drought tolerance	HAU, IRRI, VPI	August 2007	July 2009; NCE: January 2010
36	G4008.06	<i>Single nucleotide polymorphism discovery</i>	Peggy Ozias-Akins, wef October 2010; Steven J Knapp, UGA	Global	Groundnuts	• multiple traits	ICRISAT	January 2008	June 2011
37	G7009.06	<i>Development of a SNP platform for molecular breeding in elite material of chickpea</i>	Douglas Cook, UC-D	Ethiopia, Kenya, India	Chickpea		National Center for Genome Resources, ICRISAT	November 2009	October 2011

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
<b>Objective 2: Development of comparative maps within and across species and framework genetic markers for target crops</b>									
38	G3007.03	<i>Genetic and physical mapping resources produced for drought breeding in cassava</i>	Pablo Rabinowicz, UoM	Africa, Asia, Latin America	Cassava	• drought tolerance	ACGT–UoP, ACGT–UoW	August 2007	February 2010
39	G4008.07	<i>Genomic resources and mapping populations developed and assembled for pearl millet to enable trait/gene identification</i>	C Tom Hash, ICRISAT	Africa, Latin America, Asia	pearl millet	• various traits	AICPMIP, CAZRI, ILRI, RAU	January 2008	December 2009; Project under review
40	G4008.09	<i>Genomic resources and mapping populations for sweet potato developed to enable trait/gene identification</i>	Roland Schafleitner, CIP (up to July 2010)	sub-Saharan Africa	sweet potatoes	• drought and disease resistance	EMBRAPA, IIAM, INIA–Uruguay, NAARI, DArT P/L (service provider)	January 2008	December 2009; NCE: June 2010
41	G4008.47	<i>Genomic resources (ESTs, markers and maps) developed for pigeonpea to enable trait/gene identification</i>	Gregory D May, NCGR	various regions	pigeon-peas	• drought and disease resistance	ICRISAT, NRCPB, PDKV	August 2008	December 2010
<b>Objective 3: Assignment of genes and pathways to phenotypes through the convergence evidence of genome variation, expression patterns and phenotypic data</b>									
42	G3007.02	<i>Genomic dissection of tolerance to drought stress in wild barley</i>	Robbie Waugh, SCRI	various regions	barley	• drought tolerance	ICARDA, INIA–Chile, UC–R, OSU	August 2007	July 2009 NCE: July 2010
43	G3008.05	<i>Discovery and development of alleles contributing to sorghum drought tolerance</i>	Andrew H Paterson, UGA	Global	Sorghum	• drought tolerance	UGA, ARC, ICRISAT, MAU, NRCS, SARI–Ghana	November 2008	October 2011
44	G4008.08	<i>Causal relationship between whole-genome expression patterns and stress tolerance determined in rice via analysis of near-isogenic lines (NILs)</i>	Shoshi Kikuchi, NIAS	various regions	rice	• drought tolerance	IRRI	January 2008	December 2009; NCE: December 2010
45	G7009.01	<i>Examining natural variation in the transcriptional regulation of drought responses in wheat</i>	Peter Langridge, ACPFG	Global	Wheat	• drought tolerance	ACPGF, CIMMYT, ICS–CAAS	January 2009	December 2011
<b>Objective 4: Validation of genes and pathways via evaluation of under- or over-expression constructs or variants (induced or natural) of target genes</b>									
46	G3008.03	<i>Delayed senescence and drought tolerance in rice</i>	Eduardo Blumwald, UoC–Davis	Global	Rice	• drought tolerance	UoC–Davis, IRRI	November 2008	October 2011
47	G3008.04	<i>Drought from a different perspective: Improved tolerance through Phosphorous acquisition</i>	Sigrid Heuer, IRRI	Global	Rice	• drought tolerance • Phosphorous deficiency	IRRI, ICABIOGRAD, JIRCAS, UoPd/MPIMPP, ZU	November 2008	October 2011
48	G7009.02	<i>Validation of QTLs associated with drought tolerance traits in chickpea</i>	Pooran M Gaur, ICRISAT	Global	Chickpea	• drought tolerance	ICRISAT, ARS–Durgapura, DZARC, RAKCA–Sehore, RARS–Nandyal, UAS–Bangalore	January 2009	December 2011
49	G7009.04	<i>Development and evaluation of drought-adapted sorghum germplasm for Africa and Australia</i>	David Jordan and Andrew Borrell, DPI&F	Africa, Australia	Sorghum	• drought tolerance	DPI & F, Agropolis–CIRAD, IER	July 2009	June 2012

**Theme 2 – Integrated crop breeding**

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
<b>Objective 1: Crop genetic diversity</b>									
50	G3007.01	Base broadened of current crop diversity in rice using interspecific bridges with African rice	Alain Ghesquière, Agropolis—IRD	Africa, Asia	rice	• drought tolerance	ARC, CIAT, Fedearroz, IER, INERA, PAU, PhilRice, UoA	August 2007	July 2009; NCE: December 2010
51	G3008.01	Generating new wheat germplasm with enhanced drought/heat tolerance using AB genomes genetic diversity	SC Misra, IARI—ICAR	Global	Wheat	• drought/heat tolerance	CIMMYT, IARI—ICAR, PBI—UoS, UAS—Dharwad	November 2008	October 2011
52	G4006.01	Developing strategies for allele mining within large collections	NR Sackville Hamilton, IRRI	Global	Rice		IRRI, EMBRAPA, ICARDA, ICRISAT	January 2006	August 2011
53	G4008.01	Populations for multiple allelic segregation developed in rice and sorghum through multiple parent intercrossing	Hei Leung, IRRI (Project succeeded by G4008.46)			• various		January 2008	December 2009; NCE: December 2010
54	G4008.46	Sorghum MAGIC: Multi-parent advanced generation inter-cross development for gene discovery and allele validation	Tom Hash, ICRISAT	Global	Sorghum		ICRISAT, NIAB	August 2008	February 2011
55	G4008.42	DARtS developed as a genomewide molecular characterisation technology for crops with little sequence information	JC Glaszmann, Agropolis—CIRAD	various			Agropolis—IRD, CIP, CRISL, DARt P/L, ICRISAT, IITA	January 2008	December 2009; NCE: December 2010
<b>G4008.02/03/05/33:</b> Drought-related phenotyping of specific populations with high-quality molecular information implemented and Phenotyping Support Service consolidated. See below for details:									
56	G4008.02	Phenotyping sorghum reference set for drought tolerance	HD Upadhyaya, ICRISAT	Global	sorghum		ICRISAT, IER, ISRA/CERAAS, KARI, NPGRC, UAS—Dharwad	January 2008	December 2011
57	G4008.03	Precision phenotyping of the GCP spring wheat reference sample for drought	Susanne Dreisigacker, CIMMYT	and regions	wheat	• various traits	INRA—Morocco	January 2008	December 2010; NCE: March 2011
58	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
59	G4008.33	Drought tolerance phenotyping of the GCP maize inbred line reference set	James Gethi, KARI	Global	Maize	• drought tolerance	KARI, Agropolis—INRA, CIMMYT, ETH	January 2008	February 2011
60	G4008.45	A Nested Association Mapping (NAM) population of rice: laying the bases for highly efficient QTL characterisation	Mathias Lorieux, IRD/CIAT	Global	Rice	• drought tolerance	ARC	August 2008	July 2011

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
<b>Objective 2. Characterisation of segregating populations and identification of genomic regions for plant breeding</b>									
61	G3007.04:*	<i>Tailoring superior alleles for abiotic stress genes for deployment into breeding programmes – A case study based on association analysis of Alt<sub>SB</sub>, a major aluminium tolerance gene in sorghum</i>	Jurandir Vieira Magalhães, EMBRAPA	Africa and other developing regions	sorghum	• aluminium tolerance	IGD–CU, INRAN, USDA–ARS	August 2007	July 2009; NCE: December 2010
62	G4007.04	<i>Association mapping of downy mildew resistance in elite maize inbred lines in Thailand</i>	Chalermpol Phumichai and Julapark Chuwongse, BIOTEC	Asia	maize	• mildew resistance	NCSRC–KU, IICRD–KU, NSFRC	August 2007	July 2009; NCE: December 2010
63	G4007.23	<i>Field evaluation of wheat–barley introgression lines under different water regimes</i>	Márta Molnár-Láng, ARI–HAS	various regions	wheat, barley	• drought, salt and aluminium tolerance	CAAS, CIMMYT, DPSPP–EKC	December 2007	December 2010
64	G4008.15	<i>Developing potato cultivars adapted to southern Africa countries</i>	F Vilaró, INIA–Uruguay	Southern Africa countries	potato	• various traits	CIP, DARTS, EMBRAPA, IIAM, INIA–Chile, INTA–Argentina	January 2008	December 2009 NCE: November 2011
<b>Objective 3. Development and evaluation of novel breeding or molecular technologies to better serve modern plant breeding</b>									
65	G3008.06	<i>Targeting drought-avoidance root traits to enhance rice productivity under water-limited environments</i>	K McNally, IRRI	Global	Rice	• drought tolerance • water use efficiency	IRRI, ARC, BF, CSU, DRR, NagU, SUA, TNAU, UoAb, UoMi	November 2008	October 2011
66	G3008.07	<i>Basal root architecture and drought tolerance in common beans</i>	JP Lynch, PSU	Global	Beans	• drought tolerance • rooting	PSU, CIAT, IIAM, SABRN	November 2008	October 2011
67	G3008.08	<i>Breeder-friendly high-throughput phenotyping tools to select for wheat adaptive traits in drought environments</i>	Francis Ogonnaya, (ICARDA); Co-PI: M. Fernanda Dreccer, CSIRO	Global	Wheat	• drought	ICARDA, CSIRO, CIMMYT, INRA-CRRA Centre Aridoculture (Settat, Morocco), EIAR	November 2008	October 2011; NCE: June 2012
68	G4008.12	<i>Linking genetic diversity with phenotype for drought tolerance traits through molecular and physiological characterisation of a diverse reference collection of chickpea</i>	Lakshmanan Krishnamurthy, ICRISAT	Global	Chickpeas	• drought tolerance	ICRISAT, JIRCAS, UAS–Bangalore	January 2008	December 2009; NCE: September 2011
69	G4008.13:	<i>Improving drought tolerance phenotyping in cowpea</i>	Jeff Ehlers, UoC–Riverside	Mozambique, Senegal, Burkina Faso	Cowpeas	• drought tolerance	UoC–Riverside, IITA, INERA–BF, ISRA, TAMU	January 2008	December 2010
70	G4008.14	<i>Breeding for drought tolerance with known gene information</i>	Jiankang Wang, CIMMYT	various	various	• various	Agropolis–INRA, CAAS, CSIRO, ICRISAT, IRRI, UQ	January 2008	December 2009; NCE: June 2010
71	G4008.34	<i>Environmental assessment for the GCP phenotyping network</i>	Glenn Hyman, CIAT	various	various	• various	EMBRAPA, KUL, WA	January 2008	December 2009; NCE: June 2010
<b>Objective 4. Marker/allele validation in adapted germplasm under target environments</b>									
72	G4007.05	<i>Bridging genomics, genetic resources and breeding to improve wheat and barley production in Morocco</i>	Fouad Abbad Andaloussi, INRA–Morocco	Africa	wheat, barley	• various traits	CIMMYT, CU, ICARDA, UdB, UoMi	January 2007	December 2009; NCE: December 2010

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
73	G4007.06	<i>Integrating marker-assisted selection into the conventional breeding procedure for improvement of wheat (Triticum aestivum L) in the drought-prone areas of Northern China</i>	Ruilian Jing, CAAS	Asia	wheat	• drought tolerance	IDF–HAAS, LAAS, NU, NWSUAF, SAAS	August 2007	July 2010
74	G4008.10	<i>Assessment of the breeding value of superior haplotypes for Alt<sub>SB</sub>, a major Al tolerance gene in sorghum: linking upstream genomics to acid soil breeding in Niger and Mali (ALTFIELD)</i>	Robert Schaffert, EMBRAPA	Niger, Mali	Sorghum	• Aluminium tolerance	ICRISAT, INRAN	January 2008	December 2011

### Objective 5. Application of molecular markers in breeding programmes

75	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	Rice	• drought tolerance	IRRI, BAU, BF, CRRI, CRURRS, IGKV, JNKYV, NDUAT, TNAU, UAS–Bangalore, UoAI, YAAS	August 2007	March 2011
76	G4007.07	<i>Marker-assisted selection for sweet potato virus disease (SPVD) resistance in sweet potato germplasm and breeding populations</i>	Wolfgang Grüneberg, CIP	various regions	sweet potatoes	• SPVD resistance	NaCRRI	August 2007	July 2010; NCE: June 2011
77	G4008.11	<i>Dry bean improvement and marker-assisted breeding for diseases and abiotic stresses in Central America and the Caribbean</i>	Jorge A Acosta-Gallegos, INIFAP	Mexico	Beans	• drought tolerance • disease & pest resistance	INIFAP, CIAT, INTA–Nicaragua	January 2008	July 2011
78	G4008.17	<i>Application of marker-assisted selection for Striga resistance in cowpeas</i>	Jean-Baptiste Tignegre, INERA	Africa	cowpeas	• Striga resistance	IITA	January 2008	December 2009; NCE: December 2010
79	G4008.19	<i>Incorporation of an MSV-resistance gene in Mozambican maize varieties, mediated by use of MAS</i>	Mark Laing, UKZN	Africa	maize	• MSV resistance	IIAM	January 2008	December 2010

### Theme 3 – Crop information systems

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
<b>Objective 1: User Support – Ensuring that all GCP scientists have access to advice and tools to facilitate data management analysis and publication</b>									
	G8009.01.02	<i>Activity 1.1.2: Develop and deploy the Integrated Breeding Portal</i>	D González-de-León (up to December 2010), Fred Okono, GCP	Global	Global	• Global	AAFC, CIRAD, INRA and ICIS development team), BI, CAAS, CIAT, CIMMYT, Consultants, CSIRO, CU, EMBRAPA, ICRISAT, IRRI, IRRI–CRIL, KUL, other CGIAR germplasm centres, SGRP, UQ, WUR	July 2009	July 2014
	G8009.06.02	<i>Activity 3.2.2: Information Mgt</i>	A Portugal, GCP	Global	Global	• Global		July 2009	July 2014
	G8009.06.04	<i>Activity 3.2.4: Design &amp; analysis</i>	Marcos Malosetti, WUR	Global	Global	• Global		July 2009	July 2014

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
<b>Objective 2: Data curation and quality – Provide access to fully documented GCP data of certified quality for GCP partners and other interested researchers</b>									
80	G4008.31	<i>Upgrading the quality and utility of GCP phenotyping data through the development of a data input template to facilitate the storage of data in crop-specific databases</i>	Robert Koebner, CropGen International	global	global	• global	N/A	February 2008	January 2009; NCE: January 2010
81	G4008.32:	<i>Quality management procedures in GCP research laboratories promoted</i>	J Smith, FERA	Global	Global	• Global	CIMMYT, FERA	July 2008	July 2011
82	G4009.03/ G4010.06/ G4011.01	<i>Enhancement and implementation of the Crop Ontology for data integration and data interoperability</i>	Elizabeth Arnaud, Bioversity	Global	Global	• Global	CIMMYT, CIP, IRRI, CIAT, IATA, NCRI, Plant Ontology Consortium, NERC Environmental Bio-informatics Centre, University of Manchester	January 2010	December 2011
	G8009.06.03	<i>Activity 3.2.3: Data curation</i>	Arlet Portugal, GCP	Global	Global	• Global		July 2009	July 2014
<b>Objective 3: Methodology development – Bioinformatics research required to provide the methodology and informatics tools needed for GCP and MBP activities</b>									
83	G3008.09	<i>Breeding drought tolerance for rainfed lowland rice in the Mekong region</i>	Boonrat Jongdee, BRRD	Mekong Delta	Rice	• drought tolerance	BRRD, CARDI, NAFRI, UQ	November 2008	October 2011
84	G4008.21	<i>Largescale phylogenomic analyses tools developed for gene function prediction for GCP crops</i>	Mathieu Rouard, Bioversity	global	global	• global	Agropolis–CIRAD	January 2008	December 2009; NCE: February 2010
85	G4009.04/ G4010.05	<i>Dev't 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	August 2011
<b>G8009.03:**</b> A toolbox of analysis and decision-support applications to support molecular breeding developed (PIs: Graham McLaren/Diego González-de-León, GCP)									
	G8009.03.01	<i>Activity 2.2.1: Develop and deploy statistical and genetic analysis methodology for molecular breeding</i>	Activity Leader: Fred van Eeuwijk, WUR	various	various	• various	CIMMYT	July 2009	July 2014
	G8009.03.02	<i>Activity 2.2.2: Develop and deploy cross prediction and selection methodology for molecular breeding</i>	Activity Leader: Alain Charcosset, Agropolis–INRA	various	various	• various	N/A	July 2009	July 2014
	G8009.03.03	<i>Activity 2.2.3: Develop and deploy simulation tools for complex G–E systems</i>	Activity Leader: Mark Dieters, UQ	various	various	• various	CAAS, CIMMYT, CSIRO	July 2009	July 2014

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
<b>Objective 4: Informatics infrastructure – Provide facilities for data integration and sharing among GCP partners</b>									
	G8009.04.01	<i>Integrated GCP informatics platform created</i>	C Liang, IRRI wef July 2010; previous PI: Guy Davenport, CIMMYT (This project succeeds G4006.16, which ended June 2009)	Global	Global	• Global	CIMMYT, ICRISAT	July 2009	July 2014

**G8009.02:\*\* Objective 2.1:** Existing tools for data management and breeding logistics of molecular breeding available to IBP users (PI: Arllet Portugal)

	G8009.02.01	<i>Activity 2.1.1: Identify, deploy and support tools facilitating management of germplasm lists, pedigrees, intellectual property and other passport data</i>	Shawn Yates and Fran Clarke, AAFC	Global	Global	• Global		July 2009	June 2012
	G8009.02.02	<i>Activity 2.1.2: Identify, deploy and support tools for management of phenotypic characterisation and evaluation</i>	H Sanchez, CIMMYT	Global	Global	• Global		July 2009	June 2012
	G8009.02.03	<i>Activity 2.1.3: Identify, deploy and support tools for management of genotypic characterisation</i>	Trushar Shah, ICRISAT	Global	Global	• Global		July 2009	June 2012
	G8009.04.03	<i>Activity 2.3.3: Information network and configurable workflow system for molecular breeding developed and deployed</i>	G McLaren, GCP; Guy Davenport (up to August 2010), CIMMYT	Global	Global	• Global	CIMMYT, IRRI	July 2009	July 2014

#### Theme 4 – Capacity building

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

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

86	G4007.20	<i>Managing the Generation Challenge Programme in a Post-International Treaty World: A proposal for a technical training workshop and related materials</i>	Michael Halewood, Bioversity	global	global	• global	CAS–IP, EMBRAPA, IRRI	August 2007	July 2008; NCE: October 2010
87	G4008.50	<i>Delivery Plan remote learning modules</i>	Lawrence Pratt, CIMS–INCAE	global	global	• global	CU	August 2008	July 2009; NCE: August 2010
88	G4009.08	<i>Plant Breeding: concepts &amp; methods – a Learning Module</i>	Theresa Fulton, IGD–CU	Global	Global		IGD–CU, CropGen International	November 2009	June 2011

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

**Capacity-building à la carte Programme (awards in various years, ongoing in 2010)  
2010 awards**

89	G4010.04	<i>Enhancing capacity for use of advance genotyping for fine-mapping and pyramiding of major salt tolerant QTLs through MABC for the development of durable saline tolerant rice varieties</i>	Zeba I Seraj, UoD	Bangladesh	Rice	• salt tolerance	UoD, BRRI, IRRI	July 2010	June 2011
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#	Projects		Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
	Axapta No	Project Title						Start	End
<b>2009 awards (to TLI partners)</b>									
	G4009.07	<i>Capacity building à la carte 2009</i>	Carmen de Vicente, GCP (up to October 2010)			See sub-projects below		October 2009	October 2010
90	G4009.07.01	<i>Capacity-building à la carte 2009 – TLI students for analysis of drought tolerance in common bean</i>	Steve Beebe, CIAT	Ethiopia, Zimbabwe	Beans	• drought tolerance	CIAT, CBI–DAR4D, SABRN–Zambia/UoZ, SARI–Ethiopia	October 2009	October 2011
91	G4009.07.02	<i>Capacity-building à la carte 2009 – Capacity-building in modern cowpea breeding</i>	Jeffrey D Ehlers, UoC–Riverside	Senegal, Mozambique	Cowpeas	• drought tolerance	UC–Riverside, ISRA, UEM	October 2009	October 2011
92	G4009.07.03	<i>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)</i>	Rajeev K Varshney, ICRISAT	Kenya, Ethiopia	Chickpeas	• drought tolerance	EIAR, EgU, ICRISAT	October 2009	October 2011
93	G4009.07.04	<i>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</i>	Vincent Vadez, ICRISAT	sub-Saharan Africa	ground-nuts	• drought tolerance	ARI–Naliendele, CRS, ISRA, INRAN	December 2009–December 2010; NCE: December 2011	
<b>2008 awards</b>									
	G4008.39	<i>Capacity-building à la carte 2008</i>	Carmen de Vicente, GCP (up to October 2010)			See sub-projects below		April 2008	April 2010
94	G4008.39.01	<i>Enhancing MAS capacity for salt-stress rice breeding in Bangladesh</i>	MA Salam, BRRI	Asia	rice	• salt tolerance	IRRI, UoD	April 2008	March 2009; NCE: March 2010
95	G4008.39.02	<i>Improving capacity for phenotyping for abiotic and biotic stress in Burkina Faso</i>	Issa Drabo, INERA	Africa	cowpeas	• various traits	IITA, UC–R	April 2008–	April 2010
96	G4008.39.03	<i>Improving capacity for phenotyping for abiotic and biotic stress in Senegal</i>	Ndiaga Cissé, ISRA	Africa	cowpeas	• various traits	UC–R	April 2008	April 2010; NCE: December 2010
97	G4008.43	<i>Improve cowpea productivity for marginal environments in Mozambique</i>	Rogério Chiulele, UEM	Africa	cowpeas	• drought tolerance	PSU, UC–R	July 2008	June 2010
<b>2007 awards</b>									
98	G4007.13.04	<i>Characterisation of maize germplasm found in Ghana, using the bulking technique</i>	Allen Oppong, CRI–CSIR	Africa	cassava	• various traits		July 2007	July 2009; NCE: July 2010
99	G4007.13.05	<i>An integrated proteomics and genomics approach to discover salt tolerance genes</i>	Ghasem Hosseini Salekdeh, ABRII	Asia	rice	• salt tolerance	IRRI, IPK	July 2007	July 2009; NCE: August 2010

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
100	G4007.13.06	<i>Enhancing capacity of ICABIOGRAD in phenotyping and molecular analysis to develop elite rice lines suitable to Indonesian uplands</i>	Masdiar Bustamam, ICABIOGRAD	Asia	rice	• blast resistance	IRRI	July 2007	July 2009; NCE: March 2010
<b>Fellowships and travel grants</b>									
<b>Fellowships</b>									
101	G4008.37	<i>PhD in plant breeding training at the West Africa Centre for Crop Improvement</i>	Eric Y Danquah, WACCI-UoG	Africa	Global	• Global	AfricaRice–Benin, AGRA/PASS, CRI–CSIR, CU, EAST College, IER, INERA–BF, SARI–Ghana, WACCI	March 2008	February 2014
102	G4009.02.01	<i>Fellowship – Honoré Kam: Study of Burkina Faso rice landraces diversity and breeding for resistance to Rice Yellow Mottle Virus (RYMV)</i>	Kam Honoré, INERA-BF	Burkina Faso	Rice	disease resistance	CIRAD, INERA-BF, IRD, UKZN	March 2009	March 2011
103	G4010.01.01	<i>Fellowship – Armin Bhuiya: Identification of novel QTLs for salinity tolerance and pyramiding with submergence tolerance to develop improved rice varieties for Bangladesh</i>	Armin Bhuiya, BRRI	Bangladesh	Rice	• salt tolerance • submergence tolerance	BAU, BRRI, IRRI	March 2010	March 2012
<b>Travel grants</b>									
104	G4009.02.04	<i>Travel Grant – International Symposium on Genomics of Plant Genetic Resources</i>	Carmen de Vicente, GCP; Roberto Tuberosa, UNIBO	various	various	• various	CBS, CSIR, EgU, ICAR, ICRISAT, INRA, NRCRI, UTM	February 2010	May 2010
105	G4010.01.02	<i>Travel Grant – ICPBM3 International Training Workshop on Plant Molecular Breeding</i>	Carmen de Vicente, GCP; Zhikang Li, CAAS–MST	various	various	• various	AGI, BRAC, CBI, CRI–CSIR, FCRI, ICERI, IIAM, INERA, ISRA, KAgRI, RRDJ	August 2010	September 2010
<b>Faculty support</b>									
106	G4006.36	<i>Capacity-building and research project: Academic position in molecular breeding supported</i>	Mark Laing, ACCI–UKZN	Africa	Global	• Global	ACCI–UKZN, AGRA/PASS	January 2007	December 2011
<b>Objective 3: Constructing systems for ensuring product delivery</b>									
107	Capacity-building mechanisms and product pipelines established for tropical legume improvement in Africa <i>Details in the TLI section of this publication.</i> (Lead institutes: ARI–Naliendele, CRS, CBI–DR&SS, EIAR, INERA, IRAD, ISRA, LZARDI, SARI–Ethiopia, EgU)						ICRISAT, UC–R, CIAT		
	<i>G6010.01: Improve groundnut productivity for marginal environments in sub-Saharan Africa (PI: Vincent Vadez, ICRISAT)</i>								
	<i>G6010.02: Improve cowpea productivity for marginal environments in sub-Saharan Africa (PI: Jeff Ehlers, UC–R)</i>								
	<i>G6010.03: Improve common bean productivity for marginal environments in sub-Saharan Africa (PI: Steve Beebe, wef October 2010/M Blair, CIAT)</i>								
	<i>G6010.04: Improve chickpea productivity for marginal environments in sub-Saharan Africa and South Asia (PI: Rajeev K Varshney, ICRISAT)</i>								
	<i>G6010.05: Cross-cutting crop activities (drought phenotyping, data management and capacity building) (PI: Carmen de Vicente, GCP [up to October 2010])</i>								

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
108	G4008.26/ G7010.01.05	<i>A cassava breeding community of practice in Africa for accelerated production and dissemination of farmer-preferred cassava varieties resistant to pests and diseases (overlaps with cassava RI)</i>	Emmanuel Okogbenin, NRCRI	Ghana, Nigeria, Tanzania, Uganda	Cassava	• drought tolerance • pest resistance • disease resistance	CRI–CSIR, Ghana, NaCRRI, Uganda, NRCRI, NRTP–ARI <i>Collaborators</i> CIAT, IITA, CU	January 2008	December 2014
109	G4009.09	<i>The Community of Practice strengthening rice breeding programme using genotyping building strategy and improving phenotyping capacity for biotic and abiotic stresses in the Mekong region</i>	Jonaliza Lanceras-Siangliw, RGDU	Mekong region	Rice	• drought tolerance • soil acidity • disease resistance	BIOTEC, CARDI, DAR, NAFRI	November 2009	October 2012

#### Objective 4: Developing and implementing support services

110	G4008.35	<i>Toolbox of available molecular markers useful for marker-assisted selection in GCP crops (Extension: G4010.03)</i>	Veerle Van Damme, Consultant	various	various	• various	GCP	March 2008	March 2010
111	G4010.03	<i>GCP Molecular Marker Toolkit (Extends G4008.35)</i>	Veerle Van Damme, Consultant	various	various	• various	GCP	July 2010	October 2010; NCE: December 2010
112	G8009.06.06	<i>Activity 3.2.6: Genotyping Support Service (This project succeeds G4007.21, which ended in 2008, and G4009.01, which ended in 2009)</i>	Chunlin He, wef October 2010/ Humberto Gómez-Paniagua, GCP	Global	Global	• Global	<i>Beneficiaries:</i> BCKV, CIBE–ESPOL, CRISL, CSIR–CRI, EMBRAPA, INIA–Chile, INIA–Uruguay, INIFAP, IPB–UPLB, IPGR, IARI, JUCAVM, KARI, MahU, NRCRI, PGRRI, PhilRice, PROINPA, SARI–Ethiopia, TNAU, UAS, UEM, UKM, UNALM <i>Service providers:</i> BecA, CIAT, DArT P/L, DLM, ICRISAT, KBi	July 2009	July 2014
113	G4007.22.04	<i>Development and implementation of a GCP workflow and repository system</i>	Carmen de Vicente, GCP	global	global	• global	Cropster GmbH (service provider)	June 2009	July 2010

#### Objective 5: Ex ante impact analysis and impact assessment

114	G4006.13	<i>Targeting and impact analysis of GCP technologies</i>	Glenn Hyman, CIAT	global	global	• global	CIMMYT, IFPRI, IRRI	November 2006	October 2007; NCE: March 2010
115	G4008.24	<i>A strategic assessment of the capacity to develop and adopt GCP technologies</i>	Stanley Wood, IFPRI	various	various	• various	CIAT, VPI	January 2008	December 2009; NCE: April 2010

**Theme 5 – Product delivery**

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
116	G4007.01	Genotyping validation of the GCP reference sets	Jean-Francois Rami, Agropolis – CIRAD	Global	Various	• Various	Agropolis – CIRAD, BI, CIAT, CIMMYT, CIP, ICARDA, ICRISAT, IITA, IRRI, UoC–Riverside	January 2007	May 2011
117	G4010.02	Potential Benefits of Marker-Assisted Selection Technologies on Wheat, Sorghum, Cassava, and Rice, and of the Integrated Breeding Platform	George W. Norton, VPI	Global	Sorghum, Cassava, Rice	• Various	VPI, IFPRI	May 2010	December 2011

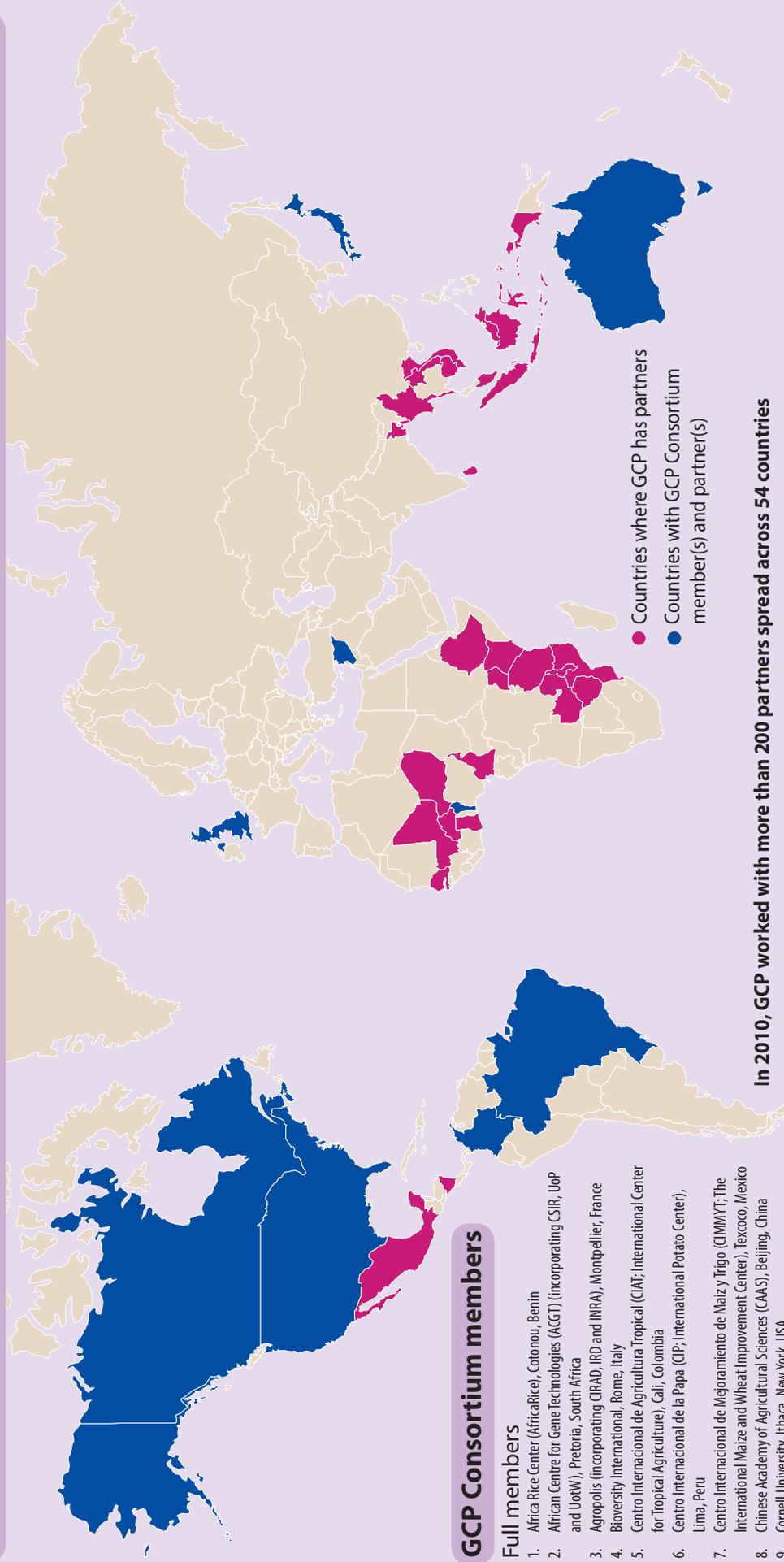
**III. Service Component – Integrated Breeding Platform**

#	Axapta No	Projects Project Title	Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
								Start	End
<b>Component 1: Integrated Breeding Portal &amp; HelpDesk</b>									
118	<b>G8009.01 Objective 1.1: Establish and manage the Molecular Breeding Platform</b>								
	G8009.01.01	Activity 1.1.1: Establishment of the Integrated Breeding Platform	Graham McLaren, GCP	Global	Global	• Global	AAFC, CIRAD, INRA and ICIS development team), BI, CAAS, CIAT, CIMMYT, Consultants, CSIRO, CU, EMBRAPA, ICRISAT, IRRI, IRRI-CRIL, KUL, other CGIAR germplasm centres, SGRP, UQ, WUR	July 2009	July 2010
	G8009.01.02	Activity 1.1.2: Develop and deploy the Integrated Breeding Portal	D González-de-León (up to December 2010), Fred Okono, GCP	Global	Global	• Global		July 2009	July 2014
	G8009.01.03	Activity 1.1.3: Establish Integrated Breeding Platform helpdesk and coordinate training and communication activities	Ndeye Ndack Diop, GCP	Global	Global	• Global		July 2009	July 2014
	G8009.01.04	Activity 1.1.4: Establish and support crop molecular breeding communities of practice	Ndeye Ndack Diop, GCP	Global	Global	• Global		July 2009	July 2014
<b>IBP Component 2: Information system</b>									
119	<b>G8009.02 Objective 2.1: Make existing tools for data management and breeding logistics available to molecular breeding projects through the MBP</b>								
	G8009.02.01	Activity 2.1.1: Identify, deploy and support tools facilitating management of germplasm lists, pedigrees, intellectual property and other passport data	Shawn Yates and Fran Clarke, AAFC	Global	Global	• Global		July 2009	June 2012
	G8009.02.02	Activity 2.1.2: Identify, deploy and support tools for management of phenotypic characterisation and evaluation	H Sanchez, CIMMYT	Global	Global	• Global		July 2009	June 2012
	G8009.02.03	Activity 2.1.3: Identify, deploy and support tools for management of genotypic characterisation	Trushar Shah, ICRISAT	Global	Global	• Global		July 2009	June 2012

#	Projects		Principal Investigator	Target Countries	Target Crops	Target Traits	Partners	Project Dates	
	Axapta No	Project Title						Start	End
120	<b>G8009.03 Objective 2.2: Develop a suite of analysis, prediction and simulation tools for MAB</b>								
	G8009.03.01	Activity 2.2.1: Develop and deploy statistical and genetic analysis methodology for molecular breeding	Activity Leader: Fred van Eeuwijk, WUR	various	various	• various	CIMMYT	July 2009	July 2014
	G8009.03.02	Activity 2.2.2: Develop and deploy cross prediction and selection methodology for molecular breeding	Activity Leader: Alain Charcosset, Agropolis–INRA	various	various	• various	N/A	July 2009	July 2014
	*G8009.03.03	Activity 2.2.3: Develop and deploy simulation tools for complex G–E systems	Activity Leader: Mark Dieters, UQ	various	various	• various	CAAS, CSIRO	July 2009	July 2014
121	<b>G8009.04 Objective 2.3: Develop an information network, decision-support tools and a workflow management system for molecular breeding</b>								
	G8009.04.01	Activity 2.3.1: Establish middleware infrastructure for networking databases and applications	C Liang, IRRI wef July 2010; Guy Davenport, CIMMYT (This project succeeds G4006.16, which ended December 2009)	various	various	• various	CIMMYT, ICRISAT	July 2009	July 2014
	G8009.04.02	Activity 2.3.2: Integration and development of visualisation and decision-support applications	H Sanchez, G Davenport (up to August 2010), CIMMYT	various	various	• various	ICRISAT	July 2009	July 2014
	G8009.04.03	Activity 2.3.3: Implement a configurable workflow system (CWS) for molecular breeding	G McLaren, GCP, Guy Davenport (up to August 2010), CIMMYT	various	various	• various	AAFC, ICRISAT	July 2009	July 2014
<b>IBP Component 3: Services</b>									
122	<b>G8009.05 Objective 3.1: Provide access to critical molecular breeding services</b>								
	G8009.05.01	Activity 3.1.1: Genetic Resources Support Service	Jean Christophe Glaszmann, Agropolis–CIRAD	Global	Global	• Global		July 2009	July 2014
	G8009.05.02	Activity 3.1.2: Marker Services	Chunlin He, wef October 2010 Humberto Gómez Paniagua, GCP	Global	Global	• Global		July 2009	July 2014
	G8009.05.03	Activity 3.1.3 Trait and metabolite services	Leader: Xavier Delannay, GCP	Global	Global	• Global		July 2009	July 2014
123	<b>G8009.06 Objective 3.2: Provide assistance with a range of molecular breeding support</b>								
	G8009.06.01	Activity 3.2.1: Breeding Plan Development	Xavier Delannay, GCP	Global	Global	• Global		July 2009	July 2014
	G8009.06.02	Activity 3.2.2: Information Management	A Portugal, GCP	Global	Global	• Global		July 2009	July 2014
	G8009.06.03	Activity 3.2.3: Data curation	A Portugal, GCP	Global	Global	Global		July 2009	July 2014
	G8009.06.04	Activity 3.2.4: Design & analysis	Marcos Malosetti, WUR	Global	Global	• Global		July 2009	July 2014
	G8009.06.05	Activity 3.2.5: Phenotyping sites & screening protocols)	Xavier Delannay, GCP	Global	Global	• Global		July 2009	July 2014
	G8009.06.06	Activity 3.2.6: Genotyping Support Service	Chunlin He, GCP	Global	Global	• Global		July 2009	July 2014
	G8009.06.07	Activity 3.2.7: IP & Policy Helpdesk	Chunlin He, GCP	Global				July 2009	July 2014



# Where in the world is GCP? The GCP network in 2010



## GCP Consortium members

### Full members

1. Africa Rice Center (AfricaRice), Cotonou, Benin
2. African Centre for Gene Technologies (ACGT) (incorporating CSIR, IOP and UoW), Pretoria, South Africa
3. Agropolis (incorporating CIRAD, IRD and INRA), Montpellier, France
4. Bioversity International, Rome, Italy
5. Centro Internacional de Agricultura Tropical (CIAT; International Center for Tropical Agriculture), Cali, Colombia
6. Centro Internacional de la Papa (CIP; International Potato Center), Lima, Peru

7. Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT; The International Maize and Wheat Improvement Center), Texcoco, Mexico
8. Chinese Academy of Agricultural Sciences (CAAS), Beijing, China
9. Cornell University, Ithaca, New York, USA
10. Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA; Brazilian Agricultural Research Corporation), Brasília, Brazil
11. Indian Council of Agricultural Research (ICAR), New Delhi, India
12. International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo, Syria

13. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India
14. International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria
15. International Rice Research Institute (IRRI), Los Baños, The Philippines
16. John Innes Centre (JIC), Norwich, UK
17. National Institute of Agrobiological Sciences (NIAS), Tsukuba, Japan
18. Wageningen University and Research Centre (WUR), Wageningen, The Netherlands

### Provisional members

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

## In 2010, GCP worked with more than 200 partners spread across 54 countries

### Developing-country partners

- Central and West Asia and North Africa**
1. Morocco
  2. Tunisia
- East Europe**
3. Bulgaria
  4. Hungary
- Latin America and the Caribbean**
5. Argentina
  6. Bolivia
  7. Chile
  8. Colombia
  9. Costa Rica
  10. Ecuador
  11. Nicaragua
  12. Peru
  13. Uruguay

- South and Southeast Asia**
14. Bangladesh
  15. Cambodia
  16. Indonesia
  17. Laos
  18. Myanmar
  19. Sri Lanka
  20. Vietnam

- Sub-Saharan Africa**
21. Burkina Faso
  22. Cameroon
  23. Ethiopia
  24. Ghana
  25. Kenya
  26. Malawi
  27. Mali
  28. Mozambique
  29. Niger
  30. Nigeria
  31. Senegal
  32. Tanzania
  33. Uganda
  34. Zambia
  35. Zimbabwe

### Newly industrialised countries

- Latin America and the Caribbean**
36. Brazil
  37. Mexico
- South and Southeast Asia**
38. China
  39. India
  40. Malaysia
  41. Thailand
  42. The Philippines
- Sub-Saharan Africa**
43. South Africa

### Industrialised-country partners

- Asia**
44. Japan
- Europe**
45. Belgium
  46. France
  47. Germany
  48. Italy
  49. Switzerland
  50. The Netherlands
  51. United Kingdom
- North America**
52. Canada
  53. USA
- Oceania**
54. Australia

## Integrated Breeding Platform (IBP) launch meeting participants, February 2010, Hyderabad, India

The Integrated Breeding Platform is envisioned as a sustainable, web-based one-stop shop for information, analytical tools and related services to design and carry out integrated breeding projects. IBP will boost crop productivity and resilience for smallholders in drought-prone environments by exploiting the economies of scale afforded by collective access to cutting-edge breeding technologies hitherto unavailable to developing-country breeders.



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