

Project Name: Improving tropical legume productivity for marginal environments
in sub-Saharan Africa and South Asia: Phase II

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International Maize and Wheat Improvement Center)

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Charitable Purpose:

To contribute to the development of improved legume varieties in sub-Saharan Africa and South Asia by advancing molecular breeding for traits of importance in both regions.

Project Description:

This proposal focuses on improving the productivity of four tropical legumes of high importance to food security and poverty reduction efforts in sub-Saharan Africa (SSA). Its overall objective is to improve the productivity of groundnut, cowpea, common bean and chickpea for SSA through the application of modern breeding approaches using the genetic resources and genomic tools developed in the first phase of the project, in close partnership with SSA countries and regional research institutions. This project will apply modern breeding for the four legume crops, will conduct high-quality phenotyping and will improve human resources and local infrastructure. The long-term objective of this project (7–12 years) is to double grain legume productivity in farmers' fields. Doing so will generate an additional income for farmers of \$370/h in groundnuts, \$160/h in cowpea, \$220/h in bean and \$250/h in chickpea, per crop cycle in the target countries of the project, where average agricultural population per capita income today is around \$120 per year.

Improving tropical legume productivity for marginal environments in sub-Saharan Africa: Phase II

A proposal submitted to the Bill & Melinda Gates Foundation by the CGIAR Generation Challenge Programme

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Acronyms and Abbreviations

AA	Andean × Andean
AB	Advanced Backcross
ABCLs	Advanced Backcross Lines
AB-QTL	Advanced backcross QTL
ACCI	African Centre for Crop Improvement, South Africa
Ad x Ai	<i>Arachis duranensis</i> and <i>Arachis lpaensis</i>
AGRA	Alliance for a Green Revolution in Africa
Agropolis–CIRAD	Agropolis–Centre de coopération internationale en recherche agronomique pour le développement, France
AM	Andean × Mesoamerican
APSIM	Agricultural Production Systems Simulator
ARI(s)	advanced research institute(s)
ARI–Naliendele	Agricultural Research Institute–Naliendele Research Station, Tanzania
BAC	Bacteria Artificial Chromosome
BC	Backcross
BC ₂ , BC ₃ , etc.	Backcross 2 nd generation, Backcross 3 rd generation, etc.
BCMNV	Bean common mosaic necrosis viruses
BCMV	bean common mosaic virus
BES-SSRs	Bac-end sequences microsatellites
BSM	Bean stem maggot
CAbMV	Cowpea aphid borne mosaic
CB	conventional breeding
CBB	Common bacterial blight
CBI	Crop Breeding Institute
cDNA	complementary DNA
CERAAS	Centre d'étude régional pour l'amélioration de l'adaptation à la sécheresse, Senegal
CG	CGIAR (see below)
CGIAR	Consultative Group on International Agricultural Research
CIAT	Centro Internacional de Agricultura Tropical (International Center for Tropical Agriculture)
CID	Carbon isotope discrimination
CIMMYT	Centro Internacional de Mejoramiento de Maíz y Trigo (the International Maize and Wheat Improvement Center)
CIP	Centro Internacional de la Papa (International Potato Centre)
cM	centimorgan
CRS	Chitedze Research Station, Malawi
CRSP	USAID-funded Collaborative Research Support Program
CSSL	chromosome segment substitution line
CT	Carbohydrate translocation
CTD	Canopy temperature depression
DAB	Drought Andean Bean
DAR4D	Department of Research and Specialist Services, Zimbabwe

DARS	Department of Agriculture Research Services, Malawi
DArT	diversity arrays technology
DFID	UK's Department for International Development
DNA	Deoxyribonucleic acid
DR & SS	Department of Research & Specialist Services, Zimbabwe
DR	Deep rooting
DREB	Drought responsive element binding
EARO	Ethiopian Agricultural Research Organization
ECABREN	Eastern and Central Africa Bean Research Network
EIAR	Ethiopian Institute of Agricultural Research
ELS	Early leaf spot
EMBRAPA	Empresa Brasileira de Pesquisa Agropecuária (Brazilian Agricultural Research Corporation)
EMU	Eduardo Mondlane University (Mozambique)
ESA	Eastern and Southern Africa
F1...etc.	first filial generation, etc.
FAO	Food and Agriculture Organisation of the United Nations
FMPV	Farmer- and market-preferred variety
FT	Flower thrips
GCP	Generation Challenge Programme of the CGIAR
GRV	Groundnut rosette virus
GWMABC	Genome-wide marker-assisted backcrossing
GWS	Genome Wide Selection
GxE	genotype by environment interaction
HI	Harvest index
IARCs	International Agricultural Research Centers
ICAR	Indian Council of Agricultural Research
ICGGC	International Chickpea Genetics & Genomics Consortium
ICIS	International Crop Information System
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
IER	Institut d'économie rurale, Mali
IIPR	Indian Institute of Pulses Research, India
IITA	International Institute of Tropical Agriculture, Nigeria
ILRI	International Livestock Research Institute
INERA–Burkina Faso	Institut de l'environnement et de recherches agricoles, Burkina Faso
INRAN	Institut national de la recherche agronomique du Niger
IPHIS	International <i>Phaseolus</i> Information System
IRAD	Institut de la recherche agronomique pour le développement, Cameroon
ISRA	Institut sénégalais de recherches agricoles, Senegal
KARI	Kenya Agricultural Research Institute
LCD	Liquid Crystal Display Projector
LD	Linkage disequilibrium
LLS	Late leaf spot
LZARDI	Lake Zone Agricultural Research and Development Institute, Tanzania
M	<i>Macrophomina</i>
MAB	marker-assisted breeding

MABC	marker-assisted backcrossing
MAGIC	multiparent advanced generation inter-cross
MARS	marker-assisted recurrent selection
MAS	marker-assisted selection
MB	molecular breeding
Mbp	million base pairs
MBP	Molecular Breeding Platform of the Generation Challenge Programme
NARS	national agricultural research system(s)
NCGR	National Center for Genome Resources, USA
NCSU	North Carolina State University, USA
NDSU	North Dakota State University
NGS	Next generation sequencing
NSF	National Science Foundation, USA
OBO	Open Biomedical Ontologies
OPA	oligo-nucleotide pooled assay
PABRA	Pan-African Bean Research Alliance
PASS	Program for African Seed Systems
PCR	Polymerase chain reaction
PDL	Product Delivery Leader
PHI	Pod harvest index
PIC	Polymorphism information content
PIs	Principal Investigators
PPI	Pod partitioning index
PVS	plant variety selection
QEI	QTL by environment interaction
qPCR	quantative PCR
QTL	quantitative trait locus/loci
RDPF	Relative duration of pod filling
RFLP	Restriction fragment length polymorphism
RGA	resistance gene analogs
RIKEN	Rikagaku Kenkyūsho (Institute of Physical and Chemical Research), Japan
RIL	recombinant inbred lines
RLD	root length density
S	<i>Striga</i>
SA	South Asia
SABRN	Southern Africa Bean Research Network
SADC	Southern African Development Community
SARI	South Agricultural Research Institute, Ethiopia
SBR	Stem biomass reduction
SCMR	chlorophyll meter reading
SDC	Swiss Agency for Development and Cooperation
SLA	specific leaf area
SNP	single nucleotide polymorphism
SP	Subprogramme
SP1, SP2 etc	Subprogramme 1, Subprogramme 2 etc.

SPAD	soil plant analytical development
SSA	sub-Saharan Africa
SSD	single seed descent
SSR	simple sequence repeat
TE	Transpiration efficiency
TLI	Tropical Legumes I Project
TLII	Tropical Legumes II Project
TNC	Total non-structural carbohydrates
TOGs	Tentative Ortholog Groups
UC–Davis	University of California–Davis, USA
UCB	Universidade Católica de Brasília, Brazil
UC–Riverside	University of California–Riverside, USA
UEM	Universidade Eduardo Mondlane, Mozambique
UoG	University of Georgia, USA
UoN	University of Nairobi, Kenya
USA	United States of America
USAID	United States Agency for International Development
USDA	United States Department of Agriculture
UTR	Untranslated Region
VPD	vapour pressure deficitWACCI West Africa Centre for Crop Improvement, University of Ghana
WCA	Western and Southern Africa

Grant Proposal – Narrative

I. Background and Rationale

General – legumes

For many of the world's poorest people, legumes are the major—and sometimes only—sources of protein and fat they consume. Grain and forage legumes account for 27% of the world's primary crop production, with grain legumes alone contributing 33% of the dietary protein nitrogen needs of humans (Vance et al. 2000). Grain legumes are also a rich source of essential vitamins, minerals, and important amino acids like lysine (Grusak 2002), and so legumes are key components in the diets of resource-poor people in the developing world, especially those who cannot afford to supplement their diets with meat. In sub-Saharan Africa (SSA), where hunger and malnutrition threaten the lives of an estimated 11 million people, consumption of legumes is higher than anywhere else in the world, except for North and South America (see Annex 1). India is the world's largest producer of chickpea—two-thirds of the global chickpea production in 2005-2007—and its largest world consumer as well. As a result, India's dependence on imports to meet its domestic demand continues to increase. Legumes also generally attract higher market prices than other staple crops, making them an important source of income for farmers. Legumes can be grown by farming in impoverished soils (legumes fix atmospheric nitrogen and enrich depleted soils), and in SSA and SA are commonly used in mixed cropping systems. The seed industries in most countries have not developed their own legume seed production programmes and in spite of their importance, the breeding of food legumes has received less attention than cereals. As a result, especially SSA countries lack seeds of varieties for different seasons and different cropping systems (<http://www.fao.org/ag/AGP/agps/abidjan/Paper5-1.htm>)

Groundnut, cowpea, common bean, chickpea

Despite the many benefits in health, income creation, and soil rehabilitation that legumes provide, in SSA, legume productivity is lower than anywhere else in the world (see Annex 2) reaching only 10-50% of yields obtained under optimal conditions. This proposal focuses on improving the productivity of four legume crops of high importance to food security and poverty reduction efforts in SSA and South Asia (SA): groundnut, cowpea, bean, and chickpea. The rationale for the selection of these crops was already discussed in the proposal for the first phase of this project.

Overall this proposal for TLI Phase II builds on the effort of the first three-year funding, i.e. it focuses on improving crop productivity by providing solutions to overcome the biotic and abiotic stresses that typically afflict these legumes in SSA. While legumes hold great potential to decrease yield gaps in SSA, this potential remains unrealised because legumes are however subject to the most severe biotic constraints (Waddington et al., 2010). The target biotic stresses depend on the specific crops and locations, with drought as the major focus for abiotic stress across the four legumes. The approach of addressing multiple constraints is very important when breeding for harsh environments, where resource-poor farmers do not have access to irrigation or pesticides, and where the accentuated biotic stresses under water-limited conditions severely hamper plant performance.

Groundnut: While China and India are the leading producers worldwide, millions of small-holder farmers in SSA grow groundnut as a food and cash crop, which accounts for 9m ha of cultivated farmland (2007 datum). While this area is 40% of the world total, this percentage represents only 25% of the total production due to low yield (950 kg/ha, versus 1.8 t/ha in Asia). The main constraints hampering higher yields and quality in Africa are intermittent drought due to erratic rainfall patterns, and terminal drought during maturation (FAOSTAT). Yield losses from drought run to millions of dollars each year (Sharma and

Lavanya 2002). A drought-related quality issue is pre-harvest contamination of seeds with aflatoxin, a carcinogenic mycotoxin produced primarily by the fungus *Aspergillus flavus*, which consequently shuts out SSA groundnuts from export markets which would be more lucrative. In addition, foliar disease rust, rosette, early leaf spot (ELS) and late leaf spot (LLS) cause devastating yield losses (50-60% yield losses by ELS-LLS, Waliyar et al., 1991; 2000; Grichar et al., 1998). To further compound the problems above, in the absence of much-needed improved varieties, outdated poorer varieties and landraces are usually cultivated.

Cowpea is the most important grain legume crop in SSA, grown by more farmers on more farmlands (>12 million ha) than any other grain legume (Timko et al., 2007). It is mostly grown in the hot drought-prone savannas and very arid Sahelian agro-ecologies, where it is often intercropped with pearl millet and sorghum (Hall, 2004). Cowpea is a key component in sustaining livelihoods of not only millions of farmers (the majority of whom are women), but also of hundreds of thousands of traders and local food processors (Langyintuo et al., 2003). Cowpea provides not only protein-rich grain that complements staple cereal and starchy tuber crops, but also provides fodder for livestock, soil improvement benefits through nitrogen fixation, and households benefits from both cash and income diversity. Cowpea 'on-farm' grain yields in SSA reach only 10–30% of their biological yield potential, due primarily to insect and disease attacks and drought (Ehlers and Hall, 1997). Improved varieties are urgently needed that will help to reduce this yield gap, taking into account existing production systems and that inputs will remain beyond the reach of resource-poor farmers (Hall et al., 1997).

Common bean is the most important food legume for direct human consumption with 23m ha grown worldwide (Broughton et al. 2003). Over 200 million people in SSA depend on the crop as a primary staple, with beans contributing to diet and incomes in over 24 countries in this region alone (Wortmann et al. 1998). Consumption is as high as 66 kg/year/person, and in many areas, common bean is the second most important source of calories after maize, as well being a major source of proteins and minerals in the diet. Typical bean yields, however, represent only 20 to 30% of the genetic potential of improved varieties due to major production risks such as insect pests, diseases and drought, which – due to climate change – is increasing in severity and frequency in the region (Funk et al. 2008). Drought affects production of common beans in most of Eastern Africa, but is especially severe in the mid-altitudes of Ethiopia, Kenya, Tanzania, Malawi and Zimbabwe, as well as in Southern Africa as a whole.

Chickpea is the world's second-largest cultivated food legume and the developing countries account for over 95% of its production and consumption (Gaur et al. 2008). It is an important grain legume in South Asia and SSA, especially in Eastern and Southern Africa. Chickpea is a dry-season legume that grows well on the residual moisture of the post-rainy season, providing a unique opportunity of enhancing legume production in Africa as it does not compete for area with other major legumes. Indeed, this feature gives farmers a second crop (where only one crop would traditionally be grown), hence increased income and better nutrition. It is an excellent source of high-quality protein, with a wide range of essential amino acids (Wood and Grusak 2007). 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. In Eastern Africa the area planted to chickpea has doubled during the past 30 years (from 210,000 ha during 1979-1981 to 420,000 ha during 2006-2008), a trend expected to continue considering the increasing demand of chickpea in domestic and international markets. There is also the possibility that the soaring fertilizer price may further push farmers, particularly resource poor farmers, to switch from cereal production to those crops that do not demand fertilizer such as chickpea. Since major consumers such as India outstrip domestic supply, there are opportunities for SSA countries to exploit a ready-made and guaranteed market. Increase in production and attractive prices in the international market have recently led to substantial increase in the export of chickpea. During 2002 to 2007, the export of chickpea by

Eastern Africa has ranged between 17 to 42%, with an average of 30%. This has provided the farmers extra income to buy other essentials and send their kids to school. Projections using the IMPACT-WATER model indicate that production will be 562000t in 2020, and that African net trade will be negative (-103 000 t) owing to increased local demand at 662 000 t, which strongly supports research for chickpea improvement in Africa. Similarly, improvement of chickpea in SA will save the revenues spent (representing on average ca. 74 million \$/year —1998 to 2007—equivalent to 186,000 tons/year) on chickpea import as predicted by the trend in chickpea consumption of the ever-growing population in India. Drought is globally the number one constraint for chickpea production, causing yield losses of around 3.7 million tons (out of a total production of 8.6 million tons) (Ryan 1997). In SSA 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 (Gaur et al. 2008).

The molecular breeding approach

This proposal promotes the application of modern breeding, which combines conventional field breeding with plant biotechnologies, to improve the productivity of four legume crops in SSA. Molecular breeding (MB) is the generic term used to describe several modern breeding strategies including: marker-assisted selection (MAS) – the selection of specific alleles for traits conditioned by a few loci; marker-assisted backcrossing (MABC) – the transfer of a limited number of loci from one genetic background to another; and, more recently, marker-assisted recurrent selection (MARS) – the identification and selection of several genomic regions involved in the expression of complex traits within a single population. The effectiveness of MB for simple traits such as some disease resistances as well as for complex traits such as tolerance to low temperature or drought has been reported in cereals (Ribaut and Ragot 2006), and in commercial crops like soybeans, where many disease resistance traits – including soybean cyst nematode which is typically hard to score phenotypically – are routinely screened with markers (Eathington et al, 2007). MB combined with conventional phenotypic selection is now widely practised by the private sector, but less so by the public sector (Dwivedi et al. 2007). The progress observed in both the private and public sectors suggests that efficient plant breeding through combining phenotypic selection (which considers genetic effects as a whole) with molecular breeding (which allows selection of favourable alleles at target loci) offers great promise for developing country agriculture. Until recently, MB demanded heavy investment in laboratory infrastructure, a limitation that can now be overcome through outsourcing to access the latest technologies. In addition, advances in Single nucleotide polymorphism (SNP) technology are a quantum leap in decreasing marker costs, making this approach extremely cost-effective.

Links with TLI Phase I and TLI

TLI Phase I aimed to both 1) build on the advances made through ongoing initiatives in developing genomic resources in some key legumes and 2) conduct genetic studies to identify markers for target traits directly relevant for SSA, with an emphasis on drought tolerance. It served as a catalyst in legume improvement by bringing together the knowledge about legume diversity recently generated through the Generation Challenge Programme (GCP), by leveraging the existing effort in genetic studies of stress tolerance, and by supporting a large effort for marker development to provide new tools for plant breeding. The endeavour from Phase I has resulted in significant increases in the numbers of genomic tools for the four legumes, markers available for specific diseases and thorough knowledge about drought tolerance traits (Annex 3). Phase I efforts have resulted in sufficient molecular markers for meaningful genetic studies in cowpea, bean and chickpea, including molecular breeding. Furthermore, relatedness between the legume species implies genome similarities, despite contrasting patterns of ecological adaptation.

TLI Phase II will emphasise the 'application' of outputs obtained during the first phase. The modern breeding approaches proposed represent pioneering efforts in the implementation of a new breeding paradigm using genomics-based resources for the four legume crops, and thus they will provide valuable experiences and lessons. Certainly high-quality phenotyping will continue to be limiting because of its critical role for accurate marker-trait associations, and the second phase of the project has a strong capacity-building component that will build on Phase I efforts to improve human resources and local infrastructure.

Achievements and lesson learnt from Phase I shape this proposal, which reflects an evolution of activities (see Annex 4) summarised in the following points:

- Elite lines identified in Activity 1 Phase I will be used as parents to develop new populations in Phase II. There will be no more characterisation of contrasting germplasm (including reference sets, apart from chickpea and confirmation of a limited number in groundnut).
- Development of groundnut genomic resources will remain an important activity, although with a relatively modest budget, and there will be very limited development of genomic resources for cowpea, common bean and chickpea, which were already significantly increased in Activity 2 Phase I.
- Markers for biotic stresses identified in Phase I will be validated through introgression into popular local germplasm
- Improved phenotypic screening methods developed in Phase I will be further streamlined in Objective 5 and they will be applied in the MARS experiments.
- Quantitative trait locus (QTL) detected for drought in Phase I, characterised by small genetic effects, trait specificity, large GxE interactions and instability across backgrounds, support the plan to use a novel breeding scheme (MARS) that allows the identification and introgression of several QTLs at a time, particularly suited to improve drought in Phase II. This approach based on allelic selection at QTL in the target population has been successfully used in the private sector, where it proved very efficient in breeding for polygenic traits (Eathington et al, 2007).
- In view of the large and diverse amount of data generated in Phase I and that this number will significantly increase in Phase II, in particular due to the MARS experiments, a strong data management component is included, which also proposes to gather phenotypic assessment data from TLII.
- Human resource development is now embedded in the crop-objectives to strength the link between learning and research. More resources are allocated in Phase II to improve NARS infrastructure, in continuation of the effort conducted in Phase I.

In the medium term, it is anticipated that TLI and TLII will merge to represent the actual integration of molecular markers into large-scale legume breeding efforts in the developing world. It was agreed that Phase II of the TL initiative would still benefit from two distinct but associated projects to fill the need for more genomic resources (mainly for groundnut), to validate elite alleles for biotic and abiotic stresses and test molecular breeding approaches. If the objectives of Phase II are achieved, merging TLI and TLII into a single project appears as a logical next step. At that time, it will be important to balance the value of having parallel initiatives for each crop (for ease of management) as opposed to keeping them together (for increased spillover across legumes). GCP might not be involved in this decision-making, but we strongly recommend that the value of coordinating data management, adopting consistent screening methodologies, building capacity across legume breeding and establishing a strong legume community be given due consideration.

Links with other GCP activities

The overall framework of this project aligns well with the changes implemented by GCP itself in the transition to Phase II. These changes are summed up by a clear focus – through seven new Challenge Initiatives (CIs) – on selected crops, traits and target countries in Africa and Asia; value-adding and building on key achievements; shifting from discovery to more applied activities; enhancing existing infrastructure and expertise; and ensuring delivery of research products. In particular, delivery is at the core of the GCP rationale for this proposal, which concentrates on the exploration and validation of modern breeding approaches (AB-QTL, MABC, MARS), while also committing to transfer clear MB outputs (Annexes 4, 5 and 6) to the Tropical Legumes II project, which will then adapt, adopt and apply them for legume breeding in harsh environments in SSA and Asia. Two of the seven CIs are devoted to two of TLI's four crops, namely cowpeas and chickpeas. The other CIs are on cassava, rice, sorghum, wheat and comparative genomics. Noteworthy are two facts: one, that the product delivery coordinator of the chickpea CI is the principal investigator for chickpea breeding in TLII and the TLI breeder as well, in an effort to build effective links between TLI and TLII; two, that GCP is in process of negotiating a complementary grant from the Indian Government to advance chickpea research for drought improvement in South Asia. The latter represents a notable development to leverage funds and amplify the expected impact of the chickpea Objective for both SSA and SA.

Besides the two CIs above, of the utmost importance for TLI Phase II are the links with the GCP Molecular Breeding Platform (MBP). This initiative will enable breeding programmes to accelerate variety development for developing countries using marker technologies for breeding, from simple marker-assisted selection to complex molecular breeding approaches (eg, MARS, GWS). The platform provides access to breeding and support services in order to access and use marker technologies, and it also promotes the creation of communities of practice on molecular breeding. In the framework of the MBP, TLI crop Objectives will be able to outsource high-throughput genotyping, contribute to the MBP database, benefit from the set of selected phenotyping sites, and will have access to appropriate analytical tools and related services to design and efficiently conduct molecular breeding experiments. The development of the Platform will be driven by the needs of 14 user cases, three of which are MB activities in TLI Objectives 2, 3 and 4.

II. Project Objectives (see Appendix A for Objectives, Activities, and Outcomes)

Overall objectives

The overall objective of this project is to improve the productivity of four tropical legume species for SSA through the application of modern breeding approaches using the genetic resources and genomic tools developed in the first phase of the project, in close partnership with sub-Saharan Africa country and regional research institutions.

Other important generic objectives specific to the second phase of the project are:

- To introgress and validate favourable alleles for biotic stresses in popular African germplasm
- To validate molecular breeding approaches in drought-prone environments to improve selection efficiency for target traits important to sub-Saharan African farmers
- To develop reliable phenotyping to guarantee accurate marker-trait associations and to refine selection indices used by breeders
- To integrate data management of all data-producing research activities in TLI, Phase I and II, to ensure availability of high-quality, well-documented and publicly available data
- To build capacity of breeding programme partners in Africa, helping to institutionalise and expand modern breeding efforts in legumes

- To promote communication between crop teams and their respective TLII partners to ensure that TLI outputs will be adopted and will have impact on TLII breeding activities

Specific objectives

Crops

Of the five objectives in this proposal, four are crop-specific, namely groundnut, cowpea, bean and chickpea:

- The main objectives for groundnut are to pursue the development of genomics resources and produce the first molecular breeding products of the crop by introgressing rust and/or rosette disease resistance QTL identified during Phase I in farmer- and market-preferred varieties (FMPVs) in partner countries. Objectives also aim to set the foundation for future MARS breeding by tapping on the recently identified sources of drought tolerance.
- Main objective for cowpea is to advance modern breeding by applying tools and knowledge for the optimisation of MARS and MABC for sub-Saharan Africa traits and environments. It will employ molecular breeding to develop lines and varieties with drought tolerance and biotic stress resistances identified from the analysis of elite x elite breeding populations.
- Main objectives for common bean is the selection of drought tolerant genotypes through MARS and Advanced Backcross using and enhancing sources of resistance in Andean and Mesoamerican genepools, respectively. Important insect and disease resistances for dryland environments will also be incorporated into the drought-tolerant line crosses.
- Main objective for chickpea is to develop drought tolerance genotypes. While so doing, this objective will develop a Multi-parent Advanced Generation Inter-Cross (MAGIC) population harnessing novel genetic diversity for broadening the genetic base, and it will increase the available genomic resources to better facilitate MABC and MARS activities in this project and for the future. Moreover, through the links with other ongoing projects (including the projects on molecular breeding for biotic stresses and on nodulation biology in chickpea recently funded by the Indian government and sponsored by the BREAD programme), the chickpea investment to develop markers, tools and MAGIC populations will serve both African and South Asian markets.

Cross-cutting activities

- Activity 1 of Objective 5 aims to identify critical traits to refine selection indices and guide breeding for superior adaptation to drought of TLI crops for target environments. Traits identified to be highly contrasting for seed yield under drought conditions across sites and years in TLI Phase I will be assessed to determine the range of variation available, and to establish closer relations between these traits and selection indices used by breeders. While so doing, an added objective will be to train NARS breeders in effective phenotyping.
- Activity 2 of Objective 5 will develop and implement a project-wide data management and publication strategy so that data from all objectives in Phases I and II will be documented and made available (after a suitable embargo for publication) for public access. This activity will also develop or refine crop ontologies for standard annotation of legume traits. This will allow integration of data across species where appropriate. Data management will be harmonised with the Molecular Breeding Platform for breeding activities in all Objectives so that this activity also sets the standard for management of molecular breeding information for tropical legumes.
- Capacity building in Phase II aims to enhance human resource capacity of SSA scientists as a powerful mechanism for technology and knowledge transfer between the North and South and, consequently, as a guaranteed means to increase the chances of adoption of the research outputs

planned. Together with improved infrastructure, which will enhance what was put in place in Phase I, NARS partners will be equipped to build on the pioneering efforts of TLI modern breeding in the public sector in Africa. The realisation of this goal will result from the combined endeavour on capacity building in breeding for drought tolerance through the detailed study of cross-legume phenotyping and on data management by cataloguing all data generated in the project, including genomic data from Objective 5 in Phase I.

III. Project Design and Implementation Plan

Each of the four crop Objectives is built around a set of complementary Activities that unite Agricultural Research Institutes (ARIs), CGIAR Centers, and National Agricultural Research Systems (NARS). Whilst activities across crop Objectives were designed in a common framework in Phase I, in this proposal for Phase II, priority has been given to the application of outputs for breeding in line with the level of advancement achieved in the first phase. This results in a framework with some commonalities among crops but with different resources allocated per activity across crops reflecting the diverse progress achieved in the first phase, which is mainly due to the intrinsic nature of the crops. Together, they encompass germplasm characterisation, targeted development of genomic resources, validation of markers for biotic stresses and identification and validation of markers for abiotic stresses through modern breeding approaches such as MARS.

The TLI Phase II project is planned around the testing and validation of research outputs and breeding approaches, with the clear purpose of their transfer to TLII breeding programmes. Accordingly, a Sub-Activity in Objective 5, Activity 3 will execute this transfer and will follow-up with breeders with regards to the usefulness and adoption of the relevant outputs. Once a marker for a target trait has been validated in Phase I, it will be transferred for application to breeding in TLII.

Overall activities across crop objectives

Germplasm characterisation

The four crop Objectives will share an Activity that deals with genetic diversity, which in the first phase focused on the study of reference collections. Now, cowpea and chickpea will harness diversity in a MAGIC population. These will be developed and shared with the wider cowpea and chickpea research communities as a long-term resource for genetic analysis and breeding. They will capture and recombine genetic diversity from elite drought-tolerant genotypes identified in TLI Phase I (cowpea) and from promising genotypes identified in Phase I of both TLI and TLII in relevant locations in SSA (Ethiopia, Tanzania and Kenya) and SA (India). Researchers will explore new sources of disease resistance and drought tolerance for groundnuts in a set of diverse germplasm selected during the first phase, while efforts for common bean will concentrate on the evaluation of diversity for deep-rooting ability. For the evaluation of diverse germplasm, care will be taken to undertake evaluations in similar maturity groups to avoid the confounding effect of precocity (drought escape) on drought tolerance.

Development of genomic resources

With low genetic polymorphism in current cultivated cultivars, groundnut thus by its nature holds back the identification and use of enough polymorphic markers, which are a very basic ingredient for molecular breeding (MB). Full implementation of MB requires not only sufficient markers, but also marker types suitable for high-throughput operations, in particular when dealing with an important number of large-size populations. SNPs fulfil these requirements and they are undeniably the marker of choice for MB. As such, the second phase of TLI will aim to develop a sufficient number of markers (SSR, SNP) for

groundnut, while it will work towards the identification of a higher number of polymorphic SNPs relevant for breeding populations (cowpea, common bean, chickpea). In cowpea, this area of focus will build upon the huge advance made in Phase I (Annex 3). In common bean, the effort will join forces with ongoing sequencing initiatives elsewhere (www.jgi.doe.gov/), where TLI will contribute selected materials of breeding interest. With the necessary markers at hand, prospects to fully benefit from MB will be enhanced.

Marker validation and molecular breeding for biotic and abiotic stresses

Groundnut research will identify new markers for disease resistance in populations developed during Phase I and will use available markers to both introgress rust and rosette resistance in farmer- and market-preferred varieties in Mali and Malawi, and confirm the efficiency of the MABC approaches. Cowpea research in the second phase will test molecular breeding approaches such as MARS and MABC to develop improved breeding lines and varieties relevant for the locations and breeding goals of African partners. Common bean activities will validate identified markers (Phase I) to deploy insect and disease resistance in drought-tolerant advanced lines for ECABREN/SABRN, will transfer drought tolerance traits from the inter-genepool crosses into the Andean genepool and will also enhance drought tolerance testing of MARS and AB-QTL breeding approaches within the preferred Andean genepool. Finally, chickpea research in Phase II will identify more suitable markers for pod borer and drought stress, and will increase the efforts initiated in Phase I for introgressing drought tolerance QTL, some of which (such as those for deep rooting), have already been identified in Phase I via MABC and MARS.

Cross-cutting activities

Special emphasis on increased capacity will be given in an Activity that will work on the identification of traits to refine selection indices and guide breeding for superior adaptation to drought in targeted environments. This activity will strengthen the knowledge base of phenotyping efforts made in each crop Objective during Phase I, and will train African breeders in effective phenotyping. It will also enable the exchange of experiences and development of common activities between crop Objectives. Linking all Objectives, the project intends to manage and catalogue the diverse data generated by Tropical legumes I as a whole, including phenotyping and genotyping data from Phases I and II. In addition, in association with the capacity-building capacity efforts carried out in Phase I (namely infrastructure and human resource development), a clear goal of Phase II for all crops is to engage African partners one step further through specific training activities, including degree education, and active participation in research on phenotyping and molecular breeding. The training of sub-Saharan Africa scientists will enhance the human capital needed to sustain and strengthen legume research and development in SSA. For all crop Objectives, personnel and institutional links exist between TLI and TLII projects, thereby paving the way for ensuring adoption of molecular breeding down the research pipeline.

Overview of the Rationale, Activities and Partners of the five Objectives

Objective 1: Improve groundnut productivity for marginal environments in sub-Saharan Africa

The limited level of groundnut genetic polymorphism restricts the use of modern breeding (Halward et al., 1992; Kochert et al., 1996; He et al., 1997; Hopkins et al., 1999; Varshney et al., 2009). Nevertheless, large phenotypic differences exist for traits such as disease resistance and drought tolerance (Nigam et al., 2005; Ratnakumar et al., 2009; Vadez et al., 2007b, 2008; Devi et al., in press[c]; Devi et al., 2009) – traits that are very much needed to enhance groundnut productivity for resource-poor farmers in SSA (Sharma and Lavanya, 2002). 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 (Chu et al., 2007). All these research activities also offer rich training ground for scientists and technicians from SSA country programmes.

This Objective will be conducted through six activities: Diversity, Molecular Tools, Diseases, Breeding, Training and Data management. Data gathered in Activity 3 of Phase I indicated that synthetics may likely offer higher levels of resistance than cultivated lines. Activity 1 will therefore assess the existing synthetics and derivatives (5–10 synthetics and two derivative populations) for disease resistance in parallel to the best cultivated germplasm. The work on drought will focus on the intermittent stress conditions of West Africa and East-Southern Africa. It will also confirm the level of drought tolerance of about 30 cultivated accessions from the reference germplasm collection and it will compare drought-adaptive traits in both types of germplasm. Promising synthetics will be tested for their 'crossability' with farmer- and market-preferred varieties, and AB-QTL populations using the promising synthetics will be initiated. Potential sources of tolerance and resistance will also be tested for agronomic traits by TLII.

Marker-assisted selection (MAS) can increase selection efficiency (Morris et al. 2003; Ribaut and Hoisington 1998), so, while this project will continue to use SSR from Phase I to ensure continuity of marker use, Activity 2 will identify SNPs to prepare for future groundnut breeding. Collaboration will be sought by tapping on ongoing SNP development efforts, while additional SNP will be generated from drought response-contrasting genotypes. Extra SSR markers will be developed in strategic genomic regions (drought, disease resistance QTL regions), and in reference points linking different genetic maps. This work will link up with other initiatives outside of TLI and the markers generated will become part of the MBP toolbox.

During Phase I, QTL for disease resistance were identified in diploid and cultivated x synthetic populations, building on previous work (Mace et al. 2006; Mondal and Badigannavar 2009), and recombinant inbred lines (RIL) populations were developed. One population per disease (rosette, rust, ELS and LLS) will be phenotyped and genotyped for QTL identification, and MABC will be used to introgress known QTL (rosette or rust resistance) in an FMPV background. New sources of disease resistance (Activity 1) will be used to create new populations in FMPV backgrounds as the base for future MARS/MABC breeding.

New breeding populations are needed given the small size of drought-related trait QTL (TE, SCMR and SLA) identified (Krishnamurthy et al., 2007; Varshney et al., 2009a), the lack of genetic polymorphism in the existing populations and the large variation of the response to drought observed in Phase I. These will involve FMPVs, which show drought sensitivity in current drought trials, and the top-ranked drought-tolerant germplasm. To avoid making crosses with low genetic polymorphism in TLII, parental genotypes of drought breeding materials of TLII would also be genotyped. While developing these populations, the relevance of phenotyping F₄ families for drought tolerance will be tested, in preparation for future MARS (Charmet et al. 1999). TLII will eventually take charge of these populations.

Training of technicians and scientists (Activity 5) will focus on molecular breeding and phenotyping for drought and disease. This involves medium-term training (4–6 months) at ICRISAT research stations as well as on-location hands-on practice in project activities at student's country of origin. This arrangement will allow long-term collaboration between trainees and trainers. Provided there are suitable candidates, two technician–scientist pairs will be targeted for each NARS. Collaboration with AGRA will be sought to ensure good coordination and complementarity of efforts. Finally, Activity 6 will deal with data management,

ie, the curation and storage of genotypic data from the reference germplasm and RIL populations, and of phenotypic data from drought and disease screening trials. Such a database will also gather the phenotypic data from TLII experiments, which will help drawing certain germplasm comparisons and performing meta-analysis of genotype response in different types of environments.

Links to other projects include the TLII project, a major partner of this Objective, where Activity 4 acts as an interface; 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 markets (Holbrook et al. 2009; Nigam et al 2009). 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 (USAID grant to ICRISAT in collaboration with the University of Florida, USA) examines water conservation traits (Devi et al., 2009a).

The lead institute of Objective 1 will be the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), which has extensive experience and expertise in conventional and modern approaches for the development and dissemination of improved groundnut varieties in Africa and Asia. The wide geographical array of partners, reflecting the extent of groundnut cultivation, represents a set of prevailing drought and disease stress conditions where groundnut is cultivated (eg, ELS in Mali; rust in Tanzania). The NARS partners overlap and complement TLII (Malawi, Tanzania). Although the NARS of Mali and Niger are not involved in TLI, the close relation with ICRISAT research stations in place, with a groundnut breeder working in both TLI and TLII, guarantees the 'spill over' effect. Senegal has a strategic involvement in the development of pre-breeding products using groundnut synthetics with likely higher disease resistance. Partners in the United States and Brazil have a long-term and highly renowned experience in developing modern breeding tools.

Objective 2: Improve cowpea productivity for marginal environments in sub-Saharan Africa

New plant breeding strategies have emerged from the genomics revolution that expedites delivery of improved crop varieties. These strategies emphasise selection of desirable genomic segments across the genome and rely on the availability of high-density genetic maps and high-throughput genotyping systems. These 'whole-genome' 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 NARS of SSA, has lagged behind due in large measure to the upfront investment in genomic tool development needed for each crop and lack of awareness and expertise by conventional breeders. In Phase I of this project 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 MBP, 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.

This Objective has five activities: 1) *Develop MAGIC population*, 2) *Develop genomic resources in support of marker-assisted breeding*, 3) *Employ marker-assisted recurrent selection (MARS) and marker-assisted backcrossing (MABC) to develop improved breeding lines and varieties*, 4) *Capacity building for modern breeding in Africa* and 5) *Curation and storage of data*. Under Activity 1, a cowpea MAGIC population will be developed as a long-term community resource for trait discovery and breeding. Under Activity 2, genomic resources will continue to be developed in support of marker-assisted breeding, including: a) Customised sets of markers suited for bi-parental MARS breeding for both TL and TLII projects, b) Optimised tools for calculation of breeding values for MARS breeding, c) QTL for drought tolerance and biotic stress resistances identified from analysis of elite x elite breeding populations and d) the effectiveness of drought tolerance QTL discovered in Phase I will be evaluated in collaboration with TLII in their breeding populations. Activity 3 will employ marker-assisted recurrent selection (MARS) and marker-assisted backcrossing (MABC) to develop improved breeding lines and varieties. Quantifiable outputs from Activity 3 will be: a) sixteen (4 lines/partner) advanced breeding lines developed with superior performance under drought, b) QTL for aphid resistance and heat tolerance identified and used in MARS breeding, and c) eight varieties (2/partner) with improved drought tolerance or resistance to biotic stresses developed using WGMABC. Activity 4 will be devoted to capacity building for modern breeding in Africa, with three African PhD students expected to be in the final stages of their degree training and eight African NARS researchers (including TLII breeders) trained in modern breeding by the end of the project. Activity 5 will organise and store data collected in both Phase I and II of TLI, in close collaboration with TLI Objective 5 to ensure standardisation of protocol across objectives.

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 of this Objective 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 Objective is linked to the TLII project through two specific activities described in Appendix G: Activity 2.5 *Drought tolerance QTL validation* in TLII breeding populations and Activity 4.1 *Train NARS breeders in modern breeding*. IITA provides the linkage point for delivery of TLI cowpea outputs to TLII countries by virtue of its leadership in cowpea breeding and seed delivery in the TLII project. The work of this Objective 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 TLI project, such as the high-throughput genotyping platform and consensus genetic map, have already been utilised in the CRSP project, and future TLI outputs will be similarly utilised. Genetic materials and

information were exchanged with a Kirkhouse Trust-funded project targeting marker-assisted breeding of cowpea for resistance to the parasitic weed *Striga gesneriodes* in several West African countries and this linkage will continue in Phase II. A link with the GCP Molecular 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 outlined in this proposal. In this objective the MBP 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.

The partners in this Objective are: 1) UC–Riverside (USA) which is responsible for the overall management of the work flow, as well as key components of germplasm development, genotyping, genotype analysis and phenotyping for heat tolerance and aphid-resistance; 2) IITA (Nigeria); 3) ISRA (Senegal); 4) INERA (Burkina Faso); and 5) Universidade Eduardo Mondlane (UEM, Mozambique). IITA, ISRA, INERA and UEM are each responsible for executing two cycles of MARS and MABC breeding. All partners listed have experience with cowpea breeding and excellent relationships with complementary projects targeting delivery of improved varieties to farmers in SSA.

Objective 3: Improve common bean productivity for marginal environments in sub-Saharan Africa

Phase II will continue to focus on drought as the primary constraint to crop production throughout Eastern and Southern Africa (Broughton et al., 2003, Beebe et al., in press, Graham et al., 2003). 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 (Funk et al., 2008). Wortmann et al. (1998) estimated that drought is the primary yield constraint to bean production throughout the region, affecting over 70 percent of the bean production area (Wortmann et al., 1998).

This Objective will comprise seven Activities: Activity 1 will evaluate the diversity of the rooting depth of parental sources; Activity 2 will validate genomic resources for use in inter- and intra-genepool crosses for drought tolerance breeding; Activity 3 will deploy biotic stress resistances in advanced breeding lines; Activity 4 will deploy drought tolerance traits into the Andean genepool through physiological screening and QTL trait transfer; Activity 5 will pyramid drought tolerance traits through marker-assisted recurrent selection (MARS) and advanced backcross (AB) breeding along with pyramiding crosses within the preferred Andean genepool; Activity 6 will undertake capacity-building for modern bean breeding in Eastern and Southern Africa; Activity 7 will deal with data storage and management.

Phase II will exploit the genetic tools and breeding populations created in Phase I for the marker-assisted selection of drought-tolerant germplasm in common beans. Tolerance to drought varies considerably in both genepools of the species and is based on several mechanisms (Beebe et al., in press; Terán et al., 2002). 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 water (Beebe et al., in press; Sponchiado et al., 1989; White et al., 1989), earliness (drought escape) (Beebe et al., in press; Rosales-Serna et al., 2004) and seed filling capacity (Beebe et al., in press; Miklas et al., 2006). 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 (Miklas et al., 2006; Beebe et al., 2008). 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-gene pool 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 (Miklas et al., 2006; Beebe et al., 2008; Schneider et al., 1997), 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 (Blair et al., 2008; Blair et al., 2009a; Blair et al., 2009b) 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 phase (Lynch, 2007; Rao, 2001).

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. Recurrent selection has proven to be valuable for concentrating alleles for drought tolerance within the Mesoamerican gene pool, and the same will be done for the large-seeded commercial varieties of the Andean gene pool. QTL transfer will be confirmed through reliable field nurseries and greenhouse screening techniques. The selection of AB-QTL and MARS parents has been coordinated with the TLII project, as will be the testing. Germplasm work stresses cream mottled, large red, red mottled seed types popular in the region, and selection will be for combining commercial characteristics with drought tolerance traits and QTL. Pyramiding crosses (multi-way crosses) within the Andean gene pool especially and in coordination with TLII will be undertaken with the lines from AB-QTL and MARS. The phenotyping and germplasm testing platforms established in various important drought sites by TLI and TLII projects will allow the generation of accurate phenotypic data on the populations.

The principal linkages to Objective 3 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 as 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 Objective 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). The partners in this programme are 1) Centro Internacional de Agricultura Tropical (CIAT), which is responsible for germplasm development in common bean and is leading the companion

project on TLII breeding and seed systems work in drought areas; and 2) the regional networks of ECABREN and SABRN, which have excellent track records of varietal releases and delivery to farmers. The individual national programmes with strong drought breeding efforts within these networks that will work with the TLI project are the Department of Agriculture Research Services (DARS), Malawi; the Department of Research & Specialist Services (DR&SS), Zimbabwe; South Agricultural Research Institute (SARI), Ethiopia; and the University of Nairobi (Kenya).

Objective 4: Improve chickpea productivity for marginal environments in sub-Saharan Africa and South Asia

Terminal drought is considered the major constraint to chickpea production. Root traits, particularly rooting depth density and root depth, have 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 (Vadez et al. 2008). 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 scope of the proposal would limit itself to assess 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.

Activity 1 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 (Mackay et al. 2007) 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. Activity 2 will coordinate the development of a SNP genotyping platform and will integrate SNPs to the genetic maps. Mapping of SNPs with already mapped SSR (Nayak et al. 2010) and DArT markers will facilitate identification of diagnostic markers associated with drought tolerance (Activity 3) and accelerate molecular breeding in Activity 4 in coordination with the MBP 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, Activity 2 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. Under Activity 3 a 'hot spot' harboring many root trait QTLs was identified in Phase I, contributing up to 30% phenotypic variation, in linkage group 5. 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 a GCP-SP3 project, meaning that another important component of drought tolerance—transpiration efficiency (TE) will be used for phenotyping the reference collection (also one intraspecific mapping population) under Activity 3 of Phase II. 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. In Phase II, Activity 3 will enhance MABC and MARS activities by appointing NARS partners as leaders of these activities 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 at the corresponding institution; 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.

Activity 4 research, with active participation of NARS partners, will have heavy emphasis on capacity building and it will address capacity in modern breeding by supporting at least one PhD and two Master students from three NARS (Kenya, Ethiopia and India). At least one training course will be organised at Patancheru (India) inviting NARS TLI and TLII team members. Data management and storage (Activity 5) will enable results from TLI (e.g. marker sequence / genotypic/ mapping data, phenotypic data, MABC data and MARS data) to be readily disseminated, which will in turn be of benefit to the wider chickpea community. This Activity will compile data in one place in collaboration with Activity 2 of Objective 5, GCP's Central Registry (<http://gcpcr.grinfo.net/>), the database of the MBP and also under the auspices of the International Chickpea Genetics and Genomics Consortium (<http://www.icrisat.org/gt-bt/ICGGC/homepage.htm> – coordinated by the Principal Investigator of this Objective).

The lead institute for this Objective will be the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), which has extensive experience and expertise in using conventional and molecular approaches in the development and dissemination of improved chickpea varieties in SSA and SA. UC–Davis (USA), NCGR (USA) and DArT P/L (Australia) will provide key expertise (through outsourcing) in genomics activities. Critical to the success of this Objective will be the full involvement of national programmes from East Africa (namely EU, Kenya and EIAR, Ethiopia) and India (IIPR, Kanpur) in various activities starting from the onset of phase II.

Objective 5: Cross-cutting crop activities (Drought phenotyping, data management and capacity building)

This Objective combines three Activities: 1) Crop comparative drought phenotyping; 2) data management and 3) project management. The rationale for combining such activities is that they each cut across the four crop Objectives and provide support towards effective implementation of their respective Activities.

Activity 1 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 (eg Kholova et al., 2009, 2009-submitted; Devi et al., 2009b), higher or better use of soil water (eg Vadez et al., 2008; Ratnakumar et al., 2009), success of reproduction or remobilisation (eg, Vadez et al., 2007; Turner et al., 2005). 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: (i) predict by modelling the effect of critical traits on crop yield across years and environments (Sinclair et al 2005); (ii) assess the available variability for those critical traits demonstrating a high probability of conferring a substantial yield advantage in representative situations; and (iii) relate such traits to phenotypes that can be easily measured by breeders. The main output is a better-equipped 'toolbox' for breeders.

This approach is important for at least two reasons: (1) breeders need to know what trait to breed for, how to phenotype it, and what probability of return is predicted; (2) breeding is progressing toward environment-specific breeding where manipulating genes beneficial for specific adaptation or characteristics will be standard. 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. Key for the experimental setup will be a lysimetric system (Vadez et al., 2008), allowing both yield and trait assessment simultaneously, in a precise and high-throughput manner, under conditions that mimic the field.

A modelling component (Sinclair, 1986) 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 Objectives. It will also greatly enrich the phenotyping network of the Molecular Breeding Platform. Existing crop simulation models for grain legumes will be adapted to the four TLI legumes.

This Activity will strengthen the quality of phenotyping performed in different crops, including training of young breeders on a long-term basis, therefore enhancing the knowledge base and approach to phenotyping. The selected experimental stations will assess crops side by side and improve the respective protocols.

The selected experimental stations will assess crops side by side and improve the respective protocols. The partnerships will involve the known expertise in modelling, and drought of T Sinclair (North Carolina State University) and will build on the TLI drought phenotyping course. Collaboration with ISRA (Senegal) will make use of the lysimetric facility developed there in Phase I. Such a facility is essential to unravel the relationships between 'process-based' traits and 'breeder' traits, can place ISRA at the forefront of drought research, and opens prospects of future association with Centre d'étude régional pour l'amélioration de l'adaptation à la sécheresse (CERAAS), Senegal, this activity will also involve CIAT, with experience and expertise in remobilisation processes, and IITA, with experience on canopy temperature aspects. There will be frequent and close collaboration with members of the four crop teams. It is expected this Objective will become the cement of the drought efforts across the crops of the project.

Activity 2 will deal with data curation and management of TLI's Phase I and II. The quality and availability of data is one of the most important indicators of success. GCP project proposal templates require researchers indicate the nature and format of the data expected from the project, and that such data be published in the GCP Central Registry or in another public database. The time and effort required to properly curate, collate, annotate and publish data in a coordinated manner are generally underestimated by researchers whose primary interest is in the results arising from data, rather than the data itself. This is especially true when data is of diverse types, requiring different storage and retrieval strategies, and when an objective is to capitalise on new IT and knowledge management tools to link diverse data for easy synthesis and use. TLI's main research Objectives 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 Objectives, 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. First, a coordination centre will be established in close collaboration with the MBP platform manager and Informatics scientist. 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 in the other sub-activities. This strategy will be aligned to the MBP project and the action plan will include the tools and technologies developed in the MBP. 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 on 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 Central Registry with the necessary metadata.

Key outputs of this Activity will be a detailed data management strategy that can be applied to other projects (such as TLII), catalogued and curated data available in public databases and knowledge management tools to allow retrieval and comparison of data across databases and data sources.

The third activity in Objective 5 will deal with the infrastructural support for partner institutions in sub-Saharan Africa and with project management. The rationale for grouping infrastructure and capacity-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 Objective 5 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 Objectives 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 Objectives.

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

The partners involved in Activity 3 will be the NARS scientists involved in the four crop Objectives, whether they participate in capacity-building activities directly or indirectly, and TLII partner institutions engaged in breeding. Other critical partners include the University of Kwazulu-Natal in South Africa through the African Center for Crop Improvement (ACCI) and the University of Ghana through the West African Centre for Crop Improvement (WACCI), both members of the Program for African Seed Systems (PASS). Here, through GCP CB efforts outside of, but parallel to, TLI, a student working on cowpea from Burkina Faso and another in chickpea from Kenya have been accepted to start their PhD programmes in 2010. Additional special linkages exist for the promotion of TLI technologies. For example, for countries such as Burkina Faso and Senegal, which are not active partners in TLII cowpea activities, the USAID-funded CRSP project underway in these countries has objectives similar to TLII, and has already adopted some of the early phase TLI outputs, such as the high-throughput genotyping platform. Very importantly, this Activity will link with the training elements and the Communities of Practice for legume molecular breeding of the MBP.

Link with other projects

Besides TLI, GCP has other ongoing legume projects and this proposal guarantees complementarities across the different projects. As mentioned earlier (in *Links with other GCP activities*), this is particularly relevant for cowpea and chickpea, which are two of the seven GCP Challenge Initiatives (CIs). CIs are comprehensive and targeted projects to which GCP will devote half of its resources in the second phase of the Programme (2009–2013). As mentioned above, links with GCP's MBP will be sustained throughout the project. In particular, strong links will be established between the Objective 5 Activity 2 (data management) and the MBP database, especially in standards and procedures, the MBP's information management and data curation services, and in training.

IV. Potential Risks*Common across crops*

While each Objective of this project has been designed using the best scientific knowledge available and building on both the progress achieved and the lessons learnt in the first phase of TLI, as with any research programme, there are potential risks that must be considered. At the experimental level, the greatest and most likely risk is crop failure at the field sites, due, for example, to excessive or insufficient rainfall. This risk can be reduced by planting the materials in different countries or different sites within the country. Political instability at the breeding or testing sites could also disrupt planting, management, or harvest. For Objectives engaged in large molecular breeding activities (such as MARS), if genotyping costs were significantly greater than estimated, the number of samples genotyped or the number of single-plex loci assayed would have to be reduced or switched to a less-costly genotyping option. This will also affect the genotyping of MAGIC populations. The implementation of MARS has a number of extra implicit risks: for example, those inherent to working with many samples, such as mix-ups; those related to poor phenotyping (because of the trait itself or the limited skills of the technician who collected the data), which in any case will result in unreliable QTL detection and as a consequence lack of genetic gain; and those related to feasibility, ie, the complex logistics behind the number of crosses, plants and environments that MARS requires. From an overarching perspective, adoption of MARS may be questioned from a sustainability standpoint, in particular where institutional support is only partial. Limited time and resources for data analysis affects all crops and research Objectives. Preventive measures have been taken to include these tasks in the workplans, in addition to Objective 5 Activity 2.

Objective-specific risks

For Objective 1, sources of resistance might be difficult to incorporate into acceptable agronomic background. In addition, there will always be the intrinsic constraint of low genetic polymorphism in groundnut, due to the fact that it is a highly self-pollinating crop, which complicates the development of a sufficient number of markers for modern molecular breeding approaches.

In Objective 2, based on polymorphism between parents, it is assumed that trait QTL exist in the elite x elite populations to be assayed for target traits. To mitigate failures during population development and advancement under Activity 3, back-up crossing and progeny development will be conducted in parallel at UC–Riverside. Insect attack at many African locations can be severe and can affect accuracy of drought phenotyping, so close attention will be paid to controlling insects with regular applications of selective/effective insecticides.

For Objective 3, populations are reaching the genotyping stage, which will make Phase II marker-intensive. Reliance will be on previously developed SSR and target SNP markers. The low polymorphism of intra-genepool comparisons can be overcome with targeted SNP development for drought genes in genomic regions that are more variable (for example 5' UTRs or inter-gene spaces). As for crosses for Activities 4

and 5, the regional bean breeders know the best combiners among commercial varieties, but if crosses for MARS do not segregate commercial types, the project may rely on off-season nurseries to increase the number of crosses and to undertake rapid generation advance with up to four seasons per year, especially with the early maturity determinate types of Andean beans.

In Objective 4, development of breeding populations at NARS have the risk or failure to complete each crossing cycle in a timely fashion due to seed set of hybrid pods or weather conditions. A similar situation may be encountered for MABC activities. Consequently, ICRISAT will make back-up crosses for these countries, and will develop three MABC crosses – one for each partner as safety back-up crosses. SNP polymorphism may be low in intraspecific crosses; in such a case, either DArT or SSR markers, developed in Phase I, will be used. Similarly, the next generation sequencing (NGS, Varshney et al. 2009) for BAC contigs based on a BAC-pool strategy and the alignment with the *Medicago* genome sequence data may fail, in which case BAC-end sequencing for selected BACs from each contig would be used.

Risks in Objective 5 are diverse depending on the Activity. Activity 1 may encounter difficulties due to slower than desirable seed transfer among teams; another possibility is that coordination and planning are sub-standard for the establishment of phenotyping facilities in Senegal, an essential partner for the project. In Activity 2, two main difficulties can be encountered, one due to data quality (poor, unreliable, disorganised) and the other to data release (limited availability). In both cases, the role of the Principal Investigator for this Activity will be essential, as well as his interactions with the data management focal point for each of the crops and the respective PIs. Related to Activity 3, a key risk is that of producing Outputs that are not pertinent to the NARS partners or to the TLII community. Close monitoring of usefulness and applicability will be exercised to detect such threat as early as possible.

V. Monitoring and Evaluation

During the first phase, GCP developed an online monitoring tool to facilitate the task of routine research progress reporting. The Senior Programme Officer may access this tool liberally. As is required for all GCP projects, TLI projects too must submit a comprehensive annual technical report every October. And since all TLI projects are contracted by GCP, this requires timely release of data to GCP or public databases.

Similar to the first phase, GCP Subprogramme Leaders (SPLs) will have an essential role in monitoring progress and achievements of TLI Phase II. The SP1 Leader will follow up research on diversity issues, and the development of markers and genomic tools are the province of the SP2 Leader. The SP3 Leader will pay special attention to marker applications to breeding and use of modern breeding schemes, and management including labelling and curation will be overseen by the SP4 Leader, while the SP5 Leader will supervise capacity-building activities and will act as the bridge with TLII, since the SP5 Leader also serves as the overall TLI Project Coordinator.

Teleconferences will be planned with the Principal Investigators to discuss arising logistics issues. Annual meetings will be organised, in which teams will report progress and revise workplans. External expertise will be provided by advisory committees to review progress. These experts will participate in the annual meeting. Moreover, SP2- and SP5-related activities may rely on a specific advisor (Review and Advisory Panel member) accessible on request. Site visits will be done by GCP research managers, in conjunction with external experts or advisors. These visits are aimed at both reviewing ongoing projects and providing GCP with feedback on its operations and progress.

A special element of TLI Phase II will be the activities on molecular breeding. These will be conducted in close collaboration with the MBP, and as such will also be monitored by the management structure in place for that project. At the overall level, as happened in Phase I, TLI Objectives will each be required to develop a delivery plan in collaboration with project partners, emphasising the usefulness of the

planned research outputs and mapping out the steps needed to ensure timely and appropriate transfer of outputs to primary users.

Given that the success of TLI Phase II is intrinsically aligned with the goals of TLII and, consequently, with the TLII adoption of outputs from TLI, the evaluation role of TLII will be essential. In consideration of this, TLI Phase II will maximise communication with TLII primary users, both informally (eg, email sharing of interim and annual reports) and via more formal avenues, such as attending each other's annual meetings, and organising exchanges related to TLI achievements useful to TLII. The degree of adoption by the TLII breeding community will be the ultimate measure of success.

VI. Organisational Capacity and Management Plan

GCP was founded as a time-bound programme to establish a global network of agricultural research institutions to create public goods from plant genetic diversity and the advanced tools of genomics science for use in plant breeding programmes. GCP's main functions are to solicit, design and support collaborative research projects and capacity-building activities under GCP's five themes toward products for enhancing public plant breeding programmes.

GCP is headquartered at the International Maize and Wheat Improvement Center (CIMMYT) in Texcoco, Mexico. The GCP Consortium consists of 22 public research institutions around the world, including nine CGIAR centers, four advanced research institutes, and nine national agricultural research systems of developed and developing countries. All GCP projects are collaborative efforts, and most involve multiple partnerships within and beyond the GCP Consortium. At present, GCP collaborates actively with more than 130 Institutions around the world. GCP's average yearly income over the last three years has been around US\$ 15 million. The largest donors are the UK's Department for International Development (DFID), the European Commission, The World Bank and the Bill & Melinda Gates Foundation. Other donors include the Swedish International Development Cooperation Agency (Sida), the Swiss Agency for Development and Cooperation (SDC), Pioneer-Hi Bred International and the Syngenta Foundation for Sustainable Agriculture.

As the primary applicant, GCP, will ensure overall management and implementation of the project. GCP's Subprogramme 5 will oversee project coordination and other SPLs will be involved in project management as described in the previous sections (4 and 7). This project will follow established GCP policies for project reporting and review. GCP will subcontract advanced research institutes, CG Centers and national programmes to collaborate and lead most of the research activities. For this project, the principal investigating institutions are: the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) [Objectives 1, 4 and Objective 5 Activities 1 and 2]; the University of California–Riverside, USA and the International Institute for Tropical Agriculture (IITA) (Objective 2); the International Center for Tropical Agriculture (CIAT) [Objective 3]; and the Generation Challenge Programme (Objective 5). More details regarding Project Investigators, Activity Leaders, and proposed key collaborators are in Appendix G, Appendix E, and Annex 7 and 8.

The TLI Phase II proposal aligns well with the changes GCP itself has undertaken in its Phase II (2009–2013). On one hand, there is a more focused research agenda, building on achievements and tangible outputs obtained in TLI Phase I, and emphasising the application of modern breeding tools and technologies for food security crops. At the same time, TLI will pay particular attention to the distribution channels of products. To better address this issue, in mid 2009, GCP recruited a full-time Product Delivery Leader (PDL) with experience in the private sector. And because the GCP's Molecular Breeding Platform is a project that actively promotes advanced breeding in the public sector, highlighting the needs of public institutions in developing countries, embarking on molecular breeding for the legumes with and for the MBP will represent a mutual two-way benefit.

Finally, GCP will provide matching funds at a level of about US\$ 3.6M over the 4 years of the project, out of which US\$ 3M will support research activities in legumes. These activities range from upstream research, (eg, understanding of basal root architecture and drought tolerance in bean), to more applied activities aiming to transfer drought QTL in chickpea or selecting for flower thrips in cowpea. GCP will also support from its own funds capacity-building activities, including degree training, in all four legumes, and will promote the use of molecular markers by legume breeders in Africa through the Genotyping Services. All these activities will be conducted in harmony with the TLI initiative, which will, in turn, create synergy across all legumes projects involving GCP partners.