LEGUME INNOVATION LAB FOR COLLABORATIVE RESEARCH ON GRAIN LEGUMES

FY 2013 – 2014 WORKPLAN

Project Code and Title: SO1.A5 Genetic improvement of cowpea to overcome biotic stress and drought constraints to grain productivity

Lead U.S. Principal Investigator (PI) and affiliated Lead U.S. University:
Philip A. Roberts, University of California, Riverside, CA 92521

Host Country and U.S. Co-PIs and Institutions:
Issa Drabo & Jean-Baptiste Tignegre, Institut de l'Environment et des Recherches Agricole (INERA), Koudougou and Kamboinse, Burkina Faso
Ibrahim Atokple & Francis Kusi, Savanna Agricultural Research Institute (SARI), Tamale, Ghana
Ndiaga Cisse, Centre National Recherches Agronomie, Bambey, Institut Senegalais de Recherches Agricole (ISRA) & CERAAS, Thies, Senegal
Timothy J. Close, Dept. Botany and Plant Sciences, University of California, Riverside, CA

I. Project Problem Statement and Justification:
The primary project focus is to 1) discover insect tolerance and resistance QTL for cowpea breeding; 2) increase African and US cowpea productivity by improved varieties with resistance to insect stresses, drought tolerance or disease resistance; 3) expand farmer marketing opportunities with improved cowpea varieties with desirable grain characteristics; and 4) provide training and capacity building in modern cowpea breeding. In addressing these primary constraints, the objectives are well aligned with Feed The Future research strategic priorities of 1) crop resistance to heat, drought, salinity and flood; 2) West African Sudano-Sahelian systems with emphasis on insect-resistant cowpea; and 3) grain legume productivity. Our plan includes the FTF focus countries Ghana and Senegal, and also Burkina Faso, which offers regional importance from an agro-ecological perspective for cowpea yield gain in the Sudano-Sahel region. Strategically, these countries represent the primary agro-ecologies underpinning cowpea production in this region.

We will employ genomics and modern breeding methods to improve cowpea for yield limiting constraints. By leveraging genomic resources developed under complementary cowpea genomics and modern breeding work funded by the CGIAR Generation Challenge Program, we will apply comprehensive modern breeding tools and methods for genetic improvement of cowpea emphasizing insect tolerance and resistance. Insect pests are seen as a major regional constraint to cowpea productivity in West Africa. The project team determined in the project planning meeting that significant gain can be made by targeting the major insect threats that occur at early (aphids), mid-flowering and pod-set (flower thrips), and later pod-filling (pod-sucking bugs) stages of the cowpea season. Although discovery work through phenotyping, genetic mapping and QTL identification needs to be done in most cases for these insect pests, some progress on resistance and tolerance donors and initial QTL identity provide good starting points in the project. High throughput SNP genotyping platforms, high density consensus cowpea genetic maps, plus numerous discovered QTL for important biotic stress resistance and abiotic drought tolerance traits are now available through our work. We are completely familiar with these technological advancements and have initial

experience in their application to modern cowpea breeding. We have also been working closely with the CGIAR-GCP Integrated Breeding Platform program development using our cowpea data as a test user case, and will bring these technological advances into the project work. The project breeding programs have a range of early generation populations carrying various target traits, providing valuable starting points for breeding advancement.

Low productivity of agriculture is central to rural and urban poverty in Africa. On-farm cowpea yields in West Africa average 240 kg/ha, even though potential yields are often five to ten times greater. Most of the loss in yield potential is due to drought, poor soil fertility, and insect pests. Cowpea varieties with increased productivity (yield per unit area) without the need for purchased inputs especially benefit poor farmers, many being women who lack access to the most productive lands. By targeting insect tolerance and combining with drought tolerance, we have the opportunity to increase cowpea productivity. Productivity is key to increasing rural incomes and new resources can then be invested in other activities that help boost total family income. Productivity increases also help reduce prices to urban consumers. Sustainable increases in cowpea productivity in Africa and the US can be achieved through development of varieties with resistance to insects, nematodes and pathogens, drought tolerance, and the ability to thrive under of low soil fertility.

To increase marketing options, new cowpea varieties must have features desired by consumers; grain appearance, cooking and processing characteristics are especially important. Large white grains with rough seed-coat are good for direct dry-milling, and can be marketed over a wide area, buffering supply and prices in the region. Regionally adapted cowpea varieties with large white grain and resistance to pests would increase the marketing opportunities of cowpea farmers and traders in both West Africa and the US. Considerable demand exists for large rough brown grain types, especially in the large urban centers and command a premium price. However standard varieties like 'Ife Brown' are susceptible to pests and diseases and require improvement.

II. Planned Project Activities for the Workplan Period (April 1, 2013 – September 30, 2014)

Objective 1: Discover QTL for insect resistance and apply in molecular breeding for target regions in West Africa and the US

Collaborators: Dr. Bao Lam Huynh, UC Riverside, USA
Dr. Clementine Dabire, INERA, Burkina Faso
Dr. Isgouhi Kaloshian, UC Riverside, USA
Dr. Barry Pittendrigh, U Illinois, USA
Dr. Manu Tamo, IITA, Benin
Dr. Christian Fatokun, IITA, Nigeria
Dr. Ousmane Boukar, IITA, Nigeria
Dr. Ibrahima Sarr, ISRA, Senegal
Mr. Joseph Batieno, INERA, Burkina Faso

Approaches and Methods:
Overall approach to sub-objectives: We have developed the necessary tools to exploit molecular breeding for cowpea. We have also worked with the CGIAR-GCP to develop a publicly available integrated breeding platform, essentially a pipeline for conducting marker-based selection from initial crossing to new variety release. Requisite tools developed include genic SNP markers, high density SNP-based genetic maps including consensus maps using African cowpea germplasm for sub-Saharan Africa

relevant breeding use, a high-throughput SNP genotyping platform for cowpea, with conversion to a format provided through an outsource genotyping service, QTL for many major biotic and abiotic stress resistance and tolerance traits (drought, heat, fungal, bacterial and viral diseases, some insects, nematodes, Striga), and accompanying software programs. These tools, documented in the Technical Application, enable selection of multiple traits simultaneously across the genome (rather than single marker-trait selection). We will apply these technologies to existing and new breeding populations, for both QTL discovery and breeding.

Breeding targets will be to develop and release varieties that have preferred large white grain type for both domestic and export markets, and rough brown types primarily for domestic markets. The primary traits for grain yield enhancement include QTL for tolerance or resistance to three target insect pests. We have already identified a series of QTL controlling biotic and abiotic stresses. We will select parent combinations and generate breeding populations from their crosses which will enable selection for progeny carrying combinations of the insect tolerance with the other traits (specifically drought tolerance, nematode, Striga and Macrophomina resistance and also some virus resistance). In California, QTL for resistance to Fusarium wilt (*Fot3-1, Fot4-1, Fot4-2*) and root-knot nematodes (*Rk, Rk2, Rkn*) will be bred in backgrounds with Lygus bug tolerance, targeting the primary biotic stress constraints to yield.

Three sub-objectives focus on aphid resistance (Obj. 1.1), flower thrips resistance (Obj. 1.2), and pod-sucking bug resistance (Obj. 1.3). Each of these foci has the same goal, to discover and validate QTL underlying the target insect tolerance/resistance traits, then to apply the QTL knowledge to breeding population development and advancement, leading to enhanced yield performance cowpea varieties.

Genotyping approach: We will apply the KASP SNP platform that we developed with the GCP IBP and LGC KBioscience for SNP genotyping both in the QTL discovery phase and for breeding. The platform has 1022 mapped SNPs providing excellent coverage across the cowpea genome. For cost efficiency, on a cost per data-point basis we can choose the number of SNPs to be tested on the number of genotypes needed for each QTL discovery population or breeding decision. We will genotype all parent and control genotypes with the full set of SNPs. Then we will select the polymorphic SNPs for a desired pair of parents and genotype the progenies (individuals or bulked families) with the polymorphic subset of SNPs. This approach can be used for genotyping RIL populations or F2:3 families for QTL mapping purposes, or for backcross populations to select the appropriate individuals (BC1F1 or BC2F1, etc.) carrying positive alleles for making the next backcross. We will employ this genotyping approach in the workplan period. The NARS breeders will grow plants in the host country, where take leaf punches at the young plant stage, place in 96-well plates, dehydrate with silica gel and then express ship to LGC KBioscience in the UK or USA. The data will be returned within a 4-week turnaround, analyzed and jointly interpreted for a breeding decision (which plants to use for crossing or to advance) for the QTL discovery or breeding advancement. Iterative rounds of genotyping and periodic phenotyping to validate will be used to foreground select the desired complement of positive QTL. Because of the high density of markers and our ability to choose the cM distance and specifically QTL flanking markers for the population-specific SNP marker subsets (using our in-house ‘SNP selector’ program available at Breedit.org), efficient genetic gain by pyramiding the target traits can be made.

Phenotyping and data handling approach: Phenotyping will be conducted under field, greenhouse and lab conditions (insect screens) will be done at NARS locations using standard test protocols. Phenotypic data analyses will be by standard ANOVA. When drought tolerance is being selected, performance testing under water-

limited conditions will be done at NARS field sites. Sites and protocols will be determined by the target insect pest (see below). We will use the CGIAR GCP Integrated Breeding Platform (IBP) tools for data recording, processing and archiving. The variables will include geographical coordinates and dates of each trial, soil and weather data, persons conducting experiments, trait dictionary language and other parameters set up in the IBP FieldBook (tool for software tablets). This data capture format allows for export into the ICI mapping and Optimas programs for QTL analyses and molecular score selection indices. These tools are now familiar to the project team members in Burkina Faso, Senegal and UC-Riverside from their use in the TL1 project, and we will train the Ghana NARS team members in their use and application.

1.1 Aphid resistance: We will test the genetic relatedness of five sources of cowpea aphid (*Aphis craccivora*) resistance. Field observations in Africa and California indicate differential effects of resistance sources on aphid populations from different cowpea production areas. Cowpea lines IT97K-556-6, KvX295-2-124-99, an IITA wild donor line, UCR01-11-52/SARC1-57-2, and 58-77 representing a set of resistance donor genotypes plus known susceptible control lines will be seed-multiplied by spring 2014. Uniform screens in field locations across all project NARS (Burkina, Ghana, Senegal) and California will be conducted in 2014 in protected and non-protected split plots, with 4-fold replication, using standard resistance assessment scales across all test sites. The uniform test design and coordination planning for the aphid resistance assessment will be developed by the project team during 2013. Additional germplasm lines will be included in the screening sites to search for more sources of resistance. The resistance donors and susceptible controls will be SNP genotyped on the KASP platform, coordinated by UCR. We will engage with Dr. B. Pittendrigh and M. Tamo (Project SO1.B1) in the characterization (molecular fingerprinting) of the aphid isolates representing the different aphid populations at each location. This will be especially valuable if, as expected, aphid biotypes are delineated on the cowpea resistance sources. Samples of aphids will be collected and stored for DNA extraction, with a view to developing a DNA sequence based fingerprint to distinguish the isolates. We will also be advised by Dr. Kaloshian at UCR who has been working on the complete aphid genome sequence.

New segregating populations and some existing ones between aphid resistant and susceptible parents will be used to phenotype screen for QTL discovery. Depending on the source, we are at different stages of QTL mapping. We are finishing a QTL discovery effort for aphid resistance in IT97K-556-6 for which one major and one minor QTL have been identified but which require further phenotypic validation. This validation test will be conducted in California during the summer 2013, using a 4-fold replicated RCBD setup, with aphid damage scores being recorded one month after planting and again at post-flowering stage. In the wild donor IITA line a RIL population has been developed for mapping QTL but will require phenotyping and genotyping. This work is being planned in collaboration with Dr. Fatokun at IITA, Nigeria under the TL1 project, but the results will directly impact the LIL breeding decisions. The QTL will be included in foreground selection in the breeding populations, with a plan to target effective resistance sources within a given NARS region (i.e., match effective resistance with preferred and adapted cowpea types the relevant production area.

Crosses of the aphid resistant line UCR01-11-52/SARC1-57-2 with drought tolerance donors will be made in Ghana followed by the first backcross, and the BC1F1 will be SNP genotyped to select individuals for the second backcross.

1.2 Flower thrips resistance: In recent work on QTL discovery, we identified and SNP-mapped loci (*Cft-1* and *Cft-2*) for flower thrips (*Megalurothrips sjostedti*) tolerance

donated by Sanzi in the cross Sanzi x Vita 7, and these loci are promising for introduction and selection in breeding progenies but require better definition through phenotyping. Additional sources of thrips tolerance are 58-77 (biparental RIL population from 58-77 x Yacine is available) and Tvx3236. In Senegal and Ghana both RIL populations will be field-phenotyped for tolerance to flower Thrips using the Jackai and Singh (1988) tolerance scale, at sites in Bambey, Njouro and Tamale during the workplan period. Additional germplasm lines will be included in the screening sites to search for more sources of resistance. Screens will be designed as a 4-replication RCBD and include the parents, and run by entomologists Ibrahima Sarr (Senegal) and Francis Kusi (Ghana). In Senegal the different tolerance sources in Sanzi, 58-77 and Tvx3236 will be intercrossed in all combinations by Dr. Cisse. In Ghana, three Sanzi-derived F3 populations segregating for seed color (including white) and flower thrips resistance are available for QTL discovery and breeding. One parent is IT97K-499-35, now the popular Ghana variety 'Songotra', a high yielding black-eye resistant to Striga but thrips sensitive which can be improved for thrips tolerance via the F3 population. The SARI team will phenotype the three F3 populations for thrips tolerance in the workplan main season using the previously described experimental protocols. The parents of these populations will be SNP-genotyped by UCR to set up marker-based progeny selections.

1.3 Pod-sucking bug resistance: The Heteropteran Coreid pod-sucking bugs (*Clavigralla tomentosicollis* complex) are a major yield suppressor in Burkina Faso, Ghana and neighboring countries. We have not yet identified genes or QTL for resistance to pod-sucking bugs but resistant cowpea accessions are available. We plan to use biparental resistant x susceptible segregating populations to map QTL and initiate their selection as a new breeding target. This work will be a focus of effort in Burkina Faso. A primary tolerance source is IT86D-716 (used in Burkina Faso); pods (maternal, F3) on F3 plants will be genotyped and phenotyped to identify the underlying QTL, using standard screens of young pods in petri dishes to score bug viability and fecundity. We will also include other potential tolerance donor lines in the initial phenotyping screens, including those in the pedigree of resistance donor IT86D-716, to broaden the knowledge base and potentially identify additional sources of tolerance. Two existing F2 populations generated from resistance donor IT86D-716 with parents Kvx771-10 and IT98K-205-8 will enable combining Striga resistance with pod-sucking bug tolerance. UCR will have the parents genotyped through KBioscience and the F2 and F3 populations will be phenotyped for pod bug resistance in Burkina Faso, in collaboration with Dr. Dabire. The F2 will be advanced to F3 early in the workplan period to provide screening resources. UCR will have the F2 and F3 populations genotyped using leaf samples collected from phenotyped plants in Burkina Faso. We will genotype single F2 plants and F3 family bulks consisting of a minimum of 12 individual plants. The phenotype and genotype data from the F2 and F3 generations will be used for QTL discovery with the ICI Mapping program, which will be conducted at UCR.

For the three insect groups (aphids, thrips, pod bugs), we will collaborate with Dr. Pittendrigh and Dr. Tamo (Project SO1.B1) to utilize our project trial sites to collect insect samples for use in molecular characterization of the insect populations.

Objective 2: Complete release and validation of advanced cowpea lines developed under the Pulse CRSP in Burkina Faso, Senegal, and US.

Collaborators: Dr. Bao Lam Huynh, UC Riverside, USA
Dr. G. McClaren, CGIAR GCP IBP

Dr. Ousmane Boukar, IITA, Nigeria
Dr. TJ Higgins, CSIRO, Canberra, Australia
Dr. Samba Thiaw, ISRA, Senegal
Dr. Mywish Maredia, Michigan State U., USA

Approaches and Methods:

2.1. A first component of this objective is to use our genotyping capability to tag the BT gene insertion for Muruca resistance with our SNP marker panel, in order to track the gene in segregating progeny in breeding populations in Burkina Faso and Ghana. We will use the insert flanking sequence information to identify the insert region and its genomic location in the genetic map. The accuracy of marking the gene with higher density flanking markers or a perfect (gene) marker scored as presence absence will be done in conjunction with the new SNP development for increased capacity in the proposed 20,000-SNP panel under other USAID funding. However, for the current work, we will use a Bt-segregating cowpea population (to be chosen in 2013) which will be field-phenotyped in Burkina Faso and genotyped with our current SNP platform of 1022 mapped SNPs. PCR will be conducted to test for gene expression. These data will be used in ICI mapping to confirm the location of nearby markers to the Bt insert on the genetic map. The phenotyping trial will be done in 4-fold replicated design in a Maruca hot-spot location in the central Burkina Faso cowpea production area (Kamboinse). Maruca damage to pods and grain yield estimates will be used to index resistance and susceptibility to pod borer damage. The Burkina Faso team has good experience with making these evaluations. The genotyping will mostly follow the same protocol as outlined under the Objective 1 work. We will use leaf samples from young field grown plants in the phenotyping plots for DNA extraction in Burkina Faso. Following shipping to KBioscience, the DNA samples will be SNP assayed and the genotype data sent to UCR for quality checking. The combined phenotype and genotype data will be analyzed for trait mapping using the ICI mapping software for QTL discovery. This should validate SNP markers flanking the Bt-insert locus, thereby enabling genotyping in the future generations to select for the Bt-insert without the need to phenotype at each generation. Depending on the quality of the phenotyping data (insect pressure sometimes variable), a second season of phenotyping may be required in main season 2015.

2.2. We plan to capitalize on the previous Pulse CRSP breeding effort by completing the release requirements of several advanced breeding lines that are in the final stages of performance testing in Burkina Faso, Senegal and California. Specifically, in Senegal there are three large white grain type cowpeas (at least 25 g /100 grains) developed by Dr. Cisse which are in the pre-release phase that could all be released as varieties. These will be grown together with the recently released white seeded CRSP variety in 20 on-farm demonstration trials in main season FY13. Combined with performance data from 2011 and 2012, this should complete the performance data required for the formal release. The demonstration trials will be conducted in the northern cowpea zone (Louga, Mekhe, Thilmakha), with plot size sufficiently large (400 to 500 m^2) to allow mechanical planting. Yield, diseases and insects incidence will be recorded. The performance data will be used to submit the release request documentation during early 2014, with release approval expected by the end of this workplan period. Breeder Seed will be increased during 2014 to supply the Foundation Seed development.

In Burkina Faso, 20 pre-release CRSP advanced lines developed by Dr. Drabo require final rounds of on-farm performance testing. Multi-location tests are needed to support the final selections for release. These trials will be completed during the 2013-2014 seasons located at Saria, Pobe, and Kamboinse in Burkina Faso. The lines will be tested for yield and grain quality, plus any disease susceptibility in trials using 4-row

plots, 5 m long and 4 reps arranged in a RCBD. Release of the best performing lines is anticipated for the project year 2015.

In California, we will field test advanced blackeye, all-white, and dry-green blackeye breeding lines for release potential. These represent CRSP developed lines and they require at least one to two years of field performance testing. The lines carry a combination of lygus bug tolerance, and root-knot nematode and Fusarium wilt resistance. For two advanced blackeyes, we will conduct on-farm large strip trails in Tulare Co. to assess commercial yield performance. The other lines will be tested at the Kearney and UCR field stations in four-row 4-fold replicated RCBD trials with the center two rows machine harvested. Yield weights, 100-seed weights and lygus damage to seed will be assayed. All yield and performance data will be analyzed by standard ANOVA.

The Senegal and Burkina Faso sites releases will represent tangible project outputs, and offer the opportunity for tracking along the impact pathway as new releases which will be entering the seed multiplication and distribution process in each country. Opportunities exist to initiate baseline data for the releases through the impact analyses under the LIL project led by Dr. M. Maredia.

Objective 3: Increase capacity of NARS in Burkina Faso, Ghana and Senegal to serve the cowpea sector.

Collaborators: Dr. Bao Lam Huynh, UC Riverside
Dr. G. McClaren, CGIAR GCP IBP
Dr Ousmane Boukar, IITA, Nigeria

Approaches and Methods:
Short-term Training: Molecular breeding for young trainee breeders and NARS scientists will be conducted. Continuous short-term training will occur through iterative data analysis and interpretation cycles using the phenotyping and genotyping data generated by each of the three Host Country partner teams (about 12 participants). To provide periodic intensive training, we will convene a training workshop in each project year, using training modules developed by the UC-R team, plus those developed by the CGIAR GCP Integrated Breeding Platform program (IBP) which is using our tropical legumes project cowpea breeding population data for the training modules development. We will plan a training workshop in conjunction with the Legume Innovation Lab Global planning meeting to be held in May 2014, and(or) earlier at UCR in conjunction with a possible GCP-TL1 training workshop. Where feasible, we will coordinate the cowpea modern breeding short-term training with the bean breeders in the Legume Innovation Lab Andean and Middle American bean breeding projects. The molecular breeding approach is complex and requires a combination of hands-on experience with self-generated data sets, augmented with periodic intensive training workshops to improve knowledge, skills and problem –solving. The technologies underlying the genotyping capability are in a state of frequent enhancement and upgrade, requiring periodic training input. Thus both young breeder trainees new to the programs and experienced breeders from the HC NARS are in need of this training. Training materials and protocols will also be used by the NARS breeders to train the technical staff in the NARS programs after NARS breeders have been trained further on the standardized electronic fieldbook, leaf assay, and field phenotyping protocols.

Degree Training: We plan to conduct degree training for two graduate students in the workplan period:

1. Arsenio Ndeve, Mozambique, male student in PhD Plant pathology program at UC Riverside, working in pathology, genetics and breeding of SE African cowpea germplasm
2. Sassoum Lo, Senegal, female student in MS Plant genetics program at UC Riverside, working in cowpea genomics and breeding

III. Contribution of Project to USAID Feed the Future Performance Indicators:

Please see the attached completed "Performance Indicators – Targets" form for FY 2013, 2014 and 2015.

IV. Outputs:

Under Objective 1.1 -- Aphid resistance
A differential cowpea panel of aphid resistance sources and control lines seed-multiplied for multi-location field screening (Project team).
A uniform test protocol designed for aphid biotype screening (Project team).
Set of F1s made from aphid resistant x drought tolerant line crosses (Ghana).
A set of first BC1 progenies will be made from the aphid x drought F1s (Ghana).
Genotyping data generated for aphid resistant parents and BC1F1s (UCR).

Under Objective 1.2 -- Thrips resistance
Two RIL populations will be phenotyped for QTL refinement in Senegal and Ghana.
F1s will be generated from thrips resistance sources intercrosses (Senegal).
Data from phenotyping 3 F3 populations with Sanzi donor parent (Ghana).
Data generated from genotyping parents of 3 F3 with Sanzi donor (UCR).

Under Objective 1.3 – Pod bug resistance
Data generated from genotyping parents, F2 and F3 populations derived from resistance donor IT86D-716 (UCR).
Two F3 populations developed from existing F2 for pod bug resistance (BF).
Data from phenotyping 2 F3 populations with IT86D-716 donor parent (BF).
Initial QTL from IT86D-716 discovered by ICI Mapping (UCR and BF).

Under Objective 2.1 – SNP markers for Bt tracking
Genotype data produced from one Bt-transgene segregating population (UCR).
Phenotype data produced from one Bt-transgene segregating population (BF).

Under Objective 2.2 – Variety releases
Release of 3 large white-seeded CRSP varieties in Senegal.
20 pre-release CRSP lines evaluated in on-farm trials (BF).
Data from one advanced yield trial of new lines (BF and Senegal).

V. Engagement of USAID Field Mission(s)

During the main cowpea season July-September in 2014, the UC-R PI and Co-PI will make field visits to the three HCs to review and coordinate field based phenotyping activities. During these HC trips, we will arrange to visit the Senegal and the Ghana country missions and also the West Africa regional mission in Accra. The mission visits will be made together with the respective Host Country PI and Co-PI plus senior NARS

administrators where feasible, and will be used to inform the mission staff of our LIL cowpea modern breeding project goals and activities in each country and in the region. In Burkina Faso, we will connect with the mission representation from Niger to inform them of our activities, and as we have done in the past, with US Consulate leaders in Ougadougou. The UC-R team will also assist the NARS PIs in developing project activity briefs for them to share directly with the US Mission staff to keep them informed and to solicit possible Mission buy-ins.

VI. Partnering and Networking Activities: We will work closely with other national and international cowpea breeders, including Drs. Ousmane Boukar and Christian Fatokun, Senior Scientists and Cowpea Breeders at IITA, Dr. Mohammed Ishiyaku of the IAR in Nigeria, and Dr. Rogerio Chiulele, Eduardo Mondlane University, Maputo, in Mozambique. We will continue to work with national extension services, World Vision International, World Bank and other NGOs to extend new cowpea technologies. Specifically in the Host Countries for this project, we will network with NGOs and farmers' cooperatives in Burkina Faso, Senegal, and Ghana. Although we do not have a formal seed systems objective in the project, the new cowpea varieties developed by the project will be fed into the NARS coordinated seed systems structure in each country. New varieties will be assured of entry and promotion in the seed systems. Exciting events are occurring to aid in this realization for seed multiplication and distribution to farmers. In Senegal, HC PI N. Cisse is working with World Bank on its new $80M commitment to the cowpea seed system, while CORAF and AGRA with Foundation support are working to advance the seed systems in Burkina Faso, Ghana and neighboring countries. HC PIs I. Drabo and I. Atokple are involved in these efforts and can promote the introduction of the new CRSP and LIL cowpea varieties. This will be especially important in the Objective 2 activities through which CRSP variety releases are planned for 2014 in Senegal and 2015 in Burkina Faso.

VII. Leveraging of CRSP Resources: Other resources leveraged from current and future funded complementary cowpea research projects include the following:

California Dry Bean Advisory Board and its Blackeye Varietal Council (funds currently and typically set at $20,000 per year) funded for cowpea breeding in California. This is a continuing, long term research arrangement in support of the UC Riverside cowpea breeding program.

The CGIAR Generation Challenge Program (GCP) Tropical Legumes I Project Phase 2 extension was funded for 4 years (May 2010-April 2014). The cowpea component of this project is lead by UC Riverside (Roberts, and Close) and includes collaborative funded cowpea breeding and research with the cowpea breeding programs in Burkina Faso (with PI I. Drabo), Mozambique (PI R. Chiulele) and Senegal (PI N. Cisse), and IITA (PI, O. Boukar). This project funded at $2.729M is applying cowpea genomic resources based on SNP genotyping for cowpea marker-assisted breeding. Use of the high throughput marker platform for major traits including insect pest, nematode and disease resistance, and drought and heat tolerance are being targeted in African breeding populations. This project provides an excellent leveraging for CRSP activities described here to be used for cowpea modern breeding. The project also links us to the GCP-Integrated Breeding Platform project which is developing a breeder's workflow system, which we will bring into the LIL project activities for data collection, analysis, interpretation and curation.

The project team plus Dr. O Boukar, IITA, Nigeria, have a proposal pending to the

USAID Climate Resilient legumes program. We are optimistic of funding approval, with a final decision likely by September 2013. This project would enable development of new cowpea genomic resources, particularly a 20,000-SNP Infinium genotyping platform, which would be developed by late 2014. We will plan to leverage this advancement by applying it to our LIL project genotyping needs, thereby enhancing the quality and efficiency of the genotyping component.

The LIL funds proposed herein will also be leveraged with opportunity funds within the Host Countries via NGOs and national sources through presentation of the LIL effort and the associated opportunities for participatory funding.

The Kirkhouse Trust is supporting a project under Dr. Cisse at ISRA on molecular breeding for Striga resistance for 3 years (July 2012 – June 2015) for $ 90,000.

VIII. Timeline for Achievement of Milestones of Technical Progress:

Please see completed "Milestones for Technical Progress" form for the workplan period.

Training/Capacity Building Workplan for FY 2013 – 2014

Degree Training:

First and Other Given Names: Sassoum
Last Name: Lo
Citizenship: Senegal
Gender: Female
Training Institution: UC Riverside
Supervising CRSP PI: Roberts and Close, UC-R
Degree Program for training: MS/PhD
Program Areas or Discipline: Cowpea genomics and breeding
If enrolled at a US university, will Trainee be a “Participant Trainee” as defined by USAID: Yes
Host Country Institution to Benefit from Training: Senegal
Thesis Title/Research Area: Cowpea molecular breeding
Start Date: 01/2014
Projected Completion Date: 12/2015
Training status: Pending
Type of CRSP Support: partial

Degree Training:

First and Other Given Names: Arsenio
Last Name: Ndeve
Citizenship: Mozambique
Gender: Male
Training Institution: UC Riverside
Supervising CRSP PI Roberts and Close, UC-R
Degree Program for training: PhD
Program Areas or Discipline: Plant Pathology, genetics and breeding
If enrolled at a US university, will Trainee be a “Participant Trainee” as defined by USAID: Yes
Host Country Institution to Benefit from Training: Mozambique
Thesis Title/Research Area: Genomewide selection for disease and drought tolerance in SE African cowpeas

Start Date: 01/2012
Projected Completion Date: 06/2016
Training status: Active
Type of CRSP Support: partial

Short-term Training:

Type of training: Molecular breeding for young trainee breeders and NARS scientists
Description of training activity: As described under capacity building Objective 3, continuous short-term training will occur through iterative data analysis and interpretation cycles using the phenotyping and genotyping data generated by each Host Country partner team. To provide periodic intensive training, we will convene a training workshop in each project year, using training modules developed by the UC-R team, or developed by the CGIAR GCP Integrated Breeding Platform program (IBP) which is using our tropical legumes project cowpea breeding population data for the training modules. We will plan the first of these training workshops to coincide with the Legume Innovation Lab Global planning meeting to be held in May 2014.
Location: TBD, linked to LIL Global meeting
Duration 3 days
When will it occur? May 2014
Participants/Beneficiaries of Training Activity
Anticipated numbers of Beneficiaries (male and female): 12 (8 male, 4 female)
PI/Collaborator responsible for this training activity: Dr. Bao Lam Huynh, UC-R
List other funding sources that will be sought (if any): Training funds through CGIAR-GCP Tropical Legumes I project and possibly USAID Climate Resilient Legumes project (if funded).
Training justification: The molecular breeding approach is complex and requires a combination of hands-on experience with self-generated data sets, augmented with periodic intensive training workshops to improve knowledge, skills and problem –solving. The technologies underlying the genotyping capability are in a state of frequent enhancement and upgrade, requiring periodic training input. Thus both young breeder trainees new to the programs and experienced breeders from the HC NARS are in need of this training.

Equipment (costing >$5,000)**:** None requested during this period.

Specific Type of Equipment to be purchased
Justification for equipment to achieve workplan objectives
Institution to benefit from equipment
Institution to purchase equipment
Amount budgeted for equipment item