

Tropical Legumes I mid-year progress summary 2007

The Tropical Legumes I project started on May 1st, 2007. To avoid missing one planting season, some project partners started activities prior to the official starting date. Other activities started in May.

A summary of activities for each of the Objectives during the first six months follows:

Objective 1: During the initial few months of the project, the reference set of ~300 accessions was identified using phenotypic and molecular information from previously funded GCP projects. These will be combined with local varieties for evaluation under field conditions for abiotic and biotic stresses to serve as baselines for improved trait phenotypes. New genomic resources are being developed from the SSR-enriched libraries and BAC-end sequencing. The AA and BB genome linkage maps were enhanced to include new molecular markers and the populations advanced towards RIL status. Mapping populations were identified for located QTLs for drought tolerance and resistance to GRD, rust, ELS and LLS. Finally, a set of farmer and consumer preferred varieties were identified in each target country and will be the basis for MABC and MARS to incorporate improved traits. In conclusion, materials were identified and the crop cycles in each country determined for the evaluation of drought and disease screenings.

Objective 2: This project has completed 2 of the 15 project milestones on or before the projected completion date, exceeding the initial numerical targets in both cases. These milestones include a 17x coverage BAC library (initially promised 14X) composed of a total of 73,728 clones (actually two libraries with 36,864 each, while initially promised 70,000) and 9 cDNA libraries (initially 6). For cDNA libraries, the additional cowpea genotypes (3) are expected to more fully capture the genetic variability in cowpea germplasm than would the smaller sample. Leaf samples from 600 genotypes (out of the 1440 expected in the future) were already collected for future SNP genotyping in this project. Germplasm has been multiplied at UC Riverside (Activity 1) for use in Activities 2-5 as follows: 320 accessions of 374 from the IITA/GCP cowpea core collection, 70 genotypes from the CRSP Core Collection and 600 recombinant inbred lines (RILs) from 6 RIL 'sets'. As for phenotyping, two RIL populations were phenotyped for resistance to two races of Fusarium wilt at UC Riverside; two RIL populations are being phenotyped for resistance to flower thrips at Niore and Bambey, Senegal and one RIL set for resistance to flower thrips and bacterial blight is phenotyped in Cameroon. Trials for drought phenotyping of almost 500 accessions have been planted by UC Riverside in Coachella, CA, by IITA at Kano, Nigeria, by INERA at Pobe and Kamboinse, Burkina Faso and by ISRA at Louga and Bambey, Senegal. Additional funding for activities has been sought for activities to establish a partnership with Mozambique and for MARS breeding.

Objective 3: In the first activity, seed was multiplied from a reference collection of common bean diversity for use in drought trials in CIAT and with ECABREN/SABRN partners. In addition, six new recombinant inbred line populations are being developed. In the second activity, for the development of genomic resources, DREB gene markers have been mapped and primer design initiated for BAC end microsatellites along with testing of amplification for cDNA and small insert based microsatellite markers. In the third activity, genetic crosses have been made for future marker assisted selection of arcelin, CBB and BCMNV resistance; while in the fourth activity seed

of QTL mapping populations has been multiplied for testing at ECABREN/SABRN sites along with phenotypic evaluation of deep rooting in greenhouse experiments. In the fifth activity, inter-gene pool populations have advanced in Zimbabwe and CIAT. Conclusions for this initial stage of the project are that i) recombinant inbred line population and marker development are underway in activities 1 and 2, respectively ii) F1 crosses have been made for activity 3 with the appropriate resistance gene sources for marker-aided gamete selection; iii) seed has been multiplied for reference collection and QTL studies in activities 1 and 4, respectively and iv) selections have been advanced for inter gene-pool crosses developed for activity 5.

Objective 4: During the initial few months of the project, the reference set of ~300 accessions was identified using phenotypic and molecular information from previously funded GCP projects. These will be combined with local varieties for evaluation under field conditions for abiotic and biotic stresses to serve as baselines for improved trait phenotypes. New genomic resources are being developed from the SSR-enriched libraries and BAC-end sequencing. Mapping populations are being phenotyped and genotyped to identify QTLs for drought tolerance and resistance to pod borers. A set of farmer and consumer preferred varieties were identified in each target country to become the basis for MABC and MARS to incorporate improved traits.

Objective 5: Research activities have focused primarily on the development of tools for the isolation of orthologous genes from the target legume species, under activity 1, and the identification of simple sequence repeat markers in groundnut, under activity 2. In Activity 1, bioinformatic tools for the identification of orthologous genes and design of oligonucleotide primers for PCR amplification and sequence analysis were developed. Our initial work has focused on the analysis of 2,880 amplicons, representing 1,545 transcript clusters. Cross-species amplification success rates were typically greater than 83% and sequencing success rates in the range of 75%, with between 800 and 1,000 orthologous amplicons obtained from each species. Based on interactions with Objectives 1-4, parental lines from mapping populations of chickpea, cowpea, common bean and diploid groundnut were selected and tested. In activity 2, a pilot scale analysis of 7500 BAC end sequences from the diploid AA groundnut BAC library revealed an abundance of repetitive elements. In spite of the challenges that this situation presents, the analysis yielded 160 SSRs that will be tested for polymorphism in both diploid and tetraploid germplasm. Also, with the goal of identifying ultra-long SSRs, genome libraries enriched for SSR motifs were constructed. 192 are currently being sequenced to evaluate the quality of these libraries. Progress in the first 4 months of the project is on track or ahead of schedule.

Objective 6: During the reporting period, activities of Objective 6 involved the organization of the kick-off meeting of the project (Safari Lodge at Rustenburg Kloof -South Africa) from 18th-22nd of September; development of delivery plans and the identification of technical and infrastructural needs of the project partners. In relation to TLII, discussions and information exchanges took place and a summary made describing the agreement reached in the following subjects: 1) focal points for germplasm issues, phenotyping, training/degree students, TLI meeting in 2008, TLII meeting, TLI teleconferences, TL webpage, common TLI-TLII press release mid-October 2007. The next months of Objective 6 will involve the fulfilment of technical and infrastructural needs of African project partners, in close collaboration with the PI of Objectives 1-4. Together with this a training course will take place on drought phenotyping for legumes, commissioned by the GCP to ICRISAT, and which is planned for the first quarter of 2008 with the attendance of the majority of African partners.

