

Tropical Legume I: Objective 2
**Improve cowpea productivity for marginal environments
in Sub-Saharan Africa**

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Progress by Objective 2 Activity and Milestone (Activity leadership in parenthesis)

Activity 1. Characterize diversity and develop germplasm for genetic studies. Milestone 1. Seed of 4 RIL populations multiplied for Activities 3 and 4 (UCR). Seed of 10 RIL populations were multiplied in greenhouses at UCR during the first project year, far exceeding the stated goal of multiplying 4 RIL sets. ***Milestone 2. 500 genotypes characterized for drought tolerance, drought germplasm identified.*** Rainy season drought phenotyping evaluations were conducted at two drought-prone sites in Burkina Faso and one in Senegal, and in irrigated 'off-season' experiments in California, Senegal, Burkina Faso and IITA-Kano. Six genotypes were identified that showed drought tolerance over multiple environments.

Activity 2: Generate genomic resources for genetic studies and breeding. Milestone 3. 14X coverage BAC library produced, 70,000 clones (UCR, UCD). Two BAC libraries were produced (*HindIII* and *MboI*) totaling 17x genome coverage (73,728 clones, ~140 kb average insert size). ***Milestone 4. 6 cDNA libraries produced, 200,000 ESTs (UCR).*** 9 cDNA libraries were produced for sequencing at the Joint Genome Institute (JGI). An initial assessment of SNP yield conducted on 384 clones from each library showed that five libraries were most relevant to African breeding programs and TL I objectives. EST sequencing was completed on these five libraries. IITA contributed 42,000 cowpea ESTs from four additional African genotypes. More than 10,000 high confidence SNPs were discovered and a subset of 1536 SNPs were chosen for the Illumina GoldenGate assay ***Milestone 5. 1000 SNP markers on map, 1440 genotypes scored (UCR).*** Design of the Illumina GoldenGate assay for 1536 cowpea SNPs was completed in June 2008 and arrival in August 2008 is expected. We increased the target number of genotypes from 1440 to 1632 DNA to accommodate additional RILs and

accessions. DNA extractions have been completed on ~1400 cowpea leaf tissue samples (~900 RILs and ~500 accessions). **Milestone 6. BAC fingerprinting and assembly of physical map (UCR, UCD).** The planned 60,000 BAC fingerprints of IT97K-499-35 have been completed, accomplishing a final depth of coverage of ~10x. **Milestone 7. BAC-end sequencing and linkage to reference genomes and maps (UCD).** The planned 30,000 BAC-end sequencing reactions from the IT97K-499-35 library have been completed; among them 4167 contain at least one SSR. Overall, our vision of nearby marker development through a complete physical map and BAC-end sequences (including SSRs) anchored to the physical and SNP-based genetic map is on track for fruition in latter 2008.

Activity 3: Identify molecular markers and genes for biotic stress resistance. Milestone 8. 2 RILs phenotyped for resistance to flower thrips (IITA, IRAD, ISRA). Thrips resistance phenotyping was conducted in Nigeria, Cameroon, and Senegal, with a total of five RIL sets between the three locations. In Senegal, significant differences were observed between the parent lines (Yacine and 58-77) and resistant check line TVx3236, but the frequency of RILs with scores as low as the resistant parent was low and there were no apparent transgressive resistant lines. In Cameroon, differences among RILs and between RIL parental lines were not significant.. **Milestone 9. 2 RILs phenotyped for resistance to pathogens (UCR, IRAD, ISRA).** Two RIL sets, CB46/IT93K-503-1 and CB46/IT97K-499-39 were phenotyped for resistance to bacterial blight, viruses, flowering and maturity dates in Cameroon. Two RIL sets, CB46/IT93K-503-1 and CB27/24-125B were phenotyped for Fusarium wilt resistance in California. These two RIL sets are also being phenotyped for root-knot nematode resistance during spring-summer 2008 in replicated plots on infested field sites in California. **Milestone 10. Molecular markers associated with resistance to biotic stresses (UCR).** No progress was anticipated until Year 2.

Activity 4: Identify molecular markers and genes for drought tolerance. Milestone 11. RILs Phenotyped for drought tolerance (UCR, IITA, INERA, ISRA). Phenotyping of RIL sets for drought tolerance were conducted in Burkina Faso, California and Senegal. In California and Burkina Faso, significant yield differences were observed among the RILs regardless of maturity classes and transgressive RILs were identified. In Senegal RIL Mouride/Bambey 21 and RIL CB46/IT93K-503-1 were phenotyped for drought tolerance, and transgressive drought tolerant RILs identified. **Milestone 12. Molecular markers associated with drought tolerance (UCR).** No progress was anticipated until Year 2.

Activity 5: Enhance locally adapted germplasm with target traits. Milestone 13. Targeted SNPs converted to easy-to-use markers (IITA). Methods to convert known SNPs into easy-to-use markers are being developed, including exploring neighboring intergenic regions which may be easier to convert. **Milestone 14. Breeding populations developed with thrips resistance and drought tolerance (UCR).** Fifteen crosses were made at UCR between several cowpea lines likely to possess drought tolerance and that have good agronomic performance. The F₁'s of these crosses were planted and F₂ seed produced by July 2008. **Milestone 15. Easy-to-use markers validated for targeted traits (IITA).** No progress was anticipated until Year 2.