# Cowpea High-Throughput SNP Genotyping, 1,000-SNP Genetic Map and Complete Physical Map

## Tropical Legumes 1, Objective 2 (Cowpea Activity 2, Genomic Resources)


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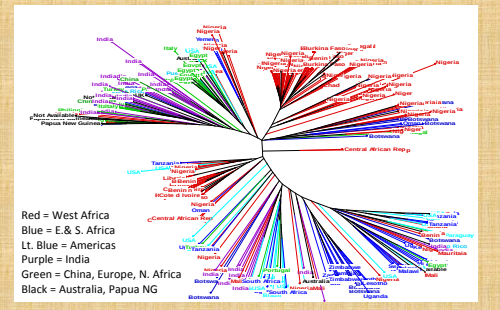
## Modern Breeding for Sub-Saharan Africa

Marker Assisted Recurrent Selection
Marker Assisted Backcrossing
Genome Wide Selection

Examples of genotype responses to drought (left) and Macrophomina (right) in field plots.

## Germplasm Diversity

Geographic representation of GCP/IITA Mini-core 370 reference set based on Neighbor Joining Analysis using DARwin




# Genomic Resources

## SNP Genotyping

1536 SNPs using Illumina GoldenGate Assay
640 accessions genotyped
7 RIL populations genotyped
Minimal tiling path BACs genotyped

## Sequence Collection

183,000 ESTs
30,000 BAC end sequences
30,000 SSRs and 10,000 high quality SNPs available

## Genetic Map

Consensus map based on 7 RIL populations
1,018 mapped SNPs
Density - 1 SNP per 0.7 cM

| Population | # RILs | SNPs | Abiotic and biotic traits |
|---|---|---|---|
| IT93K-503-1 x CB46 | 128 | 445 | Drought, Macrophomina, Fusarium |
| 524B x IT84S-2049 | 92 | 475 | Multiple traits including nematodes |
| CB27 x 24-125B-1 | 105 | 383 | CAbMV, bacterial blight |
| Yacine x 58-77 | 145 | 479 | Flower thrips |
| TVu14676 x IT84S-2246-4 | 154 | 436 | Multiple traits including insects |
| Danila x TVu7778 | 117 | 445 | Drought |
| Sanzi x Vita7 | 131 | 402 | Flower thrips |

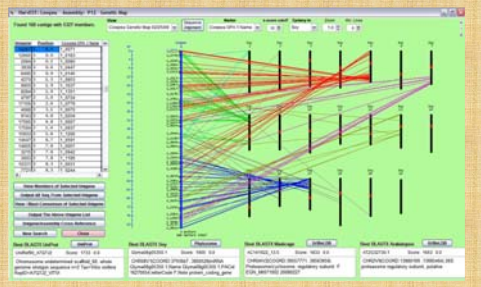
## Physical Map

African breeding line IT97K-499-35
11x genome coverage
41,182 BACs in whole-genome assembly containing 790 contigs
Physical map anchored to genetic map using SNPs in minimal tiling path
http://phymap.ucdavis.edu/cowpea

## Reference Genome Synteny:

### Soybean, Medicago and Arabidopsis

HarvEST: Cowpea displaying syntenic relationship of cowpea to soybean.
(www.harvest-web.org http://harvest.ucr.edu)



## Candidate Gene Analysis

QTL analysis
Association Mapping
Map-based positional cloning (BACs)

Visualization of genotypes at two QTL using Flapjack software.