

# **TLI-Objective 1: Improve groundnut productivity in marginal environments of sub-Saharan Africa**

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## **Principal Investigator:**

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## **Collaborating Institution(s) and Scientist(s):**

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## **B) Abstract text**

### **Context:**

Groundnut (peanut, *Arachis hypogaea* L.) is an important food and cash crop in Africa. In most countries, the crop is grown by smallholder farmers under very low input and rainfed drought-prone conditions. Lack of seed of improved varieties, poor agronomic practices, drought, diseases, and pests are the major factors limiting yield. The goal of the project's objective is to improve the disease and drought tolerance in farmer-preferred groundnut varieties using modern molecular tools, and involving African NARS. For this purpose major efforts in the following areas are needed: (1) screen a large set of representative germplasm to identify the best source of tolerance to drought and resistance to diseases for their use in breeding; (2) the development of the molecular tools, still dramatically lacking, to speed up the introgression of tolerance and resistance characteristics into farmer-preferred varieties; (3) and (4) apply the tools developed in (2) to determine the genes involved in disease resistance and drought tolerance; and (5) introgress resistance/tolerance into farmer varieties.

### **Findings and implications:**

Analysis of the molecular diversity data from a GCP-funded project with existing phenotypic data allowed the identification of a reference set of approximately 300 accessions that contain the majority of the diversity in the collection. Seed of the original plant that was genotyped has been multiplied in Year 1 for field and trait screening in Year 2.

First map in cultivated groundnut: The first genetic map of cultivated groundnut, from the cross TAG24 x ICGV86031, developed between parents contrasting for transpiration efficiency, has been assembled in the project.

Set up of the lysimetric facility at Patancheru: A large facility has been set up at ICRISAT headquarter in India. The system consists of a set of cylinders (1.2m long, 20 cm dia) filled with natural soil at common bulk density and mimicking a soil profile. Each cylinder is equipped with a collar that allows its lifting. A hanging scale allows regular weighing of the cylinders to measure plant transpiration (after limiting soil evaporation by mulching the soil surface). The system allows assessing water extraction by roots under conditions of imposed water deficit. The results from the evaluation of the reference collection of 300 genotypes has revealed a two-fold range of variation for water extraction, with known check cultivars of groundnut extracting less water than varieties known for their better drought adaptation.

#### Markers development and screening

Two hundred new SSR have been developed. Existing SSR markers have been screen in the parental lines of RIL populations involved in the project (Table)

	Nb of markers	Polymorphic markers	Polymorphic loci	Pop size
ICGV86031 x TAG24	1286	144	150	318
ICGS 44 x ICGS 76	1026	57	46	376
ICGS 76 x CSMG 84-1	633	66	40	277

Efforts are also on-going to develop DArT arrays, one with 14 parents of mapping populations, and one with 45 varied groundnut germplasm, including diploid accessions.

#### Large number of crosses developed

Many crosses have been developed in Year 1 between contrasting parents for disease resistance under activity (5). Also a collection of market- and farmer-preferred varieties has been assembled.

#### **Links:**

Phenotyping workshop at Patancheru: Organized between 3<sup>rd</sup> and 28<sup>th</sup> of March 2008 to train NARS technicians and scientists to phenotyping techniques needed to carry out the tasks of (1) and (4) (GCP-funded project G4008-27). The workshop has been the occasion to know better the African team, assess the strengths and weaknesses.

#### **Next steps and/or challenges:**

Lot of phenotyping is planned for Year 2, within Activities (1), (3) and (4), to explore the germplasm for best sources of resistance/tolerance, and to phenotype existing RIL population for QTL identification. Activity 2 will focus on sequencing the BAC library, expanded to reach about a 10X coverage, linking the genetic and physical map, developing more markers, and finalize the DArT arrays. Populations developed under (5) will be advanced. Farmer preferred varieties will be evaluated to choose the most suitable one for the introgression work.