



Genotyping Groundnut (*Arachis hypogaea*) Composite Collection Using SSR Markers



HD Upadhyaya¹, Ranjana Bhattacharjee¹, D Bertoli², D Hoisington¹, RPS Pundir¹, JFM Valls³, S Chandra¹, S Singh¹, MC Moretzsohn³, S Leal-Bertioli³ and P Guimaraes³

1. International Crops Research Institute for the Semi-Arid Tropics, Patancheru 502 324, AP, India.
2. Universidad Catolica de Brasilia (UCB), Brazil. 3. Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA), Brasília, DF - Brazil.

About groundnut

- Provides high quality edible oil (36–54%) and easily digestible protein (12–36%).
- Important oilseed crop grown in 109 countries on 26.4 million ha.
- Over two-thirds global production occurs in seasonally rainfed regions.
- Africa and Asia produced 94.2% of world groundnut (in shell) in 95.9% of the area.



Diversity for pod and seed characteristics in groundnut germplasm.

Origin and biology of groundnut

- Center of origin is the Chaco region between southern Bolivia and northwestern Argentina.
- Genus *Arachis* comprises 69 species placed in 9 sections, section *Arachis* contains cultivated groundnut.
- *Arachis hypogaea* is a tetraploid (2n=40). Some wild *Arachis* are diploid.
- Highly self-pollinated crop.

Genepool of groundnut

- Primary genepool consist of landraces of *A. hypogaea* and its wild relative, *A. monticola*.
- Secondary genepool consists of diploid species from section *Arachis* that are cross-compatible with *A. hypogaea*.
- Tertiary genepool consists of species from section *Procumbentes* that are weakly cross-compatible with *A. hypogaea*.
- Fourth genepool consists of species from remaining wild *Arachis* species classified into 7 sections.

Major centers holding germplasm

The genebank at ICRISAT in India holds the largest collection (15419 accessions from 93 countries). The other major centers are

- NSSL, Fort Collins, USA;
- USDA, Griffin, USA;
- NCSU, USA;
- Campinas & CENARGIN, Brazil;
- NRCG, Junagadh, India; and
- BORIF, Indonesia.

Development of composite collection

- A composite collection of groundnut was developed based on available phenotypic characterization, evaluation, geographic origin and taxonomic data.
- The composite collection holds 850 accessions from ICRISAT and 150 accessions from EMBRAPA, Brazil.

Selection of SSR markers

- At ICRISAT, 20 SSR markers were initially selected to pre-screen the mini-core accessions from which 10 polymorphic markers were identified.

- Ten SSR markers, each from ICRISAT and EMBRAPA, will be used to fingerprint the composite collection.

Present status of research

- Composite collection of 1000 accessions established, consisting of 184 mini-core (Upadhyaya et al. 2002) and 184 comparator mini-core from core collection (Upadhyaya et al. 2003) accessions, landraces, breeding lines, genetic stocks, and wild *Arachis* accessions.
- Accessions were planted in the field during July 2005 and leaf samples were collected from 15-day old plants for DNA extraction.
- Each day 192 samples were extracted and quantified to a concentration of 5 ng per 0.25 L.
- Genotyping of the composite collection will be done on ABI 3100.
- Data processing and analysis will be completed by December 2005.



Characterization of groundnut germplasm accessions.



Diversity for flower traits in groundnut germplasm.

Future plan

Using genotypic data a representative reference collection of 300 accessions will be selected that will be evaluated for traits associated with drought tolerance and other economic traits. The plant breeders will have access to genotypically diverse accessions to enhance the yield potential of groundnut.

List of 20 SSR markers selected for genotyping of the composite collection

13E09	17E03	18C5	19B1
1B9	2D12B	5D5	7H6
8E12	TC11A04	TC11H06	TC1A02
TC1E01	TC2D06	TC4F12	TC6E01
TC6H03	TC7C06	TC9C12	Xip373

References

- Upadhyaya HD, Bramel PJ, Ortiz R and Sube Singh. 2002. Developing a mini-core of peanut for utilization of genetic resources. *Crop Science* 42:2150–2156.
- Upadhyaya HD, Ortiz R, Bramel PJ and Sube Singh. 2003. Development of a groundnut core collection using taxonomical, geographical and morphological descriptors. *Genetic Resources and Crop Evolution* 50:139–148.