



Genotyping Groundnut Composite Collection

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About Groundnut Crop

- 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 (FAO 2004)
- Over two-thirds global production occurs in seasonally rainfed regions
- Africa and Asia produced 94.2% of world groundnut (in shell) in 95.9% area

Origin and Biology

- Chaco region between southern Bolivia and northwestern Argentina Center of origin
- *Genus Arachis* comprises 69 species placed in 9 sections. Section *Arachis* contains cultivated groundnut
- *Arachis hypogaea* is a tetraploid with $2n=40$ chromosomes. Some wild *Arachis* are diploid also
- Highly self-pollinated

Major Centers Holding Groundnut Germplasm

The genebank at ICRISAT is holding the largest collection (15419 accessions from 93 countries). The other major centers are:

NSSL, Fort Collins, USA

USDA, Griffin,

NCSU, USA

USA Campinas & CENARGIN, Brazil

NRCG, Junagadh, India

BORIF, Indonesia



Major Centers Holding Germplasm of Wild *Arachis* Species



- USDA, Griffin, USA : 498 accession
- Texas, A&M, USA : 798 accessions
- NCSU, USA : 275 accessions
- Campinas & CENARGEN, Brazil : 450 accessions
- ICRISAT, India : 453 accessions

Diversity for Pod and Seed Characteristics in Groundnut Germplasm





Geographical Pattern of Diversity in Groundnut Germplasm



- 13,342 accessions were characterized for 16 morphological and 10 agronomic traits and reaction to diseases
- Pattern of diversity was analyzed based on 14 different geographical regions
- The means for different agronomic traits differed significantly among regions
- The variances for all the traits among regions were heterogeneous
- The accessions from South America showed 100% range variation for 12 of the 16 morphological traits
- Out of the 14 geographical regions, South America also showed highest pooled diversity index



Core Collection of Groundnut Germplasm



- Core collection consists of a limited set of germplasm which represents the genetic diversity of a crop species
- At ICRISAT, we have developed a core collection of peanut consisting of 1704 accessions. This represents almost full diversity of the entire collection (Upadhyaya et al. 2003)

Mini-core of Groundnut Germplasm

- Number of accessions in core are large for easy exploitation by breeders
- To overcome this size, Upadhyaya and Ortiz (2001) suggested mini-core (1% of entire) approach
- Two stage approach
- At ICRISAT, we have developed a mini-core of groundnut germplasm that consists of 184 accessions (Upadhyaya et al. 2002)

Selection of SSR Markers

- At ICRISAT, twenty SSR markers were initially selected to pre-screen the mini-core accessions (Upadhyaya *et al.* 2002) from which ten polymorphic markers identified

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

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



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 was consisted of 850 accessions from ICRISAT and 150 accessions from EMBRAPA, Brazil

Composite Collection of Groundnut

Character	Accessions number	Character	Accessions number
ICRISAT			
Mini core	184	Early maturing	25
Mini core comparator	184	Large seeded	16
Asia minicore	50	High Shelling percentage	10
Best accessions from asia core	60	High oil content	9
Released/elite cultivar/morphological variance	36	High protein content	9
Trait specific		Interspecific derivatives	5
Resistant to biotic stresses	104	Accessions earlier genotyped (Morag Ferguon)	18
Resistant to abiotic stresses	40	Accessions of 14 Wild arachis species	52
Fresh seed dormancy	6		
EMBARPA			
Accessions of Wild arachis species	62	Cultivated accessions from diverse origin and botanical varieties	130



Future Plan

- Composite collection will be genotyped and data analyzed by January 2006
- 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



Genotyping Tier 2 Crops- Issues

- Is composite collection (1000 accessions) adequate to represent diversity of large collections such as groundnut? No
- Are 20 SSR markers sufficient to determine the genetic structure and identify alleles of interest? No
- Can the situation be rectified for tier 2 crops?
Yes
 - Groundnut composite collection should be about 2500
 - Number of markers-50



Thank you