Genotyping Pigeonpea Composite Collection Using SSR Markers

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About pigeonpea

- Pigeonpea (*Cajanus cajan* (L.) Millspaugh) is the sixth most important food legume grown as a field and/or backyard crop in over 82 countries across the globe. However, as a regular annual crop it is grown only in 19 countries on 4.4 million ha producing 3 million t of grains.
- About 92% of the area is in developing countries.
- India (3.2 million ha), Myanmar (0.48 million ha), Kenya (0.15 million ha) and Malawi (0.12 million ha) are the major pigeonpea growing countries.
- Primarily grown as dry seeds, and green vegetable.
- Pigeonpea is a good source of vegetarian protein, soil enricher, fodder, fuel wood, and is also good for arresting soil erosion.

Diversity for seed traits in pigeonpea germplasm.

Diversity for pod traits in pigeonpea germplasm.

Cajanus scarabaeoides, a wild relative of pigeonpea, has several economic traits.

Major centers holding pigeonpea germplasm

Center	Number of accessions
ICRISAT	13632
NBPGR, India	7488
University of Philippines, Philippines	433
National Biological Institute, Indonesia	200

Origin and genepool

- Pigeonpea was first domesticated in India around 2200 BC.
- Its closest wild relative is *Cajanus cajanifolius*, a native of Bastar region in southeastern India.
- Genus *Cajanus* is comprised of 32 species, *C. cajan* is the only cultivated form.
- All the species are diploid with 2n=22 chromosomes. It is an often cross-pollinated crop and accessions are heterogeneous.

Assessment of pigeonpea germplasm diversity

- In the pigeonpea collection, semi-spreading growth, green-stem color, indeterminate flowering pattern, and yellow flower were predominant among the qualitative traits.
- Accessions from Oceania were conspicuous for short-duration, short-height, smaller seeds and fewer pods.
- Accessions from Africa were taller, long-duration and multi-seeded.
- Accessions from India had medium height, higher pod number, medium-duration and high grain yield.
- The cluster analysis grouped the accessions from Oceania in cluster-1, from India and neighboring countries in cluster-2, and from Southeast Asia, Africa, and Caribbean in cluster-3 (Upadhyaya et al. in press).
- Core collection of pigeonpea (1290 accessions) has been developed to facilitate the utilization of germplasm (Reddy et al. in press).

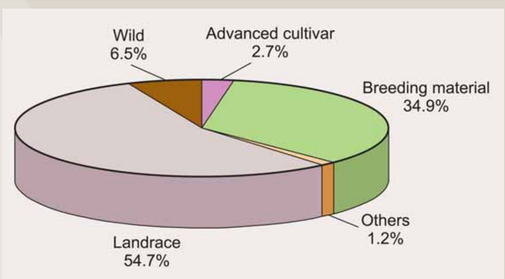
Development of composite collection

A composite collection of pigeonpea is a set of 1000 accessions, selected primarily to represent the entire collection, ecologically, taxonomically and phenotypically.

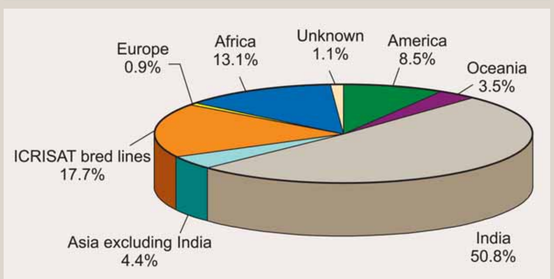
Composition of the composite collection

S No	Particular	Number of accessions
1.	Mini-core, mini-core comparators, core cluster representatives	528
2.	Trait specific accessions	270
3.	Resistant to biotic stresses	74
4.	Resistant to abiotic stresses	14
5.	Selections	29
6.	Released cultivars	16
7.	Wild species accessions	65
8.	Control cultivars	4
	Total	1000

Representation of composite collection by biological status



Representation of composite collection based on origin



Selection of markers

- Thirty SSR markers were initially selected to pre-screen the mini-core accessions, of which 20 polymorphic markers will be identified to genotype the composite collection.

Present research scenario

- The composite collection was planted in the field during August 2005.
- Considering the heterogeneity of the accessions, 12 plants per accession were randomly selected for DNA extraction, and the DNA was pooled to capture variation within accession.
- Genotyping will be done on ABI 3100.
- Data processing and analysis is likely to be completed by March 2006.

Future plan of work

Using genotypic data, a representative reference collection of 300 accessions will be formed. The reference collection will be evaluated for drought tolerance and other agronomic traits. Plant breeders will have access to genetically diverse accessions to enhance the yield potential of pigeonpea.

References

Reddy LJ, Upadhyaya HD, Gowda CLL and **Sube Singh**. (in press). Development of core collection in pigeonpea [*Cajanus cajan* (L.) Millspaugh] using geographic and qualitative morphological descriptors. Gene. Resor. and Crop Evol.

Upadhyaya HD, Pundir RPS, Gowda CLL, Reddy KN and **Sube Singh**. (in press). Geographical patterns of diversity for qualitative and quantitative traits in the pigeonpea germplasm collection. Plant Genetic Resources-Characterization and utilization.