



Genotyping Pigeonpea Composite Collection

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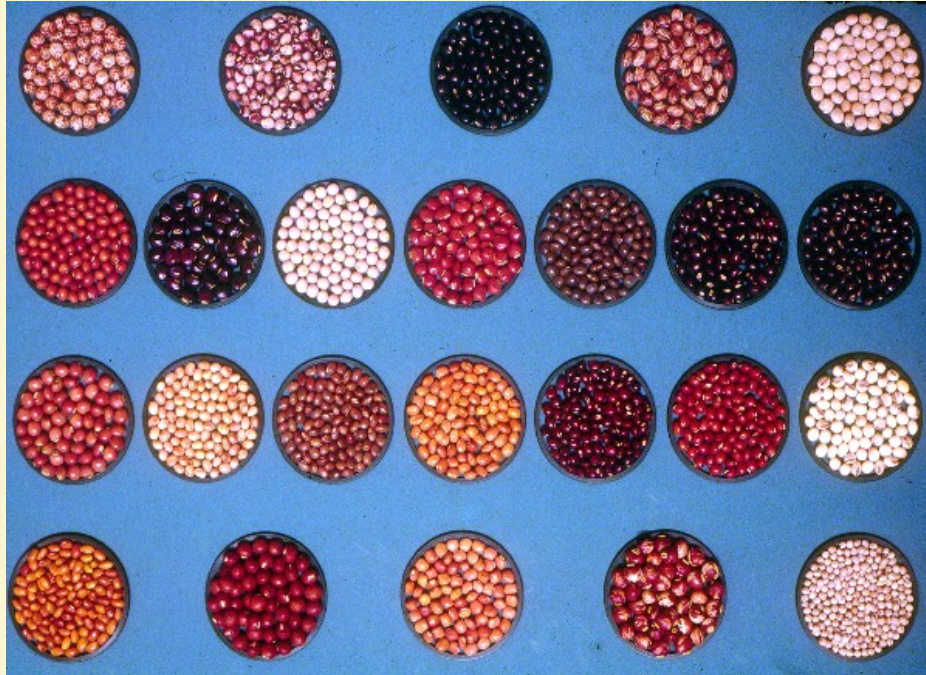
Generation Challenge Program 2005 - ARM

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About Pigeonpea Crop

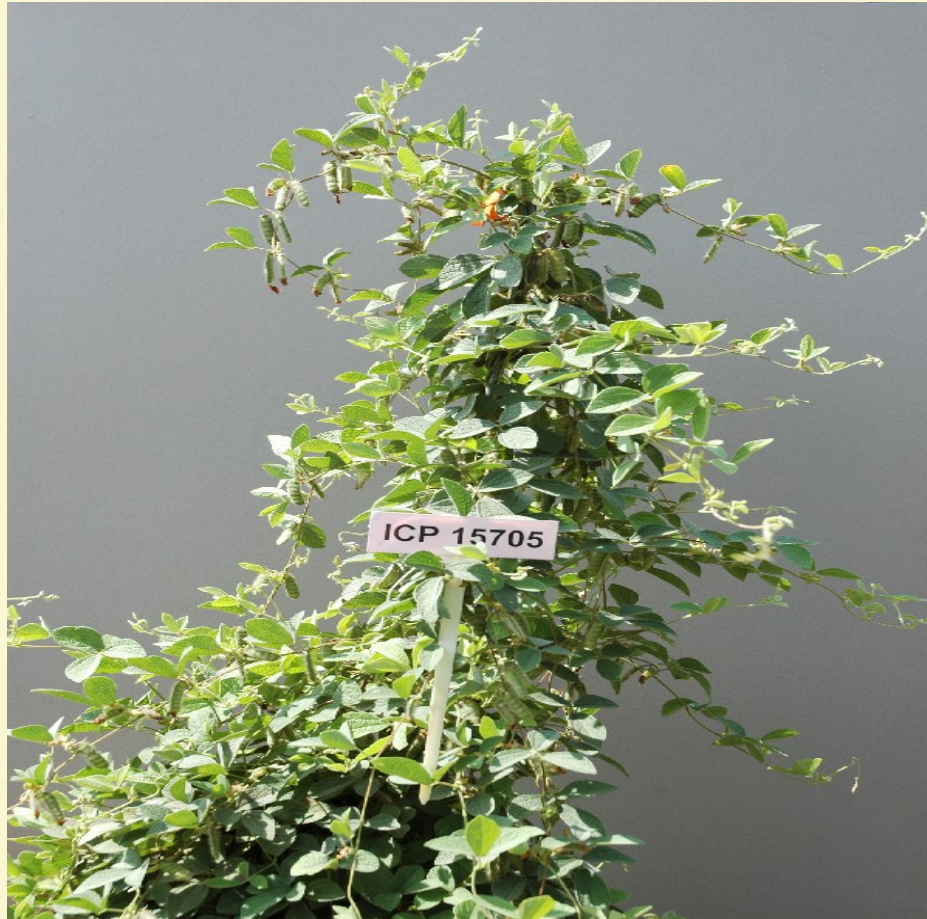
- Pigeonpea (*Cajanus cajan* (L.) Millspaugh) is sixth most important food legume grown as a field and/or backyard crop in over 82 countries across the globe. However, it is grown only in 19 countries as regular annual crop in 4.4 million hectare producing 3 million tons
- About 92% of the area is in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



Diversity for seed traits in pigeonpea germplasm



Diversity for pod traits in pigeonpea germplasm



***Cajanus scarabaeoides*, a wild relative of pigeonpea, good for several economic traits**

Major Centers Holding Pigeonpea Germplasm

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

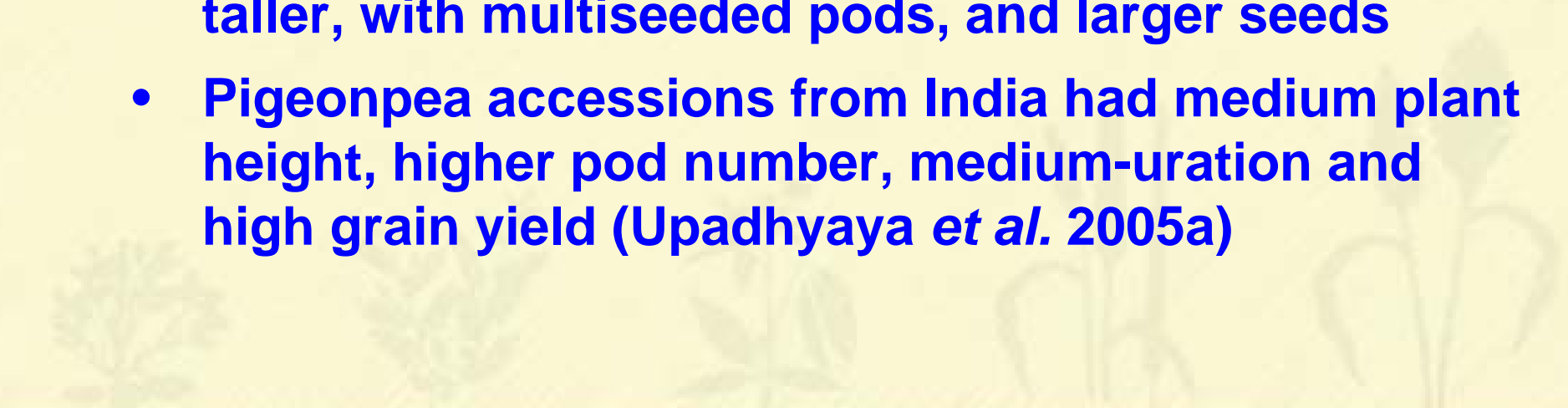
Origin and Genepool

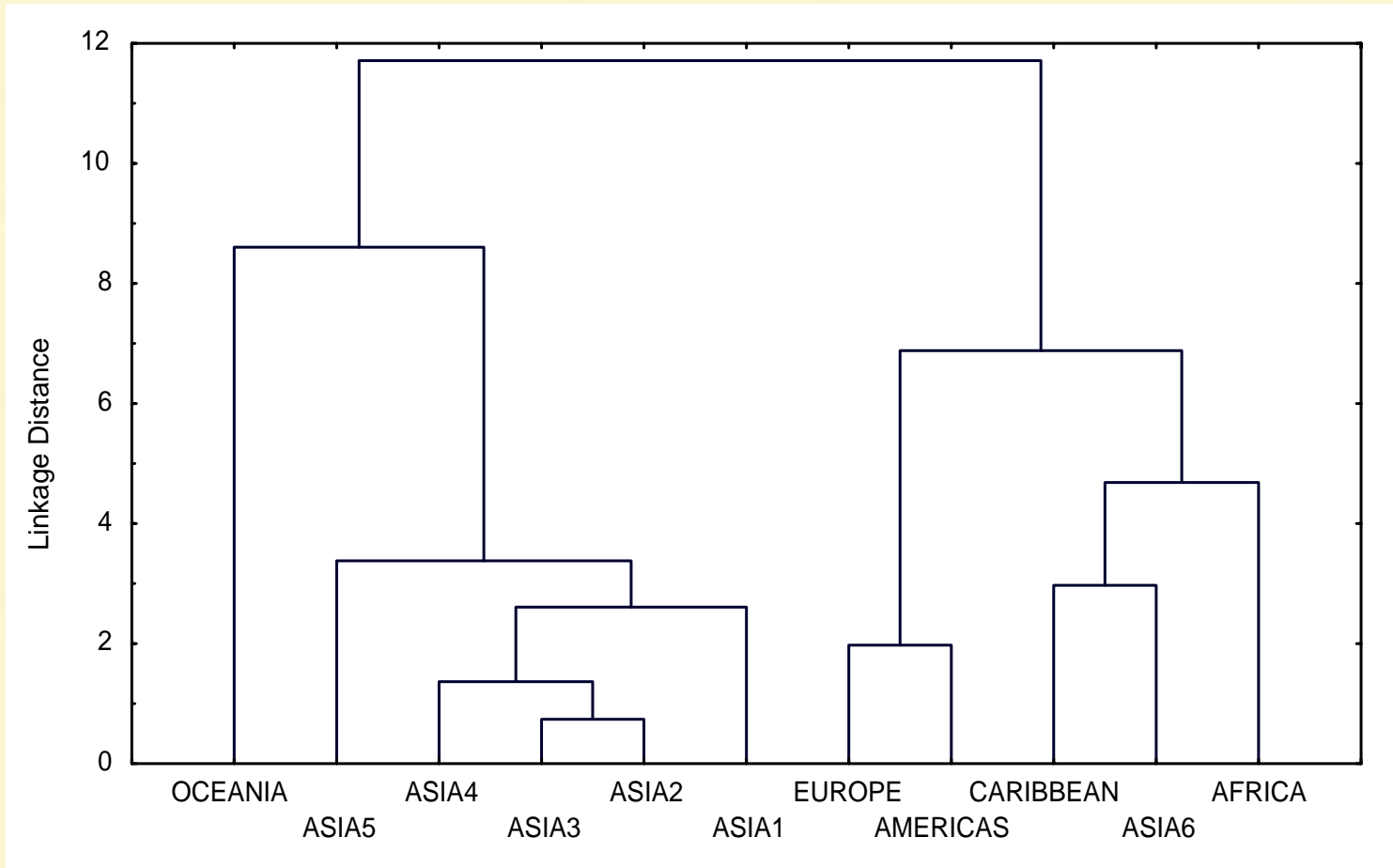
- Pigeonpea was first domesticated in India, about 2200 BC
- Its closest wild relative is *Cajanus cajanifolius*, a native of Baster region in southeastern India
- Genus *Cajanus* is comprised of 32 species, *C. cajan* is the only cultivated form
- All the species are diploid with $2n=22$ chromosomes.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




Geographical Pattern of Diversity in Pigeonpea Germplasm



- **Variances for all the traits were heterogeneous among regions**
 - **The germplasm accessions from Oceania were conspicuous by short growth duration, short height, fewer branches, pods with fewer seeds, smaller seed size, and lower seed yields**
 - **The accessions from Africa were of longer duration, taller, with multiseeded pods, and larger seeds**
 - **Pigeonpea accessions from India had medium plant height, higher pod number, medium-uration and high grain yield (Upadhyaya *et al.* 2005a)**
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Dendrogram of eleven regions in the entire pigeonpea germplasm based on first three principal components (Upadhyaya et al. 2005a)



Core Collection of Pigeonpea - Progress

- **ICRIRSAT pigeonpea core collection consists 1290 accessions (Reddy et al, 2004).**
- **Data on geographical descriptors and 14 quantitative traits of 12 153 accessions were used**
- **Phenotypic diversity in core collection assessed (Upadhyaya et al 2005b).**
- **Core collection formed the basis for mini core and composite collection.**



Development of Composite Collection

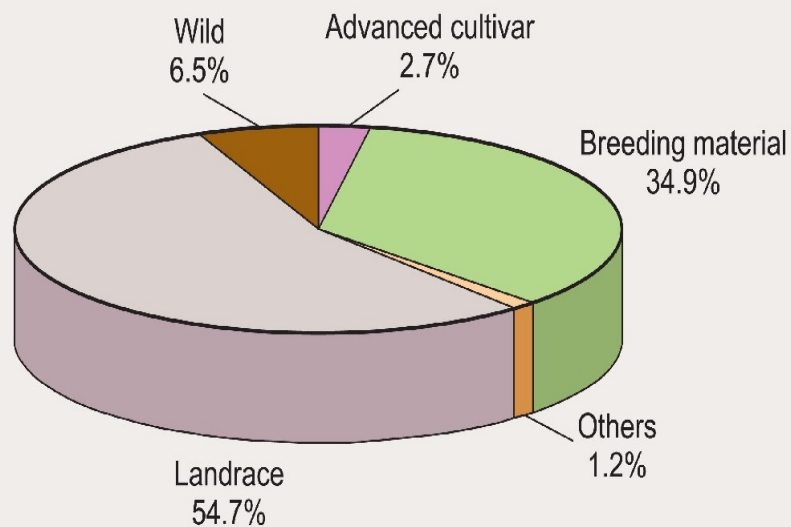
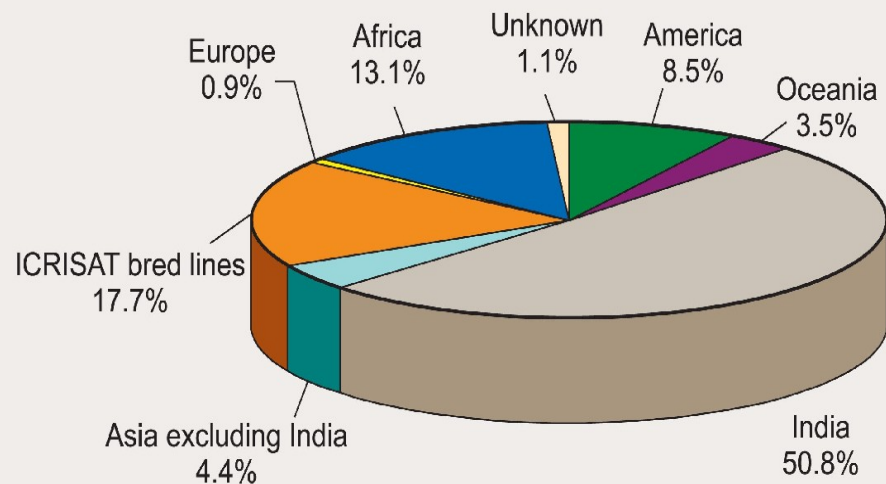
A composite collection of pigeonpea is a set of 1000 accessions, selected primarily to be the representative of the entire collection, ecologically, taxonomically, and phenotypically



Composition of the Composite Collection

Particular	Number of accessions
Mini-core, mini-core comparators, core cluster representatives	528
Trait specific accessions	270
Resistant to biotic stresses	74
Resistant to abiotic stresses	14
Selections	29
Released cultivars	16
Wild species accessions	65
Control cultivars	4
Total	1000

Representation of composite collection based on origin



Representation of composite collection by biological status


Thirty Markers Selected for Pigeonpea Germplasm Genotyping

CCB1	CCB9	PGM19	PKS34	PGM46
CCB2	CCB10	PGM23	PKS36	PGM51
CCB4	PGM3	PGM88	PGM7	PGM53
CCB5	PGM7	PGM106	PGM32	PGM62
CCB7	PGM10	PKS14	PGM38	PGM64
CCB8	PGM14	PKS23	PGM41	PGM73



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 within accession variation**
 - **Genotyping will be done on ABI 3100**
 - **Data processing and analysis is likely to be completed by March 2006**
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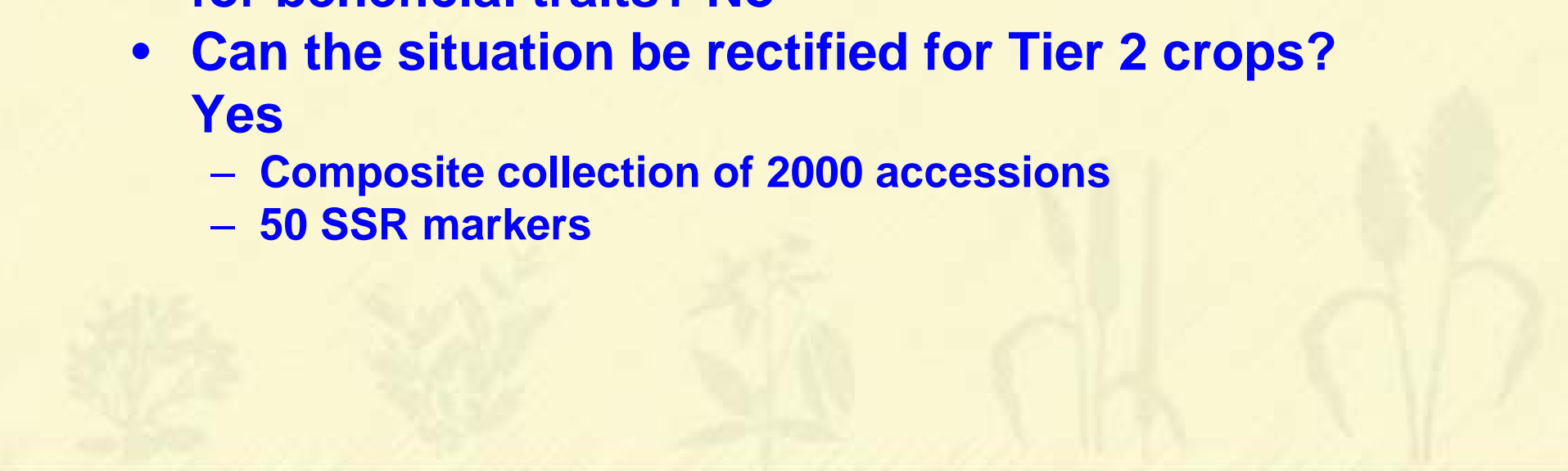
Future Plan of Work



- **Using genotypic data a representative reference collections of 300 accessions will be formed**
 - **The reference collection will be evaluated for traits associated with drought tolerance and other agronomic traits**
 - **The plant breeders will have access to genotypically diverse accessions to enhance the yield potential of pigeonpea**
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Genotyping Tier 2 Crops- Issues

- **Is composite collection (1000 accessions) of crops like pigeonpea with large collections sufficient to represent diversity? No**
 - **Is number of markers (20 SSR) sufficient to determine genetic structure and identify alleles for beneficial traits? No**
 - **Can the situation be rectified for Tier 2 crops?**
Yes
 - **Composite collection of 2000 accessions**
 - **50 SSR markers**
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Thank you