Genotyping Pigeonpea Composite Collection

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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

<table>
<thead>
<tr>
<th>Center</th>
<th>Number of accessions</th>
</tr>
</thead>
<tbody>
<tr>
<td>ICRISAT</td>
<td>13632</td>
</tr>
<tr>
<td>NBPGR, India</td>
<td>7488</td>
</tr>
<tr>
<td>University of Philippines</td>
<td>433</td>
</tr>
<tr>
<td>National Biological Institute, Indonesia</td>
<td>200</td>
</tr>
</tbody>
</table>
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).
Dendogram of eleven regions in the entire pigeonpea germplasm based on first three principal components (Upadhyaya et al. 2005a)
ICRISAT 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

<table>
<thead>
<tr>
<th>Particular</th>
<th>Number of accessions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mini-core, mini-core comparators, core cluster reps.</td>
<td>528</td>
</tr>
<tr>
<td>Trait specific accessions</td>
<td>270</td>
</tr>
<tr>
<td>Resistant to biotic stresses</td>
<td>74</td>
</tr>
<tr>
<td>Resistant to abiotic stresses</td>
<td>14</td>
</tr>
<tr>
<td>Selections</td>
<td>29</td>
</tr>
<tr>
<td>Released cultivars</td>
<td>16</td>
</tr>
<tr>
<td>Wild species accessions</td>
<td>65</td>
</tr>
<tr>
<td>Control cultivars</td>
<td>4</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>1000</strong></td>
</tr>
</tbody>
</table>
Representation of composite collection based on origin

Representation of composite collection by biological status

- India: 50.8%
- Landrace: 54.7%
- Breeding material: 34.9%
- Advanced cultivar: 2.7%
- Wild: 6.5%
- Others: 1.2%
- ICRISAT bred lines: 17.7%
- Africa: 13.1%
- Oceania: 3.5%
- Europe: 0.9%
- America: 8.5%
- Asia excluding India: 4.4%
- Unknown: 1.1%
Thirty Markers Selected for Pigeonpea Germplasm Genotyping

<table>
<thead>
<tr>
<th>CCB1</th>
<th>CCB9</th>
<th>PGM19</th>
<th>PKS34</th>
<th>PGM46</th>
</tr>
</thead>
<tbody>
<tr>
<td>CCB2</td>
<td>CCB10</td>
<td>PGM23</td>
<td>PKS36</td>
<td>PGM51</td>
</tr>
<tr>
<td>CCB4</td>
<td>PGM3</td>
<td>PGM88</td>
<td>PGM7</td>
<td>PGM53</td>
</tr>
<tr>
<td>CCB5</td>
<td>PGM7</td>
<td>PGM106</td>
<td>PGM32</td>
<td>PGM62</td>
</tr>
<tr>
<td>CCB7</td>
<td>PGM10</td>
<td>PKS14</td>
<td>PGM38</td>
<td>PGM64</td>
</tr>
<tr>
<td>CCB8</td>
<td>PGM14</td>
<td>PKS23</td>
<td>PGM41</td>
<td>PGM73</td>
</tr>
</tbody>
</table>
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.
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
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
Thank you