

Development of a Mini Core Subset for Enhanced and Diversified Utilization of Pigeonpea Germplasm Resources

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ABSTRACT

Pigeonpea [*Cajanus cajan* (L.) Millsp.], endowed with rich dietary protein in its seed, provides the much needed protein requirements of predominantly vegetarian population. Pigeonpea plays an important role in providing food, shelter, medicine and other livelihood opportunities among the rural poor. The purpose of a core collection is to provide information necessary to improve the use of genetic resources in crop improvement programs. In many crops the number of germplasm accessions in the genebanks are in several thousands. Even a core collection (consisting of 10% of total accessions) is large and becomes unwieldy to evaluate and characterize the accessions for economic traits. Hence, a mini core collection of pigeonpea, comprising 146 accessions was constituted by evaluating a core collection of 1290 accessions. Examination of data for various morphological and agronomic traits indicated that almost the entire genetic variation and a majority of coadapted gene complexes present in the core subset are preserved in the mini core subset. Due to its greatly reduced size, the mini core subset will provide a more economical starting point for proper exploitation of pigeonpea genetic resources for crop improvement for food, feed, fuel, and other agricultural and medicinal purposes.

PIGEONPEA is grown in a diverse array of cropping systems for its multiple uses (food, feed, fuel, medicine, fencing, roofing, basket making, etc.) (Nene and Sheila, 1990). Although pigeonpea is known to be grown in about 82 countries as a field and/or backyard crop in Asia, Oceania, Africa, and the Americas (Nene and Sheila, 1990), FAO statistics are available only for 19 countries, all of which are developing countries (FAO, 2005). During 2004, pigeonpea as a field crop was grown on 4.36 million ha, with a production of 3.24 million t and an average productivity of 0.74 t ha⁻¹.

Pigeonpea, which remained a less-known crop in the west until recently, is emerging more as an international crop, with the Simpson Index of diversity rising from 0.20 in 1980–81 to 0.26 in 1996–98 (Ryan and Spencer, 2001). With the advent of short-duration and high-yielding pigeonpea cultivars such as ICPL 88039, large productivity gains in the rice-wheat system in South Asia were witnessed, triggering a major geographic extension of the crop within Asia and Africa, and other regions (Shiferaw et al., 2004). Recently, pigeonpea has shown the potential to fill forage gaps in the USA during summer (Phillips and Rao, 2001; Rao et al., 2002; Rao et al., 2003). Similarly, it has been demonstrated for its utility

in soil conservation, fodder production, and other uses in China (Zong et al., 2001). Pigeonpea has potential for several other uses, such as fuel in India, medicine (see Faris and Singh, 1990), agroforestry, alley cropping, live stock feed (Remanandan et al., 1991), and soil enrichment through its efficient extraction of iron-bound phosphorous from typical Alfisols, compared to several other crops (Ae et al., 1990).

Pigeonpea is cultivated for multiple uses in a diverse array of cropping systems. The adaptation of improved genotypes to intercropping, alley cropping, multiple cropping, and multiple harvests is an important objective in pigeonpea improvement programs (Singh et al., 1990). The curative effects of various parts of pigeonpea plant have been reported in folk medicine and ayurvedic medicines worldwide, in countries such as India, Indonesia, Madagascar, West Africa, the Caribbean region, and China. Pigeonpea as whole plant, leaf juice and decoction, flowers, young pods, seeds, seed decoction, and roots are mentioned to have 39 different medicinal and cosmetic uses in 13 countries (see Faris and Singh, 1990). Morton (1976) reported the use of pigeonpea leaf decoction to cure jaundice in Cuba. Almost all villages in Bangladesh maintain pigeonpea in the kitchen gardens exclusively for its leaf juice, used to cure jaundice (L.J. Reddy, personal observation, 1999). However, no germplasm screening for higher levels of chemical constituents useful for medicinal purposes have been undertaken. In recent years, there is new found interest in pigeonpea in several countries. In the Philippines, pigeonpea is found to be a cheap source of poultry feed (Sugui et al., 2004). In China, pigeonpea has been revived for soil conservation and fodder production in some areas (Yang et al., 2001), and the utility of pigeonpea in soil conservation, as fodder, food, and vegetable production has been demonstrated (Zong et al., 2001). Pigeonpea forage yields and nutritive values during summer equaled those of other forage crops and research is underway to identify more nutritive and high yielding pigeonpea varieties well-adapted to the southern plains of the U.S. (Phillips and Rao, 2001; Rao et al., 2002; Rao et al., 2003). However, in all the above studies, only a very small number of genotypes, mostly the breeding material, have been used.

In spite of its multiple uses, pigeonpea germplasm has been used primarily for developing high grain yielding varieties of different maturity groups, as sources of resistance to major diseases and insect pests and for other simply inherited traits. Some economists have asserted that the materials in genebanks are rarely used (Wright, 1997). Usually the number of useful germplasm accessions for breeding is less than 5% and mostly less than

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Abbreviations: H', diversity index.

1% (Goodman, 1990) The prime reasons for the low use of diverse germplasm for improvement of quantitative traits in the plant breeding programs are the extended time and high costs involved in identifying these useful accessions. Also most breeders prefer to work with their own lines rather than exotic material (Cox et al., 1988; Duvick, 1995). Further, the priority of pigeonpea breeders has been to exploit the variability that has arisen from the cross-pollinated nature of the crop. A large number of the notified or released varieties in India are selections from the local landraces (Singh et al., 1990).

Developing a core collection, comprising about 10% of the entire collection and representing most of the diversity of the species, has been proposed as a means of increasing the use of germplasm more economically (Frankel, 1984). The information obtained from such a core collection can aid in judicious use of the entire collection. A pigeonpea core collection was constituted with 1290 accessions from the global germplasm available at ICRISAT (Reddy et al., 2005). Although the core collection with 1290 accessions can be screened for morphological traits, its evaluation for agronomic traits in replicated multilocation trials would be unwieldy, costly, and time consuming for breeders. Therefore, we need still a smaller set of accessions that represent almost the entire spectrum of diversity available in the core collection. In such cases a 'core of the core' (mini core subset) facilitates the screening of accessions with reasonable costs and success. The present study was undertaken to constitute a mini core subset following Upadhyaya and Ortiz (2001), which will help screen the pigeonpea germplasm in a cost effective and speedy way to find suitable genotypes for multiple uses, including crop improvement.

MATERIALS AND METHODS

From 12370 pigeonpea accessions available at ICRISAT Center, Patancheru, India, a core collection comprising 1290 accessions from 53 countries, was constituted (Reddy et al., 2005). These 1290 accessions were assessed during 2004–2005 crop season for 18 qualitative and 16 quantitative traits at the ICRISAT research farm, Patancheru (18° N lat; 78° E long, 545 m.a.s.l., and about 600 km from the sea). Sowings were done on a precision vertisol field (Kasireddipally Series isohyperthermic Typic Pellustert). The test accessions were planted in an augmented design (Federer, 1956) to evaluate the core collection accessions and to select the mini core collection. This design is considered ideal and efficient in testing large number of germplasm accessions. We used four cultivars of different maturity duration to serve as controls. The controls included extra early (ICP 11543), early (ICP 6971), medium (ICP 8863), and late maturing (ICP 7221) genotypes. The accessions along with replicated controls were evaluated in a block of 40 entries. The controls were randomized in each block, and the accessions were randomly assigned to the plots. Each block comprised nine accessions flanked by the check cultivars. The error component from an appropriate check based on the maturity duration of accessions was used in adjusting the values of the accessions.

Each plot consisted of a single four-meter row on a ridge. The distance between rows was 750 mm and between plants 500 mm. Care was taken to ensure uniform planting depth of 25 mm. Dry seed treatment with 3 g of thiram per kg seed was applied before planting to protect from seed borne diseases.

The experimental field received 20 kg N and 40 kg P₂O₅ ha⁻¹ as a basal dose and the need-based protection against diseases, insects and weeds as per research standards. The crop was planted on 30 June 2004 and harvested between Nov. 2004 and Feb. 2005, depending on the maturity of accessions.

The data on 18 qualitative (vigor, growth habit, plant pigmentation, stem thickness, flower base color, streak color, streak pattern, flowering pattern, pod color, pod shape, pod hairiness, seed color pattern, primary seed color, secondary seed color, seed eye color, seed eye color width, seed shape, and seed hilum) and 16 quantitative characters were recorded following IBPGR and ICRISAT (1993). Days to flowering and maturity, 100-seed weight, harvest index, shelling percent, and seed yield kg ha⁻¹ were recorded on plot basis. Leaf size, plant height, number of primary, secondary, and tertiary branches, number of racemes, pod bearing length, pods plant⁻¹, pod length, seeds pod⁻¹ were recorded on randomly chosen five competitive plants in a plot, avoiding the plants at the beginning and end of the alleys.

A phenotypic distance matrix was created by calculating the differences between each pair of 1290 accessions for each of the 34 traits. The diversity index was calculated by averaging all the differences in the phenotypic values for each trait divided by respective range (Johns et al., 1997). The distance matrix was subjected to the hierarchical cluster algorithm of Ward (1963) at an *R*² (squared multiple correlation value) of 0.75 by means of SAS (1989) for clustering 1290 accessions. This method optimizes an objective function because it minimizes the sum of squares within groups and maximizes the sum of squares between groups. The proportional sampling strategy was used, and from each cluster approximately 10% of the accessions were randomly selected to constitute the mini core subset. At least one accession was included from each cluster even if had less than 10 accessions.

The means of both the core and the mini core subsets were compared using the Newman-Keuls procedure (Newman, 1939; Keuls, 1952) for all the 16 quantitative traits. The homogeneity of variances between the core and mini core subsets was tested by Levene's test (Levene, 1960). The distribution homogeneity for each of the 17 morphological descriptor traits was analyzed using the chi-square test. The expected frequencies of the accessions in different classes of a trait in the mini core were based on proportion of mini core to core or mini core to entire collection. The expected frequencies were tested against observed frequencies in the mini core for goodness of fit using χ^2 test. The percentage of traits for which the core and mini core subsets differed significantly for the mean [mean difference percentage (MD%)] or for the variance [variance difference percentage (VD%)] was calculated (Hu et al., 2000). The coincidence rate (CR%) and the variable rate (VR %) were calculated to evaluate properties of the mini core subset (Hu et al., 2000). The Wilcoxon (1945) rank-sum non-parametric test was performed using the SAS NPAR 1 WAY procedure (SAS, 1989). The phenotypic correlations among different traits in the core and mini core were estimated independently to determine whether these associations, which may be under genetic control, were conserved in the mini core subset. The diversity index (*H'*) of Shannon and Weaver (1949) was used as a measure of phenotypic diversity of each trait. The index was calculated independently in both core and the mini core subsets to determine whether the diversity for each trait was retained in the mini core subset.

RESULTS AND DISCUSSION

The clustering procedure we used resulted in grouping the 1290 core subset entries into 79 clusters. The

Table 1. Comparison of number of accessions and their frequency distribution in the entire, core and mini core collections of pigeonpea from different geographical regions.

Region†	Number of accessions			χ^2 Core (<i>p</i>) vs. Mini core		χ^2 Entire (<i>p</i>) vs. Mini core	
	Entire	Core	Mini core				
Southern and Eastern Africa	992 (8.17)§	108 (8.40)§	12 (8.33)§	0.004	(0.950)¶	0.001	(0.975)¶
Western and Central Africa	207 (1.70)	29 (2.26)	5 (3.47)	0.899	(0.346)	1.630	(0.202)
Americas	188 (1.55)	29 (2.26)	3 (2.08)	0.024	(0.877)	0.026	(0.872)
Caribbean	379 (3.12)	46 (3.58)	4 (2.78)	0.279	(0.597)	0.244	(0.621)
Asia ¹	2460 (20.25)	247 (19.21)	24 (16.67)	0.560	(0.454)	1.043	(0.307)
Asia ²	1183 (9.74)	123 (9.56)	17 (11.81)	0.681	(0.409)	0.547	(0.460)
Asia ³	1399 (11.52)	143 (11.12)	17 (11.81)	0.041	(0.840)	0.002	(0.964)
Asia ⁴	4758 (39.17)	478 (37.17)	50 (34.72)	0.311	(0.577)	0.897	(0.344)
Asia ⁵	6 (0.05)	3 (0.23)	1 (0.69)	1.285	(0.257)	2.540	(0.111)
Asia ⁶	119 (0.98)	21 (1.63)	2 (1.39)	0.060	(0.807)	0.003	(0.956)
Asia ^{7,‡}	365 (3.01)	39 (3.03)	5 (3.47)	0.078	(0.780)	0.003	(0.956)
Europe	29 (0.24)	8 (0.62)	3 (2.08)	4.845	(0.028)	13.288	(0.001)
Oceania	61 (0.50)	12 (0.93)	1 (0.69)	0.094	(0.729)	0.074	(0.390)
Total	12153	1290	146	9.161	(0.689)	20.298	(0.062)

† Details of countries in each region: 1. Southern and Eastern Africa: Ethiopia, Kenya, Malawi, Mozambique, Rwanda, South Africa, Tanzania, Uganda; 2. Western and Central Africa: Cape Verde, Central African Republic, Ghana, Nigeria, Senegal, and Sierra Leone; 3. Americas: Brazil, Colombia, Guyana, Mexico, Peru, USA, and Venezuela; 4. Caribbean: Antigua and Barbuda, Barbados, Dominican Republic, Grenada, Guadeloupe, Jamaica, Montserrat, Puerto Rico, Saint Kitts and Nevis, Saint Lucia, Saint Vincent and the Grenadines, and Trinidad and Tobago; 5. Asia1: Indian north western states, Iran, and Pakistan; 6. Asia2: Indian north western states, Bangladesh, Nepal, and Myanmar; 7. Asia3: Indian central states; 8. Asia 4: Indian southern states, Maldives, and Sri Lanka; 9. Asia 5: Russia & CISs, China, and Taiwan; 10. Asia 6: Indonesia, Thailand, and Philippines; 11. Asia 7: Unknown Indian states; 12. Europe: Belgium, Germany, Italy, and United Kingdom; 13. Oceania: Australia.

‡ Data on accessions of unknown origin are also included.

§ Figures in parenthesis are percentages of accessions.

¶ *P* is the probability level of significance.

number of core entries in the clusters ranged from 1 (0.08%; in seven clusters) to 65 (5.04%; in cluster 2). The procedure we used to develop the mini core subset resulted in the selection of 146 entries from the core subset. The composition of the mini core subset reflected the predominance of accessions from southern India, Sri Lanka, and the Maldives (34.7%), followed by accessions from northwestern India, Pakistan, and Iran (16.7%), Bangladesh, Myanmar, Nepal, China, Taiwan, north eastern India (11.8%), and central India (11.8%). About 8.3% accessions in the mini core were from southern and eastern Africa, and 3.5% each from western and central Africa, and unknown Indian states. The proportions of accessions in the entire vs. core and core vs. mini core collections compared favorably (Table 1) across all the 13 regions (Upadhyaya et al., 2005).

Of the 18 morphological descriptor traits studied, there was no variation for pod hairs both in core and mini core subsets. The remaining 17 traits showed similar proportions for various descriptor states in the mini core collection indicating that the mini core represented the core collection adequately (Table 2).

Differences between the means of the core and the mini core subset for all the quantitative traits were not significant (Table 3). Variances of the core and the mini core subsets were homogeneous for all traits except secondary branches ($p = 0.049$). There were no significant differences between the medians of the core and mini core subsets for any of the 16 measurable traits (Table 4). The zero value for mean difference percentage indicated that the mini core subset adequately represented the core subset (Hu et al., 2000). For secondary branches and shelling percentage, 100% of the variation available in the core was included in the mini core. For the 11 other traits (primary branches, harvest index, plant height, days to maturity, days to flowering, raceme number, leaf size, plot yield kg ha⁻¹, 100-seed weight,

pod per plant, and tertiary branch number) the variation included in the mini core ranged from 82.3 to 96.5%. For seeds per pod 77.8% and for pod bearing length 72.2% variation was included in the mini core.

An adequate and proper sampling, essential in developing a representative core collection, should consider the conservation of phenotypic associations arising out of co-adapted gene complexes (Ortiz et al., 1998). Phenotypic correlations were conducted between all 16 quantitative traits in the core and mini core subsets, independently. Only those traits with correlation coefficients greater than 0.707 and less than -0.707 are considered as biologically meaningful (Skinner et al., 1999) as more than 50% of the variation in one trait is predicted by the other (Snedecor and Cochran, 1980). In our study, nine such meaningful relationships between

Table 2. Comparison of frequency distribution for 17 morphological descriptors between core vs. mini core and entire vs. core collection of pigeonpea.

Descriptor	Df	Core vs. mini core		Entire vs. mini core	
		χ^2 (<i>P</i>) †		χ^2 (<i>P</i>) †	
Plant vigor	6	0.357	(0.992)	0.400	(0.999)
Growth habit	3	0.352	(0.950)	0.350	(0.950)
Plant pigmentation	4	4.644	(0.326)	4.680	(0.322)
Stem thickness	6	0.272	(0.999)	0.260	(0.999)
Flower base color	5	2.452	(0.784)	2.470	(0.781)
Flower streak color	5	1.343	(0.930)	1.350	(0.930)
Streak pattern	22	26.411	(0.235)	26.550	(0.229)
Flag pattern	3	0.638	(0.888)	0.620	(0.892)
Pod color	7	7.056	(0.423)	7.090	(0.420)
Pod shape	1	0.227	(0.634)	0.210	(0.646)
Seed color pattern	11	6.408	(0.845)	6.460	(0.841)
Primary seed color	63	51.471	(0.850)	51.670	(0.845)
Secondary seed color	19	27.91	(0.085)	28.050	(0.083)
Seed eye color	21	14.889	(0.829)	14.690	(0.838)
Seed eye color width	6	2.193	(0.901)	2.220	(0.899)
Seed shape	5	2.551	(0.769)	2.540	(0.770)
Seed hilum	2	0.177	(0.915)	0.180	(0.913)

† *P* is the probability level of significance.

Table 3. Means and variances for quantitative traits recorded in the core and mini core subsets of pigeonpea at ICRISAT Center, Patancheru, India.

Trait	Means†			Variance‡			
	Core subset	Mini core subset	Significance	Core subset	Mini core subset	F value	(P)
Leaf size (cm)	18.1	18.3	NS‡	41.90	46.83	0.25	(0.6179)
Days to flowering	124.3	125.3	NS	351.60	398.80	0.81	(0.3682)
Plant height (cm)	203.1	203.8	NS	554.70	556.10	<0.001	(0.9858)
Days to maturity	184.3	184.9	NS	425.50	497.00	1.77	(0.1834)
Primary branches (no.)	14.8	14.8	NS	10.88	12.85	1.58	(0.2091)
Secondary branches (no.)	27.7	27.2	NS	47.41	60.92	3.89	(0.0486)
Tertiary branches (no.)	4.6	4.8	NS	10.62	14.56	1.33	(0.2482)
Raceme (no.)	161.8	160.5	NS	3388.90	3500.50	0.05	(0.8159)
Pod bearing length (cm)	69.6	69.0	NS	40.62	40.45	0.01	(0.9382)
Pods per plant (no.)	269.0	268.0	NS	14281.00	14766.00	0.04	(0.8343)
Pod length (cm)	5.4	5.4	NS	0.65	0.74	0.54	(0.4640)
Seeds per pod (no.)	4.0	4.0	NS	0.16	0.20	1.69	(0.1932)
100-seed weight (g)	9.2	9.4	NS	5.63	6.51	0.69	(0.4064)
Harvest index %	23.1	23.3	NS	13.58	17.96	3.53	(0.0605)
Shelling %	61.1	60.9	NS	9.83	12.48	1.31	(0.2518)
Plot yield (kg ha ⁻¹)	1480.0	1464.0	NS	267086.00	274438.00	0.04	(0.8488)

† Differences between means of core and mini core subsets tested by Newman-Keuls test and variance homogeneity by Levene's test.

‡ NS indicates nonsignificant differences at $P = 0.05$.

the agronomic traits in the core subset were found (data not shown). Except for the relationships of seeds per pod with pod length, and plot yield with pods per plant (data not shown), the rest of the five relationships (Table 5) were retained in the mini core collection. These relationships suggest that it is not necessary to measure both the related traits in future germplasm evaluations, and only easily measurable traits should be given priority. For example, days to flowering and days to maturity are correlated in the core ($r = 0.950$) and in the mini core ($r = 0.957$). So, it will be easy and sufficient if days to flowering are recorded in pigeonpea in preliminary evaluations to arrive at the days to maturity. Days to flower is more reliable in arriving at the maturity duration in pigeonpea, because frequent and heavy pod borer damage triggers fresh flower production in pigeonpea, which delays the days to maturity.

The Shannon-Weaver diversity index (H') was calculated to compare diversity in the core and mini core subsets. The index is used in genetic studies as a convenient measure of both allelic richness and allelic even-

ness. A low (H') indicates an extremely unbalanced frequency of classes for an individual trait and a lack of genetic diversity. The average H' for the 17 qualitative descriptors and 16 agronomic traits in the mini core subset was similar to the core subset (Table 6) indicating that the diversity of the core was adequately represented in the mini core subset.

The grouping of similar genotypes depends on the dissimilarity among them, which can be determined by a phenotypic diversity index. The average phenotypic diversity, minimum diversity, and maximum diversity indices in the mini core were higher compared to those in the core collection (Table 7). In the mini core, the minimum phenotypic diversity index was observed between ICP 13884 (a landrace from Puerto Rico) and ICP 14116 (a landrace from Jamaica) and the maximum phenotypic diversity between ICP 14444 (a breeding line from ICRISAT) and ICP 7426 (a landrace from Madhya Pradesh, India).

Concern about the loss of landraces, wild relatives, and cultivars led to large ex situ collections in genebanks.

Table 4. Median, range and coefficient of variation for 16 quantitative traits in core and mini core subsets of pigeonpea at ICRISAT center, Patancheru, India.

Trait	Median			Range		Coefficient of variation (%)	
	Core subset	Mini core (P) † subset	(P)	Core subset	Mini core subset	Core subset	Mini core subset
Leaf size (cm)	16.7	16.4	(0.727)	6.1–54.2	7.9–49.2	35.8	37.5
Days to flowering	124.3	126.1	(0.434)	62.5–168.7	71.7–164.9	15.1	15.9
Plant height (cm)	206.3	204.9	(0.504)	104.4–258.3	119.8–257.0	11.6	11.6
Days to maturity	182.1	182.1	(0.853)	112.8–228.3	120.5–222.5	11.2	12.1
Primary branches (no.)	14.4	14.5	(0.727)	7.6–29.4	8.3–29.4	22.3	24.2
Secondary branches (no.)	27.7	26.5	(0.170)	13.2–59.7	13.2–59.7	24.9	28.7
Tertiary branches (no.)	3.5	3.5	(0.753)	1.1–33.5	1.2–27.8	45.0	48.8
Raceme (no.)	161.7	159.2	(0.485)	44.2–366.0	44.2–326.5	36.0	36.9
Pod bearing length (cm)	69.7	69.7	(0.891)	46.9–96.1	53.3–85.8	30.2	69.6
Pods per plant (no.)	263.1	260.8	(0.600)	66.0–821.0	71.0–692.0	44.4	45.3
Pod length (cm)	5.2	5.2	(0.861)	3.1–8.8	3.8–8.8	15.0	16.0
Seeds per pod (no.)	3.9	3.9	(0.115)	2.3–5.9	2.7–5.5	10.0	11.1
100-seed weight (g)	8.6	8.6	(0.861)	5.3–20.1	5.3–17.85	25.7	27.2
Harvest index %	23.0	23.1	(0.861)	12.7–40.1	13.0–38.7	35.2	66.6
Shelling %	61.7	61.6	(0.382)	43.9–69.8	43.9–69.7	39.9	95.4
Plot yield (kg ha ⁻¹)	1493.5	1471.0	(0.549)	498.0–3191.0	498.0–2784.0	34.9	35.8

† P is the probability level of significance.

Table 5. Correlation coefficients with values greater than 0.707 between traits in the core and mini core subsets of pigeonpea at ICRISAT Center, Patancheru, India.

Traits	Core subset	Mini core subset
Days to flowering vs. Days to maturity	0.950	0.957
Secondary branch number vs. raceme number	0.780	0.743
Secondary branch number vs. pods per plant	0.728	0.703
Raceme number vs. pods per plant	0.901	0.902
Pod length vs. 100-seed weight	0.733	0.733

Genebank curators adopted the philosophy of keeping everything in absence of low cost technology to identify unique accessions. This led to the rapid growth of germplasm collections, but not of their utilization (Duvick, 1984). On the other hand, agricultural investments by the public and private sectors are extremely low in the developing countries, especially on 'orphan' crops (Nelson et al., 2004) and there is an urgent need for mechanisms to enhance agricultural development in poor agrarian societies (Mosher, 1996), where pigeonpea is an important crop.

Mini core collections, which comprise about 1% of the total collection have been recently constituted based on global germplasm available at ICRISAT in chickpea (Upadhyaya and Ortiz, 2001) and peanut (Upadhyaya et al., 2002). Recently, a mini core collection has been

Table 6. Shannon–Weaver diversity index for 17 qualitative descriptor traits and 16 quantitative traits in the core and mini core subsets of pigeonpea at ICRISAT Center, Patancheru, India.

Traits	Shannon diversity index	
	Core subset	Mini core subset
Qualitative traits		
Plant vigor	0.269	0.256
Growth habit	0.136	0.138
Plant pigmentation	0.066	0.111
Stem thickness	0.149	0.162
Flower base color	0.071	0.065
Flower streak color	0.116	0.124
Streak pattern	0.522	0.568
Flag pattern	0.085	0.083
Pod color	0.131	0.128
Pod shape	0.201	0.195
Seed color pattern	0.436	0.443
Primary seed color	0.845	0.767
Secondary seed color	0.453	0.494
Seed eye color	0.285	0.312
Seed eye color width	0.213	0.234
Seed shape	0.080	0.032
Seed hilum	0.081	0.084
Mean \pm SE	0.243 \pm 0.051	0.246 \pm 0.050
Quantitative traits		
Leaf size (cm)	0.552	0.562
Days to flowering	0.632	0.598
Plant height (cm)	0.571	0.555
Days to maturity	0.586	0.620
Primary branches (no.)	0.617	0.596
Secondary branches (no.)	0.624	0.590
Tertiary branches (no.)	0.472	0.420
Racemes (no.)	0.620	0.614
Pod bearing length (cm)	0.628	0.626
Pods per plant (no.)	0.592	0.570
Pod length (cm)	0.640	0.588
Seeds per pod (no.)	0.583	0.538
100-seed weight (g)	0.569	0.584
Harvest index %	0.623	0.604
Shelling %	0.580	0.545
Plot yield (kg ha ⁻¹)	0.605	0.606
Mean \pm SE	0.588 \pm 0.010	0.576 \pm 0.012
Mean over-all \pm SE	0.378 \pm 0.039	0.374 \pm 0.040

Table 7. Phenotypic diversity in the core and mini core collection of pigeonpea at ICRISAT Center, Patancheru, India.

Core collection	
Mean phenotypic diversity index	0.1608
Minimum phenotypic diversity index	0.005
Between	ICP 11790 and ICP 15016
Maximum phenotypic diversity index	0.5229
Between	ICP 14444 and ICP 11246
Mini core collection	
Mean phenotypic diversity index	0.1949
Minimum phenotypic diversity index	0.0458
Between	ICP 13884 and ICP 14116
Maximum phenotypic diversity index	0.5692
Between	ICP 14444 and ICP 7426

developed to represent the U.S. peanut germplasm collection, which will be useful in screening for traits that are difficult and/or expensive to measure (Holbrook and Dong, 2005). The chickpea mini core collection has been useful in identifying genotypes with deep root system that avoids drought stress (Krishnamurthy et al., 2003; Kashiwagi et al. (2005), and genotypes with high salinity tolerance (Serraj et al., 2004). Similarly, by screening a mini core collection of peanut Upadhyaya (2005) identified 18 genotypes with drought resistance traits, similar to the resistant control cultivar, but genetically diverse from them. Although multiple uses of pigeonpea are well known, screening germplasm to identify useful parents for agronomic traits has been scanty because of the costs involved in such screenings. The present mini core subset of pigeonpea facilitates screening for agronomic traits and in identifying efficient genotypes suitable for various purposes such as medicinal uses, fodder, agroforestry, alley cropping, vegetable uses, as feed for ruminants and non-ruminant animals (such as poultry and pigs), and dual purpose genotypes suitable for seed and lac production in a very cost-effective way. Also, the pigeonpea mini core can be utilized for molecular characterization to identify genetically diverse parents for use in crop improvement. The list of pigeonpea genotypes included in the mini core subset with the ICP number, cluster number, and country of origin is available on diskette, free of charge from the corresponding author. This information is also available at: www.icrisat.org/PigeonPea/MiniCorecollection.htm (verified 11 July 2006).

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