

Phenotypic diversity in the pigeonpea (*Cajanus cajan*) core collection

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Abstract The pigeonpea core collection developed at ICRISAT genebank consists of 1,290 accessions from 53 countries. The core collection, which includes selected lines in extra early, early, medium and late maturity groups was evaluated for 18 qualitative and 16 quantitative characters during the 2004 rainy season, to assess the phenotypic diversity and determine the relative importance of different characters in evaluating pigeonpea germplasm accessions. The four maturity groups differed significantly for all characters under study. The medium maturity group showed significantly higher mean number of primary, secondary and tertiary branches, number of racemes, pod bearing length, pods per plant, shelling percent and plot seed yield. Late maturity group showed significantly higher mean for leaf size, plant height, pod length, seeds per pod and 100-seed weight, indicating this group as a good source of vegetable pigeonpea. Significant positive correlations were found between number of secondary branches and pods per plant in extra early group ($r = 0.756$), late maturity group

($r = 0.776$) and entire core ($r = 0.728$) and between number of racemes and pods per plant in all maturity groups and entire core. Principal coordinate and principal component analysis showed that seven qualitative and nine quantitative traits were important in explaining multivariate polymorphism. The Shannon–Weaver diversity index (H') varied for different maturity groups and traits. Phenotypic diversity, averaged over all the 16 characters, increases from extra early group (0.36 ± 0.04) to late maturity group (0.42 ± 0.04) suggesting that medium and late maturity groups have greater diversity compared to extra early and early maturity groups.

Keywords *Cajanus cajan* · Core collection · Correlation · Phenotypic diversity · Pigeonpea · Principal component analysis

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is an important legume crop of tropics and subtropics, grown as a field as well as backyard crop in about 82 countries (Nene and Shiela 1990). As a field crop, it was grown in 19 countries, over 4.4 m ha during 2004 (FAO 2005). India, which is considered the primary center of diversity (van der Maesen 1980) has the largest area under pigeonpea (3.3 m ha) followed by Myanmar

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(0.58 m ha), Kenya (0.15 m ha), Malawi (0.12 m ha), Uganda (0.08 m ha), Tanzania (0.07 m ha), Nepal (0.03 m ha), and Dominican Republic (0.01 m ha) (FAO 2005). Pigeonpea has wide adaptability to diverse climates and soils. Because of its multiple uses as food, fodder, fuel wood, rearing lac insects, hedges, windbreaks, soil conservation, roof thatches and green manure, it plays an important role in subsistence agriculture. However, the average world productivity of pigeonpea is rather low (709 kg ha⁻¹) (FAO 2004), indicating an urgent need for improving the genetic potential of the crop.

The contribution of landraces as source material for crop improvement has been substantial. In the past, the majority of released pigeonpea cultivars have been developed through selection from landraces (Pathak 1970; Laxman Singh et al. 1990). To meet the challenges in crop improvement, efforts were made to widen the genetic base by collecting and conserving germplasm across the world, which led to assembly of large collections at national and international genebanks. The genebank at ICRISAT holds 13,632 accessions of pigeonpea including 555 accessions of wild relatives from 74 countries. Of these 9,759 accessions were acquired mainly by donations from various institutes in different countries, and 3,873 accessions by launching 99 germplasm collecting missions in 33 countries (Upadhyaya et al. 2005). The cultivated accessions (13,077) are from 66 countries. However, utilization of germplasm in crop improvement is still very limited. The accessibility and utilization of a collection is inversely related to its size (Frankel and Soule 1981). Development of a core collection is one way to enhance the use of genetic resources in crop improvement (Frankel 1984). The core collection derived from an existing entire collection comprises a chosen set of accessions that represent a wide-cross section of genetic spectrum available in a given crop species with minimum amount of duplication (Brown 1989). Core collection has value in crop improvement programs and due to its reduced size, it can be evaluated extensively with limited resources. Pigeonpea core collection comprising 1,290 accessions of cultivated pigeonpea from 53 countries was developed at ICRISAT (Reddy et al. 2005). The

main aim of the present study was to assess diversity for different morpho-agronomic characters in the pigeonpea core collection to enhance the use of genetic resources in pigeonpea improvement.

Materials and methods

The experimental material consists of the pigeonpea core collection comprising 1,290 accessions including advanced cultivars (9), breeding material (466), landraces (810) and others (5), representing 12,153 accessions that are conserved in the ICRISAT genebank (Reddy et al. 2005). The experiment was conducted at ICRISAT research farm, Patancheru (18° N, 78° E, 545 m a.s.l., and about 600 km away from the sea) in an augmented design. Four control cultivars; representing different maturity groups were used. Each control cultivar was sown after every nine-test accessions. Thus, there were four checks and 36 test accessions in a block of 40 entries. The checks used were ICP 11543 (extra early), ICP 6971 (early), ICP 8863 (medium maturing) and ICP 7221 (late maturing). Sowing was done on 30 June 2004 in rainy season on vertisols (Kasireddipally Series-Isohyperthermic-Type-Pellustert). Each accession was sown as single row of 4-meter length, spaced 75 cm apart. Plant to plant spacing within the row was 50 cm. Crop was fertilized with 20 kg N and 40 kg P₂O₅ ha⁻¹ as a basal dose. The experiment was provided with life saving irrigation and protected from weeds, pests and diseases. The crop was harvested during November to February 2005 depending on the maturity of the accessions.

The observations 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 the 'Descriptors for Pigeonpea' (IBPGR and ICRISAT 1993). Observations on all qualitative and six quantitative characters (days to 50%

flowering, days to 75% maturity, 100-seed weight, harvest index, shelling percent, and plot seed yield) was recorded on plot basis. Observations on remaining ten quantitative traits (leaf size, plant height, number of primary, secondary and tertiary branches, number of racemes, pod bearing length, pods per plant, pod length, seeds per pod) were recorded on three random plants from each plot.

Using the standard maturity classification that was developed for pigeonpea and being followed at ICRISAT (ICRISAT 1978), the accessions of core collection were grouped as extra early (<80 days to 50% flowering), early (81–100 days to 50% flowering), medium (101–130 days to 50% flowering) and late maturity (>130 days to 50% flowering) group. Days to 50% flowering refer to the number of days from the date of sowing to the date when 50% of the plants in a given plot have at least one open flower. This classification of core collection resulted in 37 accessions belonging to the extra early group, 87 accessions to the early group, 669 accessions to the medium maturity group, and 497 accessions to the late maturity group. Phenotypic proportions for the 18 qualitative traits were calculated based on accessions in each maturity group.

The data were analyzed following REML (Residual Maximum Likelihood) approach using GENSTAT 6.1. Mean, range, and variances for all quantitative traits were calculated for each of the maturity groups. The means of different maturity groups for all traits were compared using the Newman–Keuls procedure (Newman 1939; Keuls 1952). The homogeneity of variances of maturity groups was tested using Levene's test (Levene 1960). Phenotypic correlations were estimated among all traits in the entire core as well as in all maturity groups and identified number of significant and meaningful correlations. Principal coordinate analysis (PCoA) of 18 qualitative traits and principal component analysis (PCA) of 16 quantitative traits were performed to find out the relative importance of different traits in capturing the variation in core collection or its four subsets. A phenotypic distance matrix was created by calculating the differences between

each pair of accessions for each character. 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). Shannon and Weaver diversity index (H') was used as a measure of phenotypic diversity for each trait (Shannon and Weaver 1949). The index was estimated for each trait over all accessions and for all traits within each maturity group.

Results and discussion

Because pigeonpea is often cross-pollinated, variation for different characters was considerably high. Out-crossing in pigeonpea ranges from 3% to 26% and varies according to location, genotype, and intensity of insect population and time of flowering (Bhatia et al. 1981; Saxena et al. 1990; Reddy et al. 2004). Therefore, heterogeneity for almost all traits exists in the germplasm samples collected from farmer's fields. The intra-accession variation that was available in the collected accessions is maintained in the genebank. When the accessions were characterized, more than one class of traits within each accession was observed. Frequency distribution of different classes within each qualitative character, mean values, variance, character associations, principal components and diversity in four maturity groups and the entire core subset is discussed hereunder.

Qualitative characters

Vigor

Vigor of plants in accessions at 50% flowering was recorded visually as low (score 3), intermediate (score 5) and high (score 7). The medium and long duration genotypes predominant in the world collection, and show more plant vigor, due to their larger seeds and leaves. Highly vigorous accessions were predominant in the entire core (70.3%), medium maturity group (77.95%) and late maturity group (75.7%) (Remanandan et al. 1988). On the other hand, accessions with

relatively smaller seeds in the extra early and early groups showed intermediate vigor (Appendix 1).

Growth habit

It was recorded in three classes: compact, spreading and semi-spreading. In the entire core, 91.1% accessions were of semi-spreading habit followed by compact type with 8.7%. A similar pattern was exhibited in all the maturity groups. The extra early maturity group contained a larger proportion of compact cultivars (24.3%), no accessions in this and the early groups were of spreading habit. Most of the accessions in extra early and early maturity groups were the products of breeding programs, which aimed at developing early maturing, short statured and determinate varieties (Remanandan et al. 1988).

Plant pigmentation

The stem color recorded as plant pigmentation was classified into five classes (green, purple, green + purple, green + red, purple + green). About 97% of the core accessions have plants with green stem. Remaining classes are negligible and are found only in the medium and late maturity groups. Conspicuously, all accessions of extra early and early maturity groups had green stem.

Stem thickness

It was recorded visually as thin, intermediate and thick at 50% flowering. Thick stems are predominant in the entire core (90.7%), medium (95.6%), and late (96.8%) maturity groups. High proportion of accessions in the extra early group (32.4%) produced thin stems. Increase in stem thickness with maturity duration may be attributed to the longer growth period.

Flower base color

Of the six classes (yellow, orange yellow, red, light yellow, ivory and mixture of light yellow and yellow), yellow flower base color was dominant

(>95% accessions) in the core subset as well as in all maturity groups. Only the accessions that produced flowers with yellow and orange yellow flower base color were found in the extra early and early maturity groups.

Flower streak color

Color of streaks on vexillum was recorded as red, purple, yellow, none (no other color on streaks) and red (more plants without any other color to the streaks and few plants with red streaks), red and none (more plants with red streaks and few plants without any other color to the streaks), and none (all plants without any other color to the streaks). Accessions having flowers with red streaks were maximum (>88%) in the core as well as in all four maturity groups, and all accessions in the extra early group had red streaks.

Flower streak pattern

In total, 23 classes were observed for this trait in the entire core and maximum accessions were with few streaks (69.7%) followed by medium streaks (12.4%). A similar pattern was observed in all four maturity groups (Appendix 1).

Flowering pattern

Four classes, [Indeterminate (NDT), determinate (DT), and mixture of both patterns (DT+NDT, and NDT+DT)] were observed for this character with a maximum of 95.8% NDT type in the entire core. Proportion of NDT was 80.5% in the early, 97.2% in the medium and 100% in the late maturity group. On the other hand, maximum DT (48.7%) accessions were observed in the extra early group, which could be due to high proportion of targeted selection of breeding programs (Remanandan et al. 1988).

Pod color

It was recorded in eight classes (green, light green, purple and dark purple and four are heterogeneous classes in different combinations of these colors). Green pod color was predominant (>89%) in the

entire core, and in all maturity groups. The other pod color that appeared (<3%) in all the four maturity groups and in entire core was purple. All other colors appeared only in the late maturity group (Appendix 1).

Pod shape

Cylindrical pod shape was most common in the entire core (82.6%), extra early (83.8%), early (90.8%), medium (93.1%) and the late (67.2%) maturity groups. Remaining accessions had flat pods (Appendix 1).

Pod hairiness

This is a monomorphic trait and all accessions in the entire core subset had pubescent pods.

Seed color pattern

In total, 11 classes (mottled, speckled and plain and different combination of these three patterns) were observed in the core. Maximum number of accessions had plain (>59.4%) seed color pattern followed by speckled (>5.4%) in the core as well as in all maturity groups.

Primary seed color

Large diversity for primary seed color was observed in the core. A total of 64 classes (14 solitary and 50 classes having heterogeneity) were observed. In the core, accessions having orange seed color was maximum (51.0%) followed by cream (21.6%) and light cream (3.1%) seed colors. All the four maturity groups showed similar pattern as that of entire core collection (Appendix 1).

Secondary seed color

This trait was recorded in 20 classes (13 solitary and 7 heterogeneous). Absence of secondary seed color (i.e. uniformly one color of the seed coat) was more common (68.8%) in the core as well as in all the maturity groups. However, white color as secondary seed color was

observed in considerable proportions in the core (20.9%), extra early (21.6%), early (11.5%), medium (12.7%) and the late (33.2%) maturity groups.

Seed eye color

It was recorded in 22 classes (13 solitary and nine heterogeneous). Brown eye color was predominant in the core and also in all the maturity groups (>83%). Brown and reddish brown seed eye color accessions were found in all maturity groups. All seed eye colors, except cream and the mixture of purple and brown appeared in the late maturity group (Appendix 1).

Seed eye color width

Six classes (three solitary and three heterogeneous) were recorded for this trait in the entire core. Narrow eye color width was predominant (>76%) in the entire core as well as in all maturity groups.

Seed shape

In this trait, six classes (oval, square, elongate, globular and two heterogeneous classes) were recorded in the core. Oval shape was most common (>94% accessions) in the entire core and in all the maturity groups. Square shape was the other seed shape that appeared in the entire core as well as in all maturity groups in some proportion (<3.0%).

Seed strophiole

This is a primitive trait differentiating wild and the cultivated pigeonpea. It is prominent in almost all wild relatives. Observation on seed strophiole was recorded as absent or present. Maximum frequency of accessions (95.5%) in the core did not produce the strophiole. Only 4.4% in the core, 8.1% in the extra early group and 8.3% accessions in the late maturity group produced strophiole.

Quantitative characters

Range, mean and variance

REML analysis indicated that the variance components due to genotypes were significant for all quantitative characters in the entire core as well as in all the maturity groups suggesting significant variability for all traits in the core and in the four maturity groups (data not given). The mean, range and variances for 16 quantitative traits of the four maturity groups are given in Table 1. The four maturity groups differed significantly for different traits. The differences between extra early, early, medium and late maturity groups were significant for days to 50% flowering, plant height, days to 75% maturity, number of secondary branches and seed yield (Table 1). Mean values in the early group were significantly greater than in the extra early group for number of racemes, pods per plant and harvest index. Mean values in the late maturity group were significantly greater than medium maturity group for seven traits (leaf size, days to 50% flowering, plant height, days to 75% maturity, pod length, seeds per pod and 100 seed weight). The extra early group differed significantly with the late maturity group for all characters except 100-seed weight. High seed weight in the extra early group could be the result of selection by breeders in the recent years to develop short duration and determinate varieties (which can produce large seeds), adaptable to different cropping systems (Laxman Singh et al. 1990). Majority of determinate type accessions were extra early and early and are products of breeding programs (Remanandan et al. 1988). Medium maturity group having high proportion of semi-spreading and indeterminate accessions recorded significantly higher mean values for number of secondary branches, pod bearing length, shelling percent, and seed yield than all other maturity groups. In the present study, the extra early and the early maturity groups were not found promising for any of the other characters under study except days to 50% flowering, plant height and days to 75% maturity, which is in agreement with findings of Remanandan et al. (1988). Among four maturity groups, the medium maturity group was found

more promising for important agronomic characters (for e.g. number of primary, secondary and tertiary branches, number of racemes, pod bearing length, pods per plant, harvest index, shelling percent and seed yield (kg ha^{-1}). However, the late maturity group was good source for long pods and large seeds (for vegetable pigeonpea).

The variances were heterogeneous ($P < 0.0001$) for all quantitative traits, except for days to maturity and number of tertiary branches. The late maturing group recorded maximum variance for all traits, except plant height, days to 75% maturity, pod bearing length and shelling percent. Higher variance was observed in the extra early group for days to 75% maturity and shelling percent and the early group for plant height and pods per plant (Table 1).

Range of variation was highest in the early maturity group for plant height, days to 75% maturity and pod bearing length; in the medium maturity group for number of primary branches, pod length, seeds per pod, 100-seed weight, harvest index, shelling percent and seed yield; and in the late maturity group for leaf size, days to 50% flowering, number of secondary and tertiary branches number, number of racemes and pods per plant (Table 1). On the other hand, range was lowest in the extra early group for all the traits, except seeds per pod, harvest index, and shelling percent. Range for leaf size, days to 50% flowering, number of secondary and tertiary branches, racemes number and pods per plant increased with the increase in maturity duration. This increase in variation from the extra early group to the late maturity group for above traits may be attributed to the high proportion of highly photoperiod sensitive indeterminate accessions in medium and late maturity groups (Remanandan et al. 1988).

Correlations

Phenotypic correlations were estimated among all quantitative characters in all the maturity groups and in the entire core. Within the group, correlations were tested for significance (Snedecor and Cochran 1980). In the present study, 37 correlations in the extra early group, 99 in the early group, 105 in the medium group, 111 in the late

Table 1 Mean, range and variances for quantitative characters in different maturity groups of the pigeonpea core collection, at ICRISAT center Patancheru, India

Character	Mean ^a				Range				Variance ^b				F-value	P
	Extra early (37) ^c	Early (87)	Medium (669)	Late (497)	Extra early (37)	Early (87)	Medium (669)	Late (497)	Extra early (37)	Early (87)	Medium (669)	Late (497)		
Leaf size (cm ²)	13.7c	13.5c	16.3b	21.6a	6.1–19.6	6.2–34.6	7.9–44.3	10.5–54.2	11.43	23.51	22.19	52.85	13.19	<0.0001
Days to 50% flowering	72.0d	92.5c	117.9b	142.4a	62.5–80.0	80.9–100.1	100.9–130.4	130.5–168.7	23.05	26.32	47.08	80.66	23.65	<0.0001
Plant height (cm)	128.9d	167.6c	202.4b	215.9a	104.4–189.6	107.4–226.0	133.9–241.5	167.9–258.3	329.50	639.40	205.20	233.40	27.19	<0.0001
Days to 75% maturity	131.6d	156.3c	175.1b	205.5a	112.8–155.1	122.4–178.2	155.1–209.0	180.2–228.3	114.07	65.60	79.10	67.80	2.54	0.0552
Primary branches (no.)	12.8b	13.2b	15.2a	14.7a	9.5–16.5	9.4–18.4	7.6–29.4	7.7–26.4	3.28	3.11	9.43	13.87	17.76	<0.0001
Secondary branches (no.)	16.9d	23.2c	29.4a	26.9b	13.2–26.1	14.4–37.0	14.9–49.9	13.7–59.7	7.74	25.80	36.77	51.81	9.99	<0.0001
Tertiary branches (no.)	2.1b	2.8b	5.1a	4.5a	1.0–5.8	1.0–9.8	1.1–23.4	1.1–33.5	0.64	2.42	10.64	11.50	2.46	0.614
Racemes (no.)	72.6c	126.3b	171.5a	161.5a	44.2–123.7	54.0–291.4	58.6–366.0	48.7–363.3	399.10	2419.40	2245.00	4394.60	32.48	<0.0001
Pod bearing length (cm)	64.2c	72.8a	71.5a	67.0b	54.9–76.6	53.6–96.1	46.9–88.9	48.2–85.8	37.83	86.54	31.80	29.23	24.75	<0.0001
Pods per plant (no.)	102.0c	169.1b	279.0a	286.0a	70.8–240.4	75.5–352.6	69.0–674.0	66.0–821.0	1296.00	4497.70	8775.00	20170.00	44.14	<0.0001
Pod length (cm)	5.3b	5.1c	5.2cb	5.7a	4.4–7.3	3.9–7.0	3.1–8.7	4.1–8.8	0.42	0.28	0.39	0.88	20.54	<0.0001
Seeds per pod (no.)	3.8b	3.8b	3.9b	4.1a	2.3–4.6	3.2–4.7	3.1–5.9	2.7–5.5	0.15	0.08	0.10	0.21	14.53	<0.0001
100 Seed weight (g)	10.2a	9.0b	8.5b	10.2a	7.6–15.3	6.0–13.8	5.3–20.1	5.3–19.4	3.21	1.99	3.11	8.13	28.31	<0.0001
Harvest index (%)	18.7c	20.7b	23.5a	23.3a	13.9–27.2	14.1–26.8	13.9–40.1	12.7–38.7	11.33	8.86	10.33	16.30	6.94	<0.0001
Shelling percent	57.0c	59.8b	62.3a	60.0b	47.8–65.2	50.5–65.2	44.3–69.7	43.9–68.7	20.53	10.67	5.66	10.04	8.13	<0.0001
Yield kg ha ⁻¹	587.0d	895.0c	1612.0a	1472.0b	498.0–792.0	520.0–1516.0	509.0–3191.0	498.0–3078.0	7121.00	63869.00	190088.00	283406.00	29.78	<0.0001

^a Differences between means of different maturity groups were tested by Newman–Keuls test. Mean followed by same letter indicate non-significant and different letter indicate

Significant differences at $P = 0.05$

^b Variance homogeneity tested by Levene's test

^c Numbers within parenthesis indicate number of accessions in each maturity group

Table 2 Meaningful correlations ($r > 0.707$) in different maturity groups of pigeonpea core collection and in the entire core collection, at ICRISAT center, Patancheru, India

Character	Extra early	Early	Medium	Late	Core collection
Number of secondary branches vs. pods per plant	0.756	0.687	0.644	0.776	0.728
Number of racemes vs. pods per plant	0.841	0.890	0.866	0.923	0.901

maturing group and 118 in the entire core were found to be significant at 5% probability level. Similarly, 28 correlations in the extra early group, 85 in the early group, 98 in the medium maturity group, 109 in the late maturity group and 117 in the entire core were significant at 1% probability level. As more than 50% variation in one character is predicted by another character, the correlation coefficients greater than 0.707 and lower than -0.707 were considered as biologically meaningful (Skinner et al. 1999). Two such meaningful correlations were found in the entire core and in all the four maturity groups. Meaningful associations were also found between number of secondary branches and pods per plant in the extra early group ($r = 0.756$), late maturity group ($r = 0.776$) and entire core ($r = 0.728$); and between number of racemes and pods per plant in the extra early ($r = 0.841$), early ($r = 0.890$), medium ($r = 0.866$) and late ($r = 0.923$) maturity groups and entire core ($r = 0.901$) (Table 2). Magnitudes of correlations indicate maturity dependent positive associations among these characters. These results suggest that number of secondary branches and racemes per plant should be recorded ignoring the number of pods per plant, which takes relatively more time to record, to improve the seed yield (r value between number of pods and yield = 0.724).

Principal coordinates and principal components

The percentage variation explained by the first five principal coordinates (PCo) was 69.9% in the entire core, 80.5% in the extra early group, 71.9% in the early maturity group, 82.6% in the medium maturity group and 71.0% in the late maturity group. The PCo 1, the most important coordinate accounted for 34.69% in the entire core, 32.39% in the extra early group, 31.64% in the early

group, 39.46% in the medium maturity group and 38.73% in the late maturity group. Only seven traits (vigor, growth habit, stem thickness, flowering pattern, pod shape, primary seed color and secondary seed color) showed high correlation with PCo scores and occurred at least three times out of five, indicating their importance in explaining the variation.

The percentage of variation explained by the first five principal components (PC) and the vector loadings for each agronomic character and PC are given in Table 3. The first five PCs explained 78.81% variation in the entire core, 76.9% in the extra early group, 74.9% in the early group, 66.2% in the medium maturity group and 77.8% in the late maturity group and reduced the original 16 traits to 12 in the entire core and in all maturity groups, except medium maturity group. The PC1, which is most important component accounted for 38.62% variation in the entire core, 29.54% in the extra early group, 43.57% in the early group, 30.32% in the medium maturity group and 43.67% in the late maturity group. The eigen values for the entire core, extra early, early, medium and late maturity groups were 6.18, 4.73, 6.97, 4.85 and 6.83, respectively. The PC1 separates accessions on six traits (number of secondary and tertiary branches, number of racemes, pods per plant, pod length and 100-seed weight) in the entire core; on five traits (number of secondary and tertiary branches, number of racemes, pod bearing length and pods per plant) in the extra early group; on seven traits (days to 50% flowering, plant height, number of secondary branches, number of racemes, pods per plant, shelling percent and plot seed yield) in the early group; on five traits (leaf size, number of secondary branches, number of racemes, pods per plant and pod length) in the medium maturity group; and on seven traits (leaf size, number of secondary branches, number of racemes, pods per

Table 3 Vector loadings and percentage of variation explained by the first five principal components in different maturity groups of pigeonpea core collection, at ICRISAT center, Patancheru, India

Character	Principal components				
	1	2	3	4	5
<i>Entire core</i>					
Variation explained (%)	38.62	21.40	7.67	6.08	5.00
Latent root	6.18	3.42	1.23	0.97	0.80
Leaf size (cm ²)	0.244	- 0.296	0.076	- 0.077	- 0.017
Days to 50% flowering	0.029	- 0.508	- 0.089	0.114	0.039
Plant height (cm)	- 0.126	- 0.419	0.033	0.123	- 0.384
Days to 75% maturity	0.027	- 0.495	- 0.094	0.159	0.035
Primary branches (no.)	- 0.239	- 0.058	0.014	0.531	0.234
Secondary branches (no.)	- 0.322	- 0.102	- 0.206	- 0.214	0.074
Tertiary branches (no.)	- 0.189	- 0.083	- 0.395	- 0.650	0.162
Racemes (no.)	- 0.352	- 0.131	- 0.101	- 0.070	- 0.026
Pod bearing length (cm)	- 0.232	0.132	0.109	- 0.057	- 0.794
Pods per plant (no.)	- 0.339	- 0.183	- 0.088	0.003	0.014
Pod length (cm)	0.304	- 0.207	0.124	- 0.200	- 0.121
Seeds per pod (no.)	0.260	- 0.195	0.199	- 0.258	0.037
100 Seed weight (g)	0.305	- 0.147	0.083	- 0.107	- 0.109
Harvest index (%)	- 0.205	- 0.104	0.566	- 0.102	0.315
Shelling percent	- 0.215	0.038	0.566	- 0.226	0.049
Yield kg ha ⁻¹	- 0.303	- 0.174	0.213	- 0.055	- 0.037
<i>Extra early maturity group</i>					
Variation explained (%)	29.540	17.600	15.590	7.900	6.230
Latent root	4.727	2.816	2.494	1.264	0.997
Leaf size (cm ²)	0.064	- 0.427	- 0.055	0.015	0.455
Days to 50% flowering	- 0.050	0.196	- 0.473	- 0.065	- 0.234
Plant height (cm)	- 0.114	0.397	- 0.100	- 0.271	0.358
Days to 75% maturity	0.070	0.076	- 0.263	- 0.587	0.049
Primary branches (no.)	0.055	- 0.189	0.376	- 0.480	0.085
Secondary branches (no.)	- 0.419	- 0.025	- 0.001	0.166	0.136
Tertiary branches (no.)	- 0.386	- 0.019	0.054	0.245	0.049
Racemes (no.)	- 0.389	0.121	- 0.109	- 0.085	0.229
Pod bearing length (cm)	- 0.308	0.027	- 0.179	0.002	- 0.205
Pods per plant (no.)	- 0.447	0.066	0.023	0.007	0.095
Pod length (cm)	- 0.145	- 0.474	- 0.248	0.073	- 0.023
Seeds per pod (no.)	- 0.105	- 0.413	- 0.126	- 0.305	- 0.195
100 Seed weight (g)	0.027	- 0.284	- 0.486	- 0.025	0.249
Harvest index (%)	- 0.281	- 0.055	0.361	- 0.252	0.227
Shelling percent	- 0.075	- 0.280	0.241	0.094	- 0.191
Yield kg ha ⁻¹	- 0.290	- 0.046	0.058	- 0.285	- 0.536
<i>Early maturity group</i>					
Variation explained (%)	43.570	12.020	6.920	6.430	5.930
Latent root	6.970	1.923	1.108	1.029	0.949
Leaf size (cm ²)	0.101	- 0.463	- 0.348	- 0.072	- 0.359
Days to 50% flowering	- 0.294	- 0.169	0.188	0.062	- 0.323
Plant height (cm)	- 0.310	0.042	0.146	0.192	0.216
Days to 75% maturity	- 0.274	- 0.131	0.246	0.141	- 0.339
Primary branches (no.)	- 0.167	- 0.023	- 0.283	- 0.582	0.178
Secondary branches (no.)	- 0.305	0.086	0.097	- 0.358	0.022
Tertiary branches (no.)	- 0.214	- 0.029	0.265	- 0.492	0.029
Racemes (no.)	- 0.328	- 0.034	- 0.061	0.008	0.098
Pod bearing length (cm)	- 0.266	0.140	0.124	0.378	0.336
Pods per plant (no.)	- 0.325	- 0.100	- 0.051	- 0.069	0.119
Pod length (cm)	0.150	- 0.501	0.218	0.053	0.394
Seeds per pod (no.)	0.091	- 0.332	0.578	- 0.088	- 0.207

Table 3 continued

Character	Principal components				
	1	2	3	4	5
100 Seed weight (g)	0.171	-0.441	-0.025	-0.038	0.455
Harvest index (%)	-0.207	-0.276	-0.409	0.206	-0.141
Shelling percent	-0.286	-0.128	-0.140	0.141	0.101
Yield kg ha ⁻¹	-0.312	-0.226	-0.105	0.058	-0.001
<i>Medium maturity group</i>					
Variation explained (%)	30.320	11.120	10.060	8.040	6.670
Latent root	4.851	1.779	1.610	1.287	1.067
Leaf size (cm ²)	0.301	0.185	0.071	0.191	0.002
Days to 50% flowering	-0.007	0.222	0.431	0.355	0.083
Plant height (cm)	-0.250	-0.219	0.473	-0.001	0.157
Days to 75% maturity	0.096	0.159	0.456	0.112	-0.446
Primary branches (no.)	-0.197	-0.149	0.057	0.283	-0.623
Secondary branches (no.)	-0.332	0.189	-0.098	0.141	0.074
Tertiary branches (no.)	-0.194	0.411	-0.035	0.212	0.386
Racemes (no.)	-0.376	0.234	-0.043	-0.012	-0.152
Pod bearing length (cm)	-0.167	-0.178	0.422	-0.470	0.203
Pods per plant (no.)	-0.376	0.262	-0.001	0.036	-0.046
Pod length (cm)	0.314	0.335	0.130	-0.140	-0.030
Seeds per pod (no.)	0.195	0.412	-0.068	-0.008	-0.072
100 Seed weight (g)	0.299	0.131	-0.022	-0.103	0.090
Harvest index (%)	-0.148	-0.113	-0.401	0.048	-0.116
Shelling percent	-0.048	0.272	-0.034	-0.618	-0.360
Yield kg ha ⁻¹	-0.300	0.274	0.001	-0.209	0.065
<i>Late maturity group</i>					
Variation explained (%)	43.670	15.520	7.830	6.330	5.460
Latent root	6.828	2.483	1.253	1.013	0.874
Leaf size (cm ²)	0.288	-0.134	0.118	0.179	-0.156
Days to 50% flowering	0.194	-0.498	0.007	-0.006	0.225
Plant height (cm)	-0.027	-0.447	0.181	-0.195	-0.469
Days to 75% maturity	0.164	-0.516	0.051	-0.021	0.254
Primary branches (no.)	-0.221	-0.126	0.148	-0.416	0.185
Secondary branches (no.)	-0.297	-0.135	-0.237	0.222	0.009
Tertiary branches (no.)	-0.164	-0.101	-0.495	0.556	-0.010
Racemes (no.)	-0.318	-0.240	-0.055	0.138	-0.032
Pod bearing length (cm)	-0.251	0.051	0.040	-0.110	-0.596
Pods per plant (no.)	-0.303	-0.296	0.017	0.099	-0.015
Pod length (cm)	0.318	-0.041	0.116	0.242	-0.227
Seeds per pod (no.)	0.282	0.045	0.149	0.296	-0.157
100 Seed weight (g)	0.306	-0.052	0.102	0.155	-0.162
Harvest index (%)	-0.181	-0.006	0.580	0.349	0.304
Shelling percent	-0.211	0.234	0.401	0.209	0.082
Yield kg ha ⁻¹	-0.284	-0.121	0.282	0.147	-0.221

plant, pod length, 100 seed weight and yield) in the late maturity group. Considering the analyses of all maturity groups and the entire core, nine traits (days to 50% flowering, plant height, number of secondary and tertiary branches, number of racemes, pods per plant, pod length, 100-seed weight and yield) occurred at least four times in

the first five PCs, indicating their importance for characterization of pigeonpea germplasm accessions. Remaining characters (leaf size, days to 75% maturity, number of primary branches, pod bearing length, seeds per pod, harvest index and shelling percent) had no contribution in explaining variation in the first five PCs of the entire core

as well as all the four maturity groups, indicating their low importance as pigeonpea descriptors for characterization.

Diversity index

The grouping of similar genotypes depends on the dissimilarity among them, which can be determined by a phenotypic diversity index (Table 4). The average diversity was highest in the extra early group (0.2619) and lowest in the medium maturity group (0.1543). Range of phenotypic diversity was highest in the late maturity group (0.0363–0.6337) and lowest in the extra early group (0.1042–0.5769) and it was almost same in the medium maturity group (0.0007–0.5236) and the entire core (0.0005–0.5229) (Table 4). High range of phenotypic diversity in the late maturity group may attribute to indeterminate flowering pattern and high percent of out-crossing during prolonged flowering period. When compared within each maturity group between accessions, lowest phenotypic diversity index was observed between ICP 10923 and ICP 14829 in the extra early group (0.104); between ICP 12989 and ICP 6965 in the early group (0.066); between ICP 11790 and ICP 15016 in the medium maturity group (0.001); between ICP 11012 and ICP 12235 in the late maturity group (0.036); and between ICP 11790 and ICP 15016 in the entire core (0.001). Highest phenotypic diversity index was

observed between ICP 14444 and ICP 14471 in the extra early group (0.577); between ICP 16198 and ICP 7782 in the early group (0.561); between ICP 6523 and ICP 8265 in the medium maturity group (0.524); between ICP 12079 and ICP 7941 in the late maturity group (0.634); and between ICP 14444 and ICP 11246 in the entire core (0.523). Mean phenotypic diversity index was highest (0.262) between accessions of extra early group. The accessions with high phenotypic diversity index in the extra early maturity group would be useful in pigeonpea breeding programs.

The Shannon–Weaver diversity index (H') was calculated to assess the phenotypic diversity for all characters in different maturity groups and the entire core collection (Table 5). The diversity index is used as a measure of allelic richness and evenness. Low H' indicates extremely unbalanced frequency classes and lack of genetic diversity in a trait. The estimates of H' were made for each trait and four maturity groups. The diversity values were variable among traits and among maturity groups. So, the diversity within a maturity group depends upon the traits. The H' values averaged over the four maturity groups ranged from 0.04 ± 0.03 (plant pigmentation) to 0.73 ± 0.07 (primary seed color) among qualitative characters; and from 0.45 ± 0.03 (number of tertiary branches) to 0.61 ± 0.01 (number of primary branches) among quantitative characters. The H' values averaged over both qualitative and

Table 4 Phenotypic diversity index in four maturity groups of core and the core collection of pigeonpea germplasm, at ICRISAT center, Patancheru, India

Maturity group	Parameter	Diversity index	Between accessions
Extra early	Mean	0.2619	
	Minimum	0.1042	ICP 10923 and ICP 14829
	Maximum	0.5769	ICP 14444 and ICP 14471
Early	Mean	0.2289	
	Minimum	0.0657	ICP 12989 and ICP 6965
	Maximum	0.5610	ICP 16198 and ICP 7782
Medium	Mean	0.1543	
	Minimum	0.0007	ICP 11790 and ICP 15016
	Maximum	0.5236	ICP 6523 and ICP 8265
Late	Mean	0.1933	
	Minimum	0.0363	ICP 11012 and ICP 12235
	Maximum	0.6337	ICP 12079 and ICP 7941
Core collection	Mean	0.1608	
	Minimum	0.0005	ICP 11790 and ICP 15016
	Maximum	0.5229	ICP 14444 and ICP 11246

quantitative traits ranged from 0.36 ± 0.04 (extra early and early groups) to 0.42 ± 0.04 (late maturity group). In the late maturity group, possibly due to the increased out-crossing during prolonged flowering in indeterminate accessions, diversity was highest for all qualitative characters except, growth habit, stem thickness and flowering pattern. Diversity for plant pigmentation, flower base color, flower streak color, pod color and seed eye color increases with maturity duration among accessions.

Accessions in the medium maturity group were highly diverse ($H' = 0.59 \pm 0.01$) for quantitative traits followed by the late ($H' = 0.58 \pm 0.01$), early ($H' = 0.57 \pm 0.01$) and extra early ($H' = 0.53 \pm 0.02$) maturity groups. Diversity level increases from extra early group to late maturity group for leaf size, pod bearing length and pod length indicating the association of these traits with late maturity. High diversity for most of the characters in the medium and late maturing groups having

Table 5 Shannon–Weaver diversity index (H') for qualitative and quantitative characters in different maturity groups of pigeonpea core collection, at ICRISAT center, Patancheru, India

Character	Maturity group				Mean \pm SE
	Extra early (37) ^a	Early (87)	Medium (669)	Late (497)	
<i>Qualitative characters</i>					
Vigor	0.091	0.155	0.229	0.241	0.18 \pm 0.03
Growth habit	0.241	0.174	0.107	0.152	0.17 \pm 0.03
Plant pigmentation	0.000	0.000	0.032	0.114	0.04 \pm 0.03
Stem thickness	0.274	0.319	0.079	0.062	0.18 \pm 0.07
Flower base color	0.054	0.065	0.064	0.074	0.06 \pm 0.00
Flower streak color	0.000	0.048	0.057	0.191	0.07 \pm 0.04
Streak pattern	0.541	0.442	0.334	0.697	0.50 \pm 0.08
Flowering pattern	0.347	0.215	0.065	0.001	0.16 \pm 0.08
Pod color	0.054	0.027	0.059	0.225	0.09 \pm 0.05
Pod shape	0.193	0.133	0.107	0.275	0.18 \pm 0.04
Seed color pattern	0.341	0.229	0.334	0.558	0.37 \pm 0.07
Primary seed color	0.688	0.571	0.738	0.918	0.73 \pm 0.07
Secondary seed color	0.428	0.208	0.345	0.571	0.39 \pm 0.08
Seed eye color	0.054	0.186	0.218	0.368	0.21 \pm 0.06
Seed eye color width	0.149	0.123	0.146	0.286	0.18 \pm 0.04
Seed Shape	0.108	0.055	0.041	0.121	0.08 \pm 0.02
Seed strophiole	0.122	0.000	0.040	0.130	0.07 \pm 0.03
Mean \pm SE	0.22 \pm 0.05	0.17 \pm 0.04	0.18 \pm 0.04	0.29 \pm 0.06	0.21 \pm 0.03
<i>Quantitative characters</i>					
Leaf size (cm ²)	0.562	0.572	0.563	0.572	0.57 \pm 0.00
Days to 50% flowering	0.581	0.563	0.604	0.522	0.57 \pm 0.02
Plant height (cm)	0.510	0.611	0.632	0.621	0.59 \pm 0.03
Days to 75% maturity	0.567	0.580	0.601	0.564	0.58 \pm 0.01
Primary branches (no.)	0.578	0.619	0.622	0.609	0.61 \pm 0.01
Secondary branches (no.)	0.532	0.585	0.621	0.607	0.59 \pm 0.02
Tertiary branches (no.)	0.391	0.475	0.515	0.429	0.45 \pm 0.03
Racemes (no.)	0.525	0.567	0.618	0.592	0.58 \pm 0.02
Pod bearing length (cm)	0.567	0.578	0.627	0.630	0.60 \pm 0.02
Pods per plant (no.)	0.381	0.543	0.616	0.572	0.53 \pm 0.05
Pod length (cm)	0.530	0.561	0.561	0.610	0.57 \pm 0.02
Seeds per pod (no.)	0.560	0.609	0.549	0.600	0.58 \pm 0.01
100 Seed weight (g)	0.584	0.566	0.570	0.591	0.58 \pm 0.01
Harvest index (%)	0.528	0.636	0.607	0.603	0.59 \pm 0.02
Shelling percent	0.567	0.592	0.554	0.579	0.57 \pm 0.01
Yield kg ha ⁻¹	0.460	0.541	0.624	0.602	0.56 \pm 0.04
Mean \pm SE	0.53 \pm 0.02	0.57 \pm 0.01	0.59 \pm 0.01	0.58 \pm 0.01	0.57 \pm 0.01
Mean \pm SE (over all traits)	0.36 \pm 0.04	0.36 \pm 0.04	0.37 \pm 0.04	0.42 \pm 0.04	0.39 \pm 0.04

^a Numbers within parenthesis indicate number of accessions in each maturity group

maximum indeterminate accessions could be due to evolution of new variation because of prolonged out-crossing. Higher sensitivity of the crop for photoperiod and temperature during long crop growth period might have also contributed for high diversity in late maturity group. On the other hand, extra early and early maturing groups having maximum determinate type accessions, which are mostly the products of breeding programs and less sensitive to photoperiod and temperature has probably resulted in lower diversity (Saxena and Sharma 1990).

Conclusions

As evidenced in the present study, medium and late maturity groups are more promising than extra early and early groups for diversity,

particularly, for agronomic traits. However, accessions in the extra early and early maturity groups are less sensitive to temperature and photoperiod and adaptable in different cropping systems (Saxena and Sharma 1990). Days to 50% flowering, plant height, number of secondary and tertiary branches, number of racemes, pods per plant, pod length, 100 seed weight and seed yield were found as more important for characterizing pigeonpea germplasm accessions. Future germplasm collections for pigeonpea should be preferably focus on the traits mentioned above to update the present core collection. The information generated in this study could be used to reduce the size of the core collection further to develop a mini core subset (Upadhyaya and Ortiz 2001). This will provide easy access to the pigeonpea collection through replicated multiloational evaluation of mini core to identify useful parents for use in crop improvement programs.

Appendix 1 Frequency distribution of qualitative characters in different maturity groups of pigeonpea core collection, at ICRISAT center, Patancheru, India

Character	Entire core	Maturity group			
		Extra early	Early	Medium	Late
No. of accessions	1290	37	87	669	497
<i>Vigor at 50% flowering</i>					
Low	0.16	5.41			
Intermediate	29.59	94.59	88.51	22.05	24.35
High	70.25		11.49	77.95	75.65
<i>Growth habit</i>					
Compact	8.71	24.32	13.79	6.28	9.86
Spreading	0.16			0.15	0.20
Semi-spreading	91.13	75.68	86.21	93.57	89.94
<i>Plant pigmentation</i>					
Green	97.33	100.00	100.00	98.62	94.97
Green, Purple	0.63				1.61
Green, Red	1.49			1.38	2.01
Purple	0.39				1.01
Purple, Green	0.16				0.40
<i>Stem thickness</i>					
Thin	1.02	32.43	1.15		
Intermediate	8.32	67.57	41.38	4.44	3.22
Thick	90.66		57.47	95.56	96.78
<i>Flower base color</i>					
Ivory	0.24				0.60
Light yellow	0.24				0.60
Light yellow, Yellow	0.08				0.20
Orange yellow	2.51	2.70	3.45	3.06	1.61

Appendix 1 continued

Character	Entire core	Maturity group			
		Extra early	Early	Medium	Late
Red	0.08			0.15	
Yellow	96.86	97.30	96.55	96.78	96.98
<i>Flower streak color</i>					
None	4.47		2.30	1.99	8.45
None, Red	0.71			0.15	1.61
Purple	0.08				0.20
Red	94.19	100.00	97.70	97.55	88.73
Red, None	0.47			0.15	1.01
Yellow	0.08			0.15	
<i>Streak pattern</i>					
Dense streaks	4.55	8.11	5.75	3.52	5.43
Dense streaks, Few streaks	0.16			0.31	
Dense streaks, Medium streaks	0.08				0.20
Dense streaks, None	0.16				0.40
Few streaks	69.70	62.16	67.82	81.93	54.53
Few streaks, Dense streaks	0.47				1.21
Few streaks, Medium streaks	0.39	2.70	1.15	0.31	0.20
Few streaks, None	0.08			0.15	
Few streaks, Plain	0.86			0.61	1.41
Medium streaks	12.40	16.22	19.54	8.58	15.90
Medium streaks, Dense streaks	0.08		1.15		
Medium streaks, Few streaks	0.16			0.15	0.20
Medium streaks, None	0.24				0.60
Medium streaks, Plain	0.71			0.46	1.21
None	4.47		1.15	1.99	8.65
None, Dense streaks	0.08			0.15	
None, Few streaks	0.08				0.20
None, Medium streaks	0.24				0.60
None, Plain	0.31				0.80
Plain	3.61	2.70	3.45	1.68	6.24
Plain, Dense streaks	0.24	5.41		0.15	
Plain, Few streaks	0.31				0.80
Plain, Medium streaks	0.63	2.70			1.41
<i>Flowering pattern</i>					
Determinate	3.69	48.65	19.54	1.84	
Determinate, Indeterminate	0.39	2.70		0.61	
Indeterminate	95.76	48.65	80.46	97.24	100.00
Indeterminate, Determinate	0.16			0.31	
<i>Pod color</i>					
Dark purple	1.41			0.31	3.22
Dark purple, Green	0.24				0.60
Green	94.19	97.30	98.85	97.40	88.93
Green, Dark purple	0.31				0.80
Green, Purple	0.86			0.15	2.01
Light green	0.08				0.20
Purple	2.83	2.70	1.15	2.14	4.02
Purple, Green	0.08				0.20
<i>Pod shape</i>					
Cylindrical	82.57	83.78	90.80	93.11	67.20
Flat	17.35	16.22	9.20	6.74	32.80
<i>Seed color pattern</i>					
Mottled	4.79		4.60	2.45	8.25
Mottled, Plain	0.78			0.92	0.80

Appendix 1 continued

Character	Entire core	Maturity group			
		Extra early	Early	Medium	Late
Mottled, Speckled	4.40	10.81		2.15	7.65
Mottled, Speckled, Plain	0.16			0.31	
Plain	73.63	78.38	87.36	82.39	59.36
Plain, Mottled	0.55	2.70		0.46	0.60
Plain, Mottled, Speckled	0.31			0.15	0.60
Plain, Speckled	1.88	2.70	1.15	1.68	2.21
Speckled	12.09	5.41	5.75	8.12	18.91
Speckled, Plain	1.33		1.15	1.38	1.41
Speckled, Plain, Mottled	0.08				0.20
<i>Primary seed color</i>					
Brown	1.49	5.41	2.30	1.07	1.61
Brown, Cream	0.24			0.31	0.20
Brown, Grey	0.08				0.20
Brown, Orange	0.08			0.15	
Black	0.16			0.15	0.20
Black, Light grey	0.08				0.20
Cream	21.59	18.92	13.79	13.17	34.21
Cream, Brown	0.08				0.20
Cream, Black	0.16			0.15	0.20
Cream, Dark brown	0.16			0.31	
Cream, Dark purple	0.16			0.15	0.20
Cream, Grey	0.08			0.15	
Cream, Light brown	0.24			0.15	0.40
Cream, Orange	2.28	8.11	1.15	2.14	2.21
Cream, Orange, dark Grey	0.08				0.20
Cream, Purple	0.16			0.15	0.20
Cream, White	0.08			0.15	
Dark Brown	1.57	8.11	4.60	1.38	0.80
Dark brown, Cream	0.24			0.31	0.20
Dark brown, Grey	0.08			0.15	
Dark brown, Light brown	0.08			0.15	
Dark brown, Orange	0.08			0.15	
Dark brown, Purple	0.08	2.70			
Dark Grey	0.39				1.01
Dark grey, Reddish brown	0.08				0.20
Dark purple	1.10			1.07	1.41
Dark purple, Orange	0.08				0.20
Grey	1.33			0.46	2.82
Grey, Cream	0.16				0.40
Grey, Dark brown	0.08				0.20
Grey, Light cream	0.24			0.15	0.40
Grey, Orange	0.16				0.40
Light brown	3.14		1.15	2.30	4.83
Light brown, Cream	0.08				0.20
Light brown, Dark brown	0.08			0.15	
Light brown, Grey	0.16			0.15	0.20
Light brown, Light grey	0.08				0.20
Light brown, Orange	0.08				0.20
Light cream	1.18			1.07	1.61
Light grey	0.08				0.20
Light grey, Orange	0.16			0.31	
Orange	51.02	48.65	65.52	61.72	34.61

Appendix 1 continued

Character	Entire core	Maturity group			
		Extra early	Early	Medium	Late
Orange, Brown	0.08			0.15	
Orange, Cream	3.14	5.41	1.15	3.37	3.02
Orange, Cream, Grey	0.08			0.15	
Orange, Dark brown	0.39		2.30	0.31	0.20
Orange, Dark grey	0.16			0.15	0.20
Orange, Dark purple	0.31			0.31	0.40
Orange, Grey	0.47		1.15	0.31	0.60
Orange, Grey brown	0.08				0.20
Orange, Light cream	0.08				0.20
Orange, Light grey	0.16			0.15	0.20
Orange, Purple	0.47			0.61	0.40
Orange, Reddish brown	1.10	2.70	1.15	1.84	
Purple	1.57		4.60	1.68	1.01
Purple, Brown	0.08				0.20
Purple, Cream	0.16				0.40
Purple, Grey	0.08				0.20
Purple, Light cream	0.08			0.15	
Purple, Orange	0.39			0.46	0.40
Reddish brown	1.26			1.84	0.80
Reddish brown, Grey	0.08		1.15		
Reddish brown, Orange	0.47			0.77	0.20
White	0.39				1.01
<i>Secondary seed color</i>					
Brown	0.24			0.31	0.20
Cream	1.02			0.46	2.01
Dark grey	0.31				0.80
Dark grey, None	0.08				0.20
Dark purple	0.08			0.15	
Dark purple, None	0.08			0.15	
Grey	0.24				0.60
Light brown	0.94	2.70		0.31	1.81
Light cream	0.31				0.80
Light grey	0.08			0.15	
None	68.84	67.57	86.21	79.33	52.11
None, Cream	0.08				0.20
None, Light brown	0.08				0.20
None, Purple	0.08				0.20
None, White	2.75	2.70	1.15	2.76	3.02
Orange	1.49	2.70		1.38	1.81
Purple	0.08			0.15	
Reddish brown	0.31	2.70		0.31	0.20
White	20.88	21.62	11.49	12.71	33.20
White, None	2.04		1.15	1.84	2.62
<i>Seed eye color</i>					
Brown	88.38	97.30	90.80	90.96	83.90
Brown, Dark grey	0.24			0.15	0.40
Brown, Dark purple	0.08				0.20
Brown, None	0.31			0.31	0.40
Brown, Purple	0.08				0.20
Brown, White	0.08				0.20
Cream	0.08			0.15	
Dark brown	1.73		2.30	2.14	1.21
Dark grey	0.71				1.81

Appendix 1 continued

Character	Entire core	Maturity group			
		Extra early	Early	Medium	Late
Dark grey, Brown	0.08				0.20
Dark purple	1.57		3.45	1.38	1.61
Dark purple, Brown	0.39			0.46	0.40
Grey brown	0.39			0.31	0.60
Light brown	0.86				2.21
Light grey	0.31			0.15	0.60
None	2.35		2.30	1.84	3.22
None, Brown	0.24				0.60
Orange	0.24			0.31	0.20
Purple	0.86			0.46	1.61
Purple, Brown	0.24			0.46	
Reddish brown	0.71	2.70	1.15	0.92	0.20
White	0.08				0.20
<i>Seed eye color width</i>					
Large width	0.39			0.46	0.40
Large width, Narrow width	0.08				0.20
Medium width	11.77	10.81	5.75	5.36	21.33
Medium width, Narrow width	0.16			0.31	
Narrow width	87.52	89.19	94.25	93.87	77.87
Narrow width, Medium width	0.08				0.20
<i>Seed shape</i>					
Elongate	0.31		1.15	0.15	0.40
Elongate, Oval	0.08	2.70			
Oval	96.62	94.59	97.70	98.47	94.16
Oval, Square	0.08				0.20
Globular	1.73			0.77	3.42
Square	1.18	2.70	1.15	0.61	1.81
<i>Seed strophiole</i>					
Absent	95.53	91.89	100.00	98.16	91.55
Present	4.48	8.11		1.84	8.45

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