



Unlocking Morphological and Genetic Diversity in Pigeonpea [*Cajanus cajan* (L.)] Accessions for Crop Improvement

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ABSTRACT

Background: Genebanks serve as repositories for superior genes found within germplasm diversity. They play a crucial role as a source of desirable genes for crop improvement. The assessment and characterization of germplasm accessions remain essential, providing insights into identifying superior germplasm or potential donor for future breeding activities.

Methods: In the present study, 258 germplasm accessions of pigeonpea and three checks (PT 0012, BSMR 736 and Asha) were used and same evaluated in augmented block design during the *kharif* season 2022 at Zonal Agricultural Research Station (ZARS) Kalaburagi. Genetic diversity, principal component analysis and correlation studies have been done using R software version 2023.12.1.

Result: The 261 accessions were grouped into 7 clusters, with cluster three containing the largest number of accessions (87), followed by cluster four with 61 accessions. Clusters 1, 2, 5, 6 and 7 contained 54, 27, 5, 21 and 5 accessions respectively, indicating greater genetic diversity for the traits under study. Correlation analysis revealed associations between seed yield and other important traits. Principal component analysis demonstrated the relationships between various traits and their impact on variability. A concise summary of the data was provided by the first three principal components, which collectively explained 64.30% of the variation. Based on the current study, genotypes IC73883, IC73961, IC73952, IC73975 and EC843239 were found to be superior with respect to seed yield and other related traits.

Key words: Characterization of germplasm, Genetic improvement, Morphological diversity, Pigeonpea.

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp] is an important legume crop widely cultivated in Africa and Asia in diverse environments. It is a diploid ($2n = 2X = 22$) crop with a genome size of 833.07 Mbp. It belongs to the family Leguminosae and sub-family Papilionoideae. *Cajanus cajan* is the only domesticated species among *Cajanea* family. It is a crucial crop in the semi-arid tropics, cultivated across 24 countries on approximately 6.03 million hectares, yielding about 5.3 million tons annually. India dominates this landscape, accounting for 82.20 per cent of the cultivated area (5.01 million hectares) and 77.60 per cent of the total production (4.3 million tons). Other significant contributors to pigeonpea production include Myanmar, Malawi, Kenya and Tanzania, each contributing over 2 per cent. Within India, pigeonpea is grown in 25 states, covering an area of 5 million hectares and producing 4.3 million tons, resulting in a productivity rate of 861.2 kg per hectare (Food and Agriculture Organization, 2023). Key states for pigeonpea cultivation include Karnataka (0.89 million hectares) Telangana (0.30 million hectares), Uttar Pradesh (0.29 million hectares), Gujarat (0.24 million hectares), Jharkhand (0.23 million hectares), Andhra Pradesh (0.24 million hectares), Madhya Pradesh (0.25 million hectares) and Odisha (0.12 million hectares). Karnataka is the leading producer with an output of 9.48 lakh tons, followed closely by Maharashtra with 8.75 lakh tons of pigeonpea production (Indiastat, 2023).

Morphological traits play a pivotal role in determining yield in pigeonpea. Key morphological traits such as plant

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vigor, which is directly proportional to biomass production and stress tolerance are crucial. Semi-spreading types are lodging resistant and typically exhibit higher yields. Additionally, seed shape often correlates with seed size and seed weight. Understanding the relationship between morphological traits and yield is essential for the continued development of pigeonpea varieties that meet diverse needs. Furthermore, a major concern in improving pigeonpea

crops is the limited genetic foundation of contemporary cultivars. Consequently, the anticipated genetic advances in pigeonpea output have not been fully realized. Genes with beneficial features found in genebanks can be utilized to create desirable genetic variation and enhance resilience to stressors induced by climate change (Díez *et al.*, 2018). Therefore, it is crucial to explore genebanks for new germplasm to employ in pigeonpea breeding initiatives, aiming to increase cultivar productivity and climate change resilience.

The degree of genetic variability and diversity resulting from the many traits accessible to breeders to create desirable variations determines the effectiveness of breeding programmes in any given crop (Govindaraj *et al.*, 2020). Furthermore, genetic diversity studies offer an information on target trait availability and variability for the effectiveness of breeding programmes by highlighting the disparities among accessions (Mohammadi and Prasanna, 2003). Finding out the extent of genetic diversity present in the various germplasm lines is therefore essential. To gather crucial data for pigeonpea crop improvement, the current study was carried out to evaluate the morphological and genetic diversity in the pigeonpea accessions.

MATERIALS AND METHODS

The field experiment was carried out during *kharif* 2022 at Zonal Agricultural Research Station (ZARS) Kalaburagi, which is located at a latitude of 17°30' (N), 76°81' Longitude (E) and at an altitude of 443.88 meters above mean sea level and it comes under agro-climatic zone-2 (North-eastern Dry Zone of Karnataka state). A total of 261 pigeonpea accessions (Table S1) obtained from National Genebank of ICAR-National Bureau of Plant Genetic Resource (NBPGR), New Delhi including three checks PT-012, BSMR-736 and Asha were sown in augmented block design (ABD) consisting of 27 blocks. The accessions were sown in 3-meter length of 2 rows each with a row to row and plant to plant spacing of 90 and 20 cm respectively. Standard agronomic practices were followed and plant protection measures were taken as and when required by following the recommended package of practices (Anonymous, 2017).

At specific stage, the morphological traits were noted, the plant vigour observed and classified into poor (1), good (2) and very good (3) based on visual scoring. Growth habits were observed and grouped into erect and compact (1) semi spreading (2), spreading (3), trailing (4) and others (99). Determinate (1) semi-determinate (2) Indeterminate (3) and others (99) were the classes for plant habit trait. Green (1) sun red (2) purple (3) dark purple (4) and others (99) were the classes of stem color. Flower color observed and grouped into light (1) light yellow (2) yellow (3) orange yellow (4) and others (99). Streak patterns were observed and grouped as sparse streaks (3) medium streaks (5) dense streak (7) uniform coverage of second color and others (99). Seed traits

such as seed color grouped into white (1), cream (2), Orange (3), light brown (4), reddish brown (5), light grey (6), grey (7), purple (8), dark purple (9) dark grey (10) and others (99), seed shape in to oval (1), globular (2), square (3), elongate (4) and others (99). and seed eye width for all the lines were observed and scored into narrow (3), medium (5), wide (7) and others (99) (Table S2). Quantitative traits were recorded in 5 random plants from two rows of each accession, viz., days to 50 per cent flowering, plant height, primary branches, secondary branches, pod bearing length, number of seeds per pod, number of pods per plant, days to physiological maturity, seed yield and seed weight. The qualitative traits include plant vigor, growth habit, plant habit, seed eye width, seed color and seed shape. The analysis of variance (ANOVA) was carried out for all the quantitative traits. The data was analyzed using R software version 2023.12.1.

RESULTS AND DISCUSSION

The ANOVA results indicated that the mean sum of square for genotypes was highly significant ($P \leq 0.01$) for all the traits (Table 1). Based on D^2 values, the accessions were grouped into seven clusters using Tocher's method given by (Rao, 1952). Of the seven clusters, cluster three was found to be largest with 87 accessions. Cluster four with 61 accessions. Cluster one, two, five, six and seven have 54, 27, 5, 21 and 5 accessions respectively. The existence of genetic variability in these traits were also reported by (Tuntun *et al.*, 2022; Kumara *et al.*, 2013; Basavaraj *et al.*, 2023).

Variability parameters for quantitative traits

Significant variations were observed in the mean, range and coefficient of variations (Table 2). For the days to 50 per cent flowering, the range was from 77 to 188 days with a mean of 122 days. Days to physiological maturity ranged between 127.17 to 232.17 days with an average of 174.69 days. The mean plant height was 168.60 cm with a range of 84.14 to 213.65. The number of seeds per pod and the number of pods per plant showed mean values of 3.33 and 103.5, with ranges of 2.08 to 4.52 and 6.59 to 398.16, respectively. Seed yield ranged from 1.18 g to 76.34 g with a mean value of 17.05 g, while seed weight showed a mean value of 8.29 g with a range of 5.93 g to 18.93 g. Similarly, substantial variation was observed in most of the traits. Box plot analysis compared trait distribution between exotic and indigenous accessions. On an average, days to maturity, secondary branch number, plant height and seed weight were higher in exotic collections (ECs), while primary branch number, pod length and seed yield showed higher average performance in indigenous collections (ICs) (Fig 1). The major steps in crop improvement are assessing the variability for desired traits and their utilization in breeding programs (Kumar *et al.*, 2015; Tuntun *et al.*, 2022). The wide range of variability obtained was attributable to the diverse collection assessed in the study.

Table S1: Passport data of accessions used in the study.

Accession number	Source	Biological status
IC468590, IC468591	Andhra Pradesh	Landrace
EC552913	Australia	Breeding/Research material
EC552925	Bangladesh	Breeding/Research material
EC552876, EC552910	Barbados	Traditional cultivar/Landrace
IC245520, IC245560, IC74134	Delhi	Unknown
EC552862	Guadeloupe	Breeding/Research material
EC552881, EC552894, EC552903	India	Breeding/Research material
EC552886	Indonesia	Breeding/Research material
EC552890, EC552897	Jamaica	Breeding/Research material
EC552883, EC552884, EC552911, EC552912	Kenya	Breeding/Research material
IC468334, IC74097	Madhya Pradesh	Landrace, unknown
IC73866, IC73867, IC73868, IC73869, IC73870, IC73871, IC73872, IC73873, IC73875, IC73876, IC73877, IC73879, IC73880, IC73881, IC73882, IC73883, IC73884, IC73885, IC73886, IC73889, IC73891, IC73892, IC73893, IC73894, IC73896, IC73897, IC73898, IC73899, IC73901, IC73902, IC73904, IC73906, IC73907, IC73908, IC73910, IC73911, IC73912, IC73914, IC73916, IC73917, IC73919, IC73920, IC73921, IC73924, IC73925, IC73926, IC73929, IC73930, IC73931, IC73932, IC73933, IC73934, IC73935	Maharashtra	Landrace
EC552920, EC552921, EC552922	Malawi	Traditional cultivar/Landrace
EC552915, EC552916, EC552917, EC552918	Mozambique	Traditional cultivar/Landrace
EC552887, EC552889, EC552900	Myanmar	Breeding/Research material
EC552861, EC552868, EC552902	Nepal	Traditional cultivar/Landrace
EC552879, EC552880, EC552898	Nigeria	Traditional cultivar/Landrace
EC552896	Pakistan	Breeding/Research material
EC552893	Philippines	Traditional cultivar/Landrace
EC552906	Puerto Rico	Traditional cultivar/Landrace
EC552878, EC552891, EC552904	Tanzania	Traditional cultivar/Landrace
IC525370, IC525373, IC525385, IC525396, IC525402, IC525474, IC525476, IC525478, IC525482, IC525502, IC525503, IC525504, IC525507, IC525514, IC525515, IC525529, IC525531, IC525532, IC525533, IC525534, IC525552, IC525553, IC525632, IC525636, IC525653, IC525656, IC634397, IC634438	Telangana	
EC552907, EC552908, EC552909	Trinidad and Tobago	Traditional cultivar/Landrace
EC552909	Trinidad and Tobago	Traditional cultivar/Landrace
EC552899, EC843237, EC843238, EC843239, EC843240, EC843241, EC843243, EC843244, EC843246, EC843249, EC843250, EC843251, EC843255, EC843258, EC843259, EC843264, EC843265, EC843270, EC843276, EC843279, EC843280, IC525650, IC73913, IC74035, IC74036, IC7403	Unknown	Unknown
EC552872	Uganda	Traditional cultivar/Landrace
IC73922	Uttar pradesh	Unknown
EC552901	Venezuela	Breeding/Research material

To identify the amount of genetic diversity, present in the experimental material the cluster analysis has been done, these clusters represent existence of diversity between the set of accessions. In current study none of the accessions belongs to solitary cluster, the accessions congregated into a cluster which exhibit narrow range of genetic among them while, broad range of variability was

recorded between clusters. The generation of such clusters may be due to total isolation arresting the gene flow or rigorous natural or human selection for diverse adaptive complexes. The clusters generated are presented in Table 3, Fig 2.

Significant genetic diversity has also been found by previous researchers in the pigeonpea materials

Table S2: Descriptors used for agro -morphological characterization of pigeonpea accessions.

Descriptors	Code	Stage of observation	Descriptor state
Qualitative traits			
Days to 50% flowering	DAY FLW	At 50% flowering	Plot basis
Plant height	PLANT HT	At maturity stage	Average of 5 plants
Number of primary branches	PRIBRN	At flowering stage	Average of 5 plants
Number of secondary branches	SEC BRN	At maturity stage	Average of 5 plants
Pod bearing length	PBL	Poding stage	Average of 5 plants
Number of seeds per pod	NSPP	At maturity stage	Average of 5 plants
Number of pods per plant	NPPP	At maturity stage	Average of 5 plants
Seed yield per	SED YLD	At maturity stage	Per plant basis
100 seed weight	SED WT	After harvest	Average of 5 plants
Quantitative traits			
Growth habit	GRW HAB	At maturity stage	Plant growth: 1= Erect and compact, 2= Semispreading, 3= Spreading, 4= Trailing, 99= Others
Plant habit	PLT HBT	At maturity stage	Plant habit: 1= Determinate, 2= Semi determinate, 3= Indeterminate, 99= Others
Plant vigour	PLT VGR	Seedling stage	Early plant vigour: 1= Poor, 2= Good, 3= Very good, 99= Others
Stem color	STEM CLR	At maturity stage	Stem colour: 1= Green, 2= Sun red, 3= Purple, 4= Dark purple, 99= Others
Streak pattern	STRE PAT	At flowering	Streaks patterns: 3= Sparse streaks, 5= Medium streaks, 7= Dense Streaks 9= Uniform coverage of second colour 99= Others
Flower color	FLW CLR	At 50 % flowering	Base flower colors: 1= Light, 2= Light yellow, 3= Yellow, 4= Orange yellow, 99= Others
Seed color	SEED CLR	After harvest	Base seed colour: 1= White, 2= Cream, 3= Orange, 4= Light brown, 5= Reddish brown, 6= Light Grey, 7= Grey, 8= Purple, 9= Dark purple, 10= Dark gray, 99= Others
Seed shape	SEED CLR	After harvest	Seed shape: 1= Oval, 2= Globular, 3= Square 4= Elongate, 99= Others
Seed eye width	SEED EYE	After harvest	Seed eye width: 3= Narrow, 5= Medium, 7= Wide, 99= Others

Table 1: ANOVA for yield and attributing traits of pigeonpea accessions.

Source	Df	Mean sum of square									
		DF	PH	PB	SB	PBL	NSPP	NPPP	DM	SY	SW
Block (Ignoring treatments)	26	438.10**	1060.0**	11.50**	11.70**	443.80**	0.49**	2839.20**	399.10**	271.80**	4.10**
Treatment (Eliminating blocks)	260	177.80**	551.40**	8.90**	12.90**	112.20**	0.18**	2732.10**	196.10**	402.30**	3.00**
Treatment: Check	2	2709.0**	261.40	24.20**	3.50	529.60**	4.30**	105.60**	4930.00**	2912.40**	0.60**
Treatment: Test and test vs. check	258	158.20**	553.70**	8.80**	13.00**	109.00**	0.10**	2752.40**	159.40**	382.90**	3.00**
Residuals	52	0	91.44	3.7	1.10	24.30	0.04	41.80	1.80	26.90	0.05

Note: Non significant: $P > 0.05$; * $P \leq 0.05$; ** $P \leq 0.01$.

DF: Days to 50 per cent flowering; PB: Number of primary branches; NPPP: Number of pods per plant; DM: Days to maturity; SB: Number of secondary branches; SW: 100 seed weight (g); PH: Plant height (cm); PBL: Pod bearing length (cm); SY: Seed yield per (g); NSPP: Number of seeds per pod.

(Pushpavalli *et al.*, 2017). The experimental material in the current study exhibited significant genetic diversity, suggesting that it could be a valuable genetic resource for choosing diverse parents which are having higher genetic distance within the cluster for a hybridization programme that aims to isolate desirable segregants for key characteristics such as seed yield and related traits.

Correlation studies and principal component analysis

Days to 50 per cent flowering ($r = -0.25$, $P \leq 0.001$) and days to physiological maturity ($r = -0.26$, $P \leq 0.001$) have shown significant negative association with seed yield. Number of pods per plant ($r = 0.50$, $P \leq 0.001$) had a significant positive association with seed yield indicating the more the number of pods per plant will increase the seed yield. The number of seeds per pod ($r = 0.28$, $P \leq 0.001$) had a significant positive association with seed yield. Primary branches have shown a significant positive ($r = 0.28$, $P \leq 0.001$) association with seed yield. Whereas secondary branches have shown a positive ($r = 0.18$, $P \leq 0.05$) association with pod bearing length and seed yield. Plant height had shown a significant positive ($r = 0.29$, $P \leq 0.001$) association with seed yield (Fig 3). The strong correlation among some of the traits, such as days to 50% flowering and days to maturity and pods per plant, showed that sufficient weightage has to be given while exercising selection for yield.

The significant positive association shown by the traits (Number of seeds per pod, primary and secondary branches and plant height) can be used for multiple trait selection. Here the days to 50% flowering and days to physiological maturity have shown negative correlation with seed yield. Similar results were reported by (Saroj *et al.*, 2013) (Vanniarajan *et al.*, 2023; Bhadru *et al.*, 2010). In converse, a negative correlation between seed weight and seed yield has also been reported previously (Hemavathy *et al.*, 2017). The significant relationship between days to 50% flowering, days to physiological maturity, plant height, number of seeds per pod, number of pods per plant and seed yield is useful for selection for high seed yield. Direct selection for these traits would result in yield improvement.

Principal component analysis (PCA) of trait variation in pigeonpea germplasm accessions

PCA revealed the association among different traits and their contribution towards variability. The first three PCA components provided a realistic summary of the data and explained 64.29% of total variation. The first principal component (PC1) accounted for 30.05% of the total variation, whereas PC2 and PC3 accounted for 22.11% and 12.13 % variance respectively (Table 4, Fig 4). The days to 50% flowering and days to physiological maturity and seed weight were the highest and positive contributors (With contributions of 0.211, 0.209 and 0.079) on PC1. Seed yield was the only positive

contributor (0.046) on the PC2. Traits like days to 50% flowering, plant height, days to physiological maturity and seed weight were negatively correlated with PC2 exhibiting negative (-0.594, -0.351, -0.597 and -0.148) PC scores

on PC2. Number of seeds per pod, number of pods per plant seed yield and seed weight were the positive contributors (0.582, 0.086, 0.236 and 0.683) to the phenotypic variation on PC3. PCA enabled the

Table 2: Descriptive statistics for ten traits in pigeonpea accessions.

Trait	Mean	Max	Min	Skewness	Kurtosis
DF	122.05	188.00	77.00	1.29**	7.42**
PH	168.60	213.65	84.14	-0.74	4.35**
PB	11.04	18.93	3.82	0.10	3.04
SB	5.84	14.97	0.07	0.45**	2.85
PBL	42.33	76.53	2.76	-0.08	2.88
NSPP	3.33	4.52	2.08	0.16	2.85
NPPP	103.5	398.16	6.59	1.24**	8.81**
DM	174.69	232.17	127.17	0.87**	6.15**
SY	17.05	76.34	1.18	1.78**	6.68**
SW	8.29	18.93	5.93	2.6**	17.12**

Note: Max: Maximum; Min: Minimum; DF: Days to 50 per cent flowering; PB: Number of primary branches; NPPP: Number of pods per plant; DM: Days to maturity; SB: Number of secondary branches; SW: 100 seed weight (g); PH: Plant height (cm); PBL: Pod bearing length (cm); SY: Seed yield per (g); NSPP: Number of seeds per pod.

Table 3: Clustering analysis of pigeonpea accessions using D² method.

Cluster no.	No. of accession	Name of accession
I	54	ASHA, EC552921, IC73882, IC73957, IC74017, IC74119, BSMR-736, EC552922, IC73893, IC73960, IC74018, IC74122, EC552872, EC843240, IC73912, IC73964, IC74033, IC74142, EC552889, EC843250, IC73931, IC73965, IC74035, IC74015, IC74117, IC73879, IC73954, PT0012, EC552891, EC843258, IC73934, IC73966, IC74036, EC552903, EC843265, IC73938, IC73996, IC74049, EC552910, IC73868, IC73939, IC73998, IC74052, EC552915, IC73872, IC73943, IC74006, IC74086, EC552916, IC73875, IC73947, IC 74007
II	27	EC552861, EC552894, EC552906, EC552917, EC843280, IC525653, EC552883, EC552897, EC552907, EC843255, IC525552, IC73896, EC552884, EC552899, EC552908, EC843264, IC525553, EC552886, EC552900, EC552909, EC843276, IC525632, EC552893, EC552904, EC552911, EC843279, IC525636
III	87	EC552862, IC525502, IC73894, IC73925, IC73972, IC74077, EC552868, IC525507, IC73897, IC73929, IC7393, IC74078, EC552876, IC525534, IC73899, IC73930, IC74000, IC74079, EC552890, IC525656, IC73901, IC73932, IC74002, IC74084, EC552896, IC73866, IC73904, IC73933, IC74005, IC74089, EC552901, IC73871, IC73906, IC73937, IC74009, IC74098, EC552902, IC73873, IC73907, IC73940, IC74012, IC74108, EC552925, IC73876, IC73910, IC73941, IC74023, IC74110, EC843243, IC73877, IC73913, IC73945, IC74025, IC74120, EC843244, IC73880, IC73914, IC73946, IC74037, IC74121, IC468590, IC73884, IC73916, IC73953, IC74043, IC74126, IC468591, IC73885, IC73917, IC73956, IC74044, IC74134, IC525370, IC73886, IC73919, IC73962, IC74059, IC525396, IC73891, IC73920, IC73968, IC74062, IC525476, IC73892, IC73922, IC73970, IC74075
IV	61	EC552878, EC843246, IC525515, IC73911, IC74057, IC74099, EC552879, EC843259, IC525529, IC73921, IC74058, IC74100, EC552880, EC843270, IC525531, IC73924, IC74061, IC74116, EC552881, IC468334, IC525533, IC73935, IC74068, IC74131, EC552887, IC525373, IC525650, IC73951, IC74069, IC74132, EC552898, IC525474, IC73867, IC74011, IC74071, IC74133, EC552912, IC525478, IC73869, IC74019, IC74081, IC74143, EC552913, IC525482, IC73870, IC74020, IC74087, EC552918, IC525503, IC73881, IC74046, IC74088, EC843238, IC525504, IC73889, IC74055, IC74090, EC843241, IC525514, IC73902, IC74056, IC74092
V	5	EC843237, IC245520, IC245560, IC525385, IC73971
VI	21	EC843239, IC73908, IC73959, IC73973, IC73995, IC74080, EC843251, IC73926, IC73961, IC73974, IC74013, IC73883, IC73950, IC73967, IC73975, IC74014, IC73898, IC73952, IC73969, IC73993, IC74060
VII	5	EC843249, IC525402, IC525532, IC634397, IC634438

identification of important traits with high variability amount the accessions. The traits which have exhibited high contribution of principal components can be used for selection. Similar results were reported previously (Nyirenda *et al.*, 2020; Mohan *et al.*, 2021).

Qualitative traits characterization in pigeonpea germplasm accessions

The frequency distribution of the entire set was non-normal and varied among traits. In certain cases, a particular trait predominated, while it was dispersed in others. For instance,

the trait of plant vigor exhibited good plant vigor in most cases. Among the 258 genotypes, 186 accessions were found to have good plant vigor, while 57 accessions displayed very good plant vigor. The remaining accessions exhibited poor plant vigor. Semi-spreading growth habits were found in 174 accessions, while the rest, 84 accessions, were of the erect and compact type. Concerning plant habit trait, most accessions displayed an indeterminate nature, with only 3 genotypes found to be determinate. Regarding seed color, the majority of accessions (144) exhibited a reddish-brown color, followed by 29 with a light brown color,

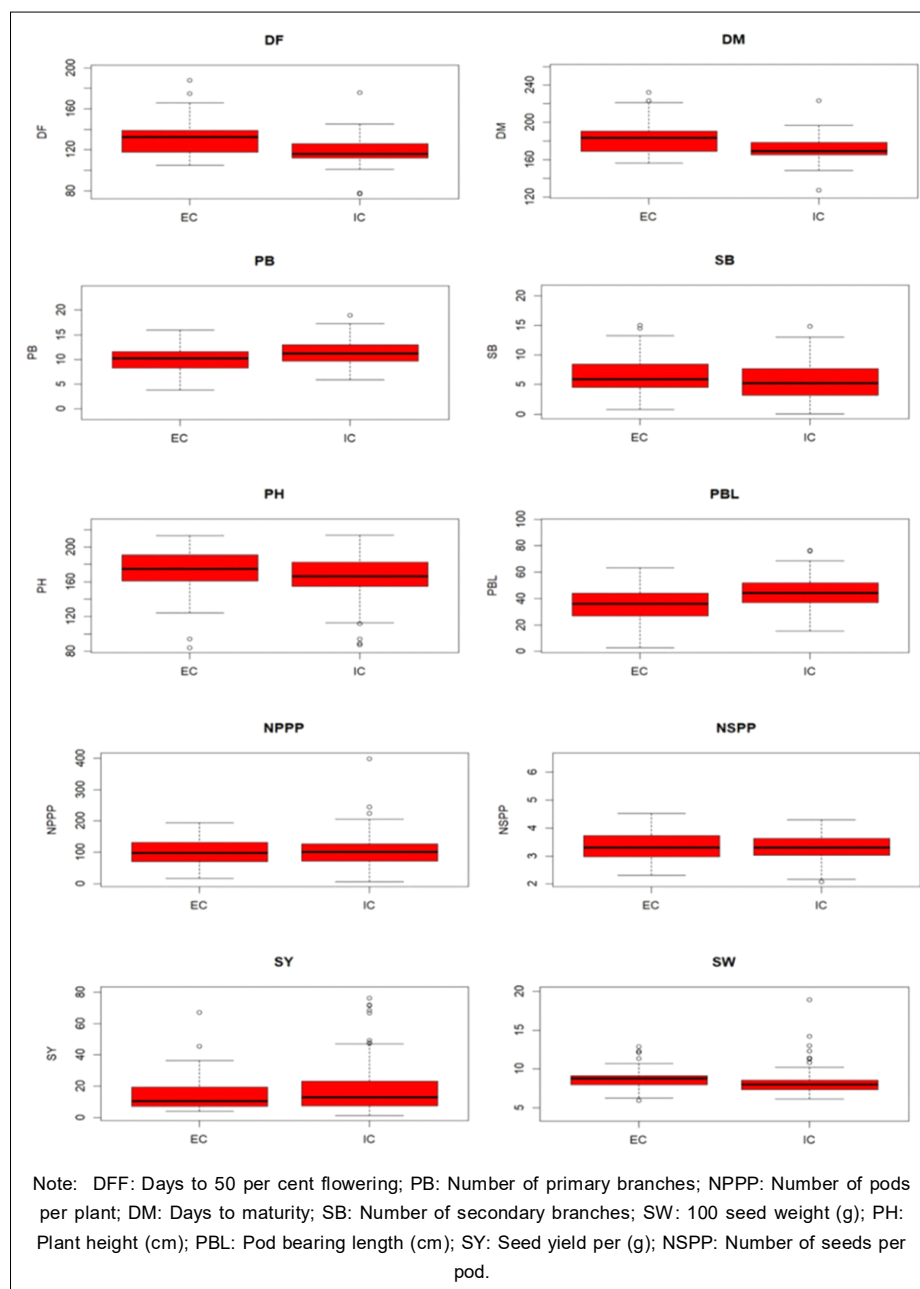


Fig 1: Boxplot depicting the variability of traits in the indigenous collection (IC) and exotic collection (EC) of the pigeonpea accessions.

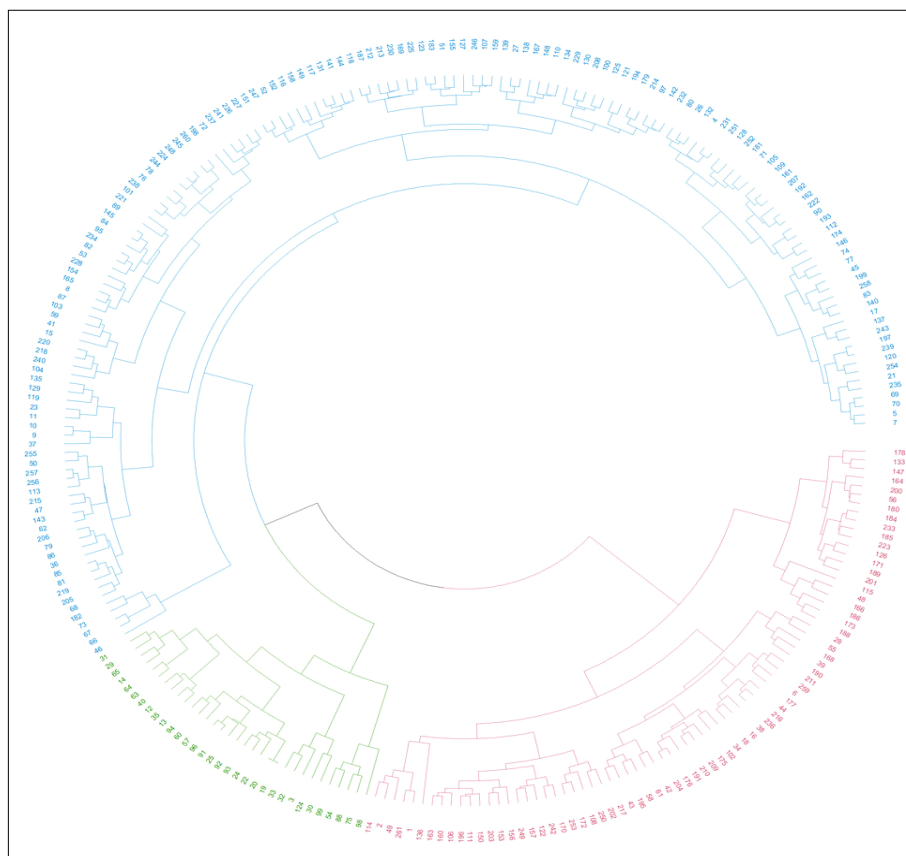


Fig 2: Clustering analysis dendrogram of 261 pigeonpea accessions.

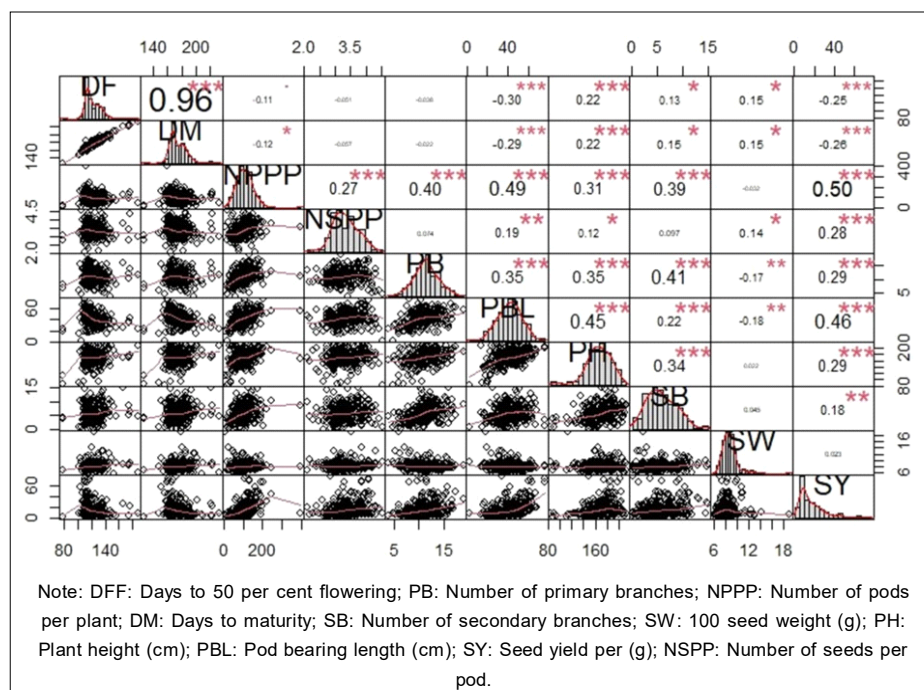


Fig 3: Correlation plot matrix of yield with associated traits.

5 genotypes with a purple color and the remaining accessions displaying mixed colors. Seed shape was categorized into oval (230), globular (16) and square (12) in this study, with the

majority of accessions having an oval seed shape. Seed eye width was found to be medium in 128 accessions, narrow in 120 accessions and wide in 10 accessions (Fig 6).

Table 4: PC scores, eigen value and per cent variance of the principal components.

Trait	PC1	PC2	PC3
DF	0.211	-0.594	-0.006
PH	-0.301	-0.351	-0.072
PBL	-0.45	-0.048	-0.101
SB	-0.275	-0.316	-0.097
NSPP	-0.438	-0.097	0.582
NPPP	-0.438	-0.097	0.086
DM	0.209	-0.597	-0.018
SY	-0.415	0.046	0.236
SW	0.079	-0.148	0.683
Eigen value	3.000	2.210	1.210
% Variance	30.050	22.110	12.130

Note: DFF: Days to 50 per cent flowering; PB: Number of primary branches; NPPP: Number of pods per plant; DM: Days to maturity; SB: Number of secondary branches; SW: 100 seed weight (g); PH: Plant height (cm); PBL: Pod bearing length (cm); SY: Seed yield per (g); NSPP: Number of seeds per pod.

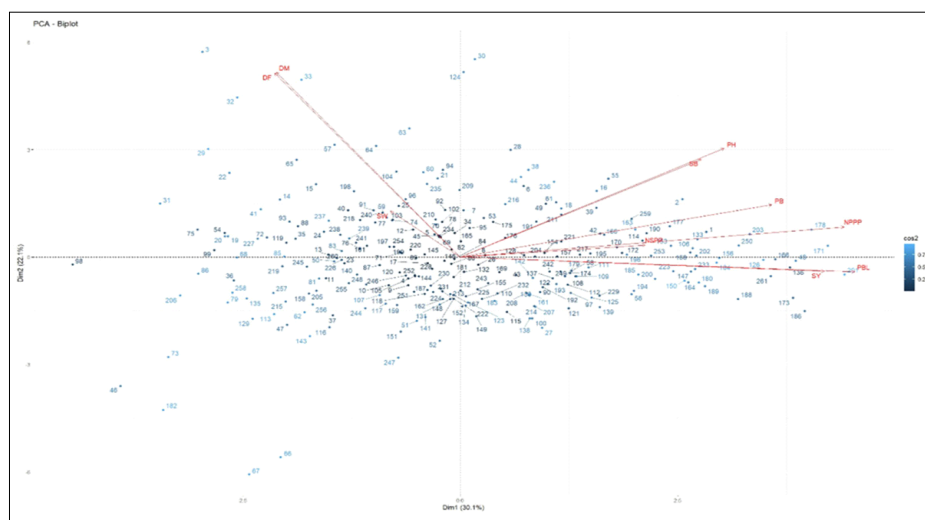


Fig 4: Distribution of pigeonpea accessions across first two principal components.



Fig 5: Photographs superior lines IC 73952 and EC 843239.



Fig 6: Frequency distribution of entire pigeonpea germplasm accessions for qualitative traits.

Identification of trait-specific pigeonpea accessions

Superior trait specific accessions IC73961, IC73952, IC73975 and EC843239 for yield and related traits were identified from this study and they are depicted in Fig 5. The identified accessions could be tested in multi-locations and seasons to confirm their performance and then can be used as a potential donor for crop improvement.

CONCLUSION

The present study involved the characterization of 261 pigeonpea accessions based on various qualitative and quantitative traits. Cluster analysis was employed to assess and elucidate the genetic diversity among the accessions. Correlation and principal component analysis (PCA) revealed associations among various morphological and yield-related traits, highlighting their contribution to the observed genetic diversity. This study also enabled the identification of trait-specific accessions. Based on per se performance, genotypes IC73883, IC73961, IC73952, IC73975 and EC843239 were identified as superior for yield and associated traits. These promising accessions can serve as valuable donors in pigeonpea breeding programs and varietal development.

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Conflict of interest

The authors declare that they have no conflicts of interest relevant to the content of this article.

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