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Assessment of Variability, Diversity and Performance of Indigenous Pigeonpea Germplasm for Yield and Nutritional Traits

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ABSTRACT

Background: Pigeon pea [*Cajanus cajan* (L.) Millsp.] is a perennial legume vital to subsistence agriculture in semi-arid tropics, providing food, fodder and soil enrichment. Genetic improvement of pigeon pea hinges on understanding the genetic variability among its genotypes.

Methods: Fifty-six pigeon pea accessions were collected from various districts in Telangana, India. Forty-five accessions were characterized for yield, quality and nutritional traits in a randomized block design with two replications during the Late-*kharif* season of 2022. Data analysis included variance, heritability, genetic advance, correlation, path coefficient analysis, cluster analysis and principal component analysis (PCA).

Result: Significant genetic variation was found among the accessions for all traits. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV), indicating substantial environmental influence. High heritability estimates and genetic advance were observed for traits such as single plant yield, pods per plant and iron content, suggesting strong selection potential. Correlation analysis revealed that traits like plant height, number of branches per plant and 100-seed weight had significant positive associations with yield. Path coefficient analysis identified pods per plant and 100-seed weight as having the highest direct positive effects on yield. Cluster analysis divided the accessions into four clusters, with cluster III showing superior performance in yield-related traits. PCA indicated that four principal components explained 69.16% of the total variability, with PC1 dominated by yield traits.

Key words: Genetic diversity, Heritability, Nutritional traits, Pigeon pea, Principal component analysis, Yield traits.

INTRODUCTION

Pigeon pea [*Cajanus cajan* (L.) Millsp.]-known as Adhaki in Sanskrit, Arhar in Hindi and Tur in Bengali-is a perennial member of the Fabaceae family. Other common names for pigeon pea include red gram, congo pea, gungo pea, and no-eye pea (Wu, 2009). It ranks as the sixth most significant grain legume crop cultivated in the semi-arid tropics of Asia, Africa and the Caribbean, thriving under various cropping systems (Mula and Saxena, 2010). Beyond its role as a food source, pigeon pea serves multiple purposes: It is used in traditional medicine, animal feed, fodder, fuel wood, hedges, windbreaks, roof thatches and green manure. Additionally, pigeon pea helps prevent soil erosion, particularly on sloping land, enriches soil organic matter and supplies nitrogen through symbiotic rhizobia, underscoring its importance in subsistence agriculture.

The cultivation of pigeon pea dates back at least 3,000 years, with India recognized as its center of origin. Historical references to this crop appear in ancient Sanskrit and Buddhist literature from 400 BC to 300 AD. The spread of pigeon pea reached East Africa and later the Americas, likely via the slave trade. Presently, pigeon pea is grown extensively in tropical and semi-tropical regions worldwide, with India being the largest producer, accounting for 63% of global production. The crop is cultivated on approximately 5.4 million hectares globally, with India alone accounting for 3.9 million hectares or 72% of the total area dedicated to pigeon pea cultivation (FAO, 2018).

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Nutritionally, pigeon pea is a rich source of protein, fiber, minerals, and vitamins. It contains 20-26% protein, 1-2% fat, 53-65% carbohydrate and 3.8-8.1% ash Ajayi *et al*. (2010); Saxena and Kumar, (2010). The seeds are particularly rich in sulfur-containing amino acids, methionine and cystine and provide essential minerals such as phosphorus, magnesium, iron, calcium, sulfur and potassium, while being low in sodium (Kunyanga *et al*., 2013). For example, 100 g of dry pigeon peas provide 117% of the daily recommended value for copper, 65% for iron, 78% for manganese, 52% for phosphorus, 15% for selenium, 13% for calcium and 25% for zinc.

Understanding the nature and extent of genetic variation in pigeon pea genotypes is crucial for plant breeding programs. The processes of collecting, conserving, and characterizing genotypes form the foundation of any crop improvement endeavor, which depends on the genetic diversity present within the gene pool. This genetic variability enables breeders to develop new and improved cultivars with desirable traits. Historically, the natural genetic variability within crop species has been harnessed to meet subsistence food requirements. Today, this variability is being leveraged to address the needs of growing populations and to produce surplus food.

Despite its numerous benefits, pigeon pea is often considered an “orphan crop” in many countries, receiving less attention and investment compared to major staple crops. Nonetheless, recognizing its importance and harnessing its genetic potential can significantly contribute to sustainable agriculture and food security.

MATERIALS AND METHODS

Plant material and collection

The experimental materials comprised pigeon pea and its wild relatives’ germplasm collected from various parts of Jayashankar Bhupalpally, Warangal, Mulug and Mahabubabad districts in Telangana during January 2020. The collection was conducted by the ICAR-National Bureau of Plant Genetic Resources Regional Station, Rajendranagar, Hyderabad, in collaboration with the Regional Agricultural Research Station, PJTSAU, Warangal. A total of 56 accessions of pigeon pea were collected during the survey, showcasing a significant level of diversity in the germplasm.

Germplasm handling and evaluation

The collected germplasm samples were homogenized and subjected to characterization, evaluation and multiplication processes at the Regional Agricultural Research Station in Warangal (RARS, Warangal). These steps were undertaken to better understand and utilize the genetic resources of pigeon pea and its wild relatives.

Experimental design and data collection

Forty-five accessions were selected based on their performance. Data for various yield, quality and nutritional characters were recorded, including days to 50% flowering, days to maturity, plant height, number of branches per plant, pods per plant, 100-seed weight (g), copper (Cu, mg/kg), zinc (Zn, mg/kg), iron (Fe, mg/kg), manganese (Mn, mg/kg), protein content (%) and single plant yield (g). Data were collected for each replication by selecting 5 random plants in each row, and mean values were estimated. The experiment was conducted during the late-*kharif* season of 2022 using a randomized block design with two replications. The replication-wise mean values of each genotype for the twelve different characters were used for statistical analysis.

Statistical analysis

Analysis of variance for each character was calculated as per the standard procedure suggested by Panse and Sukhatme (1967). Data management and all statistical analyses were performed using the R software packages.

RESULTS AND DISCUSSION

The analysis of variation revealed highly significant differences among the accessions for all the characters studied, including days to 50% flowering, days to maturity, plant height, number of branches per plant, pods per plant, 100-seed weight (g), Cu (mg/kg), Zn (mg/kg), Fe (mg/kg), Mn (mg/kg), protein content (%) and single plant yield (g), indicating the existence of considerable genetic variation in the experimental material. Examination of the variance components revealed that the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all characters studied, indicating the role of environmental variance in the total variance (Table 1).

Variability and heritability

The genotypic coefficient of variation for various characters ranged from 5.154% to 46.681%, while the phenotypic coefficient of variation ranged from 5.228% to 46.681%. High genotypic and phenotypic coefficients of variation were observed for single plant yield (g), Fe (mg/kg), and number of pods per plant. Moderate GCV and PCV were observed for protein content (%), number of branches per plant, 100-seed weight (g) and Cu (mg/kg). Low GCV and PCV values were observed for days to 50% flowering, plant height, Zn (mg/kg), Mn (mg/kg) and days to maturity. Heritability estimates are crucial for determining the heritable portion due to genetic variation. High heritability estimates, indicating that the characters are least influenced by environmental factors and can be transmitted to subsequent generations, were observed for almost all the characters studied. Moderate heritability estimates were observed for the number of branches per plant. The success of genetic advance under selection depends on the magnitude of genetic variability in the base population and the heritability of the character under consideration. Genetic advance is usually expressed as a percentage of the mean. High genetic advance as a percentage of the mean was observed for Fe (mg/kg), single plant yield (g), and pods per plant. Moderate genetic advance as a percentage of the mean was observed for plant height,

number of branches per plant, 100-seed weight (g), Cu (mg/kg), Zn (mg/kg) and Mn (mg/kg). Similar findings reported by Edukondalu *et al*., (2023); Vanniarajan *et al*. (2023); Anuj *et al*. (2018); Pushpavalli *et al*. (2018); Mallesh *et al*. (2017); Ram *et al*. (2016); Shunyu *et al*. (2013); Sharma *et al*. (2014) and Hamid *et al*. (2011).

According to Johnson *et al*. (1955), heritability along with genetic advance is mostly useful and reliable in predicting the resultant effects of selection. Selection can only be achieved when high heritability is accompanied by high genetic advance (Burton, 1952). In the present study, high estimates of heritability coupled with high genetic advance as a percentage of the mean were observed for single plant yield (g), pods per plant and Fe (mg/kg), indicating better scope for these traits for direct selection.

Correlation of attributing characters with grain yield

Genotypic and phenotypic correlations between single plant yield and other traits were depicted in (Fig 1). Single plant yield had positive and highly significant associations with plant height (r_g=0.246*, r_p=0.225*), number of branches per plant (r_g=0.540**, r_p=0.377**), number of pods per plant (r_g=0.748**, r_p=0.720**) and 100-seed weight (g) (r_g=0.231*, r_p=0.218*) at both genotypic and phenotypic levels, similar results reported by Vanniarajan *et al*. (2023) and Sharma *et al*. (2023). Conversely, significant negative relationship was observed with Mn content (mg/kg) (r_g= -0.279**, r_p=-0.259*) and Cu (mg/kg) (r_g=-0.228*, r_p= -0.181*) at both genotypic and phenotypic levels. Days to maturity (r_g=, r_p=0.011) and Fe (mg/kg) (r_g=, r_p=0.005) had slightly positive but non-significant associations at both genotypic and phenotypic levels with single plant yield.

In contrast, Days to 50% flowering (r_g= -0.006, r_p= -0.002), Zn (mg/kg) (r_g= -0.077, r_p= -0.073) and protein content (%) (r_g= -0.009, r_p= -0.009) exhibited negative and non-significant associations with single plant yield at both genotypic and phenotypic levels. These results align with findings reported by Edukondalu *et al*. (2023); Vanniarajan

Table 1: Genetic parameters of twelve characters.

Characters	GCV	PCV	h^2 (Broad sense)	Genetic advance as % of mean
Days to 50% flowering	5.154	5.228	0.972	10.468
Days to maturity	3.938	3.989	0.975	8.01
Plant height	12.852	14.319	0.806	23.763
No. of branches per plant	21.33	29.608	0.519	31.653
Pods per plant	44.557	45.061	0.978	90.759
100 seed wt (g)	19.972	20.735	0.928	39.628
Cu (mg/kg)	14.932	15.492	0.929	29.65
Zn (mg/kg)	11.088	11.092	0.989	22.832
Fe (mg/kg)	46.681	46.681	0.985	96.162
Mn (mg/kg)	11.956	12.043	0.986	24.451
Protein content (%)	21.999	22.008	0.990	45.301
Single plant yield (g)	46.415	48.467	0.917	91.564

GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation.

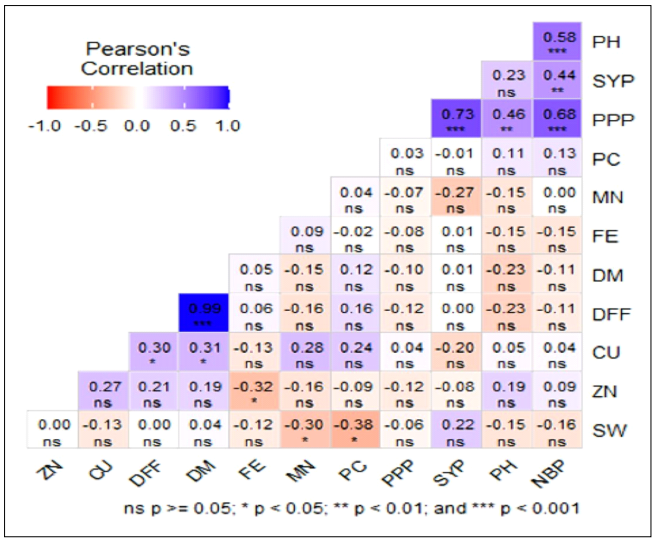


Fig 1: Correlation matrix.

Table 2: Direct and indirect effects of component characters on grain yield in pigeon pea.

Characters		DFF	DM	PH	NBP	PPP	SW	CU	ZN	FE	MN	PC
DFF	G	0.1813	0.1811	-0.0452	-0.0228	-0.0217	-0.0002	0.0558	0.0379	0.0109	-0.0300	0.0293
	P	0.1092	0.1076	-0.0241	-0.0119	-0.0131	0.0004	0.0324	0.0225	0.0065	-0.0177	0.0174
DM	G	-0.0619	-0.062	0.0149	0.0082	0.0063	-0.0019	-0.0198	-0.0117	-0.0033	0.0095	-0.0076
	P	-0.0176	-0.0179	0.0039	0.0017	0.0018	-0.0007	-0.0054	-0.0033	-0.001	0.0027	-0.0022
PH	G	-0.0033	-0.0031	0.013	0.0102	0.0064	-0.002	0.0006	0.0027	-0.0021	-0.002	0.0015
	P	0.0153	0.0151	-0.0694	-0.032	-0.0297	0.0103	-0.0032	-0.0127	0.0098	0.0098	-0.007
NBP	G	0.0416	0.0437	-0.2597	-0.3307	-0.2745	0.0652	-0.01	-0.0347	0.0587	-0.0005	-0.0505
	P	0.0032	0.0028	-0.0137	-0.0296	-0.0175	0.0039	-0.0013	-0.0023	0.0038	0.0002	-0.0033
PPP	G	-0.1308	-0.1112	0.5359	0.9063	1.0918	-0.0764	0.04	-0.1292	-0.0879	-0.0762	0.0332
	P	-0.0981	-0.0831	0.3508	0.4834	0.8192	-0.0457	0.0385	-0.0955	-0.0651	-0.0573	0.0254
SW	G	-0.0003	0.0088	-0.0448	-0.0576	-0.0205	0.2924	-0.041	0.0005	-0.0351	-0.0892	-0.1127
	P	0.0009	0.0108	-0.0393	-0.0354	-0.0148	0.2658	-0.0331	0.0003	-0.0308	-0.0792	-0.0988
CU	G	-0.1091	-0.1131	-0.0157	-0.0107	-0.013	0.0497	-0.3545	-0.0975	0.0465	-0.101	-0.0847
	P	-0.0732	-0.0743	-0.0115	-0.0105	-0.0116	0.0307	-0.2465	-0.065	0.0311	-0.0676	-0.0573
ZN	G	0.0429	0.0386	0.0423	0.0215	-0.0243	0.0004	0.0564	0.2053	-0.0665	-0.0329	-0.0189
	P	0.0245	0.0221	0.0217	0.0091	-0.0139	0.0001	0.0313	0.1189	-0.0385	-0.0188	-0.0109
FE	G	0.0052	0.0046	-0.0136	-0.0152	-0.0069	-0.0103	-0.0112	-0.0277	0.0857	0.0077	-0.0016
	P	0.0057	0.0051	-0.0136	-0.0123	-0.0076	-0.0111	-0.0121	-0.0311	0.0961	0.0086	-0.0018
MN	G	-0.0044	-0.0041	-0.0041	0.0001	-0.0019	-0.0081	0.0076	-0.0043	0.0024	0.0266	0.0012
	P	0.0073	0.0068	0.0064	0.0002	0.0032	0.0135	-0.0124	0.0072	-0.0041	-0.0453	-0.002
PC	G	0.0326	0.0248	0.0229	0.0308	0.0061	-0.0778	0.0482	-0.0186	-0.0038	0.009	0.2018
	P	0.021	0.0161	0.0133	0.0145	0.0041	-0.049	0.0307	-0.0121	-0.0025	0.0059	0.1319
SYP	G	-0.0062	0.0082	0.246	0.5401	0.7479	0.231	-0.2278	-0.0772	0.0056	-0.2791	-0.009
	P	-0.0017	0.0109	0.2245	0.3771	0.7201	0.2182	-0.1811	-0.0731	0.0055	-0.2587	-0.0087
Partial R^2	G	-0.0011	-0.0005	0.0032	-0.1786	0.8166	0.0675	0.0808	-0.0158	0.0005	-0.0074	-0.0018
	P	-0.0002	-0.0002	-0.0156	-0.0112	0.5899	0.058	0.0446	-0.0087	0.0005	0.0117	-0.0011

DFF= Days to 50% flowering; DM= Days to maturity; PH= Plant height; NBP= No. of branches per plant; PPP= Pods per plant; SW= 100 seed wt (g); CU= Cu (mg/kg); ZN= Zn (mg/kg); FE= Fe (mg/kg); MN= Mn (mg/kg); PC= Protein content (%); SYP= Single plant yield (g).

et al. (2023); Sharma *et al*. (2023); Ramasamy *et al*. (2021); Kandarkar *et al*. (2020); Narayanan *et al*. (2018); Anuj *et al*. (2018); Pandey *et al*. (2016); Hemavathy *et al*. (2019); Chaudhary *et al*. (2023).

Direct and indirect effects of attributes on grain yield

Path coefficient analysis, which splits the correlation coefficient into direct and indirect effects, was performed to gain a clear picture of the interrelationships among various component traits with yield (Table 2). In the present study, the number of pods per plant (genotypic path coefficient, 1.0918; phenotypic path coefficient, 0.8192) exhibited the maximum positive direct effect on single plant yield, followed by 100-seed weight (g) (0.2924, 0.2658), Zn content (mg/kg) (0.2053, 0.1189), protein content (%) (0.2018, 0.1319) and days to 50% flowering (0.1813, 0.1092). In contrast, the number of branches per plant (-0.3307, -0.0296), Cu content (mg/kg) (-0.3545, -0.2465), and days to maturity (-0.062, -0.0179) had negative direct effects on single plant yield.

The number of pods per plant, 100-seed weight (g), Zn content (mg/kg) and protein content (%) had significant positive direct effects on grain yield. Similar findings were observed by Edukondalu *et al*. (2023); Kandarkar *et al*. (2020) and Pandey *et al*. (2016). Conversely, the number of branches per plant, Cu content (mg/kg) and days to maturity showed low negative direct effects on single plant yield. Such direct effects were also reported by Sharma *et al*. (2023); Ramasamy *et al*. (2021); Narayanan *et al*. (2018); Anuj *et al*. (2018); Verma *et al*. (2018); Sharma *et al*. (2023); Bhadru *et al*. (2010).

Cluster analysis

The D2 analysis classified the genotypes into relatively homogeneous groups to minimize within-cluster diversity and maximize between-cluster diversity. The respective genotypes from diverse clusters can be utilized in breeding programs depending on the breeding objectives.

A set of 45 indigenous germplasm of pigeon pea was subjected to D2 analysis for twelve characters. Based on D2 values, four clusters were formed (Table 3, Fig 2). This indicated substantial diversity in the available gene pool of pigeon pea. Cluster analysis results revealed that Cluster III was the largest, consisting of 14 accessions, followed by Cluster I with 12 accessions, Cluster II with 11 accessions and Cluster IV with 8 accessions, similar results were reported by Naing *et al*. (2022). The clustering pattern demonstrated that the pigeon pea germplasm accessions collected from different locations in Telangana were genetically diverse. Hence, the genotypes studied are reliable for hybridization and selection.

The mean values for different characters were compared across the clusters and are presented in (Table 4). Results revealed that Cluster I was better for the early days

Table 3: Grouping of pigeonpea germplasm accessions in various clusters on the basis of D^2 values.

Cluster no.	No. of genotypes	Genotypes
1	12	IC-0634383, IC-0634384, IC-0634393, IC-0634407, IC-0634419, IC-0634425, IC-0634426, IC-0634428, IC-0634429, IC-0634435, IC-0634436, IC-0634437
2	11	IC-0634385, IC-0634387, IC-0634388, IC-0634395, IC-0634400, IC-0634414, IC-0634421, IC-0634427, IC-0634431, IC-0634432, IC-063443
3	14	IC-0634386, IC-0634389, IC-0634391, IC-0634392, IC-0634401, IC-0634408, IC-0634409, IC-0634410, IC-0634411, IC-0634416, IC-0634418, IC-0634420, IC-0634423, IC-0634424
4	8	IC-0634394, IC-0634398, IC-0634399, IC-0634402, IC-0634403, IC-0634412, IC-0634413, IC-0634430

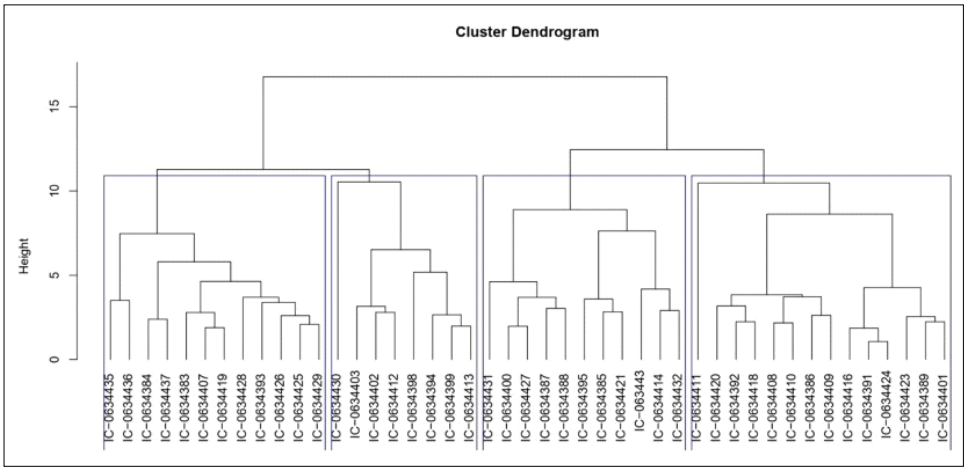


Fig 2: Dendrogram depicting genetic relationships among 45 pigeonpea accessions.

to 50% flowering and days to maturity, whereas Cluster II exhibited the highest values for 100-seed weight (g), Cu (mg/kg) and Zn (mg/kg). Similarly, Cluster III had better genotypes for plant height, number of branches per plant, pods per plant and single plant yield (g), while Cluster IV exhibited the highest values for Fe (mg/kg), Mn (mg/kg), and protein content (%). These findings align with previous studies by Edukondalu *et al*. (2024); Ranjani *et al*. (2023); Nyirenda *et al*. (2020); Ranjani *et al*. (2021) and Reddy *et al*. (2015). Similar patterns have been reported in studies of Bhatt *et al*. (2025); Kalyan *et al*. (2025); Kaur *et al*. (2023).

Principle component analysis

The scree plot illustrated the percentage of variance for each principal component, with PC1 showing 23.22% variability and an eigen value of 2.786, which then declined

Table 4: Cluster means of different characters in pigeon pea germplasm.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Days to 50% flowering	128.38	144.5	138.32	137.62
Days to maturity	169.58	185.73	179.00	178.25
Plant height	162.71	152.68	168.79	162.19
No. of branches per plant	9.00	9.36	10.79	10.12
Pods per plant	167.25	184.64	251.57	195.50
100 seed wt (g)	9.05	10.10	8.47	7.01
Cu (mg/kg)	10.72	12.65	10.12	11.12
Zn (mg/kg)	37.11	38.67	36.96	33.12
Fe (mg/kg)	168.06	146.91	178.8	193.39
Mn (mg/kg)	18.93	18.18	16.84	19.40
Protein content (%)	13.82	13.81	14.01	18.73
Single plant yield (g)	32.67	37.64	54.86	28.25

Table 5: Eigen values, % variance and cumulative eigen values of pigeon pea genotypes.

Traits	Principle component	Eigen value	Percentage of variance	Cumulative percentage of variance
Days to 50% flowering	PC1	2.787	23.225	23.225
Days to maturity	PC2	2.230	18.586	41.810
Plant height	PC3	1.814	15.118	56.929
No. of branches per plant	PC4	1.469	12.241	69.170
Pods/Plant	PC5	0.971	8.095	77.265
100 seed wt (g)	PC6	0.813	6.773	84.038
Cu (mg/kg)	PC7	0.609	5.071	89.109
Zn (mg/kg)	PC8	0.483	4.028	93.137
Fe (mg/kg)	PC9	0.403	3.362	96.499
Mn (mg/kg)	PC10	0.299	2.493	98.992
Protein content (%)	PC11	0.115	0.956	99.948
Single plant yield (g)	PC12	0.006	0.052	100.000

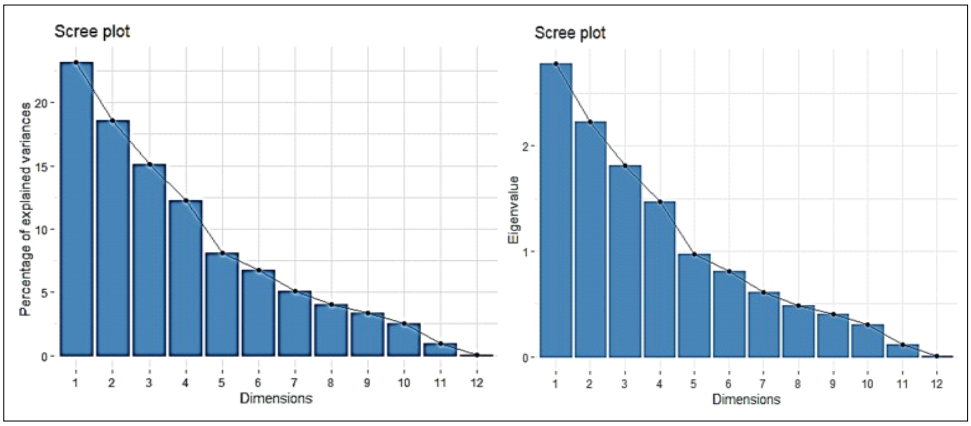


Fig 3: Screen plot.

gradually (Table 5, Fig 3). PCA on agro-morphological, yield, and nutritional components of pigeon pea indicated that four principal components (PCs) with eigenvalues greater than 1 accounted for 69.16% of the total variability. PC1 contributed 23.22%, PC2 18.58%, PC3 15.11% and PC4 12.24% (Fig 4).

Table 6: Rotated component matrix.

Traits	RC1	RC2	RC3	RC4
Days to 50% flowering	-0.085	0.975	0.024	0.040
Days to maturity	-0.075	0.971	0.003	0.036
Plant height	0.650	-0.241	0.142	0.360
No of branches per plant	0.827	-0.091	0.180	0.168
Pods per plant	0.907	-0.032	0.010	-0.08
100 seed wt (g)	-0.074	0.049	-0.778	0.060
Cu (mg/kg)	-0.041	0.357	0.519	0.410
Zn (mg/kg)	-0.027	0.194	-0.065	0.809
Fe (mg/kg)	-0.09	0.103	0.107	-0.719
Mn (mg/kg)	-0.215	-0.24	0.626	-0.120
Protein content (%)	0.170	0.230	0.598	-0.071
Single plant yield (g)	0.781	0.116	-0.356	-0.215

The rotated component matrix (Table 6, Fig 5) revealed that PC1 was dominated by yield traits like plant height, number of branches per plant, number of pods per plant, and single plant yield (g), while PC2 was associated with days to 50% flowering and days to maturity. PC3 and PC4 were primarily related to mineral and protein content traits such as Cu, Zn, Mn and protein content percentage (Table 7).

PC scores of the genotypes

Genotypes were selected based on PC scores, which can propose precise selection indices. High PC scores indicate high values for specific traits in those genotypes (Singh and Chaudhary, 1977). PC scores showed positive and negative values (Table 8) across components:

In PC1, the positive scores ranged from 0.0950 (IC-0634391) to 3.741 (IC-0634411), while negative values ranged from -0.0255 (IC-0634419) to -2.3433 (IC-063443). In PC2, the positive values ranged from 0.0057 (IC-0634412) to 1.9786 (IC-0634435) and negative values ranged from -0.0182 (IC-0634398) to -1.7855 (IC-0634414). In PC3, the positive values ranged from 0.0131 (IC-0634385) to 2.0743 (IC-0634424) and negative values ranged from -0.0169 (IC-0634395) to -2.3487 (IC-0634392). In PC4, the positive

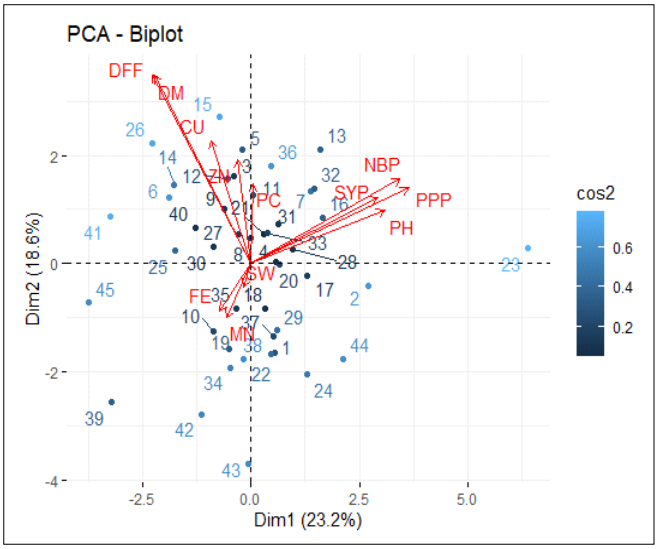


Fig 4: Biplot diagram of principal components.

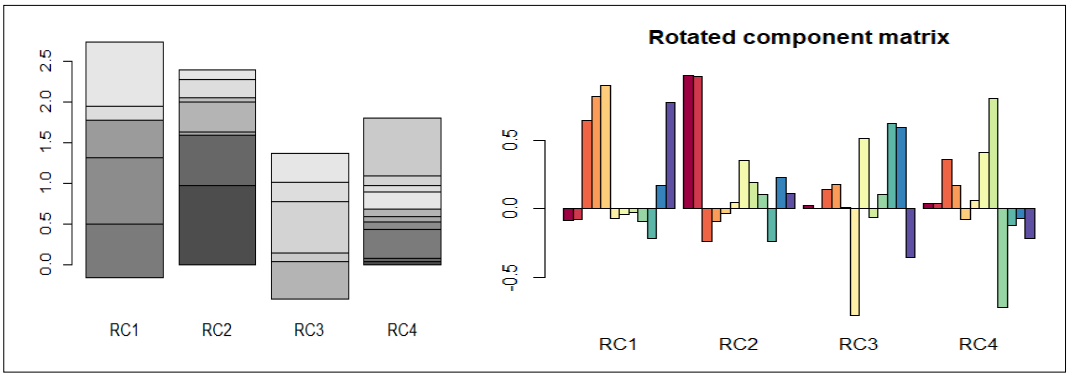


Fig 5: Rotated component matrix.

Table 7: Interpretation of rotated component matrix for the traits having values >0.5 in each PCs.

	PC1	PC2	PC3	PC4
Traits	Plant height	Days to 50% flowering	Cu (mg/kg	Zn (mg/kg)
	No. of branches per Plant	Days to maturity	Mn (mg/kg)	
	No. pods per plant		Protein content (%)	
	Single plant yield (g)			

Table 8: PC scores of pigeon pea germplasm in the study programme.

Genotypes	RC1	RC2	RC3	RC4
IC-0634383	-0.32756	-0.34597	1.076911	0.782966
IC-0634384	1.140674	-1.58729	-2.17981	-1.60486
IC-0634385	0.183398	1.978634	-1.87719	-1.32091
IC-0634386	0.502282	-0.59182	-0.28464	-0.13832
IC-0634387	0.124967	-1.61352	-0.18819	0.024398
IC-0634388	-0.7922	1.329595	-0.82742	-0.9365
IC-0634389	0.872204	0.477187	0.653058	0.435456
IC-0634391	0.095029	-0.91651	-0.27611	-0.05854
IC-0634392	0.272856	0.557814	-1.5371	-1.21674
IC-0634393	-1.00057	0.556528	-0.80021	-0.76939
IC-0634394	0.494159	-1.33869	0.669206	0.48692
IC-0634395	0.286824	-0.9743	0.273903	0.378483
IC-0634398	1.402039	-1.78551	0.771468	0.559813
IC-0634399	-0.58402	1.298212	-0.69984	-0.67239
IC-0634400	0.355249	0.597903	-0.01699	0.280904
IC-0634401	1.088649	-1.50021	-0.61334	-0.41651
IC-0634402	0.808284	-1.03564	-0.56586	-0.31841
IC-0634403	-0.1494	-0.81978	2.074361	1.957756
IC-0634407	-0.6385	0.749503	0.687329	0.546657
IC-0634408	0.389455	0.373285	-0.16049	0.130675
IC-0634409	0.686911	0.872135	-0.16214	0.058746
IC-0634410	-0.03807	0.789713	0.340411	0.385667
IC-0634411	3.741058	0.608927	0.488359	0.415951
IC-0634412	0.147092	0.289542	0.063373	0.288297
IC-0634413	-0.96412	0.005746	-0.47345	-0.27257
IC-0634414	-0.51511	0.440645	-1.02695	-0.99119
IC-0634416	-0.13321	-0.05197	1.70975	1.358135
IC-0634418	0.910361	0.586354	0.013178	0.282559
IC-0634419	-0.0256	-0.62996	0.213946	0.328876
IC-0634420	-0.3212	-0.95091	1.085173	0.786338
IC-0634421	0.459767	0.261325	1.019617	0.735333
IC-0634423	1.070231	1.456903	-2.34878	-4.29026
IC-0634424	0.209468	0.217299	-1.12259	-1.03245
IC-0634425	-0.98216	0.899165	-0.76309	-0.75987
IC-0634426	-0.47987	1.060523	0.783582	0.699884
IC-0634427	0.753333	-1.30963	0.217032	0.354404
IC-0634428	-0.36888	0.05296	0.119919	0.320161
IC-0634429	-0.6921	-0.81281	1.176882	0.871132
IC-0634430	-1.63345	-1.19351	-0.13454	0.249459
IC-0634431	-0.45709	1.709035	-0.31473	-0.18324
IC-0634432	-1.49036	0.23864	-1.40844	-1.07159
IC-0634435	-1.5848	1.266296	1.281458	1.013758
IC-0634436	-0.94725	0.241863	0.936024	0.735018
IC-0634437	0.474583	-0.01823	1.034722	0.753646
IC-063443	-2.34336	-1.43945	1.092237	0.832348

values ranged from 0.0243 (IC-0634426) to 1.9577 (IC-0634411), while negative values ranged from -0.0585 (IC-0634407) to -4.2902 (IC-0634400).

Top PC scores of positive values in each PC were selected in four principal components. Collection IC-0634411 performed well across all components. IC-0634401 and IC-0634398 excelled in yield-related traits in PC1 and PC2, while IC-0634403, IC-0634416 and IC-0634435 showed strong performance in protein and mineral content traits in PC3 and PC4. These results align with findings by Edukondalu *et al*. (2024); Dhanushasree and Hemavathy (2022); Hemavathy *et al*. (2017) and Rekha *et al*. (2013). Similar patterns of genotype performance across principal components have been reported in studies Jain *et al*. (2023); Mohanlal *et al*. (2023); Gupta *et al*. (2023) and Kumar *et al*. (2023), highlighting the effectiveness of PCA in identifying superior genotypes for breeding programs.

CONCLUSION

This study on the assessment of variability, diversity, and performance of indigenous pigeon pea germplasm for yield and nutritional traits reveals significant genetic variation among the accessions. High heritability and genetic advance for traits such as single plant yield, pods per plant, and iron content indicate strong potential for direct selection and genetic improvement. Correlation and path coefficient analyses identified key traits, including plant height, number of branches, number of pods and 100-seed weight, as crucial for yield enhancement.

Cluster analysis demonstrated substantial diversity, with the formation of four distinct clusters, highlighting the genetic divergence among the pigeon pea accessions from different locations in Telangana. Principal component analysis further reinforced the importance of yield-related traits, accounting for 69.16% of total variability, with the first principal component dominated by traits such as plant height and number of pods per plant.

These findings provide valuable insights for breeding programs aiming to develop high-yielding pigeon pea cultivars with enhanced nutritional quality. The genetic diversity observed in this study emphasizes the potential for using these accessions in hybridization and selection to achieve sustainable agricultural practices and improve food security.

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Disclaimers

The views and conclusions presented in this article are solely those of the authors and do not necessarily reflect the official policies or positions of their affiliated institutions. While the authors have made every effort to ensure the accuracy and completeness of the information provided, they do not assume any responsibility for errors, omissions, or any outcomes resulting from the use of the content.

Conflict of interest

The authors declare that there are no conflicts of interest associated with the publication of this article. The design of the study, data collection, analysis, interpretation of results, decision to publish and preparation of the manuscript were conducted independently and were not influenced by any financial or commercial relationships.

REFERENCES

Ajayi, F.T., Akande, S.R., Odejide, J.O. and Idowu, B. (2010). Nutritive evaluation of some tropical under-utilised grain legume seeds for ruminant's nutrition. *Journal of American Science*. **6(7):** 1-7.

Anuj, K., Singh, A., Kumar, R. and Singh, B. (2018). Genetic variability, character association and path analysis in pigeonpea [*Cajanus cajan* (L.) Millspaugh]. *Bulletin of Environment, Pharmacology and Life Sciences*. **7(3):** 63-68.

Bhadru, D. (2010). Correlation and path analysis for yield and its attributing traits in white coated pigeonpea [*Cajanus cajan* (L.) Millsp]. *Legume Research*. **33(3):** 196-200.

Bhatt, A., Verma, S.K., Panwar, R.K. and Reddy, S.K. (2025). Assessment of crop genetic diversity utilizing multivariate analysis in pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes. *Legume Research-An International Journal*. **48(12):** 1987-1994. doi: 10.18805/LR-5375.

Burton, G.W. (1952). Quantitative Inheritance in Grasses. In: *Proceedings of the 6th International Grassland Congress. Pennsylvania State College*. **1:** 277-283.

Chaudhary, L., Mukherjee, E. and Kumar, M. (2023). Multivariate analysis for selection of high yielding and early genotypes in pigeonpea [*Cajanus cajan* (L.) Millsp.] for north western plain zone of India. *Legume Research-An International Journal*. **46(5):** 555-561. doi: 10.18805/LR-5011.

Dhanushasree, M. and Hemavathy, A.T. (2022). Principal component analysis (PCA) in pigeonpea [*Cajanus cajan* (L.) Millsp.] germplasm. *Biological Forum-An International Journal*. **14(3):** 1318-1323.

Edukondalu, B., Reddy, V.R., Rani. T.S., Kumari, A. and Soundharya, B. (2023). Study of genetic variability for yield and yield attributes and bran oil content in maintainer lines of rice (*Oryza sativa* L.). *International Journal of Bio-resource and Stress Management*. **14(7):** 978-985.

Edukondalu, B., Reddy, V.R., Rani, T.S., Kumari, C.A. and Soundharya, B. (2023). Correlation and path analysis for yield and yield attributes in maintainer lines of rice (*Oryza sativa* L.). *International Journal of Bio-resource and Stress Management*. **14(6):** 900-908.

Edukondalu, B., Reddy, V.R., Rani, T.S., Kumari, C.A. and Soundharya, B. (2024). Genetic diversity analysis in rice maintainer lines using K-means clustering for yield and yield attributes. *International Journal of Bio-resource and Stress Management*. **15(6):** 01-07.

Edukondalu, B., Reddy, V.R., Rani, T.S., Kumari, C.A. and Soundharya, B. (2024). Assessment of variation in rice maintainer lines using principal component analysis. *Electronic Journal of Plant Breeding*. **15(1):** 270-276.

Food and Agriculture Organization of the United Nations. (2018). FAOSTAT statistical database. Retrieved May 17, 2025, from http://www.fao.org/faostat/en/#home.

Gupta, D., Muralia, S., Gupta, N.K., Gupta, S., Jakhar, M.L. and Sandhu, J.S. (2023). Genetic diversity and principal component analysis in mungbean [*Vigna radiata* (L.) Wilczek] under rainfed condition. *Legume Research*. **46(3):** 265-272. doi: 10.18805/LR-4568.

Hamid, A.H., Haque, M.M. and Islam, M.R. (2011). Genetic variability in pigeonpea [*Cajanus cajan* (L.) Millspaugh]. *Electronic Journal of Plant Breeding*. **2(1):** 117-123.

Hemavathy, A.T., Bapu, J.R. and Priyadharshini, M. (2019). Genetic variability and character association in pigeonpea [*Cajanus cajan* (L.) Millsp.] core collection. *Indian Journal of Agricultural Research*. **53(3):** 362-365. doi: 10.18805/IJARe.A-5123.

Hemavathy, A.T., Bapu, J.R.K. and Priyadharshini, C. (2017). Principal component analysis in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Electronic Journal of Plant Breeding*. **8(4):** 1133-1139.

Hemavathy, A.T., Bapu, J.R.K. and Priyadharshini, M. (2019). Genetic variability and character association in pigeonpea [*Cajanus cajan* (L.) Millsp.] core collection. *Indian Journal of Agricultural Research*. 53(3): 362-365. doi: 10.18805/IJARe.A-5123.

Jain, S.K., Sharma, L.D., Gupta, K.C., Kumar, V. and Sharma, R.S. (2023). Principal component and genetic diversity analysis for seed yield and its related components in the genotypes of chickpea (*Cicer arietinum* L.). *Legume Research*. **46(9):** 1174-1178. doi: 10.18805/LR-4489.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*. **47(7):** 314-318.

Kalyan, A., Muniswamy. S., Gore, P., Pandey, S., Tripathi, K., Gangashetty, P.I., Satheesh Naik, S.J. and Pratap, A. (2025). Unlocking morphological and genetic diversity in pigeonpea [*Cajanus cajan* (L.)] accessions for crop improvement. *Legume Research*. pp. doi: 10.18805/LR-5419.

Kandarkar, K.G., Kute, N.S., Tajane, S.A. and Ingle, A.U. (2020). Correlation and path analysis for yield and its contributing traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Journal of Pharmacognosy and Phytochemistry*. **9(4):** 1629-1632.

Kaur, H., Singh. I., Sethi, S., Bhatia, D., Gill, B.S. and Singh, S. (2023). Genetic divergence for seed yield enhancing and quality traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Legume Research- An International Journal*. **46(6):** 684-689. doi: 10.18805/LR-4739.

Kumar, A., Singh, R. and Yadav, R. (2023). Component analysis and stability of genotypes in French bean (*Phaseolus vulgaris* L.) for yield and yield attributing traits. *Legume Research*. **46(3):** 273-278.

Kunyanga, C.N., Imungi, J.K. and Vellingiri, V. (2013). Nutritional evaluation of indigenous foods with potential food-based solution to alleviate hunger and malnutrition in Kenya. *Journal of Applied Biosciences*. **67:** 5277-5288.

Mallesh, P., Nanda, H.C., Durgaraju, Ch., Kumar, C.V.S., Mohan, N. and Lee, J. (2017). Variability, heritability and genetic advance for quantitative traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *International Journal of Pure and Applied Biosciences*. **5(5):** 25-28.

Mohanlal, V.A., Saravanan, K. and Sabesan, T. (2023). Application of principal component analysis (PCA) for blackgram [*Vigna mungo* (L.) Hepper] germplasm evaluation under normal and water stressed conditions. *Legume Research*. **46(9):** 1134-1140. doi: 10.18805/LR-4427.

Mula, M.G. and Saxena, K.B. (2010). Lifting the level of awareness on pigeonpea: A global perspective. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India.

Naing, T., Verma. S.K., Yadav, H., Chauhan, C., Gautam, A., Karn, A. and Gaur, A.K. (2022). Assessment of morphological and molecular genetic diversity in pigeonpea [*Cajanus cajan* (L.) Millspaugh]. *Legume Research- An International Journal*. **45(9):** 1088-1093. doi: 10.18805/LR-4757.

Narayanan, S.L., Manivannan, N. and Mahalingam, A. (2018). Correlation and path analyses of yield and its component traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *International Journal of Current Microbiology and Applied Sciences*. **7(3):** 614-618.

Nyirenda, Y.E., Hussein, S., Mark, L., Isack, M. and Admire, S. (2020). Phenotypic divergence analysis in pigeonpea [*Cajanus cajan* (L.) Millspaugh] germplasm accessions. *Agronomy*. **10(11):** 1682. https://doi.org/10.3390/agronomy10111682.

Pandey, P., Kumar, P. and Pandey, S. (2016). Genetic association studies for yield and yield related traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Legume Research*. **39(2):** 189-193. DOI: 10.18805/lr.v0iOF.8604.

Panse, V.G. and Sukhatme, P.V. (1967). Statistical Methods for Agricultural Workers. ICAR Publication, New Delhi.

Pushpavalli, S.N.C.V.L., Yamini, K.N., Anuradha, G., Rajani, K.R., Kumar, C.S., Sudha Rani, C., Sudhakar, C., Saxena, R.K., Varshney, R.K. and Kumar, C.V. (2018). Genetic variability and correlation in pigeonpea genotypes. *Electronic Journal of Plant Breeding*. **9(1):** 343-349.

Ram, K., Kanak, S., Shrimali, T.M. and Geeta, B. (2016). A study on genetic variability, correlation and path analysis in pigeonpea [*Cajanus cajan* (L.) Millspaugh]. *International Journal of Agriculture Sciences*. **8:** 2287-2289.

Ramasamy, S.P., Aswini, M.S. and Hemavathy, A.T. (2021). Correlation and path analysis in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Indian Journal of Pure and Applied Biosciences*. **9(6):** 1-7.

Ranjani, M.S., Jayamani, P., Manonmani, S., Latha, K.R. and Sethuraman, K. (2021). Genetic analysis and diversity in early duration pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes. *Electronic Journal of Plant Breeding*. **12(2):** 540-548.

Ranjani, M.S., Vanniarajan, C., Kumar, C.V.S., Saxena, R.K. and Hingane, A.J. (2023). Genetic diversity studies in super-early pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Agricultural Science Digest*. doi: 10.18805/ag.D-5665.

Reddy, V.G., Jayalakshmi, V. and Sreenivas, T. (2015). Genetic divergence studies in pigeonpea inbreds. *Electronic Journal of Plant Breeding*. **6(2):** 515-520.

Rekha, R., Prasanthi, M., Sekhar, R. and Shanti Priya, M. (2013). Principal component and cluster analyses in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *International Journal of Applied Biology and Pharmaceutical Technology*. **4(4):** 424-430.

Saxena, K.B., Kumar, R.V. and Sultana, R. (2010). Quality nutrition through pigeonpea-A review. *Health*. **2(11):** 1335-1344.

Sharma, P., Singh, I., Khosla, G., Singh, G., Singh, S., Dhaliwal, S.K. and Singh, S. (2023). Variability and association studies for yield and yield related traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Legume Research-An International Journal.* **46(5):** 568-573. doi: 10.18805/LR-4374.

Sharma, R., Gangwar, R.K. and Yadav, V. (2014). A study on genetic variability and correlation in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *International Journal of Scientific Research*. **3(9):** 826-828.

Shunyu, V., Chaturvedi, H.P., Changkija, S. and Singh, J. (2013). Genetic variability in pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes of Nagaland. *Indian Research Journal of Genetics and Biotechnology*. **5:** 165-171.

Singh, R.K. and Chaudhary. B.D. (1977). Biometrical Methods in Quantitative Genetic Analysis. 3rd ed. New Delhi: Kalyani Publishers.

Vanniarajan, C., Magudeeswari, P., Gowthami, R., Indhu, S.M., Ramya, K.R., Monisha, K., Pillai, M.A., Verma, N. and Yasin, J.K. (2023). Assessment of genetic variability and traits association in pigeonpea [*Cajanus cajan* (L.) Millsp.] germplasm. *Legume Research*. **46(10):** 1280-1287. doi: 10.18805/LR-4442.

Verma, S.K., Bisht, C., Gaur, A.K. and Chandra, D. (2018). Study on some genetic parameters for yield and related traits in pigeonpea [*Cajanus cajan* (L.) Millspaugh] genotypes. *Chemical Science Review and Letters*. **7(25):** 70-76.

Wu, N., Fu, K., Fu, Y.-J., Zu, Y.-G., Chang, F.-R., Chen, Y.-H., Liu, X.-L., Kong, Y., Liu, W. and Gu, C.-B. (2009). Antioxidant activities of extracts and main components of pigeonpea [*Cajanus cajan* (L.) Millsp.] leaves. *Molecules*. **14(3):** 1032-1043.