



Identification of Diverse Genetic Architecture and Nutritional Protein Profiling for Yield and Attributing Traits in Pigeonpea [*Cajanus cajan* (L.) Millsp.]

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Abstract

Background: Pigeonpea [*Cajanus cajan* (L.) Millsp.] being an often cross-pollinated crop offers a wide range of genetic diversity which gives a tremendous scope for genetic improvement of economic traits. Improvement in yield and quality traits in pigeonpea is normally achieved by selecting the genotypes with desirable characters combinations existing in nature or by hybridization.

Method: The experimental material was undertaken during *Kharif* season of year 2021-22 at Research-cum-Instructional Farm, Department of Genetics & Plant Breeding, IGKV, Raipur. The experimental material for present study consisted 20 germplasm of pigeonpea. The biochemical analysis was conducted to estimate the protein content using Kjeldahl's method in each genotype. The genotypes were planted in Completely Randomized Block Design (CRBD) with 3 replications.

Result: The study reported maximum PCV (%) and GCV (%) for no. of pods/plant. High heritability was observed for characters viz., days to 50% flowering, protein content and duration of flowering. High GA (%) was observed for no. of pods/plant followed by seed yield/plant, primary branches/plant. Characters namely plant height, primary branches/plant, no. of pods/plant and no. of seeds/pods reported high and positive correlation with seed yield/plant. Path coefficient analysis showed that characters no. of pods/plant, plant height, days to maturity, days to 50% flowering protein content had direct positive effect. Genetic divergence study revealed that 20 different genotypes of pigeonpea was divided into 5 cluster also, cluster II comprised of maximum genotypes (16), while other cluster I, III, IV and cluster V had minimum entry numbers.

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Introduction

Among various leguminous crops, pigeonpea [*Cajanus cajan* (L.) Millsp.] is the second most important one in India. It has got a high nutritional value and economic uses; its every part is useful for mankind. Despite the importance, a very little research has been made towards its improvement. A number of factors are responsible for the poor productivity includes lack of improved cultivars, poor crop husbandry, pest and disease attack such as the pod borer complex (Sahu *et al.*, 2025a). Furthermore, sensitivity to abiotic stresses like water-logging and salinity also reduces pigeonpea production (Varshney *et al.*, 2010).

Extent of crop improvement programme in pigeonpea depends upon the expanse of its genetic variability, choices made for parents in hybridization and its selection procedure. The seed yield in pigeonpea is a complex trait which is highly influenced by the environmental variation. Success of yield improvement majorly depends upon its magnitude and nature of genetic variability present in the existing material, especially within diverse populations and germplasms (Sahu *et al.*, 2025b).

Such assessments of genetic variability, character association, and diversity have proven essential for breeding programs not only in pigeonpea but across a wide variety of crop species, including linseed, oat, and grass pea (Sahu *et al.*, 2016; Sahu and Tiwari, 2019; Sahu *et al.*, 2022; Mishra *et al.*, 2025b)^[6].

Materials and Methods

The presented study included 20 germplasm of pigeonpea grown in different parts of the country planted in Completely Randomized Block Design (CRBD) with 3 replications during *Kharif* season for year 2021-22 at Research-cum-Instructional Farm, IGKV, Raipur, Chhattisgarh, India. A spacing of 60 cm between plants was maintained. All agronomic practices were strictly followed. Observations were taken from randomly five plants from each replication for each genotype for characters viz., days to 50% flowering, duration of flowering, days to maturity, plant height (cm), no. of primary branches/plant, no. of pods/plant, no. of seeds/pod, 100 seed weight (g), shelling %, protein content (%) and seed yield/plant(g). The data was statistically

analysed for descriptive statistics, correlation and path analysis and genetic divergence analysis using OPSTAT and XLSTAT software.

Results and Discussion

Table 1 represented the ANOVA for seed and its component traits. Table 2 shows the genetic parameters where it is seen that maximum PCV (%) and GCV (%) was observed for traits no. of pods/plant followed by seed yield/plant. Low PCV (%) and GCV (%) was obtained for duration of flowering, days to maturity, plant height, no. of seeds/pod and 100 seed weight. High heritability was reported by days to 50% flowering, protein content, duration of flowering, low heritability was reported by plant height and shelling % and moderate heritability was reported by days to maturity and no. of seeds/pod. High GA (%) was reported by no. of pods/plant, seed yield/plant, primary branches/plant whereas, moderate GA (%) was reported by duration of flowering and 100 seed weight whereas low GA (%) was reported by days to maturity, plant height and no. of seeds/pod.

Table 1: Analysis of variance for seed yield and its attributing traits in Pigeonpea.

Source of Variation	Replication	Treatment	Error
Degree of freedom	2.00	19.00	38.00
Days to 50% flowering	13.65	1040.72**	0.81
Duration of flowering	5.72	56.35	101.90
Days to maturity	1.87	2.61**	0.62
Plant height (cm)	890.21	490.47**	194.71
Primary branches/plant	18.02	9.10**	0.58
No. of pods/plant	1357.22	27402.36**	3167.11
No. of seeds/pod	0.28	0.05**	0.035
100 seed weight (cm)	0.38	2.48*	0.161
Shelling %	456.35	165.76**	43.018
Protein Content (%)	1.71	27.02*	0.216
Seed yield/plant (g)	295.47	1343.47*	64.238

Table 2: Estimation of genetic parameters for seed yield and its component traits in Pigeonpea.

Characters	Mean	Range		PCV (%)	GCV (%)	Heritability	GA	GA (%)
		Max	Min					
Days to 50% flowering	115.15	193.33	105.33	16.187	16.169	99.767	38.309	33.269
Duration of flowering	68.967	84.00	64	6.576	6.133	86.964	8.125	11.781
Days to maturity	194.133	196	193	0.584	0.419	51.639	1.205	0.621
Plant height (cm)	184.615	337.1	252.2	9.277	5.378	33.613	11.858	6.423
Primary branches/plant	9.12	11.87	6.73	20.287	18.474	82.923	3.161	34.655
No. of pods/plant	64.405	132.53	38.13	35.957	33.045	84.459	40.292	62.561
No. of seeds/pod	3.79	3.93	3.47	4.216	3.377	64.158	0.211	5.572
100 seed weight (g)	10.143	12.44	8.83	9.528	8.666	82.715	1.647	16.235
Shelling %	42.443	52.65	20.34	21.585	15.071	48.747	9.2	21.676
Protein content (%)	20.852	24.75	14.45	14.509	14.336	97.632	6.085	29.18
Seed yield/plant (g)	67.633	125	37.33	32.751	30.532	86.907	39.656	58.634

Results of correlation analysis was presented in Table 3 displaying genotypic as well as phenotypic correlation coefficient for seed yield and its attributing trait. Duration of flowering had positive and highly significant correlation with plant height at both genotypic and phenotypic level whereas it showed positive and significant correlation with shelling %. Plant height showed positive and highly significant correlation with seed yield/plant and no. of pods/plant. Primary branches/plant reported positive and highly significant correlation with no. of pods/plant followed by

seed yield/plant, protein content and seed weight at both genotypic and phenotypic level. No. of pods/plant reported positive and highly significant correlation with seed yield/plant followed by 100 seed weight at genotypic and phenotypic level both but with no. of seeds/pod only at genotypic level. No. of seeds/pod had positive and significant correlation with seed yield/plant and shelling % at genotypic level. Positive and significant correlation was observed by shelling % at genotypic level and with seed yield/plant at phenotypic level.

Table 3: Genotypic(G) and Phenotypic(P) correlation coefficient analysis for seed yield and its component traits in Pigeonpea.

S. No	Characters		Duration of Flowering	Days to maturity	Plant height (cm)	Primary branches/plant	No. of pods/plant	No. of seeds/pod	100 seed weight (g)	Shelling %	Protein content (%)	r _{yx}
1	Days to 50% flowering	G	-0.101 ^{NS}	-0.038 ^{NS}	-0.260*	0.194 ^{NS}	-0.298*	-0.182 ^{NS}	-0.141 ^{NS}	0.168 ^{NS}	-0.179 ^{NS}	-0.302*
		P	-0.095 ^{NS}	-0.015 ^{NS}	-0.144 ^{NS}	0.178 ^{NS}	-0.266*	-0.131 ^{NS}	-0.125 ^{NS}	0.112 ^{NS}	-0.176 ^{NS}	-0.282*
2	Duration of flowering	G		-0.022 ^{NS}	0.494**	-0.434**	-0.053 ^{NS}	-0.174 ^{NS}	-0.143 ^{NS}	0.278*	0.148 ^{NS}	-0.017 ^{NS}
		P		-0.040 ^{NS}	0.362**	-0.339**	-0.037 ^{NS}	-0.153 ^{NS}	-0.131 ^{NS}	0.224 ^{NS}	0.130 ^{NS}	0.014 ^{NS}
3	Days to maturity	G			-0.199 ^{NS}	-0.409**	-0.318*	0.141 ^{NS}	-0.190 ^{NS}	-0.116 ^{NS}	0.051 ^{NS}	-0.116 ^{NS}
		P			0.087 ^{NS}	-0.223 ^{NS}	-0.231 ^{NS}	0.180 ^{NS}	-0.087 ^{NS}	-0.099 ^{NS}	0.050 ^{NS}	-0.090 ^{NS}
4	Plant height (cm)	G				-0.030 ^{NS}	0.356**	0.112 ^{NS}	0.219 ^{NS}	0.091 ^{NS}	-0.060 ^{NS}	0.515**
		P				0.039 ^{NS}	0.266*	0.148 ^{NS}	0.134 ^{NS}	-0.033 ^{NS}	-0.015 ^{NS}	0.265*
5	Primary branches/plant	G					0.509**	0.037 ^{NS}	0.374**	0.151 ^{NS}	0.317*	0.404**
		P					0.412**	0.027 ^{NS}	0.342**	0.183 ^{NS}	0.287*	0.302*
6	No. of pods/plant	G						0.263*	0.763**	0.166 ^{NS}	0.066 ^{NS}	0.963**
		P						0.216 ^{NS}	0.586**	0.044 ^{NS}	0.058 ^{NS}	0.848**
7	No. of seeds/pod	G							0.013 ^{NS}	0.277*	-0.280*	0.297*
		P							0.043 ^{NS}	0.042 ^{NS}	-0.201 ^{NS}	0.234 ^{NS}
8	100 seed weight (g)	G								0.281*	0.246 ^{NS}	-0.717**
		P								-0.246 ^{NS}	0.223 ^{NS}	0.567**
9	Shelling %	G									-0.211 ^{NS}	0.126 ^{NS}
		P									-0.146 ^{NS}	0.083 ^{NS}
10	Protein content (%)	G										0.033 ^{NS}
		P										0.036 ^{NS}

The positive and highly significant correlation of seed yield/plant are similar to the results found by Verma *et al.* (2018), Mula *et al.* (2019), Sharma *et al.* (2021), and Jatav *et al.* (2023) ^[3] for plant height; by Saroj *et al.* (2013), Devi *et al.* (2020) ^[1] and Sharma *et al.* (2021) for 100 seed weight; and by Narayanan *et al.* (2018), Devi *et al.* (2020) ^[1], Tharageshwari and Hemavathy (2020) and Sharma *et al.* (2021) for no. of pods/plant; Saroj *et al.* (2013), Kandarkar *et al.* (2020) ^[4], Tharageshwari and Hemavathy (2020) and Gupta and Sahu (2025) ^[2] for seed yield/plant.

Results from path analysis is mentioned in Table 4. Path

coefficient analysis showed that characters no. of pods/plant, plant height, days to maturity, days to 50% flowering protein content had direct positive effect whereas, shelling %, no. of seeds/pod, primary branches/plant, duration of flowering, 100 seed weight showed direct negative effect relationship with seed yield/plant. Similar findings have already been reported as positive direct effect by Thanki and Sawargaonkar (2010), Patel *et al.* (2011), Kesha Ram *et al.* (2016), Verma *et al.* (2016), and Gupta and Sahu (2025) ^[2] for no. of pods/plant on seed yield/plant and by Sodavadiya *et al.* (2009) that character like 100 seed weight.

Table 4: Genotypic path coefficient (Direct & indirect) for seed yield and its component traits in Pigeonpea.

Characters	Days to 50 % flowering	Duration of flowering	Days to maturity	Plant height (cm)	Primary branches/plant	No. of pods/plant	No. of seeds/pod	100 seed weight (g)	Shelling %	Protein content (%)	r _{yx}
Days to 50 % flowering	0.189	0.026	-0.008	-0.089	-0.047	-0.387	0.010	0.039	-0.009	-0.026	-0.302*
Duration of Flowering	-0.019	-0.256	-0.005	0.169	0.105	-0.069	0.010	0.040	-0.014	0.022	-0.017
Days to maturity	-0.007	0.006	0.209	-0.068	0.099	-0.412	-0.008	0.053	0.006	0.008	-0.116
Plant height (cm)	-0.049	-0.126	-0.042	0.343	0.007	0.462	-0.006	-0.061	-0.005	-0.009	0.515**
Primary branches/plant	0.037	0.111	-0.085	-0.010	-0.242	0.661	-0.002	-0.104	-0.008	0.047	0.404**
No. of pods/plant	-0.056	0.014	-0.066	0.122	-0.123	1.298	-0.014	-0.211	-0.009	0.010	0.963**
No. of seeds/pod	-0.034	0.044	0.030	0.038	-0.009	0.342	-0.055	-0.004	-0.014	-0.041	0.297*
100 seed weight (g)	-0.027	0.037	-0.040	0.075	-0.091	0.989	-0.001	-0.277	0.014	0.036	-0.717
Shelling %	0.032	-0.071	-0.024	0.031	-0.036	0.215	-0.015	0.078	-0.052	-0.031	0.126
Protein content (%)	-0.034	-0.038	0.011	-0.021	-0.077	0.086	0.015	-0.068	0.011	0.147	0.033

The nature and extent of genetic diversity were assessed among 20 different genotypes of pigeonpea using Euclidean method, XLSTAT software. This echoes the necessity of multivariate approaches, such as Principal Component Analysis (PCA), which have been effectively used to evaluate the diversity of indigenous and exotic pigeonpea accessions (Mishra *et al.*, 2025a) ^[5]. It was reported that 20 different genotypes of pigeonpea were divided into 5 different clusters, where cluster II was reported to have contain maximum no. of members (16) (RP-2, RP-3, RP-5, RP-7, RP-14, RP-15,

RP-17, ICP-6994, ICP-6996, ICP-7005, ICP-7373, ICP-7374, ICP-7379, C.G.Arhar-1 and C.G.Arhar-2) whereas, other cluster I, III, IV and V had minimum no. of members (1) each in it. The estimates of average intra- and inter-cluster distance for five clusters present in Table 5 revealed that the genotypes present in a cluster have little genetic divergence from each other with respect to aggregate effect of 11 characters under study, while much more genetic diversity was observed between the genotypes belonging to different clusters. The intra-cluster distance was highest for cluster II.

Table 5: Cluster means for 11 quantitative characters in Pigeonpea.

Cluster	Days to 50% flowering	Duration of flowering	Days to maturity	Plant height (cm)	Primary branches/Plant	No. of pods/plant	No. of seeds/Pod	100 seed weight (g)	Shelling %	Protein content (%)	Seed yield/plant (g)
1	110.333	71.667	193.000	286.200	11.267	132.533	3.733	12.437	44.890	20.387	125.0
2	110.708	68.479	194.271	272.084	8.961	60.935	3.727	10.050	41.818	21.282	63.85
3	193.333	66.333	194.000	257.500	10.633	38.133	3.600	9.557	47.533	18.340	38.33
4	115.00	72.333	193.333	304.300	8.533	83.067	3.733	9.707	44.500	20.403	99.667
5	113.00	73.33	194.00	337.10	8.600	59.400	3.86	10.36	42.84	17.39	68.00

Table 7 shows the intra and inter cluster distance between genotypes. The highest inter-cluster distance was found between cluster I and cluster III, followed by cluster V and cluster III. Table 6 represents cluster mean values for all the 11 characters. The highest cluster mean for days to 50% flowering was obtained for cluster III and the lowest in

cluster I. Cluster V had the highest cluster mean for duration of flowering whereas, cluster III had the lowest. The cluster mean for days to maturity was highest for cluster II and lowest for cluster I. The highest cluster mean for plant height was obtained for cluster V and the lowest in cluster III.

Table 6: Genotypes of Pigeonpea can be grouped into 5 clusters containing following genotypes of Pigeonpea.

Cluster No.	Genotypes	Name of genotypes
Cluster I	1	RP-1
Cluster II	16	RP-2, RP-3, RP-5, RP-7, RP-14, RP-15, RP-17, ICP-6994, ICP-6996, ICP-7005, ICP-7373, ICP-7374, ICP-7379, C.G. Arhar-1, C.G. Arhar-2
Cluster III	1	RP-8
Cluster IV	1	Asha
Cluster V	1	Rajeevlochan

Table 7: Estimates of average intra-(bold) and inter- clusters distance in Pigeonpea

Clusters	1	2	3	4	5
1	0.000	95.381	155.514	58.769	105.942
2		23.738	90.884	53.410	65.513
3			0.000	119.002	119.158
4				0.000	51.540
5					0.000

Primary branches/plant had highest cluster mean for cluster I and lowest for cluster IV. No. of pods/plant had highest cluster mean for cluster I and lowest for cluster III. The cluster mean for no. of seeds/pod was highest for cluster V and lowest for cluster III. 100 seed weight had highest cluster mean for cluster I and lowest for cluster III. The highest cluster mean for shelling % was for cluster III and lowest for cluster II. Protein content had highest cluster mean for cluster II and lowest for cluster I. Seed yield/plant had highest cluster mean for cluster I and lowest for cluster III.

Conclusion

The present study revealed substantial genetic variability among the 20 pigeonpea genotypes, indicating immense potential for crop improvement. Substantial genetic and nutritional variability exists among the germplasm. Selection based on the number of pods per plant and seed protein percentage offers a reliable route for simultaneous yield and quality improvement. The trait number of pods per plant emerged as the most reliable selection criterion for yield

enhancement, as it exhibited the highest phenotypic and genotypic coefficients of variation (PCV and GCV), high heritability, and the highest genetic advance. Furthermore, correlation and path coefficient analyses confirmed that the number of pods per plant, alongside plant height, consistently showed a highly significant positive correlation and a strong direct positive effect on seed yield per plant. Genetic divergence analysis successfully grouped the genotypes into five distinct clusters. The maximum inter-cluster distance was observed between Cluster I and Cluster III, suggesting wide genetic diversity between the genotypes of these groups. Genotypes from Cluster I (RP-1), which recorded the highest cluster means for key traits like seed yield per plant, number of pods per plant, and 100 seed weight, hold great promise. Utilizing genotypes from highly divergent clusters (such as Cluster I (RP-1) and III (RP-8)) as parents in future hybridization programs is highly recommended to achieve superior transgressive segregants for high-protein and develop high-yielding pigeonpea varieties.

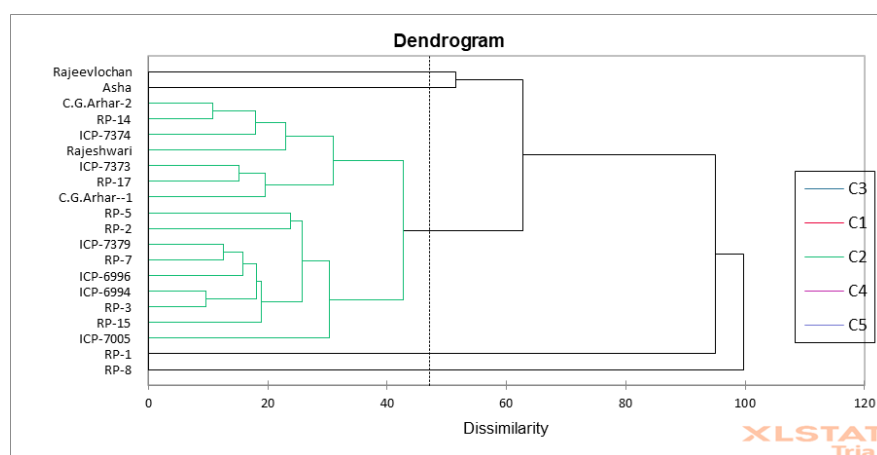


Fig 1: Dendrogram constructed using XLSTAT of 20 germplasms of Pigeonpea

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