



Plant Archives

Journal homepage: <http://www.plantarchives.org>

DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-2.414>

ASSESSMENT OF GENETIC VARIABILITY IN PIGEONPEA

Kokila Chandrakar, Mayuri Sahu*, Bhawana Sharma and Pooja Sahu

Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya,
Raipur Chhattisgarh, India 49012

*Corresponding author E-mail: mayuri.igkv@gmail.com

(Date of Receiving : 02-01-2026; Date of Revision : 26-02-2026; Date of Acceptance : 13-03-2026)

ABSTRACT

An experiment comprising 20 different genotypes including three checks viz., KRG-33, C.G. ARHAR-2 and BDN-716 of pigeonpea was conducted during *Kharif* 2024-2025 in four different environments. The present research aimed to estimate the genetic variability in 20 genotypes for yield and yield attributing traits. Observation of five plants of each genotypes in each replication were recorded in nine different quantitative characters viz., days to flowering initiation, days to maturity, plant height, number of branches per plant, number of pods per plant, seed yield per plant, 100 seed weight, plant population, seed yield per plot. High GCV and PCV values were recorded for seed yield per plant (g). Phenotypic coefficient of variation was higher than the genotypic coefficient of variation indicated that genotypes were influenced by environment also. High heritability for all the four locations were recorded for seed yield per plot and 100 seed weight, indicating the predominance of additive gene action and suggesting that direct selection for these traits would be highly effective. High heritability with high genetic advance as percentage of mean were recorded in seed yield per plant therefore selection for these traits will be effective to understand the genetic level of any genotype for future breeding programme of pigeonpea.

Keywords : Pigeonpea, Variability, Heritability, Genetic Advance.

Introduction

Pigeonpea [*Cajanus cajan*(L.) Millsp.] is a versatile food legume, serving as a lifeline to the source poor farmers in tropical and subtropical regions of Asia, Africa and Latin America. It belongs to the family 'Fabaceae' and is also known as "Arhar" or "Tur", generally used in preparing Dal which is rich in protein (24-25%) and minerals and eaten by majority of Indian vegetarian population. Pigeonpea is diploid with $2n=2x=24$ chromosomes. Pigeonpea is the most important food legume in India because it is a versatile legume that is widely used as food, feed, fodder, and fuel. Under the danger of climate change, soil degradation, and rising production costs, it has enormous potential to address the problem of worldwide pulse production (Saxena and

Sawargaonkar 2016). In the year in India, pigeonpea is cultivated in about 4.13 million hectare with total production of 3.41 million tons and productivity of 827 kg per hectare whereas in Chhattisgarh pigeonpea is cultivated in about 34.87 thousand hectare with total production of 20.75 thousand tons and productivity of 595 kg per hectare (P.C. Report - 2024-25). Genetic variability among traits is a key factor in breeding programmes, as it enables the identification and selection of desirable types. The heritability of a trait is an important measure for predicting its potential response to selection. Previous studies have emphasized that achieving genetic improvement in plants for quantitative traits requires accurate heritability estimates to design an effective breeding strategy (Allard, 1960). Broad-sense heritability

represents the ratio of genotypic variance to total phenotypic variance, indicating the proportion of variation attributable to genetic factors. Genetic advance refers to the expected improvement in a trait following the selection of superior individuals. The present investigation was carried out to evaluate the genetic variability, heritability, and genetic advance in pigeonpea (*Cajanus cajan*) genotypes. The coefficients of variation for different characters were calculated using the method proposed by Burton and De Vane (1953). Broad-sense heritability was estimated as per Burton and De Vane (1953), while the expected genetic advance was computed using the formula described by Johnson *et al.* (1955).

Materials and Methods

The experiment was conducted during *kharif* season of 2024-25 with 20 diverse genotypes viz., RPS-2016-1, RPS-2016-17, RPS-2016-31, RPS-2016-3, RPS-2016-16, RPS-2015-1, RPS-2015-40, RPS-2015-4, RPS-2015-51, RPS-2015-32, RPS-2014-34, RPS-2016-25, RPS-2015-49, ICPL 19059, ICPL 22485, ICPL 22471, ICPL 22482 including three checks namely BDN-716, C.G. ARHAR-2 and KRG-33. Material were grown in randomized block design (RBD) with three replications in four different environments viz., research cum instructional farm, department of Genetics and Plant Breeding, IGKV, Raipur (E1), S.K. CARS Kawardha (E2), CARS Kurud (E3), S.K.S. CARS Rajnandgaon (E4), Chhattisgarh. All recommended cultural practices and plant protection measures were followed to raise good crop. Five plants from each genotype were selected at random for recording observations on 9 quantitative characters viz., days to flowering initiation, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, seed yield per plant (g), 100 seed weight (g), plant population and seed yield per plot (g). The mean values computed from the observation for each replications from location were used for statistical analysis. The Analysis of variance (ANOVA) was done following the method given by Fisher (1918), The phenotypic and genotypic coefficient variability (PCV, GCV) were computed according to the suggested Sivasubramanian and Mahadevmenon (1973), heritability (h^2) and genetic advance as percentage of mean (GA) as suggested by Johnson *et al.* (1955).

Result and Discussion

The result of analysis of variance for four environments [Raipur (E1), Kawardha (E2), Kurud (E3), Rajnandgaon (E4)] are presented in table no.-1 which revealed that significant genotypic differences

existed for all the characters studied across the environments. That indicated ample amount of genetic variability present in four different environments for all the different characters.

The result on phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are presented in Table no.-2. It is clear that, in general, PCV estimates were higher than the corresponding GCV estimate for all the nine characters in all the four environments which draws a conclusion that there is influenced by environment.

It is clear that the table no.-2 that high GCV was recorded for seed yield per plot (g) (23.72%), (25.53%), (25.08%) in (E1, E3, E4), plant population (26.11%) in E2 and seed yield per pot (g) (31.22%) in E4. High PCV was recorded for number of pods per plant (23.68%), (22.36%) in (E1, E4), seed yield per plant (g) (30.09%), (26.65%), (25.53%), (20.30%) in (E4, E3, E1, E2), plant population (21.20%), (20.49%) in (E3, E4) and seed yield per plot (g) (31.22%), (22.78%) in (E4, E1). Low GCV was found for days to flowering initiation (7.51%), (6.1%), (4.40%), (4.49%) in (E3, E4, E2, E1) days to maturity (3.04%), (2.87%), (2.52%), (2.26%) in (E1, E3, E2, E4), plant height (cm) (7.36%), (5.08%), (4.65%) in (E2, E4, E1), number of branches per plant (5.68%), (4.48%) in (E1, E2), number of pods per plant (8.14%) in (E2), 100 seed weight (8.92%), (8.49%), (7.78%), (5.45%) in (E4, E3, E1, E2) and plant population (2.33%) in (E1). Low PCV was recorded for days to flowering initiation (7.25%), (6.23%), (6.01%), (4.72%) in (E3, E4, E1, E2), days to maturity (3.23%), (3.10%), (2.87%), (2.59%) in (E4, E1, E3, E2), plant height (cm) (8.51%) in (E1), number of branches per plant (5.68%), (4.58%) in (E1, E2), number of pods per plant (8.14%) in (E2), 100 seed weight (g) (8.92%), (8.49%), (7.78%), (5.45%) in (E4, E3, E1, E2) and plant population (2.33%) in (E1). High GCV and PCV was observed for seed yield per plant (g) in four environments, plant population in (E3) and seed yield per plot (g) in (E4) that indicates the sufficient amount of variation. Therefore, by selecting these traits would provide a good scope for crop improvement. Present outcome were also observed in study conducted Sahu *et al.*, (2025), Mishra *et al.*, (2025), Bhatt *et al.*, (2024) and Bathini *et al.*, (2021).

Heritability and Genetic Advance as Percentage of Mean

Heritability is the degree of phenotypic variation present is a population due to genotypic variation among the genotype in that population. It indicates the percentage of transfer of character from one generation

to another. Broad sense heritability exhibits the predominance of additive gene effect for the expression of any character. High heritability was recorded for days to flowering initiation (98.82%), (96.84%), (94%) in (E4, E3, E2), days to maturity (97.19%), (96.45%), (95.1%) in (E4, E1, E2), number of pods per plant (83.31%), (79.99%) in (E3,E4), seed yield per plant (79.28%), (69.14%), (65.92%), (62.14%) in (E1, E4, E3, E2), 100 seed weight (96.82%), (83.93%), (66.26%), (61.88%) in (E4, E1, E2, E3), plant population (69.93%), (62.24%) in (E3, E2) and seed yield per plot (84.08%), (74.22%) in (E3, E4). Low heritability was recorded for plant height (29.90%), (25.66%), (23.99%) (18.39%) in (E1, E4, E2, E3), number of branches per plant (30.27%), (11.55%), (9.15%) in (E3, E2, E1) number of pods per plant (30.67%), (15.02%) in (E2, E1), plant population (27.48%) in (E1) and seed yield per plot (22.28%) in (E1). The findings are in accordance with earlier findings of Sinha *et al.*, (2024), Akshaya *et al.*, (2023) and Vanniarajan *et al.*, (2023).

High genetic advance was recorded for number of branches per plant (28.42%) (E4), number of pods per plant (36.80%), (32.03%) in (E4, E3), seed yield per plant (g) (43.52%), (42.86%), (34.67%) (30.73%) in (E1, E4, E3, E2), plant population (37.61%), (20.76%) in (E3, E4) and seed yield per plot (g) (47.74%), (30.99%), (20. 95%) in (E4, E3, E2).The findings are in accordance with earlier findings of Sinha *et al.*, (2024), Akshaya *et al.*, (2023) and Mallesh *et al.*, (2017). High heritability combined with high genetic advance was observed for number of branches per plant in (E4), number of pods per plant (E3, E4), seed

yield per plant in four locations (E1, E2, E3, E4), plant population in (E3) and seed yield per plot in (E2, E3, E4). The findings are in accordance with earlier findings of Sahu *et al.*, (2025), Mishra *et al.*, (2025), Ekka *et al.*, (2023), Patel *et al.*, (2021) and Venkata *et al.*, (2015). High heritability combined with high genetic advance in the indication of additive gene action and selection based on this would be effective.

Summary and Conclusion

High GCV and PCV values were recorded for seed yield per plant (g). Phenotypic coefficient of variation was higher than the genotypic coefficient of variation indicated that genotypes were influenced by environment also. At all the four environments high heritability were recorded for seed yield per plot and 100 seed weight, indicating the predominance of additive gene action and suggesting that direct selection for these traits would be highly effective. Low heritability were recorded for plant height, indicating the govern by non-additive gene action and suggesting that trait heterosis breeding may be useful. High heritability with high genetic advance were recorded in seed yield per plant for all locations therefore selection for these traits will be effective to understand the genetic level of any genotype for future breeding programme of pigeonpea.

Table 1 : Pooled analysis of variance for seed yield and its attributing traits in pigeonpea (*Cajanus cajan*L.) under four different locations.

four different locations.										Mean sum of square	
Environment	Source	df	FI	DM	PH	NB	NP	SY/plant	100 SW	PP	SY/plot
Raipur	Replication	2	13.216	0.050	529.922	4.330	3183.450	80.369	0.0249	35.216	85314.528
	Genotype	19	48.943**	108.365**	736.239**	3.601*	2629.069*	249.887**	1.8341**	33.223*	258196.024*
	Error	38	10.199	1.313	322.929	1.976	1718.221	20.030	0.1100	15.550	138799.658
Kawardha	Replication	2	3.150	0.02	216.354	2.105	335.116	35.152	0.0845	15.200	124785.660
	Genotype	19	45.623**	78.543**	1702.300**	8.006**	772.750*	45.332**	1.1733**	661.665**	209276.37**
	Error	38	0.834	1.350	874.299	0.731	332.064	10.621	0.1704	109.147	42037.777
Kurud	Replication	2	0.200	6.016	437.272	5.430	140.564	23.720	1.9579	72.282	90.350
	Genotype	19	169.518**	60.332**	726.112**	4.601*	1028.608**	77.446**	1.1401*	1800.841**	260469.876**
	Error	38	0.673	17.279	433.195	1.998	64.375	11.385	0.4742	225.731	15463.402
Rajnandgaon	Replication	2	0.816	0.266	523.100	2.1250	352.827	150.388	0.0839	210.050	31977.600
	Genotype	19	80.750**	61.048**	608.008*	9.006**	4598.331**	312.696**	2.2193**	900.150**	1217734.810**
	Error	38	0.869	0.582	306.763	0.831	355.839	40.496	0.0241	230.523	126346.863

** - Significant at 5% probability level

* - Significant at 1% probability level

FI - Days to flowering initiation

NB – Number of branches per plant

DM - Days to maturity

PH – Plant height (cm)

NP – Number of pods per plant

SY/plant –Seed yield per plant (g)

100SW-100 seed weight (g)

PP- Plant population

SY/plot – Seed yield per plot (g)

Table 2 : Genetic parameters for yield and its attributing traits in pigeonpea (*Cajanuscajan* L.) under different environment

Traits	Environment	Minimum	Maximum	Grand mean	CV (%)	PCV (%)	GCV (%)	h^2 (bs) (%)	GA (as% of mean)
Days to flowering initiation	Raipur	69.00	93.00	79.96	3.99	6.01	4.49	55.87	6.92
	Kawardha	74.0	90.0	83.95	1.08	4.72	4.60	94	9.22
	Kurud	83.00	113.00	56.28	0.78	7.25	7.25	98.82	14.76
	Rajnandgaon	74.00	100.00	84.13	1.10	6.23	6.1	96.84	12.43
Days to maturity	Raipur	184.00	205.00	196.05	0.58	3.10	3.04	96.45	6.16
	Kawardha	193.00	217.00	200.65	0.57	2.59	2.52	95.1	5.07
	Kurud	186.00	205.00	15.11	2.09	2.87	2.87	47.03	2.78
	Rajnandgaon	186.00	204.00	197.91	0.38	3.23	2.26	97.19	4.60
Plant height (cm)	Raipur	183.4	301.4	251.95	7.13	8.51	4.65	29.90	5.24
	Kawardha	146.8	269.8	225.58	13.10	15.03	7.36	23.99	7.43
	Kurud	120.6	239.8	97.63	11.85	13.12	13.12	18.39	4.97
	Rajnandgaon	115.0	240.8	199.55	8.77	10.11	5.08	25.66	5.13
Number of branches per plant	Raipur	6.00	16.00	10.03	17.91	18.79	5.68	9.15	3.54
	Kawardha	9.00	17.00	13.38	12.40	13.18	4.48	11.55	3.13
	Kurud	5.6	12.6	0.86	16.14	19.32	10.32	30.27	12.05
	Rajnandgaon	6.67	15.27	10.47	8.70	18.00	15.76	76.63	28.42
Number of pods per plant	Raipur	104.00	283.00	189.85	21.83	23.68	19.17	15.02	7.32
	Kawardha	97.00	194.00	149.46	12.19	14.64	8.14	30.67	9.25
	Kurud	64.0	155.6	321.41	7.62	18.66	16.66	83.31	32.03
	Rajnandgaon	106.6	277.2	188.13	10.02	22.36	19.98	79.99	36.80
Seed yield per plant (g)	Raipur	18.28	61.04	36.88	12.13	26.65	23.72	79.28	43.52
	Kawardha	8.84	32.67	24.39	13.35	20.30	23.94	62.14	30.73
	Kurud	11.58	41.41	22.02	14.92	25.53	25.53	65.92	34.67
	Rajnandgaon	18.4	60.0	38.06	16.71	30.09	25.08	69.14	42.86
100 seed weight (g)	Raipur	7.46	11.51	9.73	3.40	8.50	7.78	83.93	14.70
	Kawardha	8.67	11.81	10.60	3.89	6.70	5.45	66.24	9.24
	Kurud	7.91	11.48	0.2	7.01	8.49	8.49	61.88	8.57
	Rajnandgaon	7.72	11.43	9.58	1.61	9.06	8.92	96.82	18.08
Plant population	Raipur	86.00	113.00	103.91	3.79	4.45	2.33	27.48	2.52
	Kawardha	69.00	153.00	125.85	8.30	13.60	10.78	62.79	17.60
	Kurud	49.0	153.0	525.03	14.31	21.83	26.11	69.93	37.61
	Rajnandgaon	62.00	167.00	103.95	14.60	20.49	14.37	49.19	20.76
Seed yield per plot (g)	Raipur	825.4	2724.7	1855.09	20.08	22.78	10.75	22.28	10.45
	Kawardha	1020.0	2303.3	1752.22	11.70	17.84	13.47	57.01	20.95
	Kurud	1022.00	2246.00	81668.82	7.14	17.89	16.14	84.08	30.99
	Rajnandgaon	1080.00	3940.00	2241.9	15.85	31.22	26.90	74.22	47.74

Reference

- Allard, R.W. (1960). Principles of Plant Breeding. 1st Edn., John Wiley and Sons Inc., New York.
- Akshaya, M., Geetha, K., Nirmalakumari, A., Sharavanan, P.T., Sithakumar, C. and Parsuraman, P. (2023). Genetic variability, correlation and principal component analysis for yield related traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Legume Research*. 5(2), 21-23.
- Anonymous (2024). Project coordinator's report 2024-25. AICRP on pigeonpea. 27-31.
- Bathini, A., Sharma, M.B., Seyie, K., Longchar, A. and Ozukum, C. (2021). Genetic variability studies in early duration pigeonpea genotypes under foothold conditions of Nagaland. *International Journal of Recent Scientific Research*, 12(09), 43017- 43019.
- Bhatt, A., Verma, S.K., Panwar, R.K., Yadav, H., Pragati, K., Kumawat, S. and Naresh, T. (2024). Assessment of genetic variability, correlation, and path coefficient for yield and its contributing traits in pigeon pea [*Cajanus cajan* (L.) Millspaugh]. *Journal of Experimental Agriculture International*, 46(8), 125-134.
- Burton G.W. and Devane E.H. (1953). Estimating heritability in tall fescue (*Festucaarundinaceae*) from replicated clonal material. *Agron. J.*, 45,478-481.
- Ekka, R.E. (2023). Study of genetic variability in pigeonpea [*Cajanus cajan* (L.) Millspaugh] genotypes. *The Pharma Innovation Journal*, 12(4), 2761-2764.

- Fisher, R. A. (1918). The correlation between relatives on supposition of mendelian inheritance trans. *Royal soc.*, **52**, 399-433.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimate of genetic environmental variability in soyabean. *Agronomy Journal*, **47**, 314-318.
- Mallesh, P., Nanda, H.C., Durgaraju, C.H., Kumar, S., Mohan, N. and Jacklee. (2017). Variability, Heritability and genetic advance for quantitative traits in pigeonpea. *International Journal of Applied Bioscience*, **5**(5), 25-28.
- Mishra A., Sahu M. and Pandey H. K. (2025). Assessment of Variability and Association among Green Forage Yield and Contributing Traits in Indigenous Genotypes of Grass Pea [*Lathyrus sativus* (L.)]. *Journal of Advances in Biology and Biotechnology* **28**,1 ,503-512.
- Patel, P.R., Sharma, M., and Patel, M.P. (2021). Study of heritability, genetic advancement, variability and character association for yield contributing characters in pigeonpea. *Emergent Life Sciences Research*, **7**(2), 1–4.
- Sahu, M., Singh S. and Singh V. (2025). Genetic variability and association pattern of yield and it's attributing characters among diallel population of pigeonpea (*Cajanus cajan* (L) MILL.S.). *Plant Archives*, **25**, 1(Supplement), 693-697.
- Saxena, K.B. and Sawargaonkar, S.L. (2016). Genetic enhancement of seed proteins in pigeonpea methodologies, accomplishment and opportunities. *International Journal of Science Research*, **4**, 3-7.
- Saxena, K.B., Singh, L and Gupta, M.D. (1990). Variation for natural out-crossing in pigeonpea. *Euphytica*, **46**, 143-148.
- Sinha, S., Kumar, N., Bhavana, P., Lal, H.C., Mahto, C.S., Kumar, B. and Kumar, J. (2024). Genetic variability estimation in forty pigeonpea germplasm for yield and yield attributing traits. *Journal of scientific research*, **30**(5), 894-900.
- Sivasubramanian, J. and Madhavmenon, P. (1973). Genotypic and Phenotypic variability in rice. *Madras Agricultural Journal*, **12**, 15-16
- Vanniarajan, C., Magudeeswari, P., Gowthami, R., Indu, S.M. Ramya, K.R., Monisha K., Pillai, M.A., Verma, N. and Yasin, J.K. (2023). Assesment of genetic variability and traits association in pigeonpea [*Cajanus cajan* L.] germplasm. *Legume Research*, **46**(10),1280-1287.
- VenkataNaresh, S., Govinda Rao, B., Ahmad, M.L. and Narasimha Rao, K.L. (2015). Genetic variability, heritability and genetic advance in pigeonpea (*Cajanus cajan* L. Millsp.) advanced lines. *The Andhra Agricultural Journal*, **62**(1), 75–78.