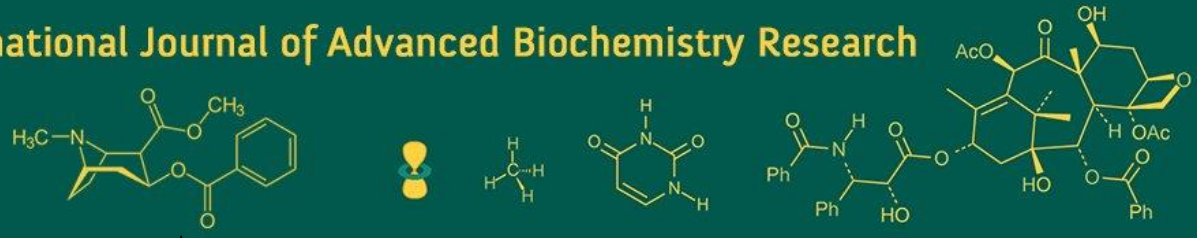
International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
IJABR 2025; SP-9(1): 926-929
www.biochemjournal.com
Received: 05-11-2024
Accepted: 08-12-2024

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Assessment of genetic variability and correlation analysis in pigeon pea (*Cajanus cajan* L.) for yield and agronomic traits

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DOI: https://doi.org/10.33545/26174693.2025.v9.i1Sl.3631

Abstract
The Experiment was conducted at Agriculture Farm, Nana Ji Deshmukh New Agriculture Campus, Mahatma Gandhi Chitrakoot Gramodaya Vishwavidyalaya, Chitrakoot, Satna to evaluate the thirty two genotypes/varieties under normal soil and rain fed condition. The experiment was laid out fallowing Randomized Block Design (RBD) with three replications during Kharif 2018. The seed yield kg/ha showed significant and positive correlation with pods/plant, secondary branches, 100-seed weight and primary branches exhibited positive correlation coefficient with seed yield kg/ha at genotypic level. The seed yield kg/ha exhibited highly significant and positive correlation with pods/plant, secondary branches and 100-seed weight exhibited positive correlation coefficient with seed yield kg/ha at phenotypic level. The characters showing significant positive correlation among yield and yield components suggested that selection would be highly effective and efficient in improving these traits. phenotypic coefficient of variation was higher than genotypic coefficient of variation. Maximum phenotypic and genotypic coefficients of variation were observed for seed yield kg/ha and number of no. of primary branches. This indicated the presence of high magnitude of genetic variability in the material for these characters.

Keywords: Variability, correlation, pigeon pea, diversity, Arhar

Introduction
Pigeon pea (*Cajanus cajan* [L.] Millsp.), also known as red gram or Arhar, is the second most important pulse crop in India after chickpea. It belongs to the family Leguminosae, with a chromosome number of 2n=22. Pigeon pea is an excellent protein source (20-22%) and is primarily consumed as dry split dhal. In 2017-18, India cultivated pigeon pea on 4.42 million hectares, yielding 4.02 million tons, with Madhya Pradesh contributing significantly (647,000 hectares; 897,000 tons; yield: 1,247 kg/ha). The crop is grown as a sole crop or intercrop with cereals and oilseeds across states like Maharashtra, Karnataka, and Madhya Pradesh.

Apart from food, pigeon pea serves as feed, fuel, fertilizer (fixing nitrogen), and material for baskets and fences. Despite its high potential yield (2,500-3,000 kg/ha), productivity remains stagnant (~700 kg/ha) due to biotic (e.g., wilt, pod borer) and abiotic (e.g., drought, erratic rainfall) stresses, coupled with limited adoption of improved management practices. Pigeon pea has also suffered a loss of genetic variability due to domestication. Breeding efforts focus on developing stress-resistant, high-yielding genotypes and analyzing genetic parameters like GCV, heritability, and genetic advance.

As pulses play a critical role in nutrition and soil health through nitrogen fixation, a holistic approach to develop region-specific varieties and technologies is essential to meet the rising demand, stabilize production, and improve per capita availability.

Materials and Methods
The Experiment was conducted at Agriculture Farm, Nana Ji Deshmukh New Agriculture Campus, Mahatma Gandhi Chitrakoot Gramodaya Vishwavidyalaya, Chitrakoot, Satna to evaluate the thirty two genotypes/varieties under normal soil and rain fed condition. The experiment was laid out fallowing Randomized Block Design (RBD) with three replications

during Kharif 2018. The experiment was sown on 29th July, 2018 and harvested on 27th, February, 2019. Each treatment was grown in 4m long 6 rows per plot spaced 90 cm apart. The plant to plant distance was maintained 25cm by thinning. Recommended agronomic cultural practices and plant protection measures were adopted to raise a best crop.
Observations were recorded for five randomly selected plants from each replication for 10 characters, including days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, seed yield per plant (g), number of seeds per pod, Appropriate variances and covariances were used for calculate phenotypic and genotypic correlation coefficients (Johnson *et al*., 1955) [3].

Result and Discussion

Genetic variability

(1.) Days to 50% flowering:
The data depicted in the table revealed that, days to 50% flowering ranged from 89.67 days (PT0704-1-2) to 108.33 days (LRG 134) and the grand mean was 95.82 days. The phenotypic and genotypic coefficients of variation were 5.65and 4.92, respectively was found low values for this character.

(2) Number of primary branches per plant
The data portrayed in table in respect of the number of branches per plant varied from 11.33 (RPS2007-105-1) to 20.00 (LRG 134) and the grand mean was 15.52. The phenotypic (16.21) and genotypic (12.81) coefficient of variation was found moderate values for this character indicating that environment has played significant role in the expression of this character.

(3.) Number of secondary branches per plant
The data portrayed in table in respect of the number of secondary branches per plant varied from 10.33 (BRGL 18-1) to 37.67 (ICPL-87119) and the grand mean was 21.29. The phenotypic (34.93) and genotypic (3.23) coefficient of variation was found high values for this character indicating that environment has played significant role in the expression of this character.

(4) Number of Pods per plant
The data expressed in table in respect of the number of pods per plant ranged from 272.00 (BDN 2013-1) to 527.00 (ICPL87119) and the grand mean was 327.53. The phenotypic (19.71) and genotypic (18.91) coefficient of variation was found high for this character indicating that environment has played significant role in the expression of this character.

(5) Plant height (cm)
The result portrayed in table exhibited that the plant height ranged from 91.33 (BRGL 18-1) to 181.33 (BDN 2013-1) and the grand mean was 124.59. The phenotypic (14.27) and genotypic (13.69) coefficient of variation was found moderate for this character indicating that environment has played significant role in the expression of this character.

(6) Days to Maturity
The data exhibited in the table revealed that days to maturity ranged from 162.67 days (AKTE 1701) to 201.33 days (LRG 134) and the grand mean was 178.99 days. The phenotypic (4.95) genotypic (4.19) coefficient of variation was found low for this character.

(7) 100-seed weight (g)
The boldest seed size was found in ICPL 87119 (13.75 g) and smallest seed size was in BDN 2013-1(9.63 g) and the grand mean was 11.43 g. The phenotypic (8.89) and genotypic (7.70) coefficient of variation was found moderate for this character indicating that environment has played significant role in the expression of this character**.**

(8.) Seed yield (kg/ha)
A large amount of variability was found for seed yield (kg/ha) ranged from 1130.99 kg/ha (RVSA 15-10) to 2873.31 (ICPL8719) and the grand mean was 1456.25 kg. The phenotypic (30.42) and genotypic (27.64) coefficient of variation was found high values for this character indicating that environment has played significant role in the expression of this character.

Correlation studies

The estimates of correlation coefficients among the 11 characters of pigeon pea genotypes at genotypic and phenotypic levels are given in Table 1 & 2.
In general, genotypic correlations were higher than phenotypic ones in magnitude for all the characters. The character which showed negative association at genotypic level also showed negative association at phenotypic level.
The seed yield kg/ha showed significant and positive correlation with pods/plant (0.701), secondary branches (0.685), 100-seed weight (0.365) and primary branches (0.267) exhibited positive correlation coefficient with seed yield kg/ha at genotypic level.
At phenotypic level, seed yield kg/ha exhibited highly significant and positive correlation with pods/plant (0.595), secondary branches (0.573) and 100-seed weight (0.251) exhibited positive correlation coefficient with seed yield kg/ha at phenotypic level.
The 100-seed weight showed significant and positive correlation with pods/plant (0.290& 0.218), secondary branches per plant (0.231 and 0.189) both at genotypic and phenotypic level.
The days to maturity showed significant and positive correlation with days to 50% flowering (0.728 and 0.572); The plant height with secondary branches per plant (0.366 and 0.331); no. of pods/plant with secondary branches per plant (0.709 and 0.677) and secondary branches per plant with primary branches (0.263 and 0.216) showed positive correlation at both genotypic and phenotypic level, respectively
The seed yield or economic yield is a complex character, which manifests from multiplicative interaction of several other characters that are termed as yield components. The genetic architecture of seed yield in pigeon pea as well as other crops is based on the balance or overall net effect produced by various yield components, interaction with one another.
Thus, selection for yield *per se* alone would not be better as such unless accompanied by the selection for various component characters responsible for conditioning it. Thus, identification of important yield components and information about their association with yield and also with each other are very useful for developing efficient breeding strategy for evolving high yielding varieties. The correlation

coefficient measures the degree of association between two variables or characters, which helps in understanding the nature and magnitude of association between yield and its components.

In the present investigation, phenotypic and genotypic correlations were estimated. The direction of phenotypic and genotypic correlations was similar for almost all the characters. In general, genotypic correlations were higher than phenotypic ones in magnitude for all the characters. The character which showed negative association at genotypic level also showed negative association at phenotypic level.

The seed yield kg/ha showed significant and positive correlation with pods/plant, secondary branches, 100-seed weight and primary branches exhibited positive correlation coefficient with seed yield kg/ha at genotypic level.

At phenotypic level, seed yield kg/ha exhibited highly significant and positive correlation with pods/plant secondary branches and 100-seed weight exhibited positive correlation coefficient with seed yield kg/ha at phenotypic level.

The strong positive correlation of grain yield with the characters mentioned above has also been reported earlier in pigeon pea. Parveen *et al*. (2011) [7] for pods per plant, harvest index and clusters per plant with seed yield, and Kumar *et al*. (1995) [6] for number of branches, number of clusters, number of pods per plant, number of seeds per plant, pod weight,

The 100-seed weight showed significant and positive correlation with pods/plant, secondary branches per plant both at genotypic and phenotypic level.

The days to maturity showed significant and positive correlation with days to 50% flowering; The plant height with secondary branches per plant; no. of pods/plant with secondary branches per plant; and secondary branches per plant with primary branches showed positive correlation at both genotypic and phenotypic level, respectively. The strong positive correlation of grain yield with above mentioned four yield components, which were highly correlated with each other, indicates the highly favorable situation for obtaining high response through selection. Therefore, selection practiced for improving these traits individually or simultaneously is likely to bring improvement in order to correlated response. This suggests that selection would be quite effective in improving yield and yield components in pigeon pea, especially in context of germplasm collections evaluated. Positive correlation among the yield components such as those noted above has also been reported by previous workers (Kingshlin and Subbraman, 1999; Sharma *et al.*, 1994; Dhamelia and Pathak, 1994; Patil *et al.*, 1989) [4, 9, 2, 8] and Kumar *et al*. (1995) [6]. Baldaniya, *et al*.(2018) for characters days to 50 percent flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, harvest index and protein content at both genotypic and phenotypic level

Table 1: Estimates of Genotypic Correlations for 08 different quantitative characters in Pigeon pea.

S. No.	Characters	Days to 50% Flowering	No. of primary branches	No. of secondary branches	No. of pods/plant	Plant height (cm)	Days to maturity	100-seed weight (g)	Seed yield (kg/ha)
1	Days to 50% Flowering	1.000							
2	No. of primary branches	-0.143^{NS}	1.000						
3	No. of secondary branches	-0.372**	0.263**	1.000					
4	No. of pods/plant	-0.126^{NS}	0.198^{NS}	0.709**	1.000				
5	Plant height (cm)	-0.246*	0.127^{NS}	0.366**	0.143^{NS}	1.000			
6	Days to maturity	0.728**	-0.018^{NS}	-0.059^{NS}	0.033^{NS}	-0.019^{NS}	1.000		
7	100-seed weight (g)	0.000^{NS}	0.074^{NS}	0.231*	0.290**	-0.008^{NS}	-0.143^{NS}	1.000	
8	Seed yield (kg/ha)	-0.016^{NS}	0.267**	0.685**	0.701**	0.166^{NS}	0.191^{NS}	0.365**	1.000

* Significant at 5% probability level,** Significant at 1% probability level

Table 2: Estimates of Phenotypic Correlations for 08 different quantitative characters in Pigeon pea.

S. No.	Traits	Days to 50% Flowering	No. of primary branches	No. of secondary branches	No. of pods/plant	Plant height (cm)	Days to maturity	100-seed weight (g)	Seed yield (kg/ha)
1	Days to 50% Flowering	1.000							
2	No. of primary branches	-0.022^{NS}	1.000						
3	No. of secondary branches	-0.317**	0.216*	1.000					
4	No. of pods/plant	-0.118^{NS}	0.155^{NS}	0.677**	1.000				
5	Plant height (cm)	-0.173^{NS}	0.117^{NS}	0.331**	0.138^{NS}	1.000			
6	Days to maturity	0.572**	-0.049^{NS}	-0.029^{NS}	0.022^{NS}	-0.013^{NS}	1.000		
7	100-seed weight (g)	-0.046^{NS}	0.069^{NS}	0.189^{NS}	0.218*	0.002^{NS}	-0.158^{NS}	1.000	
8	Seed yield (kg/ha)	-0.027^{NS}	0.165^{NS}	0.573**	0.595**	0.122^{NS}	0.115^{NS}	0.251*	1.000

* Significant at 5% probability level;** Significant at 1% probability level

Table 3: Mean, range, genotypic, phenotypic and error variance and coefficient of variation for eight quantitative characters in Pigeon pea.

S. No.	Characters	Grand mean (`X) + SE (m)	Range		Coefficient of Variation		C.V (%)
			Min.	Max.	GCV	PCV	
1	Days to 50% Flowering	95.82±1.53	89.67	108.33	4.92	5.65	2.76
2	No. of primary branches	15.52±0.89	11.33	20.00	12.81	16.21	9.92
3	No. of secondary branches	21.29±1.32	10.33	37.67	33.23	34.93	10.76
4	No. of pods/plant	326.53±10.53	272.00	527.00	18.91	19.71	5.57
5	Plant height (cm)	124.59±2.90	91.33	181.33	13.69	14.27	4.03
6	Days to maturity	178.99±2.72	162.67	201.33	4.19	4.95	2.63
7	100-seed weight (g)	11.43±0.29	9.63	13.75	7.70	8.89	4.41
8	Seed yield (kg/ha)	1456.25±107.09	1130.99	2873.31	27.64	30.42	9.09

* Significant at 5% probability level; ** Significant at 1% probability level

Conclusion

The present study highlighted the variability and correlation among different traits in pigeon pea genotypes. Significant genetic variability was observed for important traits such as seed yield, number of pods per plant, and plant height, with moderate to high phenotypic and genotypic coefficients of variation. The strong positive correlation of seed yield with traits like the number of pods per plant, secondary branches, 100-seed weight, and primary branches indicates that these traits are critical yield components. These findings suggest that selection targeting these traits can effectively improve yield in pigeon pea breeding programs. The higher genotypic correlations observed also highlight the genetic potential of the evaluated germplasm for developing high-yielding varieties.

Reference

1. Baldaniya JD, Kale BH, Mungra KS, Patel HN, Lad MD, Chauhan DA. Genetic variability, correlation and path analysis for morphological and quality traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. International Journal of Chemical Studies. 2018;6(5):2584-2587.
2. Dhamelia HR, Pathak AR. Correlation studies in segregating generations of pigeonpea. International Chickpea and Pigeonpea Newsletter. 1994;1:30-32.
3. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlations in soybean and their implications in selection. Agronomy Journal. 1955;47:477-483.
4. Kingshlin M, Subbaraman N. Character association and component analysis in F3 and full sib progenies of pigeonpea (*Cajanus cajan* (L.) Millsp.). Crop Research. 1999;18:84-88.
5. Kingshlin M, Subbaraman N, Chandirakala R. Studies of genetic parameters and selection response in biparental progenies of pigeonpea. Crop Research-Hisar. 1998;16:85-88.
6. Kumar SS, Sudharshanam A, Kumar SV, Reddy VN. Correlation and path coefficient analysis in green gram (*Vigna radiata*). Madras Agricultural Journal. 1995;82(3):160-162.
7. Parveen SI, Sekhar M, Reddi R, Reddy DM, Sudhakar P. Correlation and path coefficient analysis for yield and yield components in blackgram (*Vigna mungo* (L.) Hepper). International Journal of Applied Biology and Pharmaceutical Technology. 2011;2(3):619-625.
8. Patil HS, Deshmukh RB. Correlation and path analysis in mungbean. Journal of Maharashtra Agricultural Universities. 1988;13(2):183-185.
9. Sharma JD, Gupta VP. Selection parameters in inter-specific derivatives of urdbean x mungbean. Indian Journal of Pulses Research. 1994;7(2):174-176.