Genetic Studies on Yield and Its Components in Pigeonpea (*Cajanus cajan* L. Millsp.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Original Research Article

ABSTRACT

A field trial was carried out at the International Crop Research Institute for the Semi-Arid Tropics, Patancheru, Hyderabad during Kharif, 2023-24, with the aim of studying genetic parameters for yield and its components among pigeonpea genotypes which provides in developing an apt selection index to be included in the breeding programs. This research was conducted on 200 genotypes of Indian pigeon pea on seven traits. Data were analysed to calculate analysis of variance (ANOVA), phenotypic coefficient of variation (PCV), genetic coefficient of variation (GCV),

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broad sense heritability (h2bs) and estimated genetic progression as percentage mean using R software v 4.3.1. The results of the analysis of variance showed that there was a significant difference for days to 50% flowering, plant height (cm), hundred seed weight and seed yield per plant among the genotypes. The genotypic coefficient of variance was lower than the genotypic coefficient of variance for all the traits under selection. Higher extent of genotypic coefficient of variation is manifested by days to 50% flowering, plant height, seeds per pod, hundred seed weight and seed yield per plant. High heritability coupled with genetic advance as per cent mean was observed in seed yield per plant, number of days to 50% flowering and plant height. The results concluded that seed yield per plant, number of days to flowering up to 50%, and plant height are the traits that should be emphasized as selection indicator in Indian pigeon pea breeding programs.

1. INTRODUCTION

"Pigeonpea is a versatile crop that is cultivated across the arid and semi-arid regions of the world. It belongs to the Fabaceae family, the genus Cajanus, the species Cajan, the tribe *Phaseoleae*, and the sub-tribe *Cajaninae"* [1]. "It is an often cross-pollinated species with 11 pairs of chromosomes (2n = 2x = 22) and a genome size of 833.07 Mbp" [2]. It is commonly known as Tur or Arhar in India, and is the second most important pulse crop in the country after gram (chana). It is valued for its many uses as food, feed, fodder and fuel. On the Indian subcontinent, it is mainly consumed in the form of split dhal, while in Africa it is eaten as a whole grain. It meets the food and nutritional needs of the developing and underdeveloped countries of the world. "Globally, redgram is grown on an area of 63.57 lakh hectares with a production of 54.75 lakh tons and a productivity of 861.25 kg/ha. In India, the total area under cultivation and production of pigeonpea has been estimated at 4.23 million hectares and 3.89 million tons with a productivity of 919 kg per/ha" [3].

Since yield is a complex trait, it is influenced by multiple component characters, which are polygenically inherited and strongly influenced by environmental variation. The development of a character in a population is a result of the variability present in the population. In order to divide phenotypic variation into heritable (genetic) and non-heritable (environmental) components, the variability present in the population must be analysed. Isolating the genetic variance from the environmental variance, would improve the genotype's breeding value for accurate evaluation. Improvement of yield and productivity of pigeonpea has been an important challenge for the breeders. Last six decades of pigeonpea cultivation have displayed a retarded improvement in yield due to a narrow-cultivated gene pool diversity [3]. This necessitates the need of assessing the diversity of a wide range of genotypes for expanding the yield potential of the cultivars. Therefore, this study aimed to study genetic parameters such as phenotypic variation (PCV) and genotypic variation (GCV) of the crop and its components for 200 pigeon pea genotypes, which helps to identify suitable selection indicator and donors for inclusion in breeding programmes.

2. MATERIALS AND METHODS

The experimental material of the present study comprised 200 genotypes established at International Crop Research Institute for the Semi-arid Tropics, Patancheru, Hyderabad, during Kharif 2023-24 in an alpha lattice design with two replications. Each entry was accommodated in two rows of 3m each with a spacing of 75 cm X 15 cm. Observations were recorded on five randomly selected plants from each line in each replication except for days to 50 percent flowering, where all plants in the plot were considered. All cultivation practices were followed and timely plant protection measures were taken to avoid damage from pests and diseases. The observations were made on seven traits namely days to 50% flowering, plant height (cm), number of primary branches per plant, number of secondary branches per plant, seeds per pod, hundred seed weight (g) and seed yield per plant (g). The data collected for the different traits were subjected to various statistical analyzes.

The analysis of variance for the alpha lattice design was performed for each character with the method using the residual maximum likelihood (REML) procedure with ASREML-R v4 in the R software v 4.3.1 [4]. From ANOVA table, environmental, genotypic and phenotypic variances were estimated [5]. The phenotypic

and genotypic coefficient of variation was calculated from the ANOVA table [6]. GCV (%) and PCV (%) values were classified as described by Sivasubramanian and Madhava Menon [7]. The broad sense heritability was estimated according to method given by Allard [8]. The expected genetic advance represents the shift in a population towards the superior side under a certain selection pressure after a single generation of selection. It can be calculated according to the method proposed by Allard (1960) with a selection intensity of 5 percent and constant 'K' of 2.06 [8]. The expected genetic advance expressed as percentage of mean, was calculated according to the method proposed by Johnson et al., [5].

3. RESULTS AND DISCUSSION

3.1 Mean Performance of the Genotypes

Morphological characterization of genotypes for seven different traits, namely days to 50 % flowering (DF), plant height (cm) (PH), number of primary branches per plant (PB), number of secondary branches per plant (SB), seeds per pod (SPP), hundred seed weight (g) (HSW), yield per plant (g) (YLD) showed a wide variation. Days to 50% flowering, plant height (cm), hundred seed weight (g) and seed yield per plant (g) displayed significant genotypic variation (Table 1). This clearly indicates that there is sufficient variation among the genotypes and there is ample scope for improvement.

The mean performance of genotypes evaluated for days to 50% flowering showed that ICP 14936 (51 days) was the earliest to flower, while ICP 4231 (180.5 days) was the latest entry with a mean of 126.12 days across the panel. Plant height ranged from 88.8 (ICP 11627) to 256.6 (ICP 11833) with an average height of 191.39 cm. The number of primary and secondary branches per plant ranged from 6.2 (TS3R) to 11.6 (ICP 10276, ICP 2577), 7 (ICP 6892, GRG 152) to 18.8 (BSMR 736) with a mean of 8.16 and 11.74, respectively. Seeds per pod across the panel had a limited range from 3.32 (ICP 7803) to 4.28 (ICPL 20201) with a mean of 3.73. Hundred seed weight ranged from 6.8 g (ICP 14900) to 14.8 g (ICP 2405) with a mean of 10.2 g in the panel for all genotypes. The yield per plant also varied greatly from a minimum of 0.64 g (ICP 14294) to 77.05 g (ICP 655) with an average of 15.49 g (Table 2).

The values of the genotypic coefficient of variation were lower than those of the phenotypic coefficient of variation, indicating an effect of environment over all traits (Table 2). High values of GCV were observed for yield per plant, while moderate variance was reported for days to 50% flowering, plant height (cm), and hundred seed weight (g) indicating a greater degree of variability in these traits and thus suggesting a good scope for improvement through selection. Low values were recorded for the number of primary branches per plant, the number of secondary branches per plant and seeds per pod, suggesting that variability needs to be created by hybridization followed by selection. Similar results were reported by Galian et al. [9]; for yield per plant and plant height (cm) by Pushpavalli et al. [10]; for days to 50% flowering by Naik et al. [11]; Sahu and Ekka, (2020) for hundred seed weight (g) and seeds per pod [12]; Pashwan et al. (2021) for the number of primary branches per plant and the number of secondary branches per plant [13].

The present study showed a wide range of variability for all traits. The presence of genotypic variation alone does not indicate an improvement that could be achieved by selection. The estimation of heritability of the trait shows the relative percentage of heritable variability that allows efficient selection. High heritability was found for all traits except the number of primary and secondary branches per plant, indicating that all traits are mainly determined by additive genes and thus have the least environmental influence. The results were in accordance with those of Galian et al. (2015), Gaur et al, (2020), Patel et al. (2021) and Bhagat et al. (2022) for all traits with high heritability [9,14-16]. The number of primary branches per plant and the number of secondary branches per plant showed moderate and low heritability, respectively, indicating a greater influence of the environment on the traits, which is also explained by Pushpavalli et al. [10] and Patel et al. [15].

"The heritability value alone cannot provide information on the amount of genetic progress that would result from the selection of the best individuals. Johnson et al. (1955) suggested that the heritability estimates along with genetic gain would be more successful in forecasting the success of selecting the best individuals" [5]. In order to improve the effectiveness of the selection process, it was crucial to take the expected genetic advance into account alongside the heritability estimate. As a result, the expected genetic progress is calculated for all attributes.

Table 1. Combined analysis of variance for different traits in Pigeonpea

Description	DF	PH	PB	SB	SPP	HSW	YLD
Genotype	1508.30**	732.58**	1.303	5.240	0.019	5.141**	231.012**
Replication	0.520	374.91	1.368	1.270	0.003	0.083	12.185
Residuals	8.481	91.163	1.523	7.149	0.025	0.780	27.596

DF= Days to 50% flowering; PH= Plant Height (cm); PB= Number of Primary Branches Per Plant;
SB=Number of Secondary Branches Per Plant; SPP= Seeds Per Pod;
HSW= Hundred Seed Weight (g); YLD= Seed Yield Per plant (g)

Table 2. Genetic components of variance for pigeonpea genotypes

Trait	Minimum		Maximum		Mean	PCV	GCV	Trend of GCV	h^2 (B.S)	Trend of h^2(B.S)	GAM (%)	Trend of GAM (%)
DF	ICP 14936	51	ICP 4231		180.5	126.12	17.70	17.54	Mod	0.982	High	35.82	High
PH	ICP 11627	88.8	ICP 11833		256.6	191.39	12.77	11.77	Mod	0.849	High	22.34	High
PB	TS3R	6.2	ICP 10276, ICP 2577		11.6	8.16	15.72	4.83	Low	0.059	Mod	1.81	Low
SB	ICP 6892, GRG 152	7	BSMR 936		18.8	11.74	22.38	7.10	Low	0.111	Low	4.89	Low
SPP	ICP 7803	3.32	ICPL 20201		4.28	3.73	3.86	1.07	Low	0.077	High	0.61	Low
HSW	ICP 14900	6.80	ICP 2405		14.80	10.20	15.30	11.95	Mod	0.610	High	19.25	Mod
YLD	ICP 14294	0.64	ICP 655		77.05	15.49	67.87	61.82	High	0.829	High	115.99	High

DF= Days to 50% flowering; PH= Plant Height (cm); PB= Number of Primary Branches Per Plant; SB=Number of Secondary Branches Per Plant; SPP= Seeds Per Pod; HSW= Hundred Seed Weight (g); YLD= Seed Yield Per Plant (g)
MIN= Minimum; MAX= Maximum; GCV= Genotypic Coefficient of Variation; PCV= Phenotypic Coefficient of Variation; h^2_{bs} = Heritability (Broad sense); GAM = GA as Per Cent of Mean (%)

The genetic advance as percentage of mean was highest for yield per plant, followed by days to 50% flowering and plant height. Moderate genetic advance as percentage of mean was observed for hundred seed weight followed by low genetic advance as percentage of mean for number of primary branches per plant, number of secondary branches per plant and seeds per pod indicating higher non-additive gene action in these traits. The results were similar to the observations of Vanishree et al. [17], Saroj et al. [18]; Galian et al. for yield per plant [9], Gaur et al. (2020) for days to 50% flowering and plant height, Bhagat et al. (2022) for hundred seed weight [14,16]; Pashwan et al. (2021) and Patel et al. (2021) for number of primary branches per plant, number of secondary branches per plant and seeds per pod [13,15].

A higher heritability coupled with a high genetic advance as percentage of mean is observed for yield per plant, days to 50% flowering and plant height. This confirms higher additive gene effects and thus improvement could be achieved by direct phenotypic selection. A higher heritability with a moderate genetic advance as percentage of mean is observed for hundred seed weight and a higher heritability with low genetic advance in seeds per pod, indicating the effect of non-additive gene action. The higher heritability might be due to the favourable environment rather than the genotype. Moderate heritability with low genetic advance as percentage of mean was observed in the number of primary branches per plant, while low heritability with low genetic advance as percentage of mean was observed in the number of secondary branches per plant. These traits confirm a higher non-additive gene

action and their lower potential for improvement by selection (Table 2).

4. CONCLUSION

The findings suggest that all pigeonpea genotypes have enough variation to account for the seven variables under investigation. The value of PCV was higher than GCV, indicating a considerable influence of the environment on phenotypic expression. High heritability was observed for all traits except number of primary and secondary branches per plant, while high genetic advance as a percentage of mean for yield per plant, followed by days to 50% flowering and plant height indicated that phenotypic selection would be worthwhile. Thus, according to the results, yield per plant, days to 50% flowering and plant height are the traits that need to be prioritised for the development of the pigeonpea selection index.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Greilhuber J, Obermayer R. Genome size variation in *Cajanus cajan* (Fabaceae): a reconsideration. Plant Systematics and Evolution. 1998;212:135-141.
2. Varshney RK, Chen W, Li Y, Bharti AK, Saxena RK, Schlueter JA, Donoghue MT, Azam S, Fan G, Whaley AM and Farmer AD. Draft genome sequence of pigeonpea (*Cajanus cajan*), an orphan legume crop of resource-poor farmers. Nature Biotechnology. 2012;30(1):83.
3. FAOSTAT; 2022.
   Available:https://www.fao.org/faostat/en/data (last Access on: 15 May 2024).
4. Butler DG, Cullis BR, Gilmour AR, Gogel BJ and Thompson R. ASReml-R reference manual version 4. VSN International Ltd, Hemel Hempstead, HP1 1ES, UK; 2017.
5. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlation in soybean and their implications in selection. Agronomy Journal. 1955;47:477-483.
6. Burton GW, de Vane EM. Estimating heritability in fall fescue (*Festuaca cirunclindcede*) from replicated clonal material. Agronomy Journal. 1953;45:478-481.
7. Sivasubramaniam, S. and Madhav Menon Inheritance of short stature in rice. Madras Agriculture Journal. 1973;60:1129-1133
8. Allard RW. Principles of plant breeding, John Willey and Sons, New York; 1960.
9. Galian JL, Mohan N, Kumar CS, Mallesh P. Genetic variability studies in Pigeonpea [*Cajanus cajan* (L.) Millsp.]. The Journal of Research ANGRAU. 2015;43(3&4):1-7.
10. PushpaValli SNCVL KN. Yamini. Genetic variability and correlation in pigeonpea genotypes. Electronic Journal of Plant Breeding. 2018;9(1):343-349 (Mar 2018) ISSN 0975-928X
11. Naik SJ, Gowda B, Dinesh M, Miyan HB, Pushpa HD. Genetic analysis in advanced breeding lines (F5) of pigeonpea (*Cajanus cajan* (L.) Millisp.). BIOINFOLET-A Quarterly Journal of Life Sciences. 2013;10(1b):196-200.
12. Sahu JK, Ekka RE. Genetic variability studies in germplasm accession of pigeonpea (*Cajanus cajan* (L.) Millsp.). Journal of Pharmacognosy and Phytochemistry. 2020;9(6S):377-379.
13. Pashwan, VR., Chaurasia, A.K., Rao, D., Spandana, R., Rajkumar, M. and Surender, V., Studies on genetic variability for quantitative characters, growth and yield parameters in pigeonpea (*Cajanus cajan* L.) genotypes. J. Pharmn. Innov. 2021;10(11):269-275.
14. Gaur AK, Verma SK, Panwar RK, Estimation of genetic variability and character association for development of selection criteria in pigeonpea [*Cajanus cajan* (L.) Millspaugh]. International Journal of Chemical Studies. 2020;8(2):391-394.
15. Patel PR, Sharma M, Patel MP. Study of heritability, genetic advancement, variability and character association for yield contributing characters in pigeon pea [*Cajanus cajan* (L.) Millspaugh]. Emergent Life Sciences Research. 2021;7:1-4.
16. Bhagat P, Giri SK, Kumar K, Tiwari JK, Sinha SK. Genetic variability and association studies for seed yield and related trait in pigeonpea [*Cajanus cajan* (L.) Millsp.]. The Pharma Innovation Journal. 2022;11:2963-2966.

17. Vanisree S, Sreedhar M, Raju CS. Studies on Genetic Characteristics of Pigeon Pea and Determination of Selection Criteria with Path Co-Efficient Analysis; 2013.

18. Saroj SK, Singh MN, Kumar Ravindra, Singh Tejveer, Singh MK. Genetic variability, correlation and path analysis for yield attributes in pigeonpea. The Bioscan. 2013;8(3):941-944.

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