



Nature and Extent of Genetic Variability, Heritability and Genetic Advance in Yield, Quality and Physiological Traits in Medium Early Maturing Genotypes of Pigeonpea [*Cajanus cajan* (L.) Millsp.]

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ABSTRACT: This investigation was carried out on thirty medium early maturing genotypes of pigeonpea with three replications during Kharif, 2023 under AICRP on Pigeonpea at ARS, Ummедganj-Kota. In this study analysis of variance (ANOVA) showed a significant variability among all the sixteen characters which were studied. Genotypic coefficient of variation (GCV) was slightly less than phenotypic coefficient of variation (PCV) for all the characters. The highest GCV and PCV value was observed higher for number of primary branches per plant followed by number of secondary branches per plant, number of pods per plant and seed yield per plant. High heritability associated with high genetic advance for number of primary branches per plant, number of secondary branches per plant, number of pods per plant, seed yield per plant, harvest index, leaf area per plant and total chlorophyll content which shows that there is lesser influence of environmental factors and presence of additive gene action.

Keywords: Genetic variability, GCV, PCV, Heritability and Genetic advance.

INTRODUCTION

Pulses serve as an indispensable source of protein for the predominantly vegetarian population of many countries, including India, making a significant portion of our daily diet. In India, pulses have been described as a “poor man’s meat” and “rich man’s vegetable”. The importance of vegetable protein has been well recognized throughout the World (Anonymous, 2015). Pigeonpea [*Cajanus cajan* (L.) Millsp] holds a significant position among various food legumes, being rated highly for its biological value and belongs to the family *Fabaceae* and sub-family *Papilionaceae*. It is also known by a group of names such as Arhar, Red gram, Tur, Rahar, Angole and Cango Pea. It is an often-cross pollinated crop with diploid ($2n = 2x$) condition, having chromosome number 22 with genome size of 833.1 Mega base pairs (Varshney *et al.*, 2012).

Pigeonpea is a protein-rich crop, and its seed can be utilized to prepare a variety of meals, serving as a substitute for cowpea. In terms of nutritional content, pigeonpea seeds contain approximately 62.78g of carbohydrates, 1.49g of fats, and 21.7g of proteins per

100g. Generally, the protein content ranges from 18-29 per cent which is about three times of the value found in cereals (Techale *et al.*, 2013). India ranks the top position in pigeonpea cultivation globally with a broad area of 5.58 million hectares and a production of 4.29 Mt. This accounts for nearly 80 per cent of the total production and area dedicated to pigeonpea cultivated worldwide (FAO, 2023). In India, Uttar Pradesh, Madhya Pradesh, West Bengal, Bihar and Jharkhand contributed about 34.87 per cent, 34.55 per cent, 10.53 per cent, 8.84 per cent and 4.53 per cent, respectively (DES, MoAF & W 2022) and Rajasthan has 6320 ha area with 5680 tonnes of production with 899 kg/ha productivity (Anonymous, 2023).

Keeping in view the increasing demand of pigeonpea, there is consistent need to increase genetic seed yield potential. One of the ways to increase seed yield potential and related traits is recombination of favourable genes. To achieve this goal, understanding the extent of genetic variability among different traits and their correlations is crucial. The success of a breeding program largely hinges on the presence and understanding of genetic variability within the breeding

material. Higher the genetic variability more will be the opportunities for improvement through appropriate selection procedure. Any breeding programme rely on the variation present among the genotypes for different traits, which can be harnessed after evaluating various parameters of genetic variability like genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance.

MATERIAL AND METHOD

This experiment was carried out on thirty genotypes in Randomized block design (RBD) with 3 replications having plot size of $4 \times 1.8 \text{ m}^2$ and spacing of 60×20 cm. Observations were recorded for sixteen characters including days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, pod length (cm), 100-seed weight (g), biological yield per plant (g), harvest index (%), protein content (%), leaf area per plant (cm^2), total chlorophyll content ($\text{mg g}^{-1}\text{fw}$), relative water content (%) and seed yield per plant (g). The data were collected from five randomly selected plants from each replication. The analysis of variance for yield and yield-contributing traits was conducted following the guidelines of Panse and Sukhatme (1985). The coefficient of variation was computed according to Burton's method. Both genotypic and phenotypic coefficients of variation were determined using the formula recommended by Burton (1952). Broad-sense heritability and genetic advance were calculated following the methodology outlined by Johnson *et al.* (1955).

RESULT AND DISCUSSION

Success of any breeding programme mainly depends upon the amount of genetic variability present among the genotypes and it decides the effectiveness of selection. This study of variance among thirty medium early maturing genotypes of pigeonpea showed that the genotypes are significantly different from each other for all the sixteen characters as shown in Table 1, which revealed that the selected material for the study might be of diverse origin. The good amount of variability indicated by leaf area per plant followed by number of pods per plant, harvest index, plant height, seed yield per plant, days to maturity, number of secondary branches per plant and rest of the characters showed considerable variability. The above findings are in harmony with the findings of Sharma *et al.* (2023); Mourya *et al.* (2022); Ranjani *et al.* (2018).

In this investigation, the portion of GCV value is slightly less than that of PCV value, which indicates that there is a minor environmental influence on the expression of these characteristics. The highest GCV and PCV value was observed for number of primary branches per plant followed by number of secondary branches per plant, number of pods per plant, seed yield per plant and moderate GCV and PCV values were observed for biological yield per plant, leaf area per plant, total chlorophyll content and lowest GCV and PCV value was observed for protein content, 100-seed

weight, days to 50 per cent flowering, number of seeds per pod, relative water content, days to maturity and plant height. Whereas, high PCV and moderate GCV for seed index and moderate PCV and low GCV for pod length were observed. Similar results were also reported by Yadav *et al.* (2024); Ranjani *et al.* (2018); Mallesh *et al.* (2017); Saroj *et al.* (2015).

The estimates of heritability in broad sense were high for number of pods per plant (92.76%), days to 50 per cent flowering (92.23%), total chlorophyll content (91.79%), number secondary branches per plant (91.53%), number of primary branches per plant (90.68%), seed yield per plant (89.78%), protein content (88.59%), leaf area per plant (86.19%), harvest index (82.96%), days to maturity (77.83%), 100-seed weight (72.43%), biological yield per plant (68.91%) and pod length (64.17%). Moderate values of heritability in broad sense were observed for plant height (42.09%) and number of seeds per pod (40.38%) while, low heritability was observed for relative water content (27.26%). The above findings are in harmony with the results reported by Mourya *et al.* (2022); Rao and Rao (2020); Mallesh *et al.* (2017).

In the present study highest value of genetic advance as percentage of mean was observed for number of primary branches per plant (70.12%) followed by number of secondary branches per plant (63.16%), number of pods per plant (48.77%), seed yield per plant (41.58%), harvest index (35.48%), leaf area per plant (28.91%) and total chlorophyll content (25.73%). Moderate value of expected genetic advance as percentage of mean was observed for biological yield per plant (19.23%), pod length (16.47%), protein content (14.60%), 100-seed weight (13.04%), days to 50% flowering (12.22%) and lowest for number of seeds per pod (7.52%), days to maturity (7.24%), plant height (4.14%) and relative water content (3.71%).

In the present set of experiment material high heritability associated with high genetic advance as percentage of mean for number of primary branches per plant, number of secondary branches per plant, number of pods per plant, seed yield per plant, harvest index, leaf area per plant and total chlorophyll content. It indicates that direct selection of these traits for genetic improvement may be effective due to additive gene effect. These results are in harmony with the results reported by Rao *et al.* (2013) for number of primary branches per plant, number of secondary braches, Vanisree *et al.* (2013) for number of pods per plant, seed yield per plant and Rao *et al.* (2020) for harvest index.

Moderate genetic advance as percentage of mean coupled with high heritability for biological yield per plant, pod length, protein content, 100-seed weight, days to 50 per cent flowering. It demonstrates less environmental effect but is controlled by both additive and non-additive gene action. Hence limited genetic advancement is estimated through selection in subsequent generations. Similar findings were also reported by Rao *et al.* (2020) for 100-seed weight and Borah *et al.* (2022) for days to 50 per cent flowering.

Lowest genetic advance as percentage of mean coupled with high heritability for days to maturity revealing non-additive gene action. Whereas moderate heritability with lowest genetic advance as percentage of mean for plant height and number of pods per plant. While,

lowest heritability coupled with lowest genetic advance as per cent of mean for relative water content. The above findings are in association with Vanisree *et al.* (2013).

Table 1: Estimation of variability, heritability and genetic advance parameters for different traits in early maturing genotypes of pigeonpea.

Characters	Range		Mean	GCV%	PCV%	Heritability% Broad sense	Genetic Advance	Genetic Advance as % of mean
	Min.	Max.						
Days to 50% flowering	80	106	94.8	6.18	6.43	92.23	11.58	12.22
Days to maturity	146	171	160.98	3.98	4.52	77.83	11.66	7.24
Plant height (cm)	196.28	243.06	225.55	3.93	7.70	42.09	9.33	4.14
Number of primary branches per plant	3.86	13.84	8.37	35.74	37.54	90.68	5.87	70.12
Number of secondary branches per plant	8.66	31.1	20.29	32.05	33.50	91.53	12.82	63.16
Number of pods per plant	82.61	214.7	148.52	24.58	25.52	92.76	72.43	48.77
Number of seeds per pod	3.44	4.55	4.1	5.74	9.04	40.38	0.31	7.52
Pod length (cm)	3.67	6.02	4.88	9.98	12.46	64.19	0.80	16.47
100-Seed weight (g)	9.36	12.17	10.58	7.44	8.74	72.43	1.38	13.04
Biological yield per plant (g)	127.56	205.3	159.28	11.25	13.55	68.91	30.63	19.23
Harvest index (%)	14.29	36.11	24.83	18.91	20.76	82.96	8.81	35.48
Protein content (%)	17.65	22.77	20.4	7.53	8.00	88.59	2.98	14.60
Leaf area per plant (cm ²)	1993.49	3180.31	2517.17	15.12	16.28	86.19	93.76	28.91
Total chlorophyll content (mg g ⁻¹ fw)	1.63	2.82	2.32	13.04	13.61	91.79	0.60	25.73
Relative water content (%)	77.92	91.26	84.55	3.45	6.61	27.26	3.14	3.71
Seed yield per plant (g)	26.78	60.24	39.29	21.36	22.61	89.27	16.33	41.58

CONCLUSIONS

The ANOVA showed significant differences among thirty genotypes with respect to all sixteen characters under study. Genotypic and phenotypic coefficient of variation was highest for number of primary branches per plant followed by number of secondary branches per plant, number of pods per plant, seed yield per plant, harvest index and leaf area per plant. High heritability associated with high genetic advance as percentage of mean were observed for number of primary branches per plant, number of secondary branches per plant, number of pods per plant, seed yield per plant, harvest index, leaf area per plant and total chlorophyll content which states that weightage should be given to these characters during selection due to the presence of additive gene effect.

FUTURE SCOPE

By confirming the results of research on the genotypes for some year and location and analysing the characters that have more genetic variability, heritability and genetic advance and lesser effect of environment are to be selected for future breeding purpose.

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Conflict of Interest. None.

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