



Genetic Variability, Heritability and Genetic Advance in Pigeonpea (*Cajanus cajan* (L.) Millsp.)

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ABSTRACT

Eighty three genotypes were studied to know their performance, genetic variability {genotypic coefficient of variation (GCV)} and phenotypic coefficient of variation (PCV)}, heritability (broad sense) $\{h^2(b)\}$ and genetic advance as percent of Mean (GA as % of Mean) for yield and its contributing characters. Significant variation among the genotypes for all the 11 characters studied was observed. Wide ranges were observed for all characters days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, seed yield per plant, 100 seed weight and harvest index and protein content but for number of seeds per pod. GCV for all the characters was lesser than PCV evidencing masking effects of the environment. High PCV coupled with high GCV was observed for number of branches per plant, number of pods per plant, seed yield per plant and harvest index, indicating the presence of wider variability for these traits in the population studied. High genetic variability coupled with high $h^2(b)$ and high GA as % of mean was observed for days to 50% flowering, days to maturity, number of branches per plant, number of pods per plant, seed yield per plant and harvest index exhibiting the role of additive gene action governing the inheritance of these traits.

Key words : Coefficients of Variation, Genetic Advance, Heritability, Pigeonpea, Variability.

Pigeonpea (*Cajanus cajan* (L.) Millsp) is the most versatile food legume with diversified use as food, feed, fodder and fuel. It is the major source of protein (23%) in the cereal based vegetarian diet. Its improvement depends upon the presence of wide spectrum of variability in the germplasm and its utilization in the breeding programme. Besides genetic variability, knowledge on heritability and genetic advance measures the relative degree to which a character transmitted to its progeny, thereby helps the breeder to employ a suitable breeding strategy to achieve the objective quickly. For instance, high heritability coupled with high genetic advance indicates additive gene effect (Johnson *et al.*, 1955) and improvement could be made for that characters by simple selection based on phenotypic performance whereas low genetic advance irrespective of high or low heritability leads to non-additive gene action (Panse, 1957). In pursuit of the objective of genetic improvement of pigeonpea, 83 genotypes were utilized for estimation of genetic parameters like variability, heritability and genetic advance.

MATERIAL AND METHODS

Eighty three genotypes of pigeonpea [*Cajanus cajan* (L.) Millsp] were sown in randomized block design with three replications at the Regional Agricultural Research Station Lam, Guntur, during kharif 2008. Each genotype was represented by six rows of four meter length in each replication with a spacing of 90 cm between rows and 20 cm within row. Crop was grown as per the recommendations.

Observations on plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, seed yield per plant and harvest index were recorded on five randomly selected plants of each genotype in each replication and the average values were subjected for statistical analysis whereas days to 50% flowering, days to maturity, 100 seed weight and protein content were recorded on plot basis.

The analysis of variance and the significance of genotypic differences were tested for all the characters as per the method given by Cochran and Cox (1950). The test of significance

was carried out using 'F' table values given by Fisher and Yates (1963). Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton (1952). Categorization of the range of variation was followed as per Siva Subramanian and Menon (1973). Heritability in Broad sense [h^2 (b)] was estimated as per Allard (1960) and characterized as suggested by Johnson *et al.* (1955). Genetic advance (GA) was estimated as per the formula proposed by Lush (1940). The range of GA as per cent of mean was classified as suggested by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Significant differences for all the characters were observed, indicating considerable variation among the genotypes (Table 1). The estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability [h^2 (b)] and genetic advance as per cent of mean (GA as % of Mean) were presented in Fig. and Table 2.

Wide ranges were observed for all characters {days to 50% flowering (70-135.7), days to maturity (122.3-203), plant height (98.3-167.2 cm), number of branches per plant (7.3-21.5), number of pods per plant (36.6-393.2), pod length (3.5-6.9 cm), seed yield per plant (8.6-109.4 g), 100 seed weight (8.7-15.9 g) and harvest index (12-48.5%) and protein content (18.6-28.5%)} but for number of seeds per pod (3.3-4.5).

The phenotypic coefficients of variation for all the characters studied were greater than the genotypic coefficients of variation evidencing the masking effects of the environment. PCV and GCV were high for Branches per plant (23.8 & 21.2), pods per plant (58 & 56.1), seed yield per plant (61.9 & 60.4) and Harvest index (28.2 & 24.5); moderate for days to 50% flowering (16.2 & 16), days to maturity (13.9 & 13.3), plant height (12.2 & 10.5), pod length (10.7 & 7.5), 100-seed weight (13.7 & 10.6) and protein content (10.6 & 10.4); and low for seeds per pod (7.4 & 2.9).

High heritability coupled with high genetic advance exhibits operation of additive gene action in case of days to 50% flowering (98.2 & 32.7), days to maturity (91.9 & 26.4), number of branches per plant (79 & 38.7), pods per plant (93.7 & 111.9), seed yield per plant (95.2 & 121.4), harvest index

(75.3 & 43.8) and protein content (97.8 & 21.3). Hence directional selection for these traits in genetically diverse material could be effective for desired genetic improvement. Moderate genetic advance with high or medium heritability reveals the action of both additive and non-additive genes in case of plant height (74.7 & 18.7), pod length (48.9 & 10.8) and 100 seed weight (60.5 & 17.1) which offers the best possibility of improvement through mass selection and progeny selection. Similar results were obtained by Aher *et al.* (1996), Jag Shoran (1985), Natarajan *et al.* (1990), Basavarajaiah *et al.* (1998), Balyan and Sudhakar (1985), Khapre and Nerker (1992) and Baskaran and Muthaih (2006).

In the present study, the span of ranges are 356.6, 100.8, 80.7, 68.9, 65.7, 36.5, 14.2, 9.9, 7.2, 3.4 and 1.2 for number of pods per plant, seed yield per plant, days to maturity, plant height, days to 50% flowering, harvest index, number of branches per plant, protein content, 100 seed weight, pod length and number of seeds per pod, respectively, which reflects their variability. The differences between PCV and GCV (3.7, 3.5, 3.2, 3.1, 2.6, 1.9, 1.7, 1.5, 0.6, 0.2 and 0.2 for harvest index, number of seeds per pod, pod length, 100 seed weight, number of branches per plant, number of pods per plant, plant height, seed yield per plant, days to maturity, days to 50% flowering and protein content, respectively) denote environmental influence. Heritabilities i.e. 98.2, 97.6, 95.2, 93.7, 91.9, 78.9, 75.3, 74.7, 60.5, 48.9 and 15 for days to 50% flowering, protein content, seed yield per plant, number of pods per plant, days to maturity, number of branches per plant, harvest index, plant height, 100 seed weight, pod length and number of seeds per pod, respectively, explain the extent of the additive gene effects. Genetic advances as percent of mean (121.35, 111.9, 43.8, 38.7, 32.7, 26.3, 21.2, 18.7, 17.1, 10.8 and 2.3 for seed yield per plant, number of pods per plant, harvest index, number of branches per plant, days to 50% flowering, days to maturity, protein content, plant height, 100 seed weight, pod length, number of seeds per pod, respectively) did not follow the pattern of heritability as heritability itself is not true measure of genetic advance Johnson *et al.* (1955). In conclusion, this study helps breeder to decide breeding programme and to select material from the 83 genotypes.

Table 1. Analysis of variance for yield and yield component characters in pigeonpea [*Cajanus cajan* (L.) Millsp.].

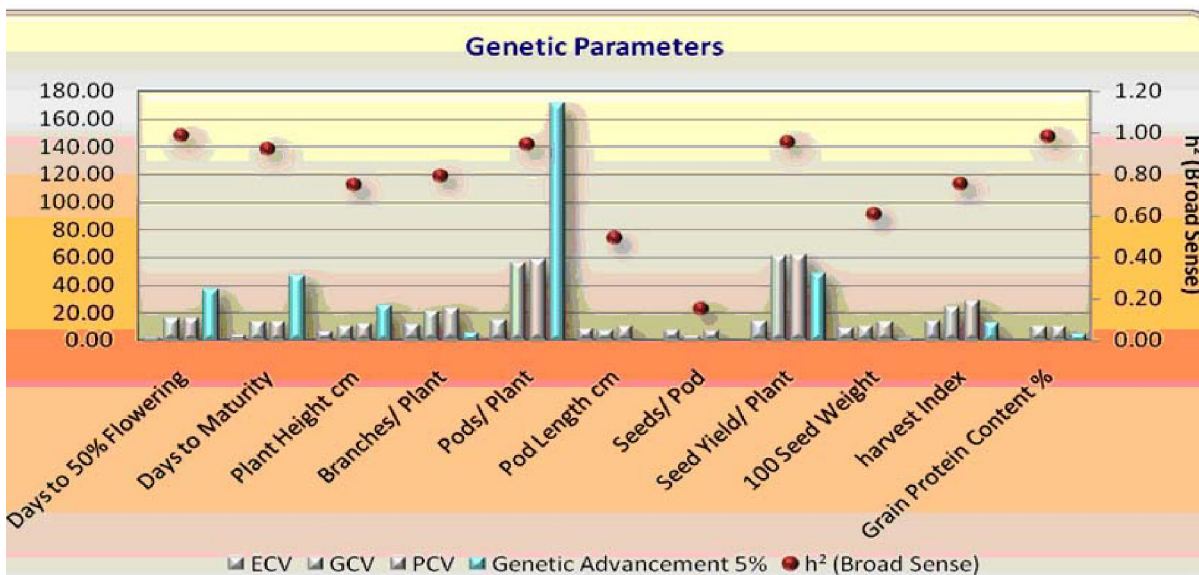
Source	d.f.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches / plant	No. of Pods/ plant	Pod length (cm)	Seeds/ pod (g)	Seed yield per plant (g)	100 seed weight (g)	Harvest index	Protein content (%)
Mean sum of squares												
Replications	2	4.14	41.73	69.37	5.74**	509.05	0.70**	0.07	6.67	1.89	21.36	0.01
Treatments	82	987.95**	1759.85**	674.84**	27.20**	22479.52**	0.48**	0.11**	1766.92**	4.66**	175.41**	18.31**
Error	164	6.07	49.97	68.50	2.22	491.40	0.12	0.07	28.99	0.83	17.27	0.13

** Significant at 1% level of probability.

Table 2. Mean, variability, heritability and genetic advance for seed yield and yield components in pigeonpea [*Cajanus cajan* (L.) Millsp.].

S. No.	Character	Mean	Range		PCV (%)	GCV (%)	Herita-bility (%) (broad sense)	Genetic advance as per cent of mean
			Minimum	Maximum				
1	Days to 50% flowering	112.83	70.00	135.66	16.18	16.03	98.18	32.72
2	Days to maturity	178.95	122.33	203.00	13.91	13.34	91.94	26.35
3	Plant height (cm)	134.99	98.33	167.20	12.18	10.53	74.69	18.74
4	Branches per plant	13.63	7.33	21.53	23.82	21.16	78.95	38.74
5	Pods per plant	152.57	36.60	393.20	57.96	56.11	93.72	111.89
6	Pod length (cm)	4.66	3.46	6.90	10.69	7.48	48.92	10.78
7	Seeds per pod	4.00	3.33	4.53	7.42	2.87	14.96	2.28
8	Seed yield per plant (g)	39.87	8.60	109.37	61.85	60.36	95.23	121.35
9	100 seed weight (g)	10.61	8.71	15.89	13.68	10.64	60.50	17.05
10	Harvest index	29.63	11.97	48.50	28.22	24.49	75.31	43.79
11	Protein content (%)	23.58	18.57	28.52	10.55	10.43	97.76	21.25

Fig 1. Environment, genotypic and phenotypic coefficients of variation, genetic advance as per cent of mean (GAM) and heritability for 11 characters in pigeonpea (*Cajanus cajan* (L.) Millsp).



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