



Genetic Variability, Heritability and Genetic Advance in Pigeonpea (*Cajanus cajan* (L.) Mill sp.) Advanced Lines

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ABSTRACT

Forty nine pigeonpea 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 13 characters studied was observed. Wide ranges were observed for all characters i.e., days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, seed yield per plant, 100 seed weight, harvest index and protein content but for pod length, number of seeds per pod and shelling percentage. GCV for all the characters was lesser than PCV evidencing masking effects of the environment. High PCV coupled with high GCV was observed for the traits viz., number of primary branches per plant, number of secondary branches per plant and number of pods per plant indicating the presence of wider variability for these traits in the population studied. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant and seed yield per plant which indicates the operation of additive gene action in the inheritance of these traits.

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

Pigeonpea (*Cajanus cajan* (L.) Millsp) 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, 49 genotypes were utilized for estimation of genetic parameters like variability, heritability and genetic advance.

MATERIAL AND METHODS

Forty nine genotypes (Table 1) 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 2010. 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 by following the recommended package of practices.

Observations on plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod length, number of seeds per pod, seed yield per plant, shelling percentage 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

The results of the present investigation showed significant differences for all the characters were observed, indicating considerable variation among the genotypes. 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 Table 2.

Wide ranges were observed for all characters (days to 50% flowering (104 for LRG 97 to 162.33 for BRG 2), days to maturity (183.33 for LRG 93 to 215.33 for LRG 104), plant height (157.25 for BDN 2010 to 298.6 cm for LRG 106), number of primary branches per plant (3.63 for ICP 8863 to 45.93 for LRG 61), number of secondary branches per plant (13.88 for PT 04-149 to 42.84 for LRG 102), number of pods per plant (156.6 for LRG 90 to 465.86 for GJP 8901), seed yield per plant (49.33 for GAUT 93-17 to 127.66 g for WRG 168), 100 seed weight (8.64 for LRG 74 to 14.29 g for LRG 100), harvest index (23.02 for NTL 554 to 34.09 % for WRG 168) and protein content (18.37 for BDN 2010 to 26.63 % for LRG 61)) but for pod length (4.06 for LRG 90 to 5.53 cm for BRG 2), number of seeds per pod (3.63 for ICP 8863 to 4.83 for BRG 2) and shelling percentage (61.24 for WRP-1 to 71.17 for LRG 61).

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 number of primary branches per plant (70.72 & 69.48), number of secondary branches per plant (36.64 & 31.25) and number of pods per plant (27.92 & 23.52) while for seed yield per plant PCV was high (21.05) and GCV was moderate (18.66) indicating the presence of wider variability for these traits in the population studied.

Moderate PCV & GCV were observed for plant height (17.58 & 16.36) where as moderate PCV but low GCV were recorded for 100-seed weight (12.31 & 6.25) and harvest index (10.67 & 7.31). Both PCV & GCV were low for days to 50% flowering (6.32 & 5.71), days to maturity (3.43 & 1.81), pod length (9.06 & 6.02), seeds per pod (7.64 & 4.44), shelling percentage (5 & 2.73) and protein content (7.32 & 6.25).

High heritability coupled with high genetic advance exhibits operation of additive gene action in case of plant height (87 & 31.36), number of primary branches per plant (97 & 98), number of secondary branches per plant (81 & 58.06), pods per plant (71 & 40.81) and seed yield per plant (79 & 34.09) indicating operation of additive gene action in the inheritance of these traits and improvement in these characters is possible through simple selection. Hence directional selection for these traits in genetically diverse material could be effective for desired genetic improvement. In the present investigation, high or medium heritability with moderate genetic advance revealed the action of both additive and non-additive genes in case of days to 50% flowering (82 & 10.63), protein content (73 & 10.99) and harvest index (47 & 10.3) which offers the best possibility for improvement of these traits through mass selection and progeny selection. Though heritability was moderate, genetic advance was low for seeds per pod (34 & 5.31) and 100 seed weight (32 & 8.09). Both heritability and genetic advance were low for days to maturity (28 & 1.98), pod length (44 & 8.2) and shelling percentage (30 & 3.07) indicating that these traits are controlled by non additive genes and further improvement of these characters would be possible through heterosis breeding. Similar results were also reported by Aher *et al.* (1996) and Khapre and Nerker (1992).

In conclusion, this study helps breeder to decide breeding programme i.e. simple selection for plant height, number of primary branches per plant, number of secondary branches per plant, pods per plant and seed yield per plant; mass selection and progeny selection for days to 50% flowering, protein content and harvest index; and heterosis breeding for seeds per pod, 100 seed weight, days to maturity, pod length and shelling percentage besides allowing to select material from the 49 genotypes.

Table 1. Source & Pedigree of the genotypes of pigeonpea (*Cajanus cajan* (L.) Millsp.).

S.No.	Geno Type	Source	Pedigree
1	JKM 250	Khargone, Madhyapradesh	NO 148 X ICP 157760
2	RVSA 07-31	Sehore, Madhyapradesh	JA 4 X JSA 73
3	SKNP 0845	S.K. Nagar, Gujarat	Selection from AG 584
4	WRG 168	RARS, Warangal	ICPL 8034 X MPG 537
5	ICP 8863	ICRISAT, Patncheru	Selection from local and race
6	BRG-2	UAS, Bangalore	Selection from Nalamangala local
7	PT00-012-1	Rahuri, Maharastra	ICP 332 X BSMR 736
8	GAUT 93-17	Vadodara, Gujarat	GAUT 87 - 20 X GAUT 84 - 21
9	CO-6	TNAU, Coimbatore	Mutant of SAI
10	GRG 2010	Gulbarga, Karnataka	Somoclonal varient from Maruthi
11	GJP 0901	Janagarh, Gujarat	LRG 41 X BDN 2
12	NTL 554	Nirmal seeds	NTL 43 X NTL 554
13	AKT- HR	PDKV, Akola	Mutant ICP 332 - 35 KR
14	JKM 249	Khargone, Madhyapradesh	Asha X ICP 15711
15	NTL 520	Nirmal seeds	NTL 530 X NTL 677
16	RVSA 07 - 24	Sehore, Madhyapradesh	JA4 X ICP 8863
17	WRG 173	RARS, Warangal	ICP 880117 X MPG 537
18	WRP-1	ARS, Gulbarga	GSI X ICP 8863
19	AKT08 - 2	PDKV, Akola	AK 261933 X BSMR 736
20	BDN 2010	ARS, Badanapur	MSMR 736 X ICP 88034
21	GJPO902	Janagarh, Gujarat	ICPL 87 X Sujatha
22	PT04 - 149	Rahuri, Maharastra	PT 00142 X PT 2002 - 6-1
23	GAUT 2003-1	Gujarat	CII X BDN 2
24	LRG 88	RARS, LAM	Selection from local collection 2009-2
25	LRG 89	RARS, LAM	Selection from local collection 2009-3
26	WRG 180	RARS, Warangal	PRG 100 X WRG 55
27	LRG 61	RARS, LAM	Asha X LRG 41 - 12- 2
28	RGT 4	ARS, Tandur	Selection from ICPL 332
29	WRG 179	RARS, Warangal	ICPL 87119 X ICPL 13257
30	LRG 52	RARS, LAM	LRG 41 X Maruthi - 15- 1
31	TRG 38	RARS, Tirupathi	ICPL TO35 X ICP 8863
32	LRG 41	RARS, LAM	Selection from Chilakaluripeta local
33	LRG 90	RARS, LAM	Selection from local collection 2009 -5
34	LRG 91	RARS, LAM	Selection from local collection 2009 -6
35	LRG 92	RARS, LAM	Selection from ICP 5546
36	LRG 93	RARS, LAM	Selection from ICP 7579
37	LRG 94	RARS, LAM	Selection from ICP 10716
38	LRG 95	RARS, LAM	Selection from local collection
39	LRG 96	RARS, LAM	Selection from ICPL 14719
40	LRG 97	RARS, LAM	Derivative of Asha X CORG 9701
41	LRG 98	RARS, LAM	Derivative of BSMR 853 X CORG 9701
42	LRG 99	RARS, LAM	Derivative of BSMR 853 X CORG 9701-2
43	LRG 100	RARS, LAM	Derivative of Lakshmi X CORG 9701
44	LRG 101	RARS, LAM	Derivative of LAM 41 X CORG 9701
45	LRG 102	RARS, LAM	Derivative of Ranga bold X CORG 9701 - 1
46	LRG 103	RARS, LAM	Derivative of Ranga bold X CORG 9701 - 2
47	LRG 104	RARS, LAM	Derivative of Ranga bold X CORG 9701 - 3
48	LRG 105	RARS, LAM	Derivative of Ranga bold X CORG 9701 -4
49	LRG 106	RARS, LAM	Derivative of Lakshmi X CORG 9701 -5

Table 2. Mean, genetic variability, heritability (broad sense) and genetic advance as percent of mean and seed yield and yield components in pignon pea (*Cajanus cajan* (L.) Millsp.).

S.No.	Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance as percent of mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Days to 50% flowering	139.34	104.00	162.33	6.32	5.71	82	10.63
2	Days to maturity	193.48	183.33	215.33	3.43	1.81	28	1.98
3	Plant height (cm)	229.73	157.25	298.60	17.58	16.36	87	31.36
4	Primary branches/ plant	16.92	3.63	45.93	70.72	69.48	97	98.00
5	Secondary branches/ plant	23.62	13.88	42.84	36.64	31.25	81	58.06
6	Pods/plant	282.87	156.60	465.86	27.92	23.52	71	40.81
7	Pod length (cm)	4.65	4.06	5.53	9.06	6.02	44	8.24
8	Seeds/pod	3.97	3.63	4.83	7.64	4.44	34	5.31
9	Shelling percentage	64.63	61.24	71.17	5.00	2.73	30	3.07
10	100 seed weight (g)	11.32	8.64	14.29	12.31	6.25	32	8.09
11	Harvest index	26.33	23.02	34.09	10.67	7.31	47	10.30
12	Grain protein content (%)	23.88	18.37	26.63	7.32	6.25	73	10.99
13	Seed yield/ plant (g)	76.95	49.33	127.66	21.05	18.66	79	34.09

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

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