

## Studies on Genetic Variability, Heritability and Genetic Advance Based on Metric and Physiological Traits in Pigeonpea [*Cajanus cajan* (L.) Millsp.].

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

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is called so as it is the preferred food by pigeons but it is now the favourite food for vegetarians. Knowledge on variability, heritability and genetic advance paves the way for breeding programme. Though considerable efforts were made in this crop on metric traits towards this goal {Satish Kumar, *et al* (2005) and Suresh, *et al* (2012)}, not much was done on physiological traits that influence the yield and stress tolerance. In pursuit of this objective, 45 genotypes were utilized for estimation of genetic parameters like variability, heritability and genetic advance.

Forty five genotypes of pigeonpea (Table 1) were sown in randomized block design with three replications at the Regional Agricultural Research Station, Lam, Guntur, during kharif, 2009-10. 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 managed as per the University recommendations. Observations were recorded on ten randomly selected plants without border effect of each genotype in each replication and the average values were subjected for statistical analysis except for days to 50% flowering, days to maturity, 100 seed weight and protein content which were recorded on plot basis. Phenotypic and genotypic coefficients of variation (PCV and GCV), Heritability in Broad sense [ $h^2$  (b)] and Genetic advance (GA) were estimated as given in Suresh, *et al* (2012).

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. The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the effect of the environment.

PCV and GCV were high for number of primary branches per plant (24.8 and 21.4), number of secondary branches per plant (40.9 and 38.3), pods per plant (26.1 and 24.3) and seed yield per plant (26.8 and 24.9). High PCV and medium GCV values were observed for harvest index (20.3 and 16.5) and LAI at vegetative stage (20.7-16.5). PCV and GCV were moderate for plant height (17.4 and 14.3), shelling percentage (14.6 and 10.8), 100-seed weight (15.3 and 12.5), LAI at flowering stage (15.6-11.8), RWC at vegetative stage (15.4 and 14.2) and RWC at flowering stage (16.9 and 16.4). PCV was moderate and GCV was low for pod length (11.4 and 7.3), SLA at vegetative stage (12.2 and 9.6), SLW at vegetative stage (10.8 and 7.8) and SLW at flowering stage (10.4 and 8.9). Low PCV and GCV were recorded for days to 50% flowering (3.8 and 3), days to maturity (3.1 and 1.9), seeds per pod (9.9 and 4.6), protein content (10 and 9.9) and SLA at flowering stage (8.3 and 5.1).

High heritability coupled with high genetic advance as per cent of mean observed for plant height (67 and 30.8), number of primary branches per plant (75 and 48.8), number of secondary branches per plant (88 and 94.7), pods per plant (87 and 59.7), 100-seed weight (67 and 27), seed yield per plant (86 and 61), grain protein content (98 and 25.9), harvest index (66 and 35.5), LAI at vegetative stage (64 and 34.8), SLW at flowering stage (74 and 20.3), RWC at vegetative stage (86 and 34.8) and RWC at flowering stage (93 and 41.7) which indicates operation of additive gene action. Hence directional selection for these traits in genetically diverse material could be effective for desired genetic improvement. High heritability and moderate {SLA at vegetative stage (61 and 19.7)} and low {days to 50% flowering (61 and 6.2)} genetic advance as per cent of mean was recorded. Moderate heritability with high {shelling

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

S.NO	GENOTYPE	SOURCE	PEDIGREE
1	JSA 73-1	Sehore	Selection from JSA 34
2	RPS 2007-109	Raipur	GWL 3 X ICPL 20071
3	BRG 9-2	Bangalore	BRG 1 X Hy3C
4	GRG 2009	Gulbarga	Mutant selection from Somaclonal varaiant
5	BRG 9-1	Bangalore	TTB 7 X ICP 8863
6	SKNP 0528	S.K. Nagar	GT 100 X ICP 9135
7	WRG 170	ARS, Warangal	WRG 27 X (LRG 30 X ICPL 87119)
8	WRG 75	ARS, Warangal	Selection from Warangal local
9	VKT 235	Khargone	KM 34 X Asha
10	ARCC V2	Nagpur	ARCC 23 X ARCC 8
11	ICP 8863	ICRISAT, Hyderabad	Selection from Maharashtra land race
12	CO 6	TNAU, Coimbatore	Mutant of SA 1
13	TAT 9629	Akola	ICPL 84008 X TT 6
14	WRP 1	ARS, Gulbarga	Selection from Gulbarga local
15	SKNP 0740	S.K. Nagar	GT 101 X GAUT 97-85
16	RPS 2007-105	Raipur	JKM 34 X Asha
17	WRG 166	ARS, Warangal	(ICPL 87119 X ICPL 13257)-p-2
18	TTB 7	UAS, Bangalore	Selection from local perennial garden type Thutogari
19	JSA 66	Sehore	ICPL 85063 X JA 4
20	VKT 244	Khargone	Amar X Asha
21	TRG 7	ARS, Tirupati	Selection from chittoor local
22	LRG-61	RARS, Lam	(Asha X LRG-41)-12-2
23	LRG-52	RARS, Lam	(LRG-41 X Maruti)-15-1
24	WRG 53	ARS, Warangal	ICP 332 X ICPL 85063
25	TRG 21	ARS, Tirupati	Selection from Kadiri local
26	11960	ARS, Tandur	Local from Allapur (Tandur area)
27	SURYA	ARS, Madhira	Selection from Madhira local
28	WRG 173	ARS, Warangal	ICP 880117 X MPG 537
29	11969	ARS, Tandur	Local from Allapur (Tandur area)
30	LRG-41	RARS, Lam	Selection from land race of Chilakaluripeta in Guntur District
31	LRG-50	RARS, Lam	(LRG-41 X Maruti)-7-1
32	LRG-56	RARS, Lam	(Ranga Bold X Maruti)-10-1
33	LRG-59	RARS, Lam	(Asha X LRG-41)-8-1
34	LRG-69	RARS, Lam	(BSMR 853 X LRG-41)-8-1
35	LRG-70	RARS, Lam	(BSMR 853 X LRG-41)-14-5
36	LRG-73	RARS, Lam	(LRG-38 X CORG 9701)-35-4
37	LRG-79	RARS, Lam	(BSMR 853 X ICPL 84031)-3-1
38	LRG-80	RARS, Lam	(LRG-30 X ICPL 84031)-3-2
39	LRG-81	RARS, Lam	(BSMR 736 X CORG 9701)-3-2
40	LRG-82	RARS, Lam	(LRG-38 X CORG 9701)-32-1
41	LRG-83	RARS, Lam	(BSMR 736 X ICPL 84031)-4-3
42	LRG-84	RARS, Lam	(LRG-38 X CORG 9701)-2-2
43	LRG-85	RARS, Lam	(LRG-30 X CORG 9701)-3-2
44	LRG-86	RARS, Lam	(TB 7 X ICPL 96047)-1-2
45	LRG-87	RARS, Lam	(LRG-41 X CORG 9701)-11-2

Table 2. Mean, genetic variability, heritability (broad sense) and genetic advance as per cent of mean for seed yield, physiological and Yield components in Pigeonpea {*Cajanus cajan* (L.) Millsp.}

S.No	Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance as per cent of mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Plant height (cm)	167	120	225	17	14	67	31
2	Days to 50% flowering	122	109	127	4	3	61	6
3	Days to maturity	177	169	185	3	2	39	3
4	Primary branches/ plant	20	8	28	25	21	75	49
5	Secondary branches/ pant	60	27	123	41	38	88	95
6	Pods/ plant	619	306	945	26	24	87	60
7	Pod length (cm)	5	4	6	11	7	40	12
8	Seeds/ pod	4	3	5	10	5	22	6
9	Shelling percentage	52	38	64	15	11	55	21
10	100 seed weight (g)	11	8	17	15	13	67	27
11	Seed yield per plant (g)	138	72	224	27	25	86	61
12	Grain protein content (%)	24	19	28	10	10	98	26
13	Harvest index	46	24	61	20	17	66	36
14	LAI at vegetative stage	3	2	5	21	17	64	35
15	LAI at flowering stage	5	3	6	16	12	57	24
16	SLA at vegetative stage ( cm <sup>2</sup> /g)	221	154	262	12	10	61	20
17	SLA at flowering stage ( cm <sup>2</sup> /g)	250	201	283	8	5	37	8
18	SLW at vegetative stage (mg/cm <sup>2</sup> )	5	4	6	11	8	52	15
19	SLW at flowering stage (mg/cm <sup>2</sup> )	4	4	6	10	9	74	20
20	RWC at vegetative stage (%)	63	46	84	15	14	86	35
21	RWC at flowering stage (%)	70	43	88	17	16	93	42

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

percentage (55 and 21) and LAI at flowering stage (57 and 23.7)}; moderate {days to maturity (39 and 3.1), pod length (40 and 12.2) and SLW at vegetative stage (52 and 14.7)}; and low {SLA at flowering stage (37 and 8.1)} genetic advance as per cent of mean was noted which indicates action of both additive and non-additive genes that offer the best possibility of improvement through mass selection and progeny selection. Both heritability and genetic advance as per cent of mean were low for number

of seeds per pod for which improvement is very difficult. Similar results were obtained by Satish Kumar, *et al* (2005) and Suresh, *et al* (2012) in pigeonpea for metric traits and Narisi Reddy and Ratna Kumari (2004), Ratna Kumari and Chamundeswari (2005), Muhammad, *et al* (2009) and Painawadee *et al* (2009) in cotton and peanut for physiological traits. In conclusion, this study helps breeder to decide breeding programme and to select material from the 45 genotypes.

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