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Studies on Genetic Parameters for Yield and its Component Traits in Pigeonpea (*Cajanus cajan* (L.) Millsp.)

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A B S T R A C T

Genetic variability was studied in pigeonpea breeding material comprising of five lines, three testers and their 15 crosses through line x tester mating design. Higher genetic variability was observed for primary and secondary branches per plant, pods per plant and seed yield per plant in crosses. In addition to these characters higher variability also observed for 100- seed weight, harvest index and phenol content in parents, indicating that greater variation in these characters offers greater scope to improve them through genetic manipulation. High heritability coupled with high genetic advance as per cent of mean was observed for secondary branches per plant, pods per plant, 100-seed weight, phenol content and seed yield per plant in crosses, while in addition to these characters, primary branches per plant, seeds per pod, pod length and harvest index in parents, indicating these characters are under the control of additive gene action. Hence, simple directional selection could be effective for improving these characters.

Introduction

Pigeonpea is a protein rich crop. It is extensively grown under rainfed conditions in India. Among the grain legumes, pigeonpea is an exception with tendency towards a high percentage of out-crossing and it can be classified as often-cross pollinated crop. A narrow genetic base, limited efforts to generate a wide genetic variability and lack of planned handling of the segregating population are responsible for poor seed yield. Accordingly the present study was undertaken to gather the information on variability, heritability and genetic advance as per cent of mean for yield and its components of pigeonpea.

Materials and Methods

The present study consists of five lines namely, ICPL-6974, ICPL-15225, ICPL-7035, ICPL-2376 and LRG-41, three testers with resistance to *Fusarium* wilt namely, ICPL-87119, ICPL-8863 and PRG-158 and their 15 crosses generated through line x tester mating design. Each strain was sown in three rows of 4m length in randomized block design with

three replications following spacing of 150 x 30 cm. Observations on 15 randomly selected plants from each entry were recorded for days to flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, pods per plant, seeds per pod, pod length (cm), 100-seed weight (g), harvest index (%), SCMR at vegetative phase, protein content (%), phenol content (%) and seed yield per plant (g).

Results and Discussion

The range and mean for fourteen characters are presented in Table 1. The highest range was recorded for pods per plant (107.00 to 606.67 and 260.67 to 1563.33) followed by seed yield per plant (50.00 to 165.33 and 67.00 to 390.00) in both parents and crosses, respectively. However, the lowest range was observed for seed protein, phenol content, pod length and seeds per pod both in parents and crosses.

Estimating of genetic parameters GCV, PCV, heritability and genetic advance are presented in Table 2. The genotypic and phenotypic coefficient of variation were high for branches per plant, pods per plant, 100-seed weight, harvest index, phenol content and seed yield per plant in parents, while in crosses it was high for branches per plant, pods per plant and seed yield per plant, indicating that these characters are highly variable and there is a great scope to improve these characters in further breeding programmes. Similar results were reported by Balyan and Sudhakar (1985) and Aher *et al.,* (1996). Very high estimates of broad sense heritability were observed for all the characters except plant height in parents, while plant height, primary branches and harvest index in crosses. Similar results were reported by Singh *et al.,* (1981) and Sidhu *et al.,* (1985). The role of additive genetic component was important for all the traits except days to flowering, days to maturity, SCMR at vegetative phase and seed protein in parents, while it was noticed for branches per plant, pods per plant, 100-seed weight, phenol content and seed yield per plant in crosses due to their high genetic advance as per cent of mean.

Table.1 Range and mean for yield and yield contributing characters in pigeonpea.

Characters	Range		Mean	
	Parents	Crosses	Parents	Crosses
Days to flowering	97.00 - 123.67	99.33 - 124.67	112.83	111.93
Days to maturity	140.00 - 181.33	142.33 - 173.67	164.58	158.22
Plant height (cm)	174.33 - 263.67	183.67 - 245.00	210.33	218.71
Primary branches per plant	7.67 - 22.67	9.67 - 25.67	16.25	17.38
Secondary branches per plant	4.00 - 35.67	13.67 - 42.00	22.13	25.27
Pods per plant	107.00 - 606.67	260.67 - 1563.33	409.42	653.69
Seeds per pod	3.40 - 5.40	3.60 - 4.53	3.98	4.00
Pod length (cm)	4.33 - 7.24	4.73 - 6.89	5.40	5.54
100-seed weight (g)	10.00 - 20.67	10.00 - 16.33	12.46	11.89
Harvest index (%)	14.86 - 32.10	17.30 - 26.03	20.66	21.54
SCMR at vegetative phase	37.70 - 45.20	39.63 - 48.07	40.98	42.76
Seed protein (%)	22.23 - 26.33	24.46 - 26.69	24.42	25.64
Phenol content (%)	3.23 - 7.55	6.02 - 8.41	5.71	7.25
Seed yield per plant (g)	50.00 - 165.33	67.00 - 390.00	101.50	158.36

Table.2 Components of variance, coefficient of variance, heritability and genetic advance as per cent of mean for various characters of pigeonpea

Characters	GCV		PCV		Heritability (%)		Genetic advance		Genetic advance as % of mean	
	Parents	F_1's	Parents	F_1's	Parents	F_1's	Parents	F_1's	Parents	F_1's
Days to flowering	9.85	7.21	10.07	7.37	95.63	95.77	22.38	16.27	19.84	14.53
Days to maturity	8.02	6.20	8.21	6.40	95.38	93.90	26.54	19.59	16.13	12.38
Plant height (cm)	13.90	9.12	18.02	12.76	59.45	51.10	46.43	29.37	22.07	13.43
Primary branches per plant	24.10	21.81	29.64	29.57	66.11	54.38	6.56	5.76	40.37	33.13
Secondary branches per plant	49.68	32.46	63.13	40.43	61.92	64.45	17.82	13.56	80.54	53.68
Pods per plant	39.20	59.69	42.26	62.46	86.03	91.35	306.62	768.26	74.89	117.53
Seeds per pod	17.01	7.08	19.20	9.04	78.53	61.37	1.24	0.46	31.05	11.42
Pod length (cm)	16.96	10.77	18.03	12.33	88.45	76.19	1.77	1.07	32.85	19.36
100-seed weight (g)	27.19	13.77	28.35	16.22	92.03	72.01	6.69	2.86	53.74	24.07
Harvest index (%)	27.66	10.50	28.72	15.20	92.77	47.69	11.34	3.22	54.89	14.94
SCMR at vegetative phase	5.28	4.74	6.37	5.21	68.72	82.91	3.69	3.80	9.01	8.89
Seed protein (%)	4.65	2.38	4.68	2.44	98.52	94.92	2.32	1.23	9.51	4.78
Phenol content (%)	23.17	11.13	23.68	11.33	95.77	96.60	2.67	1.63	46.71	22.54
Seed yield per plant (g)	38.28	62.15	45.24	65.71	71.59	89.48	67.72	191.79	66.72	121.11

High heritability coupled with high genetic advance as per cent of mean was observed for secondary branches per plant, pods per plant, 100-seed weight, phenol content and seed yield per plant both in parents and crosses. This similar results were reported by and Khapre *et al.,* (1993), Bhadru (2010). According to Panse (1957), the high heritability associated with low genetic advance may be due to dominance epistatic effect and least effect of additive genes. Such trend was observed in respect of SCMR at vegetative phase and seed protein. This was in conformity with Aher *et al.,* (1996). Appreciable amount of variability, heritability and genetic advance as per cent of mean were observed for secondary branches per plant, pods per plant and seed yield per plant both in parents and crosses, indicating the additive gene action in the control of these characters and could be improved by simple selection methods.

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