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Inheritance of yield contributing characters in pigeonpea

C.V. SAMEER KUMAR, CH. SREELAKSHMI, D. SHIVANI and M. SURESH

Agricultural Research Station, Tandur 501 141, Andhra Pradesh, India

ABSTRACT

Genetic analysis of seed yield and other important yield traits in pigeonpea genotypes was carried out using joint scaling test to determine epistasis and genetic parameters m,d,h,i,j and l. Six generations of (P_1, P_2, BC_1, BC_2, F_1 and F_2) of two cross combinations of pigeonpea (PRG 100 x ICPL 87119 and LRG 30 x ICP 8863) were studied at Agricultural Research Station, Tandur during *kharif* 2007. All the generations of each cross combinations were evaluated in a randomized block design with three replications. The mean of six generations were subjected to joint scaling test to determine epistasis and genetic parameters m,d,h,i,j and l and were estimated through three and six parameter model. Seed yield and major yield contributing parameters showed the significance of both additive, dominance and epistatic interactions. Therefore, reciprocal recurrent selection or diallel selective mating are suggested to improve the yield potential in pigeonpea.

Key words : *Cajanus cajan*, Inheritance, Pigeonpea

Pigeonpea is the second most important pulse crop in India after chickpea. Being and often cross pollinated crop, it is amenable to genetic improvement through breeding methods suitable for both autogamous and allogamous crops. Yield is one of the most important economic characters and is the product of multiplicative interaction of contributing characters. For genetic improvement of the crop, the breeding method to be adopted depends on the nature and magnitude of the gene action involved in the expression of quantitative traits.

Line x Tester analysis is used to select the parents based on their combining ability but fails to detect the epistasis, which remains the most complex problem and on which it is extremely difficult to obtain reliable results. The epistasis can be detected by the analysis of generation means using joint scaling test, which determines the nature of epistasis or accurately whether it is additive x additive, additive x dominance or dominance x dominance types of interaction. The objective of the present investigation was to obtain information on the gene effects in pigeon pea to provide a basis of selection in a breeding programme for the improvement of this crop.

MATERIALS AND METHODS

Six generations of two cross combinations *viz.*, PRG 100 x ICPL 87119 and LRG 30 x ICP 8863 were raised in a randomized block design with three replications at ARS, Tandur during *kharif* 2007. Each entry was sown in 5 m long single row plot at 1 m x 0.2 m spacing. Recommended package of practices were adopted to raise the crop. Observations on each generation were recorded for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pod clusters per plant, number of pods per plant, 100-seed weight and yield per plant. The number of competitive plants sampled were 5,50 and 30 from P_1 and P_2, F_1 and F_2, and BC_1 and BC_{II}, respectively.

The data recorded were subjected to weighted analysis of Cavalli (1952) to know the adequacy of additive - dominance model. In the presence of epistasis, the data where any of the 4,5,6 parameters are found adequate in the model of Jinks and Jones (1968) was subjected accordingly to sequential model in order to obtain more precise estimate for these parameters. The adequacy of these sequential models was tested by X^2 test, respectively.

RESULTS AND DISCUSSION

The hybrid performed better than their respective parents for all the traits in both the cross combinations. The trait mean values for F_1 generation were higher than the corresponding F_2 generation for all the characters. However, the trait mean values for the F_1 generation was higher than the corresponding mean values of BC_1 generation whereas the same for the F_2 generation was lower than the corresponding mean values of BC_{II} generation except for the characters *viz.*, test weight and seed yield in the cross PRG 100 x ICPL 87119. In the cross LRG 30 x ICP 8863, the mean performance of BC_1 generation was higher than BC_{II} generation for all the traits except for test weight. The expected mean (m) was positive for all the traits in both the cross combinations (Table 1).

Two parameter model was adequate for number of pods per plant in the cross LRG 30 x ICP 8863 and for primary branches in the cross PRG 100 x ICPL 87119 which indicated the non prevalence of non- allelic interactions (Table 2). In both the crosses, magnitude of dominance component was higher than that of additive indicating that it could be easier to select and isolate lines for most of the traits in the early generations. These results were in agreement with the earlier reports of Kandalkar (2005) and Ghokde *et al.* (1993).

For days to 50% flowering, days to maturity and test weight in both the crosses and clusters per plant, pods per plant and seed yield in the cross PRG 100 x ICPL 87119 four parameter sequential model was found fit. Non-allelic gene interactions were indicated for the above mentioned traits.

Table 1. **Mean values of six generations in two crosses of pigeonpea**

Character	Cross	P_1	P_2	F_1	F_2	BC_1	BC_2	SE±	CD (5%)
Days to 50% flowering	PRG 100 x ICPL 87119	94.13	118.40	121.46	107.07	104.67	114.70	0.79	2.49
	LRG 30 x ICP 8863	115.93	107.13	118.67	109.95	115.70	112.77	0.84	2.64
Days to maturity	PRG 100 x ICPL 87119	154.73	180.20	181.47	165.63	164.67	173.90	1.36	4.28
	LRG 30 x ICP 8863	178.27	167.73	178.67	169.95	175.77	172.77	0.87	2.75
Plant height	PRG 100 x ICPL 87119	162.96	194.22	200.48	179.30	173.82	194.16	1.01	3.17
	LRG 30 x ICP 8863	185.62	172.58	200.06	179.12	194.23	175.37	0.61	1.91
Branches per plant	PRG 100 x ICPL 87119	13.53	14.93	17.20	14.93	14.53	15.30	0.42	1.31
	LRG 30 x ICP 8863	14.20	14.53	18.00	16.55	16.16	15.40	0.29	0.95
Clusters per plant	PRG 100 x ICPL 87119	80.27	90.00	98.00	83.00	86.07	91.63	0.99	3.11
	LRG 30 x ICP 8863	76.80	88.33	92.27	82.37	78.26	90.46	1.13	3.76
Pods per plant	PRG 100 x ICPL 87119	382.53	422.00	485.66	417.32	394.77	426.40	2.59	8.19
	LRG 30 x ICP 8863	416.27	390.80	477.93	417.57	450.73	420.70	3.68	11.59
Test weight	PRG 100 x ICPL 87119	13.47	12.32	16.38	12.27	13.02	12.17	0.13	0.39
	LRG 30 x ICP 8863	8.90	12.59	12.89	10.33	10.11	12.31	0.43	1.37
Seed yield	PRG 100 x ICPL 87119	52.84	54.12	63.71	55.24	50.91	55.05	0.31	0.96
	LRG 30 x ICP 8863	52.73	54.17	62.25	53.35	58.61	55.45	0.88	2.76

For days to 50% flowering in the cross LRG 30 x ICP 8863, additive component possessing negative sign indicating the dominance , additive x additive, additive x dominance and dominance x dominance type of gene effects influencing the inheritance of the trait. Similar findings were reported by earlier research workers such as Patel *et al.* (1990), Perera *et al.* (2001) and Hooda *et al.* (2000).

There was a rare occurrence of significance of common genetic parameters assessed in one or more crosses for the same characters studied in the present investigation. A considerable variation in the relative magnitude of different genetic parameters (m), (d), (h), (i), (j) and (l) was obsedved from cross to cross for the same characters in the study, which could be ascribed to the presence of variable frequency of genes opposing and reinforcing effects in the parents involved in the crosses. (Mather and Jinks 1982, Hallauer and Mirinda 1989).

Five parameter sequential model was fit for plant height in both crosses and number of clusters per plant, number of pods per plant and seed yield in the cross LRG 30 x ICP 8863. For number of pods per plant, non-allelic interaction was deciphered. In the cross PRG 100 x ICPL 87119, (h) and (i) components exhibited opposite sign indicating the duplicatory epistatic type of gene action. In both crosses, prevalence of epistatic interactions were noticed for plant height. There was higher magnitude of dominance component compared to the additive component for these traits. These results were in agreement with the earlier reports of Oomen *et al.* (1994) and Chandra Sekhar *et al.* (1998).

In the present investigation, magnitude of (d) was relatively small to that of other gene effects indicating that additive gene is playing a major role to the inheritance of these traits. For majority of the characters, the dominance gene action was observed to be playing a major role as compared to additive gene action. It suggests that the selection for these characters in early generations may not yield fruitful yields. Breeder should postpone selection to the later generations *i.e.*, after considerable fixation of genes.

Table 2. **Estimation of genetic parameters in pigeonpea**

Character	Cross	m	d	h	i	j	l
Days to 50% flowering	C1	107.07**+ 1.58	-10.03**+2.07	25.67**+7.57	10.46+7.55	2.10+2.08	6.27+10.46
	C2	109.95**+1.21	3.00*+1.19	24.40**+5.43	7.26**+5.41	-1.40+1.23	-13.93+6.87
Days to maturity	C1	165.63**+1.64	-9.23**+2.19	28.60**+7.92	14.60+7.91	3.50+2.23	6.13+11.03
	C2	169.95**+1.22	3.00*+1.19	22.93**+5.43	-17.27**+5.41	-2.26+1.23	-11.00+6.87
Plant height	C1	179.30**+2.03	-20.34**+2.20	40.64**+9.32	18.75*+9.25	-4.71*+2.29	3.46+12.18
	C2	179.12**+1.88	18.87**+1.69	43.69**+8.33	22.73**+8.27	12.35**+1.79	-3.61+10.33
Number of branches	C1	14.93**+0.46	-0.76+0.53	2.90+2.16	-	-	-
	C2	16.55**+0.56	0.77+0.63	0.57+2.6	-	-	-
Clusters per plant	C1	83.00**+1.62	-5.56**+1.92	35.27**+7.60	23.40**+7.55	0.30+1.98	-10.53+10.23
	C2	82.37**+1.39	-12.20**+1.67	17.70**+6.59	8.00+6.47	-6.43**+1.77	4.20+9.04
Pods per plant	C1	417.32**+5.76	-31.63**+6.61	56.47*+26.88	-26.93+26.59	11.90+7.03	160.47**+36
	C2	417.57**+6.65	30.03**+9.58	147.00**+32.89	72.60*+32.77	-17.30+9.73	-52.53+46.98
100-seed weight	C1	12.27**+0.22	0.84**+0.29	4.76**+1.08	1.27+1.07	0.28+0.31	6.93**+1.49
	C2	10.33**+0.27	-2.20**+0.27	5.66**+1.23	3.51**+1.22	-0.36+0.29	-1.06+1.57
Seed yield	C1	55.24**+0.66	-4.15**+0.66	1.19+3.42	-9.04**+3.38	-3.51**+1.09	31.49**+5.02
	C2	53.35**+0.54	3.16*+0.54	23.52**+3.16	14.73**+3.05	3.88**+1.13	-11.46**+5.09

For number of clusters per plant, days to 50% flowering, days to maturity, plant height, number of pods per plant, 100-seed weight and clusters per plant. Preponderance of additive gene action over non-additive gene action was observed in both crosses. In such cases, pedigree method would be more rewarding for improvement.

The overall perusal of generation mean analysis indicated that epistasis is the integral part of genetic architecture of the material used in the present investigation. Hence, to break the gene constellations, reciprocal recurrent selection or diallel selective mating systems are required for the improvement of yield and yield attributes. further, as the duplicate type of epistasis was observed in some of the traits, so, selection intensity should be mild in the earlier and intense in the later generations to achieve the desirable improvement in that traits in pigeonpea.

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