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Genetic Analysis of Yield and Yield Components in Redgram (*Cajanus cajan* (L.) Millsp.)*

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The mode of inheritance of seven quantitative characters, was studied in two redgram crosses by a genetic analysis of the means of six generations. The yield and yield components showed the predominance of additive gene action and absence of heterosis in Cross. 1 (S. 18 X Prabhat) and a high degree of heterosis conferred by dominance and dominance X dominance effects in Cross. 2 (CO. 2 x S. 12). Reciprocal recurrent selection seems to be the ideal breeding method for crop improvement in redgram as it results in the simultaneous utilization of epistatic and non-epistatic gene effects.

In order to formulate efficient breeding programmes for selection for yield, it is essential to characterise the nature and magnitude of gene action that determine the yield and yield components. With this view, the mode of inheritance of yield and its components was studied in two redgram crosses by a genetic analysis of the means of different generations and the results are reported hereunder.

MATERIAL AND METHODS

Six generations consisting P_1, P_2 (parents), F_1, F_2, B_1 (backcross of F_1 to P_1) and B_2 (backcross of F_1 to P_2) were built up in each of the two redgram crosses viz., Cross 1 (S. 18 x Prabhat) and Cross. 2 (Co.2 x S. 12) and simultaneously raised in a randomised block design with four replications, during summer 1976. Sowing was done on ridges of 2.7 m long and 60 cm apart with a plant spacing of 30 cm. The parents and F_1 and the two backcrosses had three rows each, and the F_2 had 18 rows in each replication. The original data collected on individual plant basis for 40 random plants in parents and F_1s 200 in F_2s and 80 in each backcross over all the replications were transformed into log values and subjected to both statistical and genetic analysis as suggested by Mather and Jinks (1971). The gene effects for seven quantitative characters viz., days to first flowering, plant height, number of branches, number of clusters, number of pods, pod yield and seed yield were estimated.

RESULTS AND DISCUSSION

An examination of heterotic response of all the characters studied in Cross. 1 (Table 1) revealed significantly negative heterosis as compared to the better parent. However, the negative

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heterosis for days to first flowering (earliness) in this cross has a considerable breeding value. In Cross. 2, a high degree of heterosis was observed for all the traits except days to first flowering and plant height. The gene effects estimated from generation means (Table 2) indicated varying nature of gene action for a given character from cross to cross. The operation of duplicate type of interaction was detected for days to first flowering and plant height in Cross. 1 and for all the characters except plant height in Cross 2, as evidenced from the opposite signs of $(\hat{h})$ and $(\hat{l})$. In other cases neither $(\hat{h})$ nor $(\hat{l})$ was significantly different from zero and hence the type of interaction could not be classified (Mather and Jins, 1971).

In Cross. 1, the estimation of gene effects revealed that number of clusters, number of pods, pod yield and seed yield per plant were determined perdominantly by additive genes. The additive x dominance interaction was significantly negative. The other interaction effects besides dominance were non-significant for these characters. In respect of days to first flowering, plant height and number of branches also, considerable additive effect was detected in addition to dominance effect. The presence of significant additive effect and absence of heterosis for yield and yield components in this cross suggest that these characters *per se* would admit improvement by simple selection through pedigree breeding.

In Cross 2, the yield and yield components like number of branches, number of clusters, number of pods and pod yield manifested a high degree of heterosis, conferred by dominance and dominance x dominance effects. The dominance relationship also showed over-dominance for all the characters except plant height. This situation offers scope for the exploitation of heterosis in redgram breeding. However, some limiting factors such as lack of useable male sterile lines, fewer number of seeds per pod etc., impose certain restrictions on the large scale exploitation of heterosis in this crop. The high degree of outcrossing (Veeraswamy *et. al.*, 1973) could be advantageously utilized for developing random-mated composites, in the case of parents involved in Cross. 2. Khan (1973) also favoured the development of random mating composites in redgram.

The varying nature of gene action for a given character from cross to cross although points out the need for such detailed studies in individual crosses, it is not practicable in large scale breeding programmes. As the yield and yield components in the present study are under all the three types of gene action namely, additive, dominance and epistasis, reciprocal recurrent selection procedure seems to be the best suited method of breeding for improvement in this crop. Singh *et.al.* (1972) also suggested this procedure for yield improvement in cotton under similar situations.

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REFERENCES

KHAN, T. N. 1973. A new approach to the breeding of pigeon pea (*Cajanus cajan* (L.) Millsp.,) : Formation of Composites. *Euphytica*, 22 : 373-7.

MATHER, K. and J. L. JINKS. 1971. Biometrical Genetics. The study of continuous variation Chapman and Hall Ltd., London.

SINGH, R. B., D. K. JAIN and R. P. DAHIYA. 1972. Genetic analysis of yield characters in upland cotton (*Gossypium hirsutum*). *Indian J. Genet.*, 32 : 138-52.

VEERASWAMY, R., G. A. PALANISWAMY and R. RATHINASWAMY. 1973. Natural cross pollination in *Cajanus cajan* (L.) Millsp. and Lab-lab niger. Medikus. *Madras agric. J.* 60 1828.

Table 1. Expression of Heterosis over better parent in F_1 (Log values) (percentages)

Character	Cross 1 (S. 18xPrabhat)	Cross 2 (CO.2xS. 12)
Days to first flowering	-11.06	-0.02
Plant height (cm)	-11.10	-0.78
Number of branches per plant	-15.43	-9 69
Number of clusters per plant	-12.46	16.97
Numder of pods per plant	-17.09	12.28
Pod yield per plant (gm)	-25.32	16.33
Seed yield per plant (gm)	-23.88	20.68

Table 2. Estimates of gene effects obtained from generation means (Log values)

Character	m	(d)	(h)	(i)	(j)	(l)	(h)/(d)
Cross. 1							
Days to first flowering	1.73 ± 0.03 **	0.13 ± 0.002 **	0.44 ± 0.08 **	0.12 ± 0.03 **	0.01 ± 0.02	-0.41 ± 0.05 **	3.53
Plant height	1.69 ± 0.04 **	0.20 ± 0.01 **	0.80 ± 0.10 **	0.27 ± 0.04 **	-0.04 ± 0.03	-0.57 ± 0.06 **	4.06
Number of branches	0.84 ± 0.08 **	0.15 ± 0.01 **	1.04 ± 0.22 **	0.11 ± 0.08	0.04 ± 0.07	-0.02 ± 0.14	6.91
Number of clusters	1.51 ± 0.11 **	0.24 ± 0.02 **	0.28 ± 0.29	0.09 ± 0.11	-0.27 ± 0.09 **	-0.18 ± 0.19	1.19
Number of pods	2.08 ± 0.12 **	0.35 ± 0.02 **	0.27 ± 0.32	0.21 ± 0.12	-0.24 ± 0.10 *	-0.16 ± 0.21	0.77
Pod yield	1.44 ± 1.14 **	0.44 ± 0.02 **	0.27 ± 0.36	0.17 ± 0.14	-0.25 ± 0.11 *	-0.18 ± 0.24	0.62
Seed yield	1.37 ± 0.12 **	0.40 ± 0.02 **	-0.15 ± 0.38	-0.06 ± 0.12	-0.37 ± 0.10 **	0.10 ± 0.25	-0.40
Cross. 2							
Days to first flowering	1.67 ± 0.02 **	0.03 ± 0.003 **	0.50 ± 0.05 **	0.16 ± 0.02 **	0.01 ± 0.02	-0.31 ± 0.04 **	18.71
Plant height	1.97 ± 0.03 **	0.07 ± 0.005 **	-0.004 ± 0.08	-0.003 ± 0.03	0.05 ± 0.02 *	0.08 ± 0.05	-0.06
Number of branches	0.71 ± 0.06 **	0.01 ± 0.01 **	0.71 ± 0.15 **	0.23 ± 0.06 **	0.02 ± 0.05	-0.37 ± 0.10 **	48.77
Number of clusters	0.88 ± 0.10 **	-0.04 ± 0.02 **	2.26 ± 0.28 **	0.81 ± 0.10 **	0.16 ± 0.09	-1.11 ± 0.19 **	-58.63
Number of pods	0.89 ± 0.11 **	0.02 ± 0.02	3.17 ± 0.26 **	1.23 ± 0.10 **	0.20 ± 0.08 *	-1.66 ± 0.17 **	140.33
Pod yield	0.26 ± 0.12 *	0.07 ± 0.03 **	3.40 ± 0.31 **	1.29 ± 0.12 **	0.01 ± 0.10	-1.77 ± 0.22 **	47.45
	0.09 ± 0.12	0.05 ± 0.12 *	3.27 ± 0.31 **	1.24 ± 0.12 **	-0.06 ± 0.10	-1.68 ± 0.21 **	60.58

*Significant at 5% **Significant at 1%