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INHERITANCE OF YIELD AND ITS COMPONENTS IN SAFFLOWER (*CARTHAMUS TINCTORIUS* L.)

R. K. GUPTA AND S. P. SINGH

National Botanical Research Institute, Lucknow - 226 001

ABSTRACT

Parents, F_1, F_2, B_1 and B_2 generations of 10 crosses from 5 parents were studied to estimate the gene effects for seed yield and yield components in safflower (*Carthamus tinctorius* L.). Scaling tests suggest the non-allelic interaction for all the crosses and characters. Dominance effect (h) was more pronounced than additive effect (d) in almost all the crosses. Epistatic effects were found for all crosses. The duplicate type epistasis was more frequent than complementary. Considering the gene actions, recurrent selection may be utilized to improve the seed yield through component traits.

INTRODUCTION

Safflower is important oilseed crop having greater potential to reduce the cholesterol content in human system. For genetic improvent the knowledge of gene action involved is essential in formulating the systematic breeding programme. The study on this aspect is limited (Ramchandram and Goud 1981; Gupta and Singh 1990) in this crop. Often improvement in yield is being tried as well as contemplated without understanding the inheritance of yielding ability. Therefore, an attempt on additive -dominance model was made to examine the gene effects of 5 parents diallel.

MATERIAL AND METHODS

The experiment consisted of 10 crosses obtained from 5 parents diallel. The parents were 'EC27510' (Mexico), 'EC31367' (USA), 'EC33969' (Iran), 'Local' and 'EC27249' (Australia). Forty five genotypes including 5 parents, 10 each of F_1, F_2, B_1 and B_2 were grown in randomized block design with 3 replications. Each replication had single row of parents and F_1, 2 rows of B_1 and B_2 and 4 rows of F_2. The row length was 3.5 m with 50 x 20 cm crop geometry. Ten competitive plants/row/replication were tagged before flowering to record the data on plant height, branches/plant, capitula/plant and seed yield/plant. The analysis of variance was done according to Panse and Sukhatme (1967). The interaction components based on 6 parameter model was obtained from generation mean (Hayman 1958). Significance of genetic components were tested by corresponding standard error. Scaling test (Mather 1949) was used to test the fitness of additive-dominance model.

RESULTS AND DISCUSSION

Analysis of variances indicated significant differences among progenies for all the characters and thus data were further subjected to study the digenic interaction. The scaling test was significant for all the crosses and characters indicating the presence of inter-allelic interaction. (Table 1).

All crosses except 'EC33969' x 'Local' showed significant additive gene effect (d) for plant height, though positive significant was only in 6 crosses. Dominance (h) effect was positively significant for all the crosses. All the crosses showed significant estimates for 3 types of digenic interaction. The magnitude of additive x additive (i) was more than 10 times higher than additive x dominance (j) and dominance x dominance (1). The opposite sign of (h) and (1) revealed duplicate type epistasis for 9 crosses while cross 'EC27510' x 'EC33969' had complementary type epistasis.

For branches/plant, additive gene effect (d) was negative for all the crosses except 'EC27510' x 'EC31367' and 'EC33969 x 'Local', while dominance (h) effect was positively significant for all the 10 crosses. Considering digenic interaction, additive x additive (i) was positively significant and was much higher than that of additive x dominance (j) and dominance x dominance (l). Sign of (h) and (i) indicated the duplicate type epistasis in 7 crosses and complementary type in 3 crosses.

Positively significant (d) additive gene effect was observed in 3 crosses while dominance gene effect (h) was in all the crosses except 'EC33969. x EC27249' for capitula/plant. Sign of (h) and (i) indicated the presence of duplicate type epistasis in 9 crosses and complementary in one i.e. 'EC27510' x 'EC27249'.

The additive gene effect (d) was significant in 7 crosses for seed yield/plant and all were negative. The relative contribution of dominance gene effect (h) was much higher (10 times approximately) than that of additive gene effect. Eight crosses showed positively significant and 2 negatively significant dominance gene effect (h). Among 3 types of digenic interactions, additive x additive (i) was positively significant in 8 crosses while trend was reversed for additive x dominance (j) and dominance x dominance (l). Opposite sign of (h) and (i) showed duplicate type epistasis for all the crosses.

Safflower is self pollinated crop and out crossing was reported to 1.9 per cent (De 1973). However, frequency of out crossing may very from 5 to 10 per cent depending upon the environmental conditions and availability of pollinating insects. According to reproductive mechanism involved, mass and pedigree selections have been employed in developing cultivars of safflower. These breeding methods however imposes a serious restrictions on the population so far the manipulation of its genetic expression and flexibility is concerned. Considering different gene effect over all the characters in present material, the magnitude of dominance (h) was much

Table 1. Estimation of components of generation on 6 parameter model for seed yield in safflower

Crosses	Scaling test			m	d	h	i	j	l	Type of epistasis
	A	B	C							
EC 27510xEC 31367	**	**	**	5.77**	-.97	5.49**	3.18**	-1.96**	-13.06**	D
EC 27510xEC 33969	**	—	*	5.57**	-2.30**	13.06**	7.72**	-2.13**	-11.24**	D
EC 27510x Local	**	*	**	11.69**	-1.44*	15.48**	12.92**	-1.39*	-18.33*$	D
EC 27510xEC 27249	*	**	**	6.42**	-2.00**	10.75**	11.96**	-1.06	-18.99**	D
EC 31367xEC 33969	—	—	*	7.88**	0.52	34.67**	26.64**	1.68*	-32.58**	D
EC 31367x Local	**	—	**	10.03**	-2.48**	-6.02**	-10.40**	-1.44**	9.21**	D
EC 31367xEC 27249	**	*	**	8.99**	0.80	25.29**	16.20**	2.72**	-9.91**	D
EC 33969x Local	**	*	*	7.44**	-1.41*	16.96**	7.66**	1.28	-5.77**	D
EC 33969xEC 27249	*	**	**	7.14**	-1.45*	-2.45**	-3.06**	-.68	5.99**	D
Local x EC 27249	*	**	*	9.71**	-4.30**	20.47**	20.76**	-3.41**	-36.54**	D
SE				0.67	0.60	0.24	0.22	0.66	0.34	

higher than additive (d) gene effects. This suggests that as the inheritance of quantitative characters became more complex, the contribution of dominance (h) gene effect to their inheritance becomes greater. Further among 3 types of digenic interaction additive x additive gene effect (i) plays an important role for all the characters. The sign of two estimates i. e. (h) and (i) indicated the presence of duplicate type epistasis for all the characters except 'EC27510' x 'EC33969' for plant height, 'EC27510' x 'EC27249', 'EC33969' x 'Local' and 'EC33969' x 'EC27249' for branches/plant and 'EC27510' x 'EC27249' for capitula/plant. The presence of duplicate type epistasis may reduce the variability in F_2 and further generations thereby hammering the progress of selection. The 4 crosses showing complementary epistasis may enhance the scope of selection and thus may be exploited to increase the seed yield. Presence of epistatic gene effect indicated that this type of gene action may not be ignored in formulating any breeding programme. The character is governed by all the genes in a genome, hence it would be unrealistic to assume in any case that interallelic interaction is absent (Singh and Singh 1979). Thus, with prevailing gene action, the four crosses having complementary epistasis could be advanced to selection for high yielding genotypes. Further, the recurrent selection (Compton 1968) may be used to exploit all the types of gene effects i.e. additive, dominance and epistasis to accumulate the favourable genes and thereby releasing a greater reservoir of genetic variability to enable breeders to exercise selection upon.

REFERENCES

Compton, W. A. 1968. Recurrent selection in self polinated crops without extensive crossing. Crop Science 8: 773.

De, D. 1973. Natural crossing in Safflower (*Carthamus tinctorius* L.) M. Sc. (Ag). Thesis, Banaras Hindu University (Unpublished).

Gupta, R. K. and Singh, S. P. 1990. Genetic analysis of earliness and its inheritance in safflower (*Carthamus tinctorius* L.). Transactions of Indian Society of Desert Technology 15: 109-115.

Hayman, B. I. 1958. The separation of epistatic from additive dominance variance in generation mean. Heredity 12: 371-391.

Mather, K. 1949 *Biometrical Genetics*, Mathuen & Co. London.

Panse, V. G. and Sukhatme, P. V. 1967. Statistical methods for agricultural workerr ICAR, New Delhi.

Ramchandram, M. and Goud, I. V. 1981. Genetic analysis of seed yield, oil content and their components in safflower. Theoritical and Applied Genetics 60: 141-196.

Singh, S. P. and Singh, H. N. 1979. Genetics of seed number and its inheritance in pea. Indian Journal of Agricultural Science 49 : 401-403.