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SIMPLIFIED TRIPLE TEST CROSS ANALYSIS IN SAFFLOWER (*CARTHAMUS TINCTORIUS* L.)

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ABSTRACT

The study revealed importance of epistasis in the inheritance of yield contributing traits and possibility of its detection in Safflower. Epistasis was present for all the characters except number of main branches per plant and oil content. In presence of epistasis the estimates of genetic components would be biased. The present analysis is applicable to those four characters for which the testers had extreme phenotypes. Thus precise estimates of additive and dominance components were obtained for only number of main branches per plant. In presence of preponderance of additivity, the methods like simple selection has been advocated for further improvement in safflower.

Key words: Epistasis, simplified triple test cross, safflower, *Carthamus tinctorius*.

The selection of suitable parent is a crucial factor in any breeding programme which in turn, depends on the nature of gene action of the parents involved. Various biometrical approaches have been used for estimating different types of gene actions in crop plants. In most of the mating designs used, it is assumed that non-allelic interactions are absent, whereas the fact is often contrary to this assumption. In presence of non allelic interactions, the estimates or additive and dominance components are biased leading to the inappropriate use of breeding procedure. With the application of simplified triple test cross analysis (S. T. T. C.) [1], it has been possible to detect the epistasis and to estimate the additive and dominance components. However, choice of appropriate tester in S. T. T. C. is very crucial [2]. The present paper deals with the use of S. T. T. C. for gene action studies in safflower.

MATERIALS AND METHODS

The experimental material comprised of safflower lines, viz S-144, NS-1016, JL 281, APRR-1, B-263, EC-181287, EC181330, NRS-209, AKSF-73, FT-2, BLY-1020, BLX-1022 and BLY-1035, testers namely N.7 and BLY-652. These testers possessed the extreme phenotypes for days to flower (85, 0, 91.4) number of main branches per plant (11.2, 7.2) number, of seeds per capitulum (23.31, 31.12) and 100 seed weight (5.22, 4.28). The two testers, 13 lines and their 26 F1 hybrids were raised in a single block suggested by Mather and Jinks [3]. Data recorded on all the plants grown for eight characters and were analysed following Jinks *et al.* [1].

RESULTS AND DISCUSSION

Although data were analysed for all the characters, the analysis would be applicable only for characters with extreme phenotypes. Epistasis appeared to play a significant role in the inheritance of all the characters except number of main branches per plant and oil content (Table 1). This confirms the earlier finding in safflower [4-6].

Table 1. Test of epistasis (mean squares) for different characters in safflower

Source	d.f.	Days to flower	Plant height	No. of main branches per pl.	No. of capitula per plant	Seeds per capitulum	100 seed weight	Oil con-tent	Seed yield per plant
Epistasis $(L_{1i} + L_{2i}-P_i)$	12	4.60	13.46	0.35	10.48	3.40	0.05	1.21	17.58
Within family	340^+	1.93	3.04	0.27	4.57	1.24	0.01	0.71	1.76

$^{**}P \leq 0.01$; $^+$ The degree of freedom are less than expected due to loss of plants

The results (Table 2) further revealed that additive genetic variation was important for days to flower, plant height, 100 seed weight and seed yield per plant in the presence of epistasis suggesting the predominant role of additive gene action in the manifestation of these characters. However, these estimates were biased due to presence of epistasis.

The predominance of dominance components (H_1) was observed for number of main branches per plant, number of capitula per plant and seed per capitulum (Table 2). The importance of additive and dominance for these characters in safflower has also reported earlier [5, 7, 8].

Table 2. Estimates of additive and dominance components for different characters in safflower

Components of genetic variation	Days to flower	Plant height	No. of main branches per plant	No. of capitula per plant	Seeds per capitulum	100 seed weight	Oil contnet	Seed yield per plant
D	3.12	44.64	0.38	12.20	5.60	0.276	0.20	57.76
H_1	2.72	12.84	0.88	8.16	8.16	0.084	1.00	46.84
F	–5.99	46.8	2.6*	28.76	8.68	–0.033	–3.52	–53.60
r(sum/diff.)	0.264	–0.406	–0.698	–0.296	0.304	0.45	0.435	0.239

*P = 0.05

As the epistasis was non significant for number of main branches per plant, the analysis was applicable only for this character. The study indicated that the dominance gene action was pre-dominant for this character. It thus appears that for further improvement in this trait mearly selection would not yield any significant response in the present material. The non-significant estimates of 'F' of all the traits except number of main branches per plant indicates dominance to be ambidirectional. For number of main branches per plant, the value of 'F' was positive and significant, indicating that the increasing alleles are dominant more frequently than decreasing alleles for the traits and dominance was in one direction.

The study shows that epistasis may be an important factor in the inheritance of yield contributing traits. Genetic models neglecting epistasis may result in biased information recording genetic parameters. In general, a greater part of genetic variation was contributed by additive effects of gene for most of the traits. Thus in presence of preponderance additivity, simple breeding procedures like selection could be followed for exploitation of additive genetic components for further improvement in safflower.

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