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DETECTION OF EPISTASIS AND ESTIMATION OF COMPONENTS OF GENETIC VARIATION APPLYING MODIFIED TRIPLE TEST CROSS ANALYSIS USING TWO TESTERS IN PEA (*PISUM SATIVUM* L.)

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ABSTRACT

Fifteen lines of pea (*Pisum sativum* L.) were crossed with two testers. Genetic analysis was carried out to detect epistatis and estimate components of genetic variation for seven quantitative traits. Epistasis was detected for all the character studied. Significant estimates of both additive (D) and dominance (H) components were observed for all the characters, except for the pod length. Estimates of additive components assessed from the pure line families (D') for different characters was comparable with the D component derived from sums (L₁i + L₂i) of the triple test cross families. The F value was positive and significant for days to flowering, plant height, pods per plant, seed weight and seed yield per plant showing isodirectional nature of dominance. Significance of additive component and F parameter showing increasing effect on the character indicate that pedigree selection would be effective for the improvement of such traits.

Key words: Modified triple test cross, epistatis, additive component, dominance component, pea.

Epistasis plays a major role in the inheritance of quantitative traits in several crops, particularly in pea [1]. Consequently, the estimates of additive and dominance components of genetic variation are biased due to presence of epistasis. Kearsey and Jinks [2] devised triple test cross design to assess the epistatis in controlling the inheritance of traits. Jinks et al. [3] proposed a modified triple test cross design where only two testers instead of three are used in developing the families. This modified triple test cross detects epistasis and estimates additive (D) and dominance (H) components as well as the direction of dominance (F) with a high degree of precision. In the present investigation, the relative contribution of different genetic parameters controlling the inheritance of different traits of field pea have been studied using this modified model of triple test cross.

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Modified Triple Test Cross Analysis in Pea

MATERIALS AND METHODS

Fifteen lines, viz., VL 7, PM 5, PM 2, JP 829, JP 4, PI 280064, S 143, Rachna, HUP 7, PG 3, HFP 4, KFPD 3-2, KFPD 6, KFPD 1 and HUDP 1 were crossed with two testers of opposite nature: HUP 9 (very tall, late, leafless (afila), powdery mildew resistant, bold seeded, high yielder), and EC 33866 (dwarf, early, with normal foliage, powdery mildew susceptible, seeds small dimpled, and relatively low yielder) to generate 30 single-cross progenies (15 L₁i + 15 L₂i). The materials comprising two testers, 15 parential lines, 15 L₁i, 15 L₂ i families were grown in completely randomized block design replicated twice. The plot size of each family was a single row of 20 plants sown at 15 cm spacing in 3 m long rows at the distance of 45 cm.

Data were recorded on ten random plants selected from each of parents and the crosses in each replication on seven quantitative characters. Analysis was done following the modified triple test cross models of Jinks et al. [3].

RESULTS AND DISCUSSION

The sum of squares $(L_{1i} + L_{2i} - P_i)$ showed importance of epistasis for all the seven characters. The epistasis x block interaction was also significant for days to flowering, seeds per pod and pod length.

The analysis of variance for sums $(L_{1i} + L_{2i})$ showed that variance due to sums was important for all the traits (Table 1). However, interaction of sums x block was significant for days to flowering, pod length and seed weight. When variance due to sums for these traits were again tested with interaction item, it was found that sum item was not significant

Parameter	d.f.	days to flowering	Plant height	Pods per plant	Seeds per pod	Pod length	Seed weight	Seed yield per plant
Analysis of additive v	ariance							
Sums $(L_1 + L_2 i)$	14	117.8**	5456.2**	296.9**	0.39**	0.09	4.02**	139.9**
Sums x blocks	14	153**	11.4	4.4	0.10	0.07**	0.08**	6.1
Analysis of dominanc	e varian	ce						
Differences (L ₁ i-L ₂ i)	14	89.4**	4136.2**	203.5**	0.45	0.31**	1.88**	105.6**
Difference x blocks	14	0.7*	14.6	8.9	0.15**	0.07**	0.06**	4.7
Within families	54	0.4	225.0	10.7	0.06	0.02	0.03	8.4

Table 1. Analysis of variance for sums $(L_1i + L_2i)$ and differences $(L_1i - L_2i)$ in modified
triple test cross model in pea

*, **Significant at P = 0.05 and 0.01, respectively.

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for pod length. Thus, within family variances were the appropriate error terms for testing the significance of major components.

The test of significance of difference item $(L_{1i} - L_2 i)$ was also important for all the traits. The interaction component was important only for days to flowering, seeds per pod, pod length and seed weight. But when these interaction items were used as denominator for testing the significance of differences variance, the significance of differences item was confirmed for all the characters again.

The variance due to sums $(L_{1i} + L_{2i})$ were used for estimating additive (D) component of genetic variation, whereas the variance due to difference $(L_{1i} - L_{2i})$ item were used for estimation of dominance (H) component (Table 3). The estimates of both additive and dominance components were highly significant for all the characters, except for pod length where only dominance component was significant. In general, the estimates of additive component were greater in magnitude than the dominance component for most characters, except the seeds per pod and pod length. The presence of common alleles in the testers increases the magnitude of additive component. The additive component (D') of pure breeding lines was generally comparable to the D component derived from the sums.

The directional element F was estimated from the covariance of sums and differences and its significance was tested indirectly as the correlation r of sums and differences. When the value of r (RF) and F were considered together it was found that estimates of the directional element (F) was important and significant for days to flowering, plant height, pods per plant, seed weight and seed yield per plant (Table 2). This revealed isodirectional

Experimental material	Para- meter	Days to flowering	Plant height	Pods per plant	Seeds per pod	Pod length	Seed weight	Seed yield per plant
TTC families	D	116.3**	5431.2**	286.1**	0.33**	0.02	3.94**	131.4**
	Н	88.7**	4111.2 ^{**}	192.8**	0.30	0.24**	1.32**	97.1**
	F	121.2**	3287.9**	194.0 ^{**}	0.10	0.01**	2.43**	95.0**
	r (RF)	1.0**	0.7**	0.8**	0.24	0.07	0.83**	0.78**
	E ₂	0.4	25.0	10.8	0.06	0.02	0.03	8.4
	(H/D)	0.9	0.9	0.8	0.90	3.46	0.68	0.9
Pure breeding								
lines (P1) D		173.1	43337.0	66.4	0.38	0.29	3.26	31.5

 Table 2. Estimates of additive (D) and dominance (H) components of genetic variance and other estimates in the modified triple test cross model in pea

^{*, **}Significant at P = 0.05 and 0.01, respectively.

RF --- r value to show the significance of F parameter.

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nature of dominance, suggesting that genes with increasing effect were most predominant for these traits. The positive and nonsignificant value of F for seeds per pod and pod length suggested ambidirectional nature of dominance.

It may be argued that epistasis or dominance do not have much of the directional element. Nanda et al. [4] also did not observe the confounding effect of F with dominance for most of the traits in triple test cross analysis in wheat. However, the possibility of confounding of directional element with epistasis and dominance cannot be underrated as the component F was present along with a high coefficient of dominance and epistasis assessed for days to flowering, plant height, pods per plant, and seed yield per plant.

The dominance $(H/D)^{1/2}$ was in the range of partial dominance for most of the traits. Late flowering, tall plant height, high podding, high seed number per pod, larger seed size, and higher seed yield per plant appear to be dominant in the present investigation. Partial dominance has also been established for most of traits in pea earlier following diallel analysis [8]. Similar results [5, 7, 8] were also reported for most of the characters in triple test cross analysis in pea. The additive component (D) was important for pod length and dominance had no role in the expression of this traits. The overall degree of dominance suggested that most of the characters studies are controlled predominantly by additive gene effects, however, dominance and epistatic components also played a major role in controlling the expression of different traits which was also reported in pea [5 – 9].

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