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ADDITIVE, DOMINANCE AND EPISTATIC COMPONENTS OF VARIATION FOR SEED PROTEIN CONTENT IN PEA (*PISUM SATIVUM* L.)

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ABSTRACT

Triple test-cross (TTC) and line x tester analysis involving 16 elite lines of peas was carried out to investigate the nature of gene action and combining ability for seed protein content. Epistasis, mainly of (j+l) type, was an integral component of genetic variation. Both the triple test-cross and line x tester approaches revealed seed protein content to the governed by both additive and dominance genetic variances, the former being preponderant. The dominance was ambidirectional. The additive and dominance variances were underestimated by the line x tester analysis than by TTC analysis. Lines HPPC 84, HPPC 43, Kinnauri and HPPC 91 were good general combiners, while HPPC 91 x HPPC 63 and HPPC 43 x HPPC 63 were promising crosses on the basis of specific combining ability.

Key words: Epistasis, protein content, pea, triple test-cross analysis.

Pea (*Pisum sativum* L.) can play an important role in improving protein in diet as its protein level reaches up to 40% on dry weight basis [1]. However, the basic information on the nature of gene action and combining ability, particularly for epistatic genetic variance for this trait in peas is rather limited [2–4]. The present study aims to obtain information on combining ability and relative magnitude of additive, dominance and epistatic variances influencing the expression of protein content in peas using triple test-cross (TTC) and line x tester analyses.

MATERIALS AND METHODS

Sixteen elite lines of pea (Table 1) were crossed with Lincoln and HPCC 63 inbred testers and their F_1 (Lincoln x HPPC 63) to generate L_{1i}, L_{2i} and L_{3i} families of a triple test-cross design. The 16 parental lines (Pi) along with 48 triple test-cross families, and the two inbred testers were evaluated by growing them in a single plant completely randomized design

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during the winter of 1987–88 at the Himachal Pradesh Krishi Vishva Vidyalaya, Palampur, with the plant-to-plant distance of 40 cm. Three randomly selected plants per family were analysed for seed protein content following the method of Mckenzie and Wallace [5]. The biometrical analysis of variance of triple test-cross design was done as per [6] to detect epistasis and estimate additive and dominance components of genetic variance. The data were reanalysed after excluding L_{3i} families from the line x tester mating design of Kempthorne [7].

RESULTS AND DISCUSSION

Presence of epistasis (Table 1) was evidenced by the significance of variance ($L_{1i}+L_{2i}-2L_{3i}$). Further parti- tioning of epistasis revealed that overall epistasis (i) was not significant, while j and l types of interactions were significant for protein content. The second test of epistasis based on the variance of ($L_{1i}+L_{2i}-P_i$) also gave similar results. Therefore, inadequacy of testers cannot be ruled out for seed protein content in the present study. The overall epistasis (i) is a linear directional component and, therefore, affects means and its nonsignificance does not rule out the presence of I type interactions in the components of second degree statistics. On the other hand, j and l components of variance are nondirectional and may or may not have directional counterparts. Therefore, the epistatic variation, mainly of j+l type, appears to be an integral component of the genetic architecture of seed protein content in the present material and this component cannot be overlooked while formulating breeding programmes for the improvement of populations through hybridization in pea. The individual line analysis for epistatic effects revealed that the lines HPPC 30, HPPC 69,

Table 1. Analysis of variance for the tests of epistasis and estimates of epistatic effects for seed protein content in pea

Source	d.f.	M.S.
Tests of epistasis		
Test I:		
Epistasis ($L_{1i} + L_{2i} - 2L_{3i}$)	16	3.70*
Epistasis (i) type	1	0.79
Epistasis (j+l) type	15	3.90*
Within families error	64	0.26
Test II:		
Epistasis ($L_{1i} + L_{2i} - P_i$)	15	7.04*
Within families error	96	0.21
Estimates of epistatic effects		
Lines:		
HPPC 41		-2.79*
HPPC 65		-5.11*
HPPC 60		-1.61
HPPC 84		1.16
HPPC 67		-5.25*
HPPC 91		-1.03
HPPC 77		5.97*
HPPC 30		10.50*
HPPC 73		-0.21
HPPC 43		1.45
HPPC 69		-9.62*
HPPC 94		-3.44*
HPPC 75		3.79*
HPPC 71		-2.90*
HPPC 48		-2.93*
HHPI (Kinnauri)		2.19
SE		± 1.26

*Significant at 5% level.

HPPC 77, HPPC 67, HPPC 65, HPPC 75, HPPC 94, HPPC 48, HPPC 71, and HPPC 41 had significant epistatic effects.

The estimates of additive and dominance components from the TTC and line x tester analyses (Tables 2 and 3) indicated that both additive and dominance components, with predominance of additive genetic component, were present for protein content. The average degree of dominance was less than unity, indicating that additive genetic variance is predominant.

Similar results were reported earlier also in pea [2–4]. The directional element F was nonsignificant (Table 2), indicating the ambidirectional dominance, or the dominant alleles are dispersed between the testers. Narrow sense heritability estimate was high (Table 3). Pooni and Jinks [8] showed that the estimates of additive component of triple test-cross is more reliable and useful for cross prediction because this estimate is uncorrelated with dominance variance and has a lower sampling error even in the presence of epistasis. Our study also confirms this conclusion on the basis of two biometrical approaches and revealed that both additive and dominance genetic components have been underestimated to the extent of 52.1 and 49.8%, respectively, in the line x tester analysis.

The estimates of general combining ability (gca), specific combining ability (sca), and epistatic effects (Tables 1 and 4) revealed that the parents HPPC 84, HPPC 43, Kinnauri and HPPC 91 were good general combiners for protein content, showing no epistatic effects. The crosses HPPC 91 x HPPC 63 and HPPC 43 x HPPC 63 were most promising with one of the parents as good general

Table 2. Analysis of variance for sums ($L_{1i} + L_{2i} + L_{3i}$) and differences ($L_{1i} - L_{2i}$), and the estimates of genetic parameters for seed protein content in pea

Source	d.f.	M.S.
Analysis of sums		
Sums ($L_{1i} + L_{2i} + L_{3i}$)	15	7.80*
Within families error	96	0.26
Analysis of differences		
Differences ($L_{1i} - L_{2i}$)	15	3.44*
Within families error	64	0.16
Estimates of genetic parameters		
D		10.04
H		6.54
F		33.21
$(H/D)^{1\backslash 2}$		0.80

*Significant at 5% level.

Table 3. Analysis of variance for combining ability (line x tester approach) and estimates of genetic parameters for seed protein content in pea

Source	d.f.	M.S.
Combining ability		
Crosses	31	5.68*
Lines	15	8.26*
Testers	1	0.49
Lines x testers	15	3.44*
Error	64	0.16
Estimates of genetic parameters		
$\sigma^2 A$		4.81
$\sigma^2 D$		3.28
$(H/D)^{1\backslash 2}$		0.82
hn (%)		58.00

*Significant at 5% level.

combiners and are expected to yield transgressive segregates. The other good general combiners, but having epistatic effects, were HPPC 77, HPPC 30 and HPPC 65. The other high sca crosses, HPPC 94 x Lincoln, HPPC 71 x Lincoln and HPPC 65 x Lincoln, showed epistatic effects and are difficult to handle in segregating generations.

Under these circumstances the conventional breeding approach such as pedigree or bulk or single seed descent methods would take advantage of epistasis and dominance coupled with additive variation for the improvement of protein content if selection is delayed untill later generations when the dominance effects would have diminished. Another approach can be the sib-pollinated line selection method of Palmer [9] and the population generated from crosses can be propagated through single seed descent method with one or two intermatings.

Table 4. Estimates of general and specific combining ability effects for seed protein content in pea

Lines	Gca effects	Sca effects of crosses with	
		Lincoln	HPPC 63
HPPC 41	0.11	0.23	-0.23
HPPC 65	1.56*	0.82*	-0.82*
HPPC 60	-0.61*	-2.23*	2.23*
HPPC 84	1.93*	0.45	-0.45
HPPC 67	-3.16*	-0.56	0.56
HPPC 91	1.13*	-2.23*	2.23*
HPPC 77	2.59*	0.38	-0.38
HPPC 30	2.51*	-0.56	0.56
HPPC 73	-2.29*	0.02	-0.02
HPPC 43	1.93*	-1.72*	1.72*
HPPC 69	-3.60*	0.89*	-0.89*
HPPC 94	-2.26*	2.81*	-2.82*
HPPC 75	-0.83*	0.02	-0.02
HPPC 71	-0.32	1.40*	-1.40
HPPC 48	-0.39	-0.26	0.26
Kinnauri	1.71*	0.53	-0.53
SE (gi)	0.28	SE (Sij)	0.40
SE (gi-gj)	0.40	SE (Sij-Skl)	0.57

*Significant at 5% level.

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