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ESTIMATION OF ADDITIVE, DOMINANCE AND DIGENIC EPISTATIC INTERACTION EFFECTS FOR CERTAIN YIELD CHARACTERS IN PEA

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ABSTRACT

The components of gene effects for yield and five yield contributing characters were studied following six-parameter model of Hayman, utilizing means of six basic populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) derived after crossing seven diverse cultivars of pea. The analysis reiterated the importance of dominance (h) gene effect for yield/plant, pods/plant, and plant height. However, additive (d) effect was pronounced for yield/plant in the cross, GC 322 x B 5064, whereas all three types of gene effects (additive, dominance and epistatic interactions) were significantly involved in the crosses GC 322 x PG 3 and GC 322 x T 163 for this attribute. Among digenic epistatic interactions, additive x additive appeared to contribute more for most of the characters. Reciprocal recurrent selection is suggested for developing elite population for effective selection.

Key words: *Pisum sativum*, six-parameter model, yield characters.

The choice of plant breeding methodology for upgrading the yield potential largely depends on the availability of reliable information on the nature and magnitude of gene effects present in the population. Diallel analysis, although effective and most widely used, does not provide the estimates of nonallelic interactions. Epistasis, which is known to play a major role in the expression of heterotic potential, has been reported in pea [1–6].

Generation means analysis, which provides the estimates of the main gene actions (additive and dominance) and their digenic interactions (additive x additive, additive x dominance, and dominance x dominance), helps in understanding the performance of the parents used in the crosses and potential of the crosses to be used either for heterosis exploitation or pedigree selection. In the present paper, therefore, the six-parameter model has been utilized to study and analyse the genetical control of yield and yield controlling characters involving seven diverse cultivars of pea.

MATERIALS AND METHODS

Seven diverse cultivars of pea were intercrossed in a diallel fashion and six basic generations of each cross, namely, the two parents, P_1 and P_2, their F_1 and F_2, and backcross generations, BC_1 and BC_2 were grown in compact family block design with three replications. The parents, F_1 and backcrosses were sown in one row each, and each F_2 in five rows. The row length was 2 m, and row-to-row and plant-to-plant distances were 45 and 15 cm, respectively. Data on 10 randomly selected plants in each row were recorded for six characters (Table 1).

Mather's scaling tests A, B and C were applied in all the 21 crosses for each character to judge the adequacy of the additive–dominance model. The crosses, where the additive–dominance model was inadequate, were subjected to genetic analysis following Hayman [7], using the six-parameter model.

RESULTS AND DISCUSSION

Considering the significant deviation of A, B and C scales from zero, 10 crosses for plant height and pod length, 11 crosses for pods/plant and seed weight, and 12 crosses for seeds/pod and yield/plant showed inadequacy of the additive–dominance model, and thus, presence of epistasis in these crosses was indicated. The estimates of epistatic interaction(s) along with additive and dominance gene effects for these interacting crosses for different characters through six-parameter model (Table 1) suggested that additive (d) gene effect was significantly positive for yield/plant in the cross GC 322 x B 5064, for seeds/pod in PI 280064 x B 5064 and PI 280064 x Bonneville, for plant height in PG 3 x T 163, and for pod length in Bonneville x T 163. This clearly indicated the significant contribution of additive gene effects in the inheritance of these characters in the respective crosses. However, the dominance (h) effect was predominant in the cross A 474-288 x T 163 for pods/plant and seeds/pod, and in GC 322 x B 5064 for pods/plant.

In general, almost all the hybrids had positive dominance effect for yield/plant, pods/plant, and plant height and their magnitude was also higher than that of d, suggesting greater importance of dominance effects in the expression of these characters. The significance of only duplicate type of epistasis for these characters further confirms the prevalence of dominance effects. These results are in agreement with those of Sharma et al. [2] for pods/plant, Venkateswarlu and Singh [8] and Srivastava et al. [9] for yield/plant, and Singh and Singh [10] for both characters in this crop. The contribution of additive effect for these characters was not unidirectional and in most crosses, it had reducing (–) effect, whereas, in other increasing (+) effects.

When the sign and significance of d and h gene effects were considered for seed weight, both types of gene action were mostly negative and significant, indicating that a diminishing

Table 1. Estimates of gene effects following six-parameter model for six characters in pea

Cross	m	d	h	i	j	l	Interaction
			Plant height				
PI 280064 x A 474–288	58.3**	3.4	6.6	3.4	–10.3	5.6	—
PI 280064 x B 5064	126.1**	–9.6	102.9**	34.6	5.7	–114.1*	Duplicate
GC 322 x A 474–288	37.3**	–4.4	30.4	35.5*	6.1	–55.5**	—
GC 322 x T 163	136.2**	–45.9**	19.9	–56.3	24.8	98.0*	—
A 474–288 x Bonneville	54.6**	–0.8	26.9**	18.9*	8.9	–14.7	—
A 474–288 x PG 3	52.9**	–10.7**	30.8*	20.2	–11.1	–5.9	—
B 5064 x PG 3	135.2**	–6.1	57.0	–21.8	–44.0*	–30.2	—
B 5064 x T 163	139.8**	–49.3**	–22.0	–82.6**	–38.8	–219.2**	—
Bonneville x T 163	162.5**	–37.4**	34.0	–43.9*	16.4	22.4	—
PG 3 x T 163	136.2**	67.3**	57.7	–18.8	–43.3	74.1	—
			Pods per plant				
PI 280064 x T 163	13.3**	–6.7*	19.4**	12.2	–7.8	–14.4	—
GC 322 x A 474–288	11.8**	–9.2**	14.8	13.2	–16.2*	–35.2	—
GC 322 x B 5064	16.1**	–1.1	10.2**	–0.4	–1.7	–10.2	—
GC 3222 x Bonneville	10.2**	–3.0	10.3	10.0	–3.3	–24.2	—
GC 322 x PG 3	11.7**	–4.1*	14.9**	12.8**	–6.2	–33.0**	Duplicate
A 474–288 x B 5064	16.6**	–12.2**	24.5**	6.5	–26.2**	–6.9	—
A 474–288 x PG 3	14.0**	–2.1	15.7	11.7	–4.3	–31.9*	—
A 474–288 x T 163	12.6**	–0.9	20.7*	17.0	3.4	–26.7	—
B 5064 x Bonneville	14.2**	6.1**	13.8	7.2	14.3**	–20.7*	—
B 5064 x T 163	14.8**	11.8**	25.6**	26.7**	30.4**	–68.1**	Duplicate
Bonneville x PG 3	11.2**	5.4**	26.7**	21.1**	10.3**	–35.8**	Duplicate
			Pod length				
PI 280064 x B 5064	5.2**	–0.02	–0.5	–0.3	–0.2	–0.03	—
PI 280064 x Bonneville	6.2**	–0.8**	0.5	0.3	0.2	–1.3*	—
PI 280064 x T 163	4.9**	0.5	1.8**	1.7**	0.8	–2.0	—
GC 322 x A 474–288	6.0**	0.4	–0.3	–0.2	0.3	–1.3	—
GC 322 x Bonneville	6.7**	–0.4**	–0.4	–0.8**	0.1	1.1	—
GC 322 xPG 3	6.5**	–0.7**	0.5	0.3	–0.8**	–1.6	—
GC 322 x T 163	5.7**	0.6	0.5	0.5	0.4	–2.0	—
A 474–288 x T 163	5.1**	0.2	1.7	1.2	0.2	–0.7	—
B 5064 x T 163	4.9**	0.3	0.6	0.3	0.7	1.2	—
Bonneville x T 163	5.7**	1.3**	1.1	0.9	1.0	–0.5	—

(Contd.)

Table 1 *(contd.)*

Cross	m	d	h	i	j	l	Interaction
Seeds per pod							
PI 280064 x A 474–288	4.2^{**}	1.2^{**}	–0.6	–0.6	1.0^{*}	0.2	—
PI 280064 x B 5064	3.7^{**}	1.0^{**}	–1.0	–1.1	–0.5	0.8	—
PI 280064 x Bonneville	4.5^{*}	0.6^{**}	–0.5	–0.5	0.3	–0.4	—
PI 280064 x T 163	3.6^{**}	1.3^{**}	1.1^{*}	1.3^{*}	1.4^{*}	–1.7	—
GC 322 x A 474–288	4.1^{**}	0.1	–0.7	–0.5	–0.7	–1.4	—
GC 322 x Bonneville	4.0^{**}	0.0	1.1	1.6^{*}	–0.5	-4.4^{**}	—
A 474–288 x B 5064	3.1^{**}	–0.1	–0.2	–0.5	-1.2^{*}	0.1	—
A 474–288 x Bonneville	3.4^{**}	0.3	–0.6	–0.5	1.1	1.0	—
A 474–288 x T 163	3.0^{**}	0.2	1.2^{*}	0.7	0.5	0.4	—
B 5064 x Bonneville	3.6^{**}	-0.7^{*}	–1.4	-1.7^{*}	0.1	1.5	—
B 5064 x T 163	2.8^{**}	0.2	1.1	0.5	1.4^{*}	–0.3	—
Bonneville x PG 3	3.7^{**}	0.8	–0.5	–0.7	1.1	0.6	—
25–seed weight							
PI 280064 x GC 322	3.4^{**}	0.7^{**}	-1.7^{**}	-1.5^{**}	–0.5	2.6^{**}	Duplicate
PI 280064 x B 5064	3.3^{**}	-0.3^{*}	-1.1^{**}	-1.1^{**}	–0.1	1.5^{**}	Duplicate
GC 322 x Bonneville	4.1^{**}	–0.4	–0.2	–0.1	–0.4	–1.1	—
GC 322 x PG 3	4.7^{**}	-0.9^{**}	–0.5	–0.8	–0.9	–0.1	—
GC 322 x T 163	4.3^{**}	-0.8^{**}	0.01	0.6^{**}	–0.4	-2.4^{**}	—
A474–288 x Bonneville	3.8^{**}	-0.7^{**}	–0.8	–0.2	–0.5	–1.4	—
A 474–288 x T 163	3.6^{**}	-1.1^{**}	1.8^{*}	1.7^{*}	–0.5	–0.9	—
B 5064 x Bonneville	4.3^{**}	–0.5	–0.1	–0.5	–0.4	–0.4	—
B 5064 x PG 3	4.0^{**}	0.03	-1.5^{**}	-1.6^{**}	1.2^{**}	3.4^{**}	Duplicate
B 5064 x T 163	3.8^{**}	-0.4^{*}	0.8	0.1	0.7	2.6	—
Bonneville x PG 3	5.1^{**}	0.3	–0.2	–0.6	1.2^{**}	–0.8	—
Yield per plant							
PI 280064 x A 474–288	5.1^{**}	1.0	1.7	–1.5	1.1	5.7	—
GC 322 x A 474–288	5.4^{**}	–2.8	8.5	7.9	–6.5	-19.7^{**}	—
GC 322 x B 5064	7.8^{**}	2.4^{*}	0.8	–3.4	3.4	–0.8	—
GC 322 x Bonneville	6.0^{**}	–1.8	6.5	7.1	–2.6	–19.3	—
GC 322 x PG 3	7.6^{**}	-3.6^{**}	7.4^{*}	6.3^{*}	-6.1^{*}	-20.7^{**}	Duplicate
GC 322 x T 163	7.5^{**}	-4.3^{**}	9.1^{*}	7.5^{*}	-5.4^{**}	-17.0^{**}	Duplicate
A 474–288 x B 5064	5.6^{**}	-3.6^{**}	8.5	2.1	-7.7^{**}	–0.5	—
A 474–288 x Bonneville	5.4^{**}	–0.8	2.7	3.1	0.4	-9.9^{*}	—
A 474–288 x T 163	4.5^{*}	–2.0	11.2^{**}	9.7^{**}	0.1	–11.4	—
B 5064 x Bonneville	6.9^{**}	0.3	2.3	–0.03	3.1	–5.8	—
B 5064 x T 163	5.5^{**}	3.0	12.8^{*}	13.0^{**}	10.7^{*}	-26.6^{**}	Duplicate
Bonneville x PG 3	7.4^{**}	3.6^{**}	9.1^{*}	6.0	7.1^{*}	-12.7^{*}	Duplicate

*, **Significant at $P = 0.05$ and 0.01, respectively. Only significant interactions given.

effect due to these types of gene effect could occur in the expression of this character. However, additive x dominance interaction in the cross Bonneville x PG 3, additive x additive and dominance x dominance interactions in PI 280064 x GC 322, PI 280064 x B 5064 and GC 322 x T 163, and all three digenic interactions in B 5064 x PG 3 were observed in the inheritance of this character.

Epistatic gene effects are known to contribute a sizeable part of variation in the character which showed higher estimates of dominance effects [11]. In the present study also, higher estimates of h for yield/plant were associated with significant epistatic interaction(s) in the respective crosses. However, in certain crosses, e.g. GC 322 x PG 3 and GC 322 x T 163 for yield/plant, and B 5064 x T 163 and Bonneville x PG 3 for pods/plant, all three types of gene effect (d, h, i, j and l) were significant in the expression of both the traits.

Considering the contribution of epistatic gene effects over the crosses for a character, the additive x additive (i) interaction had enhancing effect in the expression of pods/plant, pod length, and yield/plant, which confirms the earlier report of Singh [12]. But for seeds/pod, additive x dominance interaction (j) had slightly greater effect as compared to i and l.

Comparing the magnitude of the main gene actions (d and h) along with their digenic epistatic interactions (i, j and l), the l interaction was usually higher or at least at par with i and j for all the characters. However, the sign of l gene interaction was mostly negative, indicating their reducing effect in the expression of almost all the characters.

The gene interaction, i or any digenic complementary gene interaction is fixable and thus can be exploited effectively.

The characters that are controlled by additive and additive x additive gene effects (fixable) can be improved by pedigree method of selection, while heterosis breeding may be recommended for those under the control of dominance or dominance x dominance (nonfixable) gene effects. But for exploiting all three types of gene effects, reciprocal recurrent selection may be adopted for developing elite population for selection of high yielding lines in advanced generations.

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