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Short Communication

GENETIC ANALYSIS OF CERTAIN QUANTITATIVE CHARACTERS IN FIELDPEA

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Fieldpea (*Pisum sativum* L.) is an important pulse crop of India with an average productivity of 958 kg/ha as against the world average of 1631 kg/ha [1] Thus, the yield potential of fieldpea crop can be increased much above from the present level through efficient breeding. The choice of most suitable breeding procedure depends upon the nature of gene action involved in the control of characters of economic importance. Therefore, in the present study, an attempt has been made to understand the nature and magnitude of gene effects using generation mean analysis [2].

The material for the investigation comprised three crosses of fieldpea — HUP 2 × DPFP 62; Pant P 5 × DPFP 62 and PDPD 8 × HUDP 7. The experiment with six generations was raised in completely randomized block design with three replications keeping row to row and plant to plant distances of 30 and 10 cm, respectively. From each replication, data for plant height, number of primary branches, seeds per pod and 100 seed weight recorded on five randomly selected plants from parental and F1 generation, 10 plants from backcrosses and 20 plants from F2 generation for all the three crosses. Gene effects were estimated following Generation mean analysis [2].

At least one of the scales (A, B and C) was significant for all the characters in each of the crosses studied, except for primary branches and seeds/pod in HUP 2 × DPFP 62 and primary branches in Pant P 5 × DPFP 62. This indicates inadequacy of simple additive-dominance model and significant contribution of epistatic components in the expression of characters studied.

Both additive and non-additive gene effects were important for the expression of plant height in all the crosses with duplicate type of gene interaction (Table 1). Dominance (h) effect was significant for number of primary branches in the cross HUP 2 × DPFP 62. In PDPD 8 × HUDP 7, additive × additive (i), additive × dominance (j) and dominance × dominance (1) effects were significant for this character. Seeds per pod was found predominantly under the control of non-additive

Table 1. Estimates of gene effects for certain quantitative characters in three crosses of fieldpea

Cross	Genetic parameters						Type of epistasis
	m	d	h	i	j	l	
			Plant height				
HUP 2 × DPFP 62	128.3** ± 4.8	26.8** ± 6.4	86.9** ±23.9	51.2* ±23.1	7.5 ± 7.1	-7.0 ± 34.5	Duplicate
Pant P 5 ×DPFP 62	144.0** ± 5.4	-34.0** ± 6.0	95.0** ± 25.3	60.0* ± 24.7	-39.0** ± 7.0	-146.00**±34.1	Duplicate
PDPD 8 ×HUDP 7	48.6** ± 2.4	88.7** ± 4.2	293.7** ± 13.4	230.6**±12.7	85.6**+5.1	-241.8**±21.1	Duplicate
			Primary branches				
HUP 2 × DPFP 62	6.1** ± 1.4	0.3 ± 0.3	-6.5* ± 3.4	-	-	-	-
Pant P 5 × DPFP 62	3.9* ± 1.5	-0.4 ± 0.3	0.4 ± 3.7	-	-	-	-
PDPD 8 × HUDP 7	3.7** ± 0.3	-1.1** ± 0.3	0.7 ± 0.9	0.6 ± 0.8	-1.0* + 0.4	-5.0* ± 2.3	Duplicate
			No. of seeds/pod				
HUP 2 × DPFP 62	2.9* ± 1.4	0.2 ± 0.2	1.1 ± 3.5	-	-	-	-
Pant P 5 × DPFP 62	3.4** ± 0.2	0.4 ± 0.3	-2.2* ± 0.9	-2.0* ± 0.9	0.2 ± 0.3	2.0** ± 0.4	Duplicate
PDPD 8 × HUDP 7	4.1** ± 0.2	-0.8** ± 0.3	-4.8** ± 1.1	-3.3** ± 0.9	-1.5** ± 0.3	3.8* ± 1.6	Duplicate
			100 seed weight				
HUP 2 × DPFP 62	16.4** ± 0.9	-1.4 ± 0.8	-7.8 ± 4.1	-10.0* ± 4.0	0.9 ± 0.8	24.1** ± 5.0	Duplicate
Pant P 5 × DPFP 62	16.7** ± 0.5	0.9 ± 0.8	1.1 ± 2.9	-5.4 ± 2.8	1.7 ± 1.0	14.7** ± 4.4	Complementary
PDPD 8 × HUDP 7	17.9** ± 0.9	0.8 ± 1.0	-20.7** ± 4.1	-12.0** ±4.0	3.7** ± 1.1	28.9** ± 4.1	Duplicate

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

gene effect. However, additive (d) and additive × additive (i) components were also observed to be important for this character in two crosses. Non fixable gene effects were important for the expression of seed weight in all three crosses studied. The l type of gene interaction was positive and highly significant in all the crosses suggesting its greater role in the expression of this character.

The complexity of inheritance of these quantitative characters indicated by the presence of additive, dominance and epistatic effects have earlier been reported [3].

The present investigation suggested significant contribution of both fixable and non-fixable gene effects in the inheritance of various quantitative characters studied. Also, the duplicate type of epistasis found for most the characters studied, and therefore, simple selection procedure may not be advantageous. Intermating of early segregating generations or biparental matings followed by selection in later generations could be the most effective breeding method for improvement of these quantitative characters in fieldpea.

REFERENCES

1. B. Sharma and T. N. Khan. 1996. Creating higher genetic yield potential in Fieldpea (*Pisum sativum* L.). Indian J. Genet., **56**: 371-388.
2. B. I. Hayman. 1958. The separation of epistatic from additive and dominance variation in generation means. Heredity., **12**: 371-390.
3. B. B. Singh and D. P. Singh. 1994. Generation mean analysis for yield and yield components in pea. Indian J. Pulses Res., **7**: 108-111.