



## Generation mean analysis for grain yield related traits in field pea (*Pisum sativum* L.)

G. P. Dixit, Hasan Tanveer and Subhash Chandra

Indian Institute of Pulses Research, Kanpur 208 024

(Received: January 2006; Revised: May 2006; Accepted: May 2006)

Field pea (*Pisum sativum* L.) is an important *rabi* season legume occupying an area of 0.71 million ha with an annual production of 0.73 million tonnes. During the past two decades, a number of varieties with high yield potential increased field pea productivity and it is highest among the pulse crops grown in India. But, if we compare the productivity of this crop with that in other countries, there is enough scope to further enhance its production and productivity in India.

The precise knowledge of the nature of gene action for yield attributing traits help in the choice of an effective breeding strategy to accelerate the pace of genetic improvement of grain yield. The present investigation was, therefore, carried out with an objective of assessing the nature and magnitude of gene action for grain yield and its components in field pea through generation mean analysis. The experimental material comprised of three crosses in field pea viz., IPF 14 (Tall type, non tendril)  $\times$  HUDP 16 (Dwarf type, tendril), DDR 23 (Short duration, dwarf type)  $\times$  IPF 27 (long duration, tall type) and DDR 27 (short duration, dwarf type)  $\times$  IPF 27 (long duration, tall type) involving five parents of diverse pedigree, origin and agro-climatic adaptations. Five generations, namely  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$  and  $F_3$  of these three crosses were grown in a randomized block design with three replications during *rabi* 2004-05 under irrigated conditions. Data on 50% flowering, plant height, seeds per pod, pod length, 100 seed weight, number of pods per plant and grain yield per plant were recorded on 5 plants randomly selected in  $P_1$ ,  $P_2$  and  $F_1$  generations while 20 plants were chosen in  $F_2$  and  $F_3$  generations for recording data. The scaling test [1] was applied for all the 7 characters in three crosses to test the adequacy of the additive dominance model. The gene effects and interactions for each character were estimated after Hayman [2].

Out of two scaling test (C and D), at least one scale was found significant in all the three crosses for most of the characters studies. This indicated the

presence of digenic/epistatic interactions. The estimates of mean (m) was highly significant for all the characters in all the crosses. The additive component (d) was significant for plant height, 100 seed weight in all the crosses while 50% flowering, pod length and pods per plant were found significant in two crosses i.e., DDR-23  $\times$  IPF 27 and DDR 27  $\times$  IPF 27. Grain yield per plant was found significant in the cross IPF 14  $\times$  HUDP 16. This indicates the role of additive gene action in the expression of these traits and simple pure line selection will be useful for their improvement [3].

The estimate of dominance(h) component was significant for pod length, 100 seed weight and pods per plant in cross IPF 14  $\times$  HUDP 16 while seed per pod and pods per plant were found significant is cross DDR 23  $\times$  IPF 27. In cross DDR 27  $\times$  IPF 27, dominance component was found significant for 100 seed weight and grain yield per plant. The characters 100 seed weight, pods per plant and grain yield per plant were controlled by both additive and dominance gene action. It was found that dominance component was mostly higher in magnitude than additive component and was with negative sign in few cases. It indicates the decreased expression of traits by dominance and selection would be effective during later generations only.

Among the digenic interaction effects, dominance  $\times$  dominance(I) was significant for 100 seed weight and pod per plant in the cross IPF 14  $\times$  HUDP 16, plant height and yield per plant in cross DDR 23  $\times$  IPF 27; seeds per pod in cross DDR 27  $\times$  IPF 27. The additive  $\times$  additive (i) was significant for days to 50% flowering, pod length and 100 seed weight in the cross IPF 14  $\times$  HUDP 16; days to 50% flowering and plant height in cross DDR 23  $\times$  IPF 27; plant height in cross DDR 27  $\times$  IPF 27. Additive  $\times$  additive (i) type of interaction was found significant for 100 seed weight in the cross IPF 14  $\times$  HUDP 16, but with negative sign indicating little scope of improvement through simple selection.

**Table 1.** Estimates of genetic components in three crosses of field pea

Characters	m	d	h	l	i	Epis- tasis
<b>Cross : IPF 14 × HUDP 16</b>						
50% flowering	63.90** ±0.77	-0.70 1.28	1.30 ±2.60	8.90 ±8.00	-6.50** +3.10	-
Plant height (cm)	148.10** ±9.20	56.60** ±3.70	-57.30 ±33.60	137.20 ±94.40	46.20 ±30.90	D
Seed/pod	4.00** ±0.20	-0.10 ±0.20	0.20 ±0.80	-0.80 ±2.40	0.01 ±0.90	-
Pod length (cm)	5.20** ±0.20	0.20 ±0.20	2.90** ±0.80	-4.40 ±2.70	2.70** ±9.50	D
100 seed wt (g)	18.40** ±0.80	-0.90** ±0.30	-10.50** ±3.90	23.70** ±10.50	-12.60** ±3.40	D
Pod/plant	17.50** ±1.60	-1.30 +3.30	13.40** ±6.40	42.50** ±21.30	9.10 ±8.90	-
Grain yield/pl (g)	11.20** ±1.50	-5.20** ±2.02	3.50 ±6.50	20.00 ±21.30	-5.30 ±7.00	-
<b>Cross : DDR 23 × IPF 27</b>						
50% flowering	59.60** ±1.10	-4.20** ±0.86	-8.00 ±5.90	1.70 ±15.30	-11.66** ±5.18	D
Plant height (cm)	77.70** ±2.30	-23.10** ±2.60	10.60 ±10.40	-95.88* ±20.60	-32.54** ±10.20	D
Seed/pod	4.05** ±0.31	-0.10 ±0.38	1.57** ±0.75	-3.35 ±2.68	1.60 ±1.17	D
Pod length (cm)	4.45** ±0.25	-0.49** ±0.15	0.86 ±0.77	-1.46 ±2.37	0.31 ±0.80	D
100 seed wt (g)	18.85** ±1.26	-1.29** ±0.27	-2.56 ±3.65	1.30 ±11.95	-5.25 ±3.74	D
Pod/plant	17.31** ±2.56	-8.90** ±2.51	32.09** ±2.61	24.90 ±26.52	1.60 ±8.85	-
Grain yield/pl (g)	7.26** ±1.10	-1.32 ±1.40	7.30 ±4.47	30.70** ±13.21	-0.64 ±5.05	-
<b>Cross : DDR 27 × IPF 27</b>						
50% flowering	69.99** ±0.81	-4.20** ±0.86	4.03 ±3.29	-12.47 ±8.68	-3.36 ±3.20	D
Plant height (cm)	69.05** ±2.30	-22.80** ±2.50	12.10 ±9.10	-16.40 ±24.80	-42.10** ±9.20	D
Seed/pod	3.35** ±0.13	0.01 ±0.02	-0.88 ±0.66	5.90** ±1.70	-1.28 ±0.87	D
Pod length (cm)	4.36** ±0.12	0.49** ±0.15	-0.29 ±0.05	0.59 ±1.39	-0.68 ±0.52	D
100 seed wt (g)	20.08** ±0.95	-1.29** ±0.27	6.07** ±2.62	1.05 ±8.27	-2.09 ±2.79	-
Pod/plant	22.55** ±2.74	-6.40** ±2.59	11.26 ±10.52	2.47 ±33.44	-1.33 ±11.05	-
Grain yield/pl (g)	8.36** ±1.04	-0.67 ±1.00	15.74** ±7.05	4.35 ±26.76	3.47 ±7.87	-

D = Duplicate type of epistasis

The above informations revealed that in addition to additive and dominance gene effects, the epistatic

effects are also important in the expression of the traits studied. Importance of both additive and non-additive gene effects was also reported by Tyagi and Srivastava [4], Singh and Singh [5].

The results of dominance (h) and dominance × dominance (l) type of interaction revealed that duplicate type of epistasis was prevalent for days to 50% flowering, plant height, no. of seeds/pod, pod length and 100 seed weight in the cross DDR 23 × IPF 27; days to 50% flowering, plant height, no. of seeds/pod and pod length in the cross DDR 27 × IPF 27; plant height, pod length and 100 seed wt. in the cross IPF 14 × HUDP 16. This will decrease variation in  $F_2$  and subsequent generations, and will also hinder the pace of progress through selection. Kumar and Das [6], Tyagi and Srivastava [4] and Sharma and Rastogi [7] also reported duplicate epistasis for most of the traits in field pea.

The present study revealed the importance of additive, dominance and epistatic gene effects in the inheritance of various characters studied. In this situation reciprocal recurrent selection is likely to be useful for the effective utilization of both additive and non-additive gene effects simultaneously. It will also lead towards an increased variability in later generations for effective selection by maintaining considerable heterozygosity through mating of selected plants in early segregating generations.

## References

1. Cavalli L. L. 1952. Analysis of linkage in quantitative inheritance. In: Quantitative inheritance (eds. E. C. R. Rieve and C. H. Waddington) HMSO, London: pp. 135-144.
2. Hayman B. I. 1958. The separation of epistasis from additive and dominance variation in generation mean, *Heredity*, 12: 371-391.
3. Singh B. P. and Joshi S. S. 1982. Gene mechanism for inheritance of some yield contributing characters in fieldpea. *Indian J. of Agric. Sci.*, 52: 495-499.
4. Tyagi M. K. and Srivastava C. P. 2001. Detection of epistasis and analysis of gene effects for yield and related traits in pea. *Indian J. of Pulses Res.*, 14: 20-26.
5. Singh M. N. and Singh R. B. 1990. Estimation of additive, dominance and digenic epistatic interaction effects for certain yield characters in pea. *Indian J. Genet.*, 50: 348-353.
6. Kumar H. and Das K. 1975. Analysis of gene effects and heterosis in certain productive traits in pea. *Indian J. of Agric. Sci.*, 45: 301-307.
7. Sharma M. K. and Rastogi K. B. 2001. Analysis of gene effects for agronomic and maturity characters in pea (*Pisum sativum* L.). *Legume Res.*, 24: 32-35.