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Research Article

Gene action for seed yield and its attributing traits in fieldpea (*Pisum sativum* L.)

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Abstract
Generation mean analyses were performed to estimate the nature and magnitude of gene action for yield and its component traits in six generations (P_1, P_2, F_1, F_2, B_1 and B_2) obtained from two crosses (GP 02/1108 x HFP 920 and GP 02/1108 x HFP 9907B). A considerable amount of variation was observed among parents and different generations. Individual Scaling and Joint Scaling test depicted failure of additive-dominance model for all the characters except the number of primary branches in both crosses. Six parameter model revealed a remarkable amount of fixable component though non fixable component was on a higher side in the majority of characters in both the crosses. Sufficient fixable component for the traits envisaged practising pedigree method. However, to exploit additive as well as non-additive gene effects simultaneously breeding methods like a selection from delayed generations and the bi-parental mating approach are advocated.

Keywords: Gene action, Generation means analysis, Fieldpea

INTRODUCTION

Fieldpea (*Phaseolus vulgaris* L.) is one of the six major pulse crops cultivated globally and is the third most widely grown food legume worldwide (Tyagi *et al.,* 2012; Yadav and Ravika, 2014). It is a nutrient (protein, vitamin and minerals) and protein rich (19.6%) crop, mostly used for green and dry seeds. Being a leguminous crop it ameliorates the soil health properties (Dhulgande *et al*., 2011). Seed yield in fieldpea is a complex quantitative character contributed by many other morphological as well as physiological traits. The area under fieldpea has increased but its productivity has not achieved much improvement (Sood and Kalia, 2006). There is enough scope for further enhancement of production and productivity of fieldpea in India.

The dwarf varieties have more tendrils which are modified leaves, enables the plant to stand upright (Grains Research and Development Corporation, 2018). Dwarf/ semi-dwarf genotypes combined with semi-leafless peas appear to be the most ideal plant type that would provide better tolerance to lodging and yields high (Singh and Srivastava, 2015). Lodging enhances the canopy microclimate for fungal disease development, reduces the photosynthetic ability of the plants, reduces harvest efficiency and increases harvest cost. Lodging also deteriorates the quality of seeds and pods. For these reasons, lodging can cause up to 74% yield loss in some dry pea cultivars (Amelin and Parakhin, 2003). So breeding for lodging resistance along with high yield is the most important criteria for fieldpea breeding programs. This envisages detailed genetic study of plant height, intermodal distance and number of nodes per plant because these are of paramount importance along with other conventional yield contributing traits.

The direct selection on the basis of phenotype and without considering the genotype of plant may not provide true results. Thus the knowledge of genetic architecture of genotype involving magnitude and nature of gene action of yield and its component traits is must for a breeder to choose the specific breeding and selection strategy for the development of superior and desired genotype with a higher success rate (Shashikumar *et al*., 2010). Generation mean analysis is one of the best methods which detects and measures the epistasis accurately (Sharmila *et al*., 2007).

Therefore, the present study was aimed to generate information on the nature of gene action in fieldpea to decide the efficient selection methods for the improvement of genotypes through generation mean analysis for yield and its component traits.

MATERIALS AND METHODS

Three genetically diverse parents *viz*., GP 02/1108 (dwarf), HFP 920 (medium) and HFP 9907B (tall) were utilized to generate six generations P_1, P_2, F_1, F_2, B_1 and B_2 of two crosses *i.e.* GP 02/1108 x HFP 920 and GP 02/1108 x HFP 9907B to study the genetics of seed yield and other morpho phonological traits of fieldpea. The respective F_1 generation of both the crosses was generated during the *rabi* 2016-17. In the subsequent year, the F_1's were crossed with respective parents to obtain back crosses and selfed to generate F_2's during *rabi* 2017-18. The experiment was laid out in randomized block design (RBD) with three replications during *rabi* season of 2018-19. The non segregating generations (parents and F_1's) were sown in a single row of 4 m length. Each back cross progenies was sown in two rows of 4 m length and each F_2 progenies in four rows of 4 m length. The spacing of 30 x10 cm was followed. The recommended package of practices was followed to raise a good crop. Observations were recorded on five randomly selected plants in non segregating generations (parents and F_1's), 20 randomly selected plants in each back cross and 50 plants in both the F_2's of both the crosses in all the three replications for the characters *viz*., days to flowering, days to maturity, the number of primary branches per plant, the number of secondary branches per plant, the number of nodes per plant, inter-nodal distance (cm), height of first reproductive node (cm), plant height (cm), the number of pods per plant, the number of seeds per pod, biological yield per plant (g), 100-seed weight (g), seed yield per plant (g) and harvest index (%). The individual scaling tests A, B, C and D were calculated as per the method suggested by Hayman and Mather (1955). To test the adequacy of three parameters model, Joint Scaling test was applied. The data were subjected to six parameters model (Jinks and Jones, 1958) upon failure of three parameters model.

RESULTS AND DISCUSSION

Generation mean analysis revealed each population had various nature of gene action. Therefore, the selection of breeding methods for each population was effective to improve the trait (Sathya *et al*., 2021). A considerable amount of variation was envisaged among parents and different generations for yield and various morpho-phenological traits (**Table 1**). Heterosis was not observed in F_1's. The F_1's either exhibited complete dominance or had intermediate values of the parents for almost all the characters in both the crosses. F_2 progenies of both the crosses showed reduced expression of almost all the characters observed. The mean performances of back crosses generations (B_1 and B_2) tended towards their recurrent parent for more or less all the traits in both the crosses. Such trends in the present study are in agreement with Bhardwaj and Vikram (2004), Dixit *et al.* (2006), Gomez and Ligarreto (2012), Sharma *et al.* (2013), Kosev (2015) and Parihar *et al.* (2016).

Components of mean *viz*., constant mean (m), additive gene effects (d) and dominance gene effects (h) were estimated by using generation means. The first three parameter model was used and wherever it failed, six parameter models was applied for estimation of epistasis. On simple additive-dominance model the weighted least square estimates of mean (m), additive (d) and dominance (h) effects were obtained (**Table 2**). The additive-dominance model was found to be adequate for the number of primary branches per plant in both the crosses. For all the other characters the additive-dominance model was found to be inadequate. This has also been reported in many characters by different fieldpea workers *viz*., Bhardwaj and Vikram (2004), Narayan (2006), Sharma *et al*. (2013) and Parihar *et al.* (2016).

The perusal of **Table 3** revealed the significance of additive gene effects (d) though mostly lesser in magnitude than dominance gene effects (h) for more or less all the traits except days to maturity in GP 02/1108 x HFP 9907B, 100-seed weight in both the crosses and the number of pods per plant in GP 02/1108 x HFP 920 suggested that the additive gene effects played important role in the inheritance of all these attributes and simple selection would be adequate to improve them.

The importance of additive gene effects in fieldpea was also reported by many workers for various characters and confirmed the preponderance of non-additive gene action in the inheritance of all these characters *viz.,* pod yield, plant height and days to first flowering (Gudadinni *et al*., 2017) and grain yield and yield associated traits (Nageshwar *et al*., 2020).

On the basis of six-parameter model, the epistatic gene effects were found for most of the characters, but the type and magnitude of epistatic effects varied for a character to character and cross to cross. Considering individual digenetic epistatic effects, additive x additive (i) effects appeared to be significant for days to flowering, height of first reproductive node, plant height, 100-seed weight, the number of pods per plant and seed yield per plant in cross GP 02/1108 x HFP 920; days to maturity and the number of secondary branches per plant in cross GP 02/1108 x

Table 1. Mean performance of six generations of two crosses for different morpho-phenological characters and seed yield

S. No.	Character	Cross	P_1	P_2	F_1	F_2	B_1	B_2
1.	Days to flowering	GP 02/1108 x HFP 920	63.00 ± 0.58	79.80 ± 0.34	76.13 ± 0.41	72.58 ± 0.84	71.88 ± 0.95	77.80 ± 0.89
		GP 02/1108 x HFP 9907B	67.27 ±0.36	78.93 ±0.39	73.87 ±0.71	71.14 ±1.06	69.85 ±1.09	77.23 ±1.29
2.	Days to maturity	GP 02/1108 x HFP 920	124.70 ±0.49	128.47 ± 0.33	126.67 ± 0.22	126.15 ±0.45	124.88 ± 0.46	128.45 ± 0.57
		GP 02/1108 x HFP 9907B	124.07 ±0.32	128.80 ±0.38	126.00 ±0.34	127.74 ±0.41	126.32 ±0.52	127.07 ±0.59
3.	Number of primary branches per plant	GP 02/1108 x HFP 920	2.07 ±0.26	2.40 ±0.28	2.50 ±0.33	2.53 ±0.11	2.20 ±0.16	2.53 ±0.19
		GP 02/1108 x HFP 9907B	2.27 ±0.21	2.40 ±0.23	2.33 ±0.22	2.30 ±0.09	2.20 ±0.17	2.30 ±0.12
4.	Number of secondary branches per plant	GP 02/1108 x HFP 920	3.13 ± 0.27	2.00 ± 0.24	3.00 ± 0.45	2.46 ± 0.08	2.87 ± 0.15	2.32 ± 0.15
		GP 02/1108 x HFP 9907B	3.33 ±0.22	2.40 ±0.23	2.87 ±0.33	2.23 ±0.10	2.72 ±0.15	2.30 ±0.15
5	Number of nodes per plant	GP 02/1108 x HFP 920	21.47 ± 0.98	12.87 ±0.69	18.13 ±0.47	15.71 ±0.37	16.05 ±0.65	14.17 ±0.36
		GP 02/1108 x HFP 9907B	21.00 ±0.61	15.26 ±0.35	18.13 ±0.37	17.43 ±0.40	17.03 ±0.58	15.33 ±0.61
6.	Inter-nodal distance (cm)	GP 02/1108 x HFP 920	3.07 ±0.31	8.93 ±0.43	8.27 ±0.34	4.99 ±0.22	4.03 ±0.35	5.24 ±0.30
		GP 02/1108 x HFP 9907B	3.23 ±0.26	12.60 ±0.37	13.27 ±0.43	9.14 ±0.46	5.91 ±0.67	12.23 ±0.56
7.	Height of first reproductive node (cm)	GP 02/1108 x HFP 920	28.13 ±0.10	55.93 ±1.06	35.13 ±0.63	31.17 ±1.06	26.43 ±1.26	29.48 ±1.46
		GP 02/1108 x HFP 9907B	24.80 ±0.35	71.53 ±1.25	69.06 ±1.66	63.15 ±4.15	40.82 ±3.44	84.52 ±6.59
8.	Plant height (cm)	GP 02/1108 x HFP 920	52.67 ±0.97	86.60 ±3.87	87.87 ±3.20	69.44 ±2.51	56.77 ±3.13	72.50 ±3.35
		GP 02/1108 x HFP 9907B	50.27 ±1.21	193.53 ±3.92	195.93 ±5.86	150.45 ±7.83	96.38 ±9.67	209.33 ±0.42
9.	100-seed weight (g)	GP 02/1108 x HFP 920	14.09 ±0.13	16.97 ±0.22	17.78 ±0.34	15.08 ±0.34	15.35 ±0.44	16.03 ±0.56
		GP 02/1108 x HFP 9907B	14.12 ±0.37	17.76 ±0.37	17.73 ±0.48	16.06 ±0.37	16.64 ±0.47	16.73 ±0.27
10.	Number of pods per plant	GP 02/1108 x HFP 920	26.00 ±0.29	24.07 ±0.90	29.07 ±0.85	23.79 ±1.05	26.35 ±1.42	25.17 ±1.27
		GP 02/1108 x HFP 9907B	26.53 ±0.56	23.33 ±0.89	28.00 ±0.51	23.21 ±0.86	24.97 ±1.02	23.13 ±0.72
11.	Number of seeds per pod	GP 02/1108 x HFP 920	4.40 ±0.28	5.40 ±0.23	5.47 ±0.23	4.53 ±0.17	4.60 ±0.22	4.95 ±0.26
		GP 02/1108 x HFP 9907B	4.07 ±0.39	5.73 ±0.26	6.07 ±0.39	5.03 ±0.14	4.25 ±0.23	5.27 ±0.22
12.	Biological yield per plant (g)	GP 02/1108 x HFP 920	25.14 ±1.19	36.28 ±1.61	37.30 ±0.40	36.00 ±2.09	29.79 ±1.60	35.18 ±2.55
		GP 02/1108 x HFP 9907B	26.18 ±0.72	42.63 ±0.50	43.88 ±1.22	37.27 ±1.80	31.23 ±2.02	34.67 ±2.14
13.	Seed yield per plant (g)	GP 02/1108 x HFP 920	13.06 ±0.38	18.88 ±0.37	19.33 ±0.32	17.42 ±0.78	16.36 ±0.80	18.13 ±1.06
		GP 02/1108 x HFP 9907B	13.81 ±0.44	17.28 ±0.65	18.07 ±0.66	17.18 ±0.71	16.40 ±0.92	17.44 ±0.92
14.	Harvest Index (%)	GP 02/1108 x HFP 920	60.41 ±2.66	49.72 ±2.39	54.96 ±0.90	49.12 ±1.31	56.09 ±2.19	53.28 ±2.31
		GP 02/1108 x HFP 9907B	60.65 ±2.71	40.56 ±1.66	48.26 ±2.24	41.42 ±1.48	53.59 ±1.84	51.21 ±1.72

Table 2. Individual scaling test and estimates of components of generation means (three parameter model) in two fieldpea crosses for seed yield and its attributes

S. No.	Character	Cross	A	B	C	D	m	d	h	χ2
1.	Days to flowering	GP02/1108 x HFP 920	-4.63** ±1.17	0.33 ±1.08	4.72* ±2.03	-4.51** ±1.23	71.50 ±0.18	8.23** ±0.19	4.67** ±0.31	23.05**
		GP02/1108 x HFP 9907B	-0.57 ±1.34	-3.67* ±1.56	-2.63 ±2.60	-0.80 ±1.56	73.15 ±0.15	5.87** ±0.15	-0.92* ±0.41	6.17
2.	Days to maturity	GP02/1108 x HFP 920	1.63** ±0.61	-1.77* ±0.70	1.92 ±1.13	-1.03 ±0.67	126.43 ±0.15	2.13** ±0.15	0.19 ±0.21	16.21**
		GP02/1108 x HFP 9907B	-2.57** 0.66	6.07** 0.75	0.67 1.07	2.08** 0.66	126.66 0.13	2.26** 0.14	-0.18 0.24	45.55**
3.	Number of primary branch per plant	GP02/1108 x HFP 920	0.27 ±0.31	-0.07 ±0.33	-0.44 ±0.51	0.32 ±0.18	2.25 ±0.09	0.24** ± 0.09	0.39* ± 0.20	4.09
		GP02/1108 x HFP 9907B	0.20 ±0.26	0.13 ±0.23	0.13 ±0.37	0.10 ±0.16	2.31 ±0.07	0.19** ±0.07	0.43** ±0.15	0.79
4.	Number of secondary branches per plant	GP02/1108 x HFP 920	1.00** ±0.35	0.37** ±0.14	0.89** ±0.28	0.29** ±0.11	2.29 ±0.01	-0.23** ±0.08	0.293 ±0.20	9.63*
		GP02/1108 x HFP 9907B	0.77** ±0.28	0.66* ±0.29	2.533** ±0.49	-0.55** ±0.17	2.71 ±0.08	-0.46** ±0.07	-0.54 ±0.02	29.70**
5	Number of nodes per plant	GP02/1108 x HFP 920	7.50** ±0.98	2.66** ±0.64	7.75** ±1.22	1.21* 0.60	15.27 0.26	-3.37** 0.26	1.75* 0.43	75.72**
		GP02/1108 x HFP 9907B	5.07** ±0.79	2.73** ±0.77	2.83** ±1.10	2.49** ±0.67	17.53 ±0.18	-2.45** ±0.18	0.02 ±0.29	51.04**
6.	Inter-nodal distance (cm)	GP02/1108 x HFP 920	1.27** ±0.49	6.72** ±0.47	6.56** ±0.71	0.71 ±0.37	5.91 ±0.13	2.99** ±0.13	-1.06** ±0.24	218.98**
		GP02/1108 x HFP 9907B	4.68** ±0.82	2.40 ±0.73	5.79** ±1.21	0.15 ±0.74	7.71 ±0.13	4.70** ±0.13	4.72** ±0.26	48.73**
7.	Height of first reproductive node (cm)	GP02/1108 x HFP 920	10.40** ±1.61	32.10** ±1.84	29.67** ±2.70	6.42** ±1.66	38.82 ±0.38	12.65** ±0.39	-6.03** ±0.55	404.11**
		GP02/1108 x HFP 9907B	12.23** ±4.09	-28.43** ±7.70	-18.15 ±9.79	0.97 ±6.43	48.33 ±0.37	23.55** ±0.37	20.82** ±0.99	26.76**
8.	Plant height (cm)	GP02/1108 x HFP 920	17.00** ±4.01	19.46** ±4.82	17.24* ±7.24	9.61* ±3.92	67.64 ±1.00	15.26** ±1.00	4.59 ±1.98	28.72**
		GP02/1108 x HFP 9907B	56.43** ±11.69	-26.20* ±12.70	39.85* ±19.45	-34.81** ±12.21	122.07 ±1.16	72.05** ±1.16	72.33** ±3.28	32.62**
9.	100-seed weight (g)	GP02/1108 x HFP 920	2.18** ±0.55	2.68** ±0.68	7.31** ±0.90	-1.22** ±0.57	15. 90 ±0.07	0.88** ±0.07	0.95** ±0.19	79.69**
		GP02/1108 x HFP 9907B	-0.43 0.65	1.82** 0.46	3.89** 1.05	-1.25* 0.53	16.16 0.13	1.01** 0.13	0.84** 0.27	26.37**
10.	Number of pods per plant	GP02/1108 x HFP 920	2.37 ±1.72	2.80 ±1.63	13.05** ±2.67	-3.94* ±1.64	24.70 0.26	-1.24 0.26	3.29 0.54	25.21**
		GP02/1108 x HFP 9907B	4.60** ±1.26	5.07** ±1.02	13.04** ±2.17	-1.69 ±1.23	23.90 ±0.27	-2.16** ±0.27	3.19** ±0.42	59.59**
11.	Number of seeds per pods	GP02/1108 x HFP 920	0.67* ±0.33	0.97** ±0.36	2.63** ±0.5163	-0.50 ±0.2765	4.66 ±0.0961	0.52** ±0.0961	0.41* ±0.17	27.80**
		GP02/1108 x HFP 9907B	1.63** ±0.42	1.27** ±0.37	1.80** ±0.62	0.55* ±0.24	4.64 ±0.11	0.95** ±0.12	0.74** ±0.24	20.36**
12.	Biological yield per plant (g)	GP02/1108 x HFP 920	2.85 ±1.98	3.22** ±1.09	-11.96* ±4.99	9.02* ±2.98	30.70 ±0.53	5.70** ±0.54	6.59** ±0.59	9.65*
		GP02/1108 x HFP 9907B	7.61** ±2.47	17.16** ±2.58	8.91* ±3.41	8.63** ±2.68	34.19 ±0.25	8.22** ±0.25	7.77** ±0.69	51.30**
13.	Seed yield per plant (g)	GP02/1108 x HFP 920	2.98** ±0.96	4.24** ±1.25	5.52* ±1.87	4.35** ±1.18	16.44 ±1.15	5.43** ±1.15	4.15** ±1.24	1.09
		GP02/1108 x HFP 9907B	4.08** ±1.16	5.87** ±1.19	5.52** ±1.86	6.12** ±1.11	16.50 ±1.21	3.74** ±1.21	4.42** ±1.42	0.97
14.	Harvest Index (%)	GP02/1108 x HFP 920	-9.81** ±3.00	-6.87* ±3.04	13.60** ±3.81	-11.14** ±2.37	54.12 ±0.80	-4.73** ±0.90	-4.39** ±1.05	24.94**
		GP02/1108 x HFP 9907B	-8.12** ±2.94	-20.45** ±2.56	-8.98 ±4.66	-8.29** ±2.24	51.82 ±0.79	-8.51** ±0.76	-5.59** ±1.50	65.15**

*Significance at p = 0.05 and **Significance at p = 0.01

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Table 3. Estimates of components of generation means (six parameter model) in two fieldpea crosses for seed yield and its attributes

S.No.	Character	Cross	m	d	h	I	j	l
1.	Days to flowering	GP02/1108 x HFP 920	72.58 ±0.48	-5.91** ±0.75	13.75** ±2.47	9.02** ±2.45	4.96** ±1.55	-13.32** ±3.64
		GP02/1108 x HFP 9907B	73.14 ±0.61	-7.38** ±0.97	0.37 ±3.16	1.61 ±3.31	-7.10** ±1.97	-9.84** ±3.69
2.	Days to maturity	GP 02/1108 x HFP 920	126.15 ±0.26	-3.57** ±0.42	2.12 ±1.37	2.05 ±1.35	-3.40** ±0.91	-2.19 ±2.04
		GP 02/1108 x HFP 9907B	127.74 ±0.24	-0.75 ±0.46	-4.63** ±1.34	-4.19** ±1.32	3.23** ±0.96	2.29 ±2.12
3.	Number of secondary branches per plant	GP 02/1108 x HFP 920	2.46 ±0.04	0.45** ±0.12	0.16 ±0.42	-0.47 ±0.31	-0.63 ±0.32	1.84** ±0.76
		GP 02/1108 x HFP 9907B	2.23 ±0.06	0.42** ±0.12	1.10** ±0.40	1.10** ±0.33	-0.10 ±0.30	0.33 ±0.68
4.	Number of nodes per plant	GP 02/1108 x HFP 920	15.71 ±0.21	1.88** ±0.43	-1.45 ±1.28	-2.42* ±0.20	-4.83** ±1.10	12.59** ±2.11
		GP 02/1108 x HFP 9907B	17.43 ±0.23	1.70** ±0.49	-4.97** ±1.38	-4.97** ±1.35	-2.33* ±1.06	12.77** ±2.24
5.	Inter-nodal distance (cm)	GP 02/1108 x HFP 920	4.99 ±0.13	-1.21** ±0.27	-2.16** ±0.78	-1.43 ±0.74	5.45** ±0.62	9.41** ±1.29
		GP 02/1108 x HFP 9907B	9.14 ±0.27	-6.33** ±0.50	5.06** ±1.49	-0.29 ±1.47	-3.28** ±1.04	6.37** ±2.35
6.	Height of first reproductive node (cm)	GP 02/1108 x HFP 920	31.17 ±0.61	-3.05** ±1.12	-19.73** ±3.37	-12.83** ±3.32	21.70** ±2.38	55.33** ±5.22
		GP 02/1108 x HFP 9907B	63.15 ±2.39	-43.70** ±4.29	18.95** ±6.90	-1.95 ±12.86	-40.66** ±8.62	-14.25 ±19.77
7.	Plant height (cm)	GP 02/1108 x HFP 920	69.44 ±1.45	-15.73** ±2.64	-10.99 ±8.13	-19.23* ±7.84	2.47 ±5.76	55.69** ±12.81
		GP 02/1108 x HFP 9907B	150.45 ±4.52	-112.95* ±8.21	86.65** ±24.68	9.62 ±24.42	-82.63** ±16.58	20.61 ±38.16
8.	100-seed weight (g)	GP 02/1108 x HFP 920	15.08 ±0.20	-0.69 ±0.41	4.20** ±1.16	2.44* ±1.14	3.50** ±0.83	2.42 ±1.87
		GP 02/1108 x HFP 9907B	16.06 ±0.21	-0.01 ±0.31	3.88** ±1.10	2.49* ±1.06	2.24** ±0.69	-1.10 ±1.64
9.	Number of pods per plant	GP 02/1108 x HFP 920	23.79 ±0.61	1.18 ±1.02	11.92** ±3.32	7.89* ±3.27	8.43** ±2.27	-2.72 ±5.15
		GP 02/1108 x HFP 9907B	23.21 ±0.50	1.83* ±0.72	6.44* ±2.49	3.37 ±2.46	4.87** ±1.56	6.29 ±3.60
10.	Number of seeds per pods	GP 02/1108 x HFP 920	4.53 ±0.10	-0.35 ±0.20	1.56** ±0.58	1.99** ±0.55	0.30 ±0.45	0.64 ±0.94
		GP 02/1108 x HFP 9907B	5.03 ±0.08	-1.02** ±0.18	2.07** ±0.55	-1.10* ±0.48	-0.37 ±0.46	4.00** ±0.96
11.	Biological yield per plant (g)	GP 02/1108 x HFP 920	36.99 ±1.21	-5.39** ±1.74	-17.44** ±5.98	-18.04** ±5.95	0.37 ±3.66	24.11** ±8.56
		GP 02/1108 x HFP 9907B	37.27 ±1.04	-3.44* ±1.70	-17.78** ±5.42	-17.26** ±5.36	9.55** ±3.43	42.02** ±8.10
12.	Seed yield per plant (g)	GP 02/1108 x HFP 920	17.42 ±0.45	-1.78* ±0.76	7.46** ±2.38	-7.70** ±2.37	-5.74** ±1.56	10.92** ±3.59
		GP 02/1108 x HFP 9907B	17.18 ±0.41	-1.84* ±0.75	6.49** ±2.26	-1.04 ±2.22	-0.61 ±1.57	9.59** ±3.54
13.	Harvest Index (%)	GP 02/1108 x HFP 920	49.12 ±0.76	3.82* ±1.84	17.17** ±4.89	22.28** ±4.76	-5.06 ±4.21	-30.96** ±8.27
		GP 02/1108 x HFP 9907B	48.26 ±0.85	3.38* ±1.45	13.39** ±4.76	16.59** ±4.48	-15.33** ±3.44	-42.16** ±7.45

*Significance at p = 0.05 and **Significance at p = 0.01

HFP 9907B and the number of pods per plant, the number of seeds per pod, biological yield per plant and harvest index in both the crosses. Since additive and additive x additive genetic variances are more important in the inheritance and improvement of quantitative characters in a crop like fieldpea it seems plausible to concentrate genes with complementary effects through hybridization between diverse material and subsequent selection.

The digenetic epistatic effect additive x dominance (j) effects were observed to be significant for seed yield per plant in cross GP 02/1108 x HFP 920; plant height, biological yield per plant and harvest index in cross GP 02/1108 x HFP 9907B and days to flowering, days to maturity, the number of nodes per plant, inter-nodal distance, height of first reproductive node, 100-seed weight and the number of pods per plant in both the crosses.

The dominance x dominance (l) effects were found significant for the number of secondary branches per plant, height of first reproductive node and plant height in cross GP 02/1108 x HFP 920; the number of seeds per pod in cross GP 02/1108 x HFP 9907B and days to flowering, the number of nodes per plant, inter-nodal distance, biological yield per plant, seed yield per plant and harvest index in both the crosses.

Compare of estimates obtained from the three parameter model with that of six-parameter model revealed that the estimates of (d) and (h) from three parameter model were unquestionably biased due to the presence of epistasis. This might have led to the changes both in terms of magnitude and direction of (h) and magnitude of (d) in six parameter model. The estimate (h) and (l) had an opposite sign in days to flowering, inter-nodal distance, plant height and harvest index in cross GP 02/1108 x HFP 920; the number of nodes per plant in cross GP 02/1108 x HFP 9907B and biological yield per plant in both the crosses which revealed a predominance of duplicate types of gene effects. Such epistatic effects and duplicate type of epistasis for various characters were also reported by Bhardwaj and Vikram (2004), Narayan (2006), Sharma *et al*. (2013) and Parihar *et al.* (2016). For such genetic architecture, it is suggested that the selection from delayed generations and subsequent inter mating might be a useful approach to recover or develop the desirable transgressive segregants in fieldpea.

Plant height in fieldpea, as observed in this study and reported by many workers is a quantitative character controlled by different types of allelic and non-allelic interaction, is the single most important character as it influences a number of other morpho-phenological characters. A bird eye view of the data on mean performance for F_1's, F_2's depicted increased performance in seed yield and harvest index where, the dwarf parent GP 02/1108 was involved. Genotype GP 02/1108 resulted into reduction in plant height, internodal distance and biological yield and an increased the number of primary branches per plant, the number of secondary branches per plant and the number of pods per plant. It was evident that genetic variability for the morpho-phenological traits related favourably to grain yield could be fostered through the recombination and inclusion of the dwarfing sources in crosses.

The use of dwarf genotype in hybridization resulted into reduction in plant height, internodal distance and biological yield and increased the number of primary branches per plant, the number of secondary branches per plant and the number of pods per plant. Therefore, the genetic variability for the various traits related favourably to grain yield could be fostered through recombination breeding. Enough fixable components were prevalent in both the crosses. For the traits exhibiting high fixable components and favorable association with seed yield pedigree method will be fruitful. In order to exploit additive as well as non-additive gene effects simultaneously breeding methods like a selection from delayed generations and biparental mating approach or diallel selective mating should be practised.

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