

GENE ACTION STUDIES FOR SEED YIELD AND OTHER QUANTATIVE CHARACTERS IN FIELD PEA (*PISUM SATIVUM* L.)

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Abstract: In the present study, generation mean analysis were undertaken to estimate the nature and magnitude of gene action for yield and its component traits in two crosses of field pea viz IM 9214-10 X Rachna (C-1) and IM 9214-10 X Ambika (C-2). Scaling tests revealed the presence of one or more kinds of epistatic effects for almost all the agromorphological traits. The selection of elite lines from delayed generations and subsequent inter mating might be useful approach to recover/ develop the high yielding field pea lines. The elite lines recovered from crosses IM 9214-10 X Rachna might be superior in terms of early maturity with more number of clusters per plant and seed yield per plant. Likewise, crosses *i.e.* IM 9214-10 X Ambika for plant height, number of clusters per plant and seed yield per plant; may give opportunity to isolate transgressive segregants in advanced generations.

Keywords: Epistasis, GMA, Gene effect, Inheritance, Field pea, Transgressive segregants

INTRODUCTION

Field pea is an important rabi season legume. Among the major pulse crops grown in India, field pea or dry pea (*Pisum sativum* L.) belongs to family leguminosae and sub family Papilionaceae is considered to be the native of Ethiopia, the Mediterranean and Central Asia. It is a nutritious and protein rich (19.6%) crop, mostly used for green and dry seeds. Hence, pea is categorized as vegetable type and field pea. The area of field pea in India is about 0.76 million hectares with annual production of 0.84 million tones and productivity of 1100 kg/ha. During the past two decades, a number of varieties with high yield potential increased field pea productivity and it is highest among pulse crops grown in India. But if we compare the productivity of this crop with that in other countries, there is enough scope to future enhance its production and productivity in India Dixit *et al.* (2006).

The farmers of the state are small and marginal hence, there is urgent need to give them varieties which yield better even under average agronomic management. Dwarf type has greater potential under one or two irrigations. Hence, there is need to combine together desirable gene(s) from tall and dwarf types for evolving high yielding, disease resistant and widely adopted varieties for the state of Tripura. To attain the goal, the information on genetic architecture of yield and its attributing traits is essentially needed. Hence, the present study has been undertaken to generate basic information in relation to genetic improvement in seed yield. The precise knowledge of the nature of gene action for yielding attributing traits help in the choice of an effective breeding strategy to accelerate the pace of genetics improvement of grain yield. Due to complex inheritance of seed yield and its component traits,

development of high yielding field pea varieties may be possible by studying the nature and magnitude of genetic variability present in the available stocks for different traits. The adequate information on extent of variability parameters may be helpful in the development of promising varieties through identification of yield determinants Singh *et al.* (2016). The choice of efficient breeding programmes depends on knowledge of gene action involved in expression of yield and its component traits. Several researchers Ullah *et al.* (2011); Singh *et al.* (2014a, b) studied the genetic parameters and found additive type of gene action in governing the seed yield per plant (SYP), whereas Mehandi *et al.* (2013); Bisht *et al.* (2014) observed both additive and non-additive type of gene action. Patil *et al.* (2011) performed the combining ability analysis and suggested the importance of both additive and non-additive type of gene action for SYP and its other related traits. But these methods give general idea about inheritance of traits and some time misleads. Therefore, generation mean analysis was used in present study, which may give more reliable results about inheritance of traits due to individual cross analysis. Knowledge of genetic variability and genetic nature of characters under improvement is essential and pre-requisite for launching any breeding programme to achieve the goal. Genetic improvement in relation to grain yield and harvest index is prime objective in this crop. However, yield is a complex character contributed by several morpho-physiological traits (Singh *et al.*, 2016) Hence, the knowledge relating genetic control of yield and its contributing traits is of immense use for initiating an efficient selection scheme for selecting a superior desirable genotype used in field pea breeding program for improving the seed physical quality. Keeping the above facts in mind, the present experiment was conducted (1) to

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test suitability of additive-dominance model and (2) to estimate genetic parameters such as gene effects using six basic generations in field pea.

MATERIAL AND METHOD

Genetics of seed yield and other traits of field pea were studied using the F_1 , F_2 , BC_1P_1 (BC_1) and BC_1P_2 (BC_2) of a cross between IM 9214-10 (Dwarf) as female parent (P_1) and Rachna (Tall) and Ambika (Tall) as male parents (P_2). The experiment was laid out in randomized block design (RBD) with three replications during rabi, 2013. These parents were selected from previous experiment conducted during rabi, 2012 (Singh *et al.*, 2014a) and crossed to obtain the crosses during, 2011. The F_1 seeds were subjected to back crossing and selfing during rabi, 2012. Ten competitive random plants from P_1 , P_2 and F_1 ; 15 from BC_1 and BC_2 and 60 from F_2 population were randomly selected from each family in each replication, to record the observations for agromorphological traits *viz.*, for days to first flowering, number of branches per plant, days to maturity, plant height, number of clusters per plant, pod bearing length, seed setting percent, pods per cluster, number of pods per plant, pod length, hundred seed weight and seed yield per plant. The traits *viz.*, days to first flower open and days to maturity were computed on plot basis. The observed means of the six generations and their standard errors for all the 12 characters in two crosses to test the adequacy of the additive dominance model were used to estimate the mid-parent [m], additive [d] and dominance [h] gene effects using the scaling test of Cavalli (1952). The gene effects and interactions for each characters were estimated after Hayman (1958). The significance of genetic parameters (m , [d], [h], [i], [j] and [l]) were tested using t -test. The data were subjected to generation mean analysis by using statistical package WINDOSTAT 9.1 version.

RESULT

The generation performance for crosses IM 9214-10 X Rachna and IM 9214-10 X Ambika are presented in Table 1. Components of mean *viz.*, constant mean (m), additive gene effects (d) and dominance gene effects (h) were estimated by using generation means. First three Parameter model was used and wherever it failed, six parameter model was applied for estimation of epistasis. Intra-allelic interactions *viz.*, additive \times additive (i), additive \times dominance (j) and dominance \times dominance (l) were estimated and presented in Table 2. In cross IM 9214-10 X Rachna both additive and dominance gene effects irrespective of sign were significant for plant height, pod bearing length, seed setting percent, pods per cluster and pods per plant. However, clusters per plant showed significance of additive gene effects only. Whereas dominance was found to be significant

for hundred seed weight and seed yield per plant. The additive effects were negative for plant height, pod bearing length, pods per cluster and pods per plant. On the other hand seed setting percent and pods per plant showed significance of negative dominance effects. Relatively dominance effect was greater for almost all the characters under study.

Inadequacy of additive-dominance model showed presence of epistasis for all the characters. All three types of interactions were significant for seven characters *viz.*, plant height, clusters per plant, pod bearing length, seed setting percent, pods per plant, hundred seed weight and seed yield per plant. Additive \times dominance interaction was found to be positive and significant for days to maturity where as dominance \times dominance gene interaction was found to be negative and significant for days to first flowering. All allelic and non allelic gene effects were non significant for branches per plant.

Likewise in cross IM 9214-10 X Ambika both additive and dominance gene effects were significant for plant height, clusters per plant, seed setting percent, pods per plant, hundred seed weight and seed yield per plant, whereas, dominance effect alone was significant for branches per plant days to maturity and pod bearing length. The additive effects in general were negative for all the characters except days to first flowering, days to maturity, pod bearing length and pods per plant. On the other hand dominance gene effects in general, were positive for almost all the traits except days to first flowering, days to maturity and pod bearing length. Relatively dominance effects were greater for almost all the characters under study.

Inadequacy of additive-dominance model showed presence of epistasis for all the characters. All the three types of interactions were recorded to be significant for eight characters *viz.*, plant height, clusters per plant, pod bearing length, seed setting percent, pods per plant, hundred seed weight and seed yield per plant. Both additive \times additive and additive \times dominance interactions were found to be significant for days to maturity, whereas additive \times additive along with dominance \times dominance gene interactions were significant for branches per plant. All the allelic and non allelic gene effects were non significant for days to first flowering, pods per cluster and pod length.

DISCUSSION

The present study was planned to estimate the nature and magnitude of allelic and non allelic interactions in field pea. Three elite genotypes differing in many quantitative characters were crossed in two combinations to generate variability for different traits. Six generations of each of these crosses were grown and observations recorded on twelve important characters. The discussion on the results obtained with regards to

nature of gene action are discussed here cross and character wise.

In cross IM 9214-10 × Rachna both additive and dominance gene effect irrespective of the sign were significant for plant height, pod bearing length, seed setting percent, pods per cluster and pods per plant (Table 2). However, for clusters per plant only additive effects; for hundred seed weight and seed yield per plant only dominant gene effects were found to be important. Presence of epistasis was recorded for all twelve characters in both the crosses (Table 2). Among non allelic interactions, all three types of interactions were found significant for plant height, clusters per plant, pod bearing length, seed setting percent, pods per plant, hundred seed weight and seed yield per plant whereas, for days to maturity, additive × dominance and for days to first flowering, dominance × dominance type of interactions were found significant. Duplicate type of epistasis (dissimilar sign of h & l) was observed for days to first flowering, branches per plant, plant height, pod bearing length, seed setting percent, pods per plant and hundred seed weight while, complementary epistasis (similar sign of h and l) was observed for days to maturity, clusters per plant, pod length and seed yield per plant.

The additive gene effects and additive × additive or any digenic complementary gene interaction are fixable and useful. In these populations

complementary epistasis could be exploited for the improvement of clusters per plant and seed yield per plant. Hence direct selection for these traits could be beneficial but with proper care otherwise predominance of dominant and dominant × dominant gene effects may mislead the selection. In the cross IM 9214-10 × Ambika both additive and dominance gene effects were found significant for plant height, clusters per plant, seed setting percent, pods per plant, hundred seed weight and seed yield per plant. Dominance gene effects alone were significant for branches per plant, days to maturity and pod bearing length. Interaction effects were found significant for all the characters except days to first flowering and pod length. Both additive × additive and dominance × dominance type of interaction effects were significant for branches per plant. All three types of interaction effects were found significant for days to maturity, plant height, clusters per plant, pod bearing length, seed setting percent, pods per plant, hundred seed weight and seed yield per plant. except for plant height. Clusters per plant and seed yield per plant, duplicate epistasis was found for all characters. Presence of complementary type of epistasis was observed for plant height, clusters per plant and seed yield per plant which could be exploited for improvement of grain yield in the populations under study.

Table 1. Cross wise mean performance of different generations for yield and attributes in field pea

	DFF	NBP	DM	PH	NCP	PBL	SSP	PPC	NPP	PL	SI	SYP
C-1: IM 9214-10 × RACHNA												
P ₁	43.73	3.67	121.80	60.00	4.67	7.33	68.67	1.20	8.00	4.33	18.73	5.17
P ₂	42.20	3.27	125.20	76.00	4.80	18.07	72.97	1.40	9.93	4.73	19.43	5.90
F ₁	42.40	3.67	123.53	79.67	8.80	19.33	75.33	1.53	19.03	4.33	17.70	12.07
F ₁	44.00	3.23	124.33	63.44	6.73	17.80	73.77	1.37	17.00	4.83	18.65	6.47
BC ₁	44.30	3.20	123.87	79.60	6.27	17.87	77.67	1.40	8.47	4.67	20.40	8.07
BC ₂	44.33	3.13	123.80	85.07	5.33	20.53	69.33	1.47	10.60	4.73	19.85	6.33
C-2: IM 9214-10 × AMBIKA												
P ₁	45.43	3.47	120.87	63.20	4.60	8.00	69.00	1.23	8.60	4.40	20.03	5.62
P ₂	45.13	3.67	124.20	88.67	4.47	19.53	69.67	1.43	16.33	4.70	19.28	6.40
F ₁	43.27	3.27	123.47	96.20	8.30	15.33	69.83	1.37	12.83	4.67	20.20	9.53
F ₁	43.47	3.13	124.60	65.33	4.13	15.83	72.17	1.33	9.37	4.50	19.81	6.70
BC ₁	43.80	3.53	124.03	64.17	4.50	14.00	72.33	1.43	13.70	4.43	20.73	8.30
BC ₂	43.33	3.70	123.33	71.47	5.17	13.73	76.17	1.47	9.93	4.80	21.73	10.00

DFF=Days to first flowering, NBP=No. of branches/plant, DM=Days to maturity, PH=Plant height, NCP= No. of cluster/plant, PBL= Pod bearing length, SSP=Seed setting percent, PPC=Pods/cluster, NPP=No. of pods per plant, PL=Pod length, SI=Seed index, SYP=seed yield/plant

Table 2. Estimates of gene effects and their standard errors for different characters in field pea (*Pisum sativum* L.) Cross-1

Characters	m	d	h	i	j	l	Type of epistasis
First flower (days)	44.00±0.11**	0.06±0.52	0.76±1.18	1.33±1.14	-0.76±.55	-7.93±2.22**	D
Branches /plant	3.23±.14	0.067±0.17	-0.050±.73	-0.267±.679	-0.116±.210	1.83±1.05	D
Maturity (days)	124.33±.29**	0.067±369	1.96±1.41	1.99±1.37	1.76±.45**	0.73±1.99	C
Plant height (cm)	63.44±47**	-5.46±.92**	99.57±2.69**	75.57±2.64**	14.86±.99**	-134.2±4.2**	D
Clusters/plant	6.73±.266**	0.93±.22**	0.33±1.18	-3.73±1.15**	0.99±.27**	7.60±1.47**	C
Pod bearing length (cm)	17.80±2.00**	-2.66±.45**	12.23±1.27**	5.59±1.21**	2.70±.49**	-18.33±2.1**	C
Seed setting (%)	73.76±.95**	3.33±.94**	-6.25±5.29**	-11.0±4.27**	5.78±.94**	18.76±5.42**	D
Pods /cluster	1.36±.033**	-0.06±.033**	0.48±.178**	.244±.149	0.049±.055	0.300±.272	D
Pods /plant	17.00±.20**	-2.13±.35**	-19.79±1.1**	-29.86±1.0**	-1.16±.390**	47.73±1.73**	D
Pod length(cm)	4.80±.166**	-0.060±.159	-0.73±.74	-0.53±.739	0.133±.166	-0.53±.94	D
hundred seed weight (g)	18.64±.086**	0.55±.368	4.52±.85**	5.90±.813**	0.90±.40**	-12.83±1.6**	C
Seed yield/plant	6.46±.088**	1.73±.124	9.46±679**	2.93±.43**	2.10±.138**	3.46±1.23**	D

Cross-2

Characters	m	d	h	i	j	l	Type of epistasis
First flower (days)	43.46±.067**	0.46±.58	-1.61±1.35	0.40±1.19	0.316±.62	2.43±2.66	D
Branches /plant	3.13±.133**	-0.16±.176	1.63±.74**	1.93±.64**	0.066±.22	-2.73±1.16*	D
Maturity (days)	124.60±.30**	0.699±.691	-2.73±1.98**	-3.66±1.84**	2.36±.834**	0.93±3.35	C
Plant height (cm)	65.33±.72**	-7.3±.52**	44.69±3.14**	9.93±3.08**	19.93±.59**	34.06±3.78**	D
Clusters/plant	4.13±.13**	-.66±.105**	6.56±.605**	2.80±.573**	-0.73±.159**	3.53±.783**	C
Pod bearing length (cm)	15.83±.84**	0.26±.63	-6.09±3.61**	-7.86±3.59**	6.03±.674**	11.00±4.28**	C
Seed setting (%)	72.16±1.08**	-3.83±.745**	8.83±4.70**	8.33±4.58**	-3.49±.816**	-27.0±5.61**	D
Pods /cluster	1.33±.033**	-0.033±.137	0.500±.308	0.46±.305	0.066±.139	-0.86±.57	D
Pods /plant	9.36±.712**	3.76±.517**	10.16±3.10**	9.80±3.03**	7.63±.64**	-6.46±1.99**	D
Pod length(cm)	4.50±.28**	-0.36±.21	0.58±1.24	0.46±1.2	-0.21±.23	-0.49±1.48	D
hundred seed weight (g)	19.81±.013**	-0.99±.363**	6.22±.84**	5.67±.72**	-1.37±.39**	-10.9±1.68**	C
Seed yield/plant	6.70±.25**	-1.70±.25**	13.32±1.16**	9.7±1.13**	-1.31±.28**	15.31±1.53**	D

*, ** Significant at 5 and 1 percent level of significance, C= Similar sign of h & l, D= Dissimilar sign of h & l

The [h] gene effects were greater than the [d] gene effects for all agro-morphological traits in both crosses, indicated the importance of dominance gene effects for yield and its related agro-morphological traits. The contribution of dominance gene effects varied with to cross and traits. Similar result was also observed earlier by Gawande *et al.* (2005) and Azizi *et al.* (2006). The negative and positive sign of [h] gene effects is a function of the F_1 mean value in relation to mid parent heterosis contributing to dominance gene effects (Cukadar-Olmedo and Miller, 1997). It is possible that the epistasis significantly contributed to genetic variance. Beside the additive and dominance genetic effects, epistasis components have also contributed to genetic variation with different magnitude for most of the yield and yield component traits. In such situation, the appropriate breeding method can effectively exploit the three types of gene effects.

The results obtained from present investigation reveal that seed yield in these populations were under the control of both additive and dominance gene effects. However, in both the crosses, dominance genetic variance was more prominent for seed yield. Hence careful selection for superior single plants should be operated carefully in segregating

generations. Simultaneously inter-mating among the superior segregants can also be practiced for accumulating desirable genes for higher seed yield and other traits.

REFERENCES

Dixit, G.P. (2006). Generation mean analysis for grain yield related traits in field pea (*Pisum sativum* L.). *Indian J. Genet.*, **66** (2):147-148.

Azizi, F., Rezai, A.M. and Saeidi, G. (2006). Generation mean analysis to estimate genetic parameters for different traits in two crosses of corn inbred lines at three planting densities. *J. Agric. Sci. Tech.*, **8**: 153-169.

Bisht, N., Singh, D.P. and Khulbe, R.K. (2014). Genetic variability and correlation studied in advanced inter specific and inter varietal lines and cultivars of mungbean (*Vigna radiata*). *J. Food legumes*, **27**: 155-157.

Cukadar-Olmedo, B. and Miller, J.F. (1997). Inheritance of stay green traits in sunflower. *Crop Sci.*, **37**: 150-153.

Cavalli, L.L. (1952) Analysis of linkage in quantitative inheritance. In: Quantitative inheritance (E.C.R.-Rieve and C.H.Waddington), London:pp. 135-144.

Gawande, V.L. and Patil, J.V. (2005). Gene action for seed yield and its components in mungbean [*Vigna radiata* (L.) Wilczek]. *J. Maharashtra Agric. Univ.*, **30**: 285-288.

Hayman, B.L. (1958). The separation of epistasis from additive and dominance variation in generation mean, *Heredity*, **12**: 371-391.

Mehandi, S., Singh, C.M. and Kushwaha, V.R. (2013). Estimates of genetic variability and heritability for yield and yield component traits in mungbean [*Vigna radiata* (L.) Wilczek]. *The Bioscan*, **8**: 1481-1484.

Patil, A.B., Desai, N.C., Mule, P.N. and Khandewal, V. (2011). Combining ability for yield and component characters in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Res.*, **34**: 190-195.

Singh, C.M., Singh, A.K., Mishra, S.B., Pandey, A. and Kumar, B. (2015). Detection of epistasis for yield and some important agro-morphological traits in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Genomics Genet.*, **6**: 1-7. doi: 10.5376/lgg.2015.06.0004.

Singh, C.M., Mishra, S.B. and Pandey, A. (2014a). Pattern of agro-morphological trait relationship and genetic divergence in greengram [*Vigna radiata* (L.) Wilczek]. *Electron. J. Plant Breed.*, **5**: 97-106.

Singh, C.M., Mishra, S.B. and Pandey, A. (2014b). Environmental influence on heritability and selection response of some important quantitative traits in greengram [*Vigna radiata* (L.) Wilczek]. *J. Food Legumes*, **24**: 95-98.

Ullah, H., Khalil, I.H., Iltafullah, Rahman, H. and Amin, I. (2011). Genotype \times environment interaction, heritability and selection response for yield and yield contributing traits in mungbean. *African J. Biotech.*, **10**: 475-483.

