Diallel analysis for yield and its component traits in field pea (*Pisum sativum* L. var. *arvense*)

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ABSTRACT

An experiment was carried out at Kanpur, Uttar Pradesh to study the nature of gene action in field pea (*Pisum sativum* L. var. *arvense*) through diallel analysis among ten parents and their 45 crosses. Analysis of variance showed highly significant differences among the genotypes for all traits. Variances due to parents vs. F_1s were significant for days to flowering, plant height, internodes plant^{-1}, pods plant^{-1} and 1000-grain weight. Significant additive variance for days to 50% flowering and maturity, primary branches plant^{-1} and internodes plant^{-1}, plant height and pod length was observed. Dominance component was highly significant for all the traits, and the distribution of positive and negative alleles indicated asymmetry of loci showing dominance in all the traits. The number of gene groups controlling the attributes was <1, indicating complementary action. The estimates of heritability (h^2_{ns}) and genetic advance both were high for plant height (86 and 70%) and internodes plant^{-1} (34 and 46%). High heritability with low genetic advance was found for days to maturity (62 and 6%), moderate heritability with high genetic advance was found for primary branches plant^{-1} (19 and 35%) and grain yield plant^{-1} (16 and 39%). Moderate heritability and moderate genetic advance was exhibited in pod length (27 and 15%) and low heritability with high genetic advance was found for pods plant^{-1} (9 and 40%).

Key words: Gene action, Genetic advance, Genetic components, Heritability, Field pea

Despite the largest producer of the pulses in the world, India has to import pulses every year to meet its domestic requirement. In 2011-12, India imported 3.3 million tons of pulses worth ₹ 8.8 thousand crores (DAC, 2012). Among pulses, pea (*Pisum sativum* L.) is an important *rabi* season crop, which occupies about 0.77 Mha with an annual production of 0.71 Mt, with the productivity of 915 kg ha^{-1} (Anonymous, 2012). It is a highly nutritive legume used in the form of green vegetables, soup, dal, etc. It is also used to make chapatti, having mixed with barley or wheat flour. In addition, peas are processed (canned, frozen or dehydrated) for consumption in the off season (Oelke *et al.*, 1991). So, keeping in view of its multipurpose uses, increasing demand, and limited growing area, there is needed to enhance productivity per unit area and time. In this regard, selection of suitable parents with desirable traits like yield per plant and short duration; is important for fruitful varietal development programme. Understanding of inheritance of the traits which are to be improved is pre-requisite for improvement in genotype as well as to develop an improved variety with high productivity.

The component of breeding value of the parents may include nature and magnitude of genetic variances, gene action of the traits under improvement, their heritability and genetic advance etc. It is generally expected that there will be preponderance of additive type of gene action in pea being a self-pollinated crop, the possibility of non-additive gene action cannot be ruled out. Therefore, additive and non-additive gene action needs to be assessed in the parents and their hybrids. Yield is a complex trait determined by a number of meristic and metric traits. The comprehensive study of the genetic architecture of quantitative traits of economic value is essential to improve the yield potential. The present investigation aimed to generate information on the nature of gene action in field pea to decide breeding methods for the genetic improvement of pea.

MATERIALS AND METHODS

A set of 10 parents [Rachna, Shikha, HUP 2, KPMR 522 (Jaya), KPMR 400 (Indra), HUDP 15, KPMR 516, HFP 4 (Aparna), DDR 13 and DDR 39] (Table 1) and their 45 F_1s were grown in a randomized complete block design with 3 replications at Students' Instructional Farm of C.S. Azad University of Agriculture and Technology, Kanpur (Uttar Pradesh), India, and each replication was in two tiers. Each genotype was grown in two rows of 3 m length with a row-to-row and plant-to-plant spacing of 75 cm and 10 cm, respectively. Spacing between rows was kept more than recommended for commercial cultivation, so that recording of observations would be comfortable. Recommended doses of 25 kg N, 60 kg P_2O_5 and 35 kg K_2O ha^{-1} were applied, and sufficient irrigations were

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Table 1. Varieties used for diallel crosses, their pedigree and salient features

Variety	Pedigree	Salient features
Rachna	T163 x T10	Plant tall, leafy; medium maturity; long pods; seed smooth, bold and round; 190-200 g test weight and powdery mildew resistant.
Shikha	KPMR83 x KPMR9	Plant tall, leafy, erect; medium maturity; long pods; seeds creamy white; 150-200 g test weight, and wilt and powdery mildew resistant.
HUP2	Afila Knudt x C-5064-S-143	Plant erect, tall, leafy; maturity duration 120-140 days; long pods; seeds creamy white, bold; 150-175 g test weight, and powdery mildew resistant.
KPMR 522 (Jay)	KPMR156 x HFP4	Plant dwarf, leafy, semi-spreading type; medium maturity; long pods; seeds round, creamy; 150-165 g test weight, and powdery mildew resistant.
KPMR 400 (Indra)	Rachna x HFP4	Plant dwarf; medium maturity; pods medium length; seeds white and shine; 150-175 g test weight; wilt and powdery mildew resistant.
HUDP15	PG-3(PG-3×S-143) x FC	Plant dwarf, leafy, erect type; medium maturity; pod length is medium; seed greenish, round; 140-160 g test weight; powdery mildew resistant.
KPMR 516	KPMR149 x HFP4	Plant dwarf, leafy, semi-spreading type; medium maturity; pods medium length; seeds creamy white; 180-200 g test weight; wilt resistant.
HFP 4 (Aparna)		Plant dwarf, semi-spreading type; medium maturity; pods short length; seeds white creamy, shine; 165-172 g test weight and powdery mildew resistant.
DDR 13	P465 x PH429	Plant dwarf, leafy; short duration; pod length is medium; seeds are short, rounded, greenish; 170-180 g test weight; powdery mildew tolerant.
DDR 39		Plant dwarf, leafy; early maturity; pod length medium; seeds are medium, round; 175-180 g test weight and powdery mildew resistant.

given as and when required. Manual weeding was done twice to keep plot weed-free. Analysis of variance was carried out based on the method as suggested by Panse and Sukhatme (1967). The graphical analysis was done as per Hayman (1954). The analysis was based on the variance and covariance (v_r, w_r) graph. A diallel table was prepared for each trait to calculate v_r, w_r and v_p. Related parameters were determined on the basis of the formulae suggested by Hayman (1954). 'E' was obtained from Me of the analysis of variance for design as given by Askel and Johanson (1963). A specific multiplier for each component was also calculated following the formula given by Hayman (1954). The significance of the components was tested by 't' test, using the formula suggested by Hayman (1954). A general approach to this method based on second degree statistics using the concept of $\hat{D}$ and $\hat{H}$ components of variation was suggested by Yates (1947). Heritability (ns) based on the genetic components was calculated by the formula proposed by Crumpacker and Allard (1962). The expected genetic advance was calculated by the formula of Robinson *et al.* (1949).

RESULTS AND DISCUSSION

Non-significant values of 't²' in most of the traits namely, days to maturity, primary branches plant⁻¹, plant height and pod length supported the validity of the assumptions. Significant variability was present among parents and their F_1s progenies with respect to all the traits under study (Table 2).

The graphical analysis (graphs not given) revealed that additive gene action was predominant for days to 50% flowering, days to maturity, primary branches plant⁻¹, plant height, internodes plant⁻¹ and pod length. The regression coefficient 'b' (Table 3) differed significantly from zero for days to flowering and maturity, plant height, number of internodes plant⁻¹ and thousand grain weight, while it differed significantly from unity for all the traits except days to maturity. The value of t² was found significant for days to flowering, number of internodes plant⁻¹, number of pods plant⁻¹, number of seeds pod⁻¹, 1000-grain weight and grain yield plant⁻¹, which indicates that one or more assumptions of diallel analysis made by Hayman (1954) are not fulfilled. Components of variance

Table 2. Analysis of variance for parents and F_1s in field pea

Character	Replication	Mean sum of square				
		Genotypes	Parents	F_1s	Parents vs F_1s	Error
Degree of freedom	2	54	9	44	1	108
Days to flowering	3.152	19.256**	30.128**	16.623**	37.242**	1.947
Days to maturity	12.266**	36.315**	77.861**	28.579**	2.373	1.949
Number of primary branches plant⁻¹	1.691**	1.302**	1.220**	1.336**	0.549	0.150
Plant height (cm)	18.487	1626.309**	3764.491**	1187.199**	1703.638**	15.511
Number of internodes plant⁻¹	8.570	145.611**	210.276**	134.898**	35.091**	2.926
Pod length (cm)	0.121	0.888**	1.178**	0.842**	0.295	0.113
Number of pods plant⁻¹	0.326	14.332**	6.400**	14.938**	59.082**	1.169
Number of seeds pod⁻¹	1.027*	0.906**	0.687*	0.969**	0.124	0.324
Test weight (g)	60.463	1217.125**	437.146**	1391.212**	577.154**	64.380
Grain yield plant⁻¹ (g)	0.660	5.760**	4.351**	6.169**	0.477	0.718

*, ** Significant at 0.05 and 0.01 levels, respectively.

Table 3. Value of b, sb, b-o/sb, b-1/sb and t^2 for yield traits 10-parental half diallel cross in field pea

Trait	b	Sb	b-o/sb	b-1/sb	t^2
Days to 50% flowering	0.1237	0.2299	0.54*	-3.81**	1.4941**
Days to maturity	0.8521	0.3119	2.73**	-0.47	0.6538
Primary branches plant[-1]	0.1886	0.3371	0.56	-2.41**	0.0067
Plant height (cm)	0.6486	0.2618	2.48**	-1.34**	0.0035
Internodes plant[-1]	0.3652	0.2410	1.52**	-2.63**	0.6951*
Pod length (cm)	-0.0606	0.3930	-0.15	-2.70**	0.0928
Pods plant[-1]	-0.0080	0.2507	-0.03	-4.02**	0.9820**
Grains pod[-1]	-0.0005	0.2574	0.00	-3.89**	0.8330*
1000-grain weight (g)	0.1062	0.1392	0.76**	-6.42**	8.9723**
Grain yield plant[-1] (g)	-0.0526	0.2631	-0.20	-4.00**	0.7095*

*, ** Significant at 0.05 and 0.01 levels, respectively

(Table 4) showed the presence of both additive ($\hat{D}$) as well as dominance components ($\hat{H}_1$) for days to 50% flowering, days to maturity, primary branches plant[-1], plant height, internodes plant[-1] and pod length. The traits like pods plant[-1], grains pod[-1], 1000-grain weight and grain yield plant[-1] showed presence dominance component ($\hat{H}_1$) and absence of additive component. Sharma and Sharma (2012) also found this component significant for days to flowering, pod length, number of pods plant[-1], and pod yield. Combining ability analysis also revealed highly significant gca and sca variances for all the traits. Ranjan *et al*. (2005) observed that gca and sca variances were equally important for the yield attributing traits. There was over dominance exhibited for all the traits except plant height which indicated partial dominance. Sharma *et al*. (2008) also observed more or less similar results. It was recorded that both additive and dominance genetic components are responsible for the control of characters under study. Sharma and Rastogi (2001) also reported additive as well as non-additive genetic variance for grain yield plant[-1] and its component traits. Over-dominance was observed by graphical analysis for primary branches plant[-1] and internodes plant[-1]. Complete dominance was observed for days to 50% flowering, pod length and 1000-grains weight. Partial dominance was reported for days to maturity, pods plant[-1], grains pod[-1] and grain yield plant[-1] whereas, no-dominance was observed for plant height only. On the other hand, component analysis exhibited over-dominance for all the traits studied except plant height. It may be explained that the estimates obtained through formula $(\hat{H}_1/\hat{D})^{0.5}$ gave an approximate value of the degree of dominance. Hayman (1954) suggested that in particular combinations positive, negative or complementary type of gene action and simply correlated gene distribution may seriously inflate the mean degree of dominance and convert partial dominance into apparent over-dominance. Comstock and Robinson (1952) emphasized that the degree of dominance might be biased upward either by linkage or epistasis or both. In the present study, the presence of over-dominance for most of the traits might be due to not fulfilling all the assumptions for diallel mating design, which is also witnessed by 't' test. Both graphical and component analysis revealed that over-dominance for primary branches plant[-1] and internodes plant[-1].

Table 4. Estimation of variance components for yield and its component traits in field pea

Character	Parameters						Related parameters				
	D	H_1	H_2	F	h^2	E	$(H_1/D)^{0.5}$	$H_2/4H_1$	$(4DH_1)^{0.5}+F/(HDH_1)^{0.5}-F$	h^2/H_2	r
Days to 50% flowering	9.39**	29.45**	21.09**	15.93*	4.69	0.65	1.77	0.18	2.84	0.22	-0.8935
	±3.16	±6.73	±5.72	±7.9	±3.83	±0.95					
Days to maturity	25.31**	37.54**	30.16**	24.71**	0.08	0.65	1.22	0.20	2.34	0.00	-0.3242
	±3.38	±7.19	±6.11	±7.80	±4.09	±1.02					
Primary branches plant[-1]	0.36**	1.72**	1.46**	0.45	0.05	0.05	2.20	0.21	1.81	0.04	0.2886
	±0.13	±0.28	±0.24	±0.31	±0.16	±0.04					
Plant height (cm)	1249.66**	301.16*	245.25**	395.68**	223.02**	5.17	0.49	0.20	1.95	0.91	0.2801
	±62.35	±132.71	±112.79	±143.85	±75.50	±18.80					
Internodes plant[-1]	69.12**	256.28**	191.20**	128.73**	4.28	0.98	1.93	0.19	2.87	0.02	0.2877
	±19.39	±41.27	±35.08	±44.74	±23.48	±5.85					
Pod length (cm)	0.35**	1.48**	1.10**	0.69*	0.03	0.04	2.04	0.19	2.84	0.02	0.1871
	±0.13	±0.29	±0.24	±0.31	±0.16	±0.04					
Pods plant[-1]	1.74	18.17**	16.95**	1.26	7.66**	0.39	3.23	0.23	1.25	0.45	0.2292
	±1.53	±3.25	±2.76	±3.52	±1.85	±0.46					
Grains pod[-1]	0.12	1.08**	0.84**	0.23	-0.02	0.11**	2.98	0.19	1.94	-0.02	0.5683
	±0.10	±0.20	±0.17	±0.22	±0.12	±0.03					
1000-grain weight (g)	124.26	1537.53**	1278.71**	107.47	68.43	21.46	3.52	0.21	1.28	0.05	-0.1688
	±126.24	±268.71	±228.38	±291.27	±152.87	±38.06					
Grain yield plant[-1] (g)	1.21	7.38**	5.43**	1.85	-0.02	0.24	2.47	0.18	1.89	0.00	0.0156
	±0.71	±1.52	±1.29	±1.64	±0.86	±021					

*, ** Significant at 0.05 and 0.01 levels, respectively

It might be real one and could be utilized practically; however, it could be done where loci having over-dominance effect show tight linkage.

The estimates of $\hat{F}$ value were positive for all ten traits and out of which significant values were observed for days to 50% flowering, days to maturity, plant height, internodes plant^{-1} and pod length. Significant estimates of $\hat{h}^2$ were exhibited for plant height and pods plant^{-1}. The significant and positive values of $\hat{F}$ and $\hat{h}^2$ indicated that dominant genes played a significant role in the control of these traits. The values of component were found non-significant for all the traits except grains pod^{-1} which showed environmental effect on this trait. The values of mean degree of dominance $(\hat{H}_1 / \hat{D})^{0.5}$ were higher than unity for all the traits except plant height, which showed over dominance. The value of plant height was less than unity which exhibited partial dominance. Asymmetrical distribution of positive and negative alleles among the parents, were observed for all traits as estimated values of $\hat{H}_2 / 4\hat{H}_1$ were less than the theoretical value (0.25). Graphical analysis also indicated the asymmetrical distribution of dominant and recessive alleles in the parents. The ratio $(4\hat{D}\hat{H}_1)^{0.5} + \hat{F}/(4\hat{D}\hat{H}_1)^{0.5} - \hat{F}$ observed for all traits was more than unity which indicated that the dominant alleles were distributed more frequently than the recessive alleles. The preponderance of dominant alleles was also confirmed by the positive values of for these traits. The proportion of dominant and recessive alleles among the parents determines the extent of genetic advance under directional selection. If the genes present in the population are dominant in nature, the extent of genetic advance will be high. On the other hand, genetic advance will be limited, if recessive genes are predominant. The proportion of dominant genes was fairly high for all the traits. This suggested the possibility of fairly high amount of genetic advance. The ratio of $\hat{h}^2 / \hat{H}_2$ of gene groups was found less than unity for all the traits and indicated the inheritance of these traits was governed by one major gene group. The characters exhibiting values less than unity produce little or no-dominance (Gilbert, 1958). Such a situation might have arisen due to cancellation effect of positive and negative genes. More reliance might not be placed on the ratio because it generally underestimates the number of genes and provides no information about the group of genes which are responsible for the expression of dominance. The correlation coefficient (r) between parental order of dominance (Wr + Vr) and parental measurement (Yr) was found to be negative for days to 50% flowering, days to maturity and 1000-grains weight indicating that dominant genes were mostly predominant for these traits.

High heritability (>30%) estimates were observed for plant height, days to maturity, days to 50% flowering and internodes plant^{-1}. It was due to greater contribution of additive genetic component (Table 5). High heritability estimates were also reported by Mahant *et al.* (2001). Moderate heritability (10-30%) estimates were observed for pod length, primary branches plant^{-1} and grain yield plant^{-1}. These results are in agreement with genetic analysis which indicated the greater role of non-fixable genetic effect. Ranjan *et al.* (2006) observed that most of the yield attributing traits showed high heritability and grain yield expressed high genetic advance (>30%) alongwith moderate heritability and high GCV indicating preponderance of additive gene effects. Low (<10%) estimates of heritability were observed for grains pod^{-1}, pods plant^{-1} and test weight. The high genetic advance was observed for plant height, internodes plant^{-1}, pods plant^{-1}, grain yield plant^{-1} and primary branches plant^{-1}, which indicated involvement of additive gene effects for the expression of these traits. Genetic gain was recorded moderate for test weight, pod length and grain pod^{-1}. These findings indicated the presence of additive and non-additive gene effects. Therefore, the selection would be followed in later generations. Low genetic advance was observed for days to maturity and days to 50% flowering. The selection in this set of material would not be much effective for these traits in early generations. Similar results were also reported by Sharma and Sharma (2012).

The present study revealed the significance of both additive and non-additive genetic effects in the component traits related to productivity. The genetic improvement of such traits may be based on simultaneous exploitation of both additive and non-additive components of genetic effects. For effective utilization of additive genetic effect, selective breeding may be used for the improvement of yield and its component traits in field pea. Plant height and pods plant^{-1} had considerable amount of heritability as well as genetic advance. Pedigree selection for highly heritable characters in early generations would appear to maximize progress for most of the situations.

Table 5. Mean, heritability (ns) and genetic advance for 10 characters in field pea

Character	Mean	Heritability (%)	Genetic advance	GA as percentage of mean
Days to 50% flowering	73	36.8	3.8	5.1
Days to maturity	105	62.1	5.6	5.3
Primary braches plant^{-1}	3	19.5	1.1	35.7
Plant height (cm)	57	86.2	39.9	70.2
Internodes plant^{-1}	29	34.4	13.2	46.1
Pod length (cm)	6	27.5	0.8	14.6
Pods plant^{-1}	10	8.6	4.0	39.7
Grains pod^{-1}	4	8.6	0.6	13.3
1000-grain weight (g)	166	7.5	40.6	24.4
Grain yield plant^{-1} (g)	6	15.7	2.3	39.4

Pea is an autogamous crop, for which pedigree method will be the best breeding strategies for yield improvement. However, according to availability of resources and feasibility in handling the segregating materials, this method may be employed with required modifications.

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