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Genetic analysis for gene action in field pea (*Pisum sativum* L.)

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Abstract

Cross combinations RACHNA x KPMR 940, SWATI X KPMR 940, SWATI x KPMR 940, KPMR 522 x SHIKHA, SHIKHA x KPMR 913 showed high economic heterosis for yield per plant. The high estimates of narrow sense heritability were recorded for days to flowering, days to maturity, branches per plant and moderate narrow sense heritability was observed for plant height, pods per plant, grain yield per plant, biological yield per plant, harvest index.

Keywords: Genetic, gene, pea, plant, Pisum sativum L.

Introduction

Pulses are members of the Fabaceae (Formerly Leguminosae) family and the Papilionoidea subfamily. These pulses mainly include chickpea, pigeonpea, lentil, mungbean, urdbean and field pea. Pulses have been designated as a "WONDER CROP" due to its high protein content, which makes the diet more nutritive and their symbiotic connection with nitrogen-fixing bacteria of rhizobium species, which improves soil fertility.

Pulses are the second most important component of the Indian diet after cereals. Pulses are an important source of protein for the poor as well as for the vegetarians which constitute major population of the country. India is the largest producer as well as consumer of pulses and is the largest importer in the world. The total pulse production of India was 24.42 lakh MT in 2020-21 while in 2019-20 it was 23.03 lakh MT. It includes the necessary amino acids, such as lysine and tryptophan, which are often limiting in cereals. Among the states, Uttar Pradesh is the largest producer of pea, occupying 3.60 lakh ha area under cultivation with the production of 5.6lakh tonnes and productivity of 15q./ha.

Material and Methods

The investigation was conducted at oilseed research farm, Kalyanpur of Chandra Shekhar Azad University of agriculture & technology, Kanpur during the Rabi season 2020-2021. The experimental material contains 8 germplasm lines of field pea (*Pisum sativum* var. Arvense) SWATI, RACHNA, KPMR 400, KPMR 522, SAPNA, SHIKHA, KPMR 940 and KPMR 913. The data was collected on growth and yield attributes *viz.*, days to flowering, days to maturity, plant height (cm), branches per plant, pods per plant, grains per pod, 100 seed weight(g), grain yield per plant(g), biological yield per plant(g) and harvest index (%). This material was taken from the breeders of legume section of genetics and plant breeding, Chandra Shekhar Azad University of agriculture and technology. The components of variance in diallel cross were computed using of equation as given by Hayman (1954a)^[12]. The heterosis was calculated (in percent) as increase or decrease over economic parent. The formula used, are given below:

Heterosis over economic parent (%) = $[F_1 - EP/EP] \times 100$

Coefficient of heritability (in narrow sense) in F_1 generation based on component analysis was calculated as proposed by Crum packer and Allard (1962)^[4]. The genetic advance was worked out by the formula proposed by Robinson *et al.* (1949)^[19] as:

 $\Delta GA = (k) (h^2) (\sigma_{ph})$

Result and Discussion

Components of genetic variance and gene action

The genetic component of variance for all the 10 characters were estimated using diallel mating design with two approaches *viz.*, genetic component and combining ability. The genetic component of variance namely D, H₁, H₂, h², F and E along with $(H_1/D)^{0.5}$ and related statistics was presented in (Table: 1).

The additive component (D) showed significant values for 6 characters *viz.*, days to flowering, plant height, branches per plant, pods per plant, grain yield per plant, biological yield per plant indicated the preponderance role of additive component for expression of characters. Additive component is heritable and fixable in nature and it provide ample scope for selection of superior genotype.

Dominance variance (H_1) was found significant for all the characters indicating the existence of dominant genes. Dominance variance (H_2) was also significant for 8 characters indicating the preponderance of dominant gene action which reveals the expression of non-additive gene action. That can be utilized for commercial exploitation of heterosis in the crop.

Significant and positive value of F component was found for days to flowering, branches per plant, 100 seed weight which reveals presence of dominant gene in positive direction which indicates lateness and while significant and negative value was observed for plant height, branches per plant, pods per plant which reveals the presence of recessive gene in negative direction which indicates earliness.

Significant and positive value of h^2 component for days to flowering, branches per plant, biological yield per plant and harvest index indicates that heterozygous gene combination significant distribution to the overall dominance in positive direction.

The estimates of average degree of dominance $(H_1/D)^{0.5}$ were observed for days to maturity, branches per plant, pods per plant, grains per pod, 100 seed weight, grain yield per plant, biological yield per plant and harvest index showing high degree of over dominance gene.

The estimated value of $(H_2/4H_1)$ showed symmetrical distribution of positive and negative allele in days to flowering, plant height, branches per plant, pods per plant, 100 seed weight. It was found less than 0.25 for characters like days to maturity, grain yield, biological yield and harvest index indicating asymmetrical distribution of positive and negative alleles in F1 hybrid for all characters.

The proportion of dominant and recessive gene $(4DH_1)^{0.5} + F$ / $(4DH_1)^{0.5} - F$)] indicated excess of dominant genes in days to flowering, days to maturity, branches per plants, grain yield and biological yield. Whereas, rest of characters *viz.*, days to maturity, plant height, pods per plant, grains per pod, harvest index showed excess of recessive gene effects.

The ratio of number of gene group (h^2/H_1) was found less than unity for 9 characters except for branches per plant indicating that at least one major gene group is responsible for the inheritance of characters. while in branches per plant more than one gene group is present. The above findings are in accordance with those of Singh *et al.* (2010), Ceyhan and Ali (2012), Sharma *et al.* (2015) and Tampha *et al.* (2019) ^{[23, 1, 22, ^{25]}.}

Heterosis

The term heterosis account for an increase or decrease in

performance of F1 to their parents. Heterosis, which is measured in per cent as the superiority over better or superior parent is thus important parameter in such studies. Heterosis breeding play important role in crop improvement programme for obtaining higher production especially in crops where commercial hybrids seed production is feasible. however, heterosis effect study in field pea may provide fruitful information for selection of parents for any breeding programme in order to increase productivity by isolating a desirable segregants in advance generation. The most important step in exploitation of heterosis is to know its magnitude and direction. Moll et al. (1964)^[14] observed that heterosis in yield characters was mostly dependent on genetic diversity present in the parental material. According to Griffing and Lindstarm (1954)^[9], Paterniani and Longuist (1963)^[17], the expression of heterosis is due to accumulation of the desirable genes in a hybrids plant through the crossing of parents differing in their genetic make-up. Williams and Gilbert (1960)^[26], Durate and Adams (1963)^[6] and Coyne (1965) ^[3] concluded that the genetic basis of heterosis for a complex trait is like yield could be explained by multiplicative interaction on the phenotypic level of component characters. In the present investigation, an attempt has been made to study the magnitude of heterosis for yield and yield contributing traits in diverse genotype in field pea. The results are presented in table: 2.

The negative and significant value of heterosis is considered for days to flowering, days to maturity, plant height. On the other hand, for other characters positive significant heterosis and high *per se* performance is desirable in other 7 traits.

Negative and significant cross showing economic heterosis over parent in desirable direction was shown by KPMR 522 x KPMR940, KPMR400 x KPMR 522, SAPNA x KPMR 940, RACHNA x KPMR522 for days to flowering. For days to maturity desirable cross were showed by KPMR 522 x SAPNA, KPMR 522 x KPMR 940, SAPNA x KPMR 940, KPMR 522 x SHIKHA, SHIKHA x KPMR 940 crosses. For plant height, negative heterosis which is shown by cross KPMR 400 x SAPNA.

Positive and significant heterosis with higher mean value is desirable for branches per plant, pods per plant, grains per pod, 100 seed weight, grain yield per plant, biological yield per plant, harvest index. Significant positive heterosis over economic parent was showed for branches per plant by KPMR 522 x KPMR, KPMR 400 x KPMR 940, SAPNA x KPMR 940, SAPNA x SHIKHA, RACHNA x SHIKHA, SAPNA x KPMR 913, RACHNA x KPMR 940, RACHNA x SAPNA.

Best and significant crosses for pods per plant was showed KPMR 940 x KPMR 522, RACHNA x KPMR 940, RACHNA x SHIKHA, RACHNA x KPMR 522, KPMR 522 x KPMR 940 for grains per pod desirable and significant heterosis over economic parents were showed by following cross combination KPMR 400 x KPMR 940, RACHNA x KPMR 940, KPMR 940 x KPMR 913, SAPNA x KPMR 940, KPMR 522 x KPMR 940, SWATI x KPMR 940. For 100 seed weight, significant crosses were observed by KPMR 400 x KPMR 940, SWATI x KPMR 522, SWATI x RACHNA, SWATI x KPMR 400, SWATI x KPMR 522, RACHNA x KPMR 522, RACHNA x KPMR 400, RACHNA x KPMR 940. For grain yield /per plant best combination is showed by RACHNA x KPMR940, KPMR 522 x KPMR 940, KPMR 400 x KPMR 940, KPMR 940 x KPMR 522, RACHNA x KPMR 522, RACHNA x KPMR400. For biological yield /per plant significant crosses were RACHNA x KPMR 940, SAPNA x KPMR 940, KPMR 522 x KPMR 940, KPMR 940 x KPMR 913, SWATI x RACHNA, RACHNA x KPMR 522. For harvest index best crosses observed were SWATI X KPMR 522, KPMR 400 x KPMR 522, KPMR522 x SHIKHA, KPMR 400 x KPMR913, SWATI x KPMR 400. These results are in agreement with those of Patel *et al.* (2006), Sharma *et al.* (2007), Joshi *et al.* (2015), Chauhan *et al.* (2016) and Hama –Amin T.N. (2020) ^[16, 21, 13, 2, 10].

Heritability and genetic advance

Heritability is the transmissibility of characters from parents to offsprings. It helps in partitioning the total variation into heritable and non-heritable components. The non-heritable variance includes the effect of environmental factors, which have direct bearing on the expression on genes. the heritable variance may be divided in fixable and non-fixable components. the fixable portion is due to additive and additive x additive components while, non-fixable is due to dominance and its related epistasis.

Dudley and Moll (1969)^[7] indicated the estimates of heritability and genetic variance can be useful in answering the question that plant breeder faces. Hanson (1963)^[11] while reviewing the utility of heritability in biometrical studies pointed out that estimates of heritability are influenced by method of estimation, generation of study, sample size and environment. Utility of heritability estimates depends on their reliability in predicting gain under selection.

Genetic advance refers to the advancement in mean performance of selected sample over population *i.e.* advancement in mean performance of selected population over the mean of base population in a single cycle of selection. Thus, genetic advance is based on heritability. Heritability in narrow sense is estimated for all the traits based on genetic components.

In present investigation, presented (table-3) the result revealed high and moderate heritability. The estimates of heritability in narrow sense with high value in F1s was exhibited by the characters like days to flowering (46.60%), days to maturity (31.32%) and branches per plant (32.00%) which indicated the major role of additive gene action. Medium heritability was reported in remaining characters like in plant height (22.00%), pods per plant (28.80%), seeds per pod (12.20%), 100 seed weight (14.30%), grain yield (23.90%), biological yield (27.00%) and harvest index (20.00%), which indicates the preponderance of non-additive gene action. The genetic advance as per cent over mean was taken under study and it varied from 22.16% in plant height to 1.50% in 100 seed weight. High heritability coupled with high genetic advance was observed in plant height indicate that the phenotypic variance for these traits were additive. For the rest of traits high heritability with low genetic advance was found indicating non- additive phenotypic variance for the trait. Confirming to the findings in the present investigation were also reported by Pandey et al. (2015) [15], Georgieva et al. (2016)^[8], Thakur et al. (2016)^[24], Devi et al. (2017)^[5] and Pujari et al. (2021)^[15].

Table 1: Estimates of Genetic Component of variance for 10 characters in 8 Parent Diallel Cross In Field Pea.

Estimates	Days to flowering	Days to maturity	Plant height	Branches per plant	Pods per plant	Grains per pod	100 seed wt.	Grain Yield/plant	Biological yield/plant	H.I
	17.05**	20.60	1223.71**	0.06**	1.29**	0.06	0.06	4.64**	14.02**	15.02
D SE	1.88	10.88	13.74	0.01	0.61	0.05	0.47	1.49	3.36	10.71
H_1	8.58**	34.40**	38.86**	0.07**	1.90**	0.11**	1.04**	7.94**	28.73**	38.41**
SE	1.80	10.58	13.37	0.01	0.59	0.05	0.31	1.44	3.27	10.42
H_2	14.02**	28.98**	608.94**	0.07**	2.50**	-0.02	-0.35	5.60**	19.89**	37.03**
SE	1.59	9.21	11.63	0.01	0.51	0.04	0.32	1.26	2.85	9.07
F SE	5.59**	16.59	-169.75**	0.03**	-0.26**	-0.02	1.07**	2.27	4.76	-3.31
г 5е	1.88	10.88	13.74	0.01	0.61	0.05	0.27	1.50	3.37	10.71
h2	13.44**	2.03	8.29	0.07**	0.04	0.03	0.01	0.04	7.17**	6.94
SE	1.07	6.17	7.80	0.07	0.35	0.02	0.18	0.84	1.91	6.08
E SE	0.55*	0.56	0.72	0.001	0.08	0.003	0.001	0.03	0.03	0.91
E SE	0.26	1.53	1.94	0.002	0.09	0.005	0.04	0.21	0.475	1.51
(H1/D)0.5	0.70	1.29	0.18	1.12	1.21	1.37	1.77	1.30	1.43	1.59
$H_2/4H_1$	0.40	0.21	3.92	0.25	0.33	0.26	0.25	0.18	0.17	0.24
Proportion of dominant and recessive gene	1.60	1.90	0.44	1.62	0.84	0.8	0.54	1.46	1.26	0.87
h²/H1	0.95	0.07	0.01	1.03	0.02	0.28	0.01	0.01	0.37	0.19

 Table 2: Estimates of Heterosis over Economic parent for 10 Characters in F1s.

Crosses	Dtf	Dtm	Plant Height	Branches Per plants	Pods Per plant	Grains Per pod	100 Seed wt	Grain yield	Biological yield Per plant	H.i
SWATIXRACHNA	2.29**	0.30	167.14**	-10.99**	-4.55	5.70**	2.27**	7.71**	11.58**	-3.48
SWATIXKPMR400	0.00	-0.91**	102.86**	-4.93**	0.27**	1.78**	2.60**	1.19**	-7.38**	9.24**
SWATIXKPMR522	0.00	-1.52**	111.21**	4.93**	-10.00**	5.06**	3.45**	9.65**	-5.11**	15.59**
SWATIXSAPNA	5.14**	2.13**	105.71**	8.73**	-10.45**	-0.85**	-3.61	-17.06**	-6.80**	-14.19**
SWATIXSHIKHA	5.71**	3.95**	117.50**	7.75**	-7.95**	-3.28**	-4.18	-18.15**	-13.66**	-5.21**
SWATIXKPMR 940	2.86**	1.22**	121.64**	-4.23**	-6.14**	13.03**	5.49**	10.08**	21.69**	-9.54**
SWATIXKPMR 913	4.57**	1.22**	131.43**	-9.86**	-2.05**	3.77**	-9.69	-16.51**	-8.45**	-8.81**
RACHNAXKPMR400	-0.57**	-0.91**	80.71**	0.56**	8.41**	1.71**	2.09**	10.83**	11.82**	-1.25**
RACHNAXKPMR522	-1.14**	2.74**	93.61**	3.94**	11.14**	3.70**	3.45**	16.05**	12.90**	1.95**
RACHNAXSAPNA	2.29**	0.30	87.65**	6.34**	-3.18**	2.14**	-3.73**	-7.32**	9.46**	-9.41**

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RACHNAXSHIKHA	4.57**	0.30	98.62**	11.97**	11.82**	-0.71**	-4.00**	-7.64**	-7.69**	-5.63**
RACHNAXKPMR940	1.14**	0.30	89.39**	8.87**	13.18**	17.52**	6.06**	28.03**	28.28**	2.06**
RACHNAXKPMR913	7.43**	7.90**	93.49**	4.65**	-0.45	4.91**	-4.27**	0.11**	-0.57**	-0.07
KPMR40XKPMR522	-2.29**	2.74**	3.36**	3.52**	12.27**	5.63**	0.92**	16.44**	2.81**	13.33**
KPMR400XSAPNA	4.57**	0.30	-1.57**	8.73**	2.86**	0.07**	-4.16**	-9.35**	-0.95**	-8.49**
KPMR400XSHIKHA	4.00**	2.13**	8.21**	4.93**	-1.05**	-2.71**	-3.87**	-10.56**	-6.16**	1.99**
KPMR400XKPMR940	0.00	0.91**	4.29**	13.10**	-1.82**	17.24**	3.60**	25.06**	23.96	0.41
KPR400XKPMR913	1.71**	10.03**	3.79**	5.49**	-16.59**	3.21**	-3.92**	-2.55**	-10.43**	8.75**
KPMR522XSAPNA	-4.00**	-3.04**	7.99**	8.87**	-2.32	2.85**	0.82	-1.53**	1.77**	-3.24**
KPMR522XSHIKHA	1.14**	-0.91**	16.21**	4.51**	0.23**	-0.07	0.74	-1.64	-11.90	11.64**
KPMR522XKPMR940	-3.43**	-1.22**	18.29**	16.48**	9.55**	14.25**	2.47	25.63**	18.69**	4.05**
KPMR522XKPMR913	5.14**	4.26**	18.50**	8.31**	-2.95**	7.62**	-3.69**	1.39**	-0.79**	2.13**
SAPNAXSHIKHA	11.43**	4.86**	14.79**	14.08**	-5.64**	-2.14**	-4.32**	-14.07**	-6.82**	-7.78**
SAPNAXKPMR940	-1.71**	-1.22**	13.16**	16.20**	-1.14**	4.27**	-1.09**	-5.20**	22.87**	-19.13**
SAPNAXKPMR913	10.29**	4.26**	11.85**	10.99**	-4.68	1.71**	-3.95**	-10.15**	-10.08**	0.29
SHIKHAXKPMR940	-1.14**	-0.61	21.07**	13.10**	0.68**	2.14**	-3.42**	-3.28**	13.77**	-15.53
SHIKHAXKPMR913	11.43**	6.69**	20.50**	5.63**	-6.36**	0.21**	-4.19**	-11.74**	-5.19**	-6.51**
KPMR940XKPMR913	1.14**	3.04**	14.14**	4.37**	1.86**	3.21**	-1.83*8	0.02	17.37**	-14.83
S.E.	0.60	0.61	0.70	0.02	0.21	0.01	0.007	0.14	0.14	0.79

Table 3: Estimates of Heritability and Genetic Advance in F1s for 10 Characters.

S.no	Characters	Mean	Heritability % (ns)	Genetic advance	Genetic advance over mean (%)
1.	Days To Flowering	60.31	46.60	4.02	6.6
2.	Days to maturity	111.78	31.20	3.27	2.92
3.	Plant height	72.55	22.00	16.08	22.16
4.	Branches per plants	72.553	32.00	0.17	6.88
5.	Pods per plant	2.472	28.80	0.88	6.04
6.	Grains per pod	14.553	12.20	0.094	1.94
7.	100 Seed wt	20.539	14.30	0.310	1.50
8.	Grain yield per plant	14.67	23.90	1.32	8.99
9.	Biological yield per plant	29.88	27.00	2.98	9.97
10.	Harvest index	49.23	20.00	2.54	5

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