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Genetic Analysis of Flower Initiation in Pisum Sativum L.

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A diallel F_1 and F_2 analyses (graphic, component, combining ability and combining ability over environments) involving ten diverse cultivars of pea (*Pisum sativum* L.) representing extra early, early, medium and late groups for earliness revealed the importance of both additive and non-additive gene effects. However, additive gene effects were predominant. The *per se* performance of the parents was associated with their GCA effects. All the three analyses revealed that flowering was under the control of an additive system. Heritability in the narrowsense was high indicating that improvement can be made in desired direction by simple selection procedure.

In a country like India, where vegetarian diet is predominant, pulses constitute the main source of protein. Among the several pulses grown, pea (*Pisum sativum* L.) is one of the important grain legumes cultivated throughout the world, mainly in the temperate regions.

Pea improvement work in our country has primarily been confined to selection from local variability resulting into the establishment of pure lines. Pedigree selection in hybrid progenies of single crosses has also been used in this country, but with little success after the release of T163, about 20 years back. T 163 is a high yielding, long duration and widely grown cultivar, but suffers heavy yield losses due to powdery mildew in epiphytotic years. Thus attempts must be made to increase the productivity and stability of peas by evolving efficient plant typesa nd incorporating genes for earliness to escape from the incidence the powdery mildew occurrence. The present study was therefore, undertaken to characterise the nature and magnitude of gene action for the earliness trait i.e., flower initiation.

MATERIAL AND METHODS

Diallel crosses (Non-reciprocal) were made with ten diverse cultivars of pea namely Early December (ED), Arkel (Extra early), GC 322 (early), p-206, GC-141, GC-31, Selection-2. (S_2) (medium), and T-163, T-6115 and Duke of Albany (DA) (late). The ten parents and 45 F_1 progenies were planted in a randomized block design replicated twice during 1975-76 crop season. Data on days to bloom (first flower) were recorded from ten randomly selected plants from each of the parents and F_1's from each replication. In the final experiment, 45 each of F_1's and F_2's along with their parents were planted in a Compact Family Block Design, replicated thrice at the Agriculture Research Farm, Banaras Hindu University, during *rabi* 1976-77. The seeds were sown

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15cm apart in 3 metre long rows, spaced at 60 cm. Ten plants from each of the parents and F_1's and 50 plants from each of the F_2's, from each replication were considered for recording the observations. Flowering was noted when the first flower from each selected plant opened.

The data were subjected to graphic, component and combining ability analyses. Combining ability effects were estimated by the Method-2, Model I of Griffing (1956). Combining ability analyses of the F_1's pooled over environments (Years) was done according to the Griffing's (1956) method which was further extended by Sinah (1973).

RESULTS AND DISCUSSION

The graphic analysis was done according to the method proposed by Jinks (1954). The linear regression of Wr on Vr (Wr, Vr graph) and the limiting parabola are presented in Fig.1. The non-significant t^2 values (Table 1) showed that the Wr-Vr values were homogeneous and thus the assumptions for diallel analysis (Hayman, 1654) were satisfied.

In both F_1 and F_2, the regression line intercepted the Wr axis above the origin point indicating partial dominance for this trait (Fig. 1). The regression of Wr on Vr did not differ significantly from unity, suggesting the absence of non-allelic interaction. Considering the distribution of array points along the regression line in the F_1, the cultivars GC 141, GC 322, GC 31 and S_9 exhibited higher proportion of dominant alleles, whereas Arkel and ED carried greater proportion of recessive alleles. In the F_{2s} cultivars GC 322, GC 141, CC 31 and T 6115 possessed more dominant alleles, whereas Arkel was the top recessive. However, cultivar early variety, showed concentration of dominant genes for earliness.

The estimates of both additive (D) and non-additive (H_1 and H_2) gene effects were highly significant in both the generations (Table 1). The values of $H_2/4H_1$ were far from the expected value of 0.25 indicating the asymmetrical distribution of positive and negative genes among the parents. The estimates of degree of dominance $(H_1/D)^{1/2}$ indicated the presence of partial dominance for this trait, as was also observed in the graphic analysis.

The ratio of KD/KR, being higher than unity, indicating an excess of dominant alleles in the parents for this trait and a single group of genes showing dominance was operating. Narrow sense heritability was high in both the generations.

The three sets of diallel crosses (F_1's, F_2's and F_1's pooled over two years) were subjected to combining ability analysis following Griffing's Method-2, Model-I.

The analysis of variance of combining ability (Table 2) revealed that the variances due to both GCA and SCA were highly significant in all the three populations indicating the importance of both additive and non-additive gene effects. However, the additive gene effects were predominant.

The environment played a significant role on this trait. The GCA X environment (years) interaction was

significant, whereas SCA X environment was non-significant. Five parents, ED, Arkel, GC-322, P-206 and S_2 exhibited highly significant and negative effects for days to bloom (Table 3), thus, were the desirable general combiners for earliness. ED was the best general combiner for earliness followed by Arkel. The best cross for earliness was ED X Arkel, as revealed by the highest negative and significant SCA effects (Table 3). The other promising crosses were p 206 X DA, ED X T 163, GC 322 X T 6115, GC 322 X DA, GC 141 X T 6115 and GC 141 X T 163.

Since flowering is related with pod maturity, its inheritance has been investigated with a view to produce desirable cultivars. Flowering time in pea was reported under the control of a polygenic system and the gene effects were additive (Rowlands, 1964; Koranne, 1967; Watts, *et al*. 1970; Snoad and Arthur, 1973a and Kumar and Das, 1975). Lateness was dominant to earliness (Rowlands, 1964). Three major genes S_1, S_2 and E, controlling flowering in pea were also reported by Murfet (1971a&b).

In the present study, all the three types of analyses, i. e., graphic, component and combining ability, revealed that flowering in pea was controlled predominantly by additive genes. Such traits, thus, can effectively be improved by adopting standard breeding procedures, viz. pedigree and pure-line methods.

The two best general combiners for earliness, ED and Arkel, gave the hybrid (ED X Arkel) which was the earliest, as well as showed the highest negative SCA effects for this trait. Since the SCA effects in this cross were probably due to add. X add. type of interaction, there is a chance of getting good segregates from the cross.

There is a high correlation between the *per se* performance of the parents and their GCA effects, (Table3) thus, the *per se* performance of parents may give a reasonable indication of their GCA effects.

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TABLE 1 Estimates of components of variation and genetic ratios for days to flowering in pea

Estimates of components of variation	Days to flowering	
	F1	F2
D	180.0**± 6.9	214.0**± 13.8
H1	129.8**±14.8	447.6**±117.4
H2	85.9**±12.5	385.4**± 89.8
h^2	56.6**± 8.4	11.3 ± 66.8
F	152.9**±16.0	166.7* ± 63.6
E	6.9* ± 2.1	0.7 ± 4.1
$(H1/D)^{1/2}$	0.8	0.7
H2/4H1	0.1	0.2
$\frac{(4DH1)^{1/2}+F}{(4DH1)^{1/2}-F}$	3.0	3.3
$h^2/H2$	0.6	0.6
H1-H2	43.8	62.2
Heritebility% (narrow sense)	84.0	90.6
t^2	2.4	0.9

*, **Significant at P= 0.05 and P=0.01 respectively.

TABLE 2. GCA and SCA variances and their interactions with environment (years) for days to flowering in pea.

Source of variation	DF	Days to bloom		F_2s pooled over two years
		F_2	F_3	
GCA	9	253.5**	461.3**	373.3**
SCA	45	30.6**	26.5**	28.1**
Environments	1	–	–	501.9**
GCAx Environments	9	–	–	17.6*
SCA X Environments	45	–	–	9.5
Error	108	6.9	0.7	8.2

*, **Significant at P=0.05 and P=0.01 respectively.

TABLE 3. The *Per se* performance and estimates of general and specific combining ability effects for days to flowering in pea. (only significant values are given).

Parents/Crosses	Days to Bloom					
	F_1		F_2		F_1s spooled over two years	
	per se	GCA	per se	GCA	per se	GCA
P 206	50.0	−3.5**	44.8	−3.4**	49.5	−2.6**
ED	36.0	−5.6**	36.5	−8.0**	39.0	−6.8**
GC 322	44.1	−4.4	43.1	−5.7**	43 9	−3.9
GC 141	57.4	−0.2	56 3	0.9*	55.7	0.2
GC 31	51.7	1.0	53.1	1.6	53.1	0.7
S2	51.8	−1.1	49.1	−1.4**	49.6	−1.4*
T 6115	70·7	3.9**	72.6	8.3**	64.8	3.5**
T 163	70.9	7.1**	72.4	8.2**	70.7	7.3**
DA	72.6	6.6**	72.7	6.6	66.0	3.9**
Arkel	36.3	−3.7	34.8	−7.0	39.6	3.0**
S. E. (gi)		± 0.7		± 0.2		±0.5
C. D. at 5%		2.1		0.7		1.6
P 206×T163		8.5**		4.7**		2·8*
P 206×DA		−5.7*		−4.0**		—
ED×GC 322		4.9**		6.9**		5.2**
ED×S2		7.2		3.5**		3.8*
ED×T163		—		−5.6**		−4.5*
ED×Arkel		−9.2**		−4.7**		−6.5**
GC 322×T6115		−7.2**		−6.9**		—
GC 322×DA		−6.1*		−5.8**		—
GC 141×T6115		−5.6*		−4.8*		—
GC 141×T 163		−5.8**		−2.1**		—
GC 31 ×Arkel		11.4**		6.1*		7.5**
T160 ×Arkel		5.2		6.5		4.3*
SE (Sij)		±2.4		±0.8		±1.8
GD at 5%		7.1		2.3		5·4

*, ** Significant at P=0.05 and P=0.01 respectively.

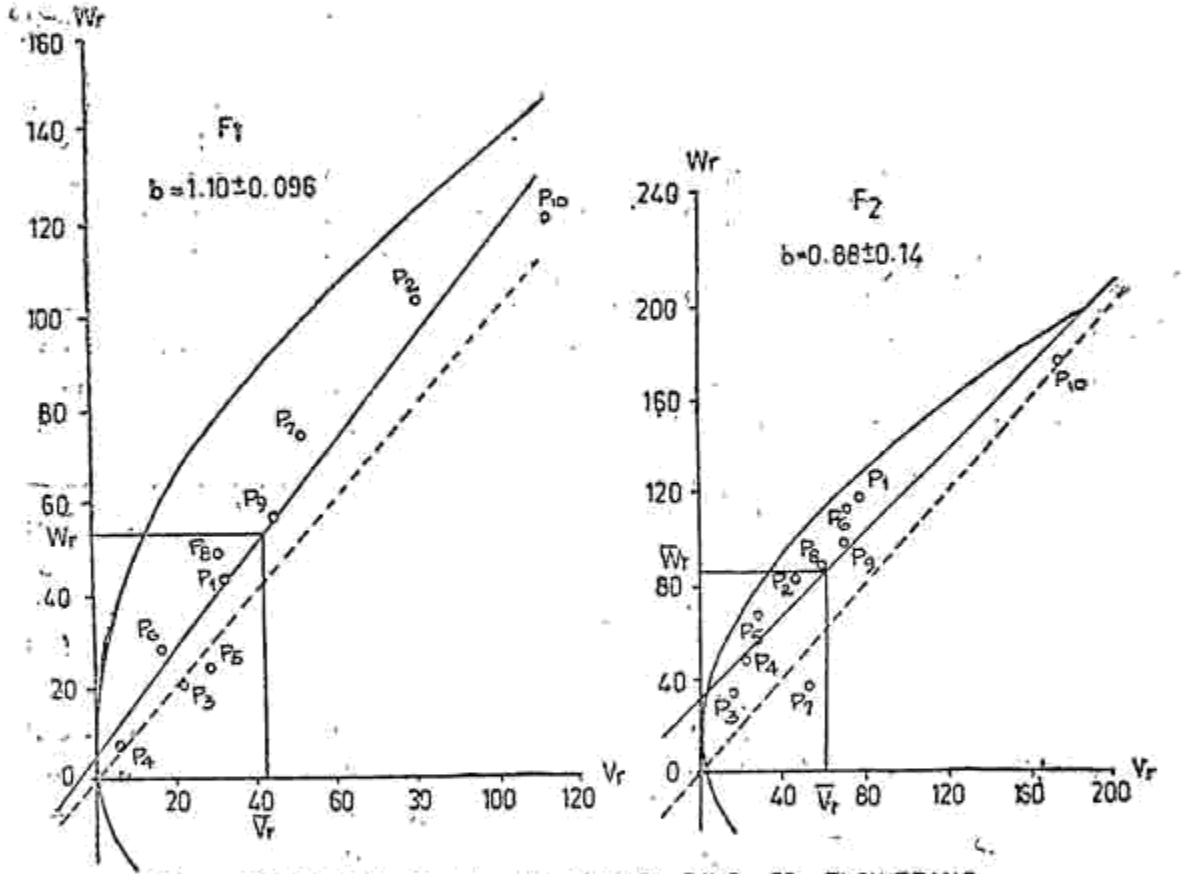

FIG.1- REGRESSION OF W_r ON V_r FOR DAYS TO FLOWERING

P_1=P206, P_2=ED, P_3=GC322, P_4=GC141, P_5=GC31, P_6=S_2, P_7=T6115, P_8=T163, P_9=DA, P_{10}=ARKEL