

COMBINING ABILITY OVER ENVIRONMENTS IN PEA

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ABSTRACT

The combining ability studies made over environments (years) revealed that both g.c.a. and s.c.a. are influenced by environments. This suggested that to have unbiased estimates of g.c.a. and s.c.a. the studies must be made over a wide range of environments. As additive gene effects were predominant, the pedigree method of breeding would be desirable for obtaining pure lines with desirable characters. Simultaneously, the diallel selective mating system among the good general combiners, may be followed to release greater genetic variability.

COMBINING ability is one of the powerful tools in identifying the best combiners which may be hybridized either to exploit heterosis or to accumulate fixable genes. However, scope of such studies is limited if they are not carried out over environments as the combining ability and inheritance of quantitative characters may vary over environments. Therefore, an attempt was made in the present study to analyse a ten parent diallel crosses over two environments (Years) for (i) combining ability \times environment (year) interaction, (ii) combining ability estimates on the data pooled over environments and (iii) the genetic systems governing these characters.

MATERIALS AND METHODS

Ten diverse cultivars of pea (*Pisum sativum* L.) namely P206, Early December (ED) GC 322, GC 141, GC 31, Selection-2 (S₂), T 6115, T 163, Duke of Albany (DA) and Arkel were crossed in all possible combinations excluding reciprocals. The ten parents and their 45 crosses were sown in a randomized complete block design with two replications at the research farm of Banaras Hindu University during two crop seasons of 1975-76 and 1976-77 *rabi*. In each replication, each of the parents and F₁S were represented by a single row of 2 m. The spacings between rows and within rows were maintained at 60 cm and 15 cm respectively. Non-experimental rows were provided all around the experiments to avoid border effects, if any. The data were recorded for days to first flowering, days to maturity, pods/plant, pod length, seeds/pod, 100-seed weight and seed yield/plant on 5 random plants per progeny from each replication. The progeny means were used for statistical analyses. The pooled analysis of combining ability was done according to Singh (1973) using method-2, model I of Griffing (1956).

RESULTS AND DISCUSSION

The analysis of variance for combining ability for the data pooled over environments revealed that both mean squares due to g.c.a. and s.c.a. were significant for all the characters studied indicating the importance of both additive and non-additive gene effects. However, additive gene effects were predominant.

The environment had a significant, role on almost all the characters. The mean squares due to g.c.a. \times environment interaction were significant for flowering, maturity, pod length and seed weight indicating that the parents were influenced by varying environments. Further, the mean squares due to s.c.a. \times environment interaction showed that the s.c.a. effects of the crosses for majority of the characters were not consistent over environments except for flowering and seeds/pod. It may, therefore, be suggested that for unbiased estimates of combining ability, the studies must be carried out over a range of environments.

The *per se* performance of the parents was closely associated with their g.c.a. effects (Table 1). Further, the g.c.a. effects revealed that the parents 'ED' and 'Arkel' for earliness; 'T 163', 'T 6115' for pods/plants; 'GC 141' and 'GC 31' for pod length; 'GC 141' and 'GC 322' for seeds/pod; 'P 206' and 'S₂' for seed weight, and 'T 163' followed by 'P 206' for seed yield were the best general combiners.

TABLE I

Mean performance and combining ability effects of parents in pea

Parent	Days to flowering	Days to maturity	Pods/plant	Pod length	Seeds/pod	100-Seed weight	Seed yield/plant
P 206	51.02	110.20	12.01	6.58	4.03	25.72	10.97
	-2.63**	-0.30	0.11	0.05	-0.33**	3.15**	0.22
ED	39.03	96.84	6.44	6.27	4.85	18.43	4.33
	-4.87**	-3.61**	-3.40**	0.04	0.17*	-0.92**	-1.69**
GC 322	43.96	104.12	7.15	6.27	4.94	19.77	6.00
	-3.95**	0.83**	-2.11*	0.15**	0.37**	-0.77**	0.06
GC 141	55.72	105.00	7.96	7.29	5.79	18.57	7.30
	0.29	0.31	-3.45**	0.48**	0.75**	-1.57**	0.11
GC 31	53.12	106.07	15.98	6.45	5.04	17.29	10.90
	0.75	0.89**	-1.86*	0.30**	0.23**	-1.79**	-0.52
S 2	49.69	103.93	13.14	6.71	4.01	24.15	8.74
	-1.45*	-0.84**	-0.62	-0.01	-0.23**	1.76**	-0.53
T 6115	64.89	113.96	20.67	5.58	4.13	19.63	10.22
	3.59**	2.70**	5.85**	-0.76**	-0.68**	-0.11	0.72
T 163	70.73	115.38	24.15	5.79	4.34	22.42	15.61
	7.32**	4.67**	5.33**	-0.29**	-0.07	0.48**	2.55**
DA	66.07	111.84	16.92	5.91	3.44	23.97	10.55
	3.95**	0.92**	2.75**	-0.19**	-0.48	1.10**	0.26
Arkel	39.67	95.76	5.95	6.91	5.06	18.46	4.99
	-3.00**	-3.92**	-2.58**	0.22**	0.26**	-1.60**	-1.18
S.E. (\hat{g}_i) \pm	0.56	0.27	0.90	0.05	0.07	0.12	0.60
S.E. ($\hat{g}_i - \hat{g}_j$) \pm	0.83	0.39	1.34	0.07	0.10	0.18	0.90

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

Upper and lower values indicate mean and g.c.a. effects respectively.

The best crosses as revealed by the s.c.a. effects were 'ED × Arkel', 'ED × 163' for earliness, 'P 206 × GC 141' and 'T 163 × Arkel' for pods/plant, 'GC 322 × T 163' and 'GC 322 × DA' for pod length, 'ED × Arkel' and 'P 206 × GC 322' for seeds/pod; 'GC 322 × T 6115' for seed weight and 'GC 322 × T 163' followed by 'T 163 × Arkel' for seed yield. It was interesting to note almost all these crosses involved one good and one poor or even a negative general combiner.

The present study revealed the importance of both additive and non-additive gene effects in the inheritance of the characters studied. Since additive gene effects were predominant, pedigree system would be the most efficient method for obtaining the desirable plant types. Simultaneously, diallel selective mating system among the parents on the basis of g.c.a. may result in breaking some undesirable linkages and release greater genetic variability.

REFERENCES

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