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Combining Ability and Gene Action Studies over Environments in Field Pea (*Pisum sativum* L.)

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Abstract: The experimental material comprising 28 F_1's, generated by crossing eight diverse lines of field pea in a half diallel fashion and their parents were evaluated in RBD in two replications at two locations during rabi, 2001-2002. The pooled analysis revealed that both gca and sca were influenced by environments which suggested that studies be conducted over environments to get unbiased estimates. The sca x E interaction was greater than gca x E interaction for most of the traits. The pooled component analysis revealed significance of both additive and dominance components. The parents Rachna, SKAU-P-4 and VL- I were found to be good general combiners for most of the traits. The best cross combinations in order by merit for seed yield were SKAU-P-4 x SKAU-P-10, VL-1 x Rachna and SKAUP-10 x Rachna. Diallel selective mating is advocated. Multiple crosses involving diverse parents can also be a viable approach for generating a wide genetic base population.

Key words: Field pea, diallel, combining ability over environments, gene action

INTRODUCTION

Most of the traits of economic importance are quantitative in nature and as such follow complex inheritance patterns. The proper understanding of the genetic systems underlying such an inheritance pattern is imperative for efficient management of available genetic variability and formulation of systematic breeding programs. The choice of parents for hybridization is one of the critical and most difficult tasks faced by plant breeders. The ability of parents to combine well depends on action, interaction and linkage relationships of genes not elucidated by mere yield performances. Combining ability studies are thus a prelude to any breeding strategy for selection of suitable genotypes for improving upon a crop species through hybridization. Besides it also elucidates the nature and extent of gene action. In fact breeding methods are dictated by action, interaction and linkage relationships of genes. Diallel analysis developed by Hayman (1954) and Griffing (1956) offers an excellent means of obtaining information on differential parental combinations in terms of general and specific combining ability, magnitude and direction of dominance and over-dominance and nature and extent of gene action. However, the scope of such studies is limited if such studies are not conducted over environments as the combining ability and inheritance of quantitative traits

vary with environments. Increasing the number of environments reduces the contribution of pooled error and additive × environment variances whereas increasing replications only reduces the pooled error (Eberhart *et al.*, 1995). A large number of studies have been carried out in garden pea but less published information on genetic architecture of quantitative traits is available in field pea. Therefore the present study was undertaken to study the combining ability estimates, combining ability × environment interaction and nature and extent of gene action in field pea.

MATERIALS AND METHODS

The present study was carried out at two locations, viz. Experimental farm of Shalimar campus of SKUAST-K and Pulses Research Station, SKUAST-K, Habak. Eight diverse lines of field pea namely SKAU-P-2, SKAU-P-4, SKAU-P-6, SKAUP-8, SKAU-P-2-1, SKAU-P-10, VL-1 and Rachna were crossed in all possible combinations without reciprocals. The 28 F_1's and eight parents were evaluated in RBD with two replications at each location during rabi 2001-2002. Each cross/parent was represented by a 3 m single row. The observations were recorded on 10 competent plants for different quantitative traits. The estimates of variance for gca and sca and their effects were computed according to Model-I (fixed effect model)

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and Method-Il (parents and crosses excluding reciprocals) as given by Griffing (1956). Combining ability analysis over environments was done following Singh (1973). Components of variance were estimated following Hayman (1954).

RESULTS

The combined analysis over environments (Table 1) revealed significant differences between genotypes. the parents and crosses interacted differentially with the environment. Crosses interacted with environment more markedly suggesting thereby that hybrids did not have the same relative performance across locations.

The pooled combining ability analysis of diallel data across environments (Table 2) revealed that variances due to general combining ability (gca) and specific combining ability (sca) were highly significant for all traits indicating importance of both additive and non-additive components. The widely used practice of assessing

relative importance of gca and sca on the basis of magnitudes of their mean squares has been found to be misleading (Arunachalam, 1976). In the present study sca variances were higher in magnitude than their corresponding gca variances indicating preponderance of non-additive gene action.

Both gca and sca interacted with environment. Interaction of gca with environment was significant for all traits except primary branches plant and harvest index where as sca x E interaction was non-significant for pod length. In all cases, sca × E variances were higher than corresponding gca × E variances which indicated that non-additive variances are more prone to environmental influences and that additive variances are relatively stable across environments. Singh and Singh (1990) also found the same trends in combining ability × environment interactions.

The perusal of gca effects of parents (Table 3) revealed that none of the parents was a good general combiner for all the traits studied. The parents Rachna

Table 1: Pooled analysis of variance for seed and other attributes in field pea (*Pisum sativum* L.)

SOV	df	No. of pods/plant	Pod length	No. of seed/pot	100 seed yield/plant (g)	Seed yield plant (g)	Biological yield/plant	Harvest index (%)
Environments	1	9.404**	0.117	2.102**	10.181**	63.786**	330.270**	144.200**
Block within environment	2	4.834**	0.949**	0.083	0.420	7.390**	142.502**	304.920**
Genotypes	35	12.458**	0.821**	0.732**	15.989**	70.998**	285.815**	18.200*
Parents	7	8.945**	0.7212**	0.4612**	17.483**	44.796**	171.714**	11.130
Hybrids	27	13.061**	0.864**	0.807**	15.794**	78.164**	318.742**	19.253**
Parents v/s hybrids	1	20.784**	0.351*	0.618**	10.797**	60.902**	195.496**	39.278**
Genotypes × environment interaction	35	10.232**	0.331*	0.623**	6.990**	15.853**	60.149**	16.453
Parents × environments	7	7.167**	0.195	0.565**	0.908**	15.502**	57.233**	22.957*
Hybrids × environments	27	11.143**	0.294	0.630**	8.819**	15.433**	60.918**	14.830
Parent v/s hybrids × environment	1	7.083**	2.292**	0.837**	0.192	29.633**	59.778**	14.777
Error	70	1.463	0.168	0.172	0.281	0.878	5.700	8.960

*, ** Significant at 5 and 1% level, respectively

Table 2: Analysis of variance for combining ability for seed yield and other attributes in field pea.

SOV	df	No. of pods/plant	Pod length	No. of seed/pod	100 seed weight (g)	Seed yield/plant (g)	Harvest indeed
gca	7	7.658**	0.462**	0.601**	12.654**	87.247**	8.897
sca	28	5.873**	0.397**	0.307**	6.829**	22.561**	9.451*
gca × E	7	5.581**	0.373**	0.353**	2.428**	3.126**	3.378
sca × E	28	4.999**	0.114	0.301	3.762**	9.126**	9.439*
$\sigma^2 g$	-	0.346	0.018	0.025	0.625	4.340	0.160
$\sigma^2 s$	-	2.570	0.156	0.110	3.344	11.061	2.485
$\sigma^2 gl$	-	0.484	0.028	0.026	0.228	0.268	0.110
$\sigma^2 sl$	-	4.268	0.029	0.215	3.621	8.687	4.958

*, ** Significant at 5 and 1% level, respectively

Table 3: Estimates of general combing ability effects for seed yield and other attributes in field pea (*Pisum sativu* L.)

SOV	No. of pods/plant	Pod length	No. of seed/pod	100 seed weight (g)	Seed yield/plant (g)	Harvest index (%)
SKAU-P-2	-0.061	-0.021	-0.280**	-0.616**	-1.866**	-0.277
SKAU-P-4	0.549**	-0.104	0.022	0.360**	-0.381*	0.061
SKAU-P-6	-0.666**	0.134*	-0.030	0.031	-1.615**	-0.367
SKAU-P-8	-0.856**	-0.103	-0.112*	-0.539**	-3.323**	-0.704
SKAU-P-2-1	-0.494**	-0.267**	-0.080	-0967**	1.608**	0.037
SKAU-P-10	0.599**	0.062	0.312**	-0.102	1.412**	-0.102
VL-1	0.446**	0.178**	0.136*	1.624**	2.084**	0.097
Rachna	0.751**	0.122**	0.078	0.211**	2.081**	1.423**
SE gi	±0.158	±0.060	±0.078	±0.078	±0.138	±0.442
Se gi-gi	±0.270	±0.091	±0.118	±0.118	±0.209	±0.669

*, ** Significant at 5 and 1% level, respectively

and VL-1 were found to be good general combiners for pod length, 100 seed weight and seed yield plant^{-1}, SKAU-P-4 was a good general combiner for 100 seed weight. The parent SKAU-P-6 was a good combiner for pod length.

The best cross combinations (Table 4) in order of merit were SKAU-P-4 × SKAU-P-10, (seed yield plant-' and 100 seed weight), VL-I × Rachna (number of pods plant-'), SKAU-P-8 × SKAU-P-2-1 (harvest index) SKAU-P-4 × SKAU-P-6 (pod length).

The pooled estimates of various genetic components of variance (Table 5) revealed that additive component [D] was significant for number of pods plant^{-1}, 100 seed weight and seed yield/plant, while as dominance

components (H_1 and H_2) were highly significant for all traits. However, the magnitude of dominance components was higher as compared to additive component indicating preponderance of non-additive gene effects. F value was non-significant for all traits which indicated that there was equal frequency of dominant and recessive alleles at the loci exhibiting dominance. The environmental component (E) was significant for number of seeds pod and harvest index only. Singh and Sharma (2001) found similar results for yield and its components in pea. The perusal of various proportions of genetic parameters revealed that the average degree of dominance was in the range of over dominance since the value of $(H_1/D)1/2$ was greater than unity for all traits. The ratio $H_2/4H_1$ was less than the

Table 4: Best Crosses based on pooled analysis in respect of *per se* performance and specific combining ability effects

Character	per se performance (value)	sca effects (value)
Number of pods/plant	VL-1 × Rachna (13.40)	VL-1 × Rachna (4.199)
	SKAU-P-4 × SKAU-P-10 (12.80)	SKA U-P-2 × SKAU-P-8 (2.516)
	SKAU-P-10 × Rachna (12.62)	SKAU-P-2 × SKAU-P-2-1 (2.219)
	SKAU-P-2 × SKAU-P4 (11.52)	SKAU-P-4 × SKAU-8 (2.056)
	SKAU-P-4 × SKAU-P-2-1 (11.00)	SKAU-P-10 × Rachim (1.699)
Pod length	SKAU-P-4 × SKAU-P-6 (7.14)	SKAU-P-4 × SKAU-P-6 (0.723)
	SKAU-P-4 × SKAU-P-10 (7.07)	SKAU-P-2 × SKAIJ-P-8 (0.707)
	SKAU-P-6 × SKAU-P-10 (6.98)	SKAU-P-2-1 × Rachna (0.463)
	SKAU-P-2 × SKAU-P-8 (6.97)	SKAU-P-2 × SKAU-P-6 (0.435)
	SKAU-P-6 × VL-1 (6.95)	SKAU-P-4 × SKAU-P-10 (0.430)
No. of seeds/pod	SKAIJ-P-6 × SKAU-P-10 (6.32)	SKAU-P-6 × SKAU-P-10 (0.662)
	VL-1 × Rachna (6.17)	SKAU-P-4 × SKAU-P-10 (0.509)
	SKAU-P-4 × SKAU-P-10 (5.97)	VL-1. × Rachna (0.477)
	SKAU-P-2-1 × SKAU-P-10 (5.97)	SKAU-P-4 × SKAU-P-2-1 (0.477)
	SKAU-P-4 × SKAU-P-2-1 (5.80)	SKAU-P-2 × SKAU-P-6 (0.404)
100 seed weight	SKAU-P-4 × SKAU-P-10 (26.66)	SKAU-P-4 × SKAU-P-10 (5.0S9)
	SKAU-P-8 × VI-I (24.36)	SKAU-P-2 × SKAU-P-6 (2.962)
	VL-1 × Rachna (24.10)	SKAU-P-8 × SKAU-P-10 (2.158)
	SKAU-P-2 × SKAU-P-6 (23.73)	SKAU-P-8 × VL-1 (1.925)
	SKAU-P-4 × Rachna (23.54)	SKAIJ-P-2 SKAU-P-8 (1.917)
Seed yield/plant	VL-1 × Rachna (19.43)	SKAU-P-4 × SKAU-P-10 (6.827)
	SKAU-P-10 × Rachna (18.07)	SKAIJ-P-10 × Rachna (6.397)
	SKAUT-2-1 × Rachna (15.85)	VL-1 × Rachna (4.910)
	SKAU-P-4 VLA (15.82)	SKAU-P-2 × SKAU-P-6 (4.610)
	SKAU-P-2-1 × VI-I (15.09)	SKAU-P-2- × SKAU-P-10 (4.071)
Harvest index	SKAU-P-2 × Rachna (52.6)	SKAU P-8 × SKAU-P-2-1 (4.214)
	SKAU-P-6 × Rachna (5 1.9)	SKAU-P-6 × SKAU-P-10 (3.892)
	SKAIU-P-6 × SKAU-P-10 (51.5)	SKAU-P-2 × Rachna (3.502)
	SKAU-P-8 × SKAUT-2-1 (51.4)	SKAIJ-P-6 × Rachna(2.792)
	SKAU-P-4 × SKAU-P-10	SKAU-P-2 × SKAU-P-8 (2.479)

Table 5: Estimates of genetic parameters and their proportions for seed yield and component traits in field pea

SOV	No. of pods/plant	Pod length	No. of seeds/pod	100 seed weight (g)	Seed yield/plant (g)	Harvest index (%)
D	1.870±0.800*	0.140±0.090	0.070±0050	4.300±2.030**	10.980±5.570*	0.540±1.860*
H_1	11.390±1.830**	0.750±0.210**	0.550±0.120**	15.440±4.660**	49.920±12.790**	13.530±2.910**
H_2	10.040±1.600**	0.660±0.190**	0.470±0.110**	11.920±4.050*	39.500±11.130**	12.870±2.530**
h^2	2.380±1.070	0.020±0.120	0.060±0.070	1.300±2.720	7.400±7.460	3.850±1.700
F	1.640±1.890	0.140±0.220	0.20±0.130	5.060±4.790	0.330±13.150	0.070±2.990
E	0.360±0.270	0.040±0.030	0.040±0.020*	0.070±0.680	0.220±1.860	2.240±0.420
$(H_1/D)1/2$	2.47	2.320	2.770	1.900	2.130	5.00
$H_2/4H_1$	0.220	0.220	0.210	0.190	0.200	0.240
$\frac{(4DH_1)1/2+F}{(4DH_1)1/2-F}$						
(KD/KR)	1.430	1.570	1.110	1.900	1.010	1.020
h^2/H_2	0.237	0.030	0.127	0.109	0.187	0.299
Habitability (ns)	0.142	0.152	0.196	0.207	0.178	0.236

*, ** Significant at 5 and 1% level, respectively

theoretical value of 0.25 indicating asymmetric distribution of positive and negative alleles in parents. There was preponderance of dominant genes in parents depicted by the value of KD/KR (more than unity for all traits). The heritability was low for most of the traits. Similar results in pea have been reported by Singh and Sharma (2001).

DISCUSSION

In the present study significant gca and sca effects were reported for most of the yield components indicating importance of both additive and non-additive gene effects. However the sca estimates were relatively greater than the corresponding estimates of gca, indicating preponderance of non-additive genetic variances. Similar results have been reported in field pea by Sachan *et al.* (2001), Dixit (2003) and Singh and Singh (2004). Hybrid breeding, though, theoretically a good approach of pea improvement has certain apparent limitations due to non-availability of efficient male sterility systems in pea thus making large scale hybrid seed production non-feasible. The heritability estimates were low in the present study therefore expected genetic gains through mass, pedigree or family selection would not yield encouraging results. Singh and Singh (2004) proposed that in case of traits with low to moderate heritability, biparental mating followed dy progeny selection would be an ideal approach for isolation of transgressive segregants and desirable recombinants. However, the good combining parents SKAU-P-4, VL-1 and Rachna can be crossed with elite genetic resources to broaden their genetic base. Further since both additive and non-additive effects are important, diallel selective mating and multiple crossing followed by recombination can also be viable approaches, which will help break tight linkages to make potential variability available for selection (Webel and Lonquist, 1967). Also the lines showing good combining ability for yield components can bee used in component breeding thereby seeking improvement in yield.

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