ESTIMATION OF COMPONENTS OF GENETIC VARIANCE AND GRAPHICAL ANALYSIS IN FIELD PEA (*PISUM SATIVUM* (L.) VAR. *ARVENSE*)

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Abstract: Genetic analysis was carried out by 8 x 8 diallel analysis (excluding reciprocals) of Field pea (Pisum sativum (L.) *var arvense*) genotypes. The results of t^2 test indicated the fulfillment of assumptions required under diallel analysis for all the characters under study except number of primary branches, grain yield (g) and harvest index (%). Narrow sense heritability was low for number of seeds per pod and most of the other trait except Days to 50% flowering and plant height which had moderate to high heritability. A higher proportion of dominant genes were observed in parent PRAKASH for affecting number of pods per plant. The parental line ADARSH was found having maximum recessive gene for increasing the protein content.

Keywords: Degree of dominance, Dialle, Fieldpea, Gene action

INTRODUCTION

For improving the genetic yield potential of the varieties and hybrids, choice of right type of parents for hybridization is important. The development of high yielding varieties with good processing quality is of immense importance. In case of grain legumes, it is not only the yield but quality parameters are also of prime concern for overcoming the protein malnutrition. Appreciable genetic diversity is the backbone of any successful hybrid/ variety development programme. The diallel analysis provides a systematic approach for identification of superior parents and crosses which is the basic material. Several reports in past have appeared which indicate that diallel analysis is the quickest method of understanding the genetic nature of quantitatively inherited traits and to ascertain the prepotency of parents. Kearsey (1965) noted that Hayman and Jinks' diallel analysis provide more information than other methods, but has more necessary assumptions. The analyses proposed by Griffing (1956a) do not provide any test to detect epistasis or linkage. Hayman and Jinks' analysis does provide such test, developed a graphical approach, using second order statistics for estimation of genetic components of variance in diallel crosses. When using Griffing's analysis to estimate variance components, it has been suggested that simple tests, such as the Wr-Vr evaluation found in Haymans' (1954b) model. The regression of array covariance (Wr) on array variance (Vr) provides geometric representation of the degree of dominance free from spurious dominance caused by non-allelic interactions.

MATERIAL AND METHOD

The present investigation consisted of eight diverse parental lines of Field pea *[Pisum sativum (L.) var arvense]* and their twenty-eight F_1s (excluding reciprocals). The parental lines *viz*., DF-1, KPMR 400, VIKAS, PRAKASH, ADARSH, IPFD 10-13, NDP-1, APARNA were selected from germplasm maintained at Centre of Excellence for Research on pulses, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, District: Banaskantha, during *rabi*, 2012 to create a diallel set. The complete set of 36 genotypes comprising eight parental genotypes and 28 F_1's were evaluated in Randomized Block Design (RBD) with three replication. The seeds of 28 F_1 hybrids were produced by hand pollination. For male and female parents, self seeds were collected during the same season. The observations were recorded both as visual assessment (Days to 50% flowering, days to maturity) and measurement on randomly selected five competitive individual plants (plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, Grain yield per plant (g), test weight (g), protein content (%), harvest index (%).

RESULT AND DISCUSSION

The analysis of variance for parents and their hybrids for different characters revealed that the variances due to genotypes were highly significant for all the characters. This indicated the presence of considerable genotypic diversity for all the characters. The parents and hybrids variances were highly significant for all the traits. The variances due to parents vs. hybrids were significant for all the traits except for days to 50% flowering, days to

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maturity and plant height indicated that F1's had heterotic effects (Table 1).

The non-significant t^2 value indicates that the additive-dominance model was adequate to explain the variation. The results of t^2 test indicated the fulfillment of assumptions required under diallel analysis for all the characters under study except number of primary branches, grain yield (g) and harvest index (%). Non-fulfillment of assumptions in these traits indicated the invalidity of the hypothesis of simple additive – dominance model of gene action and involvement of epistasis and/or linkage disequilibrium.

The estimates of D which measure the variance due to additive gene effects were significant for Days to 50% flowering, days to maturity, plant height, number of pods per plant, grain yield per plant (g) and test weight (g). Thus additive gene effects were significant for these characters. This was reflects in high heritability of Days to 50% flowering and plant height.

The H1, which measure the variance due to non-additive effects, was significant for all the characters. This clearly indicates the predominance of non-additive gene action for all the characters under study. The estimates of dominance ratio $(H1/D)^{0.5}$ greater than unity for all the traits indicating over dominance for all of the characters. Similar findings were reported by Kosev *et al.* (2013), Punia *et al.* (2013), Dalia and Naseef (2013) observed the similar findings for grain yield per plant.

The equal distribution of positive and negative genes in the parents helps the breeder in selecting particular desirable trait without loosing any other desirable traits. In the present study more or less symmetrical distribution of genes in the parental lines was observed for plant height, number of seeds per pod and test weight in present study as the value H2/4H1 was closer to 0.25. Mather and Jinks (1971) while discussing the short comings of numerical component analysis suggested that $(H1/D)^{0.5}$ at each locus is true for major degree of dominance only, where the distribution of dominance and recessive genes is symmetrical. Asymmetrical distribution of genes for may influence of over estimation of mean degree of dominance.

The values of component KD/KR indicated unequal frequency of dominant and recessive genes with higher frequency of dominant genes for all the characters studied except number of seeds per pod. Knowledge of number of genes/group of genes responsible for particular traits is important for the genetic progress through selection. The value h_2/H_2 indicated at least one group of gene was operating for all the traits of present study. Estimated narrow sense heritability was low for number of seeds per pod and most of the other trait except Days to 50% flowering and plant height which had moderate to high heritability.

The correlation between parental order of dominance (Vr + Wr) and parental mean (Yi) was positive and significant for number of pods per plant which indicated involvement of recessive alleles for increasing the mean values. Thus, recessive genes were responsible for increasing number of pods per plant. For number of seeds per pod the correlation was negative indicating role of dominant genes for increasing mean values.

The regression of Wr on Vr was desirable and near unity for number of pods per plant validity of simple additive-dominance hypothesis of gene action for this character. Whereas significant t^2 value for number of primary branches, grain yield (g) and harvest index (%) leads to failure of hypothesis for these characters. The graphical presentations for these traits were therefore not attempted.

In graphical analysis the regression line intercepted Wr axes below the origin indicated over dominance for all the characters. The wide scattering of parental array points along the regression line in the Wr-Vr graph for Days to 50% flowering, days to maturity and protein content indicated considerable genetic diversity among the parents for these traits. In graphical analysis, a higher proportion of dominant genes were observed in parent PRAKASH for affecting number of pods per plant. The parental line ADARSH was found having maximum recessive gene for increasing the protein content (Table:2).

Table 1. Analysis of variance (mean squares) for parents and hybrids for different characters in fieldpea

Source of variation	d.f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	Grain yield per plant (g)	Test weight (g)	Protein content (%)	Harvest index (%)
Replications	2	6.75	29.06	127.92	0.1	4.33	0.29	1.99	0.91	0.36	4.40
Genotypes	35	61.61**	105.36**	5613.5**	1.49**	523.96**	4.29**	256.38**	7.78**	2.72**	328.15**

Parents	7	49.08**	139.59**	5335.9**	0.54**	378.31**	0.55**	148.27**	7.87**	2.79**	142.30**
Hybrids	27	67.14**	99.98 **	5891.9**	1.76**	501.34**	5.28**	252.95**	7.94**	2.42**	366.74**
Parents vs. Hybrids	1	0.14	10.83	40.89	0.82**	2154.2**	3.78**	1105.6**	2.93*	10.21**	587.10**
Error	70	3.26	13.35	69.36	0.06	11.26	0.18	4.94	0.48	0.17	7.51

Table 2. Estimation of genetic component of variance and other parameters for various characters in Fieldpea

	Parameters	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**Number of primary branches per plant**	**Number of pods per plant**	**Number of seeds per pod**	**Grain yield per plant (g)**	**Test weight (g)**	**Protein content (%)**	**Harvest index (%)**
1	b (Wr, Vr)	0.10	0.19	0.22	0.32	0.80	-0.03	0.47	0.12	0.12	0.12
2	t_{b-0}	-0.37	-0.58	-1.08	-2.06	-2.97*	0.14	-4.13**	-0.59	-0.55	-1.74
3	t_{1-b}	3.08*	2.43*	3.71*	4.24**	0.72	4.37*	4.65**	4.05**	3.97**	12.35**
4	t^2	0.70	0.20	2.72	5.47*	0.023	1.97	9.48**	2.68	2.45	45.23**
5	D	15.24*	41.93**	1754.94*	-	122.41*	0.12	-	2.45*	0.87	-
6	H_1	85.31**	125.72**	4717.07*	-	676.96**	6.09**	-	11.10**	3.86*	-
7	H_2	44.33*	69.13*	4122.08*	-	506.69**	5.80**	-	9.25**	2.98*	-
8	F	32.53*	62.78*	207.76	-	167.97*	-0.10	-	3.33	1.38	-
9	h^2	-0.46	-0.23	-3.64	-	351.82**	0.59	-	0.40	1.64*	-
10	E	1.12	4.59	23.66	-	3.69	0.06	-	0.16	0.05	-
11	$(H_1/D)^{0.5}$	2.36	1.73	1.63	-	2.35	7.10	-	2.12	2.10	-
12	$H_2/4H_1$	0.13	0.13	0.21	-	0.18	0.23	-	0.20	0.19	-
13	KD/KR	2.64	2.52	1.07	-	1.82	0.88	-	1.93	2.21	-
14	h^2/H_2	-0.01	-0.003	-0.001	-	0.69	0.10	-	0.04	0.55	-
15	r(P, Wr +Vr)	0.15	0.23	0.40	-	0.77*	-0.05	-	0.23	0.22	-
16	Heritability	0.49	0.45	0.50	-	0.32	0.14	-	0.16	0.18	-

* and ** indicates significant at P = 0.05 and P = 0.01 levels, respectively.

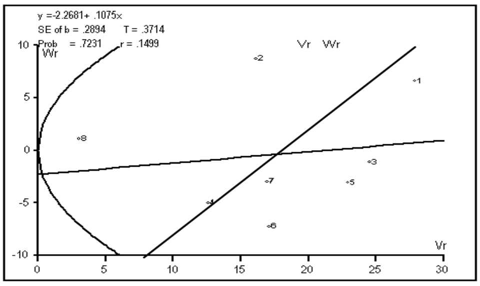

Fig 1. Wr, Vr graph for days to 50% flowering

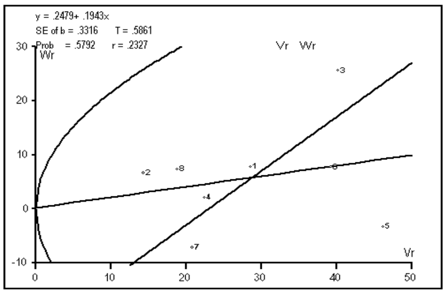

Fig 2. Wr, Vr graph for days to maturity

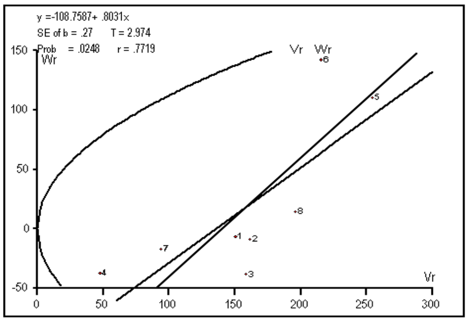

Fig 3. Wr, Vr graph for number of pods per plant

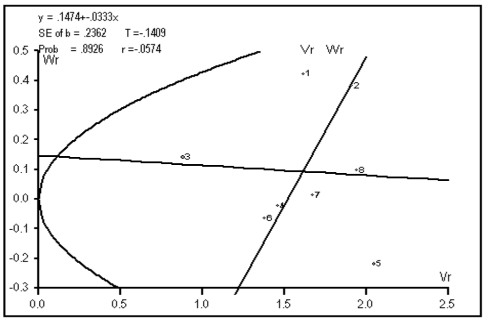

Fig 4. Wr, Vr graph for number of seeds per pod

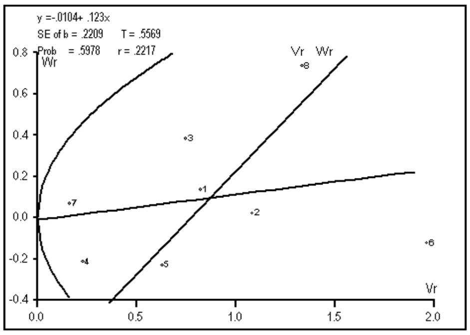

Fig 5. Wr, Vr graph for protein content (%)

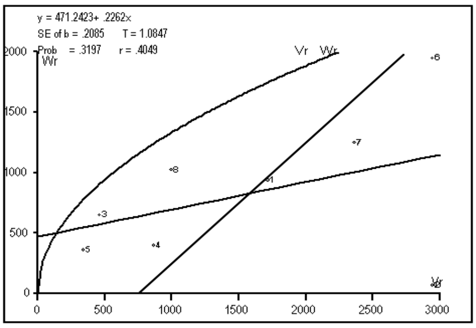

Fig 6. Wr, Vr graph for plant height (cm)

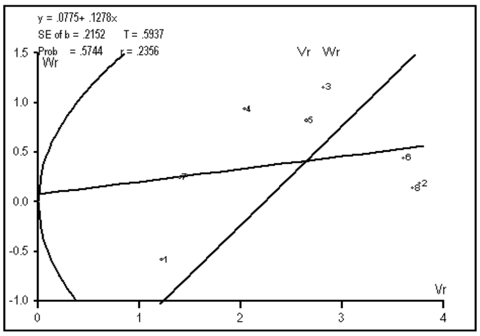

Fig 7. Wr, Vr graph for test weight (g)

Where,

1= DF-1
2 = KPMR 400
3 = VIKAS
4 = PRAKASH
5 = ADARSH
6 = IPFD 10-13
7 = NDP-1
8 = APARNA

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