ESTIMATES OF GENETIC COMPONENTS AND RELATED STATISTICS OF DIALLEL CROSS IN VEGETABLE PEA (*Pisum sativum* L.)

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ABSTRACT : The experiment was carried out at Farm of Krishi Vigyan Kendra, Pampoli, East Kameng, Arunachal Pradesh during 2012-13. Generation means analysis was carried out to estimate the nature and magnitude of gene action in order to formulate breeding strategy for identifying the segregates with desirable horticultural traits and resistant to powdery mildew disease. The testing of validity of the assumptions is based on estimated values of t^2 and regression coefficient (b) based on F_1s. It is clear from the table that t^2 was significant for pod length, pod width and 100 grain weight which reflect the failure of one or few assumptions.

Garden pea (*Pisum sativum* L.) is one of the most important cool season leguminous vegetable crops in the north east region in India. Owing to diverse agro climatic condition in Arunachal Pradesh, the crop is grown year round, generating lucrative returns to the growers. In the high altitude areas of Arunachal Pradesh, pea is grown as an off-season cash crop during summer, whereas in winter, it is cultivated in low and mid hills. Besides being a major source of plant-based dietary protein for humans and animals, this annual legume is a significant contributor to agriculture sustainability because of its ability to fix atmospheric nitrogen (Singh *et al.,* 5). Garden pea is an a autogamous crop and thus recombinant breeding is the most appropriate approach to combine various traits of interest. The most frequency used designs namely; diallele and line x tester analysis do not provide the estimates of epistatic. It is important to identity and estimate non-allelic interaction which could otherwise inflate the measure of additive and dominance components. The generation mean analysis is based on first order statistics, whereas triple test cross and biparental cross are based on second degree statistics. The matting designs such as generation mean analysis, triple test cross and biparental cross provide information about all the three components of variance *viz.,* additive, dominance and epistatic.

MATERIALS AND METHODS

The experiment was carried out at Farm of Krishi Vigyan Kendra, Pampoli, East Kameng, Arunachal Pradesh during 2012-13. The material was shown in Randomized Block Design comprising 10 treatments with 3 replications. The 45 F_1s along with their 10 parents were sown in November-2012 in a RBD with three replications for their performance in a single row length of 3.50 m maintaining row to row 50 cm and plant to plant spacing of 10 cm. Each replication comprised of 55 plots. Observations were recorded on ten randomly selected plants from both parents and F1 F_1s from each replication. The selected plants were labeled properly before flowering for recording the observations. Each replication accommodated ten plants in a row for entry. Data were collected on ten quantitative characters, *viz.,* days to flowering, days to maturity, plant length, Number of pods per plant, pod length, number of pods per plant, pod length, pod width, number of seeds per pod, length of first fruiting inter node, 100 grain weight, green pod yield per plant and yield per plant. Data were analysed as per methods described by Gardner and Eberhert (2) and Yates (7).

RESULTS AND DISCUSSION

The testing of validity of the assumptions is based on estimated values of t^2 and regression coefficient (b) based on F_1s are presented in Table 1. It is clear from the Table that t^2 was significant for pod length, pod width and 100 grain weight which reflect the failure of one or few assumptions. To different genetic

Table 1: Estimates of genetic components & related statistics for 12 characters in 10x10 diallel cross in vegetable pea

Characters	Generation	D	H_1	H_2	F	h^2	E	$(H_1/D)^{0.5}$	$(H_2/4H_1)$	$(4DH_1)^{0.5}+F$ / $(4DH_1)^{0.5}-F$	h^2/H_2
Days to flowering	F_1	64.29**	61.42**	58.05**	18.41	2.63	0.40	0.98	0.24	1.34	0.05
	SE ±	7.11	15.14	12.87	16.41	8.61	2.14				
Days to maturity	F_1	88.80**	73.42**	64.72**	-11.80	-0.18	0.62	0.91	0.22	0.86	0.00
	SE ±	5.78	12.31	10.46	13.34	7.00	1.74				
Plant length (cm)	F_1	212.57**	257.82**	235.22**	-82.26	-0.18	0.75	1.10	0.23	0.70	0.00
	SE ±	18.66	39.71	33.75	43.04	22.59	5.62				
Pod length (cm)	F_1	0.75**	2.36**	2.23**	0.01	2.01**	0.01	1.77	0.24	1.00	0.90
	SE ±	0.24	0.50	0.43	0.54	0.28	0.07				
Pod width (mm)	F_1	0.06	0.97**	0.87**	0.06	0.61**	0.03	4.02	0.22	1.26	0.70
	SE ±	0.12	0.26	0.22	0.28	0.15	0.04				
Number of seeds per pod	F_1	0.86**	1.61**	1.53**	0.18	0.61	0.23*	1.37	0.24	1.17	0.40
	SE ±	0.28	0.60	0.51	0.65	0.34	0.09				
Length to first fruiting inter node	F_1	55.70**	62.69**	58.18**	14.73	3.03	0.44	1.06	0.23	1.28	0.05
	SE ±	4.30	9.15	7.78	9.92	5.21	1.30				
Number of first fruiting node	F_1	5.14**	9.60**	6.76**	7.19**	0.26	0.33	1.37	0.18	3.09	0.04
	SE ±	0.59	1.25	1.06	1.36	0.71	0.18				
100 grain weight (g)	F_1	2.79**	0.28**	0.34**	0.07	3.23**	0.10**	0.32	0.30	1.08	9.61
	SE ±	0.04	0.09	0.08	0.10	0.05	0.01				
Grain pod yield per plant (g)	F_1	203.12**	191.18**	171.64**	54.33	348.10**	2.98	0.97	0.22	1.32	2.03
	SE ±	13.55	29.06	24.70	31.50	16.53	4.12				
Yield per plant (g)	F_1	3.95**	8.43**	7.08**	3.43**	24.85**	0.09	1.46	0.21	1.85	3.51
	SE ±	0.52	1.11	0.94	1.20	0.63	0.16				

* Significant at 5 per cent level, ** Significant at 1per cent level

components of variance *viz.,* D, H_1, H_2, F, h^2 and $\hat{E}$ along with their standard errors; mean degree of dominance $(H_1/D)^{0.5}$, the proportion of dominant and recessive genes in parents $(4H_1/D)^{0.5} + F / (4H_1/D)^{0.5} - F$ and the number of gene group which control the traits and exhibit dominance h^2/H_2 were calculated and the results are furnished in Table 1 for all the twelve characters based on F_1s. The additive component D was significant for all the characters under study except for pod width. Results are in confirmity with reports of Gupta and Singh (3) and Singh and Dhillon (6). The dominance components, H_1 and H_2 were significant for all the characters. The estimated values of H_1 were higher than H_2 for all the characters which indicated that genes are unequally distributed among parents. The F component was positive and significant only for number of 1st fruiting node and yield per plant indicating the presence of excessive dominant genes for controlling these traits. Other characters showed the presence of excess of recessive genes. The h^2 was also significant for number of pods per plant, pod length, pod width, 100-grain weight, green pod yield and yield per plant only indicating the presence of dominance. Other characters showed the presence of partial dominance. The environmental component was significant only for number of seeds per pod and 100 grain weight indicating the role of environment for expression of characters. The mean degree of

dominance revealed over dominance for all the characters under study except for days to flowering, days to maturity, 100 grain weight and green pod yield per plant where it was as partial dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$,were less than its theoretical value (0.25) for all the traits indicating that the genes were asymmetrically distributed among parent. The ratio of h^2/H_2 was less than one for all the characters indicating that at least one major gene group was responsible for controlling the characters except 100 grain weight which showed the presence of at least nine gene groups ,green pod yield (two gene groups) and yield per plant(more than three gene groups with some modifiers).The proportion of dominant and recessive genes in parents $(4H_1/D)^{0.5} + F / (4H_1/D)^{0.5}$

– F showed that more frequency of dominant groups than recessive ones were present for all the traits except days to maturity, plant length and number of pods per plant. Above findings are in consonance with reports of Askel and Johnson (1), Singh and Singh (4) and Singh and Dhillon (6).

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