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Components of genetic variation for pod yield and associated traits in garden pea (*Pisum sativum* L.)

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Abstract

Seven diverse genotypes of garden pea were crossed in a diallel mating design (excluding reciprocals) to ascertain the genetic architecture and nature of gene action involved in the inheritance of pod yield and its associated traits following Haymans' approach. The GCA and SCA variances were found significant for all the traits studied. The predictability ratio (σ^2sca/σ^2gca) was more than unity for all the traits studied except for days to 50 % flowering. Both additive (D) and non-additive (H_1, H_2) components were found significant for all the traits excepting additive component for pod yield per plant, shelling percentage, days to first picking and TSS. The mean degree of dominance revealed the presence of over dominance for all the traits which was probably due to the predominant role of non-additive genetic variation. The equal distribution of positive and negative genes in the parents was observed for days to 50 % flowering, duration of availability of marketable pods, pods per plant, seeds per pod, pod width and shelling percentage. Low narrow sense heritability estimates were observed for pod yield per plant, pods per plant, days to 50 % flowering, days to first picking, duration of availability of marketable pods and TSS. Based upon the nature of gene action as inferred from component analysis, a line of improvement of a particular trait was suggested.

Key words: Genetic variation, *Pisum sativum*, pod yield.

Introduction

Garden pea (*Pisum sativum* L.) is one of the most important leguminous vegetable, grown widely both for fresh market and processing. In recent past, several high yielding disease resistant genotypes of both early and mid maturing groups have been identified, developed and made available for commercial cultivation but still it holds future promise as the demand for high yielding strains is increasing day by day. Hence, it becomes important to study the genetic architecture of yield and yield contributing traits and their rational manipulation for the development of high yielding genotypes following appropriate breeding methodology. The knowledge of the type and magnitude of genetic variation influencing the expression of the traits of economic importance is extremely important for devising a sound breeding strategy. The component analysis besides providing information pertaining to gene action also determines the nature and extent of genetic variation present in the population which is extremely important in formulating an efficient breeding programme. The present study was therefore, designed and executed to gather information on gene action and other parameters of genetic variation influencing yield and yield contributing traits of mid maturing and diverse genotypes of garden pea.

Materials and Methods

The experimental material consisted of seven diverse genotypes of garden pea, namely Palam Priya, Azad Pea-1, Lincoln, DPP 9418-06, DPP-3, DPPLMR-41 and Pb-89 which were crossed in a diallel mating design (excluding reciprocals). The resultant 21 F_1 hybrids along with their seven parents were evaluated during Rabi, 2008-2009, in RBD with three replications at the experimental farm of Department of Vegetable Science and Floriculture, CSK HPKV, Palampur (HP). Each experimental plot comprised of two rows of 1.8m length for each parents and F_1s, accommodating 18 plants per row, with an intra and inter row distance of 10 and 45cm, respectively. The data were recorded on ten competitive plants selected at random from each treatment and each replication for days to 50% flowering, days to first picking, duration of availability of marketable pods, pod length, pod width, seeds per pod, shelling percentage, pods per plant, pod yield per plant and total soluble solids. The combining ability variances and component analyses were carried out as per the

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method outlined by Griffing (1956) and Hayman (1954).

Results and Discussion

The analysis of variance for combining ability revealed that mean squares due to general combining ability (GCA) and specific combining ability (SCA) were significant for all the traits studied (Table 1). The predictable ratio of SCA variances to GCA variances indicated the preponderance of non-additive gene action in the inheritance of all the traits studied except for days to 50 % flowering. Both additive and non-additive genetic effects were equally important in the genetic control of days to 50 % flowering. Baker (1978) clearly suggested that the relative importance of GCA and SCA in determining the progeny performance should be assessed on the basis of predictability ratio. Closer the ratio to unity, greater would be the predictability based on general combining ability. In the present study, the predictability ratio was more than unity for days to first picking, duration of availability of marketable pods, pod length, pod width, seeds per pod, shelling percentage, pods per plant, branches per plant, plant height, pod yield per plant and total soluble solids.

Table 1. Estimates of combining ability variance and components of variability

Genetic compo-nent	df	Days to 50 % flowering	Days to first picking	Duration of availability of marketable pods	Pod length	Pod width	Seeds per pod	Shelling %age	Pods per plant	Branches per plant	Plant height	Pod yield per plant	Total soluble solids
GCA	6	43.30*	99.68*	64.76*	1.59*	0.004*	0.90*	12.64*	27.99*	1.26*	64.69*	1252.99*	0.47*
SCA	21	8.30*	34.85*	10.51*	0.28*	0.001*	0.20*	8.17*	5.02*	0.37*	53.62*	210.96*	0.39*
Error	54	4.07	8.38	2.14	0.05	0.0003	0.026	1.18	1.14	0.01	5.86	33.07	0.07
σ^2 g		4.36	10.14	6.95	0.17	0.0004	0.097	1.27	2.98	0.14	6.53	135.54	0.04
σ^2 s		4.23	26.47	8.36	0.23	0.0007	0.17	6.99	3.88	0.36	47.76	177.88	0.33
Predictable ratio σ^2 sca/σ^2 gca		0.97	2.61	1.20	1.35	1.75	1.77	5.49	1.30	2.61	7.31	1.31	7.45

*Significant at 5 % level of significance

The non-significant estimates of t^2 values for all the traits studied indicated the fulfillment of the assumptions of diallel analysis. The estimates of dominance (H_1 and H_2) genetic effects were found significant for all the traits studied excepting H_2 component for days to first picking and branches per plant. However, both additive (D) and non additive (H_1 and H_2) components were found significant for all the traits studied which clearly indicated the involvement of both additive and non-additive gene effects in the expression of these traits. The results are in confirmation with the findings of earlier researchers (Sharma *et al.*, 1999 and Narayan *et al.*, 1999) who observed the active involvement of both additive and non-additive genes with varied magnitude in the manifestation of pod yield and its contributing traits in garden pea.

The mean degree of dominance $\sqrt{(H_1/D)}$ revealed the presence of over dominance for all the traits studied which was probably due to the predominant role of non-additive genetic variation. The predictability ratio of SCA variances to GCA variances (Table 1) earlier suggested the importance of dominant gene action for days to first picking, duration of availability of marketable pods, pod length, pod width, seeds per pod, shelling percentage, pods per plant, branches per plant, plant height, pod yield per plant and total soluble solids. The relative distribution of increasing and decreasing alleles in the parents as inferred from the ratio of $H_2/4H_1$ was approaching to the expected value of 0.25 for days to 50 % flowering, TSS, pods per plant, seeds per pod, duration of availability of marketable pods, pod width and shelling percentage. However, the estimates of $H_2/4H_1$ for other traits were far below the expected value of 0.25, reflecting unequal distribution of positive and negative alleles in the parents for pod yield per plant, pod length, days to first picking, branches per plant and plant height. Similar results have also been obtained by the earlier researchers (Kaur *et al.*, 2003, Singh *et al.*, 2005 and Dixit *et al.*, 2006) in garden pea.

The ratio of total number of dominant and recessive alleles in the parents was estimated by the ratio of $\sqrt{4\ DH_1} + F/\sqrt{4\ DH_1} - F$ or KD/KR. Closer the ratio to unity implies equality of number of dominant and recessive alleles in the

Table 2. Estimates of genetic components of variation for yield and yield related traits

Genetic component	Days to 50 % flowering	Days to first picking	Duration of availability of marketable pods	Pod length	Pod width	Seeds per pod	Shelling percentage	Pods per plant	Branches per plant	Plant height	Pod yield per plant	Total soluble solids
t^2	0.001	4.252	11.85	0.05	1.01	0.35	2.00	6.48	0.023	0.55	12.03	4.94
D	12.67* ± 1.94	-2.59 ± 26.74	13.30* ± 4.95	0.63* ± 0.12	0.003* ± 0.0006	0.25* ± 0.05	6.42 ± 4.85	5.45* ± 2.24	1.65*±0.34	105.55*±25.53	151.82 ± 136.05	0.05 ± 0.17
H_1	20.70* ± 4.67	130.54* ± 64.384	41.21* ± 11.91	1.20* ± 0.28	0.0038* ± 0.0016	0.75* ± 0.14	33.47* ± 11.68	17.94* ± 5.41	2.03*±0.32	227.51*±56.65	874.48* ± 327.54	1.39* ± 0.42
H_2	21.22* ± 4.11	100.72 ± 56.73	33.93* ± 10.49	0.81* ± 0.25	0.0031* ± 0.0009	0.63* ± 0.12	26.87* ± 10.29	14.52* ± 4.77	1.00±0.28	160.27*±49.92	613.85* ± 228.61	1.28* ± 0.37
F	-7.19 ± 4.65	-33.73 ± 64.15	-13.39 ± 11.87	0.22 ± 0.28	0.0018 ± 0.0016	-0.07 ± 0.14	6.65 ± 11.64	-5.82 ± 5.39	2.20*±0.32	153.67*±56.45	-303.40 ± 326.39	-0.09 ± 0.42
E	4.04±0.68	8.19±9.45	2.07±1.75	0.04±0.04	0.0003±0.0002	0.03±0.02	1.18±1.71	1.25±0.79	0.01 ±0.04	6.38±8.32	35.57±48.10	0.07±0.06
$(H_1/D)^{1/2}$	1.278	7.094	1.76	1.38	1.12	1.72	2.28	1.85	1.11	1.46	2.40	5.36
$H_2/4H_1$	0.256	0.193	0.20	0.17	0.20	0.20	0.20	0.20	0.12	0.17	0.17	0.23
KD/KR	0.637	0.044	0.55	1.29	1.73	0.84	1.58	0.54	4.03	2.96	0.41	0.70
R	0.884	0.953	0.84	0.82	0.63	0.70	0.13	0.73	0.85	-0.08	0.69	0.39
Regression (b)	0.882 ± 0.20	0.165 ± 0.02	0.39 ± 0.11	0.77 ± 0.24	0.44 ± 0.24	0.84 ± 0.38	0.07 ± 0.24	0.36 ± 0.15	0.82*±0.23	-0.06*±0.32	0.26 ± 0.12	0.17 ± 0.18
h^2(bs)	74.02	79.28	89.12	93.89	88.24	93.98	90.75	85.22	99.26	94.50	89.22	86.13
h^2 (ns)	20.97	10.79	25.41	71.88	65.57	45.80	55.46	23.81	90.37	77.85	22.39	8.43

*Significant at 5 % level of significance

parents. The ratio was almost close to unity for pod length, which exhibited symmetrical distribution of dominant and recessive alleles in the parents for this character. This ratio was much greater than unity for branches per plant, plant height, pod width and shelling percentage indicated excess of dominant gene in the parents, whereas far below than unity for pod yield per plant, pods per plant, seeds per pod, days to 50 % flowering, days to first picking, duration of availability of marketable pods and TSS which revealed that parental arrays contained excess of recessive genes for these traits. The direction of dominance (F value) for these traits was also negative which further confirmed excess of recessive genes in the parents. The positive estimates of F value for pod length, pod width, branches per plant, plant height and shelling percentage confirmed the involvement of more of dominant genes in the parents for these traits.

The narrow sense heritability estimates ranged from 8.43 for TSS to 90.37 per cent for branches per plant. Medium to high narrow sense heritability estimates were observed for branches per plant, plant height, shelling percentage, pod length, pod width and seeds per pod. Under such situation, pedigree selection for the component traits would be more useful to effect improvement in garden pea. The remaining horticultural traits viz., pod yield per plant, pods per plant, days to 50 % flowering, days to first picking, duration of availability of marketable pods and TSS depicted fairly low narrow sense heritability estimates. This clearly indicated that either hybridization or selection of better segregants in later filial generation may be taken up for bringing improvement in these traits. The correlation coefficient between $W_r + V_r$ and Y_r were positive and higher in magnitude for all the traits except for plant height and shelling percentage, which showed that higher proportion of recessive genes with positive effects were associated with these traits. The negative correlation coefficient between the parental measurement (Y_r) and parental order of dominance ($W_r + V_r$) for plant height indicated that the high expression of the character was associated with dominant genes.

The results suggested that based on gene action, the horticultural trait like pod yield per plant, pods per plant, seeds per pod, pod length, shelling percentage, days to first picking, duration of availability of marketable pods, plant height and TSS can be improved upon either through heterosis breeding which is not feasible in pea, therefore, selection of the desirable segregants in later filial generation will be more beneficial. However, to exploit both additive and non-additive genetic variances for days to 50 % flowering, pod width and branches per plant, selection involving certain degree of intercrossing may be employed in combining the desirable genes and maximizing the exploitation of genetic variability.

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