Graphical analysis of genetic variation for pod yield and earliness in garden pea

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Abstract

Seven diverse genotypes of garden pea were crossed in a diallel mating design (excluding reciprocals) to infer about the genetic architecture of pod yield and earliness following Haymans' approach. Both 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. The values of observed regression coefficient 'b' were low in magnitude and deviated from unity for days to first picking, shelling percentage, pods per plant, plant height and pod yield per plant. The regression line intersected Wr-axis below the point of origin which indicated the presence of over-dominance. The scatter of array points along the regression line clearly indicated that the parental genotypes used in the present investigation were genetically diverse. The parental arrays, DPP 9418-06 and Pb-89 possessed most of the dominant genes with positive effect, whereas, the parents DPP-3 and DPP LMR-41 had the recessive genes with increased effect on pod yield and its related traits. Both additive (D) and non-additive (H_1, H_2) components were found significant for all the traits except additive component for pod yield per plant, shelling percentage and days to first picking. 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, pods per plant and shelling percentage. Low narrow sense heritability estimates were observed for pod yield per plant, pods per plant, days to 50 % flowering and days to first picking.

Key words: Pod yield, genetic variation, graphical analysis.

Introduction

In recent past, several high yielding disease resistant genotypes of both early and mid maturing groups of garden pea have been identified, developed and made available for commercial cultivation but still breeding for new varieties holds promise, as the demand for high yielding and disease resistant genotypes is increasing day by day. Thus, it becomes imperative to study the genetic architecture of yield and yield-contributing traits so that appropriate breeding methodology can be developed for evolving desirable varieties. The knowledge of the type and magnitude of genetic variation, expression of the traits of economic importance is extremely important for devising appropriate breeding strategy. The graphical analysis of Hayman's approach besides providing information regarding the nature of genetic variation, also determines the number of genes involved in the manifestation of a particular trait. 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 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; these genotypes 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 and accommodated 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 various characters viz., days to 50% flowering, days to first picking, shelling percentage, pods per plant, plant height and pod yield per plant. The combining ability variances, graphical and component analyses were carried out as per the method outlined by Griffing (1956) and Hayman (1954).

Results and Discussion

The mean squares due to general combining ability (GCA) and specific combining ability (SCA) indicated significant differences for all the traits studied (Table 1). However, the predictability ratio of SCA to GCA variances revealed the active involvement of non-additive gene action in the inheritance of all the traits studied except for days to 50 % flowering, where both additive and non-additive genetic effects were almost equally important.

suggested the presence of excess of recessive genes influencing earliness in garden pea. The genotypes, DPP LMR-41, DPP 9418-06, Lincoln and Pb-89 contained the maximum concentration of dominant genes whereas, the parents, Azad Pea-1, DPP-3 and Palam Priya possessed more of recessive genes controlling pod yield and most of its contributing traits (Figs. 9,10). The standardized deviation graph of Yr and Wr + Vr (Figs. 3,4) revealed that the parental lines Pb-89, DPP 9418-06 and Azad Pea-1 possessed most of the recessive genes with negative effect and the parents, Lincoln, DPP-3 and DPP LMR-41 had the dominant genes with positive effect on earliness (days to 50 % flowering and days to first picking). The parental arrays, DPP 9418-06 and Pb-89 possessed most of the dominant genes with positive effect while DPP-3 and DPP LMR-41 had the recessive genes with increased effect on pod yield and its related traits (Figs.7, 8, 11 and 12). Thus, the genotypes, DPP 9418-06, Pb-89 and Azad Pea-1 can be successfully exploited either through hybridization or bi-parental mating for evolving high yielding and early maturing genotype(s) of garden pea.

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

Genetic component	df	Days to 50 % flowering	Days to first picking	Shelling percentage	Pods per plant	Plant height	Pod yield per plant
GCA	6	43.30*	99.68*	12.64*	27.99*	64.69*	1252.99*
SCA	21	8.30*	34.85*	8.17*	5.02*	53.62*	210.96*
Error	54	4.07	8.38	1.18	1.14	5.86	33.07
σ^2 g		4.36	10.14	1.27	2.98	6.53	135.54
σ^2 s		4.23	26.47	6.99	3.88	47.76	177.88
Predictable ratio σ^2 sca/σ^2 gca		0.97	2.61	5.49	1.30	7.31	1.31

*Significant at 5 % level of significance

The non-significant estimates of 't^2' values for all the traits studied indicated that Wr, Vr values were homogenous and fulfilled the basic assumptions of diallel analysis (Table 2). The values of observed regression coefficient 'b' were low in magnitude and deviated from unity for all the traits studied except for days to 50% flowering; which indicated the presence of inter-allelic interactions. The regression line intersected Wr-axis below the point of origin (Figs. 1, 2, 5, 6, 9 &10) for all the traits under study which indicated the presence of over-dominance in the manifestation of these traits. The scatter of array points (Figs. 3, 4, 7, 8, 11 & 12) along the regression line clearly indicated that the parental genotypes used in the present investigation were genetically diverse. For earliness (days to 50% flowering and days to first picking), the parental arrays, Lincoln, DPPLMR-41 and DPP-3 were very close (Fig.1, 2) to the point of origin of Wr, Vr graphs, which indicated that these parents possessed more of the dominant genes, whereas arrays, DPP 9418-06, Pb-89 and Azad Pea-1 were far away from the point of origin which

The estimates of dominance (H_1 and H_2) genetic effects were found significant for all the traits studied except H_2 component for days to first picking (Table 2). 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 genetic effects in the expression of these traits (Sharma *et al.* 1999 and Narayan *et al* 1999).

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

Genetic component	Days to 50 % flowering	Days to first picking	Shelling percentage	Pods per plant	Plant height	Pod yield per plant
t^2	0.001	4.252	2.00	6.48	0.55	12.03
D	12.67* ± 1.94	-2.59 ± 26.74	6.42 ± 4.85	5.45* ± 2.24	105.55* ± 25.53	151.82 ± 136.05
H_1	20.70* ± 4.67	130.54* ± 64.384	33.47* ± 11.68	17.94* ± 5.41	227.51* ± 56.65	874.4* ± 327.54
H_2	21.22* ± 4.11	100.72 ± 56.73	26.87* ± 10.29	14.52* ± 4.77	160.27* ± 49.92	613.8* ± 228.61
F	-7.19 ± 4.65	-33.73 ± 64.15	6.65 ± 11.64	-5.82 ± 5.39	153.67* ± 56.45	-303.4 ± 326.39
E	4.04 ± 0.68	8.19±9.45	1.18±1.71	1.25 ± 0.79	6.38±8.32	35.57 ± 48.10
$(H_1/D)^{1/2}$	1.278	7.094	2.28	1.85	1.46	2.40
$H_2/4H_1$	0.256	0.193	0.20	0.20	0.17	0.17
KD/KR	0.637	0.044	1.58	0.54	2.96	0.41
R	0.884	0.953	0.13	0.73	-0.08	0.69
Regression (b)	0.882 ± 0.20	0.165 ± 0.02	0.07 ± 0.24	0.36 ± 0.15	-0.06* ± 0.32	0.26 ± 0.12
h^2(bs)	74.02	79.28	90.75	85.22	94.50	89.22
h^2 (ns)	20.97	10.79	55.46	23.81	77.85	22.39

*Significant at 5 % level of significance

a=-2.265
b=0.882±0.208

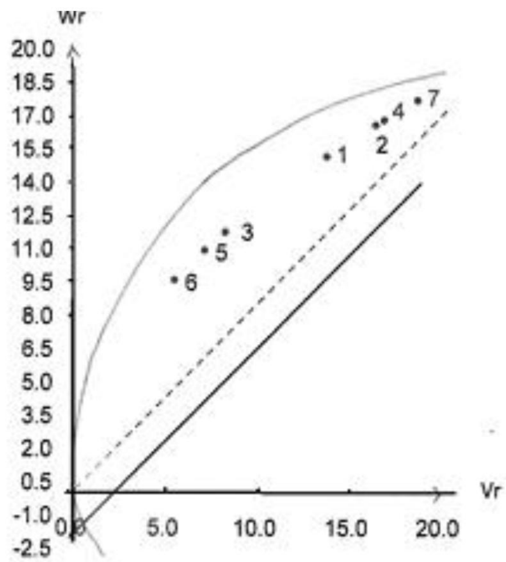

Fig. 1 Vr, Wr Graph for days to 50% flowering

a=-0.851
b=0.165±0.024

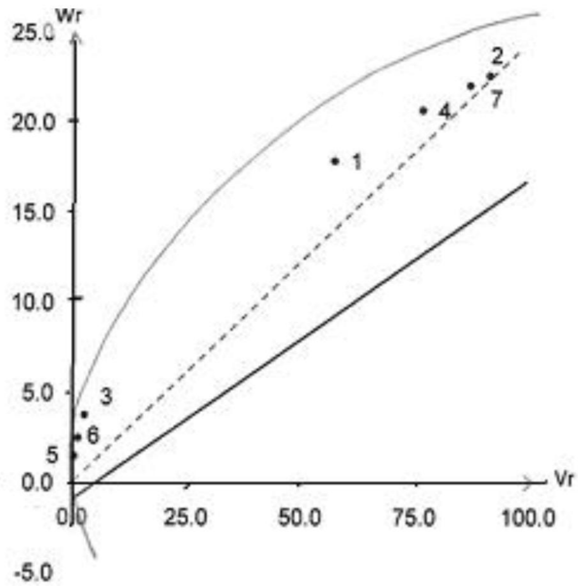

Fig. 2 Vr, Wr Graph for days to first picking

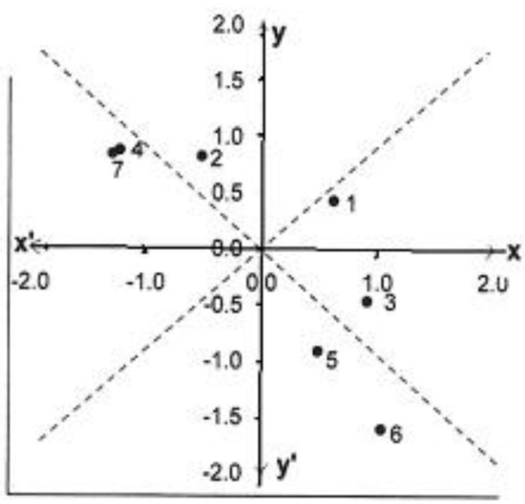

Fig. 3 Standardized deviation graph for days to 50% flowering

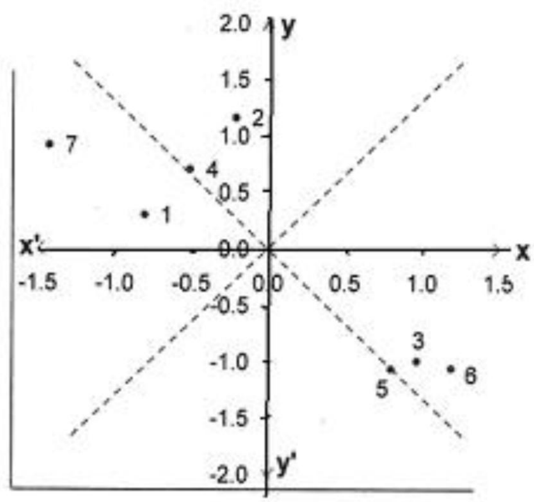

Fig. 4 Standardized deviation graph for days to first picking

a=-1.075
b=0.072±0.245

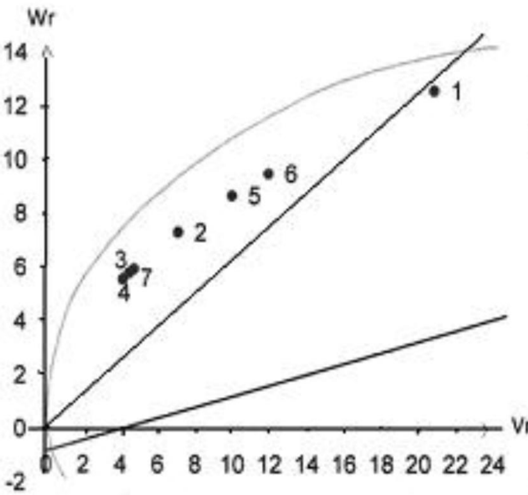

Fig. 5 Vr, Wr Graph for shelling percentage

a=-1.507
b=0.356±0.150

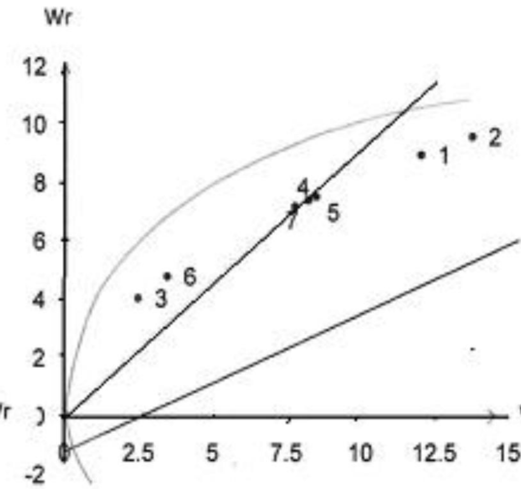

Fig. 6 Vr, Wr Graph for pods per plant

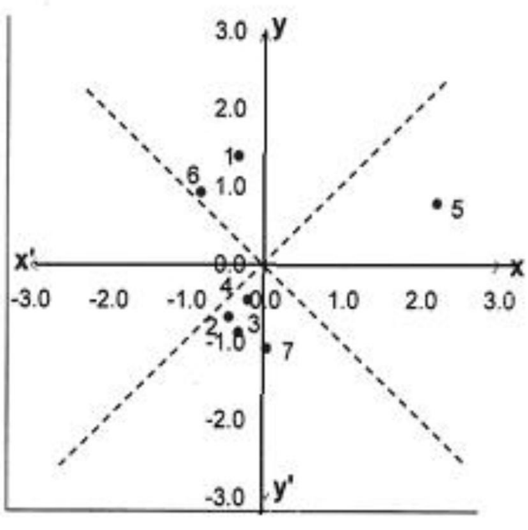

Fig. 7 Standardized deviation graph for shelling percentage

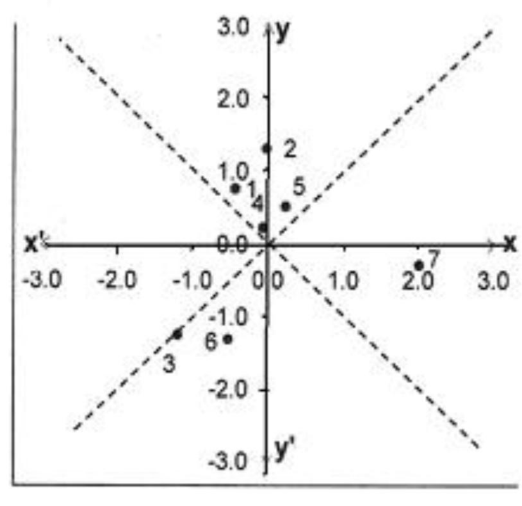

Fig. 8 Standardized deviation graph for pods per plant

a=-18.399
b=-0.065±0.322

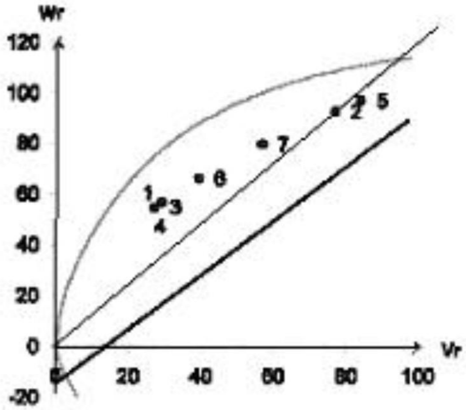

Fig. 9 Vr, Wr Graph for plant height

a=-62.903
b=0.266±0.123

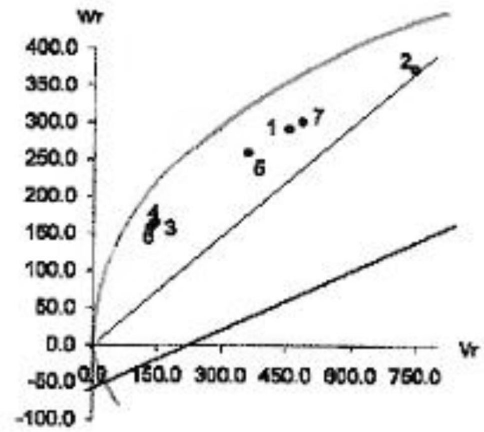

Fig. 10 Vr, Wr Graph for pod yield per plant

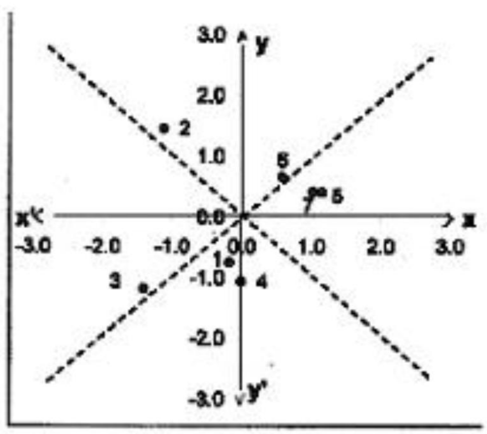

Fig. 11 Standardized deviation graph for plant height

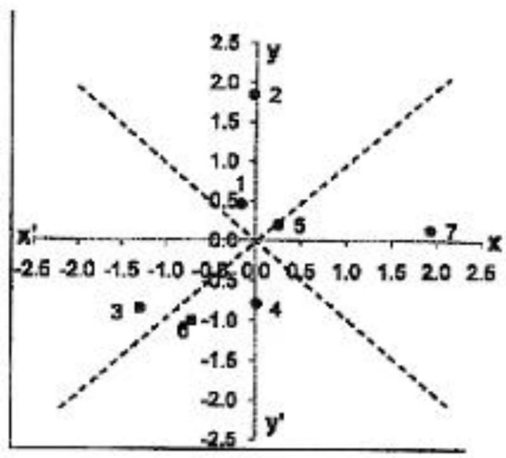

Fig. 12 Standardized deviation graph for pod yield per plant

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 relative distribution of increasing and decreasing alleles in the parents (Table 2) as inferred from the ratio of $H_2/4H_1$ was approaching to the expected value of 0.25 for days to 50 % flowering, pods per plant and shelling percentage. However, the estimates of $H_2/4H_1$ 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, days to first picking 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 revealed the ratio ($\sqrt{4DH_1} + F/\sqrt{4DH_1} - F$ or KD/KR) closer to unity signifying equal distribution of both dominant and recessive alleles in the parents. This ratio was much greater than unity for plant height and shelling percentage (Table 2) which indicated excess of dominant genes in the parents, whereas far below than unity for pod yield per plant, pods per plant and earliness (days to 50 % flowering and days to first picking) which showed that the 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 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 10.79 for days to first picking to 77.85 per cent for plant height (Table 2). Medium to high narrow sense heritability estimates were observed for plant height and shelling percentage. The remaining horticultural traits viz., pod yield per plant, pods per plant, days to 50 % flowering and days to first picking depicted fairly low narrow sense heritability estimates. This clearly indicated that either hybridization or selection of better segregants in later filial generation would be a better choice for bringing desirable improvement in these traits. The correlation coefficients 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.

Thus, based upon the results obtained from combining ability variances, graphical and component analyses of the various horticultural traits viz., pod yield per plant, pods per plant, shelling percentage, days to first picking and plant height can best be improved upon either through heterosis breeding or delayed selection of the desirable segregants. The genotypes, DPP 9418-06, Pb-89 and Azad Pea-1 were found suitable for evolving high yielding and early maturing varieties of garden pea. However, to exploit both additive and non-additive genetic variances for character like days to 50 % flowering, selection involving certain degree of intercrossing may be opted for combining the desirable genes in a single genetic background of a new variety.

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