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Genetic divergence and path analysis in early maturing garden peas

K. C. Sharma, S.Verma, Akhilesh Sharma* and Praveen Sharma*
CSK Himachal Pradesh Krishi Vishvavidyalaya
Hill Agricultural Research and Extension Centre, Bajaura - 175 125, India

Abstract

Fourteen diverse genotypes of early maturing garden pea (*Pisum sativum* L.) were evaluated for genetic divergence, correlation and path coefficient for yield and its contributing traits. On the basis of D^2 values, fourteen genotypes were grouped into six clusters. The intra and inter cluster distances among 14 genotypes revealed that cluster V showed maximum intracluster distance indicated that genotypes in this cluster are diverse. At inter-cluster level, the clusters II and VI displayed the lowest degree of divergence suggested close genetic makeup of the genotypes included amongst them. The maximum statistical distance was found between the cluster I and V followed by cluster, I and IV which indicated that the genotypes in these clusters had maximum divergence. Amongst the six characters studied, the maximum contribution towards divergence was made by number of pods per plant, followed by shelling percentage, grains per pod and pod length. The green pod yield was found to be positively and significantly associated with grains per pod and pods per plant whereas number of pods per plant recorded the maximum direct effect towards yield. Hence, these characters should be given utmost importance in the selection programme aimed at breeding for high yielding dwarf/early varieties.

Key words: *Pisum sativum* L., genetic divergence, genotype, path analysis.

Introduction

Pea (*Pisum sativum* L.), one of the most popular vegetable and pulse crops, is a rich source of protein, vitamins and minerals. In India, pea is grown in an area of about 0.27 million ha with an annual production of about 1.97 million tonnes (Rai *et al.* 2006). Pea varieties belonged to early group fetch high returns and as such it becomes important for vegetable breeders to develop varieties of garden peas through genetic improvement best suited to such conditions. Genetic improvement in turn will require information on various parameters of variability. An improvement in yield and quality in self pollinated crops like pea is normally achieved by selecting the genotypes with desired character combinations existing in nature or by hybridization. The success of hybridization programme depends upon the selection of suitable parents of diverse origin. Mahalanobis's D^2 – statistics which is based on multivariate analysis of quantitative traits is a powerful tool for measuring divergence among a set of population using the concept of statistical distance utilizing multivariate measurements. Parents identified on the basis of divergence analysis are likely to yield larger frequency of better segregants in subsequent generations. Information on correlations and path coefficients help breeders to ascertain the real components of yield and provide an effective basis of phenotypic selection. Therefore, an attempt was made to gather information on these aspects in 14 diverse genotypes of garden pea from early group.

Material and Methods

Fourteen diverse genotypes of garden pea (early group) including check 'Arkel' were grown at the Hill Agricultural Research and Extension Centre, CSKHPKV, Bajaura, Kullu (H.P.) representing the mid hill conditions of Himachal Pradesh (32.2^O N, 77^O E and 1090 m asl) in a randomized block design with 3 replications during 2004-2006. Each genotype was planted in a plot of 3 x 1.2 m with spacings of 30 cm and 5 cm between and within rows, respectively. Recommended dose of fertilizer was applied and normal package of practices were followed to raise the good crop. The observations were recorded on ten randomly selected plants from each plot on green pod yield (q/ha), pod length (cm), number of grains/pod, shelling (%), number of pods/plant and days to marketable maturity. The mean values pooled over years were used for standard statistical analysis. Genotypic and phenotypic correlation coefficients were calculated as suggested by Al-Jibouri *et al.* (1958) and path analysis by Dewey and Lu (1959). Mahalanobis's generalized distance (D^2) was used to determine the degree of divergence and the group constellations were arrived by Tocher's method as described by Rao (1952). The percentage contribution of a character towards genetic divergence was calculated as the

*Department of Vegetable Science and Floriculture, CSK HPKV, Palampur

percentage of combinations in which the character has ranked first as suggested by Singh and Chaudhary, 1985.

Results and Discussion

The analysis of variance revealed highly significant differences amongst fourteen genotypes of garden pea (early group) for all the characters studied. The D^2 values reflected wide diversity amongst the genotypes. On the basis of D^2 values, fourteen genotypes were grouped into six clusters (Table 1). Among the six clusters, cluster II had the maximum number of genotypes (4) followed by cluster I (3), while clusters III, IV and V comprised of two genotypes each. The cluster VI comprised of a solitary genotype. The composition of clusters revealed that clusters were comprised of the genotypes of heterogenous geographic origin indicated that the strains were distributed amongst the different clusters randomly irrespective of their geographical origin. Therefore, the selection of genotypes for hybridization should be based on genetic divergence rather than geographic diversity. These results are in agreement with the findings of Kalloo *et at.* (1980), Kumar *et al.* (1994) and Sureja and Sharma (2001).

Table 1. Clustering pattern based on D^2 – statistics in early peas

Clusters	No. of genotypes	Populations
I	3	VRP-6, VRP-22 and DVP-2,
II	4	DGP-207, , VL-7, DGP-17 and VP-101
III	2	DVP-1 and VRP-16
IV	2	PMR-62 and Matar Ageta
V	2	PMR-32 and VRP-5
VI	1	Arkel

The intra and inter cluster distances among 14 genotypes (Table 2) revealed that cluster V had maximum intracluster distance (4.02) indicating that genotypes included in this cluster were diverse. At intercluster level, the clusters II and VI (2.82) displayed the lowest degree of divergence suggested close genetic makeup of the tested genotypes. The maximum intercluster distance was found between the cluster I and V (9.10) followed by cluster, I and IV (7.29), which indicated that the genotypes included in these clusters had maximum divergence. Hence, intermating between the genotypes included in these clusters is expected to give transgressive segregates in the advanced generations. Kalloo *et at.* (1980) and Sureja & Sharma (2001) also suggested that the crosses between selected varieties from widely separated clusters are most likely to give desirable recombinants. The cluster VI with single genotype indicated its independent identity and importance because of various unique characters possessed by it. The magnitude of intra- cluster distance was lesser than the inter-cluster ones, indicated homogenous and heterogenous nature of the strains within and between the clusters, respectively.

Table 2. Average intra (diagonal) and inter cluster distance in early peas

Clusters	I	II	III	IV	V	VI
I	2.65	4.91	3.98	7.29	9.10	6.34
II		3.17	4.47	4.67	5.38	2.82
III			2.78	6.75	6.74	6.51
IV				3.99	5.49	4.19
V					4.02	5.36
VI						0.00

Underlined values showing intra-cluster distance

The success of breeding programme largely depends upon the degree of genetic divergence. The cluster mean values (Table 3) indicated that genotypes in cluster VI had lowest days to marketable maturity which could be helpful for breeding early and dwarf plant-type peas. The genotypes included in cluster VI also showed highest mean values for pod length (7.52 cm). Genotypes in cluster V exhibited highest mean values for green pod yield (45.67 q/ha), grains per pod (7.84), shelling percentage (40.28%) and pods per plant (20.72). Amongst the six characters studied, the maximum contribution towards divergence was made by number of pods per plant (29.68%), followed by Shelling percentage (23.08%), grains per pod (21.97%) and pod length (17.59%) thereby indicating the possibility of selection for these characters. Biju *et al.* (2001) also reported that number of pods per plant contributes more towards divergence than other traits in Indian bean, further supported the present findings. On the basis of D^2 statistics, it is suggested that a high yielding early dwarf plant-type with higher number of pods/plant could be bred by exploiting the genotypes from cluster V and VI.

Table 3. Cluster means and per cent contribution of different characters towards divergence in early peas

Characters/ Clusters	Days to maturity	Green pod yield (q/ha	Number of grains per pod	Shelling percentage	Pod length (cm)	Number of pods per plant
I	63.11	22.29	5.22	35.96	4.85	10.63
II	62.44	34.14	5.94	38.45	5.94	15.03
III	66.06	24.50	4.83	39.33	5.59	14.89
IV	67.56	34.73	6.06	43.78	6.39	15.00
V	61.56	45.67	7.84	40.28	6.86	20.72
VI	60.67	35.00	7.33	38.22	7.52	13.00
% contribution of each character towards divergence	5.49	2.19	21.97	23.08	17.59	29.68

The estimates of correlation coefficients of economic traits with yield and among themselves provide the basis for identifying the traits for ideal type and indirect selection (Al-Jibouri, 1958). The genotypic correlation coefficients were higher in magnitude than the corresponding phenotypic ones, thereby suggesting strong inherent association between various characters studied (Table 4). These results corroborate the views of Rai *et al.* (2006). At both genotypic and phenotypic levels, pod yield was found to be positively associated with grains per pod and pods per plant, indicated that traits had certain inherent relationships with pod yield. At genotypic level, the pod yield was found to be significantly correlated with shelling percentage (0.573) and pod length (0.676), suggested that improvement in these traits would result in increased pod yield. The present findings are in consonance with that of Rai *et al.* (2006), who had also reported positive and significant association of pod yield with pod length, seeds/pod and shelling percentage. The yield components mostly exhibited significant interrelationship among themselves, which indicated the need of their simultaneous selection for improvement of desirable characters.

Knowledge of correlation alone, however is often misleading as the correlation observed may not be true. Two characters may show correlation just because they are correlated with common third one. In such cases, it become necessary to study a method, which takes into account the casual relationship in addition to the degree of relationship. Path coefficient analysis is such a method that takes into account both kind of relationship. The data pertaining to path coefficient analysis (Table 5) revealed that number of pod per plant (0.772) had the highest direct effect on pod yield indicated the main contributor. Work done by Rai *et al.* (2006) also reported similar results further supported the above findings.

Thus, the present study suggested that parents must be carefully selected keeping in view the magnitude of genetic divergence. The study further suggests that number of pods per plant should be given utmost importance in selection programme for breeding high yielding dwarf/early varieties of pea. Due importance must also be given to grains/pod and shelling (%) in the selection programme for this crop.

Table 4. Correlation coefficients among different characters in early peas

Characters		Green pod yield (q/ha	Days to maturity	Number of grains per pod	Shelling (%)	Pod length (cm)
Days to maturity	P	-0.200				
	G	-0.290				
Number of grains per pod	P	0.626*	-0.289			
	G	0.850**	-0.579*			
Shelling (%)	P	0.374	-0.224	0.054		
	G	0.573*	-0.473	0.201		
Pod length (cm)	P	0.486	0.080	0.318	0.313	
	G	0.676**	-0.011	0.691**	0.522	
Number of pods per plant	P	0.795**	0.143	0.408	0.412	0.451
	G	0.867**	0.222	0.713**	0.619*	0.655**

P and G; Phenotypic and Genotypic correlation coefficient, respectively, * P = 0.05, ** P = 0.01

Table 5. Direct and indirect contribution of different characters towards green pod yield in early peas

Characters	Days to maturity	Number of grains per pod	Shelling (%)	Pod length (cm)	Number of pods per plant	Genotypic correlation coefficient with pod yield
Days to maturity	-0.319	-0.199	0.056	0.000	0.171	-0.290
Number of grains per pod	0.184	0.345	-0.024	-0.006	0.551	0.850**
Shelling (%)	0.151	0.069	-0.119	-0.004	0.477	0.573*
Pod length (cm)	0.003	0.238	-0.062	-0.009	0.505	0.676**
Number of pods per plant	-0.071	0.246	-0.074	-0.006	0.772	0.867**

Residual effect; 0.049, Underline figures indicate direct effects
* P = 0.05, ** P = 0.01

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