Multivariate analysis for yield and its contributing traits in garden pea (*Pisum sativum* L.)

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Abstract. An experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during November 2011 to March 2012 to study the multivariate analysis for yield and its contributing traits of 46 genotypes of garden pea (*Pisum sativum* L.) through principal component analysis and Mohalanobis D^2 analysis. Analysis of variance indicated that considerable genetic variability was existed among the 46 genotypes. On the basis of D^2 analysis, the genotypes were grouped into 5 clusters. Cluster II had the maximum number of 13 genotypes, while the cluster III had only 4 genotypes and cluster V had only 7 genotypes. The highest inter-cluster distance was observed between cluster III and IV (13.955), while the lowest in the cluster II and IV (3.688). The intra cluster distance was the maximum in cluster III (1.365) and minimum in cluster V (0.843). The characters: days to first flowering, days of 50% flowering, plant height and branches per plant, were found prominent towards the genetic divergence. From the results it can be concluded that the following genotypes: G17 (BD-4153), G9 (BD-4144), G25 (BD-4165), G29 (BD-4169), G34 (BD-4175), G36 (BD-4177), G44 (BD-7217) were identified as potential genotypes for higher seed yield in garden pea through hybridization.

Keywords: Genetic divergence, garden pea, *Pisum sativum* L.

INTRODUCTION

Pea is highly nutritive containing high percentage of digestible protein along with carbohydrates and vitamins. It is also very rich in minerals and excellent food for human consumption, taken either as a vegetable or in soup. Large proportion of peas are processed (canned, frozen or dehydrated) for consumption in the off season. Pea straw is a nutritious fodder. Due to its richness in protein, it is very valuable for vegetarians. Nowadays, the average production of field pea in Bangladesh has drastically reduced due to introduction of HYV rice and wheat. Thus the scope of its production as field crop has been limited. Protein and vegetable deficiency can be

overcome by developing high yielding vegetable pea in Bangladesh and there is no scope of horizontal expansion of cultivation of garden pea. So, to increase garden pea production, yield per unit area must be increased. Garden pea production can be enhanced through the development of high yielding varieties. Genetic variability with respect to genetic diversity is the prerequisite for the crop improvement through selection of high yielding progenies. Genetic diversity arises either due to geographical separation or due to genetic barriers to crossability. The quantification of genetic diversity by biometrical approaches can help choose diverse parents

Table 1. Distribution of forty six garden pea genotypes in five clusters.

Cluster	No. of member	Genotype number
I	G3, G5, G7, G12, G14, G19, G21, G26, G33, G37	BD-4137, BD-4139, BD-4142, BD-4147, BD-4150, BD-4159, BD-4161, BD-4166, BD-4174, BD-4178
II	G1, G10, G15, G18, G22, G23, G24, G28, G30, G40, G41, G43, G45	BD-4135, BD-4145, BD-4151, BD-4156, BD-4162, BD-4163, BD-4164, BD-4168, BD-4170, BD-4492, BD-6944, BD-7216, BD-7218
III	G17, G20, G42, G46	BD-4153, BD-4160, BD-7215, BARI Motor-1
IV	G2, G4, G6, G8, G11, G13, G16, G27, G31, G35, G38, G44	BD-4136, BD-4138, BD-4141, BD-4143, BD-4146, BD-4149, BD-4152, BD-4167, BD-4171, BD-4176, BD-4191, BD-7217
V	G9, G25, G29, G32, G34, G36, G39	BD-4144, BD-4165, BD-4169, BD-4173, BD-4175 BD-4177, BD-4192

for a successful hybridization program.

Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a greater heterosis than those between closely related strains (Singh, 1986) which permits to select the genetically divergent parents to obtain the desirable recombination in the segregating generations (Uddin and Choudhury, 1994). Selection of parents based on genetic divergence has become successful in several crops (Ashana and Pandey, 1980). Evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991). Therefore, the present investigation was carried out to determine the divergence among the different genotype of garden pea.

MATERIALS AND METHODS

The present experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during November 2011 to March 2012. A total of 46 garden pea germplasm along with one released variety were used in the experiment. The crop was fertilized at the rate of 10 tons of cow dung, 45 kg Urea, 62.5 kg Triple super Phosphate (TSP), 50 kg Muriate of Potash (MoP) per hectare. Half amount of urea, total amount of cow dung, TSP, MoP were applied during final land preparation. The remaining half of urea was applied as top dressing in two installments, first after 21 days and second after 42 days of sowing. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The spacing of 30 cm between line to line was maintained. Intercultural operations, such as weeding, thinning, irrigation and pest management were done uniformly in all plots when necessary.

For studying different genetic parameters and inter-relationships, ten characters were taken into consideration from the randomly selected ten plants. Mean data of each character was subjected to multivariate analysis viz, Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Canonical Vector Analysis (CVA) and Cluster Analysis (CLA) using Genstat released 13 Programme by a IBM Computer following the method of multivariate analysis of Mohalanobis (1936).

RESULTS AND DISCUSSION

Analysis of variance showed significant difference among the genotypes studied in the experiment. Thus, it indicated that considerable genetic variability existed among the 46 genotypes. The D^2 value and principal component scores also revealed a good genetic diversity among the genotypes (Islam and Islam, 2000; Vivek *et al.*, 2007).

Cluster analysis

On the basis of non-hierarchical clustering using covariance matrix, the 46 genotypes of *Pisum sativum* were grouped into five clusters (Table 1). Cluster II contained the highest number of 13 genotypes; clusters IV and I had twelve and ten genotypes, respectively. Seven genotypes were obtained by the cluster V and cluster III was constituted by four genotypes.

Even genotypes were obtained by cluster V. Cluster III was constituted by four genotypes. Principal component analysis (PCA) was carried out with 46 genotypes of garden pea. A two dimensional scattered diagram (Figure 1) was developed on the basis of the principal component score, Z_1 and Z_2 of two principal coordinates axes I and II of Figure 1. The clustering pattern obtained coincided with the apparent grouping patterns performed PCA (Figure 1.) The results obtained through PCA were confirmed by non-hierarchical clustering.

The inter and intra cluster distance of the 46 genotypes are shown in Table 2. The highest inter-cluster distance (17.842) was observed between cluster III and V followed by the cluster III with IV (13.955) and I with V (11.502). It
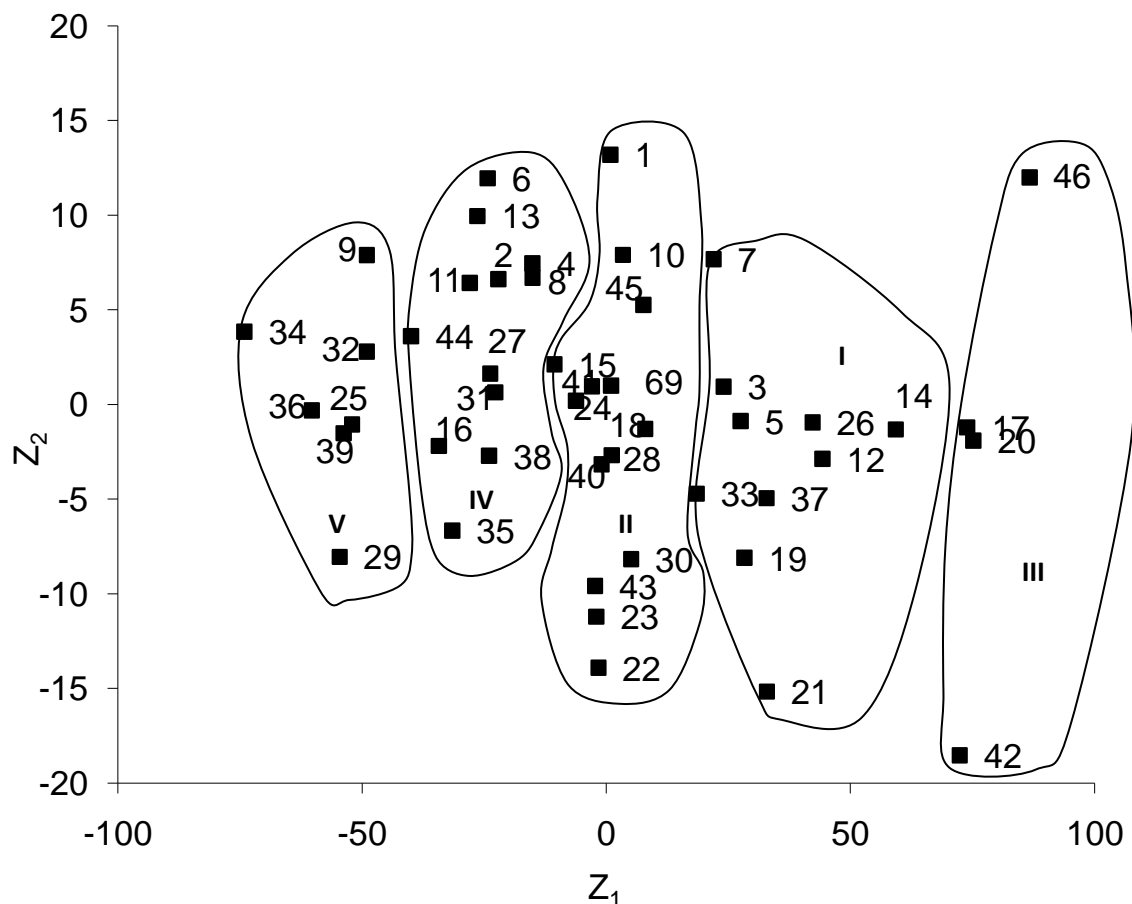
Figure 1. Scattered diagram of forty six garden pea genotypes based on their principal component scores superimposed with clustering.

Table 2. Average inter and intra cluster distance of 46 garden pea genotypes.

Cluster	I	II	III	IV	V
I	1.051				
II	4.083	0.957			
III	6.847	10.748	1.265		
IV	7.646	3.688	13.955	0.853	
V	11.502	7.458	17.842	3.897	0.843

is noted that the genotypes' grouped into this cluster were highly divergent from each other. Parent selection from highly divergent cluster distance (3.688) was observed between cluster II and IV followed by cluster IV and V (3.897); cluster I and II (4.083) suggestion close relationship among these four clusters. Moderate or intermediate distances were found between cluster II and III (10.748), and cluster I and IV (7.646).

It is mentioned that crossing involving parents belonging to the medium divergent clusters may also exhibited significant and positive heterosis (Main and Bahl, 1989). The inter cluster distance varied from 3.688 to 17.842 indicating the wide diversity among the genotypes. The intra cluster distance (1.265) was the

highest in III, while the minimum was found in the cluster V. The inter cluster distance were higher than the intra cluster distances suggesting wider genetic diversity among the genotypes of different groups.

A comparison of cluster means is shown in Table 3. Cluster II had the highest cluster mean value for days to 50% flowering (54.64), number of secondary branches per plant (6.78) and number of siliquae per plant (211.79). Cluster III obtained the highest cluster mean value of five characters viz, days to first flowering (46.58), node per plant (15.92), pod length (4.88 cm), number of seeds per plant (6.33) and hundred seed weight (10.04). This cluster was able to lead in respect of the highest cluster mean value for maximum characters. Among 10

Table 3. Cluster mean value of forty six garden pea genotypes.

Variable	Cluster				
	I	II	III	IV	V
Days to first flowering	45.40	46.54	**46.58**	46.08	45.67
Days to 50% flowering	54.17	**54.64**	54.17	54.03	54.38
Plant height	88.06	88.32	81.27	84.67	**89.25**
Number of branch per plant	9.57	10.46	8.17	11.50	**12.52**
Node per plant	15.43	15.90	**15.92**	14.64	15.86
Pod length	3.84	3.79	**4.88**	3.73	3.72
Number of pod per plant	51.53	58.97	37.50	64.89	**72.19**
Number of seeds per plant	6.17	6.23	**6.33**	6.08	6.10
Hundred seed weight	5.38	5.36	**10.04**	5.45	5.30
Seed yield	85.20	85.56	83.67	84.81	**90.62**

Table 4. Latent vectors for 10 principal component characters of 46 genotypes of *garden pea* genotypes.

Plant characters	Vectors 1	Vectors 2
Days to first flowering	0.0410	0.0317
Days to 50% flowering	-0.1180	-0.3860
Plant height	-0.0171	0.0068
Number of branch per plant	0.0827	0.0439
Node per plant	0.1472	0.0944
Pod length	-1.9129	-0.5869
Number of pod per plant	0.0502	-0.0238
Number of seed per plant	1.1142	-1.0263
Hundred seed weight	-0.0388	0.5324
Seed yield	-0.0387	-0.0151

characters, this cluster stood first for five characters. Clusters I and IV failed to show the highest values for yield or any other yield contributing characters. Cluster V obtained the highest cluster mean value of four characters viz, plant height (89.25 cm), number of branch per plant (12.52), number of pod per plant (72.19) and seed yield (90.62).

Canonical Variate Analysis (CVA) indicates that the characters having positive values in both vectors I and II contributed maximum divergence as Rahman and Munsur (2009) mentions. The characters: days to first flowering, number of branch per plant and node per plant had the positive value in both the vectors (Table 4). Therefore, these characters had the maximum, contribution towards the genetic divergence; while the characters: days to 50% flowering, pod length and seed yield had negative contribution. Hence, these characters could offer a good scope for genetic improvement in garden pea. Though the characters: number of pod per plant and number of seed per plant in vector I and plant height; hundred seed weight in vector 2 showed positive value only in one vector but negative value in other vector; also played significant role towards the genetic divergence.

According to Choudhury *et al.* (1975), selection of parents depends on the particular cluster from which the parents are selected and the relative contribution of characters to the total divergence; therefore, the parents in cluster III if crossed with cluster IV and V might exhibit heterosis as well as higher level of genetic variation. The crosses involving parents belonging to intermediate diverse parents may also have chance to produce significant and positive heterosis in the subsequent generations. Considering the magnitude of genetic distance by the contribution of different characters towards the total divergence, magnitude of cluster means for different characters and field performance; the genotypes G-9, G-25, G-29, G-34 and G-36 from cluster V, G-17 from cluster III and G-44 from cluster IV may be suitable for creating higher yield per plant through hybridization which will eventually offer more scope of selection of plants with higher per plant yield.

Conclusion

Multivariate analysis based on 10 agronomic characters indicated that the 46 genotypes were grouped into five

distant clusters. The maximum contribution of characters towards diversity was observed by days to first flowering, days of 50% flowering, plant height and branches per plant. Thus, these traits may be given high emphasis while selecting the lines for hybridization. The inter cluster distance was maximum between cluster III and V and the highest inter-cluster. The highest intra-cluster distance was found in cluster III. From the results, it can be concluded that the following genotypes *viz.,* G17 (BD-4153), G9 (BD-4144), G25 (BD-4165), G29 (BD-4169), G34 (BD-4175), G36 (BD-4177), G44 (BD-7217) were identified as potential genotypes for higher seed yield in garden pea.

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