

Multivariate Analysis of Different Pea (*Pisum sativum* L.) Genotypes

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Abstract: Forty six pea genotypes were evaluated for thirteen morphological characters during Rabi season, 2010 at Sher-e-Bangla Agricultural University, Dhaka, Bangladesh in randomized complete block design with three replications. The experiment was conducted to estimate the genetic variability in different pea genotypes. High heritability coupled with high genetic advance was recorded for hundred seed weight and pod length. This indicates that the effectiveness of selection depends on to improve these characters. Pod length, hundred seed weight, number of pods per plant, number of seeds per plant showed significant positive correlation with seed yield. The genotypes under the experiment were grouped into six clusters. The highest intra cluster distance was found in cluster III and while cluster II showed no intra-cluster distance values which revealed homogenous nature of the genotype within the cluster. The highest inter cluster distance was look-out between cluster II and V followed by II and IV. Considering genetic variability and heritability, emphasis should be given on traits during phenotypic selection and also intra and inter cluster distances for genotypic selection for developing high yielding genotypes of pea.

Keywords: Genetic Diversity, Cluster, Heritability, Correlation Coefficient

1. Introduction

Pea (*Pisum sativum* L.) is an important legume grown as a garden and field crop throughout the temperate regions of the world; it is also grown as a rabi season crop in Bangladesh [1]. Pea is very important for the nutritional quality of its seeds. Pea protein is low in sulfur containing amino acids, cysteine and methionine but rich in lysine and other essential amino acids [2]. It is the source of protein having essential amino acids (23 to 25%) that have high nutritional values for resource poor households. Moreover, some important minerals such as calcium, phosphorus and iron are present in abundant quantities in pea which are lacking in cereals [3]. Pea contains 20-25% starch, 4-10% sugar, 0.6-1.5% fat and 2-4% minerals [4]. The present nutritional status of Bangladesh is a matter of great concern because most of the people are suffering from malnutrition [5, 6] and pea can play

a vital role for meet up nutritional deficiency problem. The low yield is the main constrain for growing pea in Bangladesh. Considering the potentiality of this crop, there is a need for improvement and to develop varieties suited to specific agro-ecological conditions and also for specific end use. Genetic diversity is a major factor that determines prospects of yield improvement in future. Knowledge of genetic diversity within a crop and correlation among the yield contributing characters is essential for the long-term success of a breeding program and maximizes the exploration of germplasm resources. In order to increase yield, genetic variability is the prerequisites since it is the source of variation and raw material for yield improvement work [5]. Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm [7]. Multivariate analysis acts as a useful tool to quantify the degree of divergence between the

biological populations at genotypic level and to assess the relative contribution of different components to the total divergence both inter and intra cluster levels [8]. Therefore, the study was undertaken to assess the genetic variability and evaluate the performance of different genotypes of pea.

2. Materials and Methods

The study was conducted to assess the genetic diversity, correlation and path coefficient analysis among forty six pea genotypes. The experiment was carried out during November, 2010 to February, 2011 at the field laboratory of Sher-e-Bangla Agricultural University, located at 23° 77' N latitude, 90° 33' E longitude at an altitude of 8.6 m above sea level in Dhaka, Bangladesh. Experimental material consisting of forty six genotypes were sown in randomized complete block design with three replications; each plot consisted of a single row of 3m long with row to row distance of 50cm maintaining 10 plants per meter. Sowing was done with the help of hand drill. Ten random plants were used to take the data on days to first flowering, days to 50% flowering, plant height, number of branches per plant, number of node per plant, internode length, pod length, hundred seed weight, number of pods per plant, seeds per pod, seeds per plant, plant maturity and seed yield per plant from each plot of each replication.

Forty six pea genotypes were grouped into cluster by using Genstat v 5.5 software. The data were subjected to statistical manipulation for the analysis of variance through computer's

software M-Stat-C. The significant data were further analyzed statistically using Least Significant Difference (LSD) test at 1% probability level to compare the differences among the genotype means.

3. Results and Discussion

3.1. Analysis of Variance

The results of analysis of variance regarding various plant traits are given in Table 1. From this table it is found that in replication none of the traits showed significant differences but genotype showed significant variation for all thirteen characters studied as previously showed by [9]. Among them seeds per plant showed maximum value followed by pods per plant, plant height, days to first flowering and lowest by number of seeds per pod. So emphasis should be given on these traits for future breeding program.

Table 2 showed that all the traits have positive relation with replication except days to first flowering. Among them seeds per plant have maximum value followed by pods per plant, plant height, branches per plant. Branches per plant, number of node per plant, internode length pod length, hundred seed weight, pods per plant, number of seeds per pod, seeds per plant and seed yield per plant have positive contribution with both replication and genotype in analysis of covariance. So these characters are important to selection of parental lines.

Table 1. Analysis of variances of thirteen yield and yield related characters of pea.

Source of variation	df	Mean sum of squares												
		DFF	D50%F	PH	BPP	NPP	IL	PL	HSW	PPP	NSP	SPP	PM	SYP
Replication	2	17.35	2.23	259.96	51.26	18.45	0.05	0.02	0.53	1042.45	1.09	17584.26	16.35	34.06
Genotype	45	21.04**	2.39**	199.69**	12.55**	10.29**	0.35**	1.04**	14.11**	356.43**	0.32**	5130.64**	4.716**	14.69**
Error	90	2.28	0.55	48.16	4.07	6.24	0.07	0.04	0.19	184.65	0.16	1767.28	1.99	5.40

** significant at the 0.01 level.

DFF = Days to first flowering, D50%F = Days to 50% flowering, PH = Plant height (cm), BPP = Branches per plant, NPP = Number of node per plant, IL = Internode length (cm), PL = Pod length (cm), HSW = Hundred seed weight (g), PPP = Pods per plant, NSP = Number of seeds per pod, SPP = Seeds per plant, PM = Plant maturity, SYP = Seed yield per plant (g)

Table 2. Analysis of Covariance for yield with different yield contributing characters in pea.

Source of variation	df	Mean sum of squares					
		DFF	D50%F	PH	BPP	NPP	IL
Replication	2	-17.9241	7.819166	83.83738	41.65273	22.00753	1.160483
Genotype	45	0.761619	-1.37234	-3.7744	1.0954	1.508063	0.254039
Error	90	-0.19988	-0.21368	7.248438	0.711033	1.20303	0.256972

DFF = Days to first flowering, D50%F = Days to 50% flowering, PH = Plant height (cm), BPP = Branches per plant, NPP = Number of node per plant, IL = Internode length (cm), PL = Pod length (cm), HSW = Hundred seed weight (g), PPP = Pods per plant, NSP = Number of seeds per pod, SPP = Seeds per plant, PM = Plant maturity, SYP = Seed yield per plant (g)

Table 2. Continue.

Source of variation	df	Mean sum of squares						
		PL	HSW	PPP	NSP	SPP	PM	SYP
Replication	2	0.455574	1.653959	187.2481	3.695521	747.662	18.53919	1.653959
Genotype	45	0.889876	5.185942	30.57812	0.176801	141.8333	-3.27736	5.185942
Error	90	0.036761	0.345767	22.94188	0.19202	83.51836	-0.70156	0.345767

3.2. Genetic Variation

Genetic advance (% mean) was negligible for all the traits except hundred seed weight and pod length (Figure 1). These traits might be influenced in a small extent by the environmental factors. The expressions of other traits are mainly due to the genetic constituents rather than environmental influence. Heritability was also higher for hundred seed weight, pod length and days to first flowering which also supplemented that genetic constituents are the main source of these traits. High heritability and high genetic advance in percent of mean of these traits showed that these traits were under the control of additive gene and selection for the improvement of these traits could be effective. This finding is comparable with the results previously published by [10] and [11].

3.3. Cluster Analysis

There was much variation among the clusters compared to intra-cluster variations. The highest intra-cluster distance was observed in cluster III (0.146) and the lowest in cluster II (0.00) (Figure 2). The inter-cluster distance was maximum between cluster II and V (73.97) followed by cluster II and IV (73.19) and cluster II and VI (73.18) and the lowest inter-cluster distance was obtained between cluster I and IV (4.85)(Table 3). It is expected from the above results that the genotypes belonged to the cluster II and V; cluster II and IV and cluster II and VI having greater inter cluster distance could be effective for future breeding program to produce high yielding pea varieties. Because the genotypes from diverge cluster may be recommended for inclusion in hybridization program as they are expected to produce good segregants [11].

Sl No.	Cluster	Nearest Cluster with D ² values	Farthest Cluster with D ² values
2	II	III (70.71)	V (73.97)
3	III	I (7.11)	II (70.71)
4	IV	I (4.85)	II (73.19)
5	V	VI (5.45)	II (73.97)
6	VI	IV (5.02)	II (73.18)

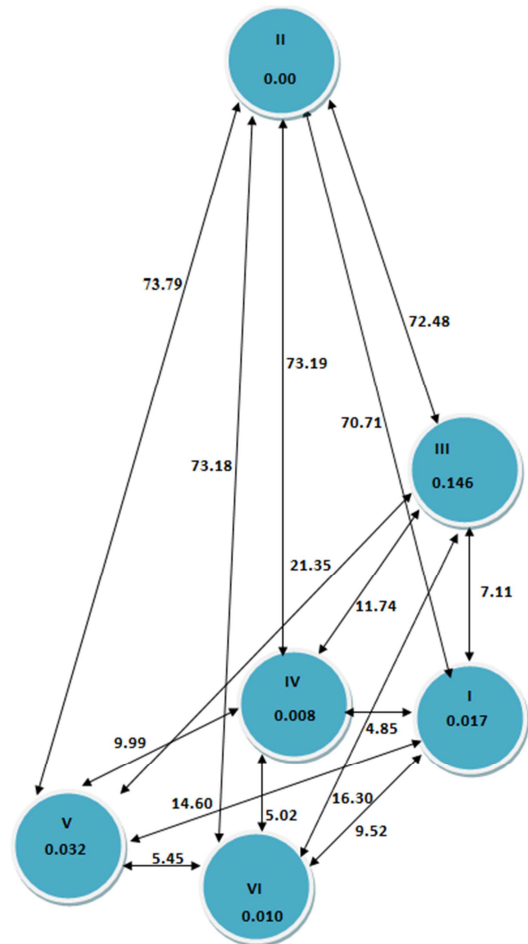


Figure 2. Diagram showing intra and inter -cluster distances (D²) of forty-six genotypes in pea.

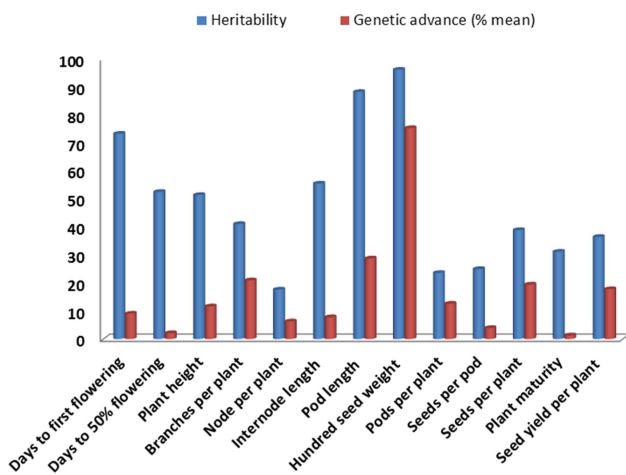


Figure 1. Heritability and genetic advance over mean in pea.

Table 3. The nearest and farthest clusters from each cluster between D² values in pea.

Sl No.	Cluster	Nearest Cluster with D ² values	Farthest Cluster with D ² values
1	I	IV (4.85)	II (72.48)

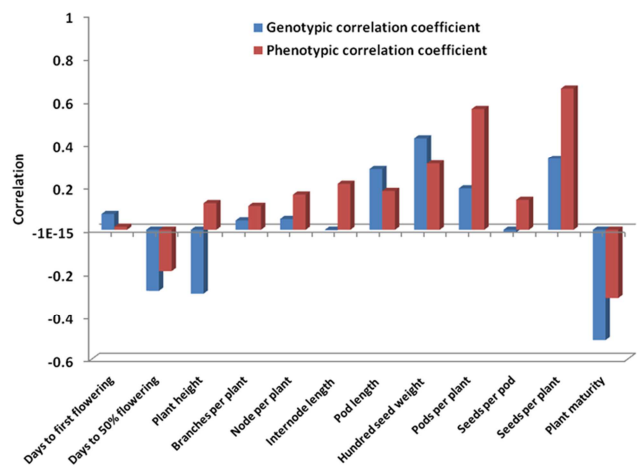


Figure 3. Genotypic and phenotypic correlation and coefficient for twelve characters of pea.

3.4. Correlation Among the Traits

Phenotypic correlation coefficients were larger in values in most of the traits as compared to their respective genotypic correlation coefficient (Figure 3). This indicates greater contribution of phenotypic factor in the development of the association. Seeds per plant, seeds per pod, pods per plant, internode length, node per plant and branches per plant showed the positive phenotypic correlation coefficient. On the other hand days to first flowering, pod length and hundred seed weight have higher phenotypic correlation coefficient than genotypic correlation coefficient. Days to 50% flowering and plant maturity have negative correlation but they showed higher phenotypic correlation coefficient than genotypic correlation coefficient. Most interestingly plant height has positive phenotypic correlation coefficient but genotypic correlation coefficient is negative. Diversity of plant height may indicate that environment have most influence in this trait.

4. Conclusion

The genotypes contributing maximum from distant clusters along with considering the analysis of variance and covariance of yield contributing characters for find the desirable traits which have active relative contribution to the heritability, genotypic and phenotypic correlation coefficient to aim at developing improved varieties.

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