Multivariate Analysis in Some Mungbean (V*igna radiata* L. Wilczek) Accessions on the Basis of Agronomic Traits

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Abstract: Thirty four diverse mungbean (*Vigna radiata* L. Wilczek) accessions were evaluated in the field experiment for 8 agronomic traits at Sher-e-Bang Agricultural University, Dhaka-1207, Bangladesh, during March 2008 to August 2008. Data were collected on quantitative and visually assed traits including days to 50% flowering, days to 80% maturity, plant height, number of pods per plant, pod length, number of seeds per pod, 1000-grain weight and grain yield per plant. All the traits were analyzed using multivariate analysis technique. Most of the important traits of mungbean genotypes under study displayed a wide range of variation. The first three principal components with Eigen values contributed 71.61% of the total variability amongst 34 accessions. Thirty four mungbean accessions were grouped into 7 clusters based on Euclidean distance. Among 8 quantitative traits, number of seeds per pod contributed maximum towards divergence. Considering the yield, growth duration and number of seeds per pod genotypes of cluster I and IV, and cluster II and IV exhibit high heterosis for yield as well as earliness, and yield as well as large number of seeds per pod, respectively.

Key words: Cluster analysis · Principal component analysis · Mungbean

INTRODUCTION

Mungbean (*Vigna radiata* L. Wilczek) is the third most important legume (pulse crop) in the Indian subcontinent. It is also one of the most important legume crops for other South Asian countries [1]. Mungbean is an important pulse crop grown in Bangladesh and it is an annual legume. On the basis of area and production mungbean's position is fifth as compared to other pulse crop grown in Bangladesh [2]. Mungbean cultivation spreads widely because of its superior digestibility and high protein content. Mungbean is cultivated in tropical, subtropical and temperate regions. In Bangladesh, it is cultivated under both in irrigated and rainfed conditions. The average yield of is very low as compared to yield in many other countries. The multivariate techniques, such as cluster analysis and principal component analysis may be an efficient tool in the quantitative estimation of genetic variation. Naidu and Satyanarayana [3] and Saxena *et al.* [4] used cluster analysis to categorize the genotypes in mungbean. Multivariate technique also plays an important role in choice of divergent parents for hybridization to exploit maximum heterosis. Falcinelli *et al.*

[5] mentioned that multivariate analysis to be a valid system to deal with germplasm collections. Grouping of genotypes by multivariate methods in the study is of practical value to the breeders of mungbean. In order to develop high yield potential cultivars of mungbean and resistant to insect and diseases, exploitation of the gene pool is of foremost importance.

Therefore, the present study were planned to evaluate the extent of genetic variation in mungbean accessions on the basis of agronomic traits using multivariate techniques to screen superior genotypes among 34 mungbean accessions for the utilization as a parent in future hybridization program.

MATERIALS AND METHODS

Thirty four mungbean accessions were evaluated for various quantitative traits in three replicated Randomized Complete Block Design (RCBD) at the experiment was carried out at the experimental farm of Sher-e-Bangla Agricultural University (SAU), Dhaka-1207, Bangladesh during March, 2008 to August, 2008 in rainfed conditions. Accession number and source of 34 mungbean genotypes

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Table 1: List of 34 mungbean accessions used in the study

Sl. No.	Accession No.	Source
G1	BARI Mung-2	BARI
G2	BARI Mung-3	BARI
G3	BARI Mung-4	BARI
G4	BARI Mung-5	BARI
G5	BARI Mung-6	BARI
G6	BD-6874	BARI
G7	BD-6875	BARI
G8	BD-6876	BARI
G9	BD-6877	BARI
G10	BD-6878	BARI
G11	BD-6879	BARI
G12	BD-6880	BARI
G13	BD-6881	BARI
G14	BD-6882	BARI
G15	BD-6884	BARI
G16	BD-6885	BARI
G17	BD-6886	BARI
G18	BD-6887	BARI
G19	BD-6888	BARI
G20	BD-6889	BARI
G21	BD-6890	BARI
G22	BD-6891	BARI
G23	BD-6892	BARI
G24	BD-6893	BARI
G25	BD-6894	BARI
G26	BD-6895	BARI
G27	BD-6896	BARI
G28	BD-6897	BARI
G29	BD-6898	BARI
G30	BD-6899	BARI
G31	BD-6900	BARI
G32	BD-6901	BARI
G33	BD-6902	BARI
G34	BD-6903	BARI

BARR = Bangladesh Agricultural Research Institute

(varieties/lines) are presented in Table 1. All the genotypes were collected from Bangladesh Agricultural Research Institute (BARI), Joydevpur, Gazipur. Three 3m row of each plot was planted with a spacing 30cm row to row and 10cm plant to plant. Pesticides were sprayed to protect the crop from pests especially white fly, a vector for Mungbean Yellow Mosaic Virus. Recommended agronomic practices were followed to raise a good crop growth. The seeds were sown on March 10, 2008. N, P and K fertilizers @ 40-60-20kg/ha were applied as a basal dose during final land preparation during the final land preparation [6]. The data were recorded on days to 50% flowering (days), days to 80% maturity (days), plant height (cm), number of pods per plant, pod length (cm), number of seeds per pod, 1000-grain weight (g) and grain yield per plant (g). Plant height (cm), number of pods per plant, grain yield per plant (g) were recorded on 10 plants sampled randomly. Pod length (cm) and number of seeds per pod were recorded on 10 pods sampled at random within each genotype. 100 seed weight (g) were recorded for each genotype. The data recorded were then subjected to analyses to determine simple statistical estimates, *i.e.*, mean, variance, broad sense heritability and genetic advance [7]. All the quantitative traits were analyzed by the procedures of cluster and principal component analyses with the help of Genstat software.

RESULTS AND DISCUSSION

Analysis of variances showed that the genotypes differed significantly for all the traits except pod length (Table 2). Sirohi and Kumar [8] reported similar results in mungbean. The estimate of genotypic variance (σ^2_g), phenotypic variance (σ^2_p), heritability (h^2_b), genetic advance (GA), genetic advance in percent of mean and coefficient of variation (CV%) for 8 different characters are given in Table 2. The coefficient of variation indicated that there were significant differences among the genotypes for the characters under study. The phenotypic variance (σ^2_p) was higher than the corresponding genotypic variance (σ^2_g) for all the characters suggesting the presence of environmental influence to some extent in the expression of these characters. Medium to high variance was observed for 1000-grain weight followed by number of pods per plant and plant height, days to maturity, grain yield per plant and days to 50% flowering. On the other hand, a small variance was observed for pod length followed by number of seeds per pod showed. Medium to high heritability was observed for all the traits except pod length (Table 3) indicated that in the present material, the scope of improvement for these traits by simple selection would be effective. High heritability coupled with high genetic advance expected in the next generation for number of pods per plant, grain yield per plant and plant height suggesting these characters are governed by additive genetic effect to a great extent and improvement of these traits would be effective through selection. Miah and Bhadra [9] reported high values for expected genetic advance for plant height and number of pods and seeds per plant.

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Table 2: Mean, standard error, range and variance for 8 traits in 34 mungbean accessions

| | | | | Variance | |
| | | | Mean Sum | --------------------------------------- | |
Traits	Mean	Range	of Square	σ^2_g	σ^2_p
Days to 50% flowering	40.27	42.67-32.00	13.63**	2.85	7.94
Days to 80% maturity	64.86	70.00-61.00	18.45**	4.36	9.72
Plant height	39.06	54.05-31.15	107.66**	32.76	42.14
Number of pods per plant	25.48	9.67-33.50	134.40**	43.30	47.79
Pod length	6.79	5.66-8.11	0.97	0.10	0.77
Number of seeds per pod	8.84	6.65-10.43	1.98**	0.47	1.13
1000-grain weight	37.77	21.41-56.03	352.32**	105.02	142.29
Grain yield per plant	11.11	5.80-15.87	24.73**	7.91	8.92

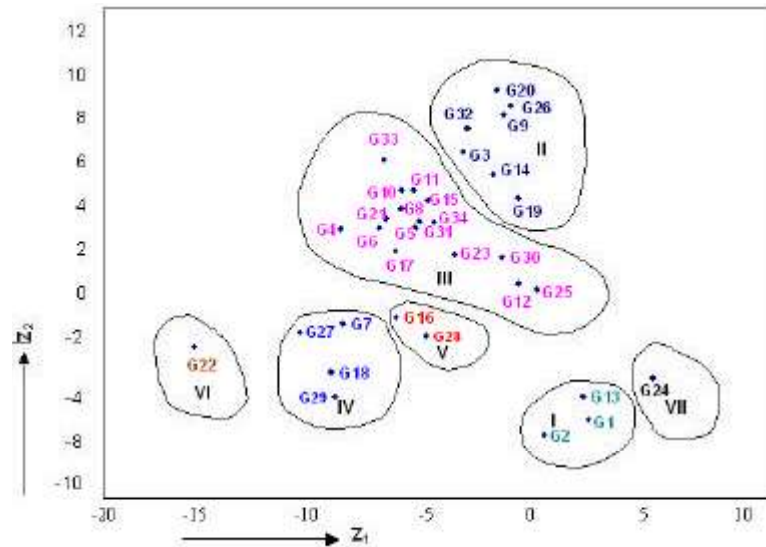**, Significant at 1% level of significance

Fig. 1: Scatter diagram of 26 Mungbean genotypes based on their principal component scores superimposed with clustering

Table 3: Heritability in broad base (h^2_b), genetic advance (GA) genetic advance in percent of mean and coefficient of variation (CV) for 8 quantitative traits in 34 mungbean accessions

| | | GA in % | | |
Traits	h^2_b	of mean	GA	CV (%)
Days to 50% flowering	35.82	1.06	2.63	5.61
Days to 80% maturity	44.88	2.88	4.44	3.57
Plant height	77.75	24.67	63.17	7.84
Number of pods per plant	90.61	12.90	50.65	8.31
Pod length	13.06	0.24	3.47	12.03
Number of seeds per pod	41.13	0.90	10.21	8.61
1000-grain weight	73.80	2.18	5.78	16.16
Grain yield per plant	88.66	5.45	49.09	9.05

Table 4: Eigen values and percentage of variation in respect of 8 traits in 34 mungbean accessions

Principal Component traits	Eigen value	Percent of Variance	Cumulative Percentage
Days to 50% flowering	2.73	34.18	34.18
Days to 80% maturity	1.61	20.12	54.30
Plant height	1.38	17.31	71.61
Number of pods per plant	0.88	11.01	82.61
Pod length	0.73	9.15	91.77
Number of seeds per pod	0.28	3.55	95.32
1000-grain weight	0.24	3.04	98.36
Grain yield per plant	0.13	1.64	100.00

Thirty four genotypes (Table 1) were grouped into 7 clusters through non-hierarchical clustering. Cluster analysis grouped genotypes together with greater genetic similarity; the clusters did not necessarily include all genotypes from same origin. Saxena et al. [4] categorized 59 genotypes using multivariate anlysis into 16 well-characterized groups. Phansak et al. [10] also clustered 15 accessions into three distinct groups. Members of each cluster are presented in Table 5. Cluster I consisted of 3 genotypes, cluster II of 7, cluster III of 16, cluster IV of

4 genotypes, cluster V of 2 genotypes, cluster VI and cluster VII of only one genotype of each. As the genotypes from various sources differed considerably, it was difficult to establish any relationship between origin and clustering pattern. Maximum number of genotypes (13) was grouped into cluster III among the clusters.

Two-dimensional scatter diagram was constructed using principal component score I as X-axis and principal component score II as Y-axis, reflecting in the relative position (Fig. 1). As per scatter diagram the genotypes were apparently distributed into seven clusters. It was

Table 5: Distribution of 34 mungbean accessions in seven clusters

Cluster	Frequency	Accession No.
I	3	G1 (BARI Mung-2), G2 (BARI Mung-3) and G13 (BD-6881)
II	7	G3 (BARI Mung-4), G9 (BD-6877), G14 (BD-6882), G19 (BD-6888), G20 (BD-6889), G26 (BD-6895) and G32 (BD-6901)
III	16	G4 (BARI Mung-5), G5 (BARI Mung-6), G6 (BD-6874), G8 (BD-6876), G10 (BD-6878), G11 (BD-6879), G12 (BD-6880), G15 (BD-6884), G17 (BD-6886), G21 (BD-6890), G23 (BD-6892), G25 (BD-6894), G30 (BD-6899), G31 (BD-6900), G33 (BD-6902) and G34 (BD-6903)
IV	4	G7 (BD-6875), G18 (BD-6887), G27 (BD-6896) and G29 (BD-6898)
V	2	G16 (BD-6885) and G28 (BD-6897)
VI	1	G22 (BD-6891)
VII	1	G24 (BD-6893)

Table 6: Cluster means for 8 traits in 34 mungbean accessions

Traits	Clusters						
	I	II	III	IV	V	VI	VII
Days to 50% flowering	34.67	40.43	40.85	41.67	40.17	41.67	39.67
Days to 80% maturity	63.11	65.05	64.90	63.50	67.00	66.33	68.00
Plant height	35.48	39.91	40.16	37.43	38.76	36.46	35.95
Number of pods per plant	13.00	29.56	27.20	24.76	22.21	31.70	10.00
Pod length	5.78	6.71	6.94	6.91	6.65	6.83	7.90
Number of seeds per pod	8.83	9.23	8.95	8.21	8.11	8.94	8.33
1000-grain weight	32.77	30.20	38.09	49.14	41.85	59.47	25.27
Grain yield per plant	7.02	10.45	11.47	13.61	13.09	13.58	5.80

Table 7: Contribution of traits towards total divergence

Traits	Vector-I	Vector-II
Days to 50% flowering	-0.13130	0.15292
Days to 80% maturity	-0.01409	0.07019
Plant height	-0.07587	0.30344
Number of pods per plant	-0.43308	0.80266
Pod length	-0.01410	0.02359
Number of seeds per pod	0.00569	0.05482
1000-grain weight	-0.85401	-0.47712
Grain yield per plant	-0.24430	0.06444

Fig. 2: Scree plot constructed for 8 principal components

also revealed that the genotypes of cluster II was more diverse from the genotypes of cluster IV, VI, VII. Eigen values of 8 principal components have been shown in the scree plot (Fig. 2). The first three components with Eigenvalues >1 contributed 71.48% of the variability amongst 34 genotypes evaluated for 8 quantitative traits. The cluster mean values are presented in Table 6. The cluster I consists of early maturing genotypes. The highest number of pods per plant was observed in cluster II, highest plant height was found in the genotypes of cluster III followed by cluster II and cluster V suggesting tallest genotypes include in this cluster, cluster IV possessed genotypes with the highest cluster mean for grain yield per plant followed by cluster VI. The cluster VI ranked first for number of pods per plant and 1000-grain weight indicating genotypes with large number of pad and larger grains are included in this cluster. The highest pod length was found in cluster VII but yield was low and also show delay maturity. Latent vectors (Vector-I and II) for different quantitative traits are presented in Table 7. Number of seeds per pod was positive for both vectors indicating this trait contributes maximum towards divergence.
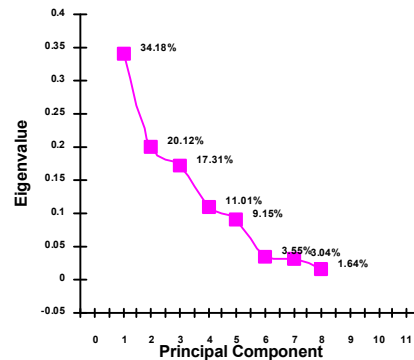
It is assumed that maximum heterosis is manifested in cross combinations involving the genotypes belonging to most divergent clusters. However, for a practical plant breeder, the objective is not only high heterosis but also to achieve high-level of production. In the present research work, the maximum distance existed between cluster II and VI; II and IV; II and I; II and VII (Fig. 1). Considering the yield and growth duration cluster I and IV exhibit high heterosis for yield as well as earliness whereas cluster II and IV exhibit maximum heterosis for yield as well as large number of seeds per pod.

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