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Full Length Research Paper

Estimation of genetic diversity of mungbean (*Vigna radiata L.* Wilczek) in Malaysian tropical environment

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To evaluate genetic diversity of 20 genotypes of mungbean, an experiment was laid out in a Randomized Complete Block Design with two replications during the period from November, 2010 to February, 2011 at the experimental field of Genetics and Molecular Biology, Institute of Biological science, University of Malaya, Kuala Lumpur, Malaysia. Eight morphological characters including plant height, number of fruiting branches per plant, number of pods per plant, number of pod clusters per plant, pod length, number of seeds per pod, 1000-seed weight and total seed yield per plant were measured. Analysis of variance showed significant differences among genotypes for all traits. A total of four groups were defined through cluster analysis and distinct genetic variations were observed among these groups. Using cluster analysis by unweighted pair group method with arithmetic mean (UPGMA) method, all genotypes were grouped into 3 main groups and 1 minor group. Cluster I consisted of 9 genotypes, cluster II of 7, cluster III of 1 and cluster IV of 3 genotypes. Principal component analysis was done to evaluate diversity and morphological traits which had more effects on diversity and three components explained near 79% of total variation among genotypes. By plot of first two components score for genotypes confirmed the result of cluster analysis.

Key words: Tropical environment, mungbean, multivariate analysis and biodiversity.

INTRODUCTION

Mungbean (*Vigna radiata* L. Wilczek) is a widely-grown, short-duration grain legume crop grown in south and Southeast Asia. It is an important source of inexpensive protein and iron, and is a good substitute for meat in most Asian diets and a significant component of various cropping systems (Rudy et al., 2006; Srinives et al., 2000). The genus Vigna has been broadened to include about 150 species; 22 species are native to India and 16 to Southeast Asia (Anon, 2010), but the largest number of species are found in Africa (Polhill and Maesen, 1985). Seven Asian Vigna species are domesticated as food crops including mung bean (*Vigna radiata*), azuki bean (*Vigna angularis*), black gram (*Vigna mungo*), jungli bean (*Vigna trilobata*), moth bean (*Vigna aconitifolia*), rice bean (*Vigna umbellata*) and creole bean (*Vigna reflexo-pilosa*) (Shanmugasundaram, 1985). Study of genetic diversity in genetic resources is a critical factor for breeders to better understand the evolutionary and genetic relationships among accessions, to select germplasm in a more systemic and effective way and to develop strategies to incorporate useful diversity in their breeding programs (Lavanya et al., 2008). In order to utilizing mung bean gene pool for development of new varieties, an exhaustive characterization of the various germplasm holdings and collections that constitute the gene pools for the crop need to be fully characterized to identify the useful genetic diversity. The crosses between the parents with maximum genetic divergence are generally the most responsive for genetic improvement (Arunachalam, 1981). With the aim to develop a successful mungbean crossing program, initially 127 mungbean genotypes were evaluated in Malaysian tropical environment and selected 20 genotypes as

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Table 1. Source of origin of 20 mungbean genotypes.

Genotype	Origin
NM-92	Pak NIAB Mung
Chakwal Mung-97	Pakistan
NM-98	Pak NIAB Mung
VC1560DxNM-92	Pakistan (parental Taiwan)
Pak-22	Pakistan
6601	Pakistan
NM-1919	Pakistan
AZRI-06	AZRI, Quetta, Pakistan
M-6	IABGR,NARC, Pakistan
SML-267	IABGR,NARC, Pakistan
40995	IABGR,NARC, Pakistan
40521	IABGR,NARC, Pakistan
40998	IABGR,NARC, Pakistan
41031	IABGR,NARC, Pakistan
40593	IABGR,NARC, Pakistan
40714	IABGR,NARC, Pakistan
41018	IABGR,NARC, Pakistan
40934	IABGR,NARC, Pakistan
5197A	IABGR,NARC, Pakistan
NM 45-10	IABGR,NARC, Pakistan

potential line. In the present study genetic diversity was evaluated among these 20 mungbean genotypes based on morphological characters through multivariate analysis.

MATERIALS AND METHODS

Experiment site

The experiment was laid out in a Randomized Complete Block Design with two replications during the period from November, 2010 to February, 2011 at the experimental field of Genetics and Molecular Biology, Institute of Biological science, University of Malaya, Kuala Lumpur, Malaysia, which is situated at 3.20°N, 101.40°E with elevation of 22 m from sea level. The climatic condition was hot and humid with frequent rain. Plants were grown in 3 m × 1 m small plots. Row to row distance was 50 cm and plant to plant distance was 10 cm. Data was collected from randomly selected plants from each plot.

Plant material

Experimental material included 20 mungbean genotypes selected from the 127 genotypes collected from different agro-ecological zones of Pakistan. A little description of these genotypes have mentioned in Table 1.

Observations

Observations were recorded on plant height, number of fruiting branches per plant, number of pods per plant, number of pod clusters per plant, pod length, number of seeds per pod, 1000-seed weight and total seed yield per plant. Weeding was done more than three times and phosphate and nitrite fertilizer applied 22 days after planting. Plants were harvested when 90% of pods changed to brown color.

Statistical methods

Analysis of variance (ANOVA) was done to know the variations among the genotypes based on the 8 morphological traits. Before doing ANOVA in normality test (Kolomogorove-Smirnove) all data showed a normal distribution, so SAS 9.1 was used for ANOVA. Means were compared by DMRT (Duncan multiple range test). Multivariate analysis, especially the principal component and cluster analyses were used to analyze these genotypes based on various traits. Cluster analysis using unweighted pair group **method** with arithmetic mean (UPGMA) (between group linkages) was used to investigate distance, similarity and relatedness of genotypes, so that similar genotypes can be classified into one group and dissimilar ones into distinct groups. Principal component analysis (PCA) was followed to understand variable independence and balanced weighting of traits, which leads to an effective contribution of different characters on the basis of respective variation.

RESULTS AND DISCUSSION

Among the 20 genotypes, the highest variation was observed for seed yield followed by 1000- seed weight and plant height. Moderate variation was observed for pods per plant and number of pod clusters per plant. Low variability was found for number of fruiting branches per

Table 2. Mean based traits variability in 20 mungbean genotypes.

Traits	Mean ± SE	Minimum	Maximum
PH	37.38 ± 1.079	26.9	57
NFB	1.708 ± 0.102	1	3.5
NP	14.397±0.916	6.33	32.25
NPC	6.493 ± 0.935	3.2	13.5
PL	6.419 ± 0.156	3.5	8.34
NSP	9.357 ± 0.219	6.89	12.12
SW	37.502 ± 1.087	24	50
SY	33.64 ± 1.756	18	60

PH: Plant height, NFB: Number of fruiting branches per plant, NP: Number of pod per plant, NPC: Number of pod clusters per plant, PL: Pod length, NSP: Number of seeds per pod, SW: 1000 seed weight SY: Total seed yield per plant.

Table 3. The Mean square values (MS) from ANOVA of yield and yield components of mungbean genotypes.

	PH	NFB	NP	NPC	PL	NSP	SW	SY
Mean Square	82.66	0.62	63.26	9.31	1.04	2.22	86.95	221.27
F Value	14.75**	3.41**	47.67**	15.59**	5.22 **	2.88*	9.94**	37.54**
CV%	6.34	25.11	8	11.90	6.97	9.4	7.88	7.22

PH: Plant height, NFB: Number of fruiting branches per plant, NP: Number of pod per plant, NPC: Number of pod clusters per plant, PL: Pod length, NSP: Number of seeds per pod, SW: 1000seed weight SY: Total seed yield per plant,* significant at 0.05 level** significant at 0.01 level.

plant, pod length, and number of seeds per pod (Table 2).

Analysis of variance

The analysis of variance showed significant differences among the genotypes for all the traits at 0.01% level except 1000-seed weight which was significant at 0.05 level (Table 3). Highest seed yield was observed in genotype 40521 followed by genotype 40714 and NM-1919 which were significantly different from other genotypes. Genotype 40593 performed lowest yield (Figure 1).

Cluster analysis

In order to maintain, evaluate and utilize germplasm effectively, it is important to investigate the extent of available genetic diversity (Mohammadi, 2003). Lee et al. (2004) considered morphological characterization as an important step in description and classification of crop germplasm because a breeding program mainly depends upon the magnitude of genetic variability (Piyada et al., 2010). Using cluster analysis by UPGMA method all genotypes were grouped into 3 main groups and 1 minor group (only 1 genotype, 41031). A dandogram based on average linkage distance for 20 mungbean genotypes was also calculated (Figure 2). Members of each cluster are shown in Table 4. Cluster I consisted of 9 genotypes, cluster II of 7, cluster III of 1 and cluster IV of 3 genotypes. The results shows that for plant height cluster II has the highest mean and cluster I has the lowest mean of plant height. For 1000-seed weight and seed yield cluster I showed high value while for number of fruiting branches per plant and number of pod clusters per plant this cluster had the lowest. Tarika et al. (2009) evaluated 9 qualitative and 21 quantitative traits in 340 diverse cultivated mungbean accessions collected at Asian Vegetable Research and Development Center. (AVRDC) to assess the extent and pattern of their diversity. The germplasm represented a wide range of diversity for most of the traits evaluated. High genetic variability was found in yield components. Penology traits such as plant height, days to flowering, and days to maturity also showed high genetic variability. Tarika Yimram et al. (2009) observed 5 major and 1 minor group when they clustered several mungbean germplasm. They described that germplasm from India and West Asia were in all major clusters, while those from Southeast Asia and other origins were mainly grouped into one cluster. They recommend that the germplasm from West Asia be exploited more in cultivar development to enrich the breeding gene pool. We also observed that the germplasms grouped in 3 major groups and those are

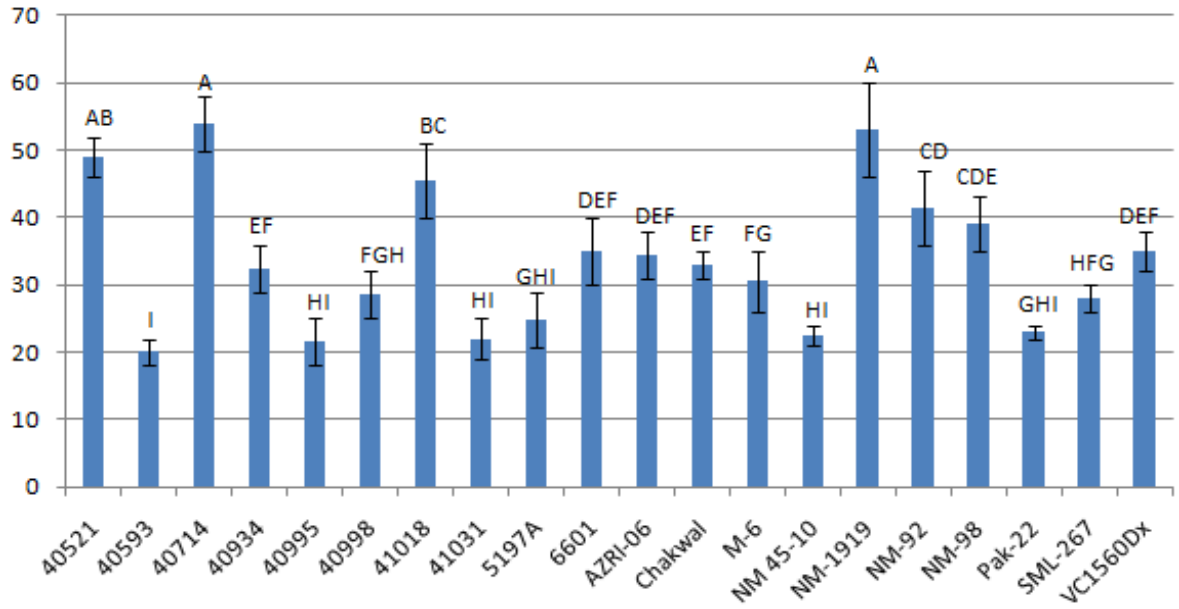

Figure 1. Mean comparison of seed yield in mungbean genotypes (Genotypes with the same letter are not significantly different at 0.05 level).

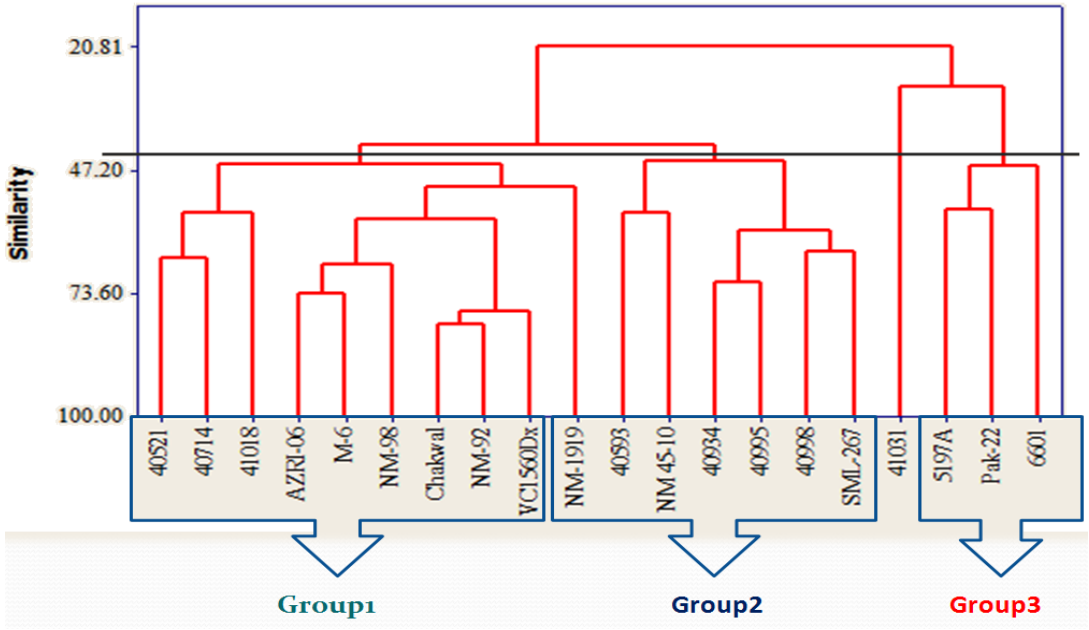

Figure 2. Dandogram based on 8 morphological traits in mungbean genotypes.

collected from different agro-ecological zones of Pakistan have wider genetic base. The mean of all traits were calculated for each groups (Table 4). Selection of proper parents is playing a vital role for a successful plant breeding program. Parents with more genetic distance can create higher variation which can increase of genetic gain in selection. So depend on breeding objective the result of cluster analysis can be applied for crossing program for mungbean improvement.

Principal component analysis

The results showed that three principal components and

Table 4. Traits mean in four Clusters group in 20 mungbean genotypes.

Group	Number of genotypes	PH	NFB	NP	NPC	PL	NSP	SW	SY
1	9	35.46	1.37	13.06	5.25	6.86	9.15	40.63	40.16
2	7	41.27	1.69	11.24	6.05	6.37	9.71	35.71	29.43
3	1	29.63	2.38	14.53	7.5	4.14	10.63	30	22
4	3	36.03	2.54	25.71	10.92	5.97	8.73	34.8	27.64

PH: Plant height, NFB: Number of fruiting branches per plant, NP: Number of pod per plant, NPC: Number of pod clusters per plant, PL: Pod length, NSP: Number of seeds per pod, SW: 1000seed weight SY: Total seed yield per plant.

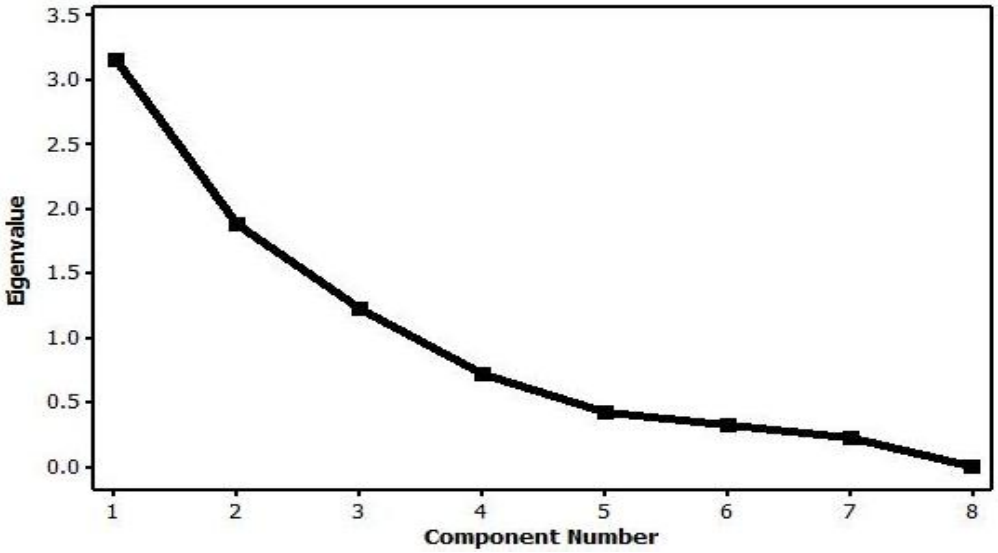

Figure 3. Scree plot constructed for 8 principal components.

Table 5. Principal components (PCs) for 8 morphological traits in mungbean genotypes.

Traits	1st component	2nd component	3rd component
PH	0.0277	-0.4488	0.5467
NFB	0.4583	0.2100	0.0501
NP	0.4134	0.3817	0.2496
NPC	0.5077	0.2072	0.2049
PL	-0.4036	0.1792	0.3986
NSP	0.1153	-0.5353	0.2215
SW	-0.3691	0.4112	-0.0681
SY	-0.2188	0.2788	0.6176
Eigenvalue	3.15	1.88	1.22
Proportion σ^2	0.3946	0.2354	0.1534
Commulative σ^2	0.3946	0.6299	0.7834

PH: Plant height, NFB: Number of fruiting branches per plant, NP: Number of pod per plant, NPC: Number of pod clusters per plant, PL: Pod length, NSP: Number of seeds per pod, SW: 1000seed weight SY: Total seed yield per plant.

factors with Eigen values more than one explained 79% of total variability (Figure 3). The first principal component (PC1) is related to number of fruiting branches per plant, number of pod per plant and number of pod cluster per plant that explained 39.4% of total variability (Table 5). The characters with greatest positive weight on second

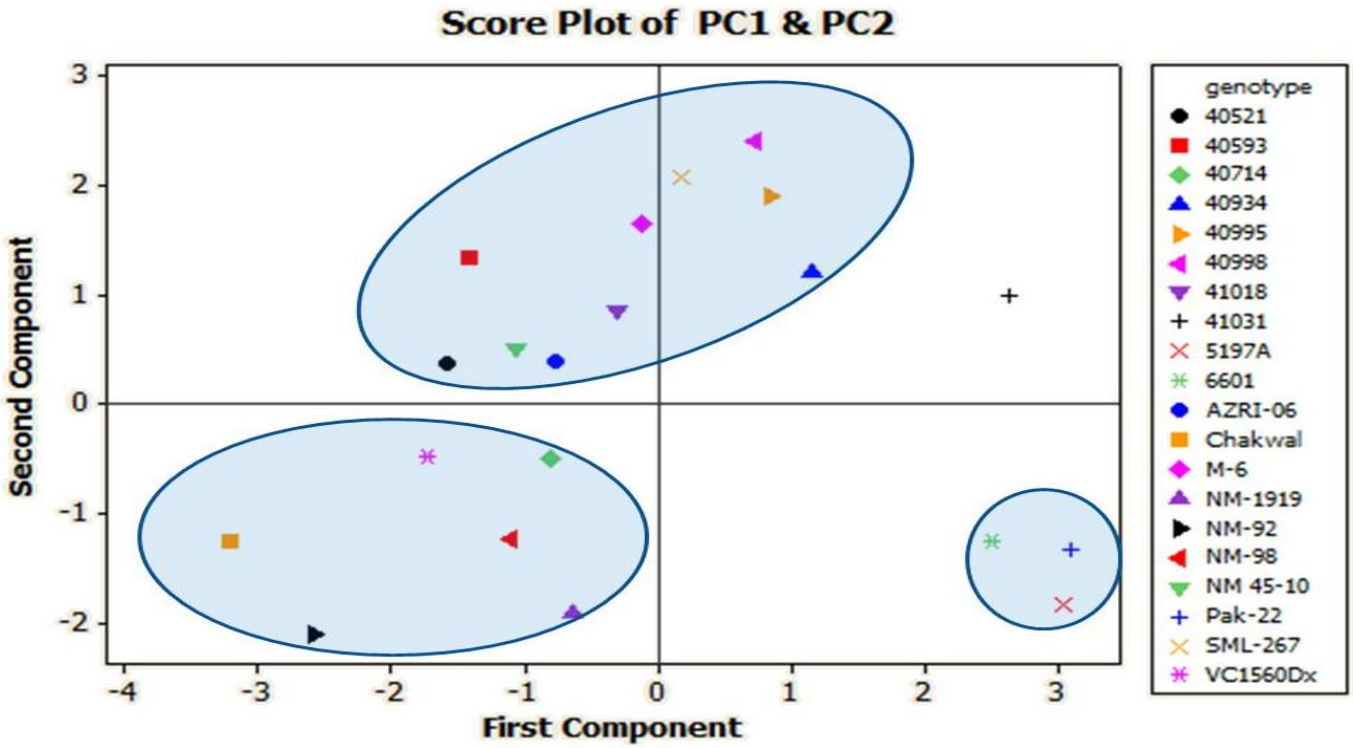

Figure 4. Scattered diagram of mungbean genotypes for first two PCs score.

principal component (PC2) were 1000 seed weight, seed yield and number of pod per plant. These findings revealed that two first components are related to yield components of mungbean. Ghafoor et al. (2001) evaluated 484 different mungbean genotypes for qualitative and quantitative traits at National Agriculture Research Council (NARC), Islamabad and observed a wide range of diversity for most of the traits, along with some accessions with unique characters which could help to identify landraces with suitable traits to be used in hybridization program for breeding to broaden genetic base. The first two components contributing 63% of the variance were plotted to observe the relationships between the clusters (Figure 4). The result of this analysis confirmed the grouping pattern which was found by cluster analysis. All clusters are clearly separated from each other.

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