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MULTIVARIATE ANALYSIS FOR QUANTITATIVE TRAITS IN MUNGBEAN [*VIGNA RADIATA* (L.) WILCZEK]

MUHAMMAD ZUBAIR, SAIF ULLAH AJMAL*, MUHAMMAD ANWAR AND A.M. HAQQANI

National Agricultural Research Centre, Islamabad, Pakistan

Abstract

Forty diverse mungbean [*Vigna radiata* (L.) Wilczek] genotypes were evaluated for 14 quantitative traits at National Agricultural Research Centre, Islamabad, Pakistan during 1999-2000 under rainfed conditions. All the traits were analyzed using multivariate analysis technique (cluster and principal component analyses). The first four PCs with eigenvalues >1 contributed 85.49% of the variability amongst genotypes. Populations with high PC_1 values were high yielding and early in maturity. The populations with high PC_2 were late in flowering and maturity, and contributed more towards vegetative growth rather than reproductive. The genotypes were categorized in four clusters based on average linkage. Clusters I, II and IV were more clearly separated from cluster III. Cluster analysis revealed that genotypes under investigation displayed a wide range of variation for most of the traits that could be exploited in breeding programme to enrich the mungbean genetic treasure.

Introduction

Mungbean has been a major pulse crop in Asia since ancient times (Paroda & Thomas, 1987). At present mungbean cultivation spreads widely because of its superior digestibility in Africa, South America, Australia and in many Asian countries, and has been identified as high yielding pulse crop (Smartt, 1990). In Pakistan it is cultivated under a wide range of ecological zones in both irrigated and rainfed conditions. During 2002-03, it was cultivated over an area of 261.4 thousand ha with 133.9 thousand tones production (Anon., 2003). The national average yield of 512.8 kg ha^{-1} is very low as compared to its potential, and yield obtained in many other countries.

The multivariate analysis, and in particular, the principal component and cluster analyses have been utilized for the evaluation of germplasm when studying various traits (Mardia *et al*., 1979; Cruz & Regazzi 1994). Variance of relatively highly heritable quantitative traits provides an estimate of genetic diversity (Rabbani *et al*., 1998). Categorization and reserves and its importance in proper genotype identification (Virmani *et al*., 1983; Ghafoor *et al*., 1992; Pezzotti *et al*., 1994; Ghafoor *et al*., 1998). Evaluation of germplasm is useful not only in selection of core collection but also its utilization in breeding programmes. Various numerical taxonomic techniques have been successfully used to classify and measure the pattern of genetic diversity in germplasm, as in mungbean (Singh, 1988), pea (Amurrio *et al*., 1995), soybean (Perry & McIntosh, 1991), alfalfa (Smith *et al*., 1995), lentil (Ahmad *et al*., 1997) and blackgram (Ghafoor *et al*., 2001). In order to develop high yielding cultivars resistant to various stresses, exploitation of the gene pool is of paramount importance. The objectives of the present study were to investigate the extent of genetic variation and relationships between various mungbean genotypes based on quantitative traits using multivariate analysis and to identify a set of agronomic attributes to be used in future breeding programme.

*Corresponding author: University of Arid Agriculture, Rawalpindi, Pakistan
E-mail: gondaldr@yahoo.com, Tel: 051-9062258, Fax: 051-9291027

Materials and Methods

Forty mungbean genotypes were evaluated for various quantitative traits in four replicated randomized complete block design at National Agricultural Research Centre (NARC), Islamabad, Pakistan (latitude 32.42° N, longitude 73.08° E and elevation 683 m above sea level) during 1999-2000 in rainfed conditions. Name, source and status of genotypes are presented in table 1. Out of forty, 27 genotypes were obtained from the Asian Vegetable Research and Development Centre (AVRDC), Taiwan and the others were of local origin collected from different research institutes of Pakistan.

Six 4m row of each genotype was planted with 10 cm intra-row spacing. The rows were 40 cm apart. 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 stand. The data were recorded on days to flower initiation (DFI), days to flowering (DF), days to pod initiation (DPI), days to maturity (DM), plant height (PH), primary branches per plant (PBPP), clusters per plant (CPP), pods per plant (PPP), pod length (PL), seeds per pod (SPP), 100 seed weight (SW), grain yield per plant (YPP) and biological yield per plant (BYPP). Days to flowering and maturity were recorded at 50% of flowering and 90% maturity, respectively. Plant height (cm), primary branches per plant, clusters per plant, pods per plant, grain yield per plant (g), and biological yield per plant (g) were recorded on 10 plants sampled randomly. Pod length (cm) and seeds per pod were recorded on 10 pods sampled at random within each genotype. 100 seed weight (g) were recorded for each genotype and harvest index (HI) was determined as economic yield expressed as percentage of total biological yield.

The data recorded were then subjected to analyses to determine simple statistical estimates, *i.e*., mean, standard deviation, variance, broad sense heritability and phenotypic correlation (Singh & Chaudhry, 1985). All the quantitative traits were analyzed by numerical taxonomic techniques using the procedures of cluster and principal component analyses (Sneath & Sokal, 1973) with the help of computer software 'Statistica' v 6.0 and 'SPSS" v 10.0 for windows. Cluster analysis was conducted on the basis of average distance k-means and genotypes in each cluster were then analyzed for basic statistics. Means of each variable were standardized prior to cluster and principal component analysis to avoid the effect due to difference in scale.

Results

Basic statistics for quantitative traits are given in table 2 that showed a considerable variability in the material under study. Medium to high variance was observed for days to flower initiation, days to flowering, days to pod initiation, days to maturity, plant height, pods per plant, biological yield per plant and harvest index. For other characters, including primary branches per plant, clusters per plant, seeds per pod, 100 seed weight and grain yield per plant, a small variance was observed. Low heritability for most of the yield contributing traits indicated that in the present material the scope of improvement for these traits by simple selection is limited and hence, more germplasm is needed to be acquired from other gene-banks to broaden the genetic base of crop. Breeding techniques like wide hybridization, mutation and other novel techniques can also help in creating genetic variation for particular traits (Ghafoor *et al*., 1998).

Table 1. Source and status of 40 mungbean genotypes tested at NARC during 1999-2000.

S.No.	Name	Status	Source	S.No.	Name	Status	Source
1.	V-1381	Exotic	AVRDC, Taiwan	21.	NCM-88	Pure line	Pakistan
2.	V-1945	Exotic	AVRDC, Taiwan	22.	VC-1163	Exotic	AVRDC, Taiwan
3.	V-3092	Exotic	AVRDC, Taiwan	23.	VC-3216	Exotic	AVRDC, Taiwan
4.	V-3976	Exotic	AVRDC, Taiwan	24.	V-3686	Exotic	AVRDC, Taiwan
5.	V-5197	Exotic	AVRDC, Taiwan	25.	VC-1973 (B)	Exotic	AVRDC, Taiwan
6.	VC-1168	Exotic	AVRDC, Taiwan	26.	VC-2755	Exotic	AVRDC, Taiwan
7.	VC-1177	Exotic	AVRDC, Taiwan	27.	VC-2764	Exotic	AVRDC, Taiwan
8.	VC-1482	Exotic	AVRDC, Taiwan	28.	VC-2768	Exotic	AVRDC, Taiwan
9.	VC-1562	Exotic	AVRDC, Taiwan	29.	VC-2778	Exotic	AVRDC, Taiwan
10.	VC-1628	Exotic	AVRDC, Taiwan	30.	E-76	Pure line	Pakistan
11.	VC-1647	Exotic	AVRDC, Taiwan	31.	E-321	Pure line	Pakistan
12.	VC-1973	Exotic	AVRDC, Taiwan	32.	M-22-24	Pure line	Pakistan
13.	V-5991-D	Exotic	AVRDC, Taiwan	33.	NM-20-21	Variety	Pakistan
14.	V-5991	Exotic	AVRDC, Taiwan	34.	NM-13-1	Variety	Pakistan
15.	NCM-87	Pure line	Pakistan	35.	M-28	Variety	Pakistan
16.	V-2773	Exotic	AVRDC, Taiwan	36.	BRM-114	Advance line	Pakistan
17.	V-2194	Exotic	AVRDC, Taiwan	37.	6601	Variety	Pakistan
18.	V-2194 (B)	Exotic	AVRDC, Taiwan	38.	71-17	Pure line	Pakistan
19.	VC-2651 (A)	Exotic	AVRDC, Taiwan	39.	k-20	Pure line	Pakistan
20.	VC-1973 (A)	Exotic	AVRDC, Taiwan	40.	s-8	Pure line	Pakistan

Table 2. Basic statistics for 14 quantitative traits in mungbean genotypes.

Traits	Mean ± S.E.	σ^2P	h^2	Minimum	Maximum
Days to flowering initiation (DFI)	40.27 ± 0.37	6.8	0.54	33.75	46.25
Days to flowering (DF)	46.00 ± 0.42	10.1	0.61	40.00	51.75
Days to pod initiation (DPI)	50.23 ± 0.31	5.8	0.57	45.75	75.00
Days to maturity (DM)	73.30 ± 0.38	9.9	0.51	68.75	79.75
Plant height (PH)	83.47 ± 1.57	108.2	0.89	64.45	101.15
Pprimary branches per plant (PBPP)	2.10 ± 0.08	0.56	0.17	1.30	3.38
Clusters per plant (CPP)	8.56 ± 2.71	5.9	0.29	5.60	13.40
Pods per plant (PPP)	21.07 ± 0.71	37.9	0.37	13.90	35.40
Pod length (PL)	7.23 ± 0.09	0.51	0.47	6.35	8.41
Seeds per pod (SPP)	9.88 ± 0.13	1.2	0.38	8.45	11.58
100 seed weight (SW)	3.36 ± 0.11	1.04	0.34	2.00	4.78
Biological yield per plant (BYPP)	51.88 ± 1.23	8136.6	0.63	38.30	72.55
Grain yield per plant (GYPP)	5.24 ± 0.17	2.40	0.30	3.41	7.40
Harvest index (HI)	10.26 ± 0.31	9.34	0.21	6.86	22.48

S.E.= Standard effort of the mean
σ^2P= Phenotypic variance
h^2 = Heritability

Correlation: Correlation results presented in table 3 revealed that days to flower initiation, days to flowering and days to pod initiation had significant positive association with days to maturity, pod length and harvest index but they showed significant negative correlation towards biological yield per plant. Days to maturity expressed significant negative correlation with primary branches per plant, clusters per plant, pods per plant, seeds per pod, biological yield and grain yield per plant. It means that increase in maturity days was not desirable as it had negative effect in most of the economically important traits. Therefore, short to medium day's maturity mungbean cultivars are suggested to be selected from the germplasm. Plant height had significant positive correlation with primary branches per plant, clusters per plant, pods per plant, seeds per

pod, biological yield per plant and grain yield per plant. Primary branches plant was significantly associated with plant height, clusters per plant, pods per plant, biological yield and grain yield. It is evident from this relationship that more primary branches will produce more clusters per plant ultimately improving the grain yield production in mungbean genotypes through their influence on pods per plant and biological yield per plant. Pods per plant showed significant positive affiliation with biological and grain yield while pod length expressed significant negative correlation with most of the traits except days to flower initiation, flowering, pod initiation, maturity and 100 seed weight. Seeds per pod had significant positive correlation with plant height and biological yield indicating the importance of this trait in mungbean genotypes. The negative correlation of 100 seed weight with biological yield and grain yield indicated limited scope for the improvement of this trait through selection. Biological yield and harvest index were positively correlated with grain yield but biological yield showed negative correlation with harvest index. This negative association of biological yield with harvest index showed physiological inefficiency for appropriate partitioning of total dry matter towards economic yield. Consequently the genotypes with low grain yield attained low harvest index and vice versa. High harvest index is very important for increasing yield potential of mungbean crop as it has strong positive association with grain yield. Malik *et al.,* (1987) and Ghafoor *et al.,* (1993) also reported similar kind of association between these two traits.

Table 3. Correlation coefficients among 14 quantitative traits in 40 mungbean genotypes.

	DF	**DPI**	**DM**	**PH**	**PBPP**	**CPP**	**PPP**	**PL**	**SPP**	**SW**	**BYPP**	**GYPP**	**HI**
DFI	0.85	0.81	0.68	0.18	0.03	-0.20	-0.17	0.34	-0.07	0.10	-0.48	-0.10	0.29
DF		0.94	0.75	0.27	-0.04	-0.20	-0.13	0.41	-0.13	0.15	-0.46	-0.00	0.37
DPI			0.79	0.18	-0.02	-0.17	-0.14	0.35	-0.25	0.20	-0.50	-0.02	0.39
DM				-0.14	-0.33	-0.41	-0.39	0.41	-0.32	0.33	-0.73	-0.26	0.32
PH					0.44	0.31	0.45	-0.32	0.56	-0.52	0.38	0.42	0.14
PBPP						0.81	0.72	-0.54	0.08	-0.51	0.40	0.47	0.18
CPP							0.93	-0.57	-0.03	-0.43	0.51	0.61	0.26
PPP								-0.53	0.06	-0.49	0.60	0.69	0.27
PL									-0.20	0.77	-0.41	-0.15	0.17
SPP										-0.50	0.37	0.22	-0.05
SW											-0.42	-0.14	0.18
BYPP												0.52	-0.28
GYPP													0.66

Correlations in *italic* are significant at p>0.05

Table 4. Four clusters grouping mungbean genotypes based on 14 quantitative traits.

Cluster	Frequency	Cluster memberships
I	15	V-3976, VC-1168, VC-1177, VC-1482, VC-1628, V-2773, VC-2651(A), VC-1973(A), NCM-88, V-3686, VC-2755, VC-2764, VC-2778, K-20, S-8
II	4	V-5197, V-5991-D, V-5991, NCM-87
III	13	V-1381, V-1945, VC-1647, VC-1973, V-2194, V-2194(B), VC-1163, VC-3216, VC-1973(B), VC-2768, NM-20-21,NM-13-1, BRM-114
IV	8	V-3092, VC-1562, E-76, E-321, M-22-24, M-28, 6601, 71-17

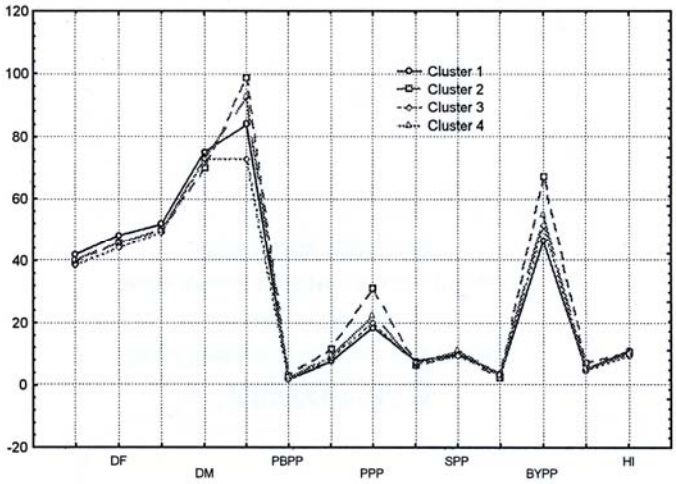

Fig. 1. Means of 14 quantitative traits of mungbean genotypes grouped in various clusters

Principal component and cluster analyses: Forty genotypes belonging to indigenous and exotic origin (Table 1) were grouped into 4 clusters based on average linkage. Members of each cluster are presented in table 4. Cluster I consisted of 15 genotypes, cluster II of 4, cluster III of 13 and cluster IV of 8 genotypes. As the genotypes from various sources differed considerably, it was difficult to establish any relationship between origin and clustering pattern. Mean values of clusters for 14 different quantitative traits are presented in Fig. 1 in order to have a clear picture of relationships among clusters. Mean values alongwith standard deviation of each cluster revealed that genotypes in cluster II were early in maturity and high yielding whereas genotypes grouped in cluster I, III and IV were late in maturity and had low to medium yield potential (Table 5). The genotypes in cluster II also exhibited highest biological yield per plant, pods per plant, clusters per plant, primary branches and plant height as compared to the genotypes of other clusters. The genotypes grouped in cluster III were early in flowering and pod initiation. This earliness in flowering and pod initiation helped the genotypes to attain maximum pod length as compared to the genotypes grouped in cluster I, II and IV. Harvest index in legumes is unpredictable and sensitive to environmental fluctuations and it is imperative to find genotypes with maximum harvest index. In this study, genotypes of cluster I exhibited comparatively more harvest index alongwith high seed weight.

Euclidean dissimilarity coefficients among four clusters ranged between 3.62 for clusters I and IV and 8.66 for clusters II and III (Table 6). A dandogram based on average linkage distance for forty mungbean genotypes was also constructed and presented in Fig. 4. Eigen values of 14 principal components have been shown in the scree plot (Fig. 2). The first four components with eigenvalues >1 contributed 85.49% of the variability amongst 40 genotypes evaluated for 14 quantitative traits (Table 7). Other PCs (5-14) had eigenvalues <1. The first PC was more related to yield and yield contributing traits (primary branches per plant, clusters per plant, pods per plant, pod length, seeds per pod, seed weight, biological yield and grain yield per plant) whereas the second PC contrast variables that related solely to vegetative growth (days to flower initiation, days to flowering, days to pod initiation, days to maturity and plant height) with those that are associated with reproductive development. The traits with greatest weight on the first component were biological yield, pods per plant, clusters per plant, pod length, seed weight, primary branches and seeds per pod, suggesting that this component reflected the yield potential of each genotype. The characters with greatest positive weight on PC_2 were days to flowering, days to pod initiation, harvest index, days to flower initiation, plant height and days to maturity. These findings revealed that second PC reflected the tendency of each genotype to emphasize vegetative growth, as opposed to reproductive. Primary branches per plant, clusters per plant, pods per plant, seed weight and grain yield per plant had also positive weight on this component. This proposed that genotypes that emphasize vegetative growth tend to have few large reproductive organs, whereas those that emphasize reproductive growth tend to have many small ones.

The first two principal components contributing more than half of the variance were plotted to observe the relationships between the clusters (Fig. 3.). Cluster I, II, and IV showed more clear separation than cluster III. Cluster III was not clearly separated which might be due to mixture of genotypes with different taxonomic traits grouped in this cluster.

Discussion

In order to maintain, evaluate and utilize germplasm effectively, it is important to investigate the extent of genetic diversity available. Smith & Smith (1989) considered morphological characterization as an important step in description and classification of crop germplasm because a breeding programme mainly depends upon the magnitude of genetic variability (Smith *et al*., 1991). For primary branches, clusters per plant, seeds per pod, 100 seed weight, grain yield per plant and harvest index, low genetic variability seemed to limit the scope of selection for these traits in the present group of genotypes. Hence the genes for these important traits should be explored from other sources through more collections from the areas of maximum diversity. Large scale testing of broad-based genotypes needs to be built up by making extensive local collection and introduction to develop a sound breeding programme (Ghafoor *et al*., 1992). Laghetti *et al*., (1998) advocated that maximum genetic conservation would be achieved by sampling populations from as many environments as possible. Subdividing the variance into its components assists the genetic resources conservation and their utilization. It enables planning for use of appropriate gene pools in crop improvement for specific plant attributes (Pecetti *et al*., 1996). Some of the genotypes possessed good genes for more than one trait and hence could be utilized directly or included in hybrid programme for varietal development. Though cluster analysis grouped genotypes together with greater genetic similarity, the clusters did not necessarily include all genotypes from same origin. Gupta *et al*., (1991), Dias *et al*., (1993), Amurrio *et al*., (1995) and Rabbani *et al.* (1998) also reported lack of association between agronomic traits and origin.

Table 5. Mean and standard deviation for four clusters based on quantitative traits.

Traits	Cluster I	Cluster II	Cluster III	Cluster IV
Days to flowering initiation (DFI)	41.95 ± 1.47	39.50 ± 3.96	38.63 ± 1.88	40.16 ± 1.61
Days to flowering (DF)	48.13 ± 1.70	45.68 ± 0.43	43.92 ± 2.43	40.56 ± 2.30
Days to pod initiation (DPI)	51.73 ± 1.40	49.88 ± 0.32	48.90 ± 2.10	49.72 ± 1.41
Days to maturity (DM)	75.07 ± 1.93	69.88 ± 0.43	72.62 ± 2.11	72.81 ± 1.79
Plant height (PH)	83.80 ± 4.47	98.58 ± 2.40	72.99 ± 5.39	92.35 ± 5.86
Primary branches per plant (PBPP)	1.86 ± 0.33	3.04 ± 0.39	1.99 ± 0.33	2.29 ± 0.40
Clusters per plant (CPP)	7.45 ± 1.05	11.74 ± 1.21	8.55 ± 0.80	9.08 ± 1.60
Pods per plant (PPP)	18.53 ± 2.78	30.91 ± 3.03	20.16 ± 1.96	22.37 ± 3.63
Pod length (PL)	7.63 ± 0.45	6.52 ± 0.12	7.13 ± 0.50	7.02 ± 0.45
Seeds per pod (SPP)	9.73 ± 0.72	10.01 ± 0.38	9.50 ± 0.71	10.70 ± 0.75
100 seed weight (SW)	3.69 ± 0.55	2.58 ± 0.14	3.48 ± 0.58	2.91 ± 0.77
Biological yield per plant (BYPP)	46.37 ± 5.84	67.41 ± 4.97	51.64 ± 3.87	54.80 ± 4.49
Grain yield per plant (GYPP)	5.02 ± 0.95	7.00 ± 0.44	4.85 ± 0.85	5.42 ± 0.95
Harvest index (HI)	10.98 ± 2.24	10.46 ± 0.17	9.49 ± 1.80	10.05 ± 1.82

Table 6. Euclidean distance among 4 clusters based on 14 quantitative traits amongst mungbean genotypes.

	Cluster I	Cluster II	Cluster III
Cluster II	7.94		
Cluster III	3.72	8.66	
Cluster IV	3.62	4.56	5.33

Table 7. Principal components (PCs) for 14 quantitative traits in mungbean genotypes.

		PC_1	PC_2	PC_3	PC_4
Eigenvalue		5.537	3.426	1.721	1.284
Proportion σ^2		39.550	24.470	12.295	9.170
Commulative σ^2		39.550	64.021	76.316	85.486
	Communalities	**Eigenvector**			
Days to flowering initiation (DFI)	0.829	-0.562	0.659	-0.261	-0.102
Days to flowering (DF)	0.925	-0.588	0.735	-0.199	-0.012
Days to pod initiation (DPI)	0.914	-0.606	0.723	-0.103	-0.117
Days to maturity (DM)	0.837	-0.797	0.416	-0.049	-0.164
Plant height (PH)	0.822	0.427	0.561	-0.507	0.260
Primary branches per plant (PBPP)	0.788	0.653	0.506	0.067	-0.318
Clusters per plant (CPP)	0.937	0.760	0.419	0.345	-0.255
Pods per plant (PPP)	0.905	0.775	0.474	0.254	-0.123
Pod length (PL)	0.804	0.732	0.029	0.235	-0.460
Seeds per pod (SPP)	0.879	0.567	0.386	0.030	-0.639
100 seed weight (SW)	0.851	0.656	0.562	0.262	-0.188
Biological yield per plant (BYPP)	0.738	0.823	-0.082	-0.036	0.229
Grain yield per plant (GYPP)	0.954	0.540	0.534	0.392	0.473
Harvest index (HI)	0.786	-0.092	0.670	0.471	0.326

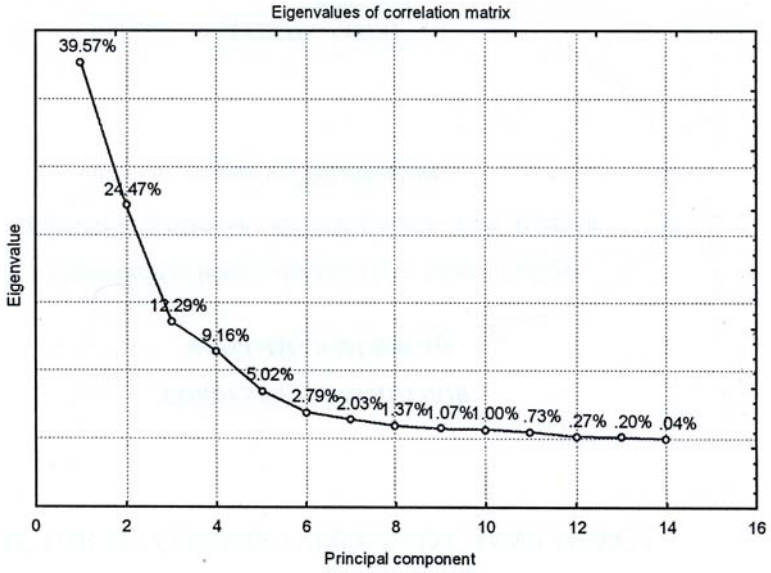

Fig. 2. Scree plot constructed for 14 principal components

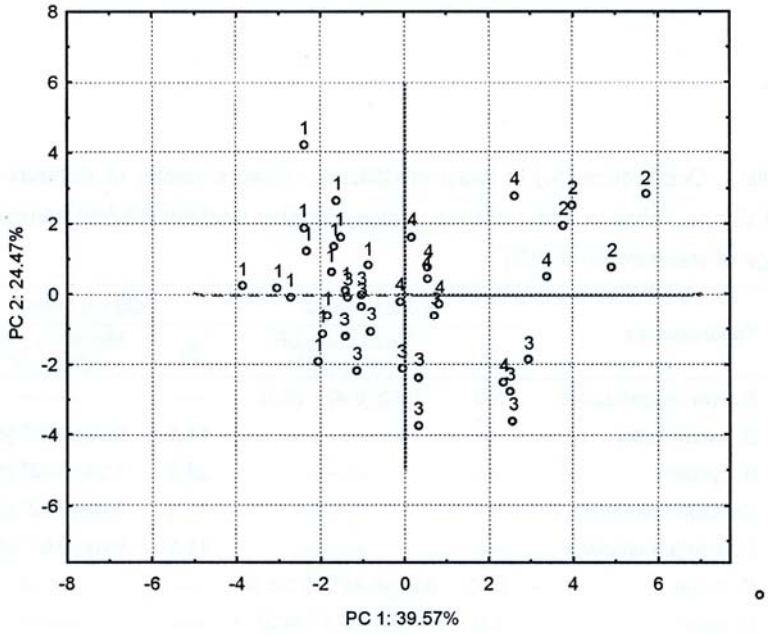

Fig. 3. Scattered diagram of mungbean genotypes for first two PCs. The digits 1, 2, 3 and 4 represent the cluster number.

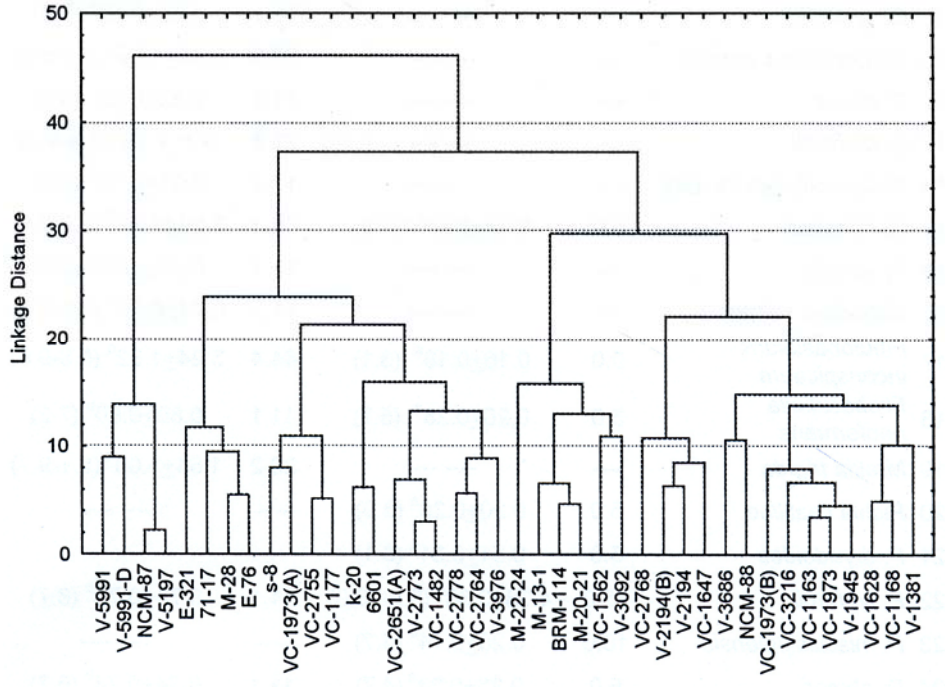

Fig. 4. Dandrogam based on 14 quantitative traits in mungbean genotypes.

The green revolution in cereals is largely supported by a tremendous increase in harvest index that enhanced cereal productivity. Similar emphasis is being given in legumes to select genotypes with appropriate harvest index. In the present set of genotypes, harvest index ranged from 7-22%, which is much lower than reported by Ghafoor *et al*., (1992) (20-30%) in mungbean. The lower harvest index in the present study is attributed to conducting the experiment under rainfed conditions. The populations with high PC_1 were characterized by high yield potential and short duration whereas populations with high PC_2 were typified by late flowering and maturity, and this component was more related to vegetative phase rather than reproductive. Falcinelli *et al*., (1988) described 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. Representative genotypes may be chosen from particular groups for hybridization programs with other approved cultivars. Several potentially important agronomic types have been identified which may be exploited for genetic potential to transfer the desirable genes and this, along with biochemical analysis, will facilitate in assembling a core collection from the large genetic resources (Singh, 1988; Clements & Cowling, 1994).

From the present research work, it was concluded that mungbean genotypes displayed a wide range of variation for most of the important traits studied. This will enable us to identify, select and combine genotypes to obtain important traits in one line with a broad genetic base. Grouping of genotypes in clusters revealed that only a portion of genetic variance has been exploited for mungbean improvement. If one of the goals is

to bring together cultivars with genetically similar characteristics, quantitative traits may be useful for grouping. Nevertheless these traits must be often used for separating genotypes when a limited range of germplasm is under consideration.

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