Multivariate analysis in some genotypes of mungbean [*Vigna radiata* (L.) Wilczek] on the basis of agronomic traits of two consecutive growing cycles

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ABSTRACT

An experiment to evaluate eleven agro morphological traits in twenty three genotypes of mungbean [*Vigna radiata* (L.) Wilczek] in the field experiment was conducted in two consecutive years 2013 and 2014. Data were recorded on quantitative as well as visually assayed agro morphological traits including days to 50 per cent flowering, days to 1st picking of pods, days to final picking, plant height (cm), number of secondary branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g), seed yield/plant (g) and harvest index (%). All the traits were analysed using multivariate statistical analysis. Most of the important evaluated traits showed a wide range of variation. Cluster analysis using UPGMA method grouped the genotypes into five clusters. The component of mungbean genotypes among different clusters was varied from two to nine genotypes. The maximum number of genotypes i.e., 9 is found in cluster III followed by cluster IV comprising of 6 genotypes. Cluster V showed the maximum mean value for plant height, branch/plant, pods/plant, seed/pod, seed yield/plant and lowest values for days to 50% maturity, 1st picking and days to maturity. Principal component analysis revealed that the first five main PCAs amounted 71.11% of the total variation among genotypes. PC1 accounts for maximum variability in the data with respect to succeeding components.

Key words: Agronomic traits, Cluster analysis, Genetic variability, Germplasm, Principal component analysis.

INTRODUCTION

Mungbean is a short duration grain legume widely grown in south and Southeast Asia. It is cultivated in tropical, subtropical and temperate regions. In India it is cultivated under both irrigated and rainfed conditions. Mungbean is a good substitute for animal protein in most Asian diets as it contains high amount of inexpensive protein and iron. It is particularly rich in leucine, phenylalanine, lysine, valine and isoleucine (Yimram *et al*., 2009). Beside its rapid growth and early maturity mungbean also has an important role in sustaining soil fertility by improving soil physical properties and associating with *Bradyrizobium* bacteria which in turn can fix atmospheric nitrogen (Joshi *et al*., 2003). At AVRDC-The World Vegetable Centre, Taiwan, where the largest mungbean collection is maintained, the majority of the germplasms were originated from India (2705), Iran (579) and Afghanistan (281) (AVRDC, 2008). Materials from India and West Asia are important sources of genetic variation for mungbean breeding, sharing about 62% of the total germplasm collected (Yimram *et al*., 2009).

Evaluation of germplasm is useful in selection of core collection as well as for breeding programs. Multivariate statistics help the researcher to summarize data and reduce the number of variables necessary to describe it (Anderson, 1972). The multivariate techniques, such as cluster analysis and principal component analysis may be an efficient tool in the quantitative estimation of genetic variation. To select germplasm in a more systemic and effective way and to develop strategies to incorporate useful diversity in their breeding programs, study of genetic diversity in genetic resources is a critical factor for breeders to better understand the evolutionary and genetic relationships among accessions (Lavanya *et al*., 2008). Multivariate technique also plays an important role in choice of divergent parents for hybridization to exploit maximum heterosis.

The objectives of present study were to investigate the magnitude of genetic variability among various genotypes of mungbean contingent on the quantitative traits using multivariate analysis and also to identify a set of agronomic attributes to be used in future breeding programme.

MATERIALS AND METHODS

Experimental site and seasons: The experiment was conducted at Experimental Farm of University of Calcutta, Baruipur, South 24 Parganas, West Bengal, India (22° N,88.26°E and 9.75m above the sea level) in two different growing seasons: March to May 2013 and mid March to 1st week of June 2014.

Experimental material and cultivation: The germplasm used in the study consisted of twenty three mungbean genotypes collected from different areas of India *viz*., NBPGR (New Delhi); Pulse & Oil Seed Research Station

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(Baharampur); & some local accessions of West Bengal. Seeds of each genotypes were sown in a single row of 2m long with 20cm of intra row and 30cm of inter row spacing with three replications. Recommended agronomic practices and plant protection measures were adopted over the two seasons to raise a good crop. Most of the cultural practices were performed according to Park. (1978).

Observed traits: Observations *viz.*, days to 50 per cent flowering [50%], days to 1st picking of pods[1st P], days to final picking [FP] were taken on row basis. For other characters *viz.*, plant height [PH] (cm),no of secondary branch per plant [B/P], number of pods per plant [P/Pt], pod length [PL] (cm),number of seeds per pod [S/P], 100 seed weight [100] (g), seed yield/plant [SY/P] (g) and harvest index [HI] (%) were observed on five randomly selected plants from each row in each sowing season. The mean values computed from the observations of both the seasons were used for statistical analysis.

Statistical Analysis: Descriptive statistics including mean, standard error (SE) and range in standard unit were calculated using SPAR 2.0 software package. Cluster analysis was performed using the unweighted pair-group method with arithmetic averages (UPGMA) based on the Euclidean distance matrix (Sneath and Sokal, 1973) and principal component analysis was done according to Rao, 1964.Both the analysis were done using IBM SPSS 16.0 software package.

RESULTS AND DISCUSSION

Variation: Descriptive statistics for all the traits are summarized in Table 1 which revealed that among these twenty three genotypes, the highest variation was found in number of pods/plant followed by seed yield/plant and plant height. Moderate variation was observed for days to final picking followed by days to 1st picking and days to 50% maturity. Low variability was found for harvest index followed by seed/pod, branch/plant, 100 seed weight and pod length.

Cluster analysis and principal component analysis: Using cluster analysis by UPGMA method all the twenty three genotypes were grouped into five major groups. Members of each cluster were presented in Table2 as well as a dendogram based on average linkage distance was also calculated (Figure 1). The component of mungbean genotypes among different clusters was varied from two to nine genotypes. The maximum number of genotypes i.e., 9 is found in cluster III followed by cluster IV comprising of 6 genotypes. Cluster I and II comprising of 3 genotypes each and cluster V consisting of 2 genotypes. Appreciable amount of variation among the cluster means for different characters presented in Table 3 also suggested the existence of diversity. Cluster V showed the maximum mean value for plant height, secondary branch/plant, pods/plant, seed/pod, seed yield/plant and lowest values for days to 50% maturity, days to 1st picking and days to final picking. At the same time cluster II exhibited the highest mean values for pod length, 100 seed weight and harvest index. These results illustrated the dependence of different clusters on their superior for different character. In order to know the combination type of agronomic traits that the mungbean genotypes would attain high grain yield as well as short maturity duration, Principal component analysis (PCA) was performed (Table 4). Figure 2 illustrated the Scree plot of the first five eigenvalues correspond to the whole percentage of the variance in the dataset. The first five main PCAs are extracted from the complicated components, the total variance of these five amounted to 71.11% with individual contribution as 24.29%, 14.15%, 12.24%, 10.53% and 9.91% respectively and had the eigen values >1. PC1 accounts for maximum variability in the data with respect to succeeding components. Similar findings are also reported by Basnet *et.al.* (2014), Md. Rahim *et al*, (2008) in mungbean. Table 4 revealed that PC1 is related to seed yield/plant, no. of secondary branch/plant, 100 seed weight and harvest index as well as the PC2 showed the highest positive values of the characters days to 1st picking, plant height, no. of pods/plant.

Table1: Mean based traits variability in 23 mungbean genotypes

Traits	Pooled Mean ± SE	Range	
		Minimum	Maximum
Plant Height	70.52 ±4.07	49.83	85
Secondary branch/plant	8.13 ±0.76	4.95	9.45
No. of Pods/plant	52.15 ±8.00	33.8	68.45
Pod Length	7.58 ±0.51	6.76	8.83
Seeds/ pod	11.05 ±0.89	9.33	13.13
100 seeds weight	3.75 ±0.66	2.7	6.67
Harvest index	16.73 ±0.96	14.78	19.05
Seed yield/plant	20.00 ±5.49	13.13	23.61
Days to 50% maturity	32.71 ±1.57	29	37.65
Days to 1st picking	57.15 ±1.64	53.73	61.85
Days to final picking	65.53 ±1.95	64.06	72.75
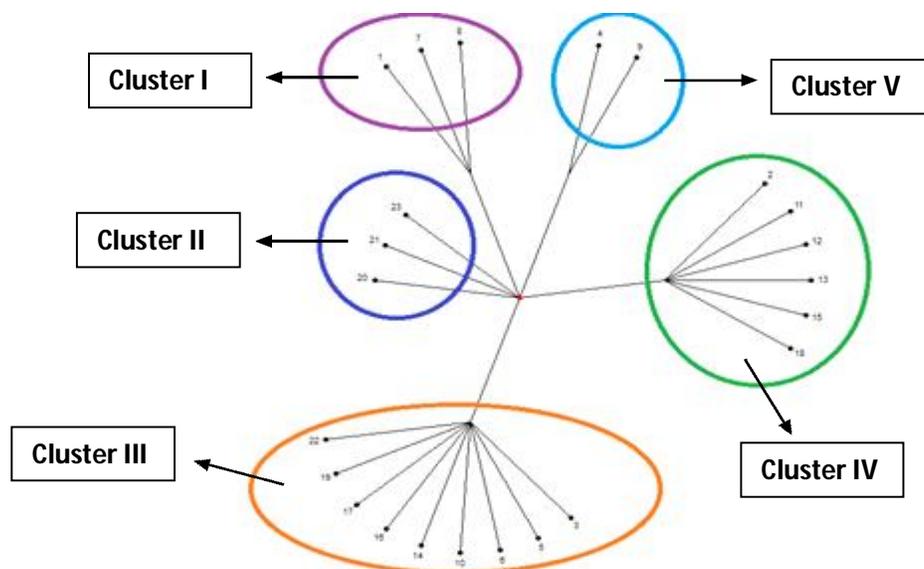
Fig 1: Dendogram derived from UPGMA cluster analysis showing genetic relationship among 23 mungbean germplasms

Table 2: Distribution of 23 mungbean germplasms in different clusters

Cluster No.	No of Genotypes	Names of Genotypes
I	3	APDM 84, ML 5, APDM 116
II	3	Baruipur Local 2, Howrah Local, Bankura Local
III	9	Purulia Local, Panna, Baruipur Local 3, Baruipur Local 1, Shona Mung 1, 24 Paragana, SML 302, PTM-11, B-1
IV	6	Shona 2, PM-2, K-851, Pusa 9632, Pusa Baisakhi, MH 981.
V	2	UPM-99-3, PS 16.

Table 3: Cluster mean for eleven quantitative characters of 23 mungbean germplasms in   different clusters

Cluster No.	Plant height	Secondary branch/ plant	No. of pods/ plant	Pod length	Seeds/ pod	100 seeds weight	Harvest index	Seed yield /plant	50% maturity	Days to 1st picking	Days to final picking
I	60.72	6.99	45.21	7.17	10.50	3.97	16.57	17.95	36.60	59.87	70.77
II	72.78	7.41	55.07	8.43	10.54	4.34	17.43	19.07	33.55	58.78	69.53
III	71.04	7.47	52.67	7.52	11.10	3.66	16.43	19.79	32.56	57.46	68.41
IV	69.36	6.19	51.90	7.63	11.58	3.41	16.84	21.08	31.25	56.02	67.23
V	83.08	8.17	61.58	7.12	12.00	3.99	16.99	22.23	30.65	54.85	66.55

Table 4: The first five principal components of 11 qualitative traits, eigenvalues, % of variance and cumulative %

|	PC1	PC2	PC3	PC4	PC5
Plant height	-0.333	0.199	-0.034	0.699	0.381
Secondary branch/plant	0.087	-0.026	0.765	0.453	-0.002
Pods/plant	-0.278	0.339	0.115	-0.065	0.496
Pod length	0.229	-0.146	0.126	-0.369	0.704
Seeds/pod	-0.546	0.560	-0.154	-0.043	0.077
100 seeds wt	0.140	-0.655	-0.285	0.461	0.003
Harvest index	0.222	0.356	0.641	-0.065	-0.305
Seed yield/plant	0.073	0.446	-0.327	0.058	-0.124
Days to 50% maturity	0.817	0.402	-0.220	0.169	0.038
Days to1st picking	0.757	0.081	0.040	0.160	0.258
Days to final picking	-0.529	0.380	-0.240	0.218	-0.145
Eigen value	2.672	1.557	1.346	1.159	1.090
% of variance	24.290	14.152	12.235	10.533	9.905
Cumulative %	24.290	38.441	50.677	61.210	71.115
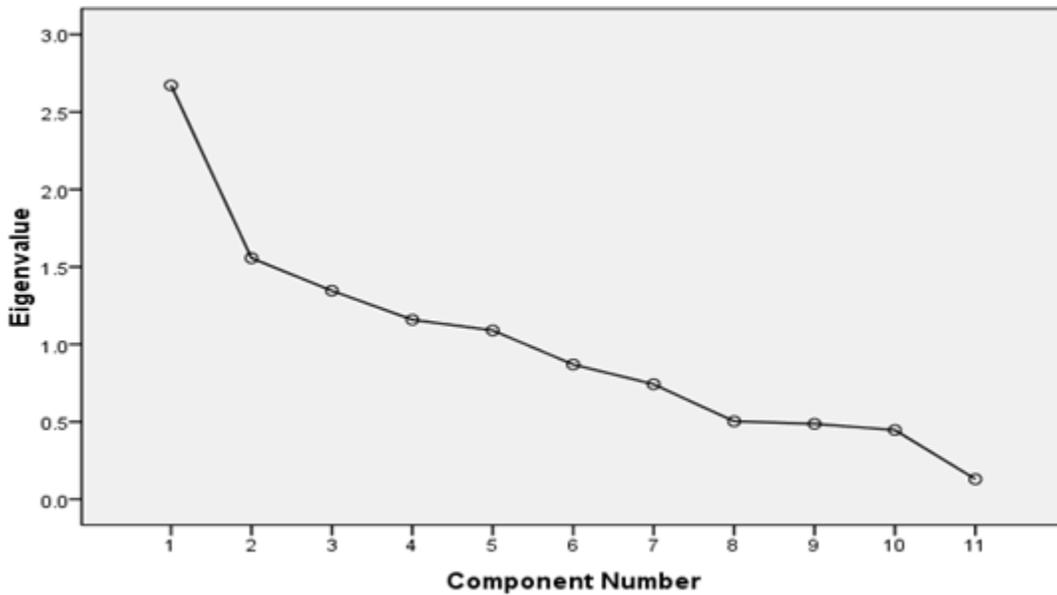
Fig 2: Scree plot constructed for 11 principal components.

To better understand the relationships among the measured traits of mungbean, the relationships are graphically displayed in a plot of PC1 and PC2 in Figure 3. In this plot, the first two PCAs mainly distinguishes the traits of S/P (seeds/pod), FP (days to final picking), P/Pt (pods/plant) and PH (plant height) as Group A from the other traits. SY/P(seed yield/plant) and HI (Harvest index) are refer to as Group B. Similar trend of grouping of traits by multivariate methods in the research is of practical value for the wheat breeders was found by Ajmal *et.al.*,2013.The other traits are grouped as: Group C, including 50% (days to 50% maturity)

and 1st P (days to 1st picking); Group D, including B (branch/plant) and PL (pod length).

In order to maintain, evaluate and utilize germplasm effectively, it is important to investigate the extent of available genetic diversity (Mohammadi and Prasanna, 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). Zaman *et.al.* 2013, suggested that if the diverse genotypes obtained from tentative groups along
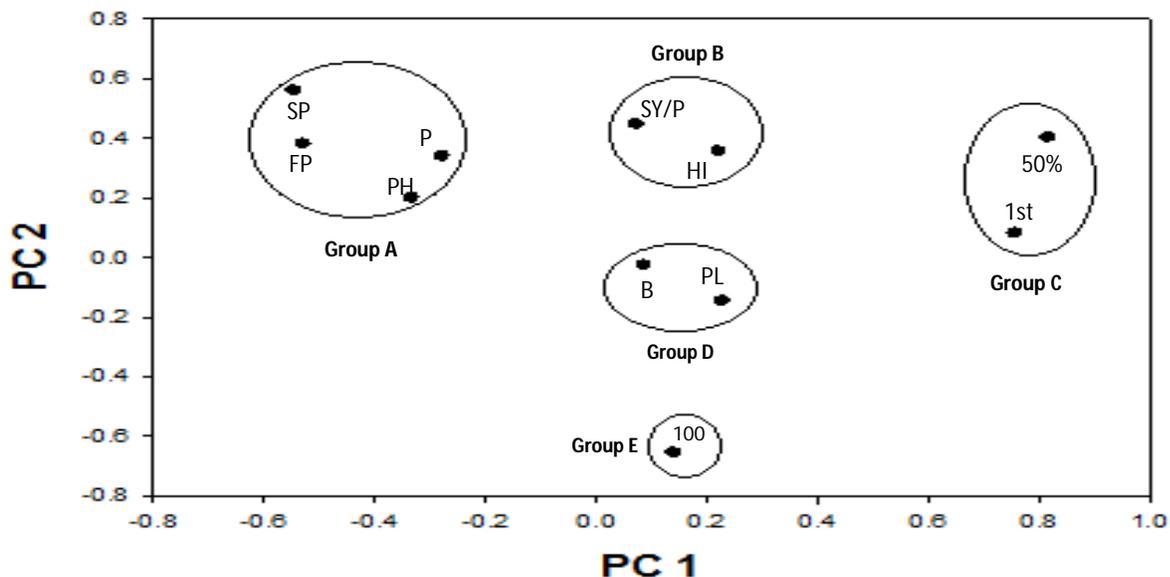

Fig 3: Plot of the first two PCAs indicating relation among various mungbean traits. For explanation of character symbols, see section Material and methods.

with the other desirable attributes are used in breeding programmes, it is expected to get better segregants for high seed yield and yield contributing traits due to non-allelic interaction. Fufa *et al.*, 2005 suggested that morphological traits of different crops have been used for estimation of genetic diversity and genetic improvement since they provide a simple way of quantifying genetic variation. Analysis of genetic diversity in Germplasm helps in classification of traits and identification of possible utility of different traits for breeding goals (Mohammadi and Prasanna, 2003). According to their similarity indices the qualitative traits involving in the multivariate analysis of the local and exotic genotypes were aligned in an appropriate manner. Basnet *et al* (2014) suggested that the genotypes grouped referring the similarity indices can be explored further at the genetic and molecular level for the crop improvement aspects employing appropriate breeding methodologies. So, according to Ajmal *et al.* (2013), the traits that form the first, second and subsequent PCAs indicated the strongest discriminatory power. In this experiment, the strongest discriminatory power was shown by seed yield/plant, days to 1st picking, plant height and pods/plant.

CONCLUSION

The mungbean genotypes exhibited a wide range of variation for most of the investigated traits. In the present study, plant height and pods/plant together were the main component of yield whereas days to 1st picking of earliness. Under this circumstances, selection should be made for increased pods/plant as well as plant height which will support in selecting superior genotypes, that may be directly used as the parent in hybridization program for the development of high yielding early maturing varieties.

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