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RESEARCH ARTICLE

Screening of Elite Mungbean Genotypes (*Vigna radiata* (L.) Wilczek) through Multivariate Analysis for Food and Nutritional Security

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Abstract: The ever-increasing urbanization to accommodate the growing population reduces substantially the agricultural land but poses a threat to meeting the requirement of proper nutrition for human health. Mungbean [*Vigna radiata* (L.) Wilczek] is a unique gift bestowed by nature to mankind, which has the potency to make up the gap of protein shortage with an inexpensive cost, but due to its low level of production as well as productivity, which in a roundabout way influences the nutritional status of people resulting in malnutrition. Therefore, enhancement of the total area under mungbean cultivation is not permissible, and an increase in the total productivity per unit area is necessary. In this manner, screening and evaluation of improved genotypes for high yield are necessary to ensure food security. But at the same time seed yield being a complex character governed by several other contributing traits, selection for the characters proves to be quite challenging. As a prerequisite for any breeding program aimed at yield enhancement presence of significant genetic diversity in a given population is highly important. In the present investigation principal component analysis was performed and the results revealed two principal components contributing to the total variance in the population. While the PC1 was predominated by yield and its attributing traits, the PC2 was mainly comprised of growth-related traits. The hierarchical (UPGMA) cluster analysis using standardized data classified the fifty-two mungbean genotypes into 4 clusters, which showed 2 major, 1 minor and one outlier. Among them, cluster II is the most fascinating, as its individual had high seed yield plant⁻¹ and related traits. The present work concluded that the identification of promising high-yielding mungbean genotypes through multivariate analysis has a good promise for future breeding programs with a view of food and nutritional security.

Keywords: Mungbean; Screening; Multivariate analysis

1. Introduction

The present unequivocal confirmation that the global population has already grown exponentially and predicted it will rise from the present to 9 billion in 2050^[1]. With

rapid urbanization and unchecked population growth ensuring food and nutritional security for the population has proved to be quite difficult even with the support of advanced technology in the field of agricultural science^[2,3]. In plant genetics resources, pulse crop species are the

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base subsistence of the world food security for a growing population. Mungbean [*Vigna radiata* (L.) Wilczek] is a unique gift presented by nature to mankind, which has the potency to make up the gap of protein shortage in view of its three-fold amount of protein as much as cereals^[4]. Besides, this crop has not only the capability to enrich soil fertility with physical and biological properties of soil health through symbiotic nitrogen fixation but also plays an important role in the economy to increase the farmer's income through the intercropping system^[5]. India alone with grown area of 3.72 million hectares and production of 1.70 million tons with productivity of 406.98 kg/ha represents around two third of global production^[6]. Thus, the overall annual production of the crop has increased yet the crop productivity has plateaued due to the non-availability of high-yielding genotypes and lack of genetic variability as well as post-harvest losses because of bruchid attack^[7]. Under the circumstances, enhancement of productivity is necessary for ensuring the food security of the population. So, there is a strong need for increasing the mungbean productivity but the current agricultural practices and the availability of sufficient land put a bar on it. Hence, an alternative approach is necessary to look for introducing improved high-yielding genotypes.

The sound knowledge of genetic diversity in genetic resources is a crucial part for plant breeders to better comprehend the evolutionary and the hereditary connections among accessions, to choose germplasm in a more organized and impressive way and to create convenient diversity in their plant breeding program^[8]. From the very beginning of agriculture genetic variability within crop species to meet subsistence food requirements has been done and now it is being utilized to surplus food for rising populations. The unavailability of stable high-yielding varieties potential is a major bottleneck for growing mungbean. Empirical selection for genotypes with high yield is difficult because of the yield complex nature controlled by polygenes. Yield is a complex trait, associated with many contributing traits which is highly influenced by the environment. Analysis of yield and related traits are also presented an intricate chain of relationships and picturized a reflection of their gene effects^[6]. Multivariate analysis such as principal component analysis and cluster analysis are statistically eligible to experiment and analyze a matrix of complicated values which can be utilized to think about the connection among traits and decide key properties and attributes that are involved in economic yield^[9]. PCA makes it conceivable to transform a given set of traits, which are either associated or not into a new system while cluster analysis is a clear and easy method to group the investigated data through their similarities by

a view of a two-dimensional vision^[10,11]. Estimation of the genetic diversity can help in the identification of genetically distant parents present in the population. Hybridization between such genetically distant parents can ensure a maximum number of recombinants expected in the segregating generation of such crosses.

Keeping these factors in view, the present investigation was conducted to determine the nature and magnitude of genetic diversity among the fifty-two mungbean genotypes for yield and yield attributing traits through multivariate analysis, particularly principal component analysis. Such analysis can clarify the association among agro-morphological traits and cluster analysis provides valuable information to screen and identify the promising high-yielding elite mungbean genotypes for future food security.

2. Materials and Methods

2.1 Experimental Material

The fifty-two mungbean genotypes were collected from different areas of India such as NBPGR (New Delhi); Pulse & Oil Seed Research Station (Berhampore); some local accessions of different districts of West Bengal and all genotypes listed in Table 1.

2.2 Experimental Site, Seasons and Cultivation

The present study was carried out at the Department of Genetics and Plant Breeding at Institute of Agricultural Science, University of Calcutta and the experimental materials consisted of fifty-two mungbean genotypes that were evaluated at Experimental Farm of University of Calcutta, Baruipur, South 24 Parganas West Bengal, India (22° N, 88.26° E and 9.75 m above the sea level) during the period of mid-March to end May in three different Years. The experiment was laid out in a Random Block Design (RBD) using three replications with the experimental plot. There were rows per plot of each genotype spaced 30 cm apart. The length distance of each row was 3 m, with plant to plant distance of 10 cm within a row. Most of the cultural practices were performed according to Park, 1978^[12].

2.3 Observed Traits

Data were collected on five randomly selected healthy harvested plants from each replication and each genotype. Pods of each plant were kept separately in an envelope and dried. Threshing was done by hand was taken to avoid a mixture of seeds. The pre and post-harvesting observations were recorded from five randomly selected plants

Table 1. List of mungbean genotypes.

Serial No.	Genotype Name	Serial No.	Genotype Name	Serial No.	Genotype Name	Serial No.	Genotype Name
1	APDM-84	14	A-82	27	IPM-99-125	40	Sukumar
2	MH-98-1	15	PM-2	28	IPM-205-07	41	PDM-54
3	B1	16	TM-98-20	29	IPM-5-17	42	Sonamung 2
4	PS-16	17	HUM-8	30	KM-139	43	CUM1
5	PTM-11	18	Sonamung-1	31	PM-11-51	44	CUM2
6	SML-302	19	Panna	32	Pusa-1431	45	CUM3
7	ML-5	20	Baruipur local	33	SML-115	46	CUM4
8	APDM-116	21	Howrah local	34	PDML-13-11	47	CUM5
9	UPM-993	22	Purulia local	35	Pusa-1432	48	CUM6
10	MC-39	23	Bankura local	36	Samrat	49	CUS1
11	Pusa Baisakhi	24	Pant mung-5	37	HUM-16	50	CUS2
12	Pusa- 9632	25	VC-639	38	MH-909	51	CUS3
13	K-851	26	Pusa Vishal	39	WBM-045	52	CUS4

from each replication on different parameters such as plant height (PH), branches plant⁻¹ (BPP), pods plant⁻¹ (PPP), pod length (PL), seeds pod⁻¹ (SPP), 100 seed weight (HSW), harvest index (HI) and seed yield plant⁻¹ (SYPP) which were determined on plot basis according to Moussa^[13] and the mean values computed from the observations of both the seasons were used for statistical analysis.

2.4 Statistical Analysis

To assess the overall variation attributed by yield attributing traits in mungbean, the descriptive statistics including mean, standard error (SE) and range in standard unit were calculated using SPAR 2.0 software package and the Principal component analysis (PCA) and k-means clustering (combined data over three seasons used for each trait) were done using IBM SPSS 20.0 while tree diagram (dendrogram) based on Unweighted Pair Group Method with Arithmetic Mean (UPGMA) method with the Euclidean distance matrix^[14] was constructed by Darwin version 6. The first two principal components were plotted against each other to find out the patterns of trait variability among the mungbean genotypes using SPSS version 20.

3. Results and Discussion

The basic statistics for eight agro-morphological traits were analyzed and summarized in Table 2 exhibited a noticeable variation present in the experimental material. Pods plant⁻¹, plant height, seed yield plant⁻¹ and harvest index showed high to medium variation whereas the rest of the traits showed low variation.

Screening is the first best step to selecting good genotypes for crop improvement. The hierarchical (UPGMA) cluster analysis constructed and classified the fifty-two mungbean genotypes into 4 clusters showing 2 major, 1

minor and one outlier in Figure 1. The genotypes were distributed in each cluster presented in Table 3 exhibited the result in a way that one genotype into cluster I contained the outlier (1.92%), 17 accessions were grouped into cluster II (32.69%), 2 genotypes made a small group into cluster III (3.85%) while 32 accessions grouped into transgressive cluster IV (61.54%). The K-Mean values were displayed in Table 4 and Figure 2 based on four clusters. Among them, cluster II constituted the most fascinating group because here each elite genotype had high seed yield as well as branches plant⁻¹, pods plant⁻¹, harvest index whereas cluster IV showed intermediate yield potency. Cluster II showed lower values in all the traits except pod length and 100 seed weight while the outlier (cluster I) was showed distinct from the other cluster because it demonstrated that the lowest seed yield plant⁻¹ as well as low branches plant⁻¹, pods plant⁻¹, harvest index. The inter-cluster distance among four cluster range between 10.57 to 28.60 based on Euclidean dissimilarity matrix presented in Table 5. The highest inter-cluster distance was found between clusters I and IV (28.60) followed by clusters I and III (26.71), clusters I and II (14.41). The closer cluster distance appeared between clusters III and IV (10.57) followed by clusters II and III (14.39) and clusters II and IV (14.63). Kahraman et al.^[11] and Darkwa et al.^[15] present similar result in common beans. Eigenvalues of eight principal components have been shown in the scree plot Figure 3. Principle component analysis (PCA) demonstrated that PC1 to PC2 had the Eigenvalues > 1 contributed traits variability 71.18% through PC1 and 28.81% through PC2 in Table 6. Seed yield plant⁻¹ and pods plant⁻¹ with maximum values closer to unity within PC1 whereas plant height and seeds plant⁻¹ close with PC2 illustrated in Figure 4. The positive and negative values in PCA

Table 2. Basic statistics for eight quantitative traits in fifty-two mungbean genotypes.

Traits	Pooled Mean \pm Standard error	Range Minimum	Maximum
PH (cm)	61.97 \pm 0.49	50.02	76.90
NBPP	3.88 \pm 0.04	2.50	4.97
NPPP	44.55 \pm 0.66	20.90	63.53
PL (cm)	7.55 \pm 0.06	6.67	9.37
NSPP	11.61 \pm 0.05	9.64	13.15
HSW (gm)	3.35 \pm 0.06	1.80	5.48
HI	24.89 \pm 0.36	17.23	32.64
SYPP (gm)	14.99 \pm 0.34	9.65	25.04

Note: PH-Plant Height, NBPP-No. of Branches per Plant, NPPP-No. of Pods Per Plant, PL-Pod Length, NSPP-No. of Seeds Per Pod, HSW-Hundred Seed Weight, HI-Harvest Index, SYPP-Seed Weight Per Plant, cm-centimeter, gm-gram.

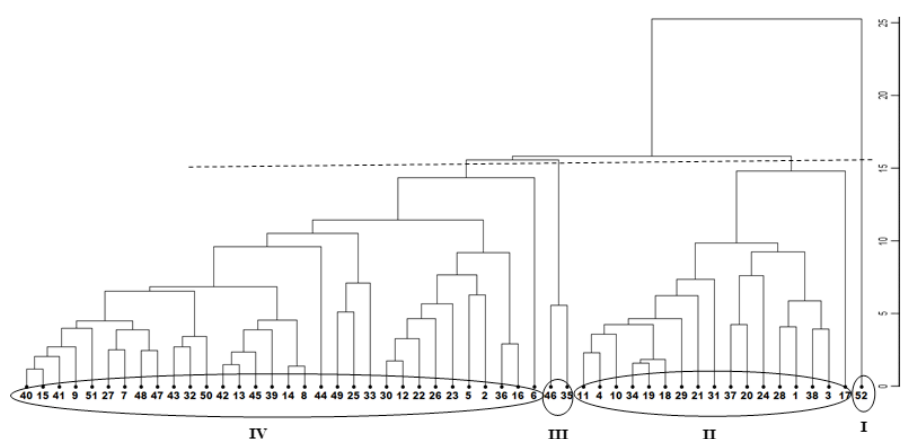


Figure 1. Dendrogram showing a cluster of 52 different mungbean genotypes.

Table 3. Cluster analysis and classification with regard to agro morphological traits of mungbean.

Cluster	No of Genotypes	Percentage of Contribution	Name of Genotypes
I	1	1.92	CUS4
II	17	32.69	Pusa Baishakhi, PS-16, MC-39, NDML-13-11, Panna, Sonamung-2, IPM-5-17, Howrah local, PM-11-51, HUM-16, Baruiপুর local, Pant mung-5, IPM-205-07, APDM-84, MH-909, B1, HUM-8.
III	2	3.85	CUM4, Pusa-1432.
IV	32	61.54	Sukumar, PM-2, PDM-54, UPM-993, CUS3, IPM-99-125, ML-5, CUM6, CUM1, Pusa-1431, CUS2, Sonali, K-851, CUM3, WBM-045, A-82, APDM-116, CUM2, CUS1, VC-639, SML-115, KM-139, Pusa-9632, Purulia local, Pusa Vishal, Bankura local, PTM-11, MH-98-1, Samrat, TM-98-20, SML-302, Pusa 1432.

represented correlation trend between the traits. These results were in trends with the findings of Pandiyan et al. Therefore, PC1 assists to select the traits such as branches plant⁻¹ and seed yield plant⁻¹ for yield improvement.

PH-Plant Height, BPP-Branches per Plant, PPP-Pods Per Plant, PL-Pod Length, SPP-Seeds Per Pod, HSW-Hundred Seed Weight, HI-Harvest Index, SYPP-Seed Weight Per Plant.

PH-Plant Height, BPP-Branches per Plant, PPP-Pods Per Plant, PL-Pod Length, SPP-Seeds Per Pod, HSW-Hundred Seed Weight, HI-Harvest Index, SYPP-Seed Weight Per Plant.

Screening is a prerequisite strategy for breeding to improve productivity so that an important crop through breeding traits variation is a necessity. Significant variation exists in the present study for yield contributing

Table 4. K-Mean performance of agro-morphological traits of four different clusters in mungbean genotypes.

Cluster	PH (cm)	BPP	PPP	PL (cm)	SPP	HSW (gm)	HI	SYPP (gm)
I	56.23 ± 3.03	2.80 ± 0.46	20.90 ± 0.17	8.70 ± 0.80	12.00 ± 0.14	4.40 ± 0.17	27.42 ± 1.66	9.65 ± 0.22
II	62.37 ± 0.69	4.01 ± 0.05	51.73 ± 0.83	7.82 ± 0.10	11.50 ± 0.08	3.59 ± 0.11	28.28 ± 0.51	20.15 ± 0.39
III	74.23 ± 1.54	3.19 ± 0.37	48.46 ± 1.47	7.26 ± 0.19	11.74 ± 0.18	2.98 ± 0.11	23.43 ± 0.63	10.65 ± 0.18
IV	61.18 ± 0.62	3.89 ± 0.05	41.22 ± 0.58	7.38 ± 0.06	11.65 ± 0.07	3.22 ± 0.07	22.96 ± 0.42	12.68 ± 0.20

Note: cm-centimeter, gm-gram

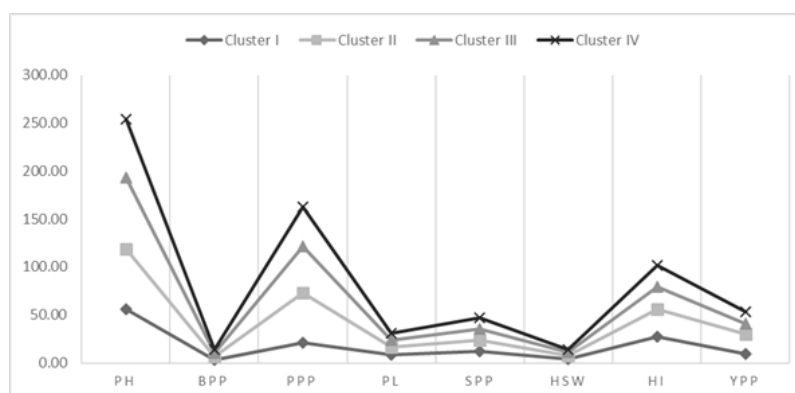


Figure 2. Means of eight quantitative traits of mungbean genotypes grouped into four clusters.

Table 5. Inter cluster distance and mean performance of agro-morphological traits of four different clusters of mungbean genotypes.

Cluster	II	III	IV
I	14.41	26.71	28.60
II		14.39	14.63
III			10.57

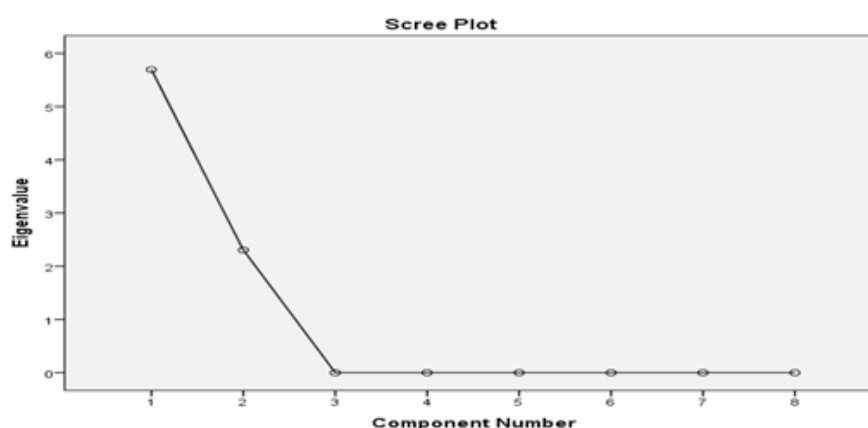


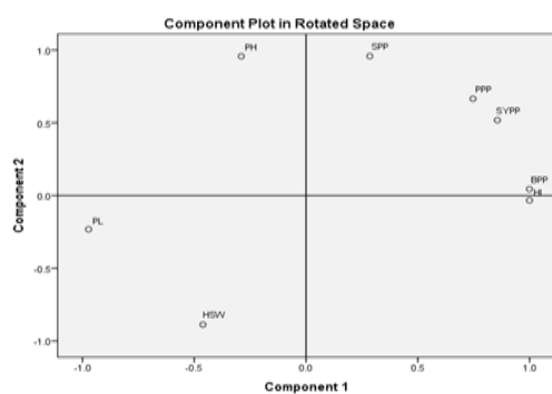
Figure 3. Scree plot constructed for eight principal components.

traits. Ghosh et al. ^[16] reported that adequate knowledge of trait variation is an imperative marker that provides a sign of the distinctive impacts which influence the aggregate variation of plant traits while variation alludes to detectable contrasts among individuals for a specific trait. The knowledge of Multivariate analysis not only indicates the

significant variance between average vectors but also provides efficient utilization for securing the genetic resources to forecast the potentiality of the breeding material by rapid authentication ^[11,17]. The nature of the distribution of the genotypes across four clusters observed in the current investigation suggested that the analysis successfully

Table 6. Two principal components with eight agro-morphological traits of mungbean genotypes.

Traits	PC1	PC2
PH (cm)	0.303	0.953
BPP	0.849	-0.529
PPP	0.992	0.126
PL (cm)	-0.933	0.359
SPP	0.777	0.629
HSW (gm)	-0.882	-0.471
HI	0.805	-0.593
SYPP	0.998	-0.057
Eigen Values	5.695	2.305
% of Variance	71.189	28.811
Cumulative %	71.189	100.000

**Figure 4.** Scattered diagram of two principal components indicating a relationship between eight agro-morphological traits.

classified the accessions based on their phenotypic performances. Similar observations were earlier reported by Basnet et al. [18]. Cluster II with seventeen elite genotypes presented the highest mean performance on seed yield plant⁻¹ as well as pods plant⁻¹ and high values for the rest of the traits and presumes that had special significance in diversification, conservation of natural resources, crop development and sustainability of production systems. Mohammad and Sharif [9] suggested that the selection of genotypes for hybridization must take into account the inter-cluster distances between different clusters as well as the intra-cluster distances among genotypes belonging to the same cluster to obtain optimum segregation during recombination. In addition to cluster analysis the principal component analysis revealed that the first principal component designated at PC1 plays a conceivable role to identify the ideotype yield enhancement traits while PC2 differentiated factors that related to vegetative growth exclusively in regenerative advancement. Pandiyan et al. [19] reported that K-Mean values showed traits ho-

mology, degree of genetic diversity and almost similar trends in principle component analysis. Hence, pods plant⁻¹, branches plant⁻¹, harvest index was considered as the most important yield attributing component which is directly reflected in the final yield and also selected seventeen elite high-yielding mungbean genotypes from cluster II which transform new opportunity to surplus food and nutrition for the rising population.

4. Conclusions

The current investigation successfully elucidated the magnitude of diversity existing within a given population of fifty-two mungbean germplasms. The study also helped in identifying seventeen germplasms distributed within the same cluster based on their high yield and promising morphological traits. Such information can be worthwhile to identify suitable parents for exploitation in future hybridization programs, and also aim for yield improvement along with other economically important traits.

Author Contributions

The first author as well as corresponding author Sanhita Ghosh took the lead in analysis, interpretation as well as writing the manuscript while co-authors Sabyasachi Kundagrami provided suggestions on experiments and Anindita Roy helped during the analysis.

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Data Availability

Data are available upon request to the corresponding author.

Conflict of Interest

The authors disclosed that they do not have any conflict of interest.

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