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Short Communication

ASSESSMENT OF GENETIC DIVERSITY IN MUNGBEAN (*Vigna radiata* L.)

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Abstract

An experiment was conducted at Sher-e-Bangla Agricultural University, Dhaka, Bangladesh to analyze the genetic diversity of fourteen mungbean varieties through Mahalanobis D^2 statistic and principal component analysis for nine quantitative traits related to yield. Based on the results of this study the varieties were grouped into four clusters by diversity (D^2) analysis where cluster IV comprised six varieties, cluster I had four varieties and cluster II and III had 2 varieties in each. The maximum inter-varietal distance was observed between G_1 and G_6 (1.288). Genetic diversity in mungbean can be explained 89.82% by the first four components, according to principal component analysis. G_1 (BARI mung1), G_2 (BARI mung2), G_6 (BARI mung6), G_7 (BARI mung7) and G_{10}(BINA moog-5) were shown to have potential for further hybridization in breeding programs, based on group distance and other agronomic performance measures.

Keywords: Cluster analysis, Genetic diversity, Mungbean, Principle component analysis.

Introduction

Mungbean (*Vigna radiata* L.) is a very common and important pulse crop belongs to the family Leguminosae sub family Papilionaceae, grown principally in the tropical and subtropical parts of the world (Bangar *et al*. 2018). Mungbean is rich in protein (24%) and sprouted mungbean is rich in calcium, iron and vitamin C (Mwangi *et al.,* 2021). Moreover, it is a short durated, well adapted, requires less water to grow and also a non-photosensitive crop (Anita *et al.,* 2025). India, Bangladesh, Pakistan, Sri Lanka, Philippines, Thailand are the main mungbean growing countries of the world (Gayacharan *et al.* 2022). In Bangladesh the production is increasing from 25000 mt to 42000 mt in the last decade (BBS, 2023). However, in spite of having various good nutritious qualities its worldwide production is 0.5 t ha^{-1} but the predictable yield potential is 2.5 to 3.0 t ha^{-1} (Gayacharan *et al,*. 2020). So there is a wide yield gap between the demand and production. Considering this factor there is a great opportunity for the breeder to improve the yield of mungbean.

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For successful breeding program genetic diversity is an essential requirement (Tabasum *et al.,* 2020). Analysis of genetic diversity is the fundamental means to detect the most diverse parents which are helpful to search out the higher transgressive segregants or heterotic hybrids (Islam *et al.,* 2020). The crosses between the genetically distant parents are capable to produce high heterotic hybrids (Falconer, 1960; Moll *et al.,* 1962; Ramanujam *et al.,* 1974; Ghaderi *et al*., 1989; Mian and Bhal, 1989). Since Mungbean is a self-pollinated crop its genetic base is narrow. So, yield improvement in mungbean from the existing germplasm is not easier. Identification of the elite mungbean germplasm will be helpful to beat the current obstruct. As such the present study was analyzed the degree and nature of genetic diversity among fourteen mungbean varieties to find out the potential parents for developing novel mungbean varieties.

Materials and Methods

Plant materials, experimental location and design

In this investigation 14 mungbean varieties were used as the plant materials, collected from three national institutes viz. Pulses Research Centre of Bangladesh Agricultural Research Institute (BARI), Gazipur Agricultural University (GAU), Salna, Gazipur, Bangladesh Institute of Nuclear Agriculture (BINA), Lalmonirhat and Barisal district (Table 1).

Table 1. List of 14 varieties of mungbean along with their sources

Sl. No.	Local name	Mark	Sources
1	BARI mung1	G_1	Pulses Research Centre, BARI
2	BARI mung2	G_2	Pulses Research Centre, BARI
3	BARI mung3	G_3	Pulses Research Centre, BARI
4	BARI mung4	G_4	Pulses Research Centre, BARI
5	BARI mung5	G_5	Pulses Research Centre, BARI
6	BARI mung6	G_6	Pulses Research Centre, BARI
7	BARI mung7	G_7	Pulses Research Centre, BARI
8	BARI mung8	G_8	Pulses Research Centre, BARI
9	BAU mung1	G_9	Department of Agronomy, GAU
10	BINA mung5	G_{10}	Plant Breeding Division, BINA
11	BINA mung8	G_{11}	Plant Breeding Division, BINA
12	BINA mung9	G_{12}	Plant Breeding Division, BINA
13	Chaitamung	G_{13}	Lalmonirhat
14	Sonamung	G_{14}	Barisal

The field investigation was carried out at the experimental plot of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh. The field was located at 90º22′ E longitude and 23º41′ N latitude, belongs to the Agro-ecological zone of the Modhupur Tract, AEZ-28. Randomized complete block design (RCBD) with three replications were followed for conducting the field experiment. The plot size was 2.5 m with single line. The distance between row to row was 30 cm and plant to plant was 10 cm. All the agronomic practices such as thinning, fertilizer application, irrigation, weeding, etc., were followed for mungbean cultivation as per the recommendation of Bangladesh Agricultural Research Institute (BARI).

Morphological parameter observation and analysis

Data were recorded on nine yield contributing characters viz. Plant height , number of leaves/plant, number of branches/plant, number of pods/plant, number of pods cluster/plant, pod length, number of seeds/pod, 1000 seed weight (g). The analyses in respect of nine different morphological traits of 14 mungbean varieties were analyzed by multivariate analyses using the GENSTAT 5.13 software program. The varieties were grouped into clusters based on Mahalanobis's D^2 statistics and canonical variate analysis.

Results and Discussion

Divergence analysis is usually performed to identify the different individual varieties for hybridization purposes. The genetic diversity analysis and clustering of the varieties were studied based on the traits studied which presented below.

Non-hierarchical clustering

By following Tocher's method (Rao, 1952) the fourteen varieties were grouped into four clusters based on the relative magnitude of Mahalanobis D^2 values (Table 2). Cluster II and Cluster III consists of two varieties, which found as the smallest cluster. Cluster IV obtained as the largest cluster composed of six varieties. Finally, cluster I composed of four varieties (Table 2). These results confirmed the clustering pattern of the varieties obtained through principal component analysis. Cluster mean values of nine different characters of 14 mungbean varieties are presented in Table 3. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. It is clear that the results obtained through PCA were supported by non-hierarchical clustering. Joshi *et al.* (2022) also studied the genetic divergence of mungbean with thirty varieties and reported about twelve clusters. Tiwari *et al.* (2022), Zhang *et al.* (2024) also reported the same results while studying about thirty six and three hundred two mungbean varietiesrespectively that corroborate with the present findings.

Table 2. Distribution of 14 mungbean varieties into four different clusters

Cluster number	Number of varieties	Percent (%)	Name of varieties
I	4	28.57	G1 , G2 , G3 , G4
II	2	14.29	G6 , G7
III	2	14.29	G5 ,G10
IV	6	42.86	G8 , G9 , G11, G12, G13, G14

Table 3. Cluster mean values of nine different characters of 14 mungbean varieties

Characters	I	II	III	IV
Plant height (cm)	52.08	43.49	47.25	42.15
No. of leaves/plant	9.53	13.11	13.05	11.16
No. of branches/plant	3.08	3.77	3.39	3.22
No. of pods/plant	10.14	18.33	11.41	13.5
No. of pod clusters/plant	5.23	5.72	6.18	5.57
Pod length/plant (cm)	8.04	10.45	10.02	8.27
No. of seeds/pod	9.25	10.83	12.5	10.44
Wt. of 1000 seeds (g)	28.58	50.84	39.83	29.11
Seed yield/plant (g)	3.23	5.05	5.1	4.24

Principal component analysis

Principal components were computed from the correlation matrix and varieties scores obtained from first components and succeeding components with latent roots greater than the unity. Eigen values corresponding nine principal component axes and percentage of total variation accounting for them obtained from the principal component analysis are presented in Table 4. It represents that the cumulative eigen values of four principal components accounted for 89.82% of the total variation among the varieties. The 1st principal component accounted for 57.45% of the total variation, the second, third and fourth components accounted for 14.09%, 10.03% and 8.25% of the total percent of variation, respectively (Table 4). For selection of the best varieties these component characters will be more helpful. Mwangi *et al.* (2021) studied the genetic divergence among seven mungbean varieties and found that first three components contributed highest (83.4%) of overall variation. Similar results were also reported by Gayacharan *et al.* (2020) and they found first five principle components (PCs) explained 91.4% of the total variation. Tiwari *et al.* (2022) also studied about mungbean results were alike.

Table 4. Eigen values, percentage of variation and cumulative percentage in respect of nine axes in 14 varieties of mungbean

Principal component axes	Eigen value	Percent variation	Cumulative % of percent variation
I	5.17	57.45	57.45
II	1.268	14.09	71.54
III	0.903	10.03	81.57
IV	0.742	8.25	89.82
V	0.517	5.74	95.56
VI	0.184	2.05	97.61
VII	0.117	1.3	98.91
VIII	0.067	0.74	99.65
IX	0.032	0.35	100

Principal coordinate analysis

Principal coordinate analysis (PCO) was performed on auxiliary principal component analysis. This analysis helps in estimating distances (D^2) for all combinations between pairs of varieties. The highest inter varietal distance was observed between the varieties G1 and G_6 (1.288). The second highest value observed between the varieties G_2 and G_6 (1.270). The tenth highest pair distance was observed between varieties G_2 and G_{11} (1.150). The lowest distance was observed between the varieties G_1 and G_2 (0.150). The second lowest observed between varieties G_{13} and G_{14} (0.185). The tenth lowest distance was observed between the varieties G_8 and G_{12} (0.394). The difference between the highest and the lowest inter-genotypic distance indicated the prevalence of variability among the 14 mungbean varieties (Table 5).

Table 5. Ten of each lower and higher inter varietal distances (D^2) between pairs of mungbean varieties

Highest 10 inter genotypic distances				Lowest 10 inter genotypic distances			
Sl	Varieties	Varieties	Values	Sl	Varieties	Varieties	Values
1	G1	G6	1.288	1	G1	G2	0.150
2	G2	G6	1.270	2	G13	G14	0.185
3	G1	G7	1.254	3	G3	G4	0.261
4	G6	G13	1.250	4	G6	G7	0.268
5	G2	G7	1.229	5	G2	G13	0.346
6	G7	G13	1.209	6	G3	G9	0.359
7	G10	G13	1.186	7	G4	G9	0.359
8	G1	G10	1.171	8	G11	G12	0.380
9	G2	G10	1.154	9	G5	G9	0.390
10	G2	G11	1.150	10	G8	G12	0.394

Conclusion

Selection of genetically divergent varieties is an essential step for the hybridization program. So, the varieties would be selected based on specific objectives. A higher heterosis could be produced from the crosses between genetically distant parents. Considering the magnitude of genetic distance and agronomic performance, the varieties G_1, G_2, G_6, and G_7 from cluster I and cluster II would be suitable for selecting the best combinations that carry the desirable characteristics by the breeders.

Author's contributions

S. S designed, conceived, and executed the experiment and drafted the manuscript; B.N.S, S.P, S.I and S.N.B edited and reviewed the manuscript; MAS supervised the experiment, analyzed the data, and edited and reviewed the manuscript.

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Conflict of Interest

All authors affirm that there are no conflicts of interest regarding this research paper.

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