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GENETIC DIVERSITY ANALYSIS AND CHARACTER ASSOCIATION IN YIELD AND YIELD CONTRIBUTING TRAITS OF MUNGBEAN (*Vigna radiata* L.)

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Abstract

An experiment was carried out at Sher-e-Bangla Agricultural University in *Kharif-1* season with 33 genotypes of mungbean (*Vigna radiata* L.) to identify genetically diverse genotypes for yield contributing characters. The genotypes were evaluated for eight yield and yield contributing characters using a Randomized Complete Block Design (RCBD) with three replications. High heritability coupled with a high genetic gain was observed in days to 50% flowering, plant height, pod length, 100 seed weight, and seed yield per plant which indicated the effect of additive genes. Selection of these traits might cause the probability of simultaneous improvement of mungbean. The genotypes were grouped into four clusters based on the D^2-value where cluster I was the largest and comprised of 13 genotypes followed by clusters III and IV with 6 genotypes in each. The highest inter-cluster distance was recorded between clusters II and IV (10.425) and the intra-cluster distance in cluster II (2.45). The lowest inter-cluster distance was found between clusters I and III (3.19). Principle component analysis revealed first four components contributed 88.77% towards genetic diversity in mungbean. Considering the magnitude of cluster means and agronomic performance the genotypes of cluster II and the genotypes of cluster IV might be suggested as parents for future hybridization programs.

Keywords: Genetic advance, Genetic variation, Heritability, Yield contributing traits.

Introduction

Mungbean (*Vigna radiata* L.) is one of the most important pulse crops belonging to the Papilionoideae subfamily of the Fabaceae and has a diploid chromosome number of 2n = 2x = 22 and is widely grown in Bangladesh but production is lower. As it is a short-duration crop, it can fit in as a cash crop between major cropping seasons. It is grown three times in a year. About 60-65% of the total mungbean is grown under the Boro rice- mungbean-Aus rice (rainfed) cropping pattern. Mungbean contains 51% carbohydrate, 24-26% protein, 4% mineral, and 3% vitamins (Afzal *et al.*, 2008). Besides providing protein in the diet, mungbean has the remarkable quality of helping the symbiotic root rhizobia to fix atmospheric nitrogen and hence enrich soil fertility (Anjum

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et al., 2006). It is covering 109000 acres with an average yield of 41000 MT (BBS, 2022). The major area of mungbean is replaced by cereals (Abedin *et al*., 1991). There are a few constraints such as several biotic and abiotic stresses, low yield, rice cultivation all year round mainly in winter (*Boro*) season which limits pulse cultivation, limited study was done on mungbean and the area covered by this crop is not satisfactory. Only a few varieties of mungbean have been developed by the Pulses Research Centre, BARI, and disseminated with the package of management technologies to the farmers for cultivation. Therefore, to improve the yield and quality of mungbean several activities like building up diverse germplasm, selection, and evaluation of genotype from germplasm, etc. should be used in the improvement program. Genetic diversity is the basic element for an efficient choice of parents for the variety development program. Genetic diversity determines the inherent potential of a cross for heterosis and the frequency of desirable recombinants in advanced generations. Therefore, the present study was conducted to study the genetic diversity for finding suitable parental groups with better performances for future breeding programs.

Materials and Methods

The experiment was carried out at the experimental field of Sher-e-Bangla Agricultural University. The experimental materials of the study consisted of 33 genotypes of mungbean (Table 1) collected from the Plant Genetic Resources Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI). The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications with a distance of plant to plant 15cm, line to line 30 cm (Krishi Projukti Hatboi, 2014), and plot to plot 2.5 m. From land preparation to all necessary intercultural operations were properly done during the cropping period (*Kharif-1*: March-June, 2017) for better growth of plants for better yield. Thinning was done 25 days after sowing and the first weeding was done during thinning and the second one after about two months of sowing. Application of fertilizers at recommended doses (Urea: 40-50 kg/ha, TSP: 80-85 kg/ha, MP: 30-35 kg/ha) by BARI (Krishi Projukti Hatboi, 2014) was done properly. Harvesting of mungbean pods was done three times after the maturity stage. The data were recorded on five selected plants from each replication of a genotype on the following characters: i. days to 50% flowering ii. plant height (cm) iii. number of branches per plant iv. number pod per plant v. pod length (cm) vi. seed per pod vii. 100 seed weight (g) viii. yield per plant (g). The data were analyzed following principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis (CA) canonical vector analysis (CVA), and Duncan‘s multiple range test (DMRT). Intra and inter-cluster distances were calculated by the method of Singh and Chaudhury (1985).In RCBD MSTAT-C was used to analyze variance and mean performance. GENSTAT 5.13 was used for multivariate analysis.

Table 1. Genotypes of mungbean

Sl.No.	Designation	Accessions	Sl. No.	Designation	Accessions
1	G1	BD-6874	18	G18	BD-6917
2	G2	BD-6875	19	G19	BD-6918
3	G3	BD-6876	20	G20	BD-6920
4	G4	BD-6878	21	G21	BD-6923
5	G5	BD-6879	22	G22	BD-6924
6	G6	BD-6896	23	G23	BD-6925
7	G7	BD-6898	24	G24	BD-6926
8	G8	BD-9835	25	G25	BD-6927
9	G9	BD-9837	26	G26	BD-6928
10	G10	BD-6900	27	G27	BD-6929
11	G11	BD-6901	28	G28	BD-6932
12	G12	BD-6902	29	G29	BD- 6933
13	G13	BD-6903	30	G30	BD-6934
14	G14	BD-6904	31	G31	BD-6935
15	G15	BD-6906	32	G32	BD-6936
16	G16	BD-6907	33	G33	BD-6937
17	G17	BD-6909			

Results and Discussion

The present experiment was conducted to study the genetic variability, character association, and genetic diversity among 33 genotypes of mungbean. Variance, heritability, and genetic advance were measured by DMRT test where days to 50% flowering showed high heritability (95.95%) with high genetic advance (6.71) (Table 2). Reddy *et al*. (2004) reported a result similar to this experiment. High heritability for hundred seed weight in mungbean was similar to Sarwar *et al*. (2004). In the case of the number of pods, 100g-seed weight, and seed yield showed high variation. Moderate variation was found in plant height, number of branches, and lower in pod length. Fetemeh *et al*. (2012) also performed a similar study in mungbean using D2 statistic.

Table 2. Estimation of genetic parameters in eight characters of 33 mungbean genotypes

Parameters	Range	Mean	Mean sum of square (MS)	σ^2p	σ^2g	σ^2e	PCV (%)	GCV (%)	ECV (%)	Heritability (%)	Genetic advance (5%)	Genetic advance (% mean)
Days to 50% flowering	7.67-19.33	14.99	33.61**	11.52	11.05	0.47	22.64	22.18	4.56	95.95	6.71	44.75
Plant height (cm)	33.20-72.87	49.32	253.09**	99.93	76.58	23.35	20.27	17.74	9.80	76.63	15.78	31.99
No. of branches per plant	1.74-3.61	2.41	0.83**	0.46	0.19	0.27	28.14	17.90	21.72	40.43	0.57	23.44
Pods per plant	6.00-22.40	11.15	49.11**	20.71	14.20	6.51	40.80	33.78	22.88	68.56	6.43	57.62
Pod length (cm)	5.42-8.98	6.43	2.24**	0.85	0.69	0.16	14.35	12.95	6.19	81.42	1.55	24.07
Seeds per pod	8.11-12.80	10.14	0.78**	1.48	0.70	0.78	11.99	8.22	8.73	47.01	1.18	11.61
100 seed weight (g)	2.01-7.30	3.11	3.18**	1.16	1.01	0.16	34.64	32.23	12.68	86.59	1.92	61.78
Seed yield per plant (g)	1.52-4.34	2.70	1.49**	0.66	0.42	0.25	30.20	23.89	18.46	62.61	1.05	38.94

σ^2p = Phenotypic variance, σ^2g = Genotypic variance and σ^2 e = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation

The principal component analysis (PCA) showed eigenvalues and percent of variation with respect to eight component characters in 33 genotypes of mungbean (Table 3). The result indicated that the first four eigenvalues for four principal coordination axes of genotypes accounted for 88.77% variation shown in Table 3. The first principal component accounted for 47.42 % of the total variation. Thirty-three genotypes were grouped into four different clusters to non-hierarchical clustering (Table 4) where cluster I had the highest number of genotypes and it was 13; clusters II, III, and IV had 8, 6, and 6 genotypes respectively.

Table 3. Eigenvalues and percent variation of eight characters of 33 genotypes of mungbean

Principal component axes	Eigenvalues	Percent variation	Cumulative % of Percent variation
I	3.320	47.42	47.42
II	1.449	20.69	68.11
III	0.814	11.63	79.74
IV	0.632	9.03	88.77
V	0.352	5.00	93.78
VI	0.234	3.35	97.14
VII	0.200	2.80	99.94
VIII	0.156	0.06	100.00

Table 4. Distribution of 33 genotypes in different clusters

Cluster no.	Genotypes	No. of populations
I	3, 5, 7, 10, 15, 19, 20, 21, 23, 27, 29, 31, 33	13
II	1, 2, 9, 12, 13, 14, 16, 17	8
III	4, 6, 11, 18, 26, 32	6
IV	8, 22, 24, 25, 28, 30	6
	Total	33

Genotypes of cluster II earned the highest cluster mean value (Table 5) for plant height (63.09), number of branches per plant (2.80), and seeds per pod (11.01) (Table 5). The genotypes included in cluster III had the highest mean value for days to 50% flowering (16.11), pods per plant (13.66), and seed yield per plant (3.18). Genotypes in Cluster IV produced the maximum cluster mean for pod length (6.90) and 100 seed weight (3.81). Konda *et al.* (2007) experiment relevant to this experiment.

Table 5. Cluster means for eight yield and yield-related characters in 33 mungbean genotypes

Characters	I	II	III	IV
Days to 50% flowering	15.77	13.13	16.11	14.67
Plant height (cm)	45.11	63.09	51.07	38.35
No. of branches per plant	2.47	2.80	2.27	1.91
Pods per plant (no.)	10.38	13.42	13.66	7.30
Pod length (cm)	6.40	6.36	6.14	6.90
Seeds per pod (no.)	9.79	11.01	10.31	9.58
100 seed weight (g)	3.18	2.80	2.69	3.81
Seed yield per plant (g)	2.48	2.97	3.18	2.33

Canonical Variate Analysis (CVA) was done to compute the inter-cluster distances. The intra and inter-cluster distance (D2) values are shown in Table 6. In this experiment, the inter-cluster distances were higher than the intra-cluster distances thus indicating broader genetic diversity among the genotypes of different groups. The highest inter-cluster distance was observed between clusters II and IV (10.425), followed by between clusters I and II (7.450). In contrast, the lowest inter-cluster distance was observed between clusters I and III (3.199). On the other hand, the maximum intra-cluster distance was found in cluster II (2.45) which contained only 8 genotypes while the minimum distance was found in cluster IV (1.73) which comprises 6 genotypes (Table 6). However, the maximum inter-cluster distance was observed between clusters II and IV (10.425) indicating genotypes from these two clusters if involved in hybridization may produce high heterosis and a wide spectrum of segregating populations.

The latent vectors (1 and 2) obtained from principal component analysis (PCA) (Table 7) showed positive values in both the vectors in case of days to 50% flowering (0.3436, 0.0356), plant height (0.3877, 0.0148), number of branches per plant (0.1007, 2.040) and pod length (0.4361, 0.8728) indicated major role of these traits in the genetic diversity.

Table 6. Intra (Bold) and inter-cluster distances (D2) for 33 genotypes

Cluster	I	II	III	IV
I	2.21	7.450	3.199	3.261
II		2.45	5.110	10.425
III			1.87	5.892
IV				1.73

Table 7. Relative contributions of the eight characters of 33 varieties to the total divergence

Principal component Accessions	Principal Component	
	Vector-1	Vector-2
Days to 50% flowering	0.3426	0.0356
Plant height (cm)	0.3877	0.0148
No. of branches per plant	0.1007	2.0940
Pods per plant	0.1420	-0.0428
Pod length (cm)	0.4361	0.8728
Seeds per pod	-0.0156	0.4476
100 seed weight (g)	-0.1844	0.0929
Seed yield per plant (g)	-0.1133	-1.5368

The higher the inter-class distance and intra-cluster distance indicated the higher the diversity present among the genotypes between and within clusters, respectively. On

the other hand, the lower inter and intra-cluster distances represent the lower diversity present among the genotypes between and within clusters, respectively. The genotypes present in the distant clusters would be used as parents in hybridization programs for gaining a wide spectrum of variation among the segregation generation.

Conclusion

The present experiment was undertaken to obtain a set of genotypes as parent materials with a wide range of diversity based on yield contributing characters for future breeding. Under the consideration of the variance, coefficient of variation, heritability, degree of magnitude of genetic distance, contribution of different traits towards the divergence, magnitude of cluster mean values for different characters and their performance, genotypes from cluster II for minimum days to 50% flowering, maximum number of pods per plant, maximum number of seeds per pod, highest plant height and genotypes from cluster IV for maximum pod length and 100 seed weight could be selected for further breeding program. So crossing between genotypes from cluster II and cluster IV can produce remarkable desired results in hybridization.

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Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

Author contributions

M. R. : Conceptualization, methodology, conduction of field research, supervision, data collection, data analysis, studying relevant scientific papers, initial drafting of manuscripts, reviewing and editing in writing, ensuring clarity and coherence and funding acquisition. M. S. H. : Conceptualization, methodology, supervision, investigation, and funding acquisition. N. Z. : supervision, funding acquisition.

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