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SHORT RESEARCH ARTICLE

Unraveling genetic diversity and yield traits in mungbean (*Vigna radiata* L.) through morpho-molecular approach

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Abstract

The present study was carried out to analyze the genetic variability in 124 genotypes of mungbean (*Vigna radiata* L.) following an augmented block design in *kharif* over two years. The analysis of variance revealed significant variation among genotypes for all the traits except the number of branches. Pearson correlation coefficients demonstrated significant correlations between several traits, notably between seed yield and traits such as the number of branches, number of pods per plant, pod length, no. of seeds per pod, and 100-seed weight. Principal component analysis (PCA) identified three principal components explaining 74.68% of the total variation. Yield-related traits predominantly influenced the first principal component (PC1); the second (PC2) by seeds per pod and days to 50% flowering, and the third (PC3) by growth-related traits such as days to flowering, days to maturity and number of branches. Cluster analysis based on morphological traits and SSR marker analysis grouped the genotypes into two distinct clusters, respectively, corroborating the morphological clustering results with SSR markers. Overall, the results of the study provide a detailed understanding of the genetic diversity and variability in morphological traits among mung bean genotypes, offering valuable insights for breeding programs and genetic improvement efforts.

Keywords*:* Morphological traits, mungbean, genetic diversity, principal component analysis, Molecular markers

Mungbean (*Vigna radiata* L.), also known as green gram, is an important legume crop in South and Southeast Asia providing plant protein for people throughout Asia (Tomooka et al. 2003). It is a good source of nutrition rich in protein, minerals, pro-vitamin A and vitamin B-complex. Globaly green gram is grown on 7.3 mha yielding an average of 721 kg/ha. Together, India and Myanmar produce 30% of the 5.3 mt of green grams produced. During 2023–2024, 3.787 mha of area was under green gram in India producing 2.916 mt with an average of 670 kg/ha. In India it is mainly cultivated in the states of Rajasthan (69.3%), Karnataka (6.4%) and Maharashtra (5.7%) during *kharif* season, while Odisha (82.4%), Andhra Pradesh (8.1%) and Tamil Nadu (4%) are the top states for *rabi* green gram cultivation (CARP-ANGRAU, 2024).It has been noticed that the genetic diversity is threatened for breeding the crops due to the destruction of wild relatives by various ecological factors and human intervention in the cultivated crop species (Wang et al. 2012; Baloch et al. 2014). It is most desirable to test experimental material of any crop across the locations and over the seasons to draw better conclusion (Banik et al. 2024). It is also useful to work out the genotype x environment interaction to understand the factors responsible for stability in yield of the genotypes (Kumar et al. 2024). To develop high yielding mung bean varieties, useful genetic diversity could be enhanced by exploiting natural genetic resources within the crop species adopting pre-breeding utilizing divergent crosses must be initiated for the designated production areas (Duc et al. 2010).

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Molecular markers, on the other hand, have also been used in mung bean to characterize DNA variation patterns within and among mung bean genotypes and closely related species (Raturi et al. 2012) and high-throughput sequencing technology allow for the analysis of samples over a shorter time course to facilitate the development of improved genotypes (Agarwal et al. 2008). Looking at its importance, the assessment of genetic diversity is vital for species diversity conservation, and crop improvement programs. The present study was, therefore, conducted to analyse genetic diversity in mung bean based on morphological and molecular markers.

A total of 124 genotypes were evaluated at Dry-land Agriculture Research Station (DARS), Budgam under field conditions in Augmented Block Design comprising of 12 blocks and each block contained ten genotypes and four checks during *kharif*-2021 and *kharif* 2022. Diversity among the mung bean genotypes was studied on the basis of various morphological traits. The plant material was planted at 30 x 15 cm maintaining row to row and plant to plant distance. The morphological traits recorded were: number of branches (NOB), days to 50% flowering (DF), plant height in cm (PH), no. pods per plant (PPP), pod length in cm (PL), no. seeds per pod (SPP), days to maturity (DM), seed yield per plant (g) (SYP) and 100-seed weight (g) (100SW).

Twenty SSR markers, namely, MAB128079, MAB128093, MAB128113, MAB128135, MB112A, MBM-0003, MBM-00201, MBM-00389, MBM-00580, MBM-01589, MBM-03131, MR7322B, MVR2, MSSR-182, MSSR-186, MSSR-217, MSSR-177, MSSR-3, MLR-738A and MSSR-4 (Abhay et al. (2020)) were used to study the diversity among the mung bean genotypes. DNA extraction (CTAB approach) using a modified version of Saghai-Maroof et al. (1984) cetyltrimethyl ammonium bromide (CTAB) approach; genomic DNA was extracted from fresh leaves of plants that were one month old.

Analysis of variance

The results of the pooled analysis of variance for the various morphological traits are summarized in Table 1. Notably, the results revealed that the genotypes, when considered independently of blocks, blocks without accounting genotypes and the blocks excluding genotypes, displayed significant variance for all the traits studied. However, the significance of genotypes when blocks were eliminated was observed for all traits except the number of branches per plant. Additionally, both the genotypes and the check varieties were found significant contributors to the observed variations in all the traits. To carry out a successful breeding programme, the degree of genetic diversity, morphological characterization of genotypes and valuable genetic resources play a pivotal role in ascertaining the genetic diversity within the mung bean. It is imperative to investigate the extent of genetic diversity for the efficient assessment, maintenance, and utilization of different genotypes (Sarkar and Kundagrami 2016; Carrillo-Perdomo et al. 2020). The present findings on significant qualitative variations observed across the examined characteristics are consistent with previously published reports (Tripathi et al. 2020; Tahir et al. 2020; Bhardwaj et el. 2025). Moderate to high phenotypic variability has been recorded for morphological traits such as seed yield per plant, number of branches, pods per plant, and 100-seed weight, while less variance among the accessions was noted in days to flowering, days to maturity and plant height with respect to the genetic parameters considered in a statistical analysis. The present study identified a few early flowering lines (range, 33 to 53 days), which matured early (Azam et al. 2018); plant height also showed significant variation; substantial variation in yield and it components has also been reported earlier by several researchers (Kindeya et al. 2020).

Descriptive statistics of various morphological traits in mung bean genotypes

The descriptive statistics for various morphological traits in mung bean genotypes is presented in Table 2. A higher number of branches per plant is regarded as a useful criterion for characterization because more number of branches having robust stature provides a better chance for a better yield. Seed yield per plant varied significantly among the different mung bean genotypes in the present study. Higher biological yield and seed yield per plant is significant because these traits were positively associated with more economic yield. Similar findings have been reported earlier in mung bean (Khajudparn and Tantasawat 2011; Sunayana et al. 2017; Patel et al. 2019) and in cowpea (Kumar and Shrikant 2016). Althogh

Correlation coefficients, principal component and cluster analyses

The findings on the correlation between the various morphological traits are given in Table 3. The utilization of a correlation matrix as a valuable tool in the selection of superior genotypes stands as a widely adopted technique for assessing the relationships between multiple variables. The results of the correlation have revealed that all nine morphological traits exhibited a significant positive correlation between different traits. The present findings on correlation in mung bean are corroborated by previous results published earlier (Parihar et al. 2018). A total of nine principal components were generated, aligning with the number of morphological traits considered. Based on these loadings, the contributions of the various morphological traits were calculated and the results are described.

The variability among the genotypes of mung bean among various morphological traits is effectively depicted in a bi-plot analysis (Fig. 1). Principal Component Analysis (PCA) was used to examine the patterns of variation and the relative importance of nine quantitative traits in explaining

Table 1. Analysis of variance of mung bean genotypes for various morphological traits

Source	Df	NOB	DF	PH	PPP	PL	SPP	DM	SYP	100SW
Blocks (ignoring treatments)	11	0.515**	9.512**	10.3**	4.631**	3.438**	1.8005**	8.238**	9.727**	2.3554**
Blocks (eliminating treatments)	11	0.07	0.36	3.9**	0.8	0.132*	0.0947**	3.07*	0.18	0.0249
Treatments (ignoring blocks)	123	1.43**	5.91**	33.7**	15.3**	1.178**	0.7510**	8.32**	4.85**	0.6777**
Treatments (eliminating blocks)	123	1.394	5.088**	33.1**	14.925**	0.882**	0.5984**	7.861**	3.997**	0.4693**
Test entries	119	0.78**	5.72**	20.2**	4.6**	1.069**	0.7652**	7.22**	3.13**	0.6511**
Checks	3	16.579**	1.67*	409.7**	19.5**	2.415**	0.4246**	13.65**	18.69**	1.8431**
Test entries vs Checks	1	33.80**	40.55**	514.7**	1272.4**	10.442**	0.0309	123.77**	1228.99**	0.3510**
Error	33	0.100	0.54	1.3	0.9	0.056	0.0743	1.41	0.14	0.0323

variability the procedure laid down by Chatfield and Collins' (1980) was followed retaining principal components with eigen values greater than one and discarding those with eigen values less than one (Supplementary Table S1). In this study, three principal components with eigenvalues (range 0.015 to 2.975) exceeding one were considered, collectively accounting for approximately 74.68% of the total variance (Table 4). Belul et al. (2014) proposed a similar criterion,

Fig.1. Bi-plot representation of various morphological traits in mung bean genotypes

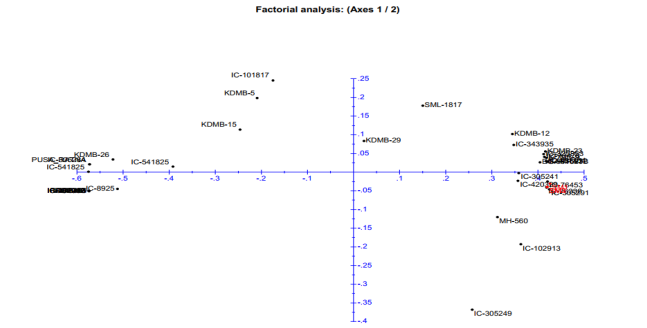

Fig. 2. Factorial analysis showing the diversity of mung bean (*Vigna radiata*) genotypes based on SSR markers

Table 2. Descriptive statistics for various morphological traits in mung bean genotypes

Trait	Mean	Range	C.V
DF	45.21	38.39-49.52	1.62
NOB	6.46	4.27-8.45	4.71
PH (cm)	47.00	37.22-58.89	2.36
PPP	17.54	9.71-24.85	4.95
PL (cm)	7.53	5.16-10.87	3.09
SPP	8.91	6.88-11.43	3.06
DM	76.74	71.20-83.70	1.53
SYP (g)	6.35	2.63-11.15	5.34
100SW (g)	4.05	2.38-6.51	4.46

emphasizing that characterizing and evaluating genetic collections for legumes should consider a proportion of variation exceeding 75% of the total variation as acceptable. The present study indicated that all examined traits significantly contributed to the variation observed in the principal components through their loading effects. Consequently, the first three principal components emerged as the most influential descriptors. These findings align with the results of Shyamalee et al. (2016), who studied and analyzed 61 mung bean genotypes.

The cluster analysis represented the total of 124 genotypes in two clusters, with a maximum number of genotypes in Cluster 1. Sen and De (2017) observed significant differences among mung bean genotypes across 13 traits, signifying the presence of considerable diversity among them; they also grouped 30 mung bean genotypes into six clusters. This suggests ample potential for selecting superior genotypes to enhance the genetic yield of mung beans. Similarly, Popoola et al. (2017) segregated 26 *Vigna vexillata* accessions into three clusters, while Musalamah et al. (2006) categorized 75 mung bean genotypes into 11

Table 3. Pearsons correlation coefficients for various morphological traits in mung bean genotypes

	PH	NOB	PPP	PL	SPP	100SW	DF	DM	SY
PH	1.00								
NOB	0.400***	**1.00**							
PPP	0.416***	0.744***	**1.00**						
PL	0.202**	0.179*	0.256***	**1.00**					
SPP	0.060	0.007	0.009	0.856***	**1.00**				
100SW	0.054	0.156*	0.060	0.262***	0.253***	**1.00**			
DF	0.281***	0.166*	0.201**	0.068	0.015	0.084	**1.00**		
DM	0.321***	0.252***	0.294***	0.192*	0.069	0.055	0.815***	**1.00**	
SY	0.360***	0.615***	0.697***	0.560***	0.400***	0.669***	0.202**	0.281***	**1.00**

major groups. In another study by

Diversity analysis based on SSR markers

All the genotypes exhibited a wide range of genetic variability in mung bean genotypes as shown by the bi-plot in Fig. 2. The various genotypes were grouped in two clusters based on the SSR as depicted by hierarchical clustering (Supplementary Fig. 1). Similar results were reported in other legume crops, such as chickpea (Upadhyaya et al. 2008). Among the twenty SSR markers used in this study, only five showed polymorphism across the mung bean genotypes studied. High polymorphism and robust repeatability are the characteristic features of the selected markers that represent genetic diversity. Bhardwaj et al. (2025) assessed the genetic diversity of 87 germplasm lines using SSR markers and reported that 19 markers out of 35 were informative, generating 35 alleles with an average of 4.11 alleles per locus. Similarly, the ISSR markers can accurately identify genetic diversity both within and between the species and therefore, they are appropriate for assessing genetic variation (Tunc et al. 2025). The PIC values obtained in the analysis gave a measure of the informativeness of each SSR marker. Breeders can use this information to select parents with diverse genetic backgrounds for hybridization, leading to the development of improved mung bean varieties with desirable traits (Govindaraj et al. 2009). Additionally, the polymorphic SSR markers identified in this study can be employed for marker-assisted selection to expedite the breeding process (Collard and Mackill 2008). In conclusion, the analysis of SSR markers has provided valuable insights into the genetic diversity and relationships among mung bean genotypes.

Authors' contribution

Conceptualization of research (AG, AAL, PAS); Designing of the experiments (MAW, MAB, ZAD); Contribution of experimental material (AG, ABS, AAL); Execution of field/ lab experiments and data collection (MR); Analysis of data and interpretation (AG, ABS); Preparation of the manuscript (AG, MR, ABS).

Table 4. Contribution of various morphological traits of mung bean genotypes in different principal components

Source	PC1	PC2	PC3
PH	3.280	6.865	0.203
NOB	9.771	12.068	15.378
PPP	11.356	9.878	17.876
PL	14.136	17.148	4.312
SPP	12.808	18.858	4.825
100SW	13.926	1.749	0.014
DF	2.472	17.503	27.854
DM	3.149	15.455	27.761
SY	29.098	0.472	1.772

Supplementary material

Supplementary Tasble S1 and Supplementary Fig. 1 are provided, which can be accessed at www.isgpb.org

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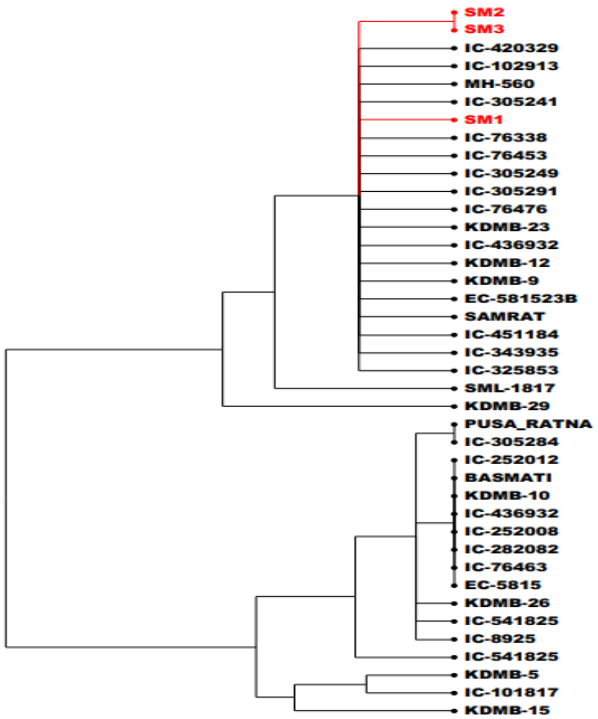
Supplementary Table S1. Eigen values of principal components for morphological traits in mung bean genotypes

Number	Eigen value	Percentage	Cumulative percentage
1	2.975	33.066	33.066
2	1.976	21.959	55.026
3	1.769	19.657	74.683
4	0.997	11.085	85.769
5	0.833	9.262	95.031
6	0.209	2.323	97.355
7	0.152	1.698	99.053
8	0.069	0.771	99.825
9	0.015	0.174	100.000



Supplementary Fig. 1. Hierarchical clustering of mung bean genotypes based on SSR markers