J. Farm Sci., 39(1): (10-13) 2026

RESEARCH PAPER

Genetic analysis of morpho-physiological and yield attributes in advanced breeding lines of mungbean (*Vigna radiata* (L.) Wilczek)

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(Received: September, 2025 ; Accepted:March,2026)

DOI: 10.61475/JFS.2026.v39i1.03

Abstract: The genetic improvement of any crop relies on the extent of genetic variability present in the breeding material, which enables the selection of superior genotypes. This study was conducted during *kharif* 2024 to assess the genetic variability and diversity among forty advanced breeding lines of mungbean. Analysis of variance demonstrated significant differences for all morpho-physiological and yield-attributing traits, confirming substantial genetic variability. Seed yield per plant and plot yield, exhibited high heritability (69.80% & 55.31%) coupled with considerable genetic advance over mean (24.28% and 25.39%), indicating the predominance of additive gene action and scope for effective phenotypic selection. Mahalanobis D^2 analysis delineated the genotypes into twelve genetically distinct clusters, with Cluster I emerging as the largest (16), followed by Clusters II and III (7) and Cluster IV (2), while remaining clusters being solitary. The major contributors to genetic divergence were NDVI 20 (15.4%), NDVI 40 (10.0%) and hundred seed weight (9.2%). The grouping of the genotypes into distinct clusters ensures the genetic diversity and extends the scope to isolate the superior genotype and to identify the clusters for appropriate decision on choice of parents for trait specific hybridization programmes. Further, the presence of desired genetic variability in the study material reasserts the scope of identifying promising genotypes and aid to mungbean improvement through careful analysis of trait associations and selection indices.

Key words: Breeding, Diversity, Mungbean, Variability

Introduction

Mungbean (*Vigna radiata* (L.) Wilczek) is the third most important crop of the tropics globally after chickpea and pigeon pea. It is indigenous to India and is predominantly cultivated in South and Southeast Asia (Nair *et al*., 2019). It is a diploid (2n = 2x = 22), self-pollinated crop known for its rapid growth and short life cycle. It has an estimated genome size of 579 Mb and classified under the family Fabaceae (Kang *et al*., 2014). It has a strong root system actively involved in fixing the atmospheric nitrogen into the soil (about 58-109 kg ha^{-1}) via symbiosis with Rhizobium. It plays a vital role in improving soil fertility and sustaining productivity. Mungbean is a rich source of vegetable protein, micronutrients and antioxidants such as flavonoids and phenolics. It serves multiple purposes including use as food, animal feed, fodder and green manure. The seeds typically contain 20-25 per cent protein and 60-65 per cent carbohydrates.

Genetic diversity assessment within germplasm collections is crucial for effectively classifying and identifying distinct genotypes that hold potential for specific breeding applications. According to Hallaur and Miranda (1988), crosses between genetically diverse parental lines result in significantly higher heterosis compared to those between closely related strains. To increase the productivity of any crops, breeders have aimed to develop better yielding cultivars and normally it is achieved by selecting desirable segregants from the segregating generation followed by hybridisation.

Material and methods

The present study was conducted at AICRP on kharif Pulses, Regional Research Station, Main Agricultural Research Station, UAS Dharwad. The experiment consisted of forty mungbean genotypes involving advanced breeding lines and appropriate check varieties. The genetic material was sourced from AICRP on *kharif* Pulses, UAS Dharwad. The test genotypes and the checks were evaluated during *kharif* 2024 in a randomised complete block design with three replications. The genotypes were sown with 30 cm x 10 cm spacing having plot size of 4.8m^2 area and recommended package of practice was followed to raise good crop.

The estimation of genetic variability parameters is fundamental in plant breeding as it provides insights into the genetic architecture of traits and helps in selecting superior genotypes for further improvement. Understanding genetic variability parameters, such as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and broad-sense heritability (h^2), is important for predicting the potential genetic advance achievable through selection for a particular trait. While GCV and PCV indicate the extent of variability present in different traits, they do not reveal the heritable portion of this variability. To determine the heritable component, it is essential to estimate heritability for the traits under consideration. When heritability is considered alongside the predicted genetic gain, it enhances the reliability of these parameters as effective tools for guiding selection in breeding programmes.

Genetic diversity analysis is a crucial step in plant breeding as it helps in the identification of diverse and appropriate parental genotypes for hybridization, which is essential for generating desirable transgressive segregants and enhancing the genetic base of breeding populations. In the present study, Mahalanobis's D^2 statistics, multivariate analysis tool was employed to assess the genetic divergence among forty mungbean genotypes based on eighteen morpho-physiological and yield-related traits.

Results and discussion

Genetic variability, heritability and genetic advance for quantitative traits

In the present investigation, the analysis of variance revealed significant differences among the genotypes for all the characters. The range, mean, coefficient of variability, heritability in broad sense and genetic advance for morpho-physiological, yield and yield attributing traits are presented in Tables 1a and 1b. High magnitudes of phenotypic as well as

Table 1a. Genetic variability parameters for morphological and yield related traits

Traits	Mean	Range		GA	CV (%)		GAM	h^2 %
		Min	Max		GCV (%)	PCV(%)		
DFF	35.51	34.00	38.00	1.71	2.79	3.33	4.82	70.21
DM	73.98	71.00	76.00	1.90	1.40	1.56	2.57	79.85
PH	66.88	54.20	83.00	10.28	9.11	11.13	15.36	67.03
NB	2.47	1.60	3.40	0.52	14.00	19.25	20.97	52.89
NCP	9.06	6.00	13.60	2.16	15.02	19.46	23.88	59.57
NPC	5.70	4.33	8.16	0.81	9.44	12.94	14.18	53.22
NPP	31.13	25.00	40.80	3.94	7.51	9.20	12.64	66.72
PL	8.46	6.80	10.80	0.68	6.12	9.53	8.10	41.24
NSPP	12.77	11.60	14.80	0.54	3.27	5.22	4.21	39.15
SYPP	9.52	6.20	12.60	2.31	14.11	16.89	24.28	69.80
HSW	4.30	3.81	5.02	0.35	4.34	4.79	8.10	82.02
PY (g)	499.00	215.00	757.00	126.70	16.57	22.28	25.39	55.31
Y ($kgha^{-1}$)	1039.00	448.00	1577.00	263.95	16.57	22.28	25.39	55.31

DFF: Days to 50 per cent flowering; DM: Days to maturity; PH: Plant height; NB: No of branches; NCP: No of clusters per pod; NPC: No of pods per cluster; NPP: No of pods per plant; NSPP: No of seeds per pod; PL: Pod length; SYPP: Seed yield per plant; HSW: Hundred seed weight; PY: Plot yield; Y: Yield.

Table 1b: Genetic variability parameters for physiological traits

Traits	Mean	Range		GA	CV (%)		GAM	h^2 %
		Min	Max		GCV (%)	PCV(%)		
SCMR 20	25.63	23.33	28.60	1.65	4.04	5.22	6.44	59.87
SCMR 40	35.41	31.04	38.67	2.56	4.31	5.30	7.22	66.10
SCMR 60	55.40	49.00	59.38	3.90	4.00	4.67	7.05	73.21
NDVI 20	0.43	0.34	0.52	0.09	10.84	11.46	21.13	89.53
NDVI 40	0.70	0.65	0.75	0.05	3.68	4.06	6.86	82.04
NDVI 60	0.81	0.75	0.85	0.04	3.01	3.45	5.41	76.15

SCMR 20: SPAD Chlorophyll Meter Reading at 20 DAS; SCMR 40: SPAD Chlorophyll Meter Reading at 40 DAS; SCMR 60: SPAD Chlorophyll Meter Reading at 60 DAS; NDVI 20: Normalized Difference Vegetation incidence at 20 DAS; NDVI 40: Normalized Difference Vegetation incidence at 40 DAS; NDVI 60: Normalized Difference Vegetation incidence at 60 DAS

Table 2. Intra and inter cluster distance of twelve clusters

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII
Cluster I	**66.36**	140.45	152.79	94.38	312.87	219.60	127.09	93.04	115.65	114.41	90.98	262.82
Cluster II		**57.83**	381.94	138.34	634.92	103.56	90.29	93.99	259.89	252.35	268.83	576.88
Cluster III			**54.60**	210.89	111.69	551.36	362.93	247.55	104.46	116.83	91.01	122.78
Cluster IV				**74.07**	318.60	232.67	149.48	93.61	127.81	227.02	171.43	333.06
Cluster V					**0.00**	880.06	620.50	412.90	173.79	277.23	246.07	124.03
Cluster VI						**0.00**	95.21	174.88	424.06	363.34	343.22	745.26
Cluster VII							**0.00**	87.58	337.52	271.33	174.06	481.29
Cluster VIII								**0.00**	195.85	163.19	153.57	382.53
Cluster IX									**0.00**	107.64	170.89	206.75
Cluster X										**0.00**	98.12	237.15
Cluster XI											**0.00**	150.06
Cluster XII												**0.00**

Note: Bold diagonal values indicate the intra cluster distance between respective cluster

Table 3. Per cent contribution of traits for diversity

Trait	Per cent contribution (%)
NDVI 20	15.4
NDVI 40	10.0
Hundred Seed Weight	9.2
NDVI 60	7.5
SCMR 60	7.0
SCMR 20	6.9
SCMR 40	6.6
Seed yield per plant	5.8
Days to Fifty Percent Flowering	4.5
Number of Pods per Plant	4.4
Number of Clusters per Pod	4.4
Days to Maturity	3.8
Plant height t	3.7
Number of Branches	2.6
Number of Pods per Cluster	2.2
Pod Length	2.1
Number of Seeds per Pod	1.9
Plot Yield	1.8

SCMR 20: SPAD Chlorophyll Meter Reading at 20 DAS; SCMR 40: SPAD Chlorophyll Meter Reading at 40 DAS; SCMR 60: SPAD Chlorophyll Meter Reading at 60 DAS; NDVI 20: Normalized Difference Vegetation incidence at 20 DAS; NDVI 40: Normalized Difference Vegetation incidence at 40 DAS; NDVI 60: Normalized Difference Vegetation incidence at 60 DAS.

genotypic coefficient of variation observed for number of branches, number of clusters per plant, seed yield per plant and plot yield. The heritability was moderate to high (range 39.5% - 89.53%). Traits like seed yield per plant, pod length and NDVI 20 had high estimate of heritability along with high genetic advance as percent of mean.This suggests that these traits are governed by additive gene action and can be improved effectively through direct selection. Thus, selection ofthesetraits would be effective for crop improvement. These results are in agreement with those reported earlier (Mallikarjuna *et al*. (2006), Suresh *et al*. (2010), Muthuswamy *et al*. (2019), Rahim *et al*. (2010) and Lal and Mishra, 2006 and Parameswarappa (2005).

Cluster analysis by Tochermethod groupedforty genotypesinto twelve clusters based on the D^2 statistics. Among these, Cluster I was the largest comprising of sixteen genotypes, followed by Clusters II and III, each with seven genotypes, Cluster IV with two genotypes, while the remaining clusters (V, VI, VII, VIII, IX, X, XI, and XII) were solitary. The mean D^2 value of intra and inter cluster distances have been tabulated in Table 2. The diagonal values provide the information about intra cluster distance whereas remaining values give inter cluster distance between two respective clusters. The maximum intra cluster distance was observed for Cluster IV (74.07) followed by Cluster I (66.36), Cluster II (57.83)

Table 4. Cluster means for eighteen traits (*kharif* 2024)

	DFF	DM	SCMR 20	SCMR 40	SCMR 60	NDVI 20	NDVI 40	NDVI 60	PH	NB
Cluster I	35.63(6)	73.98(9)	25.38(7)	35.12(7)	55.38(7)	0.42(7)	0.71(7)	0.81(7)	64.55(8)	2.58(6)
Cluster II	35.19(4)	75.10(11)	24.62(10)	33.93(10)	52.88(10)	0.38(9)	0.67(10)	0.78(9)	73.38(4)	2.26(10)
Cluster III	35.00 (3)	73.71(8)	27.18(3)	36.16(5)	58.17(2)	0.50(2)	0.73(3)	0.84(2)	65.04(7)	2.29(9)
Cluster IV	34.67(2)	72.33(2)	24.81(9)	34.47(9)	53.55(9)	0.40(10)	0.69(8)	0.79(11)	63.50(9)	2.40(7)
Cluster V	35.67(7)	73.33(3)	28.38(1)	38.44(1)	58.70(1)	0.51(1)	0.74(2)	0.84(2)	58.43(11)	2.97(3)
Cluster VI	37.00(10)	73.67(4)	24.03(12)	31.88(12)	50.90(12)	0.36(12)	0.66(12)	0.76(12)	72.67(5)	2.20(11)
Cluster VII	34.33(1)	73.67(4)	24.19(11)	33.02(11)	52.00(11)	0.37(11)	0.67(10)	0.78(9)	76.79(2)	2.80(4)
Cluster VIII	37.00(10)	73.67(4)	24.96(8)	34.80(8)	54.13(8)	0.39(8)	0.69(8)	0.79(8)	80.87(1)	2.20(11)
Cluster IX	36.33(8)	74.33(10)	26.13(4)	36.85(3)	57.66(4)	0.45(5)	0.72(5)	0.83(5)	58.07(12)	3.00(2)
Cluster X	37.67(12)	75.33(12)	26.13(4)	36.75(4)	57.29(5)	0.46(4)	0.75(1)	0.85(1)	74.97(3)	2.32(8)
Cluster XI	35.33(5)	71.67(1)	26.02(6)	36.12(6)	56.87(6)	0.45(5)	0.72(5)	0.82(6)	66.33(6)	2.67(5)
Cluster XII	36.33(8)	73.67(4)	27.22(2)	37.30(2)	57.91(3)	0.50(2)	0.73(3)	0.84(2)	59.27(10)	3.27(1)
	NCP	NPC	NPP	NSP	PL	SYPP	HSW	PY	Score	Rank
Cluster I	8.76(7)	5.69(7)	30.41(7)	12.62(10)	8..90(3)	9.33(7)	4.31(7)	478.85(8)	127	8
Cluster II	9.38(5)	5.22(11)	30.75(6)	12.96(4)	8.09(10)	8.71(9)	4.09(12)	459.57(10)	154	11
Cluster III	8.93(6)	5.92(6)	32.14(5)	12.67(8)	8.74(5)	10.30(5)	4.34(6)	575.19(2)	87	3
Cluster IV	10.70(2)	6.41(3)	34.23(4)	12.67(8)	8.30(8)	10.71(4)	4.51(3)	539.17(5)	113	7
Cluster V	8.27(8)	6.50(2)	36.60(1)	12.40(11)	9.00(2)	12.6(1)	4.73(2)	801.00(1)	60	2
Cluster VI	10.60(3)	5.40(9)	26.00(12)	12.07(12)	7.40(12)	6.47(12)	4.25(9)	253.00(12)	181	12
Cluster VII	7.20(10)	5.62(8)	29.27(9)	12.80(7)	8.50(7)	7.41(11)	4.36(5)	375.33(11)	142	10
Cluster VIII	6.53(12)	6.64(1)	35.93(2)	13.00(3)	8.00(11)	9.53(6)	4.23(10)	492.67(7)	126	9
Cluster IX	12.40(1)	5.29(10)	34.73(3)	12.87(6)	8.47(8)	11.35(3)	4.28(8)	545.00(4)	99	4
Cluster X	10.05(4)	4.37(12)	29.03(10)	12.88(5)	8.63(5)	9.21(8)	4.14(11)	548.67(3)	112	6
Cluster XI	6.70(11)	6.00(5)	27.77(11)	13.22(2)	8.78(4)	8.26(10)	4.38(4)	461.33(9)	107	5
Cluster XII	8.13(9)	6.03(4)	30.47(8)	14.67(1)	11.00(1)	12.47(2)	4.81(1)	499.00(6)	32	1

NOTE: Values in the parentheses represent the ranks across the cluster for every trait.

DFF: Days to 50 per cent flowering; DM: Days to maturity; PH: Plant height ; NB: No of branches; NCP: No of clusters per pod; NPC: No of pods per cluster; NPP: No of pods per plant; NSPP: No of seeds per pod; PL: Pod length; SYPP: Seed yield per plant; HSW: Hundred seed weight; PY: Plot yield; SCMR 20: SPAD Chlorophyll Meter Reading at 20 DAS; SCMR 40: SPAD Chlorophyll Meter Reading at 40 DAS; SCMR 60: SPAD Chlorophyll Meter Reading at 60 DAS; NDVI 20: Normalized Difference Vegetation incidence at 20 DAS; NDVI 40: Normalized Difference Vegetation incidence at 40 DAS; NDVI 60: Normalized Difference Vegetation incidence at 60 DAS

and Cluster III (54.60) whereas intra cluster distance was zero for the solitary clusters, Cluster V, VI, VII, VIII, XI, X, XI and XII. The inter cluster distance ranged between 87.58 to 880.06.

The uneven distribution with Cluster I containing 16 genotypes while Clusters V-XII being solitary which reflects the presence of both closely related and highly divergent genotypes in the population. NDVI at 20 DAS emerged as the primary contributor to genetic divergence (15.4%), highlighting the importance of early vegetative vigour in differentiating genotypes (Table 3), while physiological traits collectively contributed more to diversity than yield components which was also reported by Siddique *et al*. (2023). The wide range of inter cluster distances suggests opportunities for exploiting heterosis through strategic crosses between distant clusters. Cluster mean analysis revealed complementary strengths: Cluster XII ranked first overall with superior seed traits, Cluster V showed highest yield and Cluster III balanced multiple desirable characteristics (Table 4). These findings were in line with the findings of Ram and Saxena (2022), Sharma *et al*. (2018) and Yadav *et al*. (2024). This clear grouping enables targeted parental selection for specific breeding objectives, such as improving yield potential or seed size based on genetically distinct and complementary sources.

Conclusion

This study successfully characterizes a valuable collection of mungbean germplasm, revealing substantial genetic diversity that can be directly leveraged for crop improvement. The study concludes that direct selection for traits like seed yield per plant and pod length will be effective due to their high heritability and genetic advance. The identified clusters provide a clear roadmap for parental selection. Breeders can make strategic crosses between genetically distant clusters to generate novel variation and exploit heterosis. Physiological traits, particularly early-season NDVI, are crucial indicators of genetic diversity and should be integrated into selection criteria alongside yield components. This provides a solid foundation and a practical tool kit for mungbean breeders to develop improved, high-yielding cultivars by systematically utilizing the diverse and complementary genetic sources identified within the germplasm.

References

Hallaur A R and J B Miranda, 1988, Quantitative geneticsin maize breeding.Iowa State Univ. Press Ames.

Kang Y J, Kim S K, Kim M Y, Lestari P, Kim K H, Ha B K, Jun T H, Hwang W J, Lee T, Lee J and Shim S, 2014, Genome sequence of mungbean and insights into evolution within Vigna species. *Nature Communications,* 5(1): 544.

Lal N and R Mishra, 2006, Induced genetic variability and divergence in M_3 generation in mungbean. *Indian Journal of Pulses Research*, 1: 47-49.

Mallikarjuna Rao C, Koteswara Rao Y and Mohan Reddy, 2006, Genetic variability and path analysis in greengram. *Legume Research*, 29: 216-218.

Muthuswamy A, Jamunarani M and Ramakrishnan, P, 2019, Genetic variability, character association and path analysis studies in green gram (*Vigna radiata (L.)*Wilczek). *International Journal of Current Microbiology and Applied Sciences*, 8(04): 1136-1146.

Nair R M, Pandey A K, War A R, Hanumantharao B, Shwe T, Alam A K M M, Pratap A, Malik S R, Karimi R, Mbeyagala E K and Douglas C A, 2019, Biotic and abiotic constraints in mungbean production progress in genetic improvement. *Frontiers in Plant Science*, 10: 1340.

Parameswarappa S G, 2005, Genetic variability, character association and path coefficient analysis in green gram. *Indian Journal of Genetics and Plant Breeding*, 65: 23-27.

Rahim M A, Mia A A, Mahmud F, Zeba N and Afrin K S, 2010, Genetic variability, character association and genetic divergence in mungbean (*Vigna radiata* L. Wilczek). *Plant Omics*, 3(1): 1-6.

Ram L and Saxena A K, 2022, Estimation of genetic divergence for agro-morphological characters in mungbean (*Vigna radiata* (L.)Wilczek). *The Pharma Innovation Journal*, 11(2): 561-565.

Sharma S R, Singh D, Kumar P, Khedar O P and Varshney N, 2018, Assessment of genetic diversity in mungbean [*Vigna radiata* L. Wilczek] genotypes. *International Journal of Genetics*, 10(7): 471-474.

Siddique M E A and Hoque M A, 2023, Genetic diversity based on principal component and cluster analysis for various characters in spring wheat (*Triticum aestivum* L.) genotypes under drought condition. *Fundamental and Applied Agriculture*, 8(1): 435-446.

Suresh S, Jebaraj S, Hepziba S and Theradimani M, 2010, Genetic studies in mungbean (*Vigna radiate* (L).Wilczek). *Electronic Journal of Plant Breeding*, (6): 1480-1482.

Yadav H K, Vimal S C, Yadav S K, Chauhan P, Chourasiya V K, Kumar A, Sharma M and Pratap A, 2024, Assessment of genetic diversity in mungbean (*Vigna radiata* L.). *Journal of Advances in Biology and Biotechnology*, 27(6): 101-107.