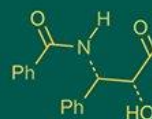


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Assessment of genetic variability, heritability and genetic divergence for yield and yield contributing traits in Mungbean (*Vigna radiata* L. Wilczek)

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Abstract

The present investigation was conducted to assess the magnitude of genetic variability and genetic divergence among 27 mungbean genotypes. The experiment was carried out during the Late Kharif 2025 season at the College of Agriculture, Navsari Agricultural University, Bharuch. The experimental material was evaluated in a Randomized Block Design (RBD) with three replications to ensure precise and dependable estimation of the traits under study. The analysis of variance indicated highly significant differences among the genotypes for all the characters, suggesting the presence of considerable genetic variability. Moderate to high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for branches per plant, clusters per plant, pods per cluster, pods per plant, and 100-seed weight, indicating substantial variability for these traits. In contrast, low GCV and PCV values were observed for days to 50% flowering, days to maturity, plant height, seeds per pod, pod length, and crude protein content. Seed yield per plant exhibited low GCV but moderate PCV, indicating a relatively greater influence of environmental factors. High heritability coupled with high genetic advance as percent of mean was observed for branches per plant, clusters per plant, pods per cluster, pods per plant, and 100-seed weight, suggesting the predominance of additive gene action and the effectiveness of direct selection for these traits. Conversely, days to 50% flowering, plant height, seeds per pod, pod length, and crude protein content exhibited moderate heritability along with low genetic advance as percent of mean, indicating limited scope for improvement through simple selection. Seed yield per plant showed moderate heritability accompanied by moderate genetic advance as percent of mean, reflecting the involvement of both genetic and environmental factors in its expression. Genetic divergence analysis grouped the 27 mungbean genotypes into eight distinct and non-overlapping clusters. Cluster I contained the highest number of genotypes (10), followed by Cluster II with eight genotypes, while Clusters III and IV comprised three and two genotypes, respectively. Clusters V, VI, VII, and VIII each consisted of a single genotype and, therefore, exhibited zero intra-cluster distance. Among the characters studied, pods per plant, clusters per plant, pods per cluster, branches per plant, and 100-seed weight contributed the greatest proportion of genetic divergence, indicating their major role in differentiating the genotypes.

Keywords: Genetic variability, heritability, genetic divergence, mungbean

Introduction

Mungbean (*Vigna radiata* (L.) Wilczek) is recognized as the third most important pulse crop in India after chickpea and pigeonpea (red gram). It represents a self-pollinated legume. Taxonomically placed in the family Fabaceae and the subgenus *Ceratotropis* of the genus *Vigna*. The crop is a diploid species ($2n = 22$) with an estimated genome size of 579 Mb (Arumuganathan and Earle, 1991) [4]. Mungbean is recognized as an excellent source of high-quality protein and plays a significant role in improving nutritional security, particularly in developing countries. The seeds contain high levels of lysine, leucine, and threonine, including essential minerals and vitamins, although they contain relatively lower amounts of methionine, tryptophan, and tyrosine. During germination, the synthesis of ascorbic acid (vitamin C) increases along with enhanced levels of riboflavin and thiamine. Owing to its nutritional value and easy digestibility, mungbean is consumed in various forms such as dal, sprouts, snacks, sweets, and several traditional food preparations (Datta *et al.*, 2012) [6].

According to the latest agricultural statistics, mungbean occupies covering nearly 35.43 lakh hectares in India, recording a production of 16.07 lakh tonnes with an average yield of 453 kg/ha. In Gujarat, the crop is cultivated over approximately 66.48 thousand hectares, producing 35.18 thousand tonnes with an average productivity of 529.09 kg/ha (Anonymous, 2024-25). The crop is believed to have originated in India and Central Asia, which were identified as primary centres of diversity by Vavilov (1939) [20]. Mungbean is a warm-season crop that requires about 90-120 frost-free days for successful growth and development. A characteristic feature of mungbean is its indeterminate growth habit, resulting in non-synchronous flowering and pod maturity. Consequently, harvesting is generally recommended when approximately 50-70 percent of the pods have matured, at which time the seed moisture content is usually between 13 and 15 percent. Genetic divergence is a useful technique in selecting diverse parents for purposeful hybridization programme. A successful breeding program requires careful consideration of the genetic factors influencing multiple quantitatively traits. This involves evaluating genetic parameters such as the genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), genetic advance (GA) along with genetic advance as a percentage of the mean (GAM) in mungbean germplasm under the arid South Gujarat so that promising genotypes could be identified for a breeding program to enhance the development of high-yielding varieties of mungbean for South Gujarat. Also, find out the pattern of genetic divergence among mungbean germplasm so that suitable divergent parents may be use for breeding programme to enhanced high yield.

Materials and Methods

The experimental material for the current study includes 27 mungbean genotypes viz., AM-15-3-2, AM-15-7-2, AM-15-8-1, AM-15-26-1, AM-15-48-4, AM-15-48-11, AM-15-52-1, AM-K18-6, AM-K18-11, AM-K18-14, AM-K18-16, AM-K18-19, AM-K18-22, AM-K18-23, AM-S19-1, ANDGG 1804, ANDGG 1805, ANDGG 1807, ANDGG 1808, ANDGG 1810, ANDGG 2011, ANDGG 2020, ANDGG 2029, AM-S22-9, AM-S22-10, GAM 5 and GAM 6. These genotypes were evaluated for different quantitative traits in RBD (Randomized Block Design) during late *Kharif*-2025 with spacing 45 x 15 cm in three replications at College Farm, College of Agriculture, Navsari Agricultural University, Bharuch. All the recommended agronomic and crop management practices were uniformly followed throughout the crop growth period until harvest. At physiological maturity, observations were recorded on five randomly selected plants from each genotype in every replication for days to 50% flowering, days to maturity, plant height (cm), branches per plant, clusters per plant, pods per cluster, pods per plant, seeds per pod, pod length (cm), 100-seed weight (g), crude protein content (%), and seed yield per plant (g). Standard statistical procedure was used for the analysis of variance (Panse and Sukhatme, 1978) [12], phenotypic and genotypic coefficient of variation (Burton, 1952) [5], heritability and genetic advance (Allard, 1960), genetic advance as percent of mean (Johnson *et al.*, 1955) [8], Mahalanobis D² (Rao, 1952) [16] analysis was performed in variability and Biotoool package in R Studio software.

Results and Discussion

The success of any crop improvement programme primarily depends on the availability of adequate genetic variability in the breeding material. A wider range of genetic variation provides greater opportunities for effective selection and the identification of superior genotypes with desirable traits. In the present investigation, the mungbean genotypes exhibited substantial variation in their mean performance for all the characters evaluated. This variability was further validated by the analysis of variance, which revealed highly significant differences among the genotypes for all the traits studied ($p < 0.05$), indicating the existence of considerable genetic diversity within the experimental material (Table 1). Through Assessment of par se performance of mean data it was showed that the evaluated twenty seven genotypes, ANDGG 2011, ANDGG 2029, ANDGG 1808 and AM-15-26-1 were high yielding genotypes and ANDGG 1808, ANDGG 1807 and ANDGG 2020 were identified as most promising early genotypes based on days to 50% flowering while AM-K18-23, AM-15-48-11 and AM-K18-22 were found early for maturity. Plant height (cm) was superior in genotypes GAM 6, AM-S22-10 and ANDGG 2029. Branches per plant was high in genotypes ANDGG 2011, ANDGG 1808 and AM-15-48-4 while genotypes AM-15-26-1, ANDGG 1808 and ANDGG 2011 reported maximum clusters per plant. Maximum pods per cluster was recorded in genotypes AM-K18-6, AM-S22-10 and ANDGG 1810 while highly pods per plant in genotypes AM-15-26-1, ANDGG 2029 and AM-15-3-2. High seeds per pod was recorded by ANDGG 2011, AM-15-3-2 and ANDGG 2029 while longest pod length ANDGG 2029, ANDGG 1810 and AM-15-7-2. Genotypes ANDGG 2011, AM-K18-11 and ANDGG 1807 were superior in respect of 100-seed weight. AM-15-48-4, GAM 6 and AM-15-48-11 were high in protein content.

Moderate to high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for branches per plant, clusters per plant, pods per cluster, pods per plant, and 100-seed weight. Comparable findings for branches per plant, pods per cluster, and pods per plant by Yoseph *et al.* (2022) [21] and Rahangdale *et al.* (2023) [14]. For cluster per plant by Tabasum *et al.* (2010) [19]. While, Nalajala *et al.* (2022) [10] observed similar results for 100 seed weight.

Low estimates of genotypic and phenotypic coefficient of variation were observed for the traits like days to 50% flowering, days to maturity, plant height, seeds per pod, pod length and crude protein content. Similar results were observed by Ahmad *et al.* (2014) [1] for days to 50% flowering, days to maturity and plant height. For seeds per pod and crude protein content similar results were observed by Joshi *et al.* (2021) [9] and Salman *et al.* (2023) [17] for pod length. Traits seed yield per plant was recorded low genotypic and moderate phenotypic coefficient of variation. Similar results were observed by Ahmad *et al.* (2014) [1]. (Table 2)

High estimates of heritability were recorded by branches per plant (76.60%), clusters per plant (87.41%), pods per cluster (85.35%), pods per plant (89.80%) and 100-seed weight (76.64%). Whereas, moderate amount of heritability was recorded by days to 50% flowering (55.51%), plant height (44.95%), seeds per pod (39.80%), pod length (46.40%), crude protein content (52.48%) and seed yield per plant

(51.68%). While, low amount of heritability was observed on days to maturity (27.99%).

The high genetic advance expressed as percent of mean was obtained for branches per plant (24.95%), clusters per plant (39.11%), pods per cluster (40.24%), pods per plant (50.80%) and 100-seed weight (22.03%). seed yield per plant (14.12%) reported moderate genetic advance expressed as percent of mean. Whereas the low genetic advance expressed as percent of mean was recorded for characters days to 50% flowering (5.34%), days to maturity (1.97%), plant height (8.73%), seeds per pod (6.05%), pod length (8.27%) and crude protein content (4.82%).

High heritability accompanied by high genetic advance as a percentage of the mean was observed for branches per plant, clusters per plant, pods per cluster, pods per plant, and 100-seed weight. These results indicate that additive gene effects predominantly control these traits, making them highly amenable to improvement through direct selection. The present results align with observations made by Rahangdale *et al.* (2023) ^[14] for branches per plant, clusters per plant, pods per cluster and pods per plant and Prasanna *et al.* (2013) ^[13] for 100-seed weight. Seed yield per plant showed moderate heritability coupled with moderate genetic advance as percent of mean. Similar findings were earlier reported by Singh *et al.* (2021) ^[18].

Moderate estimates of heritability accompanied by low genetic advance as a percentage of the mean were observed for days to 50% flowering, plant height, seeds per pod, pod length, and crude protein content. These findings imply that the expression of these traits is largely governed by non-additive gene effects and environmental influences, thereby limiting the effectiveness of selection in the early generations. These findings are consistent with the observations of Salman *et al.* (2023) ^[17] for days to 50% flowering, Alom *et al.* (2014) ^[2] for plant height, Pandey *et al.* (2007) for seeds per pod, Jagdhane *et al.* (2017) ^[7] for pod length and Joshi *et al.* (2021) ^[9] for crude protein content. While low heritability with low genetic advance as% of mean were observed in characters days to maturity. Earlier studies by Yoseph *et al.* (2022) ^[21] and Salman *et al.* (2023) ^[17]. (Figure 1 & 2; Table 3)

Results of the present investigation showed that 27 genotypes of mungbean were distributed among eight different clusters using Tocher's clustering method. 27 genotypes combined to produce eight clusters. Table 4 lists the clusters' composition and Figure 3 represent the eight clusters and inter and intra cluster distance among them (Table 5). Rao *et al.* (2006) ^[15] carried out similar type related to genetic divergence study on 60 mungbean genotypes and grouped them into eight distinct clusters using Tocher's method. With 10 genotypes, Cluster I emerged as the largest cluster, whereas Cluster II was the second largest, comprising eight genotypes. Cluster III included three genotypes, indicating moderate divergence from the other clusters, while cluster IV contained only two genotypes, representing the most genetically distinct group among all the clusters. There was only one genotype present in each of the isolated cluster's V, VI, VII and VIII. The inter-cluster and intra-cluster distances are shown in Table

5. The maximum inter-cluster distance ($D = 286.16$) was found between clusters VIII and VI, followed by that between VI and III ($D = 284.34$) and VII and VI ($D = 198.28$). The minimum inter-cluster distance was observed between clusters VI and I ($D = 63.13$). The highest intra-cluster distance ($D = 47.72$) was found for (cluster-I) followed by cluster II showed an intra-cluster distance ($D = 43.09$). Cluster III had an intra-cluster distance of ($D = 35.53$), indicating moderate diversity within the cluster. The lowest intra-cluster distance was recorded in cluster IV ($D = 33.76$), suggesting that the two genotypes in this cluster were relatively more similar genetically. The four clusters viz., V, VI, VII and VIII contained a single genotype and therefore, their intra-cluster distance was zero. Selection of parents based on large inter-cluster and intra-cluster distances for hybridization gives a range of useful combinations for the development of high yielding mungbean varieties.

The cluster mean values for the 12 characters are presented in Table 6, which revealed considerable variation among the clusters for all the traits studied. Cluster V recorded the highest mean value for days to 50% flowering (38.34), whereas the lowest mean was observed in Cluster III (35.23). For days to maturity, Cluster II exhibited the highest mean (78.75), while Cluster VI recorded the lowest (72.67). The maximum plant height (45.60 cm) was observed in Cluster VIII, whereas Cluster VI recorded the minimum mean plant height (31.17 cm). Cluster VII exhibited the highest mean for branches per plant (3.80), while the lowest value was recorded in Cluster IV (2.65). The highest mean number of clusters per plant (4.80) was observed in Cluster I, whereas Cluster VI recorded the lowest value (2.17). Similarly, Cluster IV registered the highest mean for pods per cluster (5.13), while the lowest mean was observed in Cluster VI (2.63). With respect to pods per plant, Cluster VIII recorded the highest mean (28.73), whereas Cluster VI exhibited the lowest value (12.80). The maximum mean number of seeds per pod was recorded in Cluster VII (11.87), while Cluster II showed the minimum value (10.46). For pod length, Cluster II exhibited the highest mean (9.54 cm), whereas Cluster VI recorded the lowest mean (6.95 cm). Seed yield per plant was highest in Cluster VII (8.74 g) and lowest in Cluster V (6.53 g). The highest mean value for 100-seed weight was observed in Cluster VII (5.28 g), while Cluster IV recorded the lowest value (3.54 g). For crude protein content, Cluster V exhibited the highest mean (25.69%), whereas the lowest mean was recorded in Cluster VIII (23.70%).

The analysis of character contribution to genetic divergence revealed that pods per plant (22.5%) contributed the highest proportion to the total genetic divergence, followed by clusters per plant (16.4%), pods per cluster (14.6%), branches per plant (9.2%), 100-seed weight (8.8%), days to 50% flowering (5.7%), crude protein content (4.8%), seeds per pod and plant height (4.1% each), pod length (4.0%), seed yield per plant (3.3%), and days to maturity (2.7%) (Table 7). Collectively, these characters accounted for 100% of the total genetic divergence observed among the experimental genotypes (Figure 8).

Table 1: Analysis of variance (mean sum of square) for various characters in mungbean

Source of variation	Degree of freedom	Mean of sum square					
		Days to 50% flowering	Days to maturity	Plant height	Branches per plant	Clusters per plant	Pods per cluster
Replication	2	0.16	0.38	8.42	0.05	0.02	0.08
Genotypes	26	6.29**	11.10**	29.38**	0.59**	1.17**	1.88**
Error	52	1.33	5.13	8.51	0.05	0.05	0.10
S. Em. ($\pm$)		0.67	1.31	1.69	0.13	0.13	0.18
CD at 5%		1.89	3.71	4.78	0.38	0.38	0.52
CV (%)		3.11	2.91	7.00	7.65	7.71	8.76
Source of variation	Degree of freedom	Mean of sum square					
		Pods per plant	Seeds per pod	Pod length	100 seed weight	Crude protein content	Seed yield per plant
Replication	2	1.62	1.26	0.36	0.07	1.10	0.66
Genotypes	26	74.05**	1.19**	0.83**	0.89**	2.39**	1.78**
Error	52	2.70	0.40	0.23	0.09	0.55	0.42
S.Em. ($\pm$)		0.95	0.36	0.28	0.17	0.43	0.38
CD at 5%		2.69	1.03	0.79	0.49	1.22	1.06
CV (%)		8.77	5.73	6.34	7.21	3.08	9.22

Table 2: Range and genotypic and phenotypic variance of 12 traits in mungbean

Sr. No.	Characters	Range		Mean	Variance		
		Minimum	Maximum		Genotypic	Phenotypic	Environmental
1.	Days to 50% flowering	33.00	41.00	36.99	1.66	2.98	1.33
2.	Days to maturity	72.67	80.00	77.73	1.99	7.12	5.13
3.	Plant height (cm)	36.13	47.20	41.68	6.95	15.47	8.52
4.	Branches per plant	2.50	3.80	3.05	0.18	0.23	0.05
5.	Clusters per plant	2.10	4.40	3.00	0.37	0.42	0.05
6.	Pods per cluster	2.60	5.43	3.64	0.59	0.69	0.10
7.	Pods per plant	12.53	29.50	18.74	23.78	26.48	2.70
8.	Seeds per pod	9.01	11.87	11.02	0.26	0.66	0.40
9.	Pod length (cm)	6.73	8.93	7.60	0.20	0.43	0.23
10.	100-seed weight (g)	3.17	5.28	4.17	0.27	0.36	0.09
11.	Seed yield per plant(g)	5.69	8.74	7.05	0.45	0.87	0.42
12.	Crude Protein Content (%)	22.62	25.69	24.16	0.61	1.16	0.55

Table 3: Genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean for 12 traits in mungbean

Sr. No.	Characters	GCV%	PCV%	Heritability Broad Sense (%)	Genetic Advance	Genetic Advance (% of mean)
1.	Days to 50% flowering	3.48	4.67	55.51	1.97	5.34
2.	Days to maturity	1.82	3.43	27.99	1.53	1.97
3.	Plant height	6.33	9.44	44.95	3.64	8.73
4.	Branches per plant	13.84	15.82	76.60	0.76	24.95
5.	Clusters per plant	20.31	21.72	87.41	1.17	39.11
6.	Pods per cluster	21.15	22.89	85.35	1.46	40.24
7.	Pods per plant	26.02	27.46	89.80	9.52	50.80
8.	Seeds per pod	4.66	7.38	39.80	0.66	6.05
9.	Pod length	5.90	8.66	46.40	0.62	8.27
10.	100-seed weight	12.38	14.33	74.64	0.91	22.03
11.	Seed yield per plant	9.54	13.27	51.68	0.99	14.12
12.	Crude protein content	3.23	4.46	52.48	1.16	4.82

Table 4: Distribution of twenty seven genotypes of mungbean in different clusters as per the Tochers method

Cluster	Total number of Genotypes	Name of the genotypes
I	10	AM-K18-16, AM-K18-22, ANDGG 1807, ANDGG 1810, ANDGG 1804, AM-S19-1, AM-15-8-1, AM-15-48-11, AM-S22-9 and AM-15-52-1
II	8	AM-K18-11, AM-K18-14, GAM 5, GAM 6, AM-K18-19, ANDGG 1805, AM-15-7-2 and ANDGG 2020
III	3	AM-15-3-2, AM-15-26-1 and AM-K18-11
IV	2	AM-K18-6 and AM-S22-10
V	1	AM-15-48-4
VI	1	AM-K18-23
VII	1	ANDGG 2011
VIII	1	ANDGG 2029

Table 5: Average Intra and Inter-Cluster distances amongst 27 genotypes of mungbean

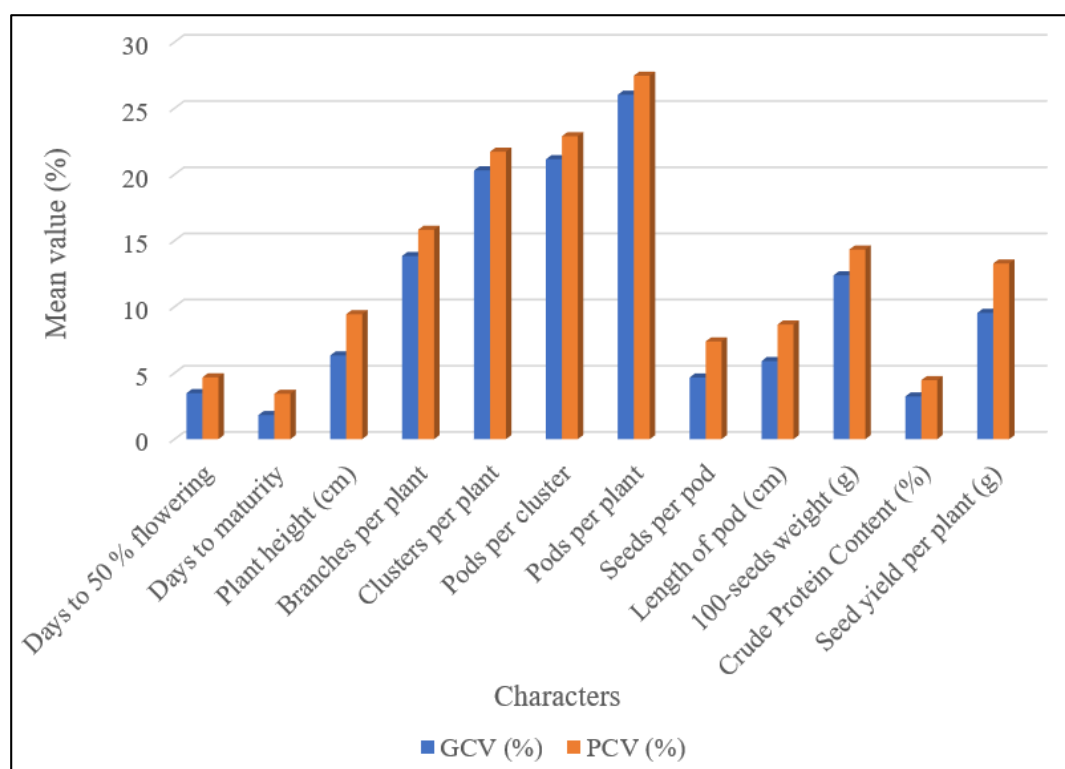
Cluster	I	II	III	IV	V	VI	VII	VIII
I	47.72	67.51	181.23	89.15	86.73	63.13	119.82	168.76
II		43.09	114.47	133.68	92.60	108.22	87.19	144.74
III			35.53	196.43	97.91	284.34	66.51	63.32
IV				33.76	115.21	173.15	154.49	162.18
V					0.00	129.16	66.35	68.07
VI						0.00	198.28	286.16
VII							0.00	70.45
VIII								0.00

Table 6: Cluster Mean of different characters in mungbean

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Seeds per pod	Pod length (cm)	100-seed weight (g)	Crude protein content (%)	Seed yield per plant (g)
I	37.40	77.87	42.05	2.90	4.80	3.56	15.26	11.17	7.60	4.05	24.06	6.78
II	37.13	78.75	41.23	2.90	3.35	3.15	18.28	10.46	9.54	4.30	23.91	6.81
III	35.23	77.56	39.07	3.60	4.03	3.84	28.39	11.53	7.25	4.29	24.27	7.90
IV	36.67	78.17	43.88	2.65	2.48	5.13	17.87	10.67	7.34	3.54	24.01	6.89
V	38.34	75.67	45.37	3.63	2.67	4.13	24.23	11.13	7.71	4.13	25.69	6.53
VI	37.67	72.67	31.17	3.10	2.17	2.63	12.80	11.17	6.95	3.70	25.04	6.69
VII	36.00	77.33	45.38	3.80	3.73	4.37	20.40	11.87	7.84	5.28	25.33	8.74
VIII	36.67	75.33	45.60	3.47	3.17	4.40	28.73	11.67	8.93	4.60	23.70	8.58

Table 7: Independent character contribution towards total divergence in 12 characters of mungbean

Sr. No.	Character	Percent of contribution (%)
1	Days to 50% flowering	5.7
2	Days to maturity	2.7
3	Plant height (cm)	4.1
4	Branches per plant	9.2
5	Clusters per plant	16.4
6	Pods per cluster	14.6
7	Pods per plant	22.5
8	Seeds per pod	4.1
9	Pod length (cm)	4.0
10	100-seed weight (g)	8.8
11	Crude Protein content (%)	4.8
12	Seed yield per plant (g)	3.3

**Fig 1:** GCV (%) and PCV (%) of various traits of mungbean

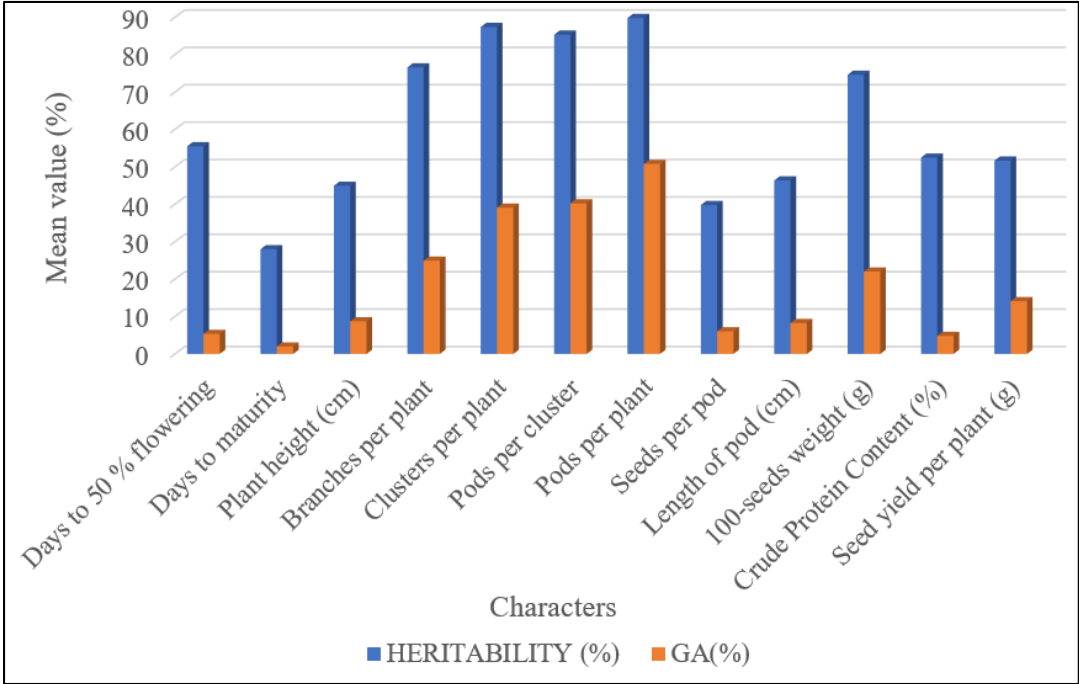


Fig 2: Heritability (%) and genetic advance (%) of various traits of mungbean

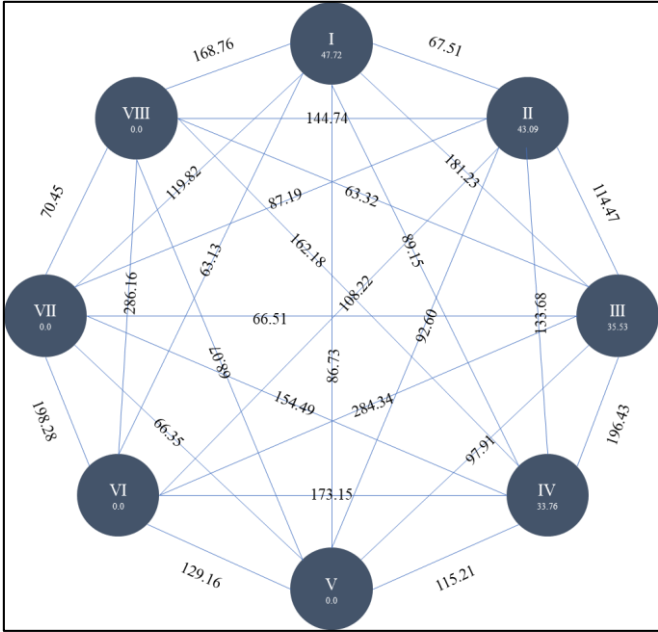


Fig 3: Inter and intra cluster (D^2) distances among eight clusters of mungbean

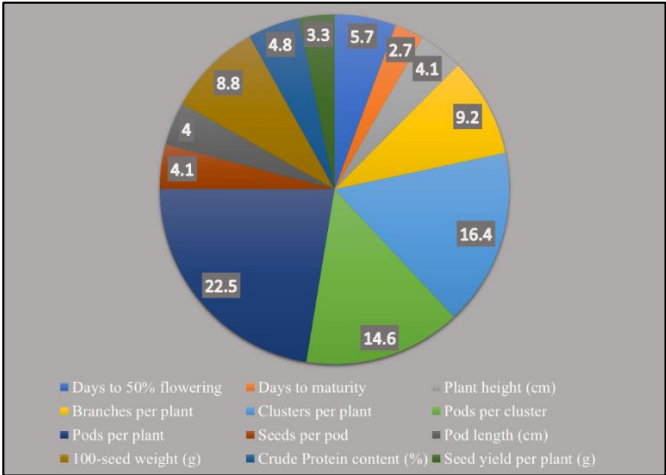


Fig 4: Relative contribution of various characters towards divergence

Conclusion

The experimental material exhibited sufficient genetic variability, indicating considerable potential for the development of early maturing and high-yielding mungbean genotypes. Based on mean performance, the genotypes ANDGG 2011, ANDGG 2029, and ANDGG 1808 were identified as promising elite genotypes for yield improvement while maintaining desirable quality attributes. High heritability coupled with high genetic advance as a percentage of the mean was recorded for branches per plant, clusters per plant, pods per cluster, pods per plant, and 100-seed weight, suggesting the predominance of additive gene action and indicating that these traits can be effectively improved through direct selection. Considering the maximum inter-cluster distance, hybridization between the genotypes of Cluster VIII (ANDGG 2029) and Cluster VI (AM-K18-23), as well as between Cluster VI (AM-K18-23) and Cluster III (AM-15-3-2, AM-15-26-1, and AM-K18-11), is recommended to generate broad genetic variability and obtain superior recombinants for yield enhancement in mungbean. Among the traits studied, pods per plant, clusters per plant, pods per cluster, branches per plant, and 100-seed weight contributed the greatest proportion of genetic divergence, highlighting their importance in the selection of diverse parental lines for future breeding programmes.

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References

- Ahmad HB, Rauf S, Rafiq CM, Mohsin AU, Shahbaz U, Sajjad M. Genetic variability for yield contributing traits in mung bean (*Vigna radiata* L.). J Glob Innov Agric Sci. 2014;2(2):52-54.
- Alom KM, Rashid MH, Biswas M. Genetic variability, correlation and path analysis in mungbean (*Vigna radiata* L.). J Environ Sci Nat Resour. 2014;7(1):131-138.
- Ministry of Agriculture and Farmers Welfare. Agricultural estimates 2024-25 [Internet]. New Delhi: Ministry of Agriculture and Farmers Welfare; 2024-2025 [cited 2025 Jun 2]. Available from: <https://agriwelfare.gov.in/en/AgricultureEstimates>
- Arumuganathan K, Earle ED. Nuclear DNA content of some important plant species. Plant Mol Biol Rep. 1991;9(3):208-218.
- Burton GW. Quantitative inheritance in grasses. In: Proceedings of the 6th International Grassland Congress. 1952;1:277-283.
- Datta S, Gangwar S, Kumar S, Gupta S, Rai R, Kaashyap M, et al. Genetic diversity in selected Indian mungbean [*Vigna radiata* (L.) Wilczek] cultivars using RAPD markers. Am J Plant Sci. 2012;3(8):1085-1091.
- Jagdhane NM, Suresh BG, Ram BJ, Yadav P. Genetic variability and character association for seed yield in mungbean [*Vigna radiata* (L.) Wilczek]. J Pharmacogn Phytochem. 2017;6(4):1388-1390.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agron J. 1955;47(7):314-318.
- Joshi DP, Parmar LD, Patel RS. Estimation of variability, correlation and path coefficient in mungbean [*Vigna radiata* (L.) Wilczek] genotypes for seed yield and its attributing characters. Pharma Innov J. 2021;10(11):1734-1740.
- Nalajala S, Singh NB, Jeberson MS, Sastry EVD, Yumnam S, Sinha B, et al. Genetic variability, correlation and path analysis in mung bean genotypes (*Vigna radiata* L. Wilczek): an experimental investigation. Int J Environ Clim Change. 2022;12(11):1846-1854.
- Pandey MK, Srivastava N, Kole CR. Selection strategy for augmentation of seed yield in mungbean (*Vigna radiata* L. Wilczek). Legume Res. 2007;30(4):243-249.
- Panse VG, Sukhatme PV. Statistical methods for agricultural workers. New Delhi: Indian Council of Agricultural Research; 1978.
- Prasanna BL, Rao PJM, Murthy KGK, Prakash KK. Genetic variability, correlation and path coefficient analysis in mungbean. Environ Ecol. 2013;31(4):1782-1788.
- Rahangdale S, Lakhani JP, Singh SK, Sharma S, Barela A, Kumar P, et al. Study of selection criteria and genetic variability in mungbean (*Vigna radiata* L. Wilczek) genotypes for seed yield and its contributing traits. Environ Ecol. 2023;41(1):145-151.
- Rao CM, Rao YK, Reddy M. Genetic variability and path analysis in mungbean. Legume Res. 2006;29(3):216-218.
- Rao CR. Diversity: its measurement, decomposition, apportionment and analysis. Indian J Stat Ser A. 1952;14:1-22.
- Salman MAS, Anuradha C, Sridhar V, Babu ER, Pushpavalli SNCVL. Genetic variability for yield and its related traits in green gram [*Vigna radiata* (L.) Wilczek]. Legume Res. 2023;46(6):700-704.
- Singh G. Genetic variability, correlation and path analysis in mungbean [*Vigna radiata* (L.) Wilczek]. Int J Agric Sci. 2021.
- Tabasum A, Saleem M, Aziz I. Genetic variability, trait association and path analysis of yield and yield components in mungbean [*Vigna radiata* (L.) Wilczek]. Pak J Bot. 2010;42(6):3915-3924.
- Vavilov NI. The origin, variation, immunity and breeding of cultivated plants. Waltham (MA): Chronica Botanica; 1939.
- Yoseph T, Mekbib F, Fenta BA, Tadele Z. Genetic variability, heritability, and genetic advance in mung bean [*Vigna radiata* (L.) Wilczek] genotypes. Ethiop J Crop Sci. 2022;9(2):113-115