



Plant Archives

Journal homepage: <http://www.plantarchives.org>DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2025.v25.no.2.403>

GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD-RELATED TRAITS IN MUNGBEAN (*VIGNA RADIATA* L. WILCZEK) UNDER INDIAN AGROCLIMATIC CONDITIONS

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(Date of Receiving-17-07-2025; Date of Acceptance-30-09-2025)

ABSTRACT

Mungbean (*Vigna radiata* (L.) Wilczek) is a vital pulse crop with high nutritional value, yet its productivity in India remains suboptimal due to limited genetic improvement. The present study was conducted during the kharif season of 2024–2025 at IARI, New Delhi, using 21 diverse mungbean genotypes evaluated in a randomized block design for six yield-related traits. Analysis of variance revealed significant differences among genotypes for all traits, indicating substantial genetic variability. The phenotypic coefficient of variation (PCV) consistently exceeded the genotypic coefficient of variation (GCV), suggesting environmental influence on trait expression. High heritability coupled with high genetic advance was observed for number of pods per plant (67.9%, 46.1%) and number of seeds per pod (77%, 36.9%), indicating the predominance of additive gene action. Biomass exhibited the highest heritability (99.9%) and genetic advance (97.3%), reflecting its strong genetic control and high selection potential. In contrast, grain yield showed moderate heritability (42.8%) with substantial environmental influence, highlighting the need for indirect selection through stable yield-contributing traits. Overall, the findings confirm the presence of considerable variability among genotypes and identify pods per plant, seeds per pod, and biomass as key selection criteria for enhancing mungbean yield.

Key words : Mungbean, Genetic variability, Genetic advance, Selection.

Introduction

Mungbean (*Vigna radiata* (L.) R. Wilczek), also known as green gram, is a promising legume contributing to global food security and sustainable agricultural systems (Manjunatha et al. 2023). It is a diploid ($2n = 22$), predominantly self-pollinated species characterized by a short growth cycle of 60–70 days and a compact genome of approximately 579 Mb (Khanbo et al. 2024). The seeds are nutritionally dense, containing 20–30% protein and 60–70% carbohydrates, in addition to essential vitamins and minerals (Nair and Schreinemachers, 2020). When consumed in combination with cereals, mungbean provides a balanced amino acid composition, making it a vital

dietary component, particularly in Southeast Asian countries (Nair et al., 2013). The crop is highly valued for its easily digestible protein and absence of antinutritional factors. Moreover, mungbean exhibits several biofunctional properties, including detoxifying, hypolipidemic, hypoglycaemic, anticancer, antihypertensive and immunomodulatory effects (Reddappa et al., 2025).

Despite its significant agronomic value and diverse uses, mungbean is cultivated on nearly 7 million hectares in the tropics and subtropics, accounting for about 8.5% of the global pulse area, with an annual production of 3 million tons and an average productivity of 721 kg per

hectare (Reddappa *et al.*, 2025). In India, mungbean is an important pulse crop, yet its productivity remains comparatively low relative to other leading mungbean-producing nations. Several factors contribute to this gap, including low yield potential, suboptimal crop management practices, variation in plant growth habits, susceptibility to pod shattering and lodging, late or indeterminate maturity, high vulnerability to insect pests and diseases, and issues related to grain quality (Nair and Schreinemachers, 2020). Therefore, enhancing mungbean production in India requires the development of improved cultivars alongside the adoption of better crop management practices.

Genetic variability serves as the basis of crop improvement, as it determines the scope for selection and genetic gain in desirable traits (Sarkar *et al.*, 2025). The success of plant breeding relies on the presence of sufficient heritable variation within a population, enabling the identification of superior genotypes for yield and adaptability (Premakumar *et al.*, 2024). Yield-related traits such as seed yield are typically quantitative in nature, governed by multiple genes and strongly influenced by environmental conditions. Therefore, separating genetic effects from environmental influences is critical for accurate evaluation. Parameters such as the genotypic and phenotypic coefficients of variation (GCV and PCV) provide valuable measures of variability, while heritability estimates indicate the proportion of phenotypic variation attributable to genetic factors (Gayacharan *et al.*, 2020). Genetic advance further reflects the potential improvement achievable through selection. A combination of high heritability with high genetic advance generally suggests the predominance of additive gene action, implying that direct selection could be highly effective for crop improvement (Manjunatha *et al.*, 2023). Assessment of these genetic parameters offers valuable guidance in breeding programs by enabling precise identification of promising traits and genotypes.

In this study, variability, heritability, and genetic advance were analyzed in mungbean with emphasis on key yield-related traits contributing to productivity. The findings are expected to aid in the development of superior, high-yielding mungbean varieties. Previous research has demonstrated that estimates of genetic parameters for yield and its components vary considerably across studies, reflecting differences in heritability, inter-trait associations, and variability. This underscores the importance of recognizing that genetic variability exists within propagative material and remains essential for further genetic improvement of yield and other agronomically significant traits.

Materials and Methods

Experimental Site and Design

A field experiment was carried out during the kharif season of 2024–2025 at the research farm of the Indian Agricultural Research Institute (IARI), New Delhi. The experiment comprised 21 diverse mungbean [*Vigna radiata* (L.) Wilczek] genotypes (Table 1) evaluated in a Randomized Block Design (RBD) with appropriate replications. Each genotype was sown in a single row, maintaining a row-to-row spacing of 30 cm and plant-to-plant spacing of 15 cm. Standard agronomic practices were followed to raise a healthy crop.

Table 1 : Genotypes evaluated in the study.

S. no	Genotype	S. no	Genotype
1	APM1	12	APM12
2	APM2	13	APM13
3	APM3	14	APM14
4	APM4	15	APM15
5	APM5	16	APM16
6	APM6	17	APM 17
7	APM7	18	APM 18
8	APM8	19	APM19
9	APM9	20	APM 20
10	APM10	21	APM 21
11	APM11		

From each genotype in every replication, five plants were randomly selected (excluding border plants) and tagged for recording observations. The mean values of these plants were used for further statistical analysis. Data were collected on the following traits

Plant hight

Plant height (cm) was measured at the time of physiological maturity. The measurement was taken from the soil surface (base of the stem) to the tip of the main shoot using a measuring scale.

Number of pods per plant

After maturity, the total number of fully developed pods on each tagged plant was counted manually and recorded.

Number of seeds per plant

All pods from each sampled plant were threshed separately. The seeds obtained from each plant were counted to determine the total number of seeds per plant.

100 seed weight

From the threshed seeds of each plant, a random sample of 100 seeds was drawn and weighed using an electronic balance with 0.01 g precision. This was

recorded as the 100-seed weight.

Seed yield per plant (g)

The total seed weight of each sampled plant after complete threshing and cleaning was recorded using an electronic balance. This was considered as seed yield per plant

Biomass per plant (g)

After harvesting, the entire above-ground plant (stem, leaves, and pods) of each sampled plant was oven-dried at 70°C until a constant weight was obtained. The dried weight was recorded as biomass per plant.

Results and Discussion

In present study, we have evaluated 21 diverse mungbean genotypes for 6 yield associated traits with 3 replications in randomised block design. The analysis of variance (ANOVA) revealed significant differences among the genotypes for all the studied traits. Plant height, number of pods per plant, number of seeds per pod, 100-seed weight, grain yield, and biomass all showed highly significant variation, indicating the presence of substantial genetic variability in the experimental material, ANOVA results were presented in Table 2 and descriptive statistics were present in Table 2. The results confirm that the studied population harbors considerable variability, which can be effectively utilized in selection and crop improvement programs. Similar reports were found in studies by Makeen *et al.* (2007) and Dhunde *et al.* (2021).

Plant height

Plant height across the genotypes exhibited considerable variability, with values ranging from 15 cm (AMP1) to 35.33 cm (AMP11) and an overall mean of 26.98 cm. The descriptive statistics further revealed a standard deviation of 5.41 and a range of 20.33, indicating moderate variation among the genotypes. The tallest plants were recorded in AMP11, AMP17, AMP12, and AMP18, all exceeding 32 cm, while the shortest plants were observed in AMP1, AMP2, AMP4 and AMP8, all below 23 cm (Fig. 1). Plant height exhibited phenotypic variance (38.33) and genotypic variance (24.78). with PCV 22.9, GCV 18.4, The trait showed high heritability (64.6%) with genetic advance (30.55%), Table 3 indicating that additive gene action may plays a major role in its expression, the results were aligned with previous reports by Ali *et al.* (2010) and Reddappa *et al.* (2025).

Number of pods per plant

The number of pods per plant varied widely among the genotypes, ranging from 15 (AMP10) to 42.33

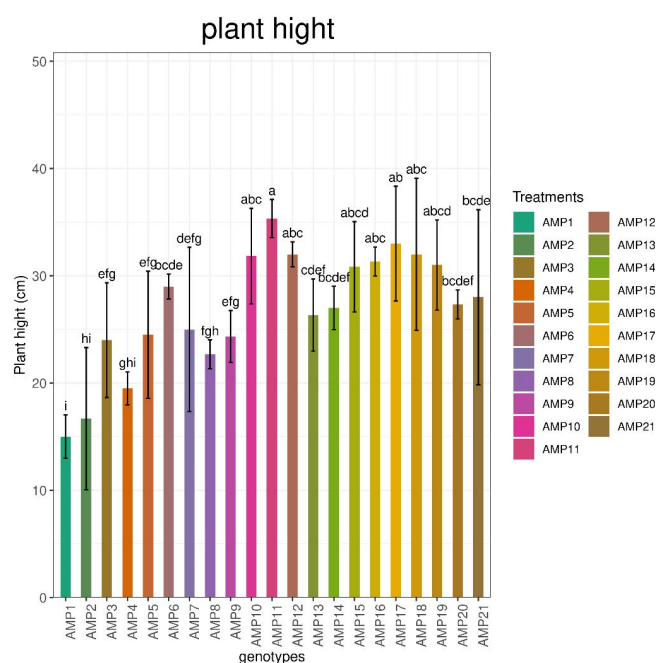


Fig. 1 : Bar graph of genotypes plant height.

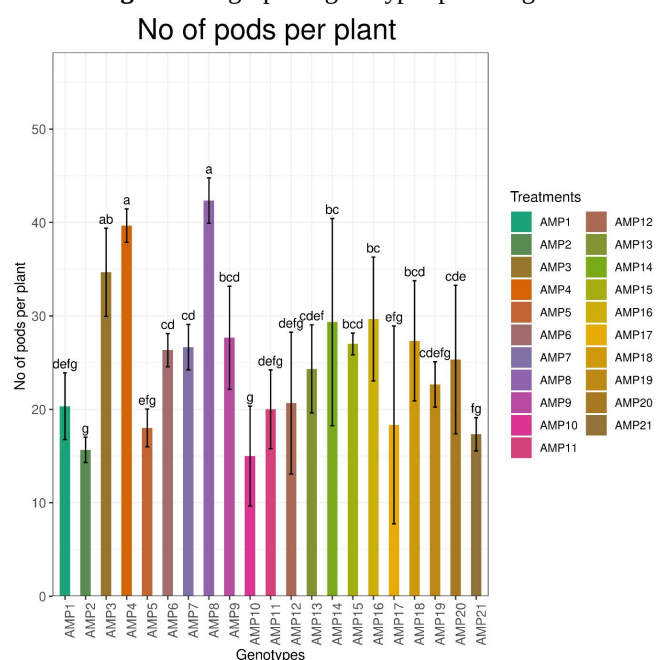


Fig. 2 : Bar graph of genotypes with No of pods per plant.

(AMP8), with a mean of 25.16 pods. The descriptive statistics revealed a standard deviation of 7.35 and a range of 27.33, indicating high variability in this trait. The genotypes AMP8, AMP4, AMP3, and AMP16 recorded the maximum pod numbers, well above the population mean, while AMP10, AMP2, AMP21 and AMP5 exhibited the lowest pod numbers Fig. 2. Number of pods per plant recorded relatively high genotypic variance (46.70) and phenotypic variance (68.74). PCV 18.59 and GCV 32.95 With heritability of 67.9% and genetic advance of 46.12% Table 3, similar results are reported by Makeen *et al.* (2007), Asari *et al.* (2019), Abhisheka and Mogali

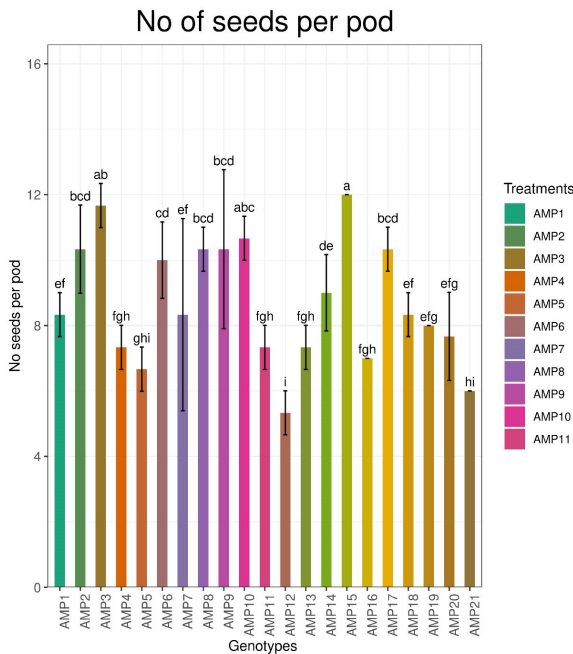


Fig. 3 : Bar graph of genotypes with No of seeds per pod.

Table 2 : ANOVA of plant height, Number of pods per plant, No of seed per plant, 100 seed weight, Grain yield, Biomass.

Trait	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Plant height	20	1757.984	87.899	6.485	0
Number of pods per plant	20	3243.079	162.154	7.358	0
No seeds per pod	20	207.651	10.383	11.049	0
100 seed weight	20	22.33	1.117	5.033	0
Grain yield	20	937.296	46.865	3.244	0.001
Biomass	20	55881.53	2794.076	3542.309	0

Table 3 : Descriptive statistics of analysed traits.

Descriptive statistics	Mean	Minimum	Maximum	Standard Deviation	Range
Plant height	26.98	15	35.	5.41	20.333
Number of pods per plant	25.15	15	42.3	7.35	27.333
No seeds per pod	8.68	5.33	12	1.86	6.667
100 seed weight	4.42	3.69	6.2	0.61	2.507
Grain yield	9.83	4.12	16.9	3.9	12.787
Biomass	64.5	18.0	130.	30.5	111.994

(2020).

Number of seeds per pod

The number of seeds per pod showed a mean of 8.68, with values ranging from 5.33 (AMP12) to 12 (AMP15). The descriptive statistics indicated a standard deviation of 1.86 and a range of 6.67, suggesting moderate variability among the genotypes. The highest seed numbers were recorded in AMP15, AMP3, AMP10, and

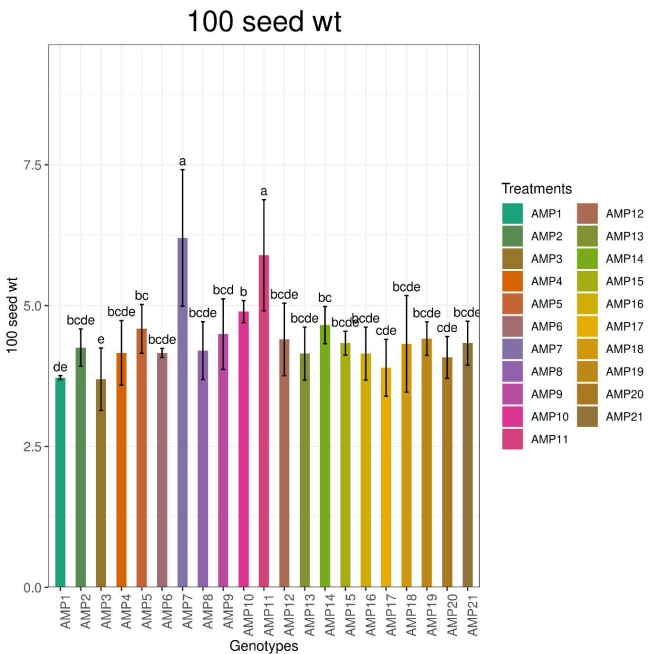


Fig. 4 : Bar graph Genotypes with 100 seed weight.

AMP2/AMP8/AMP9/AMP17, all of which performed above the population mean. On the other hand, AMP12, AMP21, AMP5, and AMP16 showed the lowest seed numbers per pod, falling well below the mean (Fig. 3).

The number of seeds per pod had moderate genotypic variance (3.15), with PCV 11.167 and GCV 23.28 and high heritability (77%) A genetic advance of 36.93% Table 3 study aligned with previous reports of Bansod *et al.* (2021) and Manjunatha *et al.* (2023).

100 seed weight

The 100-seed weight exhibited a mean of 4.42 g, with values ranging from 3.69 g (AMP3) to 6.20 g (AMP7). The descriptive statistics showed a standard deviation of 0.61 and a range of 2.51, indicating relatively low variability compared to other traits. The heaviest seeds were recorded in AMP7, AMP11, AMP10, and AMP14, all performing well above the population mean, while the lightest seeds were observed in AMP3, AMP1,

AMP17, and AMP20 (Fig. 4).

For 100-seed weight, both genotypic variance 0.29 and phenotypic variance 0.52 variances. With PCV 16.29 and GCV 12.337 Heritability was 57.3% and with a genetic advance of 19.24%. Table 3 results are aligned with Mohammed *et al.* (2020).

Grain yield

Grain yield among the genotypes displayed wide

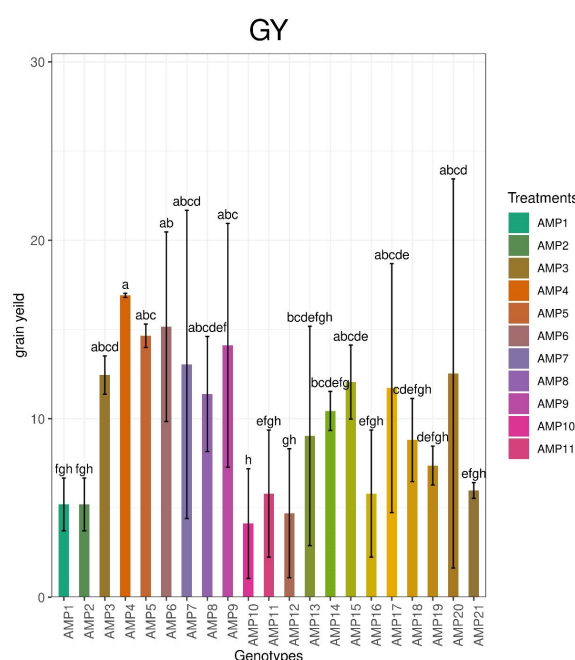


Fig. 5 : Bar graph of Genotypes with grain yield.

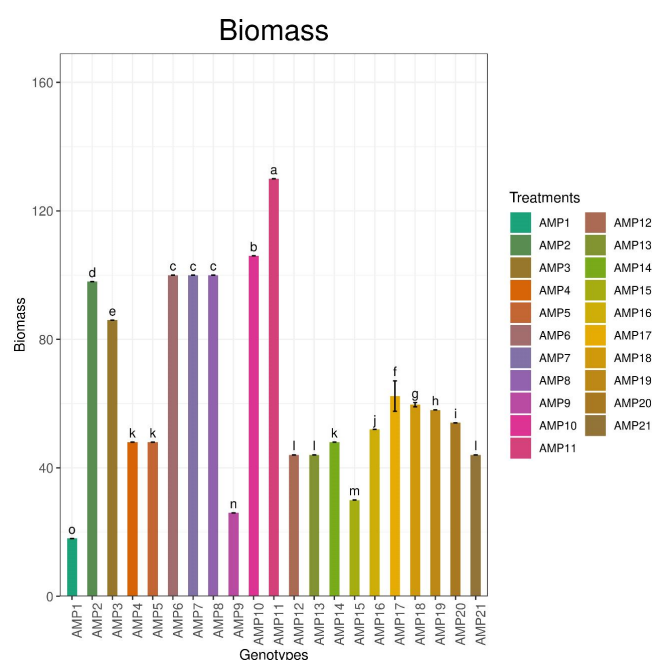


Fig. 6 : Bar graph of Genotypes with Biomass.

Table 4 : Variance components and genetic advance and heritability of analysed traits.

Column1	Genotypic variance	Phenotypic variance	Env. variance	CV(%)	PCV (%)	GCV (%)	Heritability	Genetic adv(%) (i=5%)
Plant height	24.782	38.335	13.553	13.643	22.945	18.448	0.646	30.556
Number of pods per plant	46.706	68.743	22.037	18.659	32.955	27.164	0.679	46.125
No seeds per pod	3.148	4.088	0.94	11.167	23.286	20.434	0.77	36.938
100 seed weight	0.298	0.52	0.222	10.642	16.292	12.337	0.573	19.243
Grain yield	10.806	25.253	14.447	38.656	51.107	33.432	0.428	45.051
Biomass	931.096	931.885	0.789	1.376	47.275	47.255	0.999	97.305

variation, with values ranging from 4.12 g (AMP10) to 16.91 g (AMP4), and a population mean of 9.83 g. The descriptive statistics indicated a standard deviation of 3.95 and a range of 12.79, suggesting substantial diversity for this trait. The highest yielding genotypes were AMP4, AMP6, AMP5, and AMP9, all of which exceeded the population mean by a considerable margin, while the lowest yields were recorded in AMP10, AMP12, AMP1, and AMP2 (Fig. 5).

Grain yield showed phenotypic variance (25.25) and genotypic variance (10.81), along with high PCV (51.1%) and GCV (33.4%). genetic advance (45.05%), the heritability (42.8%) indicates a strong influence of environment on yield expression (Table 2). Similar reports found by Panigrahi (2016) and Asari *et al.* (2019).

Biomass

Biomass production exhibited the widest variation

among all measured traits, with values ranging from 18.01 g (AMP1) to 130.01 g (AMP11) and an overall mean of 64.57 g. The descriptive statistics showed a high standard deviation (30.52) and a broad range (111.99), confirming the existence of strong variability within the population. The highest biomass was recorded in AMP11, AMP10, AMP8, and AMP6/AMP7, all of which greatly surpassed the population mean, whereas AMP1, AMP9, AMP15, and AMP12 represented the lowest biomass producers (Fig. 6). Biomass displayed the highest genotypic (931.09) and phenotypic (931.89) variances with environmental influence and PCV 47.375, GCV 47.25 Heritability was (79.9%), coupled with the highest genetic advance (77.3%) (Table 3). Similar result reported by Makeen *et al.* (2007), Mohammed *et al.* (2020) and Dhunde *et al.* (2021).

Conclusion

The evaluation of 21 mungbean genotypes demonstrated significant genetic variability for all studied traits, providing ample scope for selection and improvement. Traits such as number of pods per plant, number of seeds per pod, and biomass showed high heritability along with high genetic advance, suggesting that they are governed by additive gene action and can be effectively improved through direct selection. Grain yield, although highly variable, was more strongly influenced by environmental factors, indicating that indirect selection via stable yield components would be more effective for genetic improvement. Overall, this study highlights the potential of exploiting genetic variability for yield-related traits to develop high-yielding and stable mungbean cultivars, which can contribute to enhancing pulse productivity and food security in India.

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