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RESEARCH ARTICLE

Unravelling genetic variability for yield and contributing characteristics in green gram [*vigna radiata* (L.) wilczek] germplasm

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Abstract

Mungbean [*Vigna radiata* (L.) Wilczek] is an essential crop for food, feed, and income generation in rice-based farming systems across Southeast Asia and other regions. Its popularity stems from its good taste, high nutritional value and ease of digestion, making it a promising crop for enhancing livelihoods. However, despite its significance, mungbean productivity remains low, primarily due to environmental stresses and a lack of sufficient genetic variability. This study examines the variability, heritability, phenotypic and genotypic coefficient of variation and genetic advance among yield-contributing traits in green gram germplasm. A total of 450 germplasm lines were evaluated alongside check varieties, revealing significant variation, with the analysis of variance showing notable differences across nearly all traits. The mean sum of squares for the germplasm was highly significant for all phenotypic traits. Several traits exhibited high estimates of heritability and genetic advance, *viz.,* the number of branches/ plants, number of clusters/ plants, number of pods/ clusters, pod length, test weight and seed yield/plant, indicating their potential for direct selection in breeding programs. These findings suggest that additive gene effects play a dominant role in controlling these traits, with minimal environmental influence, making simple phenotypic selection an effective approach. The results provide valuable insights for advancing green gram breeding programs focused on improving yield and quality through targeted hybridization and trait selection.

Keywords

germplasm; heritability; mungbean; PCV; traits; variability

Introduction

Green gram, also known as Mungbean and scientifically classified as *Vigna radiata* (L.) Wilczek var. *radiata* is a significant leguminous crop valued for its nutritional richness and rapid growth. It is predominantly cultivated in South Asia, Southeast Asia and Australia (1). This hardy legume contributes to improved soil fertility by producing up to 40 kg of nitrogen per hectare, making it a vital crop in intercropping systems. When grown alongside cereals, mungbean enhances the availability of nitrogen and carbon in the soil for subsequent crops. This intercropping practice reduces the nitrogen requirement of the following grain crop by nearly 25% compared to the

recommended dosage (2). Green gram thrives in hot, dry climates and is highly valued for its rich protein content, making it an essential food source in many developing countries.

In India, green gram cultivation spans approximately 5.13 million hectares (3), yet the crop's average productivity is relatively low, yielding about 601 kg/ha. It is the third-most important pulse crop in the country (4). Due to declining pulse productivity, prices have surged, making pulses unaffordable for many economically disadvantaged individuals. However, green gram germplasm accessions have accumulated beneficial traits, including resistance to environmental stresses such as pests, diseases, temperature fluctuations, drought, *etc*. Natural selection plays a critical role in the evolution of the crop. Over time, green gram has developed a range of agronomic traits, including yield-contributing factors like pod count, biological (grain) yield and maturity duration. Grain yield is a complex trait influenced by the interaction of various component characteristics (5) and it serves as the primary criterion for evaluating crop improvement. Yield is the primary criterion for assessing crop improvement. The ultimate goal of any crop improvement efforts is to enhance seed yield by developing high-yielding varieties that are also disease-resistant.

Selecting superior parental lines with desirable heritability and genetic advancement for various traits is crucial for any yield improvement program. Assessing genetic variability using key metrics, such as genotypic and phenotypic coefficients of variation, heritability and genetic gain, is essential to initiate an effective breeding strategy. Moreover, genetic diversity studies are invaluable for categorizing genotypes into distinct groups, enabling the selection of superior parents from highly divergent groups for breeding purposes. Thus, the objective of this study is to evaluate genetic variability, heritability and genetic gain in a large collection of green gram germplasm accessions.

Materials and Methods

The current study was conducted using green gram germplasm, consisting of 450 accessions evaluated under field conditions. These germplasms were obtained from the National Pulses Research Centre (NPRC) in Vamban, Pudukkottai, Tamil Nadu, ensuring broad genetic diversity representative of various geographic regions. Each test entry was planted in a single row following the Augmented Block Design II. A fixed number of standard checks were replicated across all blocks, while the test entries were randomly assigned to the remaining plots without replication. The entries were sown with row spacing of 30 cm and plant spacing of 10 cm at the NPRC farm during *Rabi* 2024 (Fig. 1), situated at an altitude of 93 meters above mean sea level, at 10°36 N latitude and 78°90 E longitude. According to the augmented RCBD design, ten check genotypes *viz*., VGG-20-157, VGG-17-036, CO-9, VGG-20-227, CO-8, VGG-20-235, VBN-7, VBN-5, VBN-4 and VBN-6 were replicated randomly after every 40 test entries of germplasms to enhance the reliability and interpretability of the experimental results. The recommended agricultural practices, including balanced fertilization, efficient water management and crop rotation, were followed to support optimal plant health and growth strategies (6).

Data were collected from five randomly selected plants for ten phenotypic traits, *viz*., days to 50% flowering (DOF), plant height (PH), number of branches/plant (NOB), number of pods/cluster (NOC), number of clusters/pod (NOPC), pod length (PL), number of pods/plant (TOPP), number of seeds/pod (NOSP), test weight (100 SW) and seed yield/plant (SPY). Statistical analysis of these
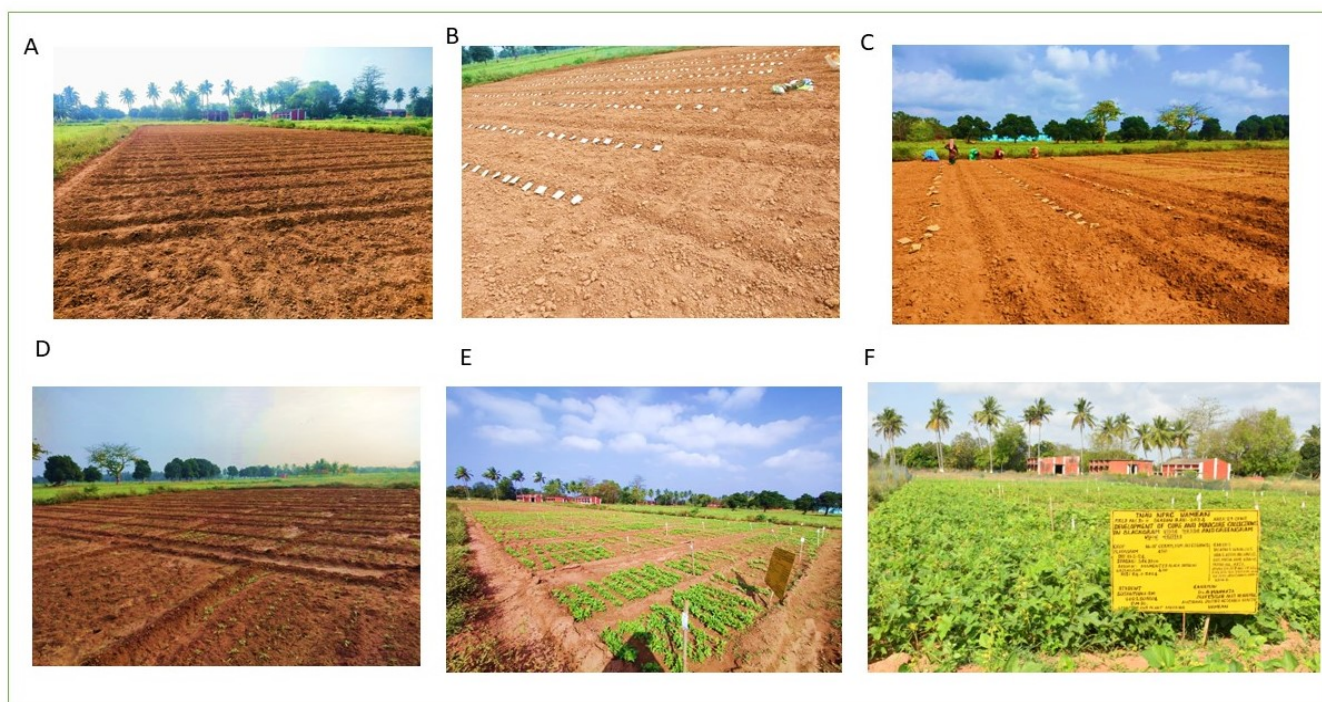

Fig. 1. Illustration on raising green gram germplasm in an experimental field - (A)- Layout preparation; (B) Arrangement of germplasm seeds in a proper single line; (C) Sowing with spacing of 30 x 10 cm; (D) Life irrigation a day after sowing; (E) Seedling stage cultivation practices; (F) A whole view of green gram germplasm before harvesting

observations was performed using the R v3.5.1, following the analysis of variance method outlined by (7) to evaluate trait variability. The genotypic and phenotypic variances were calculated using the formula provided by (8). To estimate the genotypic and phenotypic coefficients of variation, the procedures described by (9,10) were applied. Broad-sense heritability (h2b) was determined according to the method suggested by (11), while genetic advance was estimated using the formulas established by (8). This comprehensive methodology ensured a robust evaluation of genetic variability and potential for selection.

Formulas for calculating genetic variability,

Phenotypic coefficient of variation (PCV) = $\dfrac{\sqrt{\sigma^2 p}}{Mean}$ (Eqn. 1)

Where, $\sigma^2 p$ = Phenotypic variance

Genotypic coefficient of variation (PCV) = $\dfrac{\sqrt{\sigma^2 g}}{Mean}$ (Eqn. 2)

Where, $\sigma^2 g$ = Genotypic variance

Heritability in broad sense (h^2) = $\dfrac{\sigma^2 g}{\sigma^2 p} \times 100$ (Eqn. 3)

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

Genetic advance (GA) = $k \times \sigma_g \times \dfrac{h^2}{100}$ (Eqn. 4)

Where,

k = Selection differential (based on the desired percentage of selected individuals)

σ_g = Standard deviation of genotypic variance

h^2= Heritability expressed as percentage

Results and Discussion

Components of variance and variation coefficients

Genetic variability was assessed by analysing the mean performance of quantitative traits from five randomly chosen competitive plants in both the germplasm and check entries. Statistical analysis was performed using R v3.5.1 and the mean values for ten traits were analysed through variance analysis, aligned with the experimental design. A significant level (p<0.01) of genetic variability was observed among the experimental materials across all ten quantitative traits, as evidenced by the mean sum of squares for each attribute associated with the genotypes Table 1. The variance analysis highlighted substantial

variation across nearly all germplasm, indicating that the study material possesses adequate variability. These findings are consistent with those reported by (12-14). The observed variability confirmed that the green gram germplasm under investigation is suitable for further research Table 1.

Estimation of Genotypic and Phenotypic coefficient of variation

To assess how environmental factors interact with yield-related traits, it is essential to estimate the Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) (15). A comparison revealed that the PCV values were higher than the GCV values for all characters (Fig. 2), indicating the influence of environmental factors on these traits, as also noted in the study by (16). The genotypes showed significant differences across all traits analysed (Table 2). Based on the coefficient of variation, the highest variability was observed in SPY (31.46), followed by the NOB (24.49) and the TOPP (23.59).

The GCV value ranged from 4.50 % (DOF) to 45.94 % (NOB). High GCV values were recorded for NOB (45.94), TOPP (45.87), SPY (41.88), PL (41.22), 100 SW (32.09), NOC (24.62) and NOPC (25.14). Moderate GCV values were observed for the NOSP (13.76) and PH (13.02), while the lowest GCV was found in DOF (4.50) Table 2.

The PCV values ranged from 8.28 % (DOF) to 53.52 % (SPY). High PCV values were noted for SPY (53.52), NOB (51.97), TOPP (51.82), PL (41.70), 100 SW (37.51), NOC (32.71), NOPC (30.30), PH (21.42). A moderate PCV range was observed for NOSP (15.20), while DOF exhibited the lowest PCV (8.28) (Table 2).

The highest estimated values of both PCV and GCV were observed for SPY, as reported by (17,18). Traits such as NOB, TOPP, PL, 100 SW, NOC and NOPC were similarly analysed by (19). A moderate range of PCV and GCV was found in NOSP, which is in line with the results reported by (20). DOF exhibited low values for both PCV and GCV, a result consistent with the findings of (21-24). The high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) suggest considerable potential for genetic improvement through the careful selection of these traits, which can contribute to the development of high-yielding varieties. Conversely, the low values for both GCV and PCV values for days to flowering (DOF) indicate a limited range of variation among the genotypes for these traits, suggesting that simple selection techniques may have limited success in improving these characteristics.

Table 1. Summary of analysis of variance (ANOVA) for grain yield and component traits of green gram germplasm accession

Sources of variation	DF	DOF	PH	NOB	NOC	NOPC	TOPP	PL	NOSP	100 SW	SPY
Block (eliminating Treatments)	8	7.35 [ns]	267.70**	0.88**	4.42*	0.83**	95.31**	0.18 [ns]	0.57 [ns]	0.24 [ns]	6.88**
Treatment: Check	9	18.62*	375.70**	1.13**	3.99*	1.76**	133.90**	1.56**	1.64**	0.96**	4.69 [ns]
Treatment: Test	449	10.06*	108.00**	0.95**	4.37**	0.90**	142.65**	10.09**	2.59**	1.20**	6.06**
Error	72	7.09	68.11	0.21	1.89	0.28	30.86	0.23	0.47	0.32	2.35

[ns] P > 0.05; * P <= 0.05; ** P <= 0.01; ns: Non-significant; Df: Degree of freedom; DOF: Days to 50% flowering; PH: Plant height; NOB: Number of branches/plant; NOC: Number of clusters/plant; NOPC: Number of pods/plant; TOPP: Number of pods/plant; PL: Pod length; NOSP: Number of seeds/pod; 100 SW: 100 test weight; SPY: seed yield/plant.

Broad sense heritability (h²)

Heritability values ranged from DOF (29.53%) to 9.68% for PL. The highest heritability estimates were observed for traits such as PL (97.68%), NOSP (82.01%), TOPP (78.37%), NOB (78.14%), 100 SW (73.19%), NOPC (68.81%) and SPY (61.22%). Moderate heritability was noted for NOC (56.67%) and PH (36.94%), while DOF (29.53%) exhibited a low heritability range (Table 2).

Similar findings have been reported for high heritability in NOPC by (12,25), TOPP by (26), and for 100 SW TOPP (27). Additionally,(28) reported high heritability for NOB, NOPC, TOPP and SPY. For effective selection, a trait should exhibit both high heritability and significant genetic advance to ensure consistency in breeding outcomes (8). The high heritability observed suggests that additive gene effects are likely responsible for these traits, increasing the probability of successful selection. Therefore, for traits governed by additive effects, pedigree or modified pedigree selection methods are recommended for future breeding approaches.

Genetic advance (GA)

The examination of genetic advance for all the quantitative traits analysed revealed values ranging from 1.35 % (NOPC) to 19.31 % (TOPP). A moderate genetic advance was observed for TOPP (19.31%), a result also reported by (28).

In contrast, other traits exhibited lower genetic advances, such as PH (7.92%), PL (6.40%), SPY (3.11%), NOSP (2.72%), NOC (2.44%), DOF (1.93%), 100 SW (1.66%), NOB (1.57%) and NOPC (1.35%) (Table 2). These results are consistent with previous studies (29) on DOF, PL and 100 SW. For traits like PH and NOB, similar findings were observed in the study by (30).

Genetic advance as percent of mean (GAM)

An examination of the GA for each quantitative trait revealed values ranging from 5.04 % (DOF) to 84.04 % (PL). The highest genetic advance was observed for traits such as PL (84.04%), NOB (83.79%), TOPP (83.79%), SPY (67.59%), 100 SW (56.63%), NOPC (43.02%), NOC (38.24%) and NOSP (25.71%). A moderate genetic advance was recorded for PH (16.32%), while DOF (5.04 %) exhibited a low genetic advance (Table 2). These findings align with previous studies by (31) for NOB and (20) for TOPP and SPY. The moderate genetic advance observed for PH is consistent with the results reported by (12,32) for TOPP.

The combination of high heritability with both the highest and lowest genetic advances was noted in traits such as NOPC, TOPP, PL, NOSP, 100 SW and SPY. Similar results were reported in studies by (33) for TOPP, (34) for NOB and (35) for SPY. Traits like NOPC and SPY showed comparable findings in the study by (22).

Table 2. Assessment of Variability, Heritability, and Genetic Advance for Different Traits in green gram germplasm accessions.

Trait	Coefficient of variation			h² (%)	GA (%)	GAM (%)	Mean	CV (%)
	PCV%	GCV%	ECV%					
DOF	8.28	4.50	6.95	29.53	1.93	5.04	38.32	7.02
PH	21.42	13.02	17.01	36.94	7.92	16.32	48.52	16.80
NOB	51.97	45.94	24.30	78.14	1.57	83.79	1.87	24.49
NOC	32.71	24.62	21.53	56.67	2.44	38.24	6.39	21.72
NOPC	30.30	25.14	16.92	68.81	1.35	43.02	3.14	16.53
TOPP	51.82	45.87	24.10	78.37	19.31	83.78	23.05	23.59
PL	41.70	41.22	6.36	97.68	6.40	84.04	7.62	6.34
NOSP	15.20	13.76	6.45	82.01	2.72	25.71	10.59	6.40
100 SW	37.51	32.09	19.42	73.19	1.66	56.63	2.92	19.03
SPY	53.52	41.88	33.33	61.22	3.11	67.59	4.60	31.46

DOF: Days to 50% flowering; PH: Plant height; NOB: Number of branches/plant; NOC: Number of clusters/plant; NOPC: Number of pods/plant; TOPP: Number of pods/plant; PL: Pod length; NOSP: Number of seeds/pod; 100 SW: 100 test weight; SPY: seed yield/plant.
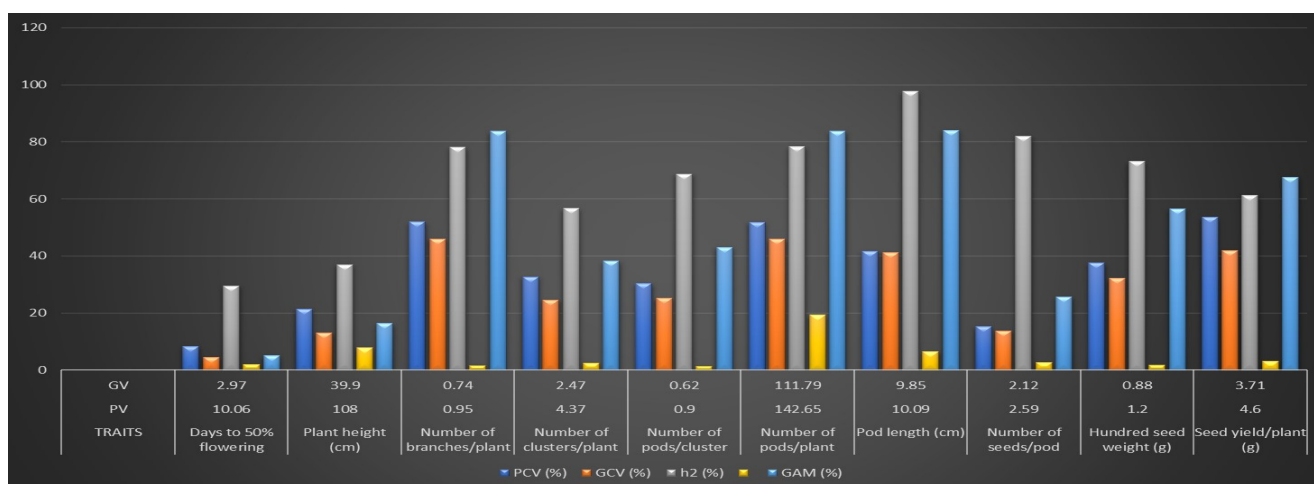

Fig. 2. Graphical representation of genetic variability for different traits in green gram germplasm

Conclusion

A wide range of variability was observed across all traits among the germplasm utilized in this study, indicating significant differences among them. The results suggest that traits showing high PCV, GCV, heritability and genetic advance as a percentage of the mean, *i.e.,* number of branches (NOB), number of clusters (NOC), number of pods (TOPP), pod length (PL), test weight (100 SW) and seed yield/plant (SPY), should be prioritized in future selection processes. Therefore, this germplasm can be effectively utilized for crop improvement strategies. The insights gained from this study will inform the development of future breeding programs focused on incorporating traits such as disease resistance and increased yield in green gram.

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Authors' contributions

SSM carried out variability studies, and manuscript drafting. YA made corrections and revised the manuscript. SSM performed statistical analysis. VC, MC & RR suggested with some comments and supervised. All authors contributed to the article and approved the submitted version.

Compliance with ethical standards

Conflict of interest: The authors declare that there are no conflicts of interest associated with this research.

Ethical issues: None

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