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Genetic variability, heritability and genetic advance for yield and its component traits in green gram (*Vigna Radiata* L. wilczek)

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Abstract

The present investigation was undertaken to assess genetic variability, heritability, and genetic advance for yield and its component traits in green gram (*Vigna radiata* L. Wilczek). The experiment was conducted during the Kharif season of 2025 at the Research Farm, Department of Genetics and Plant Breeding, AKS University, Satna, Madhya Pradesh. Thirty green gram genotypes were evaluated in a Randomized Block Design with three replications under recommended agronomic practices. Observations were recorded on eleven quantitative characters, namely days to first flowering, days to 50% flowering, number of primary branches per plant, pod length, number of clusters per plant, number of pods per plant, number of seeds per pod, 100-seed weight, biological yield per plant, harvest index, and seed yield per plant. Genetic variability was assessed using genotypic and phenotypic coefficients of variation, while heritability (broad sense) and genetic advance were estimated to determine the effectiveness of selection. The study was designed to identify traits exhibiting substantial genetic variability and favorable inheritance patterns that could be utilized for the improvement of seed yield in green gram breeding programmes. The information generated from this investigation provides a basis for selecting superior genotypes and identifying promising yield-contributing characters for future crop improvement.

Keywords: Green gram, *vignaradiata*, genetic variability, heritability, genetic advance, seed yield, quantitative traits, plant breeding

Introduction

Green gram (*Vigna radiata* L. Wilczek), commonly known as mung bean or moong, is one of the most important pulse crops cultivated in tropical and subtropical regions of the world. It is valued for its short growth duration, high nutritional quality, easy digestibility, and ability to improve soil fertility through biological nitrogen fixation. The crop contains approximately 24-25% protein and serves as an economical source of dietary protein, vitamins, and minerals, particularly in vegetarian diets. Owing to its adaptability to diverse agro-climatic conditions and suitability for multiple cropping systems, green gram plays a significant role in sustainable agriculture and food security.

India is the largest producer and consumer of green gram, where the crop is cultivated extensively in states such as Madhya Pradesh, Maharashtra, Rajasthan, Uttar Pradesh, Karnataka, and Andhra Pradesh. Despite its economic and nutritional importance, the productivity of green gram remains comparatively low due to the narrow genetic base of cultivated varieties, susceptibility to biotic and abiotic stresses, and the complex inheritance of seed yield. Therefore, the development of high-yielding cultivars possessing desirable agronomic traits is a major objective of green gram improvement programmes.

Seed yield is a complex quantitative character governed by the combined effects of several yield-contributing traits and influenced by both genetic and environmental factors. Consequently, the success of any breeding programme largely depends on the availability of sufficient genetic variability in the breeding material. Assessment of genetic variability provides information on the extent of existing variation among genotypes and helps breeders identify promising traits for selection. Parameters such as the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are widely used to estimate the magnitude of variability present in different quantitative characters. Heritability is an

important genetic parameter that measures the proportion of phenotypic variation attributable to genetic factors. However, heritability alone is not an adequate criterion for effective selection because it does not indicate the expected improvement through selection. Therefore, heritability is commonly interpreted together with genetic advance, which predicts the expected gain from selection. High heritability associated with high genetic advance generally indicates the predominance of additive gene action and suggests that selection based on phenotypic performance would be effective for genetic improvement.

The identification of traits exhibiting substantial genetic variability, high heritability, and high genetic advance is essential for developing efficient breeding strategies aimed at improving seed yield and related characters in green gram. Such information enables plant breeders to select superior genotypes and utilize them effectively in hybridization and selection programmes.

In view of the importance of genetic variability and inheritance studies, the present investigation was undertaken during the Kharif season of 2025 at the Research Farm, Department of Genetics and Plant Breeding, AKS University, Satna (Madhya Pradesh). Thirty green gram genotypes were evaluated under a Randomized Block Design with three replications to estimate genetic variability, heritability, and genetic advance for yield and its component traits. The information generated from this study is expected to contribute to the identification of promising breeding materials and to facilitate the development of high-yielding green gram cultivars.

Materials and Methods

Experimental Site

The present investigation was conducted during the Kharif 2025 season at the Research Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, AKS University, Sherganj, Satna, Madhya Pradesh, India. The experimental farm is situated at 24°58' N latitude and 80°83' E longitude, at an altitude of approximately 322 m above mean sea level. The region falls under the semi-arid subtropical agro-climatic zone and experiences hot summers, moderate monsoon rainfall, and cool winters.

Experimental Material

The experimental material comprised 30 genetically diverse green grams (*Vigna radiata* L. Wilczek) genotype obtained from the Department of Genetics and Plant Breeding, AKS University, Satna. The genotypes represented diverse genetic backgrounds and were evaluated for genetic variability and yield-related traits.

Experimental design and crop management

The experiment was laid out in a Randomized Block Design (RBD) with three replications. Each replication consisted of thirty experimental plots representing the thirty genotypes. Individual plots measured 1.20 × 2.00 m, maintaining a spacing of 40 cm between rows and 20 cm between plants. A total of 90 plots were maintained with an overall plant population of approximately 2700 plants.

A recommended fertilizer dose of 20:40:20 kg N:P₂O₅:K₂O ha⁻¹ was applied. All recommended agronomic practices, including irrigation, intercultural operations, weed management, and plant protection measures, were followed uniformly throughout the crop growth period to ensure

healthy crop establishment and minimize environmental variation.

Data recording

Observations were recorded on five randomly selected competitive plants from each plot, excluding border plants, to minimize experimental error. Data were collected for the following eleven quantitative characters:

1. Days to first flowering
2. Days to 50% flowering
3. Number of primary branches per plant
4. Pod length (cm)
5. Number of clusters per plant
6. Number of pods per plant
7. Number of seeds per pod
8. 100-seed weight (g)
9. Biological yield per plant (g)
10. Harvest index (%)
11. Seed yield per plant (g)

The mean values of five plants were used for statistical analysis.

Statistical analysis

Analysis of variance (ANOVA) was carried out according to the procedure described by Pandey and Sukhumi (1985) to determine the significance of difference among the types.

The extent of genetic variability was estimated through the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) following the method of Burton and De Vane (1953) [2]. Broad-sense heritability was computed according to Hanson *et al.* (1956) [4], while the expected genetic advance under selection and genetic advance as a percentage of mean were estimated using the procedure suggested by John *et al.* (1955).

These genetic parameters were used to assess the magnitude of variability and to identify traits governed predominantly by additive gene action for effective selection in green gram breeding programmes.

Results and Discussion

Genetic variability, heritability and genetic advance

The estimates of genetic parameters, including grand mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), environmental coefficient of variation (ECV), and coefficient of variation (CV), for eleven quantitative characters are presented in Table 4.1. The analysis revealed the existence of considerable variability among the thirty green gram genotypes for all the characters studied, indicating ample scope for selection and genetic improvement.

The phenotypic coefficient of variation (PCV) was consistently higher than the corresponding genotypic coefficient of variation (GCV) for all the characters, suggesting that environmental factors contributed to the expression of these traits. However, the relatively narrow differences between PCV and GCV for most characters indicated that the environmental influence was comparatively low and that the observed variability was predominantly genetic in nature. Similar observations have been reported by Mohammed *et al.* (2020) [10], Karthik *et al.* (2022) [7], Kumar *et al.* (2022) [9], Navya *et al.* (2023) [11], Jain *et al.* (2024) [15], and Sharma *et al.* (2024) [14].

Among the eleven characters, the highest GCV was recorded for number of pods per plant (23.64%), followed by biological yield per plant (22.34%), seed yield per plant (21.85%), 100-seed weight (19.82%), and number of clusters per plant (18.46%). These traits also exhibited correspondingly high PCV values of 26.21%, 24.81%, 23.52%, 20.74%, and 21.17%, respectively. The high magnitude of GCV and PCV indicates the presence of substantial genetic variability and suggests that these traits possess considerable potential for improvement through direct selection. Similar findings have been reported by Wesly *et al.* (2020), Karthik *et al.* (2022) [7], Kumar *et al.* (2022) [9], Navya *et al.* (2023) [11], Jain *et al.* (2024) [5], and Rai *et al.* (2026) [13]. Moderately high GCV values were observed for number of primary branches per plant (15.62%), number of seeds per pod (10.75%), days to 50% flowering (9.86%), harvest index (9.56%), and days to first flowering (8.72%). Their corresponding PCV values ranged from 11.32% to 17.48%, indicating moderate variability coupled with a limited environmental influence. These results suggest that sufficient genetic variation exists for these characters and that improvement through selection is feasible. Similar trends were reported by Abhisheka and Mogali (2020) [1], Mohammed *et al.* (2020) [10], Kumar *et al.* (2022) [9], and Sharma *et al.* (2024) [14].

The lowest GCV (7.84%) and PCV (8.41%) were observed for pod length, indicating comparatively lower variability for this trait. Nevertheless, the narrow difference between GCV and PCV suggests that pod length is less affected by environmental conditions and can be effectively improved through careful selection. Similar observations were documented by Talukdar *et al.* (2020) and Karthik *et al.* (2022) [7]. The environmental coefficient of variation (ECV) was relatively low for pod length (2.95%), days to first flowering (2.98%), number of seeds per pod (3.54%), and days to 50% flowering (4.32%), indicating minimal environmental influence on the expression of these traits.

Conversely, relatively higher ECV values were recorded for number of pods per plant (11.98%), biological yield per plant (10.79%), and number of clusters per plant (10.38%), suggesting a comparatively greater environmental contribution. Nevertheless, the predominance of genetic variability over environmental variability for these traits indicates their suitability for selection.

The coefficient of variation at the 5% level ranged from 3.05% for number of seeds per pod to 15.09% for number of clusters per plant. The comparatively low experimental coefficients of variation observed for most characters demonstrate good experimental precision and indicate that the data generated during the investigation were reliable.

Overall, the present investigation demonstrated substantial genetic variability among the evaluated green gram types. Traits such as number of pods per plant, biological yield per plant, seed yield per plant, 100-seed weight, and number of clusters per plant exhibited high genetic variability and therefore represent promising selection criteria for yield improvement. The comparatively narrow differences between GCV and PCV across all traits further indicate that phenotypic performance is a dependable indicator of genotypic potential. Consequently, these traits may be effectively utilized in breeding programmes aimed at developing high-yielding green gram cultivars.

The present findings are in close agreement with those reported by Mohammed *et al.* (2020) [10], Wesly *et al.* (2020) [16], Dhunde *et al.* (2021) [3], Karthik *et al.* (2022) [7], Kumar *et al.* (2022) [9], Navya *et al.* (2023) [11], Jain *et al.* (2024) [5], Sharma *et al.* (2024) [14], Srivastava *et al.* (2025) [15], Khot *et al.* (2025) [8], and Rai *et al.* (2026), who also report ed high estimates of GCV and PCV for seed yield, pods per plant, biological yield, and related yield-contributing traits, indicating the predominance of additive gene action and the effectiveness of direct phenotypic selection for the improvement of green gram.

Table 1: Mean, Range, Genotypic, Phenotypic, environmental variances, and coefficient of variation for eleven quantitative characters in green gram

S. N.	Characters	Grandmean	Range		GCV	PCV	ECV	CV@5%
			Min.	Max.				
1	Days to 1 st flowering	36.97	34	40	8.72	9.15	2.98	4.73
2	Days to 50% flowering	40.97	38	44	9.86	10.54	4.32	7.12
3	Number of primary branches/plants	4.98	4.2	5.7	15.62	17.48	7.26	10.28
4	Pod length (cm)	9.12	8.4	9.8	7.84	8.41	2.95	3.89
5	Number of clusters per plants,	13.05	11.2	15	18.46	21.17	10.38	15.09
6	Number of pods per plants,	31.48	27.2	35.8	23.64	26.21	11.98	14.85
7	Number of Seed/pods	12.18	11	13.4	10.75	11.32	3.54	3.05
8	100 seed Weight (g)	43.57	40.6	46.4	19.82	20.74	6.15	3.13
9	Biological Yield (g)	31.42	27.3	35.8	22.34	24.81	10.79	7.02
10	Harvest index	38.31	35.8	40.7	9.56	10.84	5.1	6.88
11	Seed yield per plant (g)	12.11	9.8	14.5	21.85	23.52	8.72	7.31

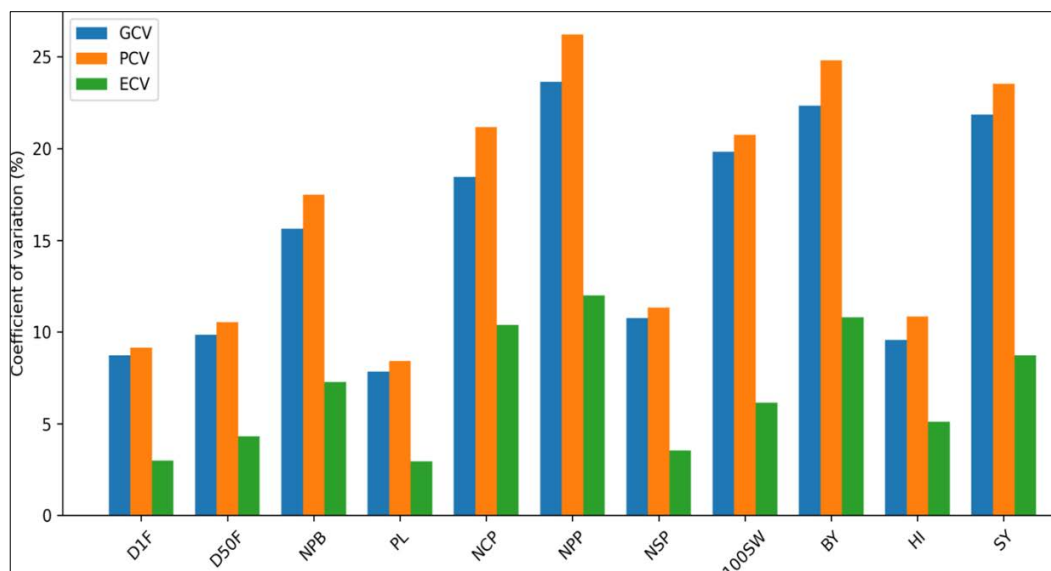


Fig 1: Genotypic, phenotypic, and environmental variances, and coefficients of variation for eleven quantitative characters in greengram

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