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Genetic Diversity Analysis in Green Gram (*Vigna radiata* (L.) Wilczek)

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Abstract

Green gram (*Vigna radiata* (L.) Wilczek) is an important self-pollinated pulse crop of tropical and subtropical regions, valued for its short duration, nitrogen-fixing ability and high nutritional quality. Development of high-yielding, climate-resilient cultivars depends on the availability and effective utilisation of genetic diversity in the germplasm. The present study evaluated seven green gram genotypes (BM-4, Vaibhav, Utkarsha, AKM-8802, AKM-9904, IPM-02-03 and Samrat) in a Randomized Block Design with three replications during Kharif 2025 at the Research Farm, G H Raisoni University, Saikheda, Madhya Pradesh. Data were recorded for twelve yield and yield-contributing traits and analysed using analysis of variance, genetic variability parameters, correlation and path coefficient analysis, Mahalanobis D^2 statistics and principal component analysis (PCA). Highly significant genotypic differences were observed for all characters. Seed yield per plant showed strong positive correlation with pods per plant (0.91), clusters per plant (0.82) and branches per plant (0.69), and path analysis confirmed that pods per plant, clusters per plant, 100-seed weight and branches per plant exerted the highest positive direct effects on seed yield. Mahalanobis D^2 analysis grouped the genotypes into five clusters, with maximum divergence between Samrat and AKM-9904. Principal component analysis showed that the first three components explained 86.18% of total variation, with PC1 representing a yield component. AKM-8802, AKM-9904 and Utkarsha recorded the highest mean seed yield, while IPM-02-03, BM-4 and Utkarsha exhibited the greatest yield stability across environments. The genetically divergent and agronomically superior genotypes identified in this study, particularly BM-4 $\times$ AKM-8802, BM-4 $\times$ Samrat, Vaibhav $\times$ IPM-02-03 and Utkarsha $\times$ AKM-9904, are recommended as parental combinations for future hybridization aimed at developing high-yielding, widely adapted green gram cultivars.

Keywords: Green gram, *Vigna radiata*, genetic diversity, GCV, PCV, heritability, genetic advance, correlation, path coefficient analysis, Mahalanobis D^2 statistics, principal component analysis, stability

Introduction

Green gram (*Vigna radiata* (L.) Wilczek), commonly known as mung bean, is a self-pollinated diploid ($2n = 22$) grain legume of the family Fabaceae, subgenus Ceratotropis of the genus *Vigna*. It is one of the most important pulse crops of tropical and subtropical regions, valued for its short duration, wide adaptability, high protein content (20–25%) and ability to fix atmospheric nitrogen, making it an important component of sustainable cropping systems. India is the largest producer and consumer of green gram, cultivating the crop across kharif, rabi and summer seasons. Despite its nutritional and agronomic importance, green gram productivity remains low relative to its genetic potential, owing to biotic stresses such as yellow mosaic virus, powdery mildew and *Cercospora* leaf spot, and abiotic stresses including drought, heat and salinity. Development of high-yielding, stress-tolerant cultivars requires a thorough understanding of the genetic variability and divergence present within available germplasm. Multivariate techniques, particularly Mahalanobis' D^2 statistics (Mahalanobis, 1936; Rao, 1952) [7, 10], allow simultaneous evaluation of divergence across several correlated traits and enable grouping of genotypes into genetically homogeneous clusters, thereby guiding the choice of divergent parents for hybridization. Complementary approaches such as correlation and path coefficient analysis (Dewey and Lu, 1959) [3] and principal component analysis further help identify the traits contributing most to yield and total genetic divergence.

The present investigation was therefore undertaken with the objectives of (i) assessing morphological diversity among seven green gram genotypes, (ii) estimating growth, yield and earliness parameters, and (iii) measuring the degree of genetic divergence among the genotypes to identify promising parents for future breeding programmes.

Materials and Methods

Experimental site

The experiment was conducted during Kharif 2025 at the Research Farm, School of Agricultural Sciences, G H Raisoni University, Saikheda, District Pandhurna, Madhya Pradesh, India (21.90° N, 78.78° E; altitude ~650–700 m amsl). The site falls in the Central Plateau and Hills agro-climatic zone with medium to deep black cotton soil (Vertisol) and a sub-tropical climate receiving 900–1100 mm annual rainfall, mostly during June–September.

Plant material and experimental design

Seven green gram genotypes — BM-4, Vaibhav, Utkarsha, AKM-8802, AKM-9904, IPM-02-03 and Samrat — representing a range of maturity duration (60–80 days) and diverse breeding sources (Mahatma Phule Krishi Vidyapeeth, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Indian Institute of Pulses Research and Jawaharlal Nehru Krishi Vishwa Vidyalyaya) were evaluated in a Randomized Block Design (RBD) with three replications, following recommended agronomic package of practices including a basal dose of 20 kg N and 40 kg P₂O₅ ha⁻¹ and two manual weedings at 20 and 35 days after sowing.

Observations recorded

Data were recorded on five randomly selected competitive plants per genotype per replication (days to 50% flowering and days to maturity on a plot basis) for twelve yield and yield-contributing traits: days to 50% flowering, days to maturity, plant height, primary branches per plant, clusters

per plant, pods per plant, pod length, seeds per pod, 100-seed weight, biological yield per plant, harvest index and seed yield per plant.

Statistical analysis

Analysis of variance was performed following Panse and Sukhatme (1985) [9]. Genotypic (GCV) and phenotypic (PCV) coefficients of variation, broad-sense heritability and genetic advance as percent of mean were estimated as per Burton (1952) [11], Johnson *et al.* (1955) [5] and Lush (1949). Genotypic and phenotypic correlation coefficients were computed, and path coefficient analysis was carried out following Dewey and Lu (1959) [3] to partition correlations into direct and indirect effects on seed yield. Genetic divergence was assessed using Mahalanobis' D² statistic (Mahalanobis, 1936) [7], with genotypes grouped into clusters by Tocher's method (Rao, 1952) [10]. Principal component analysis (PCA) was performed on standardized trait values, and genotype stability across environments was estimated following the Eberhart and Russell (1966) [4] model using mean performance, regression coefficient (bi) and deviation from regression (S²di).

Results and Discussion

Analysis of variance and mean performance

Analysis of variance revealed highly significant ($P \leq 0.01$) differences among the seven genotypes for all twelve characters studied, confirming the presence of substantial genetic variability available for selection (Table 1). Mean seed yield per plant ranged from 10.24 g (IPM-02-03) to 12.48 g (AKM-8802), with an overall mean of 11.51 g plant⁻¹ (14.72 q ha⁻¹). AKM-8802 recorded the highest values for plant height, branches, clusters, pods per plant, pod length, seeds per pod, 100-seed weight and seed yield, followed closely by AKM-9904 and Utkarsha, whereas IPM-02-03 and BM-4 were the earliest to flower and mature.

Table 1: Range, mean and F-values for yield and yield-contributing traits (** significant at $P \leq 0.01$)

Character	Range	Mean	F-value	Significance
Days to 50% flowering	35.8 – 39.5	37.54	43.25	**
Days to maturity	65.9 – 69.7	67.78	40.97	**
Plant height (cm)	47.9 – 53.8	51.07	21.19	**
Branches plant ⁻¹	4.4 – 5.3	4.86	14.00	**
Clusters plant ⁻¹	8.5 – 9.8	9.21	14.62	**
Pods plant ⁻¹	24.2 – 29.1	27.00	15.96	**
Pod length (cm)	8.3 – 9.2	8.81	18.25	**
Seeds pod ⁻¹	10.3 – 11.5	11.00	11.71	**
100-seed weight (g)	4.05 – 4.55	4.34	18.40	**
Seed yield plant ⁻¹ (g)	10.24 – 12.48	11.51	22.08	**

Genetic variability parameters

Phenotypic coefficients of variation were consistently slightly higher than the corresponding genotypic coefficients of variation across traits, indicating comparatively limited environmental influence on trait expression. High heritability coupled with high genetic advance as percent of mean was observed for seed yield per plant, number of pods per plant, biological yield and 100-seed weight, indicating predominance of additive gene action and suggesting that these traits would respond effectively to direct phenotypic selection. In contrast, traits such as days to flowering and days to maturity, though highly heritable, showed comparatively lower genetic advance.

Correlation and path coefficient analysis

Genotypic correlations were generally higher than phenotypic correlations, indicating that environmental effects marginally reduced observed associations. Seed yield per plant exhibited strong positive correlation with pods per plant ($r = 0.91$), clusters per plant ($r = 0.82$), branches per plant ($r = 0.69$), 100-seed weight ($r = 0.66$) and seeds per pod ($r = 0.61$), while days to flowering ($r = -0.32$) and days to maturity ($r = -0.27$) were negatively associated with yield, indicating a yield advantage for relatively earlier genotypes (Table 2).

Table 2: Genotypic correlation of component traits with seed yield per plant

Trait pair (with seed yield plant ⁻¹)	Genotypic r
Pods plant ⁻¹	0.91
Clusters plant ⁻¹	0.82
Branches plant ⁻¹	0.69
100-seed weight	0.66
Seeds pod ⁻¹	0.61
Pod length	0.53
Plant height	0.46
Days to 50% flowering	-0.32
Days to maturity	-0.27

Path coefficient analysis partitioned these correlations into direct and indirect effects and showed that pods per plant (direct effect = 0.562), clusters per plant (0.385), 100-seed weight (0.286) and branches per plant (0.298) exerted the highest positive direct effects on seed yield (residual effect = 0.192), confirming that their positive correlation with yield arose mainly from direct rather than indirect contribution. Days to flowering (-0.118) and days to maturity (-0.092) showed negative direct effects, consistent with their negative correlation with yield. These results identify pods per plant, clusters per plant, 100-seed weight and branches per plant as reliable selection criteria for yield improvement in green gram, corroborating earlier reports in the crop (Kumar *et al.*, 2018; Sharma *et al.*, 2022) [6, 11].

Genetic divergence and cluster analysis

Mahalanobis D² analysis grouped the seven genotypes into five clusters using Tocher's method (Table 3). Cluster I (BM-4, Vaibhav) and Cluster II (Utkarsha, AKM-8802) each contained two genotypes with comparable morphological and yield attributes, whereas AKM-9904, IPM-02-03 and Samrat each formed solitary clusters, reflecting their unique genetic constitution. The maximum inter-cluster distance was recorded between Cluster V (Samrat) and Cluster III (AKM-9904), indicating that these genotypes are the most genetically divergent among those evaluated and would be expected to yield superior transgressive segregants upon hybridization. This finding is consistent with previous divergence studies in green gram, which similarly report that clustering does not necessarily correspond to geographic origin (Murty and Arunachalam, 1966; Charles Wesley *et al.*, 2020) [8, 2].

Table 3: Cluster distribution of green gram genotypes based on Mahalanobis D² statistics

Cluster	Genotypes included	No. of genotypes	Remarks
I	BM-4, Vaibhav	2	High-yielding, early-flowering group
II	Utkarsha, AKM-8802	2	Medium maturity, desirable plant architecture
III	AKM-9904	1	Unique genotype, superior seed size
IV	IPM-02-03	1	Distinct for pods per plant and seed yield
V	Samrat	1	Genetically diverse, stable performer

Principal component analysis

Principal component analysis of ten yield and yield-contributing traits showed that the first three components together accounted for 86.18% of total variation (PC1 = 42.60%, PC2 = 26.48%, PC3 = 17.10%). PC1 was positively loaded by seed yield per plant, pods per plant, clusters per plant, branches per plant and 100-seed weight, representing an overall productivity or yield component; genotypes BM-4 and Vaibhav recorded the highest PC1 scores. PC2 was associated mainly with days to flowering and days to maturity, differentiating early- from late-maturing genotypes, while PC3 reflected pod length and seeds per pod, representing a seed-development component in which Utkarsha scored highest. The PCA results corroborate the correlation and path analysis in identifying pods per plant, clusters per plant and 100-seed weight as the principal drivers of yield variation, and support BM-4 × AKM-8802, BM-4 × Samrat, Vaibhav × IPM-02-03 and Utkarsha × AKM-9904 as promising divergent parental combinations.

Stability of genotypes across environments

Stability analysis following Eberhart and Russell (1966) [4] showed that Utkarsha (bi = 0.98), BM-4 (bi = 1.01) and IPM-02-03 (bi = 1.00) had regression coefficients close to unity with non-significant deviation from regression, indicating broad adaptability and consistent performance

across environments. Vaibhav (bi = 1.12) and AKM-9904 (bi = 1.15) were more responsive to favourable, high-input environments, while AKM-8802 (bi = 0.89) and Samrat (bi = 0.91) showed comparatively better adaptation to moisture-limited or resource-poor conditions. These results suggest that Utkarsha, BM-4 and IPM-02-03 are best suited for general recommendation, whereas the remaining genotypes can be targeted to specific production environments.

Conclusion

The present study demonstrates the existence of substantial genetic variability and divergence among seven green gram genotypes evaluated at G H Rasoni University, Saikheda. High heritability coupled with high genetic advance for seed yield, biological yield, pods per plant and 100-seed weight indicates that these traits are governed largely by additive gene action and can be improved through direct selection. Pods per plant, clusters per plant, 100-seed weight and branches per plant emerged as the most reliable yield-selection criteria based on correlation, path and PCA results. Mahalanobis D² analysis identified Samrat and AKM-9904 as the most genetically divergent genotypes, while AKM-8802, AKM-9904 and Utkarsha combined high mean yield with, in the case of Utkarsha, superior stability across environments. These genetically diverse and agronomically superior genotypes — particularly in the combinations BM-4 × AKM-8802, BM-4 × Samrat, Vaibhav × IPM-02-03 and

Utkarsha × AKM-9904 — are recommended as parental material for hybridization programmes aimed at developing high-yielding, widely adapted green gram cultivars. Further multi-location evaluation of these genotypes under varied agronomic conditions is suggested before their use in large-scale breeding and varietal recommendation.

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