

International Journal of Plant & Soil Science

Volume 38, Issue 11, Page 134-141, 2026; Article no.IJPSS.169342
ISSN: 2320-7035

Assessment of Genetic Divergence and Yield-related Traits in Green Gram (*Vigna radiata* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: https://doi.org/10.9734/ijpss/2026/v38i116409

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://pr.sdiarticle5.com/review-history/169342

Original Research Article

Received: 04/09/2026
Accepted: 31/10/2026
Published: 03/11/2026

Abstract

Green gram is an important pulse crop, but the identification of diverse parental material remains relevant to improving yield-related traits. This investigation assessed genetic divergence among 48 green gram genotypes using 15 quantitative characters, including seed yield per plant. The genotypes were evaluated in a randomised block design with three replications at B. N. College of Agriculture, Assam Agricultural University, Biswanath Chariali. Observations were obtained from five randomly selected plants per replication, and divergence was assessed using Mahalanobis D^2 statistics and Tocher's clustering method. The genotypes were grouped into six clusters. Cluster III contained the largest number of genotypes (19), followed by cluster IV (16), cluster II (8), cluster I (3) and clusters V and VI (one each). The greatest intra-cluster distance was recorded in cluster IV (144.76), whereas the largest inter-cluster distance occurred between clusters I and V (301.82). Seeds per pod contributed most to divergence (27.93%), followed by 100-seed weight (20.45%); together, these traits accounted for 48.38% of the total. Cluster VI recorded the highest mean seed yield per plant (54.81), while cluster V had the highest mean number of seeds per pod (12.00). These findings identify

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Cite as: *Doley, R., Zaman, S., Sarma, M. K., Bhuyan, J., Das, D. P., & Borah, S. R. (2026). Assessment of Genetic Divergence and Yield-related Traits in Green Gram (Vigna radiata L.). International Journal of Plant & Soil Science, 38(11), 134–141. https://doi.org/10.9734/ijpss/2026/v38i116409*

contrasting clusters and yield-related traits that may inform preliminary parent selection. However, the performance of proposed crosses requires further evaluation before their breeding value can be established.

Keywords: Green gram; genetic divergence; Mahalanobis D² statistic; Tocher's method; cluster analysis; yield components.

1. Introduction

Green gram [*Vigna radiata* (L.) Wilczek], commonly known as mung bean or moong bean, is an important self-pollinated legume belonging to the family Fabaceae, with a diploid chromosome number of 2n = 22. It is valued for its short growth duration, adaptability to diverse growing conditions and high nutritional value. Its seeds contain approximately 24% protein and 63% carbohydrates, along with essential minerals such as iron and zinc, making it an important component of human nutrition (Nair *et al.,* 2013).

In addition to its nutritional significance, green gram contributes to sustainable agriculture through biological nitrogen fixation and its suitability for crop rotation and intercropping systems (Nair *et al.,* 2019). However, its productivity is constrained by various biotic and abiotic stresses, inadequate availability of quality seeds and limited adoption of improved varieties. These constraints emphasize the need to develop high-yielding and widely adapted genotypes to enhance crop productivity (Nair *et al.,* 2019).

The evaluation and characterisation of available germplasm for genetic variability and divergence constitute essential steps in crop improvement (Degefa *et al*., 2014). Assessing the extent of genetic diversity and determining the contribution of individual traits to overall divergence provide valuable information for identifying superior genotypes and selecting diverse parents for hybridization. Mahalanobis' D^2 statistic is widely used to estimate genetic divergence based on multiple quantitative characters (Mahalanobis, 1936), while Tocher's method facilitates the grouping of genotypes into distinct clusters (Rao, 1952). Furthermore, assessing intra- and inter-cluster distances and the contribution of individual characters to divergence can assist in formulating effective breeding strategies (Singh & Chaudhary, 1985). Thus, the continuous development and adoption of improved varieties are necessary to address emerging production challenges and sustain crop productivity. Studies applying multivariate clustering to mungbean germplasm have reported differences in cluster composition and in the relative contributions of yield-associated traits across the collections examined (Yadav *et al*., 2024; Saini *et al*., 2026). These observations reinforce the need to interpret divergence estimates in relation to the particular genotypes and quantitative characters evaluated.

Recent assessments of mungbean germplasm indicate that phenotypic characterisation can distinguish accessions with contrasting agronomic characteristics, while molecular analyses provide additional evidence about genetic relationships. In an SSR-based assessment, local mungbean collections were more diverse than the released varieties included in the study, suggesting that underutilized germplasm may broaden the parental pool (Gayacharan *et al*., 2025). A separate investigation using both morphological and molecular markers also demonstrated the value of considering complementary sources of diversity information in mungbean improvement (Gull *et al*., 2025).

Genome-wide association analysis has identified genetic markers associated with phenological and yield-related agronomic traits in mungbean, providing a possible link between conventional phenotypic evaluation and molecular breeding approaches (Manjunatha *et al*., 2023). Moreover, a multi-environment study combining agronomic characters with SSR markers identified differentiated mungbean groups and promising breeding material (Rohilla *et al*., 2026). These findings support multivariate characterization as an initial step in parent selection, although the usefulness of selected combinations must subsequently be assessed through crossing and progeny evaluation. A recent multivariate assessment identified variation in flowering, maturity and seed-related traits among mungbean genotypes (Irfan *et al*., 2025). Multi-environment evaluation has also demonstrated that genotype-by-environment interactions influence yield-related performance (Sodedji *et al*., 2026), while genome-wide association analysis has identified loci associated with phenological and yield traits (Zaman *et al*., 2026). Together, these studies provide complementary contexts for interpreting phenotypic diversity without replacing germplasm-specific divergence analysis.

However, the pattern of genetic divergence and the relative contributions of the 15 quantitative characters have not yet been established for the 48 green gram genotypes examined in the present investigation. Characterising this particular collection is therefore necessary to identify contrasting groups and informative yield-related traits for preliminary parental selection.

Therefore, the present investigation was undertaken to assess the magnitude of genetic diversity among green gram genotypes, classify them into distinct clusters and determine the contribution of individual characters towards genetic divergence, thereby providing a basis for selecting suitable genotypes for future breeding programmes.

2. Materials and Methods

2.1 Experimental Design and Observations

The experiment was conducted at the experimental field of B. N. College of Agriculture, Assam Agricultural University, Biswanath Chariali, using 48 green gram genotypes procured from NBPGR, New Delhi, in a randomised block design (RBD) with three replications and a spacing of 30 cm × 10 cm. Recommended cultural practices were followed for irrigation, weeding and fertilisation.

Observations were recorded for 15 quantitative traits from five randomly selected plants in each replication. The mean values of the five plants for each trait were used for statistical analysis. The traits studied included days to initial flowering, days to 50%

flowering, plant height, number of primary branches per plant, days to initial maturity, days to 50% maturity, number of clusters per plant, number of pods per cluster, pod length, number of pods per plant, number of seeds per pod, fruit-setting capacity, 100-seed weight, seed yield per plant and harvest index.

2.2 Statistical Analysis

Data were processed using INDOSTAT software.
Genotypes were grouped into clusters based on their D^2 values using Tocher's method, as described by Rao (1952). The average intra- and inter-cluster distances were calculated from the squared D^2 values of all possible genotype pairs within each cluster, following Singh and Chaudhary (1985).

3. Results and Discussion

3.1 Genetic Diversity Present in the Genotypes with Respect to the Traits under Study

In the present investigation, 48 green gram genotypes were distributed among six clusters (Table 1; Fig. 1). The largest number of genotypes was observed in cluster III (19), followed by cluster IV (16), cluster II (8) and cluster I (3); clusters V and VI each contained one genotype. The intra-cluster distance ranged from 0 in clusters V and VI to 144.76 in cluster IV. The intra-cluster distance was zero for clusters V and VI because each consisted of a single genotype.

The minimum inter-cluster distance was recorded between clusters I and II (60.06), indicating a close relationship and similarity in most of the characters, whereas the maximum inter-cluster distance occurred between clusters I and V (301.82), indicating greater divergence between these clusters (Table 2; Fig. 2). Thus, genotypes from these clusters may be considered for intervarietal hybridisation to obtain potentially useful recombinants. These results were consistent with the reports of Gadakh *et al.* (2013) and Rekha *et al.* (2015).

The uneven distribution of accessions among clusters suggests that the germplasm evaluated here was not uniformly differentiated across the measured characters. Previous Mahalanobis D^2 analyses have likewise identified distinct groups among mungbean genotypes, although the number and composition of clusters differed between germplasm sets (Sen & De, 2017; Manivannan *et al*., 2020). The six clusters in the present experiment should therefore be interpreted as a description of this particular collection rather than a general classification of mungbean diversity.

The substantial separation between clusters I and V identifies a potentially useful contrast for selecting parents with different trait combinations. Nevertheless, large multivariate distance alone does not demonstrate heterosis or ensure desirable segregants. Integrating divergence estimates with individual trait performance and, where feasible, marker-based relationships may provide a more informative basis for prioritizing crosses (Gull *et al*., 2025; Rohilla *et al*., 2026).

Table 1. Clustering pattern of 48 green gram genotypes by Tocher's method.

Cluster	Number of entries	Genotypes
Cluster I	3	IC-76378, IC-252012, IC-2029
Cluster II	8	IC-305291, IC-305284, IC-8422, IC-1082, IC-76477, IC-472064, IC-76361, IC-76366
Cluster III	19	IC-334271, IC-763502, IC-76338, IC-472115, IC-252008, IC-76322, IC-148477, IC-76453, IC-39402, IC-76474, IC-296169, IC-39385, IC-121203, SGC-20, IC-548268, IC-39449, IC-305241, SGC-16, IC-472070
Cluster IV	16	IC-76370, IC-76414, IC-472063, IC-325853, IC-76503, IC-76464, IC-397142, IC-148500, IC-47210, IC-76476, IC-522044, IC-10187, IC-472077, IC-39603, IC-76466, IC-8915
Cluster V	1	IC-285532
Cluster VI	1	IC-76444

3.2 Contribution of Characters Towards Divergence

Among the 15 characters studied, the greatest contribution to divergence was made by seeds per pod, followed by 100-seed weight, harvest index, days to 50 *per cent* flowering, pod length, clusters per plant, pods per cluster, number of primary branches, days to initial flowering, fruit-setting capacity, plant height, days to initial maturity, pods per plant, yield per plant and days to 50 *per cent* maturity (Table 3). Major contributions of individual traits to genetic divergence in green gram were reported by Das *et al*. (2010) for seeds per pod, Panigrahi and Baisakh (2014) for 100-seed weight, and Prakash and Shekhawat (2012) for days to 50 *per cent* flowering. Therefore, characters contributing most to divergence should be considered in hybridisation programmes.

According to Table 3, seeds per pod (27.93%) and 100-seed weight (20.45%) together accounted for 48.38% of the recorded divergence, indicating that these reproductive traits were important discriminators within the present collection. However, the relative contribution of individual traits varies according to the population and characters assessed. In other mungbean studies, shelling percentage and seed yield per plant (Sen & De, 2017), or the number of branches (Manivannan *et al*., 2020), made the greatest contributions to multivariate divergence.

Yield-associated variation in pods per plant, seeds per pod and seed weight has also been described in other mungbean populations (Gull *et al*., 2025; Dhasarathan *et al*., 2026). Parental screening should therefore consider these traits alongside flowering time, maturity and yield (Manjunatha *et al*., 2023).

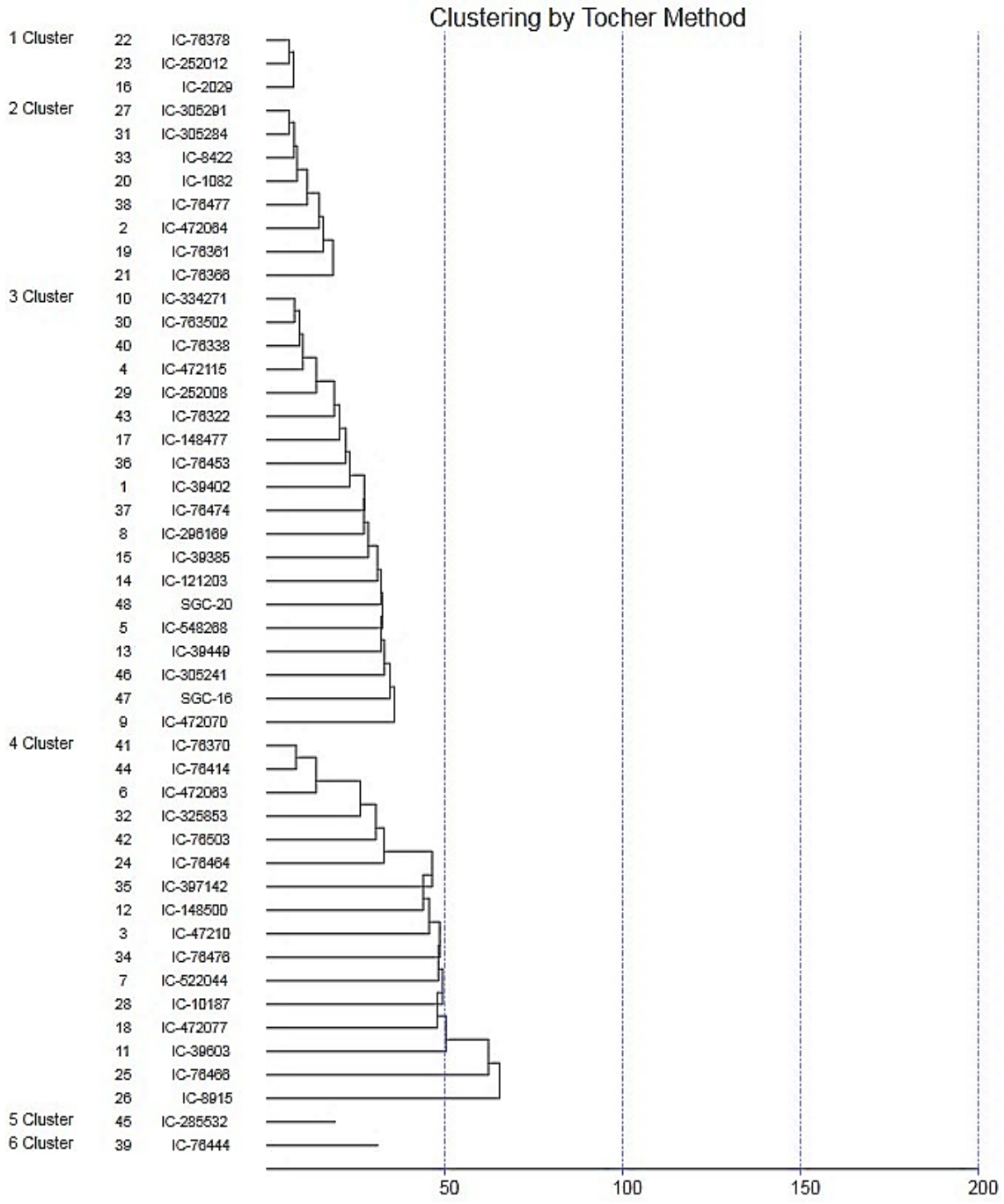


Fig. 1. Dendogram of 48 green gram genotypes based on cluster constructed by tocher's method

Table 2. Average inter and intra-cluster distances for yield and yield related characters in 48 green gram genotypes

Clusters	I	II	III	IV	V	VI
I	**25.59**	60.06	113.00	101.78	301.82	271.35
II	60.06	**44.59**	103.36	95.69	226.16	215.46
III	113.00	103.36	**84.65**	138.47	166.98	209.47
IV	101.78	95.69	138.47	**144.76**	268.51	235.90
V	301.82	226.16	166.98	268.51	**0.00**	158.06
VI	271.35	215.46	209.47	235.90	158.06	**0.00**

* *Diagonal values indicate intra-cluster distances*

* *Above and below diagonal values indicate inter-cluster distances*

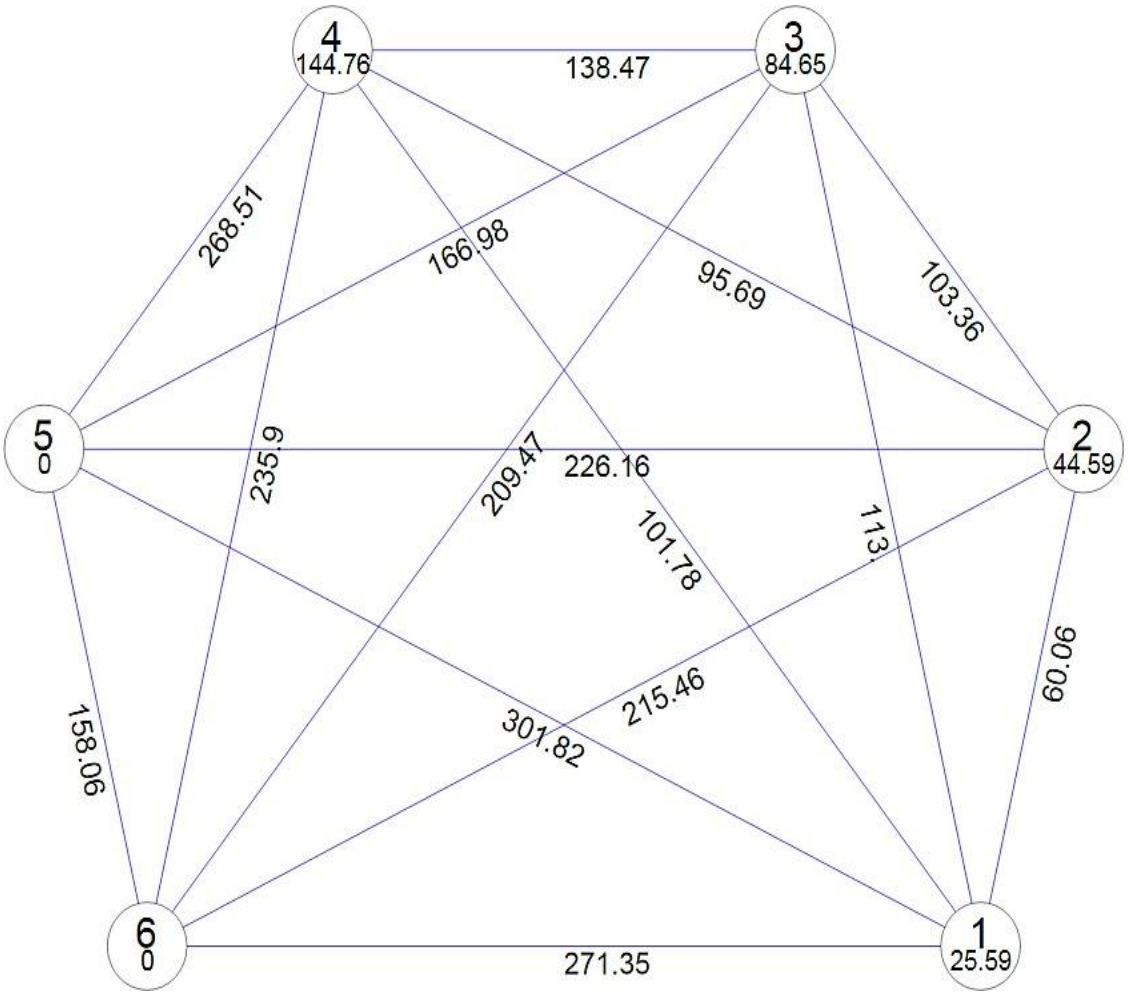


Fig 2. Mahalanobis *inter se* distance (inter and intra-cluster d² values)

Table 3. Per cent contribution of each character towards divergence in green gram genotypes evaluated in field condition.

Sl. No.	Characters	Contribution (%)
1	Days to initial flowering	3.99 %
2	Days to 50 % flowering	7.71 %
3	Plant height	2.04 %
4	Number of primary branches	4.34 %
5	Days to initial maturity	1.77 %
6	Days to 50 % maturity	0.21%
7	Number of clusters per plant	7.18 %
8	Number of pods per cluster	4.43 %
9	Pod length	7.27 %
10	Pods per plant	0.62 %
11	Seeds per pod	27.93 %
12	Fruit setting capacity	3.46 %
13	100 seed weight	20.45 %
14	Harvest Index	8.33 %
15	Yield per plant	0.27 %

3.3 Analysis of cluster means

The genotypes were grouped into six clusters, and cluster means for 15 yield-related parameters were ranked according to the desired trait values (Table 4). The cluster with the most desirable mean was assigned rank 1, followed by ranks 2, 3, 4 and so on. For days to initial flowering, days to 50 *per cent* flowering, days to initial maturity and days to 50 *per cent* maturity, the ranking was reversed, with the lowest mean assigned rank 1. Accordingly, cluster VI, with an overall score of 26.5 across the 15 characters, ranked first, indicating a comparatively favourable combination of trait means in this cluster.

Table 4. Cluster means for yield and yield related characters in 48 green gram genotypes

Clusters	DIF	D50%F	PH	PB	DIM	D50%M	C/P	P/C	PL	P/P	S/P	FSC	100SW	Y/P	HI	Overall score	Rank
I	37.56 (6)	43.00 (6)	60.44 (6)	4.27 (6)	59.56 (6)	65.56 (3)	4.24 (6)	2.47 (6)	7.02 (5)	10.60 (6)	7.78 (6)	27.08 (6)	3.21 (3)	13.12 (6)	2.67 (6)	83	6th
II	35.83 (1)	41.08 (1)	74.13 (4)	5.61 (1)	57.79 (3)	64.75 (2)	4.68 (4)	3.47 (5)	7.09 (4)	15.64 (4)	8.08 (5)	31.40 (5)	3.15 (4)	16.37 (5)	4.01 (5)	53	4th
III	37.40 (5)	42.53 (4)	77.76 (3)	5.53 (2.5)	59.49 (5)	66.09 (6)	4.44 (5)	3.56 (3)	6.77 (6)	15.14 (5)	10.20 (3)	34.17 (3)	3.25 (2)	20.47 (4)	5.02 (3)	59.5	5th
IV	36.65 (2)	42.69 (5)	73.55 (5)	5.47 (4)	59.04 (4)	65.83 (5)	5.05 (2)	3.48 (4)	7.43 (2)	16.76 (3)	8.87 (4)	32.62 (4)	3.26 (1)	21.00 (3)	4.90 (4)	52	3rd
V	37.00 (3.5)	41.67 (2)	84.33 (2)	5.13 (5)	57.67 (1.5)	65.67 (4)	4.93 (3)	4.67 (2)	7.27 (3)	21.33 (2)	12.00 (1)	37.00 (2)	2.03 (6)	20.26 (2)	5.19 (2)	41	2nd
VI	37.00 (3.5)	42.33 (3)	87.87 (1)	5.53 (2.5)	57.67 (1.5)	64.33 (1)	7.87 (1)	5.80 (1)	7.53 (1)	37.93 (1)	11.87 (2)	43.69 (1)	2.97 (5)	54.81 (1)	13.40 (1)	26.5	1st

** Figures in parenthesis, indicate the ranks based on cluster mean, highest (1) to lowest (6) except for DF and DM where the highest mean is given a score (6) and lowest mean is given a score (1). The overall score is the summation of rank number for 15 characters*

Among the 48 genotypes studied, IC-472063, belonging to cluster IV, was the earliest to attain initial flowering and 50 per cent maturity, whereas IC-305291 of cluster II was the earliest to attain 50 per cent flowering and initial maturity. Genotype IC-39402 of cluster III exhibited the greatest plant height among the genotypes. Genotype IC-76444 of cluster VI exhibited the highest values for clusters per plant, pods per cluster, pods per plant, fruit-setting capacity, 100-seed weight, yield per plant and harvest index. IC-47210 and IC-397142 of cluster IV had the greatest pod length. IC-285532 of cluster V had the highest number of seeds per pod, and IC-397142 of cluster IV had the highest 100-seed weight.

The cluster means in Table 4 show complementary trait profiles: cluster VI had the highest mean seed yield per plant (54.81), harvest index (13.40) and number of pods per plant (37.93), whereas cluster V had the highest mean number of seeds per pod (12.00). These descriptive differences suggest that parent selection may benefit from considering both divergence and yield components (Sen & De, 2017; Dhasarathan *et al*., 2026).

Clusters V and VI each comprised a single genotype, so the corresponding cluster means represent the phenotypes of individual accessions rather than averages over multiple genotypes. Their favourable values are therefore useful for preliminary prioritization but are insufficient on their own to establish stable superiority across growing environments. Additional multi-environment assessment and progeny testing would be required before making stronger breeding recommendations; complementary marker-based assessment may also help refine parental selection (Gayacharan *et al*., 2025; Rohilla *et al*., 2026).

4. Conclusion

The evaluation of 48 green gram genotypes for 15 quantitative characters revealed measurable divergence within the germplasm collection. Mahalanobis D^2 analysis separated the genotypes into six clusters, with clusters III and IV containing most of the accessions. The greatest inter-cluster distance was observed between clusters I and V, followed by those between clusters I and VI and clusters IV and V. Seeds per pod and 100-seed weight accounted for nearly half of the recorded divergence, indicating their importance in differentiating the genotypes examined. Cluster VI exhibited the highest mean seed yield per plant, harvest index and number of pods per plant, whereas cluster V had the highest mean number of seeds per pod. These differences suggest that parental selection should consider both inter-cluster divergence and the performance of individual yield-related characters. Genotypes from the more divergent clusters may be considered as candidates for crossing, provided that their agronomic attributes are suitable for the intended breeding objectives. The findings offer an initial basis for planning crosses, but the usefulness of particular combinations should be established through progeny evaluation and testing under additional growing conditions.

5. Limitations

The investigation was restricted to 48 genotypes evaluated at one experimental location, with three replications and measurements of 15 quantitative characters. The resulting divergence estimates describe this specific germplasm collection and may not represent performance across other environments. Clusters V and VI each contained only one genotype, limiting interpretation of their cluster means. The analysis relied on phenotypic traits and did not include molecular-marker validation. No crossing experiments, progeny assessments or multi-environment trials were reported; therefore, heterosis, genetic stability and the breeding value of proposed parental combinations remain unconfirmed.

Declaration of AI Use

This manuscript was prepared through the intellectual contributions of the author(s) to the study design, data analysis, interpretation of results, and scholarly content. Grammarly and ChatGPT were used solely to assist with grammatical refinement and reference formatting during manuscript revision. The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

Competing Interests

Authors have declared that no competing interests exist.

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