International Journal of Agriculture and Food Science 2025; 7(11): 41-45

ISSN Print: 2664-844X
ISSN Online: 2664-8458
NAAS Rating (2025): 4.97
IJAFS 2025; 7(11): 41-45
www.agriculturaljournals.com
Received: 15-09-2025
Accepted: 17-10-2025

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Assesement of genetic diversity in green gram [*Vigna radiata* L. (Wilczek.)] for breeding potential

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DOI: https://www.doi.org/10.33545/2664844X.2025.v7.i11a.941

Abstract
The present study was conducted to explore genetic divergence among 30 greengram genotypes during the *kharif* 2024 season at the Research Farm, Faculty of Agriculture, Tantia University, Sriganganagar. These genotypes were sown in randomized block design with three replications. Data were recorded for eleven yield and yield contributing traits. Genetic divergence analysis using D^2 statistics grouped thirty greengram genotypes into eight distinct clusters, indicating considerable genetic diversity. Cluster II comprised the highest number of genotypes (10). The highest intra-cluster distance was observed in Cluster III, while the greatest inter-cluster distance occurred between Clusters IV and VI, suggesting these as ideal individuals for hybridization to exploit heterosis. Cluster IV exhibited superior mean performance for various traits, making it a valuable parent for breeding programs. These findings provide a useful framework for the selection of diverse and promising genotypes in greengram improvement programmes.

Keywords: D^2 statistics, Genetic divergence, Germplasm, Mungbeen

1. Introduction

The greengram, or mungbean [*Vigna radiata* (L.) Wilczek], is also referred to as a mash bean, munggo, choroko, celera bean and golden gram. It is a member of the Papilionaceae subfamily of the Fabaceae family. Greengram, pollination is primarily self-pollinated. Number of chromosomes: 2n = 2x = 22. Greengram, provide 347 kcal energy, 1.2g of total fat, 1246 mg of potassium, 63g of total carbohydrates, 16g of dietary fiber, 7g of sugar, 24g of protein and 8%, 37%, 13%, 20% and 47% of vitamin C, iron, calcium, vitamin B6 and magnesium respectively. (U.S.D.A, 2018). Greengram are legume plants that fix atmospheric nitrogen (58-109 kg per hectare) because of their symbiotic relationship with *Rhizobia* (Graham and Vance, 2003) [3]. Greengram, total production in Rajasthan is 816.392 thousand tons, with a productivity of 344.868 kg/ha. According to Rajasthan State during 2023-2024, the overall area is 2367.261 thousand hectares (Rajasthan Government, 2024).

The evaluation of genetic diversity in green grams for breeding potential is the focus of current research. The type of diversity in the germplasm for a given character determines whether genetic improvement in that character is successful. Determining the relative quality of several genotypes in relation to various features is another benefit of the examination. Information about the traits that are positively connected with one another and with seed yield is provided via character association. D^2 statistics (Mahalanobis, 1936) is a useful tool for assessing the degree of genotypic divergence. It also provides the chance to find possible parents for a successful breeding plan.

2. Materials and Methods

The experimental material comprised twenty-one diverse greengram genotypes along with nine check varieties. Name of the genotypes are provided in the table 1. The experiment was carried out in a Randomized Block Design with three replication, during *kharif* 2024 - 2025 at the Research Farm, Faculty of Agriculture, Tantia University, Sri ganganagar. Row to row and plant to plant distance was 30 cm x 15 cm. As per recommendation all plant protection measures and agronomic practices were followed for better crop growth and development. Observations were recorded on five randomly selected plants from each genotype in each replication. Days to 50% flowering and days to maturity were recorded on a plot basis. The observations were recorded on eleven quantitative traits, days to 50% flowering, days on maturity, plant height, number of primary branches per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, biological yield per plant, seed yield per plant and harvest index. The genetic divergence has been estimated using Mahalanobis' D^2 statistic and genotypes were grouped into different clusters following Toucher's method (Rao, 1952) [10].

Table 1: Name of genotypes

1.	IC- 39269	16.	IC- 102792
2.	IC- 39288	17.	IC- 102821
3.	IC- 39300	18.	IC- 102857
4.	IC- 39328	19.	IC- 103014
5.	IC- 39352	20.	IC- 103059
6.	IC- 39399	21.	IC- 103204
7.	IC- 39409	22.	MH. 421
8.	IC- 39454	23.	SML-668
9.	IC- 39492	24.	SML- 832
10.	IC- 39608	25.	GANGA- 1
11.	IC- 39610	26.	GANGA - 8
12.	IC- 52073	27.	VIRAT (IPM 205-7)
13.	IC- 52076	28.	ML- 683
14.	IC- 52081	29.	ML- 818
15.	IC- 52082	30.	MH. 2-15

3. Results and Discussion

The results indicate a high level of genetic diversity within the germplasm, Based on Mahalanobis D² statistics and Tocher's method of clustering, the thirty green gram genotypes were grouped into eight distinct clusters, reflecting a broad range of genetic divergence among the accessions (Table 2 and Fig 1). Cluster II emerged as the largest cluster, comprising 10 genotypes primarily consisting of IC lines, indicating a high degree of genetic similarity among these entries. Cluster I followed closely with 9 genotypes, including both released varieties and advanced breeding lines. Cluster III included 5 genotypes, while Clusters IV, V, VI, and VII were singleton clusters, each consisting of only one genotype. These solitary genotypes were genetically distant from all others. Cluster VIII contained 2 genotypes, forming a small but genetically distinct group.

The intra-cluster D² values (Table 3 and Fig. 2), which reflect the genetic diversity among genotypes within a cluster, ranged from 0.00 to 8.34. Clusters IV, V, VI and VII recorded zero intra-cluster distances. In contrast, Cluster III exhibited the highest intra-cluster distance of 8.34, followed by Cluster VIII with 8.12, Cluster II with 6.89, and Cluster I with 6.22. These values indicate a relatively high level of genetic variation among the genotypes grouped within these clusters, making them potentially valuable sources for selection within the cluster itself.

The highest inter-cluster distance was observed between Cluster IV and Cluster VI (17.93), Other combinations with high divergence include Cluster III and Cluster VI (17.56) and Cluster VI and Cluster VIII (16.92). Cluster IV and Cluster VII (15.75), Cluster III and Cluster V (14.74), Cluster I and Cluster VIII (14.53) and Cluster V and Cluster VIII (14.51). These high values indicate a significant level of genetic dissimilarity between the genotypes of these clusters and suggest that genotypes from these distant clusters are likely to be most effective when used as parents in hybridization programs due to the potential for producing transgressive segregants (Murthy and Arunachalam, 1966). The least inter-cluster distance was observed between Cluster V and Cluster VI (7.61), followed by Cluster V and Cluster VII (7.81). The significant variation in inter-cluster D² values confirms the presence of wide genetic diversity among the greengram genotypes evaluated. This diversity provides ample opportunities for breeders to exploit heterosis by choosing genetically distant parents for hybridization (Meena *et al*., 2021) [7].

Table 2: Composition of clusters

Clusters	Number of genotypes	Composition of cluster
I	9	VIRAT-(IPM205-7), ML-818, GANGA-8, SML-668, GANGA-1, ML-683, MH-421, SML-832, MH-2-15
II	10	IC-39269, IC-52082, IC-39610, IC-39300, IC-39352, IC-52076, IC-103014, IC-39492, IC-52081, IC-102792
III	5	IC-39454, IC-39608, IC-39399, IC-39409, IC-102857
IV	1	IC-39288
V	1	IC-39328
VI	1	IC-52073
VII	1	IC-102821
VIII	2	IC-103059, IC-103204

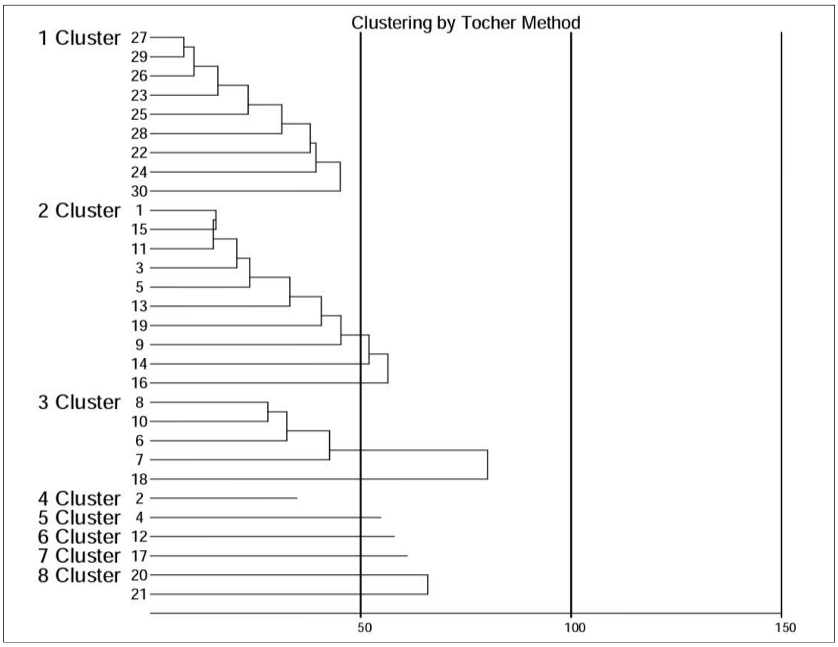

Fig 1: Cluster Diagram Based on Genetic Divergence Among Genotypes Using Mahalanobis D² Statistics

Table 3: Average intra (in bold) and inter cluster D^2 value

Clusters	I	II	III	IV	V	VI	VII	VIII
I	6.22	10.16	10.66	12.19	9.92	13.26	9.73	14.53
II		6.89	10.04	9.20	9.74	12.79	10.44	10.33
III			8.34	11.52	14.74	17.56	13.10	12.25
IV				0.00	12.67	17.93	15.75	13.71
V					0.00	7.61	7.81	14.51
VI						0.00	9.02	16.92
VII							0.00	13.00
VIII								8.12

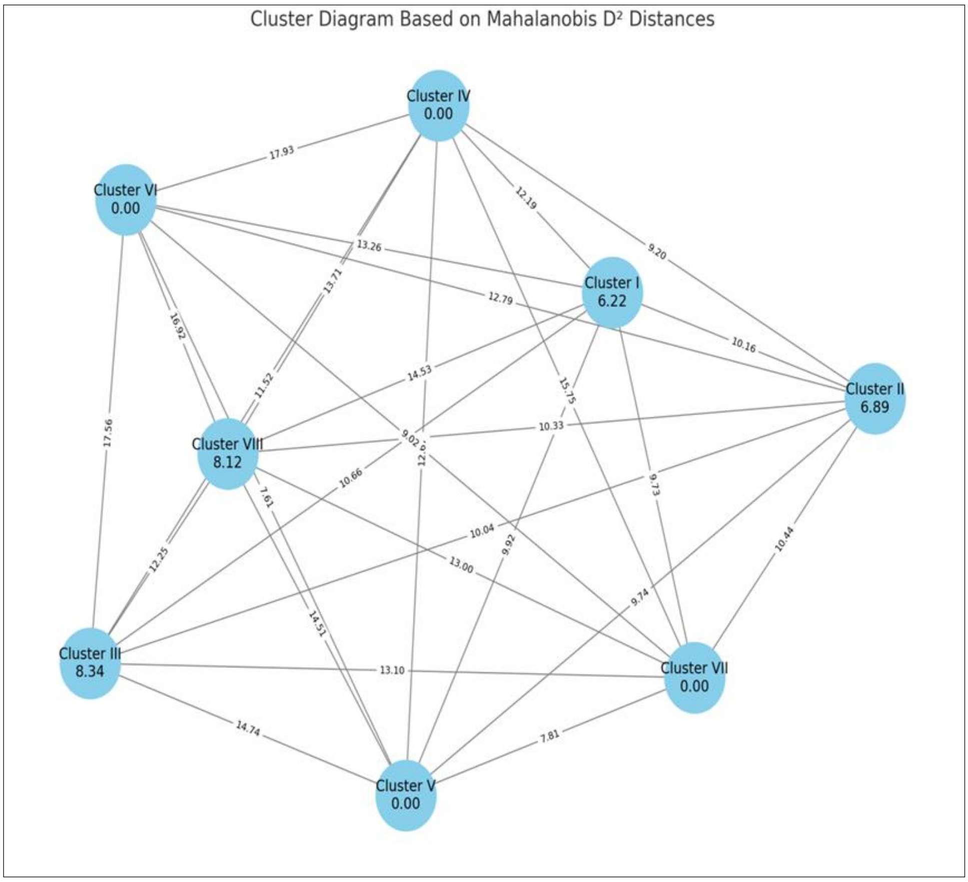

Fig 2: Clustering Pattern of greengram Genotypes Based on Multivariate D² Statistics

The analysis of trait contributions to total genetic divergence among greengram genotypes (Table 4) revealed that pods per plant had the highest contribution (25.05%), followed by days to maturity (15.86%) and days to 50% flowering (12.87%), indicating that these traits played a major role in differentiating the genotypes and are therefore critical for selection in breeding programs (Kole *et al*., 2021) [4]. Harvest index (11.96%), branches per plant (10.34%) and biological yield per plant (8.05%) also showed considerable contributions, highlighting their importance in yield-related trait divergence. In contrast, traits like seeds per pod (0.69%) and pod length (1.61%) contributed minimally, suggesting limited variability among genotypes for these characters. These findings emphasize the need to focus on highly contributing traits for efficient selection and genetic improvement in greengram (Rai *et al*., 2023) [9].

The analysis of cluster means for yield and its associated components revealed substantial variability among the eight clusters, indicating the presence of diverse genotypic groups. Mean values of clusters for all the 11 characters have been presented in (Table 5). Cluster IV exhibited the highest seed yield per plant (9.22 g), followed closely by Cluster I (8.75 g) and Cluster V (8.24 g). Notably, Cluster IV also recorded the highest values for pod length (9.20 cm), seeds per pod (12.90) and biological yield per plant (26.43 g), its relatively high harvest index (34.95%), indicating efficient partitioning of assimilates toward economic yield (Kole *et al*., 2021) [4]. Cluster I demonstrated an early flowering habit (40.04 days to 50% flowering) along with the second-highest seed yield (8.75 g), highest number of pods per plant (29.93) and good seed weight (5.97 g). The early maturity and high biological yield (25.83 g) of this cluster further support its suitability in breeding programs aiming for resilience in water-limited environments (Singh *et al*., 2022). Clusters II and III, with moderate seed yields (6.77 g and 6.71 g, respectively), showed contrasting traits. Cluster II exhibited the highest days to flowering (47.90) and maturity (80.03), indicating a late-growing type. In contrast, Cluster III, displayed a high pod length (8.59 cm), suggesting potential for selection based on pod size to meet market preferences (Rai *et al*., 2023) [9]. Cluster V containing the single genotypes, emerged as another promising group with high plant height (51.60 cm) and a high harvest index (37.58%). Cluster VI, represented the tallest plants (54.73 cm) but the lowest seed yield (5.41 g), likely due to fewer branches and pods per plant (16.53). This observation suggests that tall plant stature alone does not guarantee higher productivity (Kumar *et al*., 2020). Cluster VII recorded intermediate seed yield (6.75 g) and the highest pod length (9.22 cm), making it useful for programs focused on pod traits. Meanwhile, Cluster VIII had the lowest seed yield (4.93 g), biological yield (17.04 g) and harvest index (29.03%). Although not directly useful for yield enhancement, these genotypes may carry unique traits such as early flowering or stress tolerance suitable for introgression (Sharma and Singh, 2022) [11].

Table 4: Contribution of different characters towards total divergence

Characters	Number of times appearing in first ranking	Per cent contribution
Days to 50 per cent flowering	56	12.87
Days to maturity	69	15.86
Plant height (cm)	23	5.29
Branches per plant	45	10.34
Pods per plant	109	25.05
Pod length (cm)	7	1.61
Seeds per pod	3	0.69
100-seed weight (g)	13	2.99
Biological yield per plant	35	8.05
Harvest index (%)	52	11.96
Seed yield per plant (g)	23	5.29

Table 5: Mean values for yield and its components in various clusters

Clusters	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Primary Branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	100-seed weight (g)	Biological yield per plant	Harvest index (%)	Seed yield per plant (g)
I	40.04	70.22	49.04	3.07	29.93	8.16	11.99	5.97	25.83	34.06	8.75
II	47.90	80.03	44.21	2.21	18.63	8.16	10.86	5.60	20.48	33.51	6.77
III	50.07	83.87	38.99	2.60	29.91	8.59	10.10	5.30	20.37	33.09	6.71
IV	52.33	86.00	43.33	2.73	16.93	9.20	12.90	5.62	26.43	34.95	9.22
V	39.00	67.00	51.60	2.33	15.80	8.50	11.73	5.42	21.88	37.58	8.24
VI	37.00	67.33	54.73	2.00	16.53	7.40	12.19	5.66	14.35	37.58	5.41
VII	38.00	67.00	52.67	1.93	24.27	9.22	10.00	5.34	20.93	32.28	6.75
VIII	43.50	80.17	34.20	1.63	18.07	8.61	9.90	5.32	17.04	29.03	4.93

4. Conclusion

Overall, the study highlights the value of selecting genotypes from genetically diverse and high-performing clusters such as IV (IC-39288), I (VIRAT, SML-668, etc.) and V (IC-39328) for hybridization. This approach can aid in trait complementation and yield enhancement in greengram breeding programs. Genetic divergence analysis revealed distinct clusters with considerable variability, with Cluster IV being the most promising for breeding high-yielding and nutrient-rich varieties. Other clusters also offer useful traits for targeted improvement. Overall, these findings provide valuable guidance for breeders to utilize key yield components and genetic diversity to develop superior greengram varieties.

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