International Journal of Bio-resource and Stress Management https://ojs.pphouse.org/index.php/IJBSM

Crossref

IJBSM January 2024, 15(1): 01-08 **Article** AR5013

Research Article *Natural Resource Management*

DOI: HTTPS://DOI.ORG/10.23910/1.2024.5013

Delineating the Genetic Variability and Diversity in Green Gram [*Vigna radiata* (L.) Wilczek] Genotypes

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0009-0006-6862-3257

ABSTRACT

This study evaluated 44 green gram genotypes collected from the AICRP on MULLaRP to investigate genetic variability and divergence. During *kharif* (July–October, 2020), the genotypes were assessed for various morphological traits. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation, indicating significant variability. Clusters plant^{-1}, pods plant^{-1}, and seed yield plant^{-1} exhibited the highest genetic and phenotypic coefficient of variation. High heritability was observed for 1000-seed weight, clusters plant^{-1}, pods plant^{-1}, and seeds pod^{-1}, suggesting the influence of additive genetic factors. Genetic advance as a % of the mean was particularly notable for clusters plant^{-1}, pods plant^{-1}, and seed yield plant^{-1}. Further analysis using Mahalanobis D^2 statistics resulted in the classification of genotypes into seven clusters, with Cluster I being the largest. Cluster IV and VI showed the highest inter-cluster distance, indicating substantial genetic divergence. Notably, Cluster III represented by AKM 1801 displayed superior characteristics such as high mean values for pod length, seeds pod^{-1}, 1000-seed weight, and seed yield per plant, making it a potential candidate for green gram improvement programs. In terms of genetic diversity, 1000-seed weight contributed the most, followed by clusters plant^{-1} and chlorophyll content. These findings highlight the importance of these traits in shaping the genetic diversity observed among the green gram genotypes.

KEYWORDS: Cluster, D^2, divergence, genetic variability, green gram, heritability

***Citation* (VANCOUVER):** Mahla et al., Delineating the Genetic Variability and Diversity in Green Gram [*Vigna radiata* (L.) Wilczek] Genotypes. *International Journal of Bio-resource and Stress Management,* 2024; 15(1), 01-08. HTTPS://DOI.ORG/10.23910/1.2024.5013.

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

RECEIVED on 11th November 2023 RECEIVED in revised form on 05th January 2024 ACCEPTED in final form on 16th January 2024 PUBLISHED on 30th January 2024

1. INTRODUCTION

Green gram, scientifically known as *Vigna radiata* (L.) Wilczek, is a leguminous crop that reproduces through self-pollination and belongs to the Fabaceae family. Its origin is believed to be in the Indian subcontinent. Green gram is primarily cultivated in arid and semi-arid regions of countries such as Afghanistan, India, Korea, Myanmar, Pakistan, Philippines, and Sri Lanka (Sharma and Dhanda, 2014). In India, green gram holds significant importance as a pulse crop, following chickpea and pigeon pea (Sridhar et al., 2022). Typically, it is cultivated during the *kharif* season, serving as a sole crop or intercropped, as well as during the *rabi* and summer seasons (Shweta, 2013; Kaur et al., 2015). This crop requires low maintenance due to its minimal water requirements and short growth duration, while also possessing the ability to improve soil fertility. Its short growth cycle allows for easy incorporation into various crop rotations and intercropping systems throughout the country (Nayak et al., 2022). Notably, green gram possesses the remarkable ability to fix atmospheric nitrogen due to the presence of root nodules (Wanga et al., 2017), making it useful as a green manure and cover crop in various regions of the country.

Green gram is highly regarded in the human diet due to its substantial protein content (23%) and other valuable nutritional qualities, therefore it is also known as the "poor man's meat" (Reddy, 2009; Kumar et al., 2023). It is often considered a vegetable alternative for individuals with limited resources, thanks to its rich protein content. Additionally, green gram serves as a plentiful source of minerals, vitamin A, riboflavin, thiamine, and several antioxidants, including flavonoids, phenolic acids, caffeic acid, and cinnamic acid. It is also cultivated as a fodder crop to feed livestock.

The productivity of green gram falls short of its potential due to various limitations, including a lack of exploitable genetic variability, cultivation on marginal lands, exposure to biotic and abiotic stresses, and the unavailability of superior varieties (Rahman and Al-Mansur, 2009; Kumar et al., 2011; Panigrahi and Baisakh, 2014). The availability of genetic diversity in the germplasm accessions provides a good opportunity to plant breeders to develop new and improved cultivars with desirable characteristics (Tabasum et al., 2010; Kaur et al., 2015; Das and Barua, 2018). Improving the quantitative traits of any crop through breeding requires a thorough understanding of the crop's existing variability and the heritability of desirable traits found in the breeding material (Dey et al., 2021; Tolwani and Shukla, 2022). To establish an effective breeding program, it is essential to analyse various parameters of genetic variability such as phenotypic and genotypic coefficient of variation, heritability, and genetic advance (Devi et al., 2022). Assessing genetic diversity aids in the identification of diverse genotypes and the selection of parents for breeding programs. Genetically diverse parents having with combining ability for desirable recombinant for specific trait improvement followed by appropriate selection in segregating generation in a self-pollinated crop like green gram would result in the development of improved cultivars (Katiyar et al., 2009; Singh et al., 2014; Rekha et al., 2015; Patel et al., 2021). Employing multivariate statistics proves highly valuable for estimating genetic diversity, offering reliable insights into the actual genetic distances among tested genotypes. Among the various multivariate techniques, cluster analysis utilizing Mahalanobis generalized distance (D^2) statistics and principal component analysis (PCA) stands out as commonly used methods to assess the variability of quantitative traits and to identify the superior genotypes (Lavanya et al., 2008; Sneha et al., 2020). Keeping this objective in mind, the current experiment was conducted to evaluate the genetic diversity among the studied green gram genotypes.

2. MATERIALS AND METHODS

The experiment conducted during the *kharif* (July-October, 2020) at SKNAU in Jobner, Rajasthan. The research material consisted of forty-four genotypes obtained from the AICRP on MULLaRP (Mung, Urd, Lentil, Lathyrus, Rajmah, and Pea) at the RARI in Durgapura, Jaipur. The genotypes were grown in a Randomized Block Design with three replications, with each plot consisting of two rows and measuring 2.50 meters in length, with a spacing of 30×10 cm^2.

Data was collected from five randomly selected plants of each genotype for ten different traits, including plant height, branches $plant^{-1}$, clusters $plant^{-1}$, pods $cluster^{-1}$, pods $plant^{-1}$, pod length, seeds pod^{-1}, seed yield $plant^{-1}$, protein content, and chlorophyll content. Additionally, traits such as days to 50% flowering, days to maturity, and 1000-seed weight were recorded on a plot basis.

The mean values of all the recorded traits were analyzed using analysis of variance (ANOVA) to determine the significance of differences among the genotypes, following the statistical method recommended by Panse and Sukhatme (1985). Genotypic, phenotypic, and error variances were estimated using formulas proposed by Burton (1952) and Johnson et al. (1955). Genotypic and phenotypic coefficients of variation were calculated using the formula suggested by Burton and Devane (1953). Broad-sense heritability was determined using the formula proposed by Hanson et al. (1956). Genetic advance, expressed as a % of the mean

for each trait, was predicted using the formula provided by Johnson et al. (1955). Furthermore, Mahalanobis D^2 statistics (Mahalanobis, 1936) were applied to the data to analyze the genetic diversity among the genotypes. The genotypes were then grouped into different clusters using Tocher's method, as suggested by Rao (1952).

3. RESULTS AND DISCUSSION

Significant genetic variation was observed among the genotypes for all thirteen studied traits, as indicated by the analysis of variance (Table 1). Mean, range, GCV, PCV, heritability and genetic advance as % of mean for all the characters are presented in Table 2. The phenotypic coefficient of variation was generally higher than the genotypic coefficient of variation, implying the influence of environmental factors on trait expression. Clusters plant^{-1}, pods plant^{-1}, and seed yield plant^{-1} exhibited high genotypic and phenotypic variation, consistent with previous studies reported by Hemavathy et al. (2015), Sandhiya and Saravanan (2018), Muthuswamy et al. (2019), Nayak et al. (2022) and Sridhar et al. (2022). Conversely, traits such as seeds pod^{-1}, days to 50% flowering, days to maturity, pod length, and 1000-seed weight showed lower coefficients of variation similar to findings of Makeen et al. (2007), Anand et al. (2016), Bhutia et al. (2016), Thakur et al. (2022). In contrast, Jain et al. (2024) reported a moderate genotypic and phenotypic coefficient of variation for the trait viz., days to 50% flowering, while Payasi et al. (2015) observed high coefficients of variation for days to maturity and pod

Table 1: Analysis of variance showing mean square of various characters in green gram

Sl. No.	Characters	Sources of variation		
		Replication	Genotypes	Error
		(d.f.=2)	(d.f.=43)	(d.f.=86)
1.	Days to 50% flowering	05.37	05.64**	01.97
2.	Days to maturity	01.66	15.37**	03.27
3.	Plant height (cm)	66.12	123.70**	22.07
4.	Branches plant^{-1}	00.33	00.36**	00.14
5.	Clusters plant^{-1}	01.09	08.90**	00.63
6.	Pods cluster^{-1}	00.01	00.43**	00.10
7.	Pods plant^{-1}	00.36	51.28**	03.91
8.	Pod length (cm)	00.09	00.69**	00.23
9.	Seeds pod^{-1}	01.06	00.60**	00.48
10.	1000-seed weight (g)	02.45	39.07**	01.05
11.	Seed yield plant^{-1} (g)	00.53	03.19**	00.50
12.	Protein content (%)	00.57	03.00**	00.62
13.	Chlorophyll content (SPAD meter)	26.10	83.17**	08.99

** Significant at (p=0.05) level of significance

Table 2: Mean, range, genotypic and phenotypic coefficient of variation, heritability (broad sense) and genetic advance as percentage of mean for different characters in green gram

Sl. No.	Characters	Mean	Range	GCV (%)	PCV (%)	Heritability in broad sense (%)	Genetic advance as % of mean
1.	Days to 50% flowering	42.00	40.00–46.00	02.65	04.28	38.40	03.39
2.	Days to maturity	61.00	57.00–66.00	03.30	04.45	55.20	05.06
3.	Plant height (cm)	53.83	42.16–73.17	10.81	13.90	60.50	17.33
4.	Branches plant^{-1}	03.37	02.67–04.20	07.95	13.69	33.70	09.51
5.	Clusters plant^{-1}	07.12	04.27–11.00	23.30	25.85	81.30	43.28
6.	Pods cluster^{-1}	02.64	02.00–03.53	12.56	17.30	52.70	18.78
7.	Pods plant^{-1}	18.09	11.13–27.47	21.97	24.53	80.20	40.51
8.	Pod length (cm)	07.94	06.91–09.16	04.94	07.77	40.50	06.48
9.	Seeds pod^{-1}	12.21	11.20–13.07	01.61	05.90	74.00	00.90
10.	1000-seed weight (g)	42.61	34.17–50.40	08.36	08.69	92.40	16.54
11.	Seed yield plant^{-1} (g)	05.77	03.54–08.40	16.44	20.48	64.40	27.17
12.	Protein content (%)	20.71	18.72–22.71	04.30	05.74	56.10	06.64
13.	Chlorophyll content (SPAD meter)	41.89	33.47–54.83	11.87	13.86	73.30	20.94

length. Heritability was high for 1000-seed weight, clusters plant^{-1}, pods plant^{-1}, seeds pod^{-1}, chlorophyll content, seed yield plant^{-1} and plant height, suggesting the dominance of additive genetic factors and potential for selection. Tabasum et al. (2010), Garje et al. (2014), Hemavathy et al. (2015) and Sofia et al. (2017) reported similar findings. Additionally, Kumar et al. (2010) found comparable results for 100-seed weight, Anand et al. (2016) for seed yield plant^{-1}, plant height, and pods plant^{-1}, and Susmitha and Jayamani (2018) for plant height and 100-seed weight. Moderate heritability was observed for protein content, pods cluster^{-1}, days to maturity, days to 50% flowering, pod length, and branches plant^{-1}. Anand et al. (2016) and Choudhary et al. (2017) observed such results for days to 50% flowering, while Kumar and Katiyar (2015) found comparable findings for branches plant^{-1}, and Mohammed et al. (2020) reported similar results for pod length. In contrast, Makeen et al. (2007) reported the highest heritability for protein content.

High genetic advance, expressed as a % of the mean, was found for clusters plant^{-1}, pods plant^{-1}, and seed yield per plant, while low values were observed for branches plant, pod length, days to 50% flowering, days to maturity, and seeds pod^{-1}. Similar findings were reported by Tabasum et al. (2010), and Hemavathy et al. (2015), Garje et al. (2014) and Bhutiya et al. (2016). Traits with high heritability and moderate to high genetic advance, such as seed yield plant^{-1}, 1000-seed weight, clusters plant^{-1}, pods plant^{-1}, and chlorophyll content, are less influenced by environmental factors and thus suitable for selection (Kanavi et al., 2023).

The genotypes were further subjected to D^2 statistics and classified into seven clusters using Tocher's method (Table 3 and Figure 1). Cluster I was the largest, comprising 29 genotypes, followed by cluster II with 10 genotypes. Clusters III, IV, V, VI and VII had one genotype each. The intra and inter cluster distance between different clusters is mentioned in table 4 and figure 2. The intra-cluster distance ranged from 0.00 to 23.07, with the highest distance observed within cluster II (23.07), followed by cluster I (16.50). In the other clusters, the intra-cluster distance was zero. The inter-cluster distance between clusters varied from 14.77 to 106.15. The largest inter-cluster distance was between cluster IV and cluster VI (106.15), followed by cluster III and cluster VI (103.48), and cluster II and cluster IV (68.12). Conversely, the smallest distance was observed between cluster III and cluster IV (14.77). High inter-cluster distance indicates significant divergence between genotypes of different clusters, suggesting their potential use in future applications. Conversely, small inter-cluster distance signifies close proximity between genotypes. Similar findings were reported by previous studies.

Table 3: Clustering pattern of different genotypes in different clusters

Clusters	No. of genotypes	Genotypes
I	29	ML 2575, ML 818, ML 2482, NDMK 17-07, IPM 312-394-1, IPM 14-49-5, RMG 268, MH 1142, MSJ 158, MH 318, MH 125, GP 12, IGKM 06-10-7, JLPM 504-20-27, VGG 17-043, GP 14, IPM 409-4, OBGG 103, MH 1703, GP 18, IGKM 05-18-2, BWMCG 31, IPM 02-3, IPM 410-3, PMD 14-10, Pusa BM 5, MH 421, OBGG 104, GP 19
II	10	PM 1618, RMG 492, MH 2-15, RMG 62, RMG 975, VGG 17-038, GP 55, ML 2459, Pusa M 1971, VGG 4604
III	1	AKM 1801
IV	1	DGGV 80
V	1	MGG 389
VI	1	Pusa M 1972
VII	1	PM 16-23

Table 4: Average intra and inter-cluster distance based on corresponding D^2 values

Cluster	I	II	III	IV	V	VI	VII
I	16.50	30.60	27.96	27.67	24.38	49.32	32.40
II		23.07	59.79	68.12	44.82	30.20	35.77
III			00.00	14.77	48.81	103.48	43.74
IV				00.00	26.69	106.15	47.58
V					00.00	45.00	49.14
VI						00.00	53.33
VII							00.00

The cluster means for the thirteen studied traits were presented in Table 5. Cluster I had the lowest mean value for 50% flowering (41.23), indicating its suitability for early maturation. Cluster VI exhibited the highest mean values for days to maturity (65.00), while cluster V showed the highest mean values for plant height (73.17), pods cluster^{-1} (3.13), and protein content (922.71). Cluster VII had the highest mean values for branches plant (4.00), clusters plant^{-1} (9.930), pods plant^{-1} (22.40), and chlorophyll content (54.02). Cluster III displayed the highest mean values for pod length (8.89), seeds pod^{-1} (13.07), 1000-seed weight (50.50), and seed yield plant^{-1} (6.70). Clusters III, V,

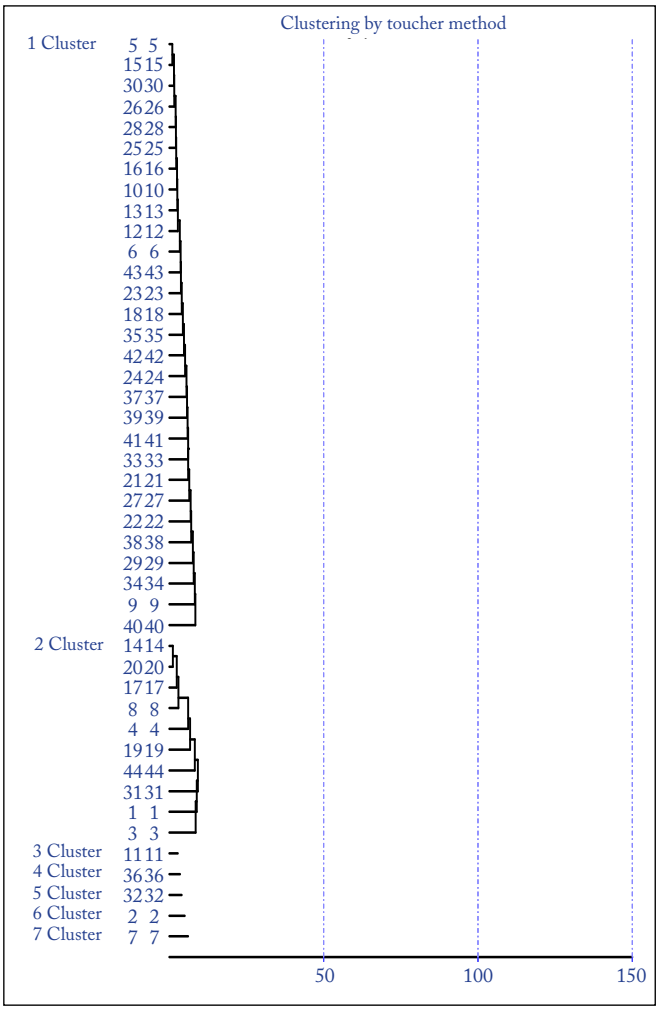

Figure 1: Clustering of genotypes by Tocher's method

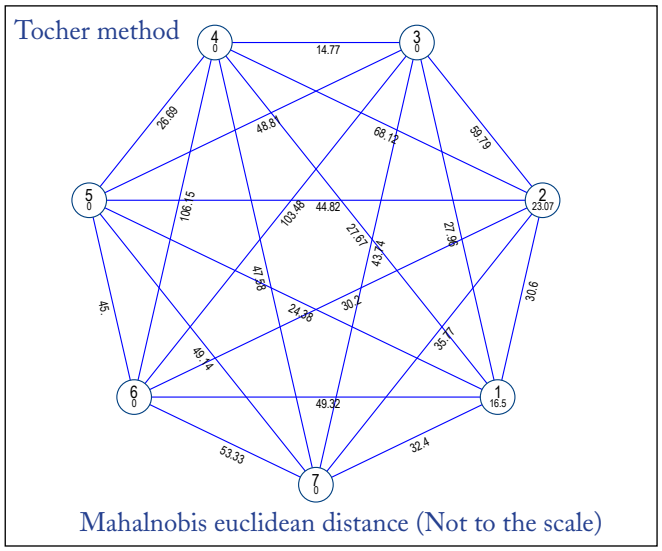

Figure 2: Cluster diagram

and VII showed high mean values for traits significantly contributing to crop yield. Genotypes with high mean values in these clusters hold potential for the breeding program of green gram.

The relative % contribution of individual traits towards total diversity was determined using the rank average method, as shown in table 6. The highest % contribution was attributed to 1000-seed weight (46.51%), followed by clusters per plant (917.65%) and chlorophyll content (10.99%). Similar conclusions were recorded by Manivannan (2002), Sharma et al. (2018), Das and Baisakh (2019) and Mounisha et al. (2022), emphasizing the significant contribution of 1000-seed weight to divergence. On the other hand, seeds pod^{-1},

Table 5: Mean values of genotypes present in different clusters for different characters

Characters	Clusters						
	I	II	III	IV	V	VI	VII
Days to 50% flowering	41.70	41.23	41.67	42.00	41.33	43.00	46.00
Days to maturity	60.94	60.13	59.67	58.67	60.67	65.00	62.33
Plant height (cm)	52.35	53.54	50.97	61.15	73.17	62.97	66.61
Branches plant^{-1}	03.29	03.57	03.40	03.13	03.13	03.60	04.00
Clusters plant^{-1}	06.54	08.77	06.53	05.60	06.53	07.53	09.93
Pods cluster^{-1}	02.69	02.51	02.27	02.80	03.13	02.47	02.33
Pods plant^{-1}	17.15	21.05	15.07	15.13	17.20	18.40	22.40
Pod length (cm)	07.92	07.84	08.89	08.64	08.63	07.80	07.41
Seeds pod^{-1}	12.23	12.01	13.07	12.73	12.93	12.27	11.67
1000-seed weight (g)	43.57	39.31	50.40	48.97	40.83	34.17	43.80
Seed yield plant^{-1} (g)	05.52	06.62	06.70	05.99	04.90	04.66	05.33
Protein content (%)	20.83	20.45	19.24	22.41	22.71	19.12	19.09
Chlorophyll content (SPAD meter)	40.78	44.73	37.03	42.50	36.73	42.72	54.02

Table 6: Relative contribution of each character towards divergence

Sl. No.	Characters	Times ranked 1st	Contribution %
1.	Days to 50% flowering	6	00.63
2.	Days to maturity	39	04.12
3.	Plant height (cm)	56	05.92
4.	Branches plant^{-1}	3	00.32
5.	Clusters plant^{-1}	167	17.65
6.	Pods cluster^{-1}	14	01.48
7.	Pods plant^{-1}	32	03.38
8.	Pod length (cm)	16	01.69
9.	Seeds pod^{-1}	1	00.11
10.	1000-seed weight (g)	440	46.51
11.	Seed yield plant^{-1} (g)	32	03.38
12.	Protein content (%)	36	03.81
13.	Chlorophyll content (SPAD meter)	104	10.99

branches plant^{-1}, and days to 50% flowering had the least contribution to genetic divergence. The study concluded that there is considerable diversity among the genotypes, which can be harnessed to improve specific traits through future breeding programs.

4. CONCLUSION

The analysis of variance revealed significant genetic variation among studied traits in green gram genotypes. Traits like clusters plant^{-1}, pods plant^{-1} and seed yield plant^{-1} showed high variation. Additive genetic factors dominated traits such as 1000-seed weight, clusters plant^{-1}, and seed yield plant^{-1}, suggesting their potential for selection in breeding. D^2 statistics classified genotypes into clusters, indicating significant divergence between them. The study underscores ample genetic variation, offering prospects for targeted breeding to enhance green gram traits and overall productivity.

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