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Genetic diversity for yield, yield components and nutritional traits in greengram [*Vigna radiata* (L.) Wilczek]

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Abstract

The research work was undertaken to assess the genetic diversity among forty-five greengram (*Vigna radiata* (L.) Wilczek) genotypes using Mahalanobis' D² statistics. The experiment was laid out in an Alpha Lattice Design with three replications, evaluating ten quantitative and four nutritional traits. Based on multivariate analysis, the genotypes were grouped into five distinct clusters, with cluster I comprising 37 genotypes, cluster II with five genotypes and clusters III, IV, and V were solitary with one genotype in each cluster. Maximum inter-cluster distance was observed between Clusters IV and V (1328.76), indicating wide genetic divergence and high potential for heterotic combinations. Cluster mean analysis revealed Clusters III and V were superior for several yield and nutritional traits. Seed yield per plant, Pods per plant, Test weight, Iron content, Pod length and Branches per plant contributed significantly to total genetic divergence, together accounting for 59.36% of the total variability. The study underscores the importance of these traits in selection and hybridization programs and identifies genetically diverse parents for the development of high-yielding, nutrient-rich greengram cultivars.

Keywords: Genetic diversity, greengram, nutritional traits and seed yield

Greengram (*Vigna radiata* (L.) Wilczek), belongs to the family Fabaceae with chromosome number 2n = 2x = 22 and is known for its short-duration life cycle, nitrogen-fixation ability, and rich protein content (~24–26%). Being a short-duration, self-pollinating annual legume, it not only supplements the income of resource-poor farmers but also provides a valuable source of easily digestible protein (Pramod et al., 2024). However, its productivity is often challenged by biotic and abiotic stresses, emphasizing the need for genetically diverse varieties that can adapt to varied environments (Nair et al., 2019). Greengram a vital legume crop of Asia, especially India, exhibits a considerable range of genetic variability across its germplasm. Genetic diversity represents the full spectrum of genetic attributes contained in the genome of a species. In crop improvement programs, it is a key resource that provides the raw material for selection and breeding. Genetic diversity in greengram is essential for crop improvement, as it provides a wide range of traits such as high yield, early maturity, resistance to pests like bruchids, diseases like yellow mosaic virus, and tolerance to stresses like drought and salinity. It also plays a key role in sustainable agriculture by helping to stabilize production under changing climatic conditions and reducing the risk of crop failure due to epidemics. In breeding programs, genetically diverse parental lines are valuable for hybridization, as they can produce vigorous offspring and help in developing superior varieties through the expression of desirable traits.

The present investigation was carried out at Regional Agricultural Research Station, Lam, Guntur during *Rabi*, 2024-2025 with 45 greengram genotypes. (**Table 1**) The experiment was laid out in Alpha Lattice Design replicated thrice and the data was recorded on ten quantitative traits and four nutritional traits to study the nature and magnitude of genetic diversity among the genotypes by multivariate analysis with D^2 statistic.

Each genotype was sown in paired rows, with a row length of 4 m and spacing of 30 × 10 cm (inter-row × intra-row). Observations on days to 50% flowering and days to maturity were recorded on a plot basis for each replication. Data on plant height (cm), number of branches per plant, number of clusters per plant, number of pods

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Table 1. List of greengram genotypes along with parentage and origin

S.No.	Genotype	Parentage	Origin
1	LGG 598	MGG 295 X P 109	Andhra Pradesh
2	LGG 612	TM 96-2	Andhra Pradesh
3	LGG 625	Sipai x P115	Andhra Pradesh
4	LGG 631	LGG 460 x TM 96-2	Andhra Pradesh
5	LGG 636	LGG 450 x P 109	Andhra Pradesh
6	LGG 691	LGG 460 x IPM 409-4	Andhra Pradesh
7	LGG 695	LGG 450 x VGG	Andhra Pradesh
8	LGG 696	LGG 450 x VGG	Andhra Pradesh
9	LGG 767	LGG 460 x MH 421	Andhra Pradesh
10	LGG 771	LGG 450 x IPM 409-4	Andhra Pradesh
11	LGG 777	LGG 407 X MH 1121	Andhra Pradesh
12	PUSA 1842	IPM 2-23 x Pusa vishal	New Delhi
13	PUSA 16-41	IPM 99-125 x Pusa vishal	New Delhi
14	PUSA M 2171	MH 318 x Mash 114	New Delhi
15	PUSA 9072	Pusa 106 x 10-215	New Delhi
16	PUSA M 19111	Pusa 105 x Pusa Vishal	New Delhi
17	PUSA VISHAL	Sel. NK 92	New Delhi
18	VBN – 2	VGG 4 x MH 309	Vamban
19	VBN – 4	PDM 139 x BB 2664	Tamil Nadu
20	OBGG 57	Mutant of OUM11-5	Orrisa
21	OBGG 58	VC 1560 x VC 20236370-92	Orrisa
22	OBGG 106	NM 94 x ML 1628	Orrisa
23	AKM 12-28	PKU Green Gold x BM 2003-2	Maharashtra
24	AKM 8802	MH 1 x PIMS 4	Maharashtra
25	AKM 8803	PIM 5 X MH 1	Maharashtra
26	VGG 14-001	Sel from Pusa EM 1401	NPRC, Vamban
27	VGG 15-038	VBN (Gg) x ML 1451	NPRC, Vamban
28	VGG 17-43	VBN (Gg)2 x IPM 205-7	NPRC, Vamban
29	IPM 205-7	IPM 02-1 x EC 398889	IIPR, Kanpur
30	IPM 13-6	IPM 02-14 x LGG 460	IIPR, Kanpur
31	MGG 373	Madhira mung x MGG 341-9	ARS, Madhira
32	MGG 389	Madhrimung x ML 267	ARS, Madhira
33	MH 1142	MH 421 (Muskan) x BDYR 2)	Haryana
34	MH 1857	Satya x MH 318	Haryana
35	BM – 4	Mutant of T 44	Maharashtra
36	TM 96-2	Kopergaon x TARM-2	Maharashtra
37	NMK 1508	Meha x GM 4	NAU, Navsari
38	GGG -1	Sel. From RFM 13-18	ARS, Ghantasala
39	RMG 1087	RMG 492 x MUM 2	RARS, Durgapura
40	TMB 146	TM 98-80 x SML 668	Mumbai
41	LGG 574 ©	LGG 460 x P 101	Andhra Pradesh
42	IPM 2-14 ©	IPM 99-125 x Pusa bold 2	Uttar Pradesh
43	LGG 600 ©	MGG 295 x P 109	Andhra Pradesh
44	LGG 607 ©	MGG 295 x COGG 912	Andhra Pradesh
45	LGG 630 ©	LGG 460 x P 109	Andhra Pradesh

per plant, pod length (cm), number of seeds per pod, test weight and seed yield per plant (g) were collected from three replications, using five randomly selected plants per replication. For nutritional analysis, standard biochemical methods were followed. Protein content (%) and vitamin C content (mg/100g) were estimated as per the procedures outlined by Sadasivam and Manickam (1996*)*. Iron (mg/g) and zinc content (mg/g) were estimated using the method described by Tandon (1999). Mahalanobis (1928) D^2 analysis was used for assessing the genetic divergence among the test genotypes. Group constellation was performed according to the method suggested by Tocher (Rao, 1952).

Based on D^2 values, 45 greengram genotypes were grouped into five clusters (**Table 2**) on the assumption that genotypes within the cluster have similar D^2 values among themselves than those from groups belonging to two different clusters. Cluster I had the highest number of genotypes (37 genotypes) and cluster II had 5 genotypes and the other three clusters had single genotype each i.e. mono-genotypic cluster. Grouping of genotypes into different clusters based on genetic diversity differs from geographical diversity. The genotypes belonging from similar geographical background, were grouped into different clusters based on genetic diversity, from this it was evident that both geographical and genetic diversity different from one another.

The average intra- and inter-cluster D^2 values (**Table 3 and Fig. 1**) were estimated as per Singh and Chaudhary (1977) and the nearest and farthest clusters for each of the five clusters are shown in **Table 4a&4b**. Intra-cluster D^2 values ranged from 0.00 (Clusters III, IV and V) to 143.14 (Cluster I), indicating varying degrees of genetic variability within clusters. Clusters III, IV, and V, each with a single genotype, showed zero intra-cluster distance. Maximum inter-cluster divergence was observed between Clusters IV and V (1328.76), followed by Clusters IV and I (866.52), and Clusters III and V (849.51), indicating their potential for hybridization. Based on Falconer's (1964) principle, crosses between genetically distant clusters may result in high heterosis and a broad spectrum of segregants. Hence, hybridization between divergent clusters, especially those involving Clusters IV and V, is recommended for breeding programs. Cluster means indicate average performance of all genotypes present in a particular cluster for a trait. Cluster mean analysis revealed considerable variation among clusters for all the traits (**Table 5**). Cluster III and V showed superiority for several yield and nutritional traits, highlighting their potential for selection and hybridization in breeding programs. Cluster III, in particular, emerged as one of the most promising clusters, exhibiting superior mean performance for traits like key yield-contributing like clusters per plant, pods for plant and nutritional traits like protein, iron, zinc and Vitamin C.

Table 2. Clustering pattern by Tocher's method of 45 greengram genotypes

Cluster number	Number of genotypes	List of genotypes
I	37	LGG 631, IPM 13-6, LGG 612, VBN 2, LGG 625, VGG 14-001, LGG 636, VGG 17-43, AKM 8802, PUSA 9072, LGG 598, MGG 373, LGG 696, PUSA M 2171, MH 1857, MGG 389, PUSA 1842, AKM 8803, TM 96-2, LGG 630, RMG 1087, LGG 777, LGG 767, TMB 146, LGG 771, LGG 691, BM 4, AKM 1228, OBGG 106, OBGG 58, MH 1142, IPM 2-14, VBN 4, VGG 15-038, NMK 1508, GGG 1 and LGG 600
II	5	IPM 205-7, LGG 607, PUSA VISHAL, PUSA 16-41, OBGG 57
III	1	LGG 695
IV	1	PUSA M 19111
V	1	LGG 574

Table 3. Cluster-wise average intra- (bold) and inter-cluster D^2 and D statistics for 45 greengram genotypes

	Cluster distances				
Cluster	**Cluster I**	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**
Cluster I	**143.14 (11.96)**	584.45 (24.17)	554.09 (23.53)	866.52 (29.43)	513.71 (22.66)
Cluster II		**115.86 (10.76)**	472.82 (21.74)	465.37 (21.57)	831.21 (28.83)
Cluster III			**0.00 (0.00)**	211.17 (14.53)	849.51 (29.14)
Cluster IV				**0.00 (0.00)**	1328.76 (36.45)
Cluster V					**0.00 (0.00)**

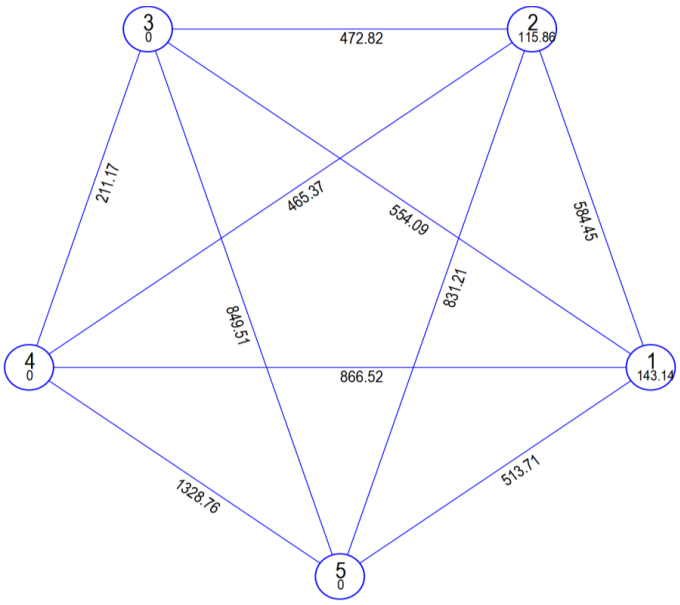

Fig.1. Euclidean distance–based intra- and inter-cluster analysis of 45 greengram genotypes across five clusters

Table 4a. Tocher's method–based identification of nearest and farthest clusters among 45 greengram genotypes using D^2 values

Cluster Number	Nearest cluster	Farthest cluster
I	V (513.71)	IV (866.52)
II	IV (465.37)	V (831.21)
III	IV (211.17)	V (849.51)
IV	III (211.17)	V (1328.76)
V	I (513.71)	IV (1328.76)

Table 4b. Tocher's method–based cluster mean values of five clusters in greengram genotypes

Character	DFF	DM	PH	BPP	CPP	PPP	PL	SPP	TW	PC	ZINC	IRON	VIT C	SYP
Cluster I	42.11	67.15	24.50	1.50	4.50	10.20	5.98	9.81	3.13	22.13	21.74	58.95	69.85	2.09
Cluster II	42.73	67.60	23.97	1.67	4.60	10.60	6.11	9.37	3.23	22.00	14.76	193.1	63.07	2.25
Cluster III	44.34	66.67	21.40	2.27	5.67	15.07	7.00	11.13	3.08	26.19	61.23	143.1	92.3	3.44
Cluster IV	38.67	67.00	27.33	1.27	4.53	10.47	7.87	12.07	3.11	20.80	58.16	179.23	46.13	2.00
Cluster V	48.00	71.00	36.00	3.90	3.00	12.00	7.40	12.40	3.40	22.10	16.70	73.5	52.3	5.24

DFF- Days to 50% flowering; DM- Days to maturity; PH - Plant height (cm); BPP - Branches per plant; CPP- Clusters per plant; PPP- Pods per plant; PL- Pod length (cm); SPP- Seeds per pod; TW- Test weight (g); PC- Protein content (%); ZINC- Zinc content (mg/kg); IRON- Iron content (mg/kg); VIT C- Vitamin C (mg/100g); SYP-Seed yield per plant (g).

Among the 14 traits studied, Six characters *viz*.,seed yield per plant (13.50%), Pods per plant (11.20%), Test weight (9.87%), Iron content (8.90%), Pod length (8.00) and Branches per plant (7.89) contributing to 59.36 % of total diversity showed notable contributions (**Table 5**) and the rest of the diversity (40.64%) was contributed by the other eight characters. The characters branches per plant, clusters per plant, pods per plant, pod length, seeds per pod, test weight, iron content, and seed yield per plant together accounted for 72.34% of total genetic divergence, indicating their importance for genetic improvement. The success and usefulness of Mahalanobis' D^2 analysis in quantifying genetic divergence in greengram was already indicated by Panigrahi and Baisakh (2014), Mahalingam *et al.* (2018), Wesly *et al.* (2020), Goyal *et al.* (2021), Mohan *et al.* (2021), Gopal *et al.* (2022), Varma *et al.* (2022), , Nayak *et al.* (2022), Bindu *et al.* (2023), Mounisha *et al.* (2023),

Table 5. Contribution of different characters towards genetic divergence in 45 greengram genotypes

S.No.	Source	Contribution (%)	Times ranked 1st
1	Days to 50% flowering	3.84	38
2	Days to maturity	4.42	44
3	Plant height	3.76	38
4	Branches per plant	7.89	79
5	Clusters per plant	6.20	62
6	Pods per plant	11.20	112
7	Pod length	8.00	80
8	Seeds per pod	6.78	68
9	Test weight	9.87	99
10	Protein content	3.52	35
11	Zinc content	6.12	61
12	Iron content	8.90	89
13	Vitamin C	6.00	60
14	Seed yield per plant	13.50	135

Srivastava *et al.* (2024) and Shekhawat and Mukhram (2025). The effectiveness of this method lies in its ability to classify genotypes into distinct clusters based on multivariate traits, thereby enabling the identification of genetically diverse parents for crop improvement programmes.

Genetic diversity analysis using Mahalanobis' D^2 statistics grouped the genotypes into five clusters, reflecting significant genetic divergence. Maximum inter-cluster distance observed between Clusters IV and V suggests that crosses involving these clusters could potentially yield superior recombinants with enhanced heterosis. Cluster mean analysis highlighted genotypes in Clusters III and V as promising sources of favorable traits, particularly for yield and nutritional quality.Importantly, characters such as seed yield per plant, pods per plant, test weight, iron content, pod length and branches per plant showed the highest contributions to genetic divergence, with eight key traits together accounting for 59.36 % of total variability. These findings emphasize the relevance of these traits in guiding selection and hybridization strategies. Overall, the study provides valuable insights into trait relationships and diversity patterns that can be harnessed in greengram breeding programs to develop high-yielding and nutrient-rich cultivars.

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