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Assessment of Genetic Diversity in Greengram (*Vigna radiata* L.) Using Metroglyph Analysis

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

Pulses like greengram are essential for sustainable agriculture and global food security due to their high protein, complex carbohydrates, fiber, vitamins, and minerals. However, their genetic diversity is underexplored, with existing studies mainly focusing on conventional methods. This study aims to estimate the variability parameters for 16 quantitative characters of greengram to classify the genotypes using Metroglyph analysis and assess genetic divergence to identify divergent parents for future hybridization programs using 45 greengram genotypes using Randomized Block Design replicated thrice. Among 45 genotypes of greengram on the basis of mean performance MGG-351(12.959) followed by MGG-347(43.16 q/ha), VBN -2 (41.12 q/ha), GM-3(40.8 q/ha) and MGG-385(39.8 q/ha) were found superior for grain yield. High GCV and PCV is recorded for Harvest Index and Number of primary branches. High heritability coupled with genetic advance as percent

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of mean are recorded for number of primary branches, harvest index (%), number of seeds per pod, biological yield per plant, seed index, number of pods per plant, number of clusters per plant. On the basis of Metroglyph analysis, the total index score was varied from 24 (SHAKTI) to 38 (SIKHA) with a mean of 31.84. Among the 45 germplasm lines, the genotypes GM-3, MGG-385, SML-1663 and MGG-371were observed as high yielder and identified for higher index score. Scatter diagram plotted with Plant Height and Harvest Index has revealed that 5 clusters could be distinguished on the basis of morphological variation. Cluster -1 was represented by 24 genotypes, Cluster -2 was represented by 10 genotypes, Cluster-3 was represented by 7 genotypes, Cluster-4 was represented by 3 genotype, Cluster -5 was represented by 1 genotype. From those complexes, the germplasm lines, SIKHA and MGG-371 recorded high index score and fell into different cluster, hence used as parents in hybridization for getting desirable transgressive segregants.

Keywords: Greengram; GCV; PCV; heritability; genetic advance; metroglyph analysis.

1. INTRODUCTION

Pulses, including crops like chickpeas, lentils, dry beans, and peas, are essential for sustainable agriculture and food security due to their high protein content and nutritional benefits (Bhatty, 2016). They improve soil fertility through nitrogen fixation, reducing the need for synthetic fertilizers and enhancing soil health (Dwivedi et al., 2020). Pulses also serve as valuable rotation crops, boosting productivity, suppressing weeds, and mitigating pest pressures (McGee et al., 2019). Their deep roots aid nutrient cycling and water management, contributing to agroecosystem efficiency (McGee et al., 2019). Pulses are vital for global food security, offering affordable nutrition and fostering sustainability.

Greengram (*Vigna radiata* L.) is grown for its edible seeds, especially in Asia, Africa, and the Americas. It holds agricultural importance due to its high nutritional content, adaptability to diverse climates, and role in sustainable farming (Singh et al., 2019). Rich in protein, essential amino acids, vitamins, and minerals, green gram supports food security and nutrition (Bhardwaj et al., 2020). It thrives in tropical and subtropical regions with warm, humid climates and well-drained soil (Singh et al*.,* 2019). Its short growth cycle and nitrogen-fixing ability enhance soil fertility and productivity, making it ideal for intercropping and crop rotation (Bhardwaj et al., 2020).

India is the world's largest producer of green gram, with cultivation across all states. In 2021-22, green gram was grown on approximately 40.38 lakh hectares, yielding 31.5 lakh tonnes, with a productivity rate of 783 kg/ha, contributing 11% to the country's total pulse production. In the Kharif season of 2022-23, production reached 17.5 lakh tonnes from 33.37 lakh hectares (1st advance estimates). Andhra Pradesh contributed 4.74% of national production, cultivating 0.97 lakh hectares and producing 0.83 lakh tonnes in 2021-22. For 2022-23, cultivation covered 0.08 lakh hectares, yielding 0.04 lakh tonnes with a productivity of 493 kg/ha.

Green gram displays significant genetic diversity, crucial for breeding programs aimed at improving traits like yield, disease resistance, and stress tolerance (Singh et al., 2019). Research focuses on utilizing molecular markers, morphological analysis, and multivariate techniques to develop cultivars suited to specific agro-ecological conditions. This legume enhances soil fertility through nitrogen fixation, reducing the need for synthetic fertilizers, and serves as an excellent rotational crop in tropical and subtropical regions (Bhardwaj et al., 2020). Its short growth cycle and adaptability to diverse soils optimize land use, improve productivity, and help break pest cycles, reducing pesticide reliance. Additionally, green gram is rich in protein, fiber, vitamins, and minerals, promoting digestive health and offering numerous health benefits, including anti-inflammatory and antioxidant effects (Satheesh & Chidambara Murthy, 2019). It's a versatile, nutritious food option in both traditional and modern diets.

Genetic variability is crucial for crop improvement programs, providing the basis for selecting and breeding varieties with desirable traits. It can be analyzed through statistical parameters like Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability, and genetic advance. GCV represents genetic variability, while PCV includes environmental factors, with high values indicating greater potential for genetic improvement.

Table 1. List of genotypes used in this study

NO.	GENOTYPES LIST	NO.	GENOTYPES LIST
1	MGG-347	24	MGG-295
2	VBN -2	25	PUSHA-105
3	GM-3	26	CO-8
4	MGG-385	27	VBN-3
5	MGG-351	28	SML-1663
6	MGG-348	29	LGG-460
7	KM-2	30	SM-02-103
8	RM-12-11	31	LGG-407
9	MGG-2	32	TM-96-2
10	KM-11-564	33	IPM-2-3
11	VEENA	34	WGG-42
12	IPM-205-7	35	PUSA BAISAKI
13	MGG-371	36	JALGAON781
14	Su-Urd-113	37	WGG37
15	ML-131	38	LGG-450
16	R-288-8	39	ML-131
17	SIKHA	40	SM2029
18	AMULYA	41	BM2002-4
19	SHAKTI	42	SPM 2040
20	MH421	43	RM 12-13
21	IPM-2-14	44	K-851
22	CO-7	45	SAMRAT-CHECK
23	VIRAT		

Heritability measures the extent of genetic influence on traits, and genetic advance estimates the expected gain from selection. Metroglyph analysis is a graphical method for visualizing genetic diversity, helping to classify genotypes and select diverse parents for breeding programs. This study aims to estimate variability parameters, classify genotypes, and identify divergent parents for hybridization using 45 genotypes of Green gram.

2. MATERIALS AND METHODS

The investigation was carried out during *Kharif* 2023 at the Field Experimentation Center of the Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh. A total of 45 green gram genotypes were sown in July using a Randomized Block Design with three replications, maintaining a row spacing of 30 cm and plant spacing of 10 cm. The recommended agricultural practices were followed throughout the experiment. The study focused on assessing key genetic parameters such as heritability, correlation, path analysis, and genetic diversity, all aimed at improving seed yield in green gram.

3. RESULTS AND DISCUSSION

The analysis of variance revealed the existence of significant differences among the genotypes for all the characters studied. Hence, the data of all the 16 characters which showed significant differences among the entries were subjected to further statistical analysis.

Out of 45 genotypes of Greengram evaluated for various characters, all genotypes found to be superior for seed yield per plant in MGG-347 (43.15 g), VBN -2 (41.12 g), GM-3 (40.83 g), MGG-385 (39.86 g), MGG-351 (38.90 g), MGG-348 (38.32 g), KM-2 (38.03 g), RM-12-11 (37.18 g), MGG-2 (36.61 g), KM-11-564 (36.12 g), VEENA (34.63 g), IPM-205-7 (34.40 g) exhibited highest seed yield per plant. And the genotypes SML-1663 (62 days) followed by VBN -2 (63.37 days), KM-11-564 (63.67 days), LGG-407 (64 days), MH421 (64.33 days), LGG-460 (65.17 days), MGG-351 (65.26 days), RM-12-11 (65.28 days), BM2002-4 (65.63 days), SAMRAT-CHECK (65.72 days), VEENA (66.16 days) and GM-3 (66.48 days) have shown early maturity among 45 Greengram genotypes. The genotypes BM2002-4, RM-12-11, MGG-351, LGG-460, MH421, LGG-407, KM-11-564, VBN -2 and SML-

1663 have shown minimum days to maturity & all the genotypes have shown maximum seed yield per plant than Check variety (SAMRAT) used in this study. Therefore, these genotypes may be used in future breeding programme to develop superior varieties with desirable economic traits beneficial for mankind by creating variability by hybridization followed by selection.

A wide range of phenotypic coefficient of variation (PCV) was observed for all the traits ranged from days to maturity (7.585) to harvest index (23.437). Higher magnitude of PCV was recorded for harvest index (23.437), number of primary branches (22.802), while medium magnitude of PCV is recorded for number of seeds per pod (19.396), biological yield per plant (18.641), seed index (17.388), number of pods per plant (15.733), seed yield per plant (15.426), number of clusters per plant (15.265), number of seeds per plant (14.367), pod length (14.26), number of secondary branches (12.321), plant height (10.099). Lower magnitude of PCV is recorded for number of pods per cluster (8.591), days to 50% pod setting (7.695), days to 50% flowering (7.632), days to maturity (7.585).

A wide range of genotypic coefficient of variation (GCV) was observed for all the traits ranged from days to maturity (4.386) to harvest index (22.234). Higher magnitude of GCV was recorded for harvest index (22.234), number of primary branches (21.937), while medium magnitude of GCV is recorded for number of seeds per pod (17.516), biological yield per plant (16.201), seed index (14.932), number of pods per plant (13.87), number of clusters per plant (13.655), seed yield per plant (11.839), number of seeds per plant (11.776), pod length (11.643), number of secondary branches (10.582). Lower magnitude of GCV is recorded for number of pods per cluster (8.492), plant height (8.245), days to 50% flowering (5.135), days to 50% pod setting (5.045), days to maturity (4.386).

In light of recent advancements, the results of this study align closely with previous research findings of Sreethy et al., 2017, Yadav et al., 2017, Sandhiya et al., 2018, Susmitha et al., 2018, Mariyammal et al., 2019, Anuradha et al., 2019, Vadivel et al., 2020, Tamalapakula et al., 2021.

The perusal of the Table 4 revealed the estimates of heritability (%) in broad sense for 14 characters studied, which range from days to maturity (33.435) to number of pods per cluster (97.716). Heritability was recorded for number of pods per cluster (97.716), number of primary branches (92.559), harvest index (90), number of seeds per pod (81.557), number of clusters per plant (80.012), number of pods per plant (77.718), biological yield per plant (75.536), number of secondary branches (73.772), seed index (73.742), number of seeds per plant (67.184), pod length (66.671), plant height (66.651). Medium heritability was recorded for seed yield per plant (58.901), days to 50% flowering (45.282), days to 50% pod setting (42.989). Low heritability was recorded for days to maturity (33.435).

A perusal of genetic advance (Table 4) revealed that it was Medium in harvest index (16.852). Low estimate of genetic advance as percent of mean was recorded for plant height (9.782), biological yield per plant (8.749), number of seeds per plant (4.063), number of primary branches (3.758), days to maturity (3.66), days to 50% pod setting (3.147), number of secondary branches (2.958), number of pods per plant (2.923), days to 50% flowering (2.542), number of seeds per pod (2.428), seed yield per plant (1.831), number of clusters per plant (1.764), pod length (1.449), number of pods per cluster (1.215), seed index (1.006).

High estimate of genetic advance as percent of mean was recorded for number of primary branches (43.477), harvest index (43.452), number of seeds per pod (32.587), biological yield per plant (29.006), seed index (26.414), number of pods per plant (25.189), number of clusters per plant (25.161). Medium estimate of genetic advance as percent of mean was recorded for number of seeds per plant (19.883), pod length (19.585), number of secondary branches (18.724), seed yield per plant (18.717), number of pods per cluster (17.293), plant height (13.866). Low estimate of genetic advance as percent of mean was recorded for days to 50% flowering (7.119), days to 50% pod setting (6.814), days to maturity (5.224).

High heritability coupled with genetic advance as percent of mean are recorded for number of primary branches, harvest index (%), number of seeds per pod, biological yield per plant, seed index, number of pods per plant and number of clusters per plant, indicated that most likely the heritability might be due to additive gene effect and selection may be effective in segregating generation's improvement of these traits.

In light of recent advancements, the results of this study align closely with previous research findings of Patel et al., 2011, Das et al., 2015, Baishak et al., 2016, Sreethy et al., 2017, Ramcahandra et al., 2017, Chandra et al., 2017, Sandhiya et al., 2018, Susmitha et al., 2018, Mariyammal et al., 2019, Anuradha et al., 2019, Vadivel et al., 2020, Sineka et al., 2021, Tamalapakula et al., 2021, Dhunde et al., 2021.

From the Metroglyph Analysis, it is revealed that maximum variability was in Plant height (59.78-81.83) followed by Days to maturity (62-76.59), Days to 50% Flowering (31.43-39.88) and Harvest Index (16.77-54.79). These traits thus were most variable for classificatory analysis in Greengram.

The total index score was varied from 24 (SHAKTI) to 38 (SIKHA) with a mean of 31.84. It indicates that germplasm lines have variations. In the present investigation, it is interesting to note that high seed yielding genotypes were found with highest index score. Among the 45 germplasm lines, the genotypes GM-3, MGG-385, SML-1663 and MGG-371, were observed as high yielder and identified for higher index score.

In light of recent advancements, the results of this study align closely with previous research findings of Abbas et al., 2010, Ghulam Abbas et al., 2011, Jha et al., 2011, Sahu et al., 2014, Hemant Sahu et al., 2014, Ahmad et al., 2019, Win et al., 2020, Lal et al., 2022.

The frequency diagram of index score for 45 greengram genotypes revealed that only one genotype had index score 38 and 24, respectively. Eight genotypes had index score 32. The scatter diagram revealed that 5 clusters could be distinguished on the basis of morphological variation.

Cluster -1 was represented by 24 genotypes with Plant Height and Harvest Index

Cluster -2 was represented by 10 genotypes with Plant Height and Harvest Index

Cluster-3 was represented by 7 genotypes with Plant Height and Harvest Index

Cluster-4 was represented by 3 genotypes with Plant Height and Harvest Index

Cluster-5 was represented by 1 genotype with Plant Height and Harvest Index

Table 2. ANOVA for 16 quantitative characters of greengram (*Vigna radiata* L.) genotypes

Sl.No.	**Source**	**Mean Sum of Squares (MSS)**		
		Replication	**Treatment**	**Error**
	Degrees of freedom	**2**	**44**	**88**
1	Days to 50% flowering	12.1550	14.154**	4.064
2	Days to 50% pod setting	10.2840	23.485**	7.199
3	Days to maturity	40.470	47.115**	18.794
4	Plant height	36.9720	118.432**	16.929
5	Number of primary branches per plant	0.2420	11.076**	0.289
6	Number of secondary branches per plant	2.6850	9.379**	0.994
7	Number of clusters per plant	0.6850	2.978**	0.229
8	Number of pods per plant	0.8690	8.517**	0.743
9	Pod length	0.7550	2.597**	0.371
10	Number of seeds per pod	0.4830	5.494**	0.385
11	Number of pods per cluster	0.629**	1.076**	0.008
12	Number of seeds per plant	0.8960	20.199**	2.828
13	Biological yield per plant	18.7360	79.368**	7.734
14	Seed Index	0.2460	1.086**	0.115
15	Harvest Index	17.9550	231.329**	8.261
16	Seed yield per plant (q/ha)	2.5140	4.961**	0.936

and ** are Significant at 5 percent and 1 percent level of significance respectively

Table 3. Mean performance of 45 greengram genotypes for 16 characters during Kharif-2023

S No.	Genotypes	DFF	D50%PS	DM	PH	NPB	NSB	NCP	NPP	PL	NSPo	NPC	NSPl	BYP	SI	HI	SYP
1	MGG-347	33.25	49.42	72.73	61	8.2	13.98	5.18	10.21	7.73	7.51	7.65	19.11	24.06	3.76	35.03	43.15
2	VBN -2	34.44	45.36	63.37	74.1	12.2	17.7	7.79	11.25	8.33	8.89	7.4	17.29	26.92	4.74	37.63	41.13
3	GM-3	38.5	50.76	66.48	79.6	11.8	16.95	6.03	14.57	7.01	5.07	6.27	20.61	38.98	3.6	44.34	40.84
4	MGG-385	38.25	47.01	75.08	75.5	10.1	14.96	6.32	10.46	6.94	6.36	7.6	21.81	31.13	3.93	38.48	39.87
5	MGG-351	36.33	43.28	65.26	74.5	8.9	15.27	5.95	8.07	7.95	6	7.42	17.42	23.04	3.5	41.27	38.91
6	MGG-348	36.77	45.99	75.14	81.3	12.1	14.82	7.89	8.96	8.09	5.11	6.99	20	32.4	4.81	47.99	38.32
7	KM-2	39.66	46.96	74.41	60.6	8.4	14.72	5.66	13.17	7.81	8.14	7.75	21.9	29.6	3.71	46.66	38.04
8	RM-12-11	37.25	49.82	65.28	76.1	7.8	14.13	7.22	10.47	8.25	6.83	6.11	21.76	39.09	4.35	42.08	37.19
9	MGG-2	35.1	45.9	69.42	76.7	5.5	17.63	5.27	10.67	5.97	7.9	6.79	16.92	27.17	3.45	35.63	36.61
10	KM-11-564	34.6	50.57	63.67	72.5	12	13.21	5.37	8.45	8.02	5.27	7.03	22.91	26.28	5	48.32	36.12
11	VEENA	33.9	46.15	66.16	75.3	5.2	15.29	6.35	10.79	8.74	5.94	6.63	19.49	29.81	4.06	54.79	34.63
12	IPM-205-7	35.5	43.72	71.7	79.4	11.4	18.9	8.7	8.26	8.66	6.29	7.92	20.92	30.58	4.1	46.1	34.4
13	MGG-371	37.66	48.14	68.66	66.4	10.6	14.95	7.14	14.98	5.69	8.04	7.43	24.62	34.6	4.54	50.27	33.92
14	Su-Urd-113	34.22	43.9	73.5	66.6	12	16.31	7.22	8.97	5.79	6.45	7.5	18.08	28.98	4.12	44.11	33.73
15	ML-131	33.33	49.73	73.16	67.7	7.7	17.85	7.52	9.41	5.62	6.5	6.19	17.32	34.89	3.15	49.49	33.36
16	R-288-8	36.75	52.2	72.75	72.8	6.2	15.61	7.81	10.52	7.36	7.28	7.22	17.54	26.4	3.1	49.15	33.3
17	SIKHA	39.88	49.87	76.59	81.61	9.33	17.13	8.01	14.6	7.92	9.1	6.27	19.11	30.27	4.13	33.45	33.08
18	AMULYA	37.44	46.67	71	63.63	8.2	17.77	6.47	11.87	6.99	7.7	7.74	21.1	29.8	3	27.83	33.07
19	SHAKTI	38.44	47.34	72	60.9	5.34	16.32	5.93	10.53	6.57	7.1	6.22	17.77	22.87	2.9	20.22	33.07
20	MH421	31.43	42	64.33	75.14	8.6	13.26	7.6	12.93	7.16	8.07	7.91	20.81	20.6	4.06	35.98	32.87
21	IPM-2-14	33.44	42.67	70.67	64.18	8.33	13.85	7.87	13	7.22	8.8	7.6	22.03	27.47	4.56	40.16	32.63
22	CO-7	38.11	47.33	70.67	67.45	8.07	18.44	6.53	11.73	5.98	9	7.77	18.68	24.53	2.8	30.31	32.4
23	VIRAT	34.77	45	69	71.84	7.8	15.62	7.4	12.73	6.33	8.03	6.19	17.42	26.93	3.6	22.08	32.3
24	MGG-295	34.62	45.33	68.33	74.05	8.6	15.14	7.13	13.2	7.18	9.34	6.47	20.9	20.13	3.56	37.88	32.04
25	PUSHA-105	37.44	47.33	71.67	67.01	8.46	16.43	7.4	12.27	7.22	8.2	6.59	21.49	26.4	4.3	37.92	31.85
26	CO-8	37.1	46.66	71.33	59.78	5.53	13.98	6.53	11.47	5.76	6.77	7.64	16.06	29.33	3.9	20.31	31.83
27	VBN-3	39.43	48	71.33	69.77	8	18.12	5.87	11.67	7.33	7.39	7.06	24.58	33.73	2.83	16.77	31.73
28	SML-1663	35.1	42	62	74.62	9.2	17.78	8.2	13.93	7.45	9.45	7.35	24.05	27.13	4.33	43.76	31.67
29	LGG-460	32.86	41	65.17	70.97	8.73	18.27	8	12.87	7.58	9.13	7.69	22.11	24.07	4.1	38.71	31.64
30	SM-02-103	34.44	42.67	67.83	72.42	8.07	18.2	6.47	11.73	6.56	8.57	6.92	21.63	28.13	3.2	29.13	31.24
31	LGG-407	34.1	44.33	64	81.83	11.33	13.99	8.4	13.07	7.33	9.67	7.46	16.82	33	4.46	38.98	29.75
32	TM-96-2	34.77	44.67	69.5	64.82	6.8	16.91	6.07	10.13	6.56	7.77	6.16	23.93	27.47	2.76	22.7	29.6

S No.	**Genotypes**	**DFF**	**D50%PS**	**DM**	**PH**	**NPB**	**NSB**	**NCP**	**NPP**	**PL**	**NSPo**	**NPC**	**NSPl**	**BYP**	**SI**	**HI**	**SYP**
33	IPM-2-3	37.11	43	69.33	65.89	8.07	13.12	7.93	12.87	7.43	9.49	7.29	17.08	32	4.16	37.24	29.59
34	WGG-42	35.1	44.67	68.33	71.17	8.93	14.09	8.2	14.33	7.59	9.67	6.8	16.65	29.67	4.1	37.8	29.3
35	PUSA BAISAKI	38.77	50.27	74.67	74.88	8.94	14.97	6.73	11.78	8.57	7.68	6.59	24.93	33.42	3.2	35.91	28.64
36	JALGAON781	36.23	43.71	72.1	78.9	9.2	15.12	8.07	11.37	5.72	5.83	6.1	20.13	36.52	4.6	46.21	28.64
37	WGG37	34.44	46.05	75.24	70.6	5.4	13.45	7.98	12.42	8.73	7.02	7.37	22.5	31.77	4.04	44.01	28.37
38	LGG-450	35.42	47.41	75.13	69.86	6.84	13.67	8.21	11.41	8.36	6.47	7.02	22.68	30.49	3.75	41.17	28.21
39	ML-131	31.43	46.22	75.35	76.3	10.4	14.55	6.89	10.89	8.35	8.26	7.74	22.22	32.22	3.01	38.23	28.21
40	SM2029	34.25	43.63	69.56	69.4	10	13.16	8.63	10.87	8.37	6.51	7.19	22.67	29.12	4.26	37.93	27.86
41	BM2002-4	35.15	51.24	65.63	62.8	9.9	16.28	7.65	11.29	8.54	5.29	7.75	23.77	40.06	3.86	38.45	27.44
42	SPM 2040	38.6	48.15	74.93	62.2	7.4	15.08	6.23	11.9	8.25	5.12	6.44	21.88	38.1	3.09	44.23	27.31
43	RM 12-13	32.7	45.04	75.16	68.1	6.7	18.36	6.13	11.18	8.06	8.56	6.29	16.04	40.04	4.4	43.31	26.99
44	K-851	33.44	44.5	69	61.3	9.2	18	5.69	12.28	8.23	7.22	6.43	23.23	40.39	3.35	41.19	26.64
45	SAMRAT-CHECK	35.5	42.5	65.72	63.3	7.5	17.6	5.83	12.75	7.66	6.47	6.22	19.64	27.69	3.2	52.02	24.64
Mean		35.71	46.18	70.05	70.55	8.64	15.8	7.01	11.61	7.4	7.45	7.03	20.43	30.16	3.81	38.78	9.78
Range	**Minimum**	31.43	41	62	59.78	5.2	13.12	5.18	8.07	5.62	5.07	6.1	16.04	20.13	2.76	16.77	24.64
	Maximum	39.88	52.2	76.59	81.83	12.2	18.9	8.7	14.98	8.74	9.67	7.92	24.93	40.39	5	54.79	43.15
CV		5.65	5.81	6.19	5.83	6.22	6.31	6.82	7.43	8.23	8.33	1.3	8.23	9.22	8.91	7.41	9.89
SEm		1.16	1.55	2.5	2.38	0.31	0.58	0.28	0.5	0.35	0.36	0.05	0.97	1.61	0.2	1.66	0.56
CD at 5%		3.27	4.35	7.03	6.68	0.87	1.62	0.78	1.4	0.99	1.01	0.15	2.73	4.51	0.55	4.66	1.57
CD at 1%		4.33	5.77	9.32	8.85	1.16	2.14	1.03	1.85	1.31	1.33	0.2	3.62	5.98	0.73	6.18	2.08
Replication		NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	S	NS	NS	NS	NS	NS
Treatment		S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S

DFF- Days to 50% Flowering, D50%PS – Days to 50% Pod Setting, DM – Days to Maturity, PH – Plant Height, NPB – Number of Primary Branches, NSB – Number of Secondary Branches, NCP – Number of Clusters per Plant, NPP – Number of Pods per Plant, PL - Pod Length, NSPo – Number of Seeds per Pod, NPC – Number of Pods per Cluster, NSPl – Number of Seeds per Plant, BYP – Biological Yield per Plant, SI - Seed Index, HI – Harvest Index, SYP – Seed Yield per Plant

Table 4. Estimates of genetic parameters for 14 quantitative characters in greengram

Sl.No.	Characters	GCV	PCV	h^2 (Broad Sense)	Genetic Advance 5%	Genetic Advance as % of Mean 5%
1	Days to 50% flowering	5.14	7.63	45.28	2.54	7.12
2	Days to 50% pod setting	5.05	7.70	42.99	3.15	6.81
3	Days to maturity	4.39	7.59	33.44	3.66	5.22
4	Plant height	8.25	10.10	66.65	9.78	13.87
5	Number of primary branches per plant	21.94	22.80	92.56	3.76	43.48
6	Number of secondary branches per plant	10.58	12.32	73.77	2.96	18.72
7	Number of clusters per plant	13.66	15.27	80.01	1.76	25.16
8	Number of pods per plant	13.87	15.73	77.72	2.92	25.19
9	Pod length	11.64	14.26	66.67	1.45	19.59
10	Number of seeds per pod	17.52	19.40	81.56	2.43	32.59
11	Number of pods per cluster	8.49	8.59	97.72	1.22	17.29
12	Number of seeds per plant	11.78	14.37	67.18	4.06	19.88
13	Biological yield per plant	16.20	18.64	75.54	8.75	29.01
14	Seed Index	14.93	17.39	73.74	1.01	26.41
15	Harvest Index	22.23	23.44	90.00	16.85	43.45
16	Seed yield per plant (q/ha)	11.84	15.43	58.90	1.83	18.72

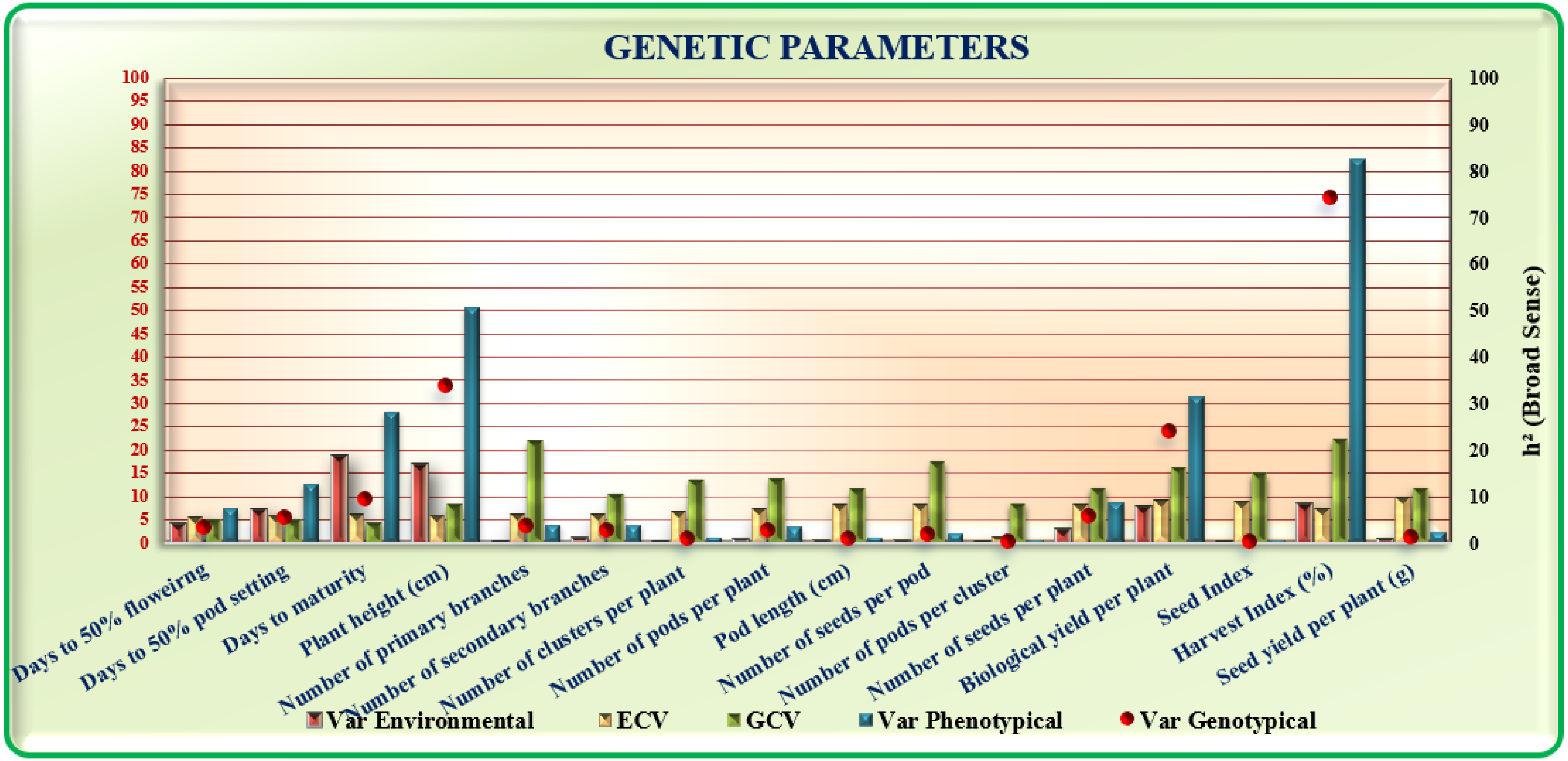

Fig. 1. Bar diagram deplicting GCV, PCV, heritability and genetic advance for 16 quantitative characters of greengram

Table 5. Range variability and class intervals of 16 quantitative characters

S No.	Character	Range of Mean	Score 1	Sign	Score 2	Sign	Score 3	Sign
			Value <		Value from - to		Value >	
1	Days to 50% flowering	31.43-39.88	33.54	○	33.54-37.88		37.88	
2	Days to 50% pod setting	41-52.2	43.38	○	43.38-48.98		48.98	
3	Days to maturity	62-76.59	66.09	○	66.09-74.01		74.01	
4	Plant height	59.78-81.83	64.27	○	64.27-76.83	○	76.83	○
5	Number of primary branches	5.2-12.2	6.72	○	6.72-10.57		10.57	
6	Number of secondary branches	13.12-18.9	14.03	○	14.03-17.57		17.57	
7	Number of clusters per plant	5.18-8.7	6.01	○	6.01-8.01		8.01	
8	Number of pods per plant	8.07-14.98	9.92	○	9.92-13.29	○	13.29	○
9	Pod length	5.62-8.74	6.47	○	6.47-8.33		8.33	
10	Number of seeds per pod	5.07-9.67	6.10	○	6.1-8.8	○	8.80	○
11	Number of pods per cluster	6.1-7.92	6.43	○	6.43-7.62		7.62	
12	Number of seeds per plant	16.04-24.93	17.84	○	17.84-23.03		23.03	
13	Biological yield per plant	20.13-40.39	25.02	○	25.02-35.31		35.31	
14	Seed Index	2.76-5	3.21	○	3.21-4.41		4.41	

S No.	Character	Range of Mean	Score 1	Sign	Score 2	Sign	Score 3	Sign
			Value <		Value from - to		Value >	
15	Harvest Index	16.77-54.79	30.00	○	30-47.56	○	47.56	○
16	Seed yield per plant	7.4-12.96	8.50	○	8.5-11.07	⊘	11.07	⊘

Table 6. Mean and index scores for yield and yield-contributing characters in greengram

S No.	Genotypes	DFF	D50%PS	DM	PH	NPB	NSB	NCP	NPP	PL	NSPo	NPC	NSPl	BYP	SI	HI	SYP	Total Index Score
1	MGG-347	1	3	2	1	2	1	1	2	2	2	3	2	1	2	2	3	30
2	VBN -2	2	2	1	2	3	3	2	2	3	3	2	1	2	3	2	2	35
3	GM-3	3	3	2	3	3	2	2	3	2	1	1	2	3	2	2	3	37
4	MGG-385	3	2	3	2	2	2	2	2	2	2	2	2	2	2	2	3	35
5	MGG-351	2	1	1	2	2	2	1	1	2	1	2	1	1	2	2	3	26
6	MGG-348	2	2	3	3	3	2	2	1	2	1	2	2	2	3	3	2	35
7	KM-2	3	2	3	1	2	2	1	2	2	2	3	2	2	2	2	2	33
8	RM-12-11	2	3	1	2	2	2	2	2	2	2	1	2	3	2	2	2	32
9	MGG-2	2	2	2	2	1	3	1	2	1	2	2	1	2	2	2	3	30
10	KM-11-564	2	3	1	2	3	1	1	1	2	1	2	2	2	3	3	1	30
11	VEENA	2	2	2	2	1	2	2	2	3	1	2	2	2	2	3	1	31
12	IPM-205-7	2	2	2	3	3	3	3	1	3	2	3	2	2	2	2	2	37
13	MGG-371	2	2	2	2	3	2	2	3	1	2	2	3	2	3	3	2	36
14	Su-Urd-113	2	2	2	2	3	2	2	1	1	2	2	2	2	2	2	2	31
15	ML-131	1	3	2	2	2	3	2	1	1	2	1	1	2	1	3	2	29
16	R-288-8	2	3	2	2	1	2	2	2	2	2	2	1	2	1	3	2	31
17	SIKHA	3	3	3	3	2	2	3	3	2	3	1	2	2	2	2	2	38
18	AMULYA	2	2	2	1	2	3	2	2	2	2	3	2	2	1	1	1	30
19	SHAKTI	3	2	2	1	1	2	1	2	2	2	1	1	1	1	1	1	24
20	MH421	1	1	1	2	2	1	2	2	2	2	3	2	1	2	2	1	27
21	IPM-2-14	1	1	2	1	2	1	2	2	2	3	2	2	2	3	2	2	30
22	CO-7	3	2	2	2	2	3	2	2	1	3	3	2	1	1	2	2	33
23	VIRAT	2	2	2	2	2	2	2	2	1	2	1	1	2	2	1	2	28

S No.	Genotypes	DFF	D50%PS	DM	PH	NPB	NSB	NCP	NPP	PL	NSPo	NPC	NSPl	BYP	SI	HI	SYP	Total Index Score
24	MGG-295	2	2	2	2	2	2	2	2	2	3	2	2	1	2	2	2	32
25	PUSHA-105	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	32
26	CO-8	2	2	2	1	1	1	2	2	1	2	3	1	2	2	1	1	26
27	VBN-3	3	2	2	2	2	3	1	2	2	2	2	3	2	1	1	2	32
28	SML-1663	2	1	1	2	2	3	3	3	2	3	2	3	2	2	2	2	35
29	LGG-460	1	1	1	2	2	3	2	2	2	3	3	2	1	2	2	2	31
30	SM-02-103	2	1	2	2	2	3	2	2	2	2	2	2	2	1	1	1	29
31	LGG-407	2	2	1	3	3	1	3	2	2	3	2	1	2	3	2	2	34
32	TM-96-2	2	2	2	2	2	2	2	2	2	2	1	3	2	1	1	2	30
33	IPM-2-3	2	1	2	2	2	1	2	2	2	3	2	1	2	2	2	2	30
34	WGG-42	2	2	2	2	2	2	3	3	2	3	2	1	2	2	2	2	34
35	PUSA BAISAKI	3	3	3	2	2	2	2	2	3	2	2	3	2	1	2	2	36
36	JALGAON781	2	2	2	3	2	2	3	2	1	1	1	2	3	3	2	2	33
37	WGG37	2	2	3	2	1	1	2	2	3	2	2	2	2	2	2	2	32
38	LGG-450	2	2	3	2	2	1	3	2	3	2	2	2	2	2	2	2	34
39	ML-131	1	2	3	2	2	2	2	2	3	2	3	2	2	1	2	1	32
40	SM2029	2	2	2	2	2	1	3	2	3	2	2	2	2	2	2	2	33
41	BM2002-4	2	3	1	1	2	2	2	2	3	1	3	3	3	2	2	2	34
42	SPM 2040	3	2	3	1	2	2	2	2	2	1	2	2	3	1	2	3	33
43	RM 12-13	1	2	3	2	1	3	2	2	2	2	1	1	3	2	2	3	32
44	K-851	1	2	2	1	2	3	1	2	2	2	2	3	3	2	2	2	32
45	SAMRAT-CHECK	2	1	1	1	2	3	1	2	2	2	1	2	2	1	3	3	29

Table 7. Classification of 45 genotypes into five complexes in scattered diagram

Complex	Name of complex	No. of lines	Name of lines	Range and average score
I	Higher plant height with higher harvest index	24	VBN -2, GM-3, MGG-385, MGG-351, MGG-348, RM -12-11, MGG-2, KM-11-564, IPM-205-7, R-288-8, SIKHA, MH421, CO-7, MGG-295, SML-1663, LGG-460, LGG-407, WGG-42, PUSA BAISAKI, JALGAON781, WGG37, LGG-450, ML-131 and SM2029	26.00-38.00 (33.00)
II	Lower plant height with lower harvest index	10	MGG-347, KM-2, Su-Urd-113, IPM-2-14, PUSHA-105, IPM-2-3, BM2002-4, SPM 2040, RM 12-13 and K-851	30.00-34.00 (31.70)
III	Lower plant height with moderate harvest index	7	AMULYA, SHAKTI, VIRAT, CO-8, VBN-3, SM-02-103 and TM-96-2	24.00-32.00 (28.42)
IV	Lower plant height with higher harvest index	3	MGG-371, ML-131 and SAMRAT-CHECK	29.00-36.00 (31.33)
V	Higher plant height with very high harvest index	1	VEENA	31.00

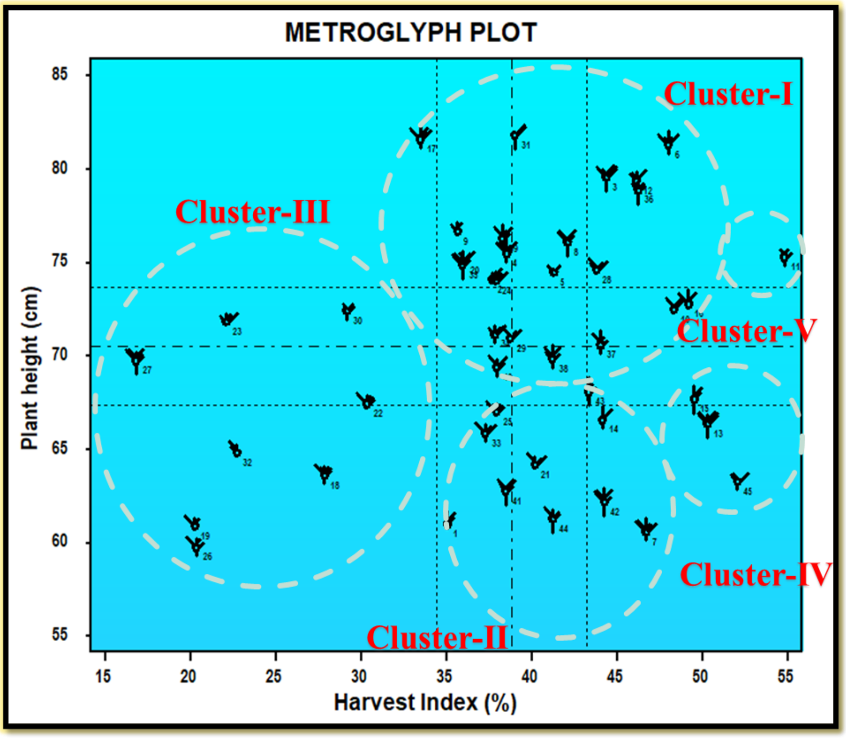

Fig. 2. Scatter diagram of Metroglyph Analysis

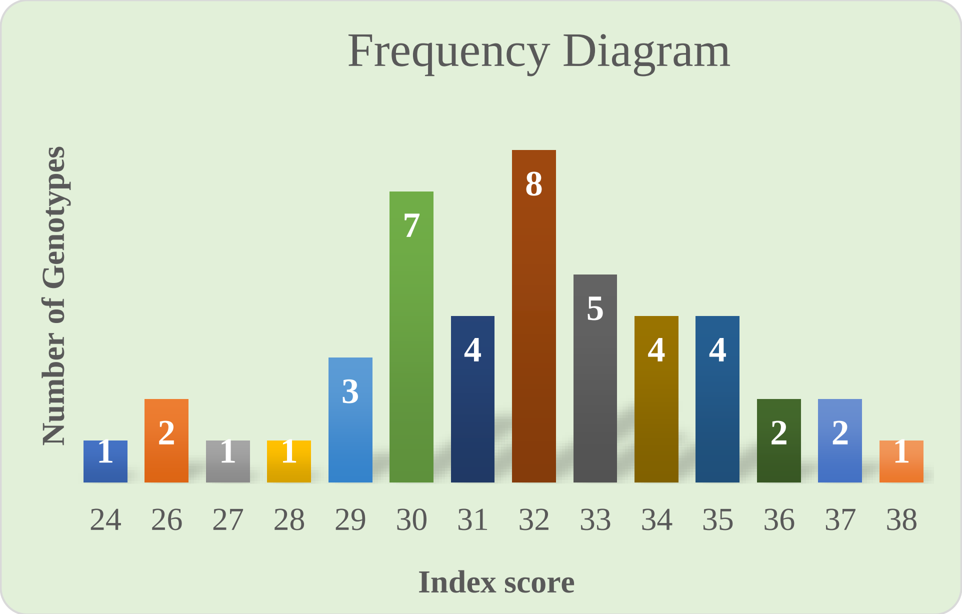

Fig. 3. Frequency diagram of index score for 45 greengram genotypes

4. CONCLUSION

From present investigation, it is concluded that among 45 genotypes of Greengram on the basis of mean performance MGG-351(12.959) followed by MGG-347(43.16 q/ha), VBN -2 (41.12 q/ha), GM-3(40.8 q/ha) and MGG-385(39.8 q/ha) were found superior for grain yield. High GCV and PCV is recorded for Harvest Index Number of primary branches. High heritability coupled with genetic advance as percent of mean are recorded for number of primary branches, harvest index (%), number of seeds per pod, biological yield per plant, seed index, number of pods per plant, number of clusters per plant. On the basis of Metroglyph analysis, the total index score varied from 24 (SHAKTI) to 38 (SIKHA) with a mean of 31.84. Among the 45 germplasm lines, the genotypes GM-3, MGG-385, SML-1663 and MGG-371were observed as high yielder and identified for higher index score. Scatter diagram plotted with plant height and harvest index has revealed that 5 clusters could be distinguished on the basis of morphological variation. Cluster -1 was represented by 24 genotypes, Cluster -2 was represented by 10 genotypes, Cluster-3 was represented by 7 genotypes, Cluster-4 was represented by 3 genotype, Cluster -5 was represented by 1 genotype. From those complexes, the germplasm lines, SIKHA and MGG-371 recorded high index score and fell into different cluster, hence used as parents in hybridization for getting desirable transgressive segregants.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

Abbas, G., Asghar, M. J., Shah, T. M., & Atta, B. M. (2010). Genetic diversity in mungbean (*Vigna radiata* (L.) Wilczek) germplasm. *Pakistan Journal of Botany*, 42(5), 3485-3495.

Ahmad, H. B., Rauf, S., Chattha, W. S., Hussain, B., Hussain, I., & Rasool, I. (2019). Diversity analysis of mungbean (*Vigna radiata*) germplasm using a semi-graphical technique. *South African Journal of Plant and Soil*, 36(5), 393-396.

Anuradha, N., Patro, T. S. S. K., & Kumar, S. R. (2019). Study on genetic variability, heritability and correlation analysis for grain yield and yield attributing traits in green gram [*Vigna radiata* (L.) Wilczek.]. *International Journal on Conservation of Science*, 7, 2050-2052.

Baisakh, B., Swain, S. C., Panigrahi, K. K., Das, T. R., & Mohanty, A. (2016). Estimation of genetic variability and character association in micro mutant lines of greengram [*Vigna radiata* (L.) Wilczek] for yield attributes and cold tolerance. *Legume Genomics and Genetics*, 7.

Bhardwaj, J., Anuradha, V., & Nadarajan, N. (2020). Genetic diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes based on agro-morphological traits and simple sequence repeat markers. *Indian Journal of Agricultural Sciences*, 90(7), 39–46.

Bhatty, R. S. (2016). Pulse Foods: Processing, Quality, and Nutraceutical Applications. Academic Press.

Chandel, D., Anchra, S., Kumar, A., Kumar, R., Kothyari, H. S., & Sharma, N. K. (2024). Assessment of Genetic Variability for Agroeconomic Traits in Green Gram: GENETIC VARIABILITY IN GREEN GRAM. *Annals of Arid Zone*, 63(2), 155-159.

Chandra, G. S., Lavanya, G. R., & Kulkarni, S. D. (2017). Studies on Genetic diversity in Greengram (*Vigna radiata* L. Wilczek) for seed yield characters. *Journal of Pharmacognosy and Phytochemistry*, 6(6), 1765-1767.

Das, R. T., & Barua, P. K. (2015). Association Studies for Yield and its components in Green Gram. *International Journal of Agriculture*, *Environment and Biotechnology*, 8(3), 561-565.

Desai, V. K., Parmar, L. D., Chaudhary, A. R., & Chaudhary, N. B. (2020). Genetic variability, correlation, path coefficient and stability analysis for yield and its attributing traits in summer greengram [*Vigna radiata* (L.) Wilczek] accessions. *International Journal of Current Microbiology and Applied Sciences*, 9(6), 2942-2955.

Dwivedi, S. L., Lammerts van Bueren, E. T., Ceccarelli, S., Grando, S., Upadhyaya, H. D., Ortiz, R., & Sahrawat, K. L. (2020). Diversifying Food Systems in the Pursuit of Sustainable Food Production and Healthy Diets. *Trends in Plant Science*, 25(11), 1096–1107.

Garje, U. A., Bhailume, M. S., & Nagawade, D. R. (2013). Genetic diversity analysis of green gram (*Vigna radiata* (L.) Wilczek.). *The Bioscan*, 8(4), 1477-1480.

Ghulam Abbas, G. A., Asghar, M. J., Shah, T. M., & Atta, B. M. (2010). Genetic diversity in mungbean (*Vigna radiata* L.) Wilczek germplasm. *Pakistan Journal of Botany*, 2010,. 42(5), 3485-349

Harsh, P., & Priyal, P. (2023). Genetic variability and correlation in green gram [*Vigna radiata* (L.) R. Wilczek]. *Plant archives*, 23(2), 144-8.

Hemant Sahu, H. S., Satyapal Singh, S. S., Jairam Amadabade, J. A., & Anupam Barh, A. B. (2014). Genetic divergence study in advanced breeding lines of mungbean in tarai region. *Electronic Journal of Plant Breeding*, 5(4), 657-663

Hemavathy, A. T., Shunmugavalli, N., & Anand, G. (2015). Genetic variability, correlation and path co-efficient studies on yield and its components in mungbean [*Vigna radiata* (L.) Wilezek]. *Legume Research-An International Journal*, 38(4), 442-446.

Jain, N., Sikarwar, R. S., Tripathi, M. K., Tiwari, S., Rahangdale, S., & Barela, A. (2024). Assessment of genetic variability, heritability and genetic advance for seed yield and its contributing traits in greengram [*Vigna radiata* (L.) Wilczek]. *International Journal of Environment and Climate Change*, 14(3), 250-256.

Jayaprada, A., Lavanya, R., Babu, R., Naga, C. H., Krishna, S., & Reddy, T. S. (2021). Genetic variabitity, heritability and genetic advance for yield and yield contributing traits of greengram, *Journal of AgriSearch*, 8(2), 89-94.

Jha, U. C., Singh, D. P., Paul, P. J., & Lavanya, G. R. (2011). Metroglyph analysis for morphological variation in chickpea (*Cicer arietinum* L.). *Madras Agricultural Journal*, 98(apr-jun), 1.

John Kingsly N. B., Aravinth, R. (2024). Studies on genetic diversity in green gram (*Vigna radiata* L. Wilczek) for yield and its attributing traits. *Euphytica* 220, 12

Khatik, C. L., Dhaka, S. R., Uddin, A., Chandra, K., Khan, M. A., Attar, S. K., ... & Kumawat, S. (2022). Estimates of Genetic variability for seed yield and its component characters in green gram (*Vigna radiata*, fabaceae). *Asian Journal on Agriculture, Extension, Economics and Sociology*, 40(10), 992-997.

Kumar, K., Prasad, Y., Mishra, S. B., Pandey, S. S., & Kumar, R. (2013). Study on genetic variability, correlation and path Analysis with grain yield and yield attributing traits in green gram [*Vigna radiata* (L) Wilczek]. *The Bioscan*, 8(4), 1551-1555.

Majhi, P. K., Mogali, S. C., & Abhisheka, L. (2020). Genetic variability, heritability, genetic advance and correlation studies for seed yield and yield components in early segregating lines (F3) of greengram [*Vigna radiata* (L.) Wilczek]. *International Journal of Chemical Studies*, 8(4), 1283-1288.

Mariyammal, I., Pandiyan, M., Vanniarajan, C., Kennedy, J. S., & Senthil, N. (2019). Genetic variability in segregating generations of greengram (*Vigna radiata* L. Wilczek) for quantitative traits. *Electronic Journal of Plant Breeding*, 10(1), 293- 296.

McGee, R. J., Douglas, C. L. Jr., & Wood, C. W. (2019). Legumes in Crop Rotations. *Agronomy Journal*, 111(1), 1–14.

Nayak, G., Lenka, D., Dash, M., & Tripathy, S. K. (2022). Genetic diversity and protein analysis in greengram. *Biological Forum – An International Journal*, 14(2): 994- 999.

PATEL, S. R., Patel, K. K., & Parmar, H. K. (2011). Genetic variability, correlation and path analysis for seed yield and its components in green gram [*Vigna radiata* (L.) Wilczek] (Doctoral dissertation, *ANAND AGRICULTURAL UNIVERSITY*).

Priyanka, B., Singh, D. P., & Khulbe, R. K. (2018). Metroglyph analysis for morphological variation in advanced lines and cultivars of intervarietal and interspecific crosses in blackgram (*Vigna mungo* L. Hepper). *Environment and Ecology*, 36(1), 175-180.

Priyanka, S. L., Satyanarayana, N. H., Babu, J. S., & Ramesh, D. (2023). Genetic Variability Studies for Yield and Nutritional Quality Traits in Greengram [*Vigna radiata* (L.) Wilczek]. *The Andhra Agriculture Journal,* 70 (1): 062-065

Ramachandra, P., & Lavanya, G. R. (2017). Variability, heritability genetic advance and correlation coefficients for yield component characters and seed yield in Greengram (*Vigna radiate* (L.) Wilczek). *Journal of Pharmacognosy and Phytochemistry*, 6(4), 1202-1205.

Ramakrishnan, C. D., Savithramma, D. L., & Vijayabharathi, A. (2018). Studies on genetic variability, correlation and path analysis for yield and yield related traits in greengram (*Vigna radiata* (L.) Wilczek). *International Journal of Current Microbiology and Applied Sciences*, 7(3), 2753-2761.

Sahu, H., Singh, S., Amadabade, J., & Barh, A. (2014). Genetic divergence study in advanced breeding lines of mungbean in tarai region. *Electronic Journal of Plant Breeding*, 5(4), 657-663.

Salman, M. A. S., Anuradha, C., Sridhar, V., Babu, E. R., & Pushpavalli, S. N. C. V. L. (2023). Genetic variability for yield and its related traits in green gram [*Vigna radiata* (L.) Wilczek]. *Legume Research-An International Journal*, 46(6), 700- 704.

Sandhiya, V., & Shanmugavel, S. (2018). Genetic variability and correlation studies in greengram (*Vigna radiata* L. Wilczek). *Electronic Journal of Plant Breeding*, 9(3), 1094-1099.

Sasipriya, S., Parimala, K., Eswari, K. B., & Balram, M. (2022). Principal component analysis and metroglyph of variation among sesame (*Sesamum indicum* L.) genotypes. *Electronic Journal of Plant Breeding*, 13(4), 1234-1242.

Sharma, H. K., Singh, D. P., Kumar, A., & Shrotria, P. K. (2013). Evaluation of F4 progenies emanated from an interspecific hybridization of mungbean and blackgram. *Legume Research-An International Journal*, 36(3), 191-199.

Sineka, T., Murugan, E., Sheeba, A., Hemalatha, G., & Vanniarajan, C. (2021). Genetic relatedness and variability studies in greengram (*Vigna radiata* (L.) Wilczek). *Electronic Journal of Plant Breeding*, 12(4), 1157-1162.

Singh, A., Rajput, R., Singh, R., Kumar, P., & Kumar, A. (2019). Genetic diversity analysis in green gram (*Vigna radiata* L. Wilczek). *Journal of Pharmacognosy and Phytochemistry*, 8(4), 164–168.

Sreethy, T. S., Lavanya, G. R., Arya, P., & Jahagirdar, J. E. (2017). Genetic variability, trait association and path analysis of yield and yield components in greengram [*Vigna radiata* (L.) Wilczek]. *Research on Crops*, 18(4), 711-717.

Susmitha, D., & Jayamani, P. (2018). Genetic variability studies for yield and its contributing traits in greengram [*Vigna radiata* (L.) Wilczek]. *Electronic Journal of Plant Breeding*, 9(2), 716-722.

Tamalapakula, T. A. J., Lavanya, G. R., Babu, V. R., Krishna, C. N. S., & T Sudheer, Reddy (2021). Genetic variability, heritability and genetic advance for yield and yield contributing traits of greengram: Variability in yield and yield contributing traits of greengram. *Journal of Agri Search*, 8(2), 89-94.

Thonta, R. (2023). Analysis of genetic variability, heritability and genetic advance for growth and yield attributes in green gram (*Vigna radiata* L. Wilczek). *International Journal of Statistics and Applied Mathematics*. SP-8(3): 43-47.

Udayasri, S., Lavanya, G. R., & Lal, G. M. (2022). Estimation of variability and genetic divergence in greengram [*Vigna radiata* (L.) Wilczek] for yield characters. *International Journal of Plant Soil Science*, 34(23), 49-56.

Vadivel, K., Mahalingam, A., & Manivannan, N. (2020). Genetic analysis on the extent of variability among the greengram (*Vigna radiata* (L.) Wilczek) genotypes. *Electronic Journal of Plant Breeding*, 11(02), 686-689.

Wesly, K. C., Nagaraju, M., & Lavanya, G. R. (2020). Estimation of genetic variability and divergence in Greengram *Vigna radiata* (L.) germplasm. *Journal of Pharmacognosy and Phytochemistry*, 9(2), 1890-1893.

Win, K. S., Win, S., Htun, T. M., & Win, N. K. K. (2020). Characterization and evaluation of mungbean [*Vigna radiata* (L.) Wilczek] germplasm through morphological and agronomic characters. *Indian Journal of Agricultural Research*, 54(3), 308-314.

Yadav, R., Ram, B. J., Suresh, B. G., & Lavanya, G. R. (2017). Studies on genetic variability, character association for yield and yield components in green gram (*Vigna radiata* L. Wilczek). *Journal of Pharmacognosy and Phytochemistry*, 6(4), 1988-1991.

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