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Genetic variability studies on yield and its components in greengram (*Vigna radiata* [L.] Wilckzek)

P J S Pramod, N Hari Satyanarayana, J Sateesh Babu and K Jaya Lalitha
Department of Genetics and Plant Breeding, Acharya N G Ranga Agricultural University,
Agricultural College, Bapatla-522101, Andhra Pradesh, India.

ABSTRACT

The present investigation was undertaken by utilizing 30 greengram genotypes for eleven quantitative traits *viz*., days to 50 % flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, pod length (cm), test weight (g) and seed yield per plant (g) in greengram during *Rabi,* 2023-24 at RARS, Lam, Guntur, Andhra Pradesh. This study aims to understand genetic variability, heritability and genetic advance in greengram. Analysis of variance revealed the presence of significant differences among the genotypes for all the traits studied. The estimates of genetic parameters revealed high phenotypic and genotypic coefficient of variations recorded for number of branches per plant, number of clusters per plant, number of pods per plant and seed yield per plant. High broad sense heritability accompanied with high genetic advance as per cent of mean was observed for the characters number of branches per plant followed by number of clusters per plant, number of pods per plant, seed yield per plant, test weight, plant height and number of pods per cluster indicating additive gene action for these traits and selection would be effective.

Keywords: *Broad sense heritability, Genetic advance, Greengram and Variability.*

Green gram (*Vigna radiata* (L.) Wilczek) is one of the important pulse crops grown in India. It belongs to the subgenus Ceratotropis in the genus Vigna. Greengram is a self-pollinating diploid grain legume (2n = 22) and it is a major source of dietary protein for the predominantly vegetarian population of India. Greengram also called mungbean was originated in India. In the human diet, particularly for most of the vegetarian population, mungbean a legume, is a cost-effective and hundred gram of green gram seeds contains energy (234 cal), protein (24.6%), fat (1.0%), fiber (2.2 g), carbohydrates (57.5%), calcium (0.08 g), phosphorus (0.045 g) and iron (5.7 mg), vitamin B (300 mg) and thiamin (0.525 mg) (Salman *et al*., 2023). Apart from the high nutritional content, soil fertility restoration through biological nitrogen fixation is a key factor for sustainable agriculture (Dhunde *et al*., 2021). In India, during 2022-23 greengram is cultivated in an area of 5.55 million hectares, with a production of 3.17 million tonnes with a productivity of 570 kg/ha. The major greengram cultivating states are Rajasthan, Madhya Pradesh, Karnataka, Maharashtra, Odisha, Tamilnadu, Bihar, Andhra Pradesh and Uttar Pradesh having of about 90% of the total area and production. (IIPR, 2024). To meet out the ever-increasing demand for greengram, there is a need to break the yield barriers by developing high yield and biotic/abiotic resistant varieties. Yield is a complex character which is influenced by many dependent characters. The dependent characters which are associated with yield component traits are themselves interrelated. Selection based on yield may not be rewarding, therefore improvement in yield is possible through selecting yield component traits which show close association with yield. Variability can be used effectively to develop high yielding cultivars through hybridization followed by selection. Genetic advance studies give an idea about the gene action and breeding programme to be adopted.

MATERIAL AND METHODS

The material for the present study comprised of 30 promising greengram genotypes including 4 checks namely COGG 912, OUM 11-5, VBN 5 and IPM 2-14 that were obtained from All India Coordinated Research Project in MullaRP, ICAR-IIPR, Kanpur, Uttar Pradesh, India as presented in Table 2. Thirty greengram gemotypes were laid out in a randomized block design with three replications. Each genotype was grown in paired rows, where each row measured four meters in length with inter-row spacing of 30 cm x 10 cm. The data were recorded on five randomly selected plants of each replication for nine quantitative characters *viz.,* plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, pod length (cm), test weight (g) and seed yield per plant (g) but in case of days to 50% flowering and days to maturity, the observations were recorded on plot basis. The data was subjected to statistical analysis to estimate the analysis of variance, genotypic and phenotypic coefficients of variation, heritability in broad sense and genetic advance as per cent of mean were calculated as per standard procedures.

RESULTS AND DISCUSSION

The analysis of variance (Table 1) revealed that mean squares due to genotypes were highly significant for days to 50 % flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, pod length (cm), test weight (g) and seed yield per plant (g) indicating the presence of sufficient amount of variability in the experimental material used. These results are in agreement with the findings of Salman *et al*. (2023) indicating adequate genetic variability among the genotype which provide ample scope for identifying genotypes with desirable character to improve yield, provided the material be subjected to sensible pressure. It reveals that the selection of superior genotypes for development of new varieties may be helpful. The magnitude of PCV was slightly greater than GCV this indicated that phenotypic variability may be considered as reliable measure of genotypic variability. Similar results were concluded by Salman *et al*. (2023).

Significant GCV and PCV were recorded for number of branches per plant (25.16 and 25.68), number of clusters per plant (23.51 and 24.29), number of pods per plant (28.46 and 29.52) and seed yield per plant (31.47 and 33.68). Identical results were also reported by Jain *et al*. (2024). Similar results for number of clusters per plant, number of pods per plant and seed yield per plant were reported by Salman *et al*. (2023) and Revathi and Lal (2023). Moderate value for GCV and PCV was observed for plant height (14.96 and 17.76), number of pods per cluster (11.88 and 14.40) and test weight (12.80 and 15.15). The moderate GCV and PCV for plant height and test weight was reported by Azam *et al.* (2018). The characters showed moderate GCV and PCV indicated that selection would be effective based on the heritable nature of these characters. Low value for GCV and PCV was observed for days to 50% flowering (5.22 and 7.59), days to maturity (2.53 and 4.79), number of seeds per pod (5.31 and 8.63) and pod length (6.70 and 9.14). Low values of GCV and PCV indicated low range of variation for traits in the genotypes, thus offering little scope for further improvement of these characters through simple selection. Kumawat *et al.* (2022) and Sineka *et al.* (2021) reported low values for pod length. Thonta (2023) and Salman *et al.* (2023) reported low values for days to 50 % flowering, days to maturity and seeds per pod.

High heritability (>60 %) in broad sense accompanied by high genetic advance as percent of mean (>20 %) estimates (Table 2) were observed for number of branches per plant (95.91 % and 50.72 %)followed by number of clusters per plant (93.68 % and46.89 %), number of pods per plant (92.94 and 56.49), seed yield per plant (87.32 and 60.58), test weight (71.32 % and 22.28 %), plant height (70.98 % and 25.97 %) and number of pods per cluster (67.7 % and 20.08 %). High heritability coupled with high genetic advance as per cent of mean indicates that most likely the heritability is due to additive gene action and selection may be effective. A similar conclusion is derived by Jain *et al.* (2024) number of branches per plant, number of clusters per plant, number of pods per plant, seed yield per plant and test weight. Moderate heritability (30 %-60 %) in broad sense accompanied by moderate genetic advance as percent of mean (10 %-20 %) estimates (Table 2) were observed for pod length (53.69 % and 10.12 %). A similar conclusion is derived by Jain *et al.* (2024) and Gajanan and Lal (2022). Moderate heritability is due to favourable influence of environment rather than genotype and selection for

Table 1: Classification of genetic parameters

S. No.	Classification	GCV/PCV	H^2 (bs)	GAM
1	High	>20%	> 60%	>20%
2	Moderate	10–20%	30–60%	10–20%
3	Low	<10%	< 30%	<10%

Estimates: GCV- Genotypic coefficients of variation, **PCV**- Phenotypic coefficient of variation, **H^2 (bs)-** Heritability in broad sense and **GAM-** genetic advance as per cent of mean

Table 2. Name, parentage and origin of greengram genotypes employed in the study

S.No.	Genotype	Parentage	Origin
1	OBGG 110	NM 94 x ML 1628	Odisha
2	COGG 912	MGG 336 x COGG 902	Tamil Nadu
3	OUM 11-5	Mutant of Dholi	Odisha
4	VBN 5	VBN (Gg) 2 x ML 1451	Tamil Nadu
5	VGG 20-234	VBN 4 x VGG 17-015	Tamil Nadu
6	PM 2015	PM 2 x UM 2	Uttarakhand
7	KM 2401	KM 2328 x M 2195	Uttar Pradesh
8	IGKM 2021-1	Pusa Vishal x HUM 12	Chattisgarh
9	RVSM 22-13	HUM 1 x CZMK 1-1	Madhya Pradesh
10	LGG 685	LGG 460 x IPM 409-4	Andhra Pradesh
11	DGG 214	IPM 2-14 x IPM 2-17	Karnataka
12	MI 2023-1	JM-SML 668 x PDM 139	Madhya Pradesh
13	IPM 2-14	IPM 99-125 x Pusa Bold 2	Uttar Pradesh
14	Pusa 23-71	TM 97-25 x PM 5	New Delhi
15	RVSM 22-3	ML 131 x TMB 37	Madhya Pradesh
16	RM 03-79	TM 96-2 x VC 3670	Chhattisgarh
17	ML 2844	ML 267 x ML 1354	Punjab
18	MGG 514	MGG 347 x SM 131	Telangana
19	RMG 1164	IPM 02-3 x COGG 912	West Bengal
20	OBGG 107	NM 94 x ML 1628	Odisha
21	BCM 20-05	MH 3-18 x EC 369223	West Bengal
22	MI 13-47	JM 721 x ML 422	Madhya Pradesh

Table 3: Analysis of Variance (ANOVA) for eleven traits in greengram

Source	df	DFF	DM	PH	NBP	NCP	NPC	NPP	NSP	PL	TW	SYP
Treatment	29	14.978 **	15.773 **	126.393 **	0.89 **	5.359 **	0.353 **	59.222 **	1.529 **	0.968 **	0.711 **	6.444 **
Replication	2	0.419	14.608	6.101	0.017	0.057	0.151	4.564	0.007	0.381	0.024	0.062
Error	58	4.048	7.282	15.16	0.012	0.118	0.048	1.462	0.541	0.216	0.084	0.298

CHARACTERS: DFF-Days to 50% flowering, **DM**-Days to maturity, **PH**-Plant height (cm), **NBP**-Number of branches per plant, **NCP**-Number of clusters per plant, **NPC**-Number of pods per cluster, **NPP**-Number of pods per plant, **NSP**-Number of seeds per pod, **PL**-Pod length (cm), **TW**-Test weight (g) and **SYP**-Seed yield per plant (g).

Table 4: Estimates of variability, heritability and genetic advance as per cent of mean for seed yield and other traits in greengram

Trait	Mean	Maximum	Minimum	GCV	PCV	h^2	GA	GA as % of Mean
DFF	36.55	46.86	30.46	5.22	7.59	47.37	2.71	7.41
DM	66.39	72.7	60.04	2.53	4.79	27.99	1.83	2.76
PH	40.71	62.4	23.28	14.96	17.76	70.98	10.57	25.97
BPP	2.15	3.55	1.38	25.16	25.68	95.91	1.09	50.72
NCP	5.62	10.24	3.86	23.51	24.29	93.68	2.64	46.89
NPC	2.69	3.78	1.69	11.88	14.4	67.7	0.54	20.08
NPP	15.42	30.62	8.78	28.46	29.52	92.94	8.71	56.49
NSP	10.81	13.01	8.96	5.31	8.63	37.84	0.73	6.74
PL	7.47	9.53	4.77	6.7	9.14	53.69	0.76	10.12
TW	3.57	5.25	2.65	12.8	15.15	71.32	0.8	22.28
SYP	4.55	8.31	1.54	31.47	33.68	87.32	2.76	60.58

such traits may not be rewarding. Moderate heritability (30 %-60 %) in broad sense accompanied with low genetic advance as percent of mean (<10 %) estimates (Table 2) were observed for days to 50 % flowering (47.37 % and 7.41 %) and number of seeds per pod (37.84 % and 6.74 %). Similar conclusion is derived by Salman *et al.* (2023) and Revathi and Lal (2023) for days to 50% flowering and Tamalapakula *et al.* (2021) for number of seeds per pod. Low heritability (<30 %) in broad sense accompanied with low genetic advance as percent of mean (<10 %) estimates (Table 2) were observed for days to maturity (27.99 % and 2.76 %). Similar conclusion was reported by Salman *et al.* (2023), Prajapati *et al.* (2022) and Yoseph *et al.* (2022). It indicates that the character is highly influenced by environmental effects and selection would be ineffective.

Heritability of a metric character is a parameter of particular significance to the breeder as it measures the degree of resemblance between the parents and the off-springs and its magnitude indicates the efficacy with which a genotype can be identified by its phenotypic expression. Characters with high heritability suggest that the selection would be more effective.

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