

Genetic Analysis in Green Gram [*Vigna radiata* (L.) Wilczek]

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Abstract

The investigation “Genetic Analysis in Green gram [*Vigna radiata* (L.) Wilczek]” was undertaken to study the direct and indirect effects of different characters on seed yield of green gram, to group the various genotypes into various clusters. Data was collected on ten morphological characters measured on 25 genotypes of green gram evaluated in randomized block design with two replications during summer 2023. The observations were recorded on green gram yield and yield contributing characters viz., days to 50% flowering (No.), days to maturity (No.), plant height (cm), plant spread (cm), number of primary branches (No.), number of pods plant⁻¹ (No.), number of clusters plant⁻¹ (No.), number of pods cluster⁻¹ (No.), number of pods plant⁻¹ (No.), number of seeds pod⁻¹ (No.) and seed yield plant⁻¹ (g). The analysis of variance showed existence of considerable variability for all ten characters. A wide range of variability was observed for almost all the characters studied. Medium GCV and PCV were found in this study for number of primary branches, number of pods plant⁻¹, number of pods cluster⁻¹, number of seed pod⁻¹ suggesting excellent potential for improvement through selection. High magnitude of heritability (b.s.) along with genetic gain as a per cent mean was observed in number of primary branches, number of pods plant⁻¹, number of seed pod⁻¹. As these characters could be significantly governed by additive gene action and direct selection of these character could be rewarded. Correlation studies at both genotypic and phenotypic levels number of primary branches, number of pods plant⁻¹, number of cluster plant⁻¹, number of pods cluster⁻¹, number of seeds pod⁻¹ exhibited significant positive correlation with seed yield plant⁻¹.

Key words : Variability, heritability, correlation, green gram, yield.

The green gram is a significant crop in India among the pulses. *Vigna radiata* (L.) Wilczek, is one of the most significant pulse crops produced in our country. Green gram originated on the Indian subcontinent (Vavilov, 1926 and Candolle, 1886). It is also called mungbean, golden gram, moong, or chop suey bean. It is botanically classified as a member of the Leguminosae family and the Papilionaceae subfamily. It is a highly self-pollinated crop with somatic chromosomal number $2n=2x=22$ (Dana, 1980).

Green gram is a major pulse crop in India, and it is thought to have originated in India. It is

a short-term legume crop used mostly as a fallow crop in rotation with rice. Green gram, like leguminous pulses, enriches soil nitrogen content. It is primarily grown in Asia, although cultivation has recently spread to Africa and America. India accounts for more than 70% of the world's green gram production. In India, green gram covered around 15.93 lakh ha (39.38 lakh acres) in 2023-24, compared to 15.57 lakh ha (38.47 lakh acres) in 2022-23. Rajasthan has 13.99 lakh ha (34.57 lakh acres), Karnataka 1.14 lakh ha (2.83 lakh acres) and Madhya Pradesh 0.25 lakh ha (0.61 lakh acres), Haryana produces 0.16 lakh hectares (0.41 lakh acres) of green gram followed by Gujarat (0.13 lakh ha (0.32 lakh acres). According to the government's third advance estimate, green

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gram production in 2022-23 will be 3.74 million tonnes.

Any plant breeding programme focused at increasing yield and related characteristics should consider parent selection. They are genetic diversity reserves that frequently adjust to local soil types, climatic conditions, and so forth. They include many valuable genes, including those involved in adaptation. As a result, it is critical to identify potential lines and land races and integrate them in crosses with the appropriate mating pattern.

The genetic makeup and genetic divergence of hybridizing populations influence how genes work in crop improvement programs. Genetic divergence is critical due to the germplasm's diverse origins and productive potential. Divergence analysis gives useful information about the kind and extent of genetic variation. As a result, the first step toward assisting effective breeding operations is a thorough characterisation of the germplasm. To achieve deliberate hybridization by heterosis breeding, the breeder must choose the right parents (Yatung *et al.*, 2014).

Materials and Methods

The material for the present study consisted of 25 genotypes of green gram collected from following sources.

The data collected on individual characters were subjected to the method of analysis of variance commonly applicable to the Randomized Block Design (Panse and Sukhatme, 1985).

Results and Discussion

In this results obtained from the research entitled "Genetic Analysis in Green gram [*Vigna radiata* (L.) Wilczek]" which was carried out on Post Graduate Institute Farm, MPKV, Rahuri,

during summer-2023 with an objectives to study genetic variability, correlation of twenty five genotypes of green gram.

Analysis of Variance : Analysis of variance for all ten character is presented in Table 2. The mean of square due to genotype have high significant difference for all characters *viz.*; days to 50% flowering, days to maturity, plant height, plant spread, number of primary branches,

Table 1. List of twenty five genotypes of green gram

Genotype	Source	Genotype	Source
JLPM2311	BM-2003-2	JLPM2324	PKVAKM-1
JLPM2312	BM-2002-1	JLPM2325	BM-4
JLPM2313	Phule Chetak	JLPM2326	Vaibhav
JLPM2314	TARM-1	JLPM2327	RAM-141
JLPM2315	AKM-12-14	JLPM2328	TAM-127
JLPM2316	AKM-16-08	JLPM2329	BM-2021-4
JLPM2317	BM-2021-1	JLPM2330	PM-702-1
JLPM2318	BM-2021-2	JLPM2331	PM-809-12
JLPM2319	PM-504-20-27	JLPM2332	PM-809-12
JLPM2320	PM-402-2-1	JLPM2333	PM-811-4
JLPM2321	PM-818-8	JLPM2334	PM-707-27
JLPM2322	PM-811-17	JLPM2335	PM-504-20-27
JLPM2323	PKV-Green gold		

Table 2. Analysis of variance for twenty five different characters of green gram

Characters	Mean sum of squares		
	Repli- cation	Geno- type	Error
Days to 50 per cent flowering	1.620	13.970**	1.370
Days to maturity	2.880	14.041**	2.171
Plant Height (cm)	119.810**	10.913*	4.643
Plant Spread	1.729	26.692**	4.049
Number of primary branches	0.072	0.753**	0.078
Number of pods plant ⁻¹	1.216	11.640**	1.874
Number of cluster plant ⁻¹	0.204	1.282**	0.386
Number of pods cluster ⁻¹	0.125	0.411**	0.117
Number of seeds pod ⁻¹	0.352	3.357**	0.412
Seed Yield plant ⁻¹	0.005	0.701**	0.169

*, ** - signs indicates significant at 5 and 1 per cent level of significance, respectively.

number of pods plant⁻¹, number of clusters plant⁻¹, number of pods cluster⁻¹, number of pods plant⁻¹, number of seeds pod⁻¹ and seed yield plant⁻¹ indicating that sufficient variability were found in the genotypes studied for these characters because of diverse genotypes.

These results were confined by Makeen *et al.* (2007), Katiyar *et al.* (2015), Kate *et al.* (2017), Muthuswamy *et al.* (2019), Wesly *et al.* (2020), Dhunde *et al.* (2021), Rahangdale *et al.* (2023).

Genotypic and Phenotypic Coefficients of Variation

Genetic variability is source of heritable enhancement in any crop. Estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) as per suggestion of Burton (1952) is presented in Table 3. Number of primary branches (13.76%) had shown a medium estimates of GCV accomplished by number of pods per cluster (12.54%), number of pods plant⁻¹ (11.88%), number of seed pod⁻¹ (11.13%). While plant spread (9.70%), number of cluster plant⁻¹ (8.57%), seed yield plant⁻¹ (7.14%), days to 50% flowering (6.18%), days to maturity (3.72%) and plant height (3.39%) showed a low GCV. Number of pods cluster⁻¹ (16.81%) had exhibited medium estimates of pcv accompanied by number of primary branches (15.27%), number of pods plant⁻¹ (13.97%), number of seed pod⁻¹ (12.60%), number of cluster plant⁻¹ (11.70 %), plant spread (11.30%). While seed yield per plant (9.14%), days to 50% flowering (6.82%), plant height (5.35%), days to maturity (4.35%) exhibited low pcv. In the present investigation the phenotypic coefficient of variation (PCV) for all the studied characters were higher than genotypic coefficient of variation (GCV) indicating that variation is not only due to genotypes but also due to environmental influence. Similar results were obtained earlier by Tabasum *et al.* (2010) in green gram for plant height, pods per plant, total plant weight and seed yield, Kate *et al.*

(2017) studied green gram for secondary branches plant⁻¹, primary branches plant⁻¹, pods plant⁻¹ and grain yield plant⁻¹, Mohammed *et al.* (2020) in green gram for days to maturity.

Heritability (b.s.) : Estimates of broad sense heritability are presented in Table 3. Genotypic coefficient of variation (GCV) alone does not signify proportion of total heritable variation. High broad-sense heritability values are helpful in determining the right characters for selection and in enabling breeders to choose superior genotypes based on the phenotypic expression of quantitative traits; these values used in conjunction with genetic advancement would be more reliable than heritability alone (Johnson *et al.*, 1955).

Days to 50% flowering (82.14%), number of primary branches (81.15%), number of seed pod⁻¹ (78.12%), plant spread (73.66%), days to maturity (73.21%), number of pods plant⁻¹ (72.26%), seed yield plant⁻¹ (61.07%) showed high magnitude of heritability (b.s.). While number of pods cluster⁻¹ (55.58%), number of cluster per plant (53.66%) and plant height (40.30%) exhibits medium heritability.

Table 3. Estimates of variability parameters for seed yield and yield contributing characters of twenty five green gram genotypes

Character	GCV (%)	PCV (%)	Heritability (bs) (%)	Genetic advance of mean (%)
Days to 50 per cent flowering	6.18	6.82	82.14	11.54
Days to maturity	3.72	4.35	73.21	6.56
Plant Height (cm)	3.39	5.35	40.30	4.44
Plant Spread	9.70	11.30	73.66	17.15
No. of primary branches	13.76	15.27	81.15	25.54
No. of pods plant ⁻¹	11.88	13.97	72.26	20.81
No. of cluster plant ⁻¹	8.57	11.70	53.66	12.93
No. of pods cluster ⁻¹	12.54	16.81	55.58	19.26
No. of seeds pod ⁻¹	11.13	12.60	78.12	20.27
Seed yield plant ⁻¹	7.14	9.14	61.07	11.50

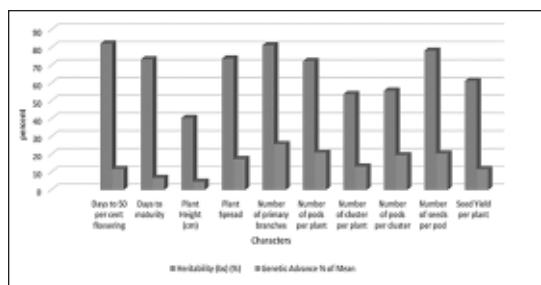
Similar results were obtained earlier by Singh *T. et al.* (2009) in green gram for days to 50 per cent flowering, days to maturity, number of pods per plant, Tabasum *et al.* (2010) used green gram to number of plant height, clusters plant⁻¹, pods plant⁻¹, pods cluster⁻¹, Katiyar *et al.* (2015) on green gram with seed yield plant⁻¹, days to flowering and plant height, Mohammed *et al.* (2020) conducted number of primary branches plant⁻¹, days to 50% flowering, days to maturity, seed yield plant⁻¹, number of pods plant⁻¹ and the number of seeds pod⁻¹.

This study depicted high heritability for all character except plant height, number of cluster plant⁻¹ and number of pods cluster⁻¹ indicating that these traits are governed by additive gene action and had less environmental influence in their expression and direct phenotypic selection can be followed for these characters in breeding programme for development of high yielding genotypes.

Genetic Advance as Per cent of Mean :

Genetic advance as per cent of mean of ten characters of twenty five genotypes of green gram ranged from 4.44% to 25.54%. High estimates of genetic advance as per cent of mean was obtained in number of primary branches (25.54%) followed by number of pods plant⁻¹ (20.81%), number of seeds pod⁻¹ (20.27%). Whereas a moderate genetic advance as per cent of mean were observed for number of pods cluster⁻¹ (19.26%) followed by plant spread (17.15%), number of cluster plant⁻¹ (12.93%) and days to 50% flowering (11.54%), seed yield plant⁻¹ (11.50%). The character days to maturity (6.56%) and plant height (4.44%) showed low genetic advance as per cent of mean.

The traits such as number of primary branches, number of pods plant⁻¹ and number of seeds pod⁻¹ showed high heritability and high



Graphical comparison of heritability and expected genetic advance as percent of mean for ten character of green gram

genetic advance as a percentage mean, which indicates these characters could be prominently governed by additive gene action and direct selection of this traits could be rewarded.

It is supported by similar findings of Kate *et al.* (2017) in green gram for plant height, days to maturity, pods per plant, days to 50 flowering, secondary branches plant⁻¹, grain yield plant⁻¹ and primary branches plant⁻¹. Muthuswamy *et al.* (2019) for number of primary branches plant⁻¹, number of clusters plant⁻¹, number of pods cluster⁻¹, number of pods plant⁻¹, 100-seeds weight and seed yield plant⁻¹, in green gram. Mohammed *et al.* (2020) in green gram with number of primary branches plant⁻¹, seed yield plant⁻¹, plant height, number of pods plant⁻¹, 100 seed weight and days to 50% flowering.

The character days to maturity shown high heritability coupled with low genetic advance, therefore selection of such character is not rewarding because of presence of non-additive genetic action and heterosis breeding is use.

Conclusion

All of the green gram genotypes that were investigated had highly significant differences that may be used in practical applications.

Medium GCV and PCV were found in this study for number of primary branches, number of pods per plant, number of pods per cluster, number of seed per pod suggesting excellent potential for improvement through selection. High magnitude of heritability (b.s.) along with genetic gain as a per cent mean was observed in number of primary branches, number of pods per plant, number of seed per pod. As these characters could be significantly governed by additive gene action and direct selection of these character could be rewarded.

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