



## **Estimation of Variability and Genetic Divergence in Greengram [*Vigna radiata* (L.) Wilczek] for Yield Characters**

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### **Authors' contributions**

*This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.*

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## **ABSTRACT**

The present investigation consists of 20 genotypes of Greengram including one check, which were grown in the Field Experimentation Centre of the Department of Genetics and Plant breeding, SHUATS, Prayagraj during *Kharif* 2021 following RBD with three replications. The data were recorded on 13 characters to study the amount of genetic variability, Genetic Advance, Genetic advance as percent mean in the greengram genotypes. Based on the mean performance genotype MODAL-L532 followed TOR-2 and SANGU-1972 were identified as best genotypes for seed yield per plant. High significant variation was obtained for all characters studies. High heritability estimates were observed for Number of primary branches, Seed yield, harvest index followed by number of pods per plant, number of secondary branches, biological yield, number of seeds per plant, number of seeds per pod, 100 seed weight, days to 50% flowering, days to maturity, days to 50% pod setting, and plant height. High values for heritability indicates that it may be due to higher contribution of genotypic components. High genetic advance as percent of mean was recorded high for seed yield, harvest index, biological yield, number of pods per plant, number of primary branches, number of seeds per plant, number of secondary branches, number of seeds per pod, hundred seed weight, plant height, days to 50% flowering, days to 50% pod setting, days to maturity. Metroglyph analysis shows, analysis of variance indicated that significant variations among the 20 lines for thirteen characters. The scatter diagram revealed that three complexes

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could be distinguished on the basis of morphological variation. Maximum number of genotypes falls in cluster I (10) and II (9) followed by cluster III (1). The germplasm lines, OLTS-B2, MODAL-L532, S/9-1179, SLTS-B2, recorded high index score and fell into different clusters can be crossed to have maximum variability of good combination of characters. Thus, the use of these genotypes in future breeding programme is suggested.

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

## 1. INTRODUCTION

Greengram [*vigna radiata* (L) Wilczek] ( $2n=2x=22$ ) belongs to the family leguminaceae, also known as mungbean, green bean, moong bean, golden gram is an excellent source as easily digestible proteins with low flatulence which complements the staple rice diet in Asia. The major portion of seeds is utilized in making dal, curries, soup, sweets and snacks. The sprouted seeds contain an increased amount of Thiamine, Niacin and Ascorbic acid, thus mung bean sprouts are increasingly becoming popular in certain vegetarian diets [1-5]. The grains contain approximately 25-28% protein, 1.02-1.05% oil. 3.5-4.5% fibre, 4.5-5.5% ash and 60-65% carbohydrates on dry weight, Greengram also contains vitamin-A ((94mg), vitamin-C (8mg), iron (7.3mg), calcium (124mg), magnesium (189mg), phosphorus (367mg) potassium (1246mg), zinc (3mg) and foliate (549mg). Unlike other pulses, it free from flatulent effects in stomach. Hence, it is fed to babies and as a coalescent to elders.

Greengram is widely cultivated throughout South Asia including India, Pakistan, Bangladesh, Srilanka, Thailand, Cambodia, Vietnam, Indonesia, Malaysia and South China. In India, it is a third most important pulse crop after chickpea and pigeon pea (Prasad 2016). It is grown mainly as a *kharif* season crop. However, its cultivation in *rabi* season is restricted to the eastern and southern parts of the country [6-9]. The crop is popular because of its suitability richer [10-13]. Due to short duration it fits in rotation, intercropping and mixture, low water requirement, soil fertility and is flavoured for consumption due to its easy digestibility and low production of flatulence (Shil and Bandopadhyaya, 2007).

Greengram is an semierect to erect, fast-growing annual, herbaceous legume reaching 25-100 cm in height. It has a well developed deep rooted and its stems are diffusely branched from the base. The leaves are alternate, five and trifoliate with five leaflets 5-12 cm long and 2-10 cm wide. Around 10-25 flowers are borne in axillary

clusters or racemes. The flowers are greenish to bright yellow with a grey tinged keel, 1-1.75cm in diameter. The flower is a typically papilionaceous with 5 sepals, five petals 10 diadelphous (9+1) stamen and monocarpillary with hairy stigma.

Greengram is an excellent source of protein. It is rich in lysine and deficient methionine and legume, which is free from anti-nutritional factor [14-17]. The range for protein content is fairly wide (20-24% per 100gm of dry grain). Temperature of 28-33degrees optimum for seed germination and plant growth [18,19].

The goals of greengram breeding programme depend on the intended use of germplasm under development. Yield received the greatest attention cultivars development as it does I other crop species [20-22]. Genetic improvement of yield and yield components are, nevertheless, the most difficult to achieve due to the complex nature of the inheritance and the numerous environment factors that influence yield and its genetic basis of variation in greengram [23-26].

Further, to improve the productivity, information about the nature and magnitude of genetic divergence would help selection of diverse parents, which upon hybridisation might lead to effective gene recombination [27-30]. The present study was under taken to select the divergent parent for future hybridisation programme.

Metroglyph and Index score analysis is the technique was developed by Anderson [31] to investigate the pattern of morphological variation in Greengram genotypes.

The main features of Metroglyph analysis are given below:

- Analysis is based on first order statistics and therefore, results are statistically morereliable and robust.
- Analysis is possible from both replicated as well as non-replicated data. The analysis is simple.
- The pattern of variability is depicted by glyph on the graph.

## 1.1 Objectives

1. To determine the extent of genetic variation for quantitative traits in Green gram.
2. To identify divergence parents of Greengram germplasm for future hybridization programmes.
3. To evaluate the genetic potential by Metroglyph analysis for yield and yield contributing characters in Greengram.

## 2. MATERIALS AND METHODS

The present investigation was carried out in the Field Experimentation Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad, U.P during *Kharif-2021*. A randomized block design was adopted with three replications and row to row spacing is 30cm and plant to plant spacing is 10cm with plot size of 1m x 1m.

The observations were recorded on five randomly selected plants from each replication for 13 different quantitative traits. Analysis of variance showed significant differences for all the 13 characters viz., 1) Days to 50 Percent Flowering, 2) Days to 50 % pod setting, 3) Days to Maturity, 4) Plant height, 5) Number of primary branches, 6) Number of clusters per plant, 7) Number of pods per plant, 8) Pod length, 9) Number of seeds per pod, 10) Biological yield per plant, 11) Harvest index, 12) Seed yield per plant, 13) 100 Seed weight.

**Chart 1. Experimental details**

Crop	Greengram
Season	<i>kharif, 2021</i>
Experimental design	Randomized Block Design (RBD)
No. of Replications	3
No. of genotypes	20
Plot size	1x1 m <sup>2</sup>
Net area	63 sq.mt
Gross area	84.5 sq.mt
Spacing	30x10 cm
Date of sowing	14/07/2021
Fertilizer Dose	20:40:20 (N: P: K) kg/ha
Date of Harvesting	09/10/2021

The analysis of variance was worked out to test the differences among genotypes by F-test. It

was carried out according to the procedure of Randomized Complete Block Design for each character as per methodology advocated by Fisher, [32]. ANOVA helps in partitioning the total variance in to three component viz., replication, treatment and error.

## 3. RESULTS AND DISCUSSION

The abundant scope for improving these characters including grain yield per plant provided the material is subjected to judicious selection programme. Due to diverse source of material taken as well as environmental influence affecting the phenotypes the presence of variability might be large.

The mean values, coefficient of variation (C.V. ), standard error of the mean (Sem+), critical difference (C.D.) at 5% and 1%, and range of 22 genotypes are shown in which demonstrated a large range of variance for all characteristics tested. MODAL-L532 (8.533gm), TOR-2 (7.69), SANGU-1972 (7.563), PUSA-L489 (7.44).

### 3.1 Variability

The variability is classified as low if coefficient of variation (<10%), moderate (10-20%) and high (>20%). High PCV and GCV were observed for harvest index (26.27), seed yield per plant (13.84). Moderate PCV and GCV were observed for the biological yield (16.05), seed index (15.44). Moderate PCV and GCV were observed for the seed yield per plant (16.12), Number of seeds per pod (11.479), Plant height (11.351). Low PCV and GCV were observed for primary branches (6.54), number of seeds per pod (5.36).

### 3.2 Heritability

The heritability classified as low (<30%), medium (30-60%) and high (>60%) by Johnson *et al.*, (1955). In the present investigation traits having the higher heritability number of clusters per plant (92.44%), harvest index (89.00%). Medium heritability observed for number of primary branches per plant (48.15%), days to 50% flowering (41.68%). Low heritability values were recorded for days to maturity (38.62%), plant height (24.75%) and number of seeds per plant (28.17%).

The high heritability values of the considered traits in the present study indicated that those

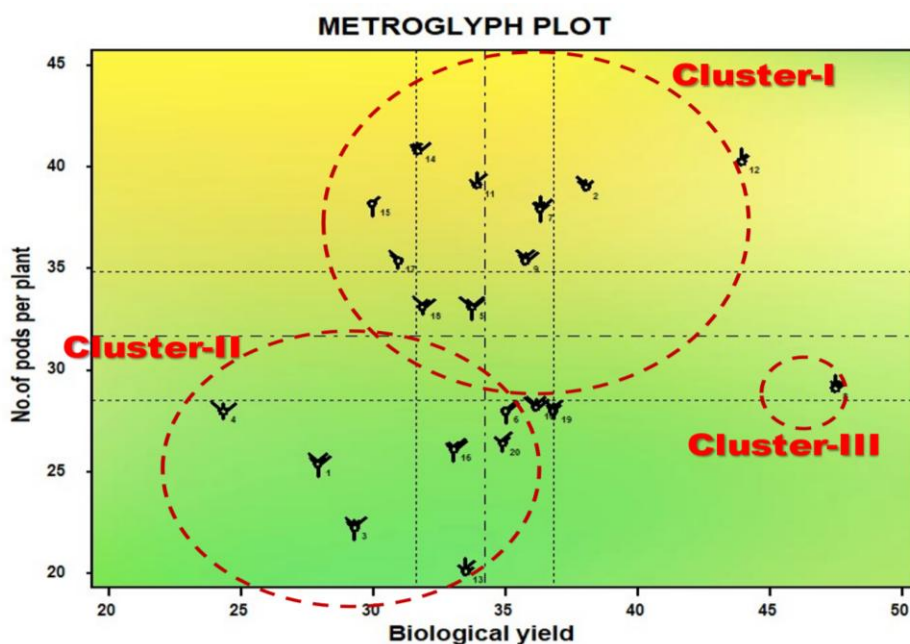


Fig. 1. Scattered diagram of Metroglyph analysis showing 20 genotypes of Greengram

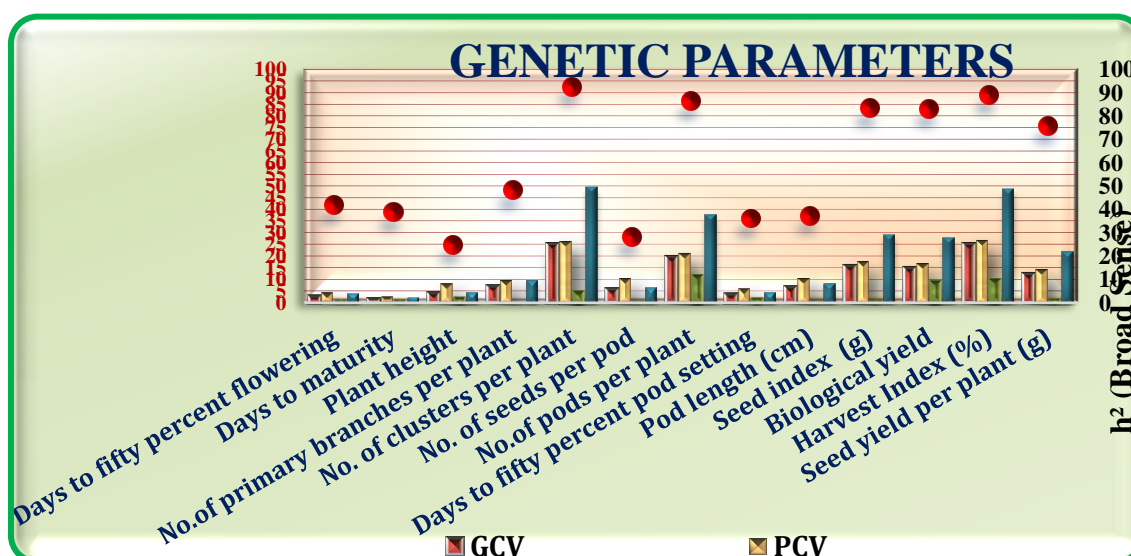


Fig. 2. Graph depicting GCV, PCV, genetic advance and heritability for 13 quantitative characters of greengram genotypes

were less influenced by the environment and thus help in effective selection of the traits based on the phenotypic expression by adopting simple selection method and suggested the scope of genetic improvement.

### 3.3 Genetic Advance as Percent Mean (5%)

The estimation of genetic advance as percent mean is classified as low (<10%), moderate (10

to 20%) and high (>20%) proposed by Johnson et al. (1955).

In the present study, high estimates of heritability coupled with high genetic advance as percent of mean was observed for harvest index (89.008, 48.17%), no. of clusters per plant (92.44, 49.33), seed yield per plant (75.73, 21.59%), no. of pods per plant (86.43, 37.20%), biological yield (83.08, 27.48%) and days to 50% flowering (41.68, 3.409%). Respectively suggesting that

**Table 1. Analysis of Variance for 13 quantitative characters of Greengram genotypes**

Source	Mean sum of squares		
	Replication	Treatment	Error
Degrees of freedom	2	19	38
Days to 50% flowering	1.4680	2.307**	0.734
Days to maturity	2.5240	3.644**	1.262
Plant height	12.0610	24.421*	12.292
Number of per branches plant	0.0370	0.109**	0.029
Number of clusters per plant	0.2670	18.184**	0.482
Number of seeds per pod	0.2630	1.491*	0.685
Number of pods per plant	5.0830	119.759**	5.952
Days to 50% pod setting	8.0280	10.795**	4.012
Pod length (cm)	0.9140	1.151**	0.415
Seed index	0.0050	1.163**	0.073
Biological yield per plant	0.7240	80.266**	5.101
Harvest index	0.1420	86.555**	3.422
Seed yield per plant	0.2880	2.16**	0.208

\*\* and \* indicates significance at 1% and 5% level of significance respectively

**Table 2. Genetic parameters for 13 quantitative characters in Greengram genotypes**

Sl. no.	Characters	GCV	PCV	h <sup>2</sup> (Broad sense)	Genetic advancement	Gen. Adv as % of mean
1	Days to fifty percent flowering	2.563	3.97	41.681	0.963	3.409
2	Days to maturity	<b>1.408</b>	<b>2.265</b>	38.629	1.141	<b>1.802</b>
3	Plant height	3.846	7.73	<b>24.751</b>	2.061	3.942
4	No. of primary branches per plant	6.54	9.424	48.15	<b>0.233</b>	9.348
5	No. of clusters per plant	<b>24.91</b>	25.907	<b>92.447</b>	4.811	<b>49.338</b>
6	No. of seeds per pod	5.365	10.108	28.174	0.567	5.867
7	No. of pods per plant	19.428	20.896	86.438	<b>11.796</b>	37.208
8	Days to fifty percent pod setting	3.318	5.527	36.038	1.859	4.103
9	Pod length (cm)	6.238	10.24	37.104	0.621	7.827
10	Seed index (g)	15.449	16.933	83.237	1.133	29.035
11	Biological yield	14.635	16.056	83.084	9.399	27.481
12	Harvest Index (%)	24.786	<b>26.272</b>	89.008	10.231	48.172
13	Seed yield per plant (g)	12.046	13.842	75.736	1.446	21.596

there was preponderance of additive gene action governing the inheritance of this character and offers the best possibility of improvement through simple selection. Hence selection of these characters can bring enhancement in black gram production and productivity.

### 3.4 Metroglyph Analysis

The scatter diagram revealed that three complexes could be distinguished on the basis of morphological variation. Complex-II was represented by 9 genotypes with Moderate biological yield per plant with low number of pods per plant.

Anderson's metroglyph analysis is a simple technique and is used for preliminary grouping of genotypes. According to this technique the 20 Greengram germplasm lines formed three complexes. The number to each complex was allotted on the basis of index score.

The range of variability for characters, their values for index score and signs with rays are. The plant height (47.23-57.30) followed by days to maturity (61.33-65.00), days to 50% flowering (26.67-30.00), harvest index (14.40-33.69), biological yield (24.30-47.45) and no. of pods per plant (20.13-40.27). These traits thus were most variable for classificatory analysis in greengram.

**Table 3. Distribution of genotypes in different complex in Metroglyph analysis**

Complex	Name of complex	No. of genotypes	Name of lines	Range and average score
I	Moderate Biological yield with Moderate Number of pods per plant	10	PUZ – P3, BULL – 7 , MODAL – L532, SLTS –B2, PUSA – L488, PUSA - L487, PUSA – L485, L.T - 879, BULL - 89, ONGS - 90	24.00-28.00(26.00)
II	Moderate Biological yield with Low Number of pods per plant	9	S/9 - 1179, SANGU - 1972, BLS – L381, PUSA – L 489, BSP – L490, PUSA – L486, TOR - 2, PUSA-L484, ML-337	25.00-29.00(25.88)
III	Higher Biological yield with Low Number of pods per plant	1	OLTS – B2	29

**Table 4. Index scores and signs used for characters for metroglyph analysis of 20 genotypes of Greengram**

Sl. no.	Character	Range of mean	Score 1 Value <	Sign	Score 2 Value from - to	Sign	Score 3 Value >	Sign
1	Days to fifty percent flowering	26.67-30	27.37	○	27.37-29.13	○	29.13	○
2	Days to maturity	61.33-65	62.20	○	62.2-64.4	○	64.40	○
3	Plant height	47.23-57.3	49.43	○	49.43-55.13	○	55.13	○
4	No.of primary branches per plant	2.13-2.8	2.31	○	2.31-2.69	○	2.69	○
5	No. of clusters per plant	5.13-15.6	7.29	○	7.29-12.21	○	12.21	○
6	No. of seeds per pod	8.73-10.67	8.96	○	8.96-10.37	○	10.37	○
7	No.of pods per plant	20.13-40.8	25.39	○	25.39-38.02	○	38.02	○
8	Days to fifty percent pod setting	42.33-49	43.42	○	43.42-47.21	○	47.21	○
9	Pod length (cm)	6.89-8.94	7.32	○	7.32-8.56	○	8.56	○
10	Seed index (g)	3-5	3.28	○	3.28-4.52	○	4.52	○
11	Biological yield	24.3-47.45	29.03	○	29.03-39.37	○	39.37	○
12	Harvest Index (%)	14.4-33.69	15.87	○	15.87-26.61	○	26.61	○
13	Seed yield per plant (g)	5.23-8.53	5.85	○	5.85-7.54	○	7.54	○

- **Complex –I** was represented by ten genotypes and characterized by Moderate biological yield with moderate number of pods per plant. It indicated that majority genotypes included in this complex were having medium total index score than that of average index score of this complex.
- **Complex-II** was represented by nine genotypes and characterized by Moderate biological yield with low number of pods per plant. It indicated that majority genotypes included in this complex having high total index score than that of average index score of this complex.
- **Complex-III** was represented by one genotype and characterized by higher biological yield with lower number of pods per plant. These genotypes were having high total index score than that of average index score of this complex.

#### 4. CONCLUSION

From the present investigation it is concluded that among 20 Greengram genotypes based on the mean performance MODAL-L532 (8.53g) was found to be superior in seed yield per plant. Harvest index had recorded with high estimates of GCV and PCV and high heritability values were recorded for no. of clusters per plant. High estimates of heritability coupled with high genetic advance as percent of mean was observed for no of pods per plant. BSP-L490, OLTS-B2, MODAL-L532 and S/9-1179 recorded high index scores and included different complexes, hence used as parents for getting good transgressive segregants for yield improvement of greengram.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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