

STUDY ON GENETIC DIVERGENCE USING  $D^2$  ANALYSIS IN GREENGRAM

(*Vigna radiata* (L.)Wilczek)

**ABSTRACT**

The purpose of the present study was to evaluate the genetic variability parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance, as well as to study genetic divergence and identify suitable parents for divergence among 53 different Greengram genotypes, including one check variety. The experiment was conducted during the kharif 2022-2023 at the experimental farm of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology, and Sciences in Prayagraj, Uttar Pradesh. A randomized block design with three replications was employed for the study. Thirteen characteristics were observed and recorded, which include: days to 50% flowering, days to 50% pod initiation, days to maturity, plant height, number of primary branches per plant, number of clusters per plant, pod length, number of seeds per pod, biological yield, harvest index, seed index and seed yield per plant. IPM-2-14 exhibited the highest mean performance in terms of seed yield per plant, followed by MGG-385, among all the genotypes. The PCV values were consistently higher than the corresponding GCV values for all traits, indicating the influence of environmental factors on trait expression. The number of pods per plant and number of clusters per plant recorded the highest GCV and PCV values. The number of pods per plant exhibited both high heritability and genetic advance. 53 genotypes were categorized into six clusters through  $D^2$  analysis. Cluster I had the maximum number of genotypes, the maximum intra cluster distance was observed in cluster IV, inter cluster distance between cluster III and was observed in cluster VI. The highest cluster mean was recorded by Cluster VI for plant height. The Percentage contribution of characters was maximum by seed yield per plant followed by the number of pods per plant and number of clusters per plant towards genetic divergence.

**Keywords:** Green gram, Phenotypic, Genotypic, Heritability, Divergence, Cluster

## 1. INTRODUCTION

Greengram [*Vigna radiata* (L.) Wilczek] is one of the important pulse crop because of its short growth duration, adaptation to low water requirement and soil fertility and is widely cultivated and consumed throughout India. Greengram is popularly known as moong or greengram or golden gram, belongs to family Fabaceae and sub family Papilionaceae with diploid chromosome number  $2n=2x=22$ .

The important greengram growing states in the country are Orissa, Maharashtra, Andhra Pradesh, Madhya Pradesh, Gujarat, Rajasthan and Bihar. Green gram is an important pulse crop which comes up well in humid tropics, semi-arid and arid regions. It is cultivated worldwide, mainly in Asian countries, viz, Bangladesh, China, India, Indonesia, and Myanmar. In global scenario, India contributes about 25 to 28 percent of total production in pulses. (Kumar *et al.*, 2019).

Though greengram is considered as an important pulse crop in India, production and productivity levels are very low to meet the nutrient demand of people and the reason behind this low production and productivity are sowing on marginal and sub-marginal land under the rainfed situation, lack of high yielding genotypes, low seed replacement ratio of improved high yielding varieties, imbalanced use of plant nutrients. Thus, the availability of pulses is quite lower than the actual recommendation of WHO, which is 29.2kg/capita/year. Hence, the production and productivity potential of pulses must be increased substantially. Among the pulses, green gram plays a vital role to meet these demands since its short growth

period and suitability to various niche and cropping systems. The crop is self-pollinated and fully self-fertile. It is a small herbaceous annual plant growing to a height of 30 to 120 cm with a slight tendency to twining in the upper branches. The central stems are erect while the side branches are semi-erect. The leaves are 5-10 cm long trifoliate with long petioles.

Both the stems and leaves are covered with short hair. The pods are linear, sometimes curved, round and slender with short pubescence. The seeds are small and nearly globular. The colour of seed is usually green. Mungbean is a short-day, warm- season crop, grown mainly in the semi-arid to sub humid tropics and tropics with 600 to 1000 mm of annual rainfall. It requires 22 to 35 degree celsius mean temperature during crop production and elevations not exceeding 1800 to 2000 m above mean sea level. For a high yield, a warm climate and deep, well drained loam or sandy loam soils are desired.

The crop is popular because of its suitability for multiple cropping systems. Due to its short life cycle of 60-75 days, it fits well into the intensive cropping systems, inter cropping, rotation and mixture. It is grown mainly as a kharif season crop. However, with the development of early maturing varieties, there is a great scope and possibility of increasing area and production of spring and summer mung bean. However, the productivity of mung beans is still very low.

There are three subgroups of *Vigna radiata* one is cultivated (*Vigna radiata* genus *Vigna sp. radiata*), and two wilds (*Vigna radiata* subsp. *Sublobata* and *Vigna radiata* subsp. *glabara*) (Asari *et al.*, 2019). The origin of greengram [*Vigna radiata* (L.) Wilczek] is Indian subcontinent according to De Candolle (1886), Vavilov (1926) and Zukoveskij (1962). Since India has a wide range of genetic diversity of cultivated, as well as of weedy wild type of greengram, it is considered as the region of its first domestication. It is widely cultivated through the Asia, including India, Pakistan, Bangladesh, Sri Lanka, Thailand, Cambodia, Vietnam, Indonesia, Malaysia and South China. Sprouts of greengram is equivalent to fresh fruit in respect of nutrient content as it contains vitamins A, B, C, E and minerals such as iron, calcium, phosphorous. It is rich in vitamin B and regarded as a remedy for Beriberi, whereas sprouts contain vitamin C and E. Besides, there is an increase in the thiamine, riboflavin, niacin content as ascorbic acid is synthesized with sprouting. It is highly nutritive and is considered a healthy food, it constitutes an important place in vegetarian diets. The protein of greengram is rich in lysine which is deficient in most of the cereal grain. To improve the protein level and quality of protein, the genetics of protein or its constituents may provide useful clues for further desired improvement (Kamble *et al.*, 2017).

Yield is a complex trait and depends on various components characters, which have a positive and negative correlation with yield and among themselves. It is governed by polygenes, hence known to be highly influenced by the environment

(Allard, 1960).

In any breeding programme aimed at genetic amelioration of yield, genetic diversity is the basic requirement. Effective hybridization programs between genetically diverse parents will cause a substantial amount of heterotic response in F1 hybrid and therefore the broad spectrum of variability in segregating generations. So, selection of parents for hybridization plays an important role in breeding. Evaluation of large number of germplasms for genetic diversity is of great importance in selection of parents for hybridization. After realizing the importance of germplasm in the development of desirable varieties, breeders are now interested in diverse forms from various sources to further improve the yield potential of the genotypes. The quantification of genetic diversity through a biometrical procedure like  $D^2$  statistics.

(Mahalanobis, 1936) has made it possible to choose genetically diverse parents. Principal component analysis (PCA) is also a powerful tool to measure genetic variability and diversity among genotypes with respect to characters studied together.

Keeping in view the above-mentioned facts, the present experiment “Study on Genetic Divergence using  $D^2$  analysis in Greengram (*Vigna radiata* (L.) Wilczek)” was carried out with the following

1. To evaluate genetic variability and heritability among greengram genotypes
2. To study about genetic diversity for morphological characters
3. To identify divergence parent for future hybridization program

## **MATERIALS AND METHODS**

The investigation on “**Study on Genetic Divergence using D<sup>2</sup> analysis in Green gram (*Vignaradiata* (L.)Wilczek)**” was carried out at Crop Research Farm, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom

University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh during *Kharif*, 2022. The spacing adopted was 30 x 10 cm. Observations on Days to 50% flowering, Days to 50% pod initiation, Days to maturity, Plant height (cm), Number of primary branches per plant, Number of clusters per plant, Number of pods per plant, Pod length (cm), Number of seeds per pod, Biological yield per plant (g), Harvest Index (%) and Seed Index (%), Seed yield per plant (g). The experimental field was laid out in Randomized Block Design (RBD). The experiment comprised of 3 Replications with 53 genotypes

Chart1 : List of the genotypes.

S.No.	Genotypes	S.No.	Genotypes	S.No.	Genotypes
1.	MGG-385	19.	SPM-20-47	37.	SML-1638
2.	KM-2	20.	GM-3	38.	TS-16
3.	MGG-295	21.	SM-20-103	39.	LGG-460
4.	ML-131	22.	SM-2029	40.	LGG-407
5.	VBN-3	23.	ML-337	41.	TM-96-2
6.	VEENA	24.	TYPE-51	42.	IPM-2-3
7.	RM-12-13	25.	PHULE MOONG-9339	43.	VIRAT
8.	MGG-347	26.	ML-331	44.	SHIKA
9.	R-288-8	27.	BM-2002-1	45.	MH-421
10.	IPM -2-14	28.	T-44	46.	SAKTHI
11.	WGG-42	29.	PDM-139	47.	AMULYA
12.	MGG-371	30.	SHWETA	48.	PUSA BISAKHI
13.	IPM-205-7	31.	SPM-2040	49.	PUSA-105
14.	MGG-351	32.	CO-7	50.	SM-20-108
15.	MGG-348	33.	JALGOON-781	51.	SML-1668
16.	K-851	34.	VBN-2	52.	LGG-450
17.	MGG-2	35.	CO-8	53.	SAMRAT (CHECK)
18.	KM-11-564	36.	PHULE MOONG - 95418		

## RESULTS AND DISCUSSIONS:

### 3.1 Analysis of variance

Analysis of variance for the thirteen quantitative traits has been presented in Table 2. A perusal of

Table 1. revealed that the lines exhibited highly significant differences among thirteen traits *viz.*, days to 50% flowering, days to 50% pod initiation, days to maturity, plant height (cm), number of primary branches, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, biological yield per plant, harvest index, seed index (g), seed

yield per plant (g).

### 3.2. GENETIC VARIABILITY

The estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) from experiment were given below in Table 2.

#### 1 Phenotypic Coefficient of Variation

The range for Phenotypic Coefficient of Variation (PCV) varies from 25.994 % in number of pods per plant to 3.703 % in the case of days to 50 % pod initiation. The PCV estimates in all the characters indicated that the

phenotypic variability was low (<10%) for days to 50% pod initiation (3.703), days to maturity (4.08), pod length (8.204), number of seeds per pod (9.208), biological yield (9.697), seed index (8.972) and zyield per plant (8.984).

The phenotypic variability was moderate (10-20%) in the case of days to 50 % flowering (10.056), Plant height (16.145), number of primary branches per plant (15.468), number of clusters per plant (18.899) and harvest index (12.637). The phenotypic variability was high (>20%) in the case of number of pods per plant (25.994). Similar results are reported by **Anonymous (2019)** for number of pods per plant ,days to maturity, biological yield, seed yield per plant , plant height, number of cluster per plant while **Divya Ramakrishnan (2018)** for number of primary branches, days to 50% pod initiation, harvest index, days to 50% flowering, number of primary branches and pod length.

### 1 Genotypic Coefficient of Variation (GCV)

The range for Genotypic Coefficient of Variation (GCV) varies from 25.019 % in number of pods per plant to 1.728 % in case of days to 50 % pod initiation. The GCV estimates in all the characters indicated that the genotypic variability was low (<10%) for days to 50% pod initiation (9.635), days to 50 % pod initiation (1.728), days to maturity (2.99), pod length (3.289), number of seeds per pod (5.535), biological yield (5.867), seed index(5.694) and seed yield per plant (5.374). The phenotypic variability was moderate (10-20%) in the case of plant height (14.102), number of primary

branches per plant (14.128), number of clusters per plant (17.38) and harvest index (10.281). The phenotypic variability was high (>20%) in the case of number of pods per plant (25.019).

Similar results are reported by **Garje, U. A., (2011)**. days to 50% pod initiation, number of seed per plant, biological yield, pod length, harvesting index, days to maturity, seed index, number of cluster per plant

### 3.3 Heritability

The heritability for all 13 characters were estimated. The heritability in broad sense ( $h^2$ ) ranged from 92.634% in the case of number of pods per plant to 16.072% in the case of pod length. The magnitude of heritability was found to be moderate (30-60%) for number of seeds per pod (36.126), biological yield per plant (36.601), seed index (40.278) and seed yield per plant (35.788). High heritability (>60%) was found for days to 50% flowering (91.803), days to maturity (53.967), plant height (76.293), number of primary branches per plant (83.427), number of clusters per plant (84.571), number of pods per plant (92.634), and harvest index (66.192).

Similar results are reported by **Degefa, et al , (2014)** biological yield per plant, days to 50% flowering, plant height, number of pods per plant, seed index, days to maturity, numbers of cluster perplant.

### 3.4 Genetic advance

The expected genetic advance for different characters ranged from 16.403% in the case of plant height to 0.203% in the case of pod length. Lowest to moderate values of expected genetic advance (<20) were found for all the characters; days to 50% flowering (7.151), days to 50% pod initiation (0.923), days to maturity (3.058), plant height (16.403), number of primary branches per plant (1.983), number of clusters per plant (1.872), number of pods per plant (4.003), pod length (0.203), number of seeds per pod (0.42), biological yield per plant (2.376), harvest index (3.435), seed index (0.3) and seed yield per plant (0.423).

Similar results are reported by **Mishra, S. P., (2018)** seed yield per plant, number of primary branches per plant, plant height, harvest index, while **Ramachandra, P.(2017)** number of pods per plant, biological yield, days to maturity, pod length.

#### 3.4. D<sup>2</sup> Analysis for Genetic Divergence

Simultaneous variation in all 13 characters of 53 greengram genotypes was verified for evaluating the nature of genetic divergence among them following Mahalanobis D<sup>2</sup> statistics.

##### **Intra and Inter-cluster distance**

Average intra- and inter-cluster distances (D<sup>2</sup>) values among the six clusters were calculated and are presented in Table 4. The lowest intra-cluster distance was associated with cluster I (14.98) followed by cluster II (21.93) and the highest intra-cluster distance was associated with cluster IV

(24.47). Cluster III, V and VI had no intra-cluster distance since those three were represented by a single genotype each.

From the average inter-cluster distance, it was evident that the most divergent clusters were III and VI (279.51) followed by clusters I & VI (176.69), cluster II & III (125.25), cluster V & VI (116.56), and cluster IV & VI (106.19). On the other hand, the least inter-clusters distance was observed between clusters I & V (32.46) followed by clusters I & III (35.46).

**Table 1. Analysis of variance for 13 morphological characters in Green gram**

Sl.No.	Source	Mean Sum of Squares (MSS)		
		Replication	Treatment	Error
	Degrees of freedom	2	52	104
1.	Days to 50% flowering	2.717	40.552**	1.172
2.	Days to 50% pod initiation	10.063	6.079**	3.313
3.	Days to maturity	11.679*	15.848**	3.538
4.	Plant height (cm)	11.999	275.124**	25.823
5.	Number of primary branches per plant	0.198	3.551**	0.221
6.	Number of clusters per plant	0.379	3.109**	0.178
7.	Number of pods per plant	0.018	12.552**	0.324
8.	Pod length (cm)	0.06	0.497*	0.316
9.	Number of seeds per pod	0.186	0.548**	0.203
10.	Biological yield per plant (g)	5.357	17.207**	6.298
11.	Harvest Index (%)	3.183	14.75**	2.146
12.	Seed Index (%)	0.018	0.236**	0.078
13.	Seed yield per plant (g)	0.107	0.566**	0.212

**Table 2. Genotypic Parameters for 13 Quantitative traits in Green gram genotypes**

<b>S.No.</b>	<b>Characters</b>	<b>GCV (%)</b>	<b>PCV (%)</b>	<b>h<sup>2</sup> (Broad Se nse)</b>	<b>Genetic Advance</b>	<b>Gen. Adv as % of Mean</b>
<b>1</b>	<b>Days to 50% flowering</b>	9.635	10.056	91.803	7.151	19.017
<b>2</b>	<b>Days to 50% pod initiation</b>	1.728	3.703	21.771	0.923	1.661
<b>3</b>	<b>Days to maturity</b>	2.99	4.08	53.697	3.058	4.513
<b>4</b>	<b>Plant height</b>	14.102	16.145	76.293	16.403	25.374
<b>5</b>	<b>Number of primary branches perplant</b>	14.128	15.468	83.427	1.983	26.583
<b>6</b>	<b>Number of clusters per plant</b>	17.38	18.899	84.571	1.872	32.925
<b>7</b>	<b>Number of pods per plant</b>	25.019	25.994	92.634	4.003	49.604
<b>8</b>	<b>Pod length</b>	3.289	8.204	16.072	0.203	2.716
<b>9</b>	<b>Number of seeds per pod</b>	5.535	9.208	36.126	0.42	6.853
<b>10</b>	<b>Biological yield per plant</b>	5.867	9.697	36.601	2.376	7.311
<b>11</b>	<b>Harvest Index</b>	10.281	12.637	66.192	3.435	17.231
<b>12</b>	<b>Seed Index</b>	5.694	8.972	40.278	0.3	7.444
<b>13</b>	<b>Seed yield per plant</b>	5.374	8.984	35.788	0.423	6.623

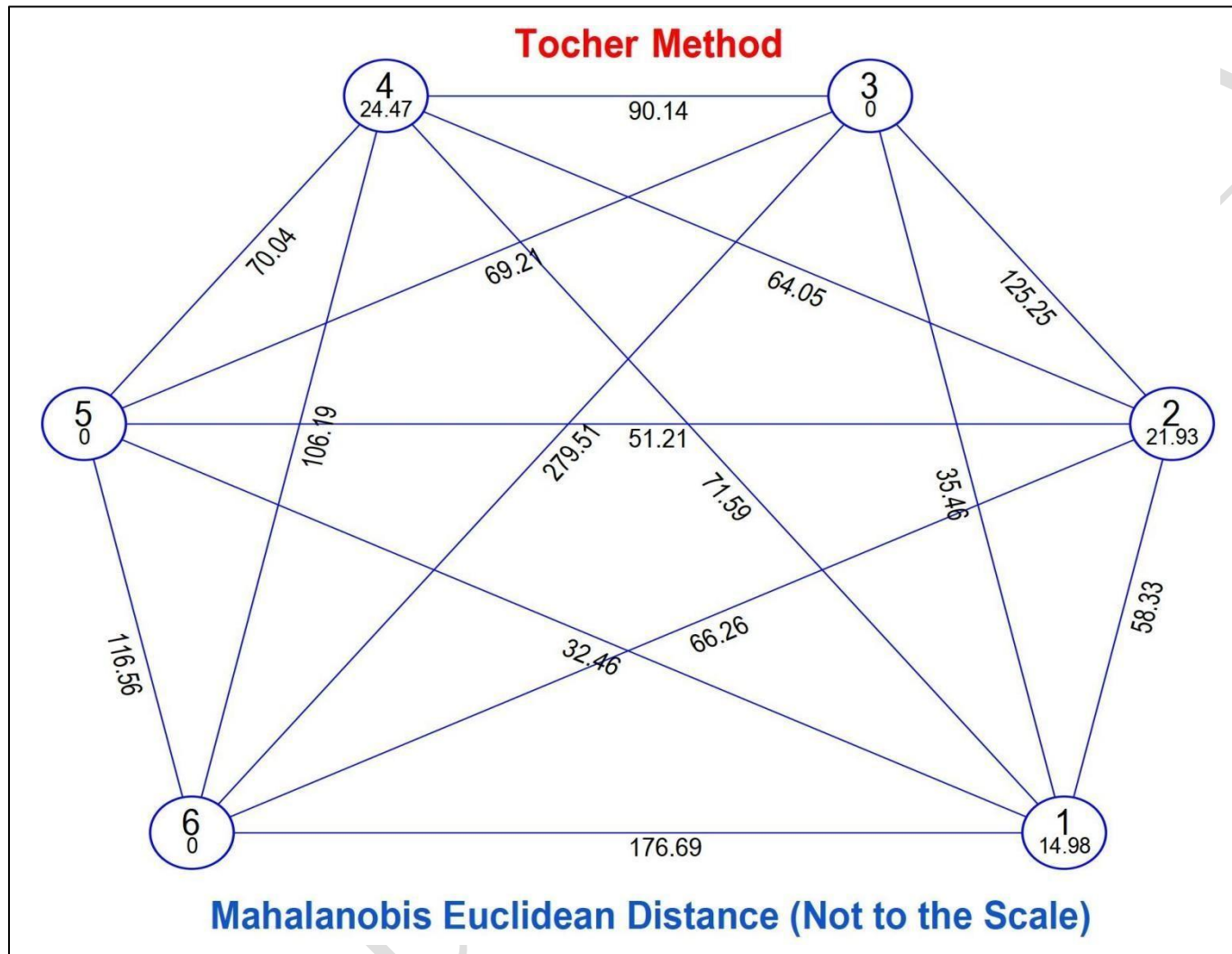
.Table 3. Distribution of 53 Green gram Genotypes into different Clusters based on D<sup>2</sup> Statistic

Cluster Group	No. of genotypes	List of Genotypes
<b>Cluster I</b>	36	MH-421, PDM-139, SML-1638, PUSA-BAISAKHI, SHWETHA, SHIKHA, MGG-2, PHULE MOONG -95418, PUSA-105, SAMRAT(CHECK), T-44, MGG-371, BM-2002, LGG-460, VIRAT, SPM-2040, SHAKTI, IPM-2-3, KM-11-564, SM-20-108, AMULYA, KM-2, SM-20-103, JALGAAN-781, K-851, TS-16, MGG-351, MGG-295, VBN-3, MGG-348, CO-7, VBN-2, ML-337, CO-8, VEENA & MGG-385
<b>Cluster II</b>	9	MGG-347, SM-2029, SPM-20-47, R-288-8, LGG-450, SMI-1668, RM-12-11, WGG-42 & GM-3
<b>Cluster III</b>	1	ML-131
<b>Cluster IV</b>	5	LGG-407, PHULE MOONG-9339, TYPE-51, TM-96-2 & ML-331
<b>Cluster V</b>	1	IPM-2-14
<b>Cluster VI</b>	1	IPM-205-7

**Table 4.. Inter and Intra cluster distance of 53 Genotypes of Green gram**

<b>Cluster Distances</b>						
	<b>Cluster I</b>	<b>Cluster II</b>	<b>Cluster III</b>	<b>Cluster IV</b>	<b>Cluster V</b>	<b>Cluster VI</b>
<b>Cluster I</b>	<b>14.98</b>	58.33	35.46	71.59	32.46*	176.69
<b>Cluster II</b>		<b>21.93</b>	125.25	64.05	51.21	66.26
<b>Cluster III</b>			<b>0.00</b>	90.14	69.21	279.51**
<b>Cluster IV</b>				<b>24.47</b>	70.04	106.19
<b>Cluster V</b>					<b>0.00</b>	116.56
<b>Cluster VI</b>						<b>0.00</b>

Fig.1: Diagram showing the Mahalanobis Euclidean distance



**Table 5. Cluster Mean of 13 Biometrical Traits of 53 Green gram Genotypes**

<b>Cluster Means : Tocher's Method</b>													
	<b>Days to 50% flowering</b>	<b>Days to 50% podinitiation</b>	<b>Days to maturity</b>	<b>Plant height</b>	<b>Number of primary branches per plant</b>	<b>Number of clusters per plant</b>	<b>Number of pods per plant</b>	<b>Pod length</b>	<b>Number of seeds per pod</b>	<b>Biological yield per plant</b>	<b>Harvest Index</b>	<b>Seed Index</b>	<b>Seed yield per plant</b>
<b>Cluster I</b>	36.00	55.72	68.01	62.27	7.09	5.35	7.28	7.38	5.97	32.40	19.90	4.05	6.36
<b>Cluster II</b>	38.37	54.74	66.19	60.88	8.76	6.82	11.34	7.51	6.47	33.09	19.04	3.97	6.20
<b>Cluster III</b>	40.00	56.00	68.33	62.03	6.33	3.87	4.40	8.51	6.28	26.48	24.57	3.85	6.31
<b>Cluster IV</b>	46.60	56.00	68.73	82.92	6.99	5.58	8.08	7.85	6.47	33.10	20.36	4.08	6.73
<b>Cluster V</b>	36.67	58.67	70.67	70.60	9.33	6.93	6.34	7.48	6.39	33.18	21.87	3.75	7.26
<b>Cluster VI</b>	42.00	52.33	64.33	89.30	10.40	8.73	12.53	7.65	6.39	33.34	20.80	3.84	6.76

## CONCLUSION

On the basis of finding generated from the present investigation, following conclusions can be drawn, which may be considered for improvement in greengram crop in future breeding programmes. The wide range of genetic variability observed for most of the characters as evidenced by significant variances due to genotypes signifying that, it could be helpful in selection of better germplasm. The phenotypic coefficients of variation were slightly higher than genotypic coefficients of variation which suggest the role of environment in governing these traits. Similarly, the magnitude of GCV and PCV was observed high for the characters viz., number of pods per plant and number of clusters per plant. The genetic diversity assessed using Mahalanobis's  $D^2$  statistics among 53 greengram genotypes, which were grouped into six clusters. From the studies of percent contribution of thirteen characters towards total divergence, it can be concluded that, seed yield per plant contributed highest for divergence followed by number of pods per plant, number of clusters per plant, number of seeds per pod, biological yield, number of primary branches per plant, pod length, harvest index, days to maturity, seed index, plant height, days to 50% pod initiation and days to 50% flowering. The objective of identifying divergence parents can be concluded by considering the genotypes of cluster III and cluster VI for further studies.

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