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Original Research Article

Genetic Diversity Estimation among the Cultivated Green Gram Genotypes [*Vigna radiata* (l.) Wilczek]

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A B S T R A C T

Green gram is the second major pulse crop with contributing 25-28% of total production in India. A field experiment was conducted during *Summer* season of 2019 under Research and Development Unit, Shreeoswal seeds and chemical ltd, Chittorgarh-khargone-Bhusawal Highway, near shubham warehouse, Neemuch-458441 (M.P.) to study the genetic divergence among 12 Green gram genotypes and observations on 14 traits were recorded. The analysis of variance indicated that significant variation was present among the different genotypes of the Green gram for all the morphological traits under study. Genetic divergence assessed using D^2 statistics for characters enabled grouping of all the genotypes in four different clusters. Among these four clusters, cluster I was the major with 5 genotypes followed by cluster II with 5 genotypes. Cluster III and IV were solitary. Maximum differences among the genotypes within the same cluster (intra-cluster) were shown by cluster II (67.91) followed by cluster I (54.09) whereas Solitary clusters III and IV showed zero intra-cluster distances. Diversity among the clusters varied from 94.89 to 733.47 inter-cluster distances. Cluster III and IV showed maximum inter cluster distance (733.47).

Keywords

Green gram, Genetic divergence, Analysis of variance, D2 analysis, Cluster analysis, Inter and intra-cluster distance

Introduction

Green gram [*Vigna radiata* (L.) Wilczek] comes under majority of the popular and worthy crops of the world, as its cultivation is most importantly done in Asian countries as Pakistan, Afghanistan, Korea, Philippines, Sri Lanka, Myanmar, Korea and significantly in India (Sharma and Dhanda, 2014). The generic cognomen of prefix *Vigna* had given after the name of Botany professor "Dominico Vigna" at Pisa (1609-1714) and the suffix word radiata derived from a Latin word "radius" which means, "radiating in every direction from the centre" as like as the spokes of a wheel, whereas it actually indicate the pods position on peduncle. The crop is also well known with the different names such as *moong, mung, mungo, Chickasaw pea, Oregon pea and Golden gram* (Chatterjee and Randhawa, 1952).

India has been considered as the domesticated country of Green gram (Vavilov, 1926) as its genus has been composed of more than 150 species, possess a considerable importance among the developing countries of the world. There are three most important botanical varieties that have been recognized named as *V. radiata*

var. *radiata*, var. *sublobata* and var. *setulosa* based upon the phylogeny of "*Phaseolus Vigna* complex", represented over a monograph. These three are distributed in India, among the twenty-two other species, Indonesia and Southern China (Polihill and Van der Masesen, 1985). There is no actual centre of origin provided for Green gram but according to Verdcourt (1970), *Vigna radiata* var. *sublobata* considered as the wild form of green gram which meant for "undoubtedly the wild form of mung".

At global scenario, India is contributing about 25 to 28 percent of total production in pulses. India is the primary producer of green gram contributes about 75 percent of the world production. In India, mung bean is cultivated as the third major pulse crop after chick pea and red gram. The states, viz, Andhra Pradesh, Maharashtra, Gujarat, Orissa and Tamil Nadu are major producers of green gram. In *kharif* season green gram is cultivated about 70 percent and remaining 30 percent in summer or *Rabi* season. The major pulse crops grown in the country under varied range of agro-climatic conditions are chick pea, green gram, black gram, pigeon pea and lentils. As per reports of FAO 2016 total production of pulses was 17.5 MT cultivated under 24.8 million ha area, which was estimated highest of all till now. Even after this much production, as per FAO 2016 India is still importing 3.6 MT of pulses per year sharing 32 percent of global imports. As of this, there is necessary to increase the productivity by varietal improvement in the pulse crops to meet hunger and demand of public in India.

Genetic diversity estimation and its relationships among the various germplasm accessions are importantly efficient for evaluating them. Now days, various tools are available for identifying the variations among the genotypes for days to maturity, days to reproductive phase, number of secondary branches, number of pods plant^{-1}, number of cluster plant^{-1}, number of grains pod^{-1} and seed yield (g) plant^{-1} and also for molecular characterization. However, morphological characterization considered as the former step for providing description and classification among different accessions of germplasm (Loganathan *et al.*, 2001b).

The D^2 analysis exhibit diversity on the basis of phenotypic expression of the different traits which restricts the resolving power mainly because of small number of variables available and some of them are developmental traits.

Materials and Methods

The present experimental research was conducted during the *Summer* season of 2019, at main experimental farm in Research and Development Unit, Shreeoswal seeds and chemical ltd., Neemuch at the latitude and longitude range of 24°29'25" N and 74°53'52" E respectively, to analyze the genetic diversity among the Green gram genotypes. The experimental area occupied was quite uniform in respect of topography and fertility with Black soil. Source and pedigree of material are given in Table 1.

The material used for the experiment consists of 12 genetically diverse genotypes and the field experiment will laid out in Randomized Block Design (RBD) with three replications. The row to row spacing within the ridges containing same germplasm will 50 cm and interspacing between two rows containing different germplasm will 100 cm. The spacing between plant to plant will be 10 cm. Seeds were sown with a depth of 4-5 cm with maximum of 2 seeds/hill and length of 200cm for each row. All the recommended agronomical practices and plant protection measures were adopted to raise the healthy

crop. The data was recorded on days to 75% flowering, days to reproductive phase, days to maturity, plant height (cm), number of branches per plant, number of secondary branches per plant, number of clusters per plant, number of pods per plant, length of the pod (cm), number of grain per pod, pod density, 100-seed weight (g), yield per plant (g) and yield per plot (g).

The data on morphological traits was subjected to analysis of variance on the basis of model described by Panse and Sukhatme (1985) for individual characters. The replicated data were subjected to genetic divergence analysis using Mahalanobis's D^2 - statistic (Mahalanobis, 1936).

Results and Discussion

The analysis of variance for all the morphological characters under study is presented below (Table 2). The mean differences due to genotypes were significant for all the characters indicating the presence of genetic variability in the material under study. Similar findings were reported by (Sinha *et al.*, 2018 and Garg *et al.*, (2017).

A method suggested by Tocher (Rao, 1952) was used to group the genotypes into different clusters based on the D^2 values. Twelve genotypes were grouped into four clusters. Among the cluster, cluster I and II was the biggest with 5 genotypes and Cluster II, IV were solitary. The clustering pattern and the distribution of genotypes into different clusters are presented in Table 3 (Fig.1).

The average D^2 value of intra and inter cluster distances are given in Table 4 (Fig. 2). Maximum differences among the genotypes within the same cluster (intra-cluster) were shown by cluster II (67.91) followed by cluster I (54.09). Solitary clusters III, IV showed zero intra-cluster distances. Diversity among the clusters varied from 94.89 to 733.47 inter-cluster distances. Cluster IV and III showed maximum inter cluster distance (733.47) followed by that between cluster I and IV (394.03), cluster II and III (337.00). The lower inter-cluster distance was noticed between cluster I and II (151.49) followed by that between cluster II and IV (131.01), cluster I and III (94.89). The perusal of mean in table 4 revealed that inter-cluster distances were greater than intra-cluster distances revealing considerable amount of genetic diversity among the genotypes studied. Genotypes belonging to clusters with maximum intra-cluster distance are genetically more divergent and hybridization between divergent clusters is likely to produce wide variability with desirable sergeants Gadakh *et al.*, (2013) and Garje *et al.*, (2013).

The cluster means and general mean values for fourteen characters of 12 genotypes have been represented in Table 5. The data revealed that differences in cluster means had existed. Cluster I comprised of 5 genotypes which were characterized as having above average values for days to 75% flowering, plant height, primary branches, pod density, 100 seed weight. Cluster II had 5 genotypes that indicate the above average values for days to 75% flowering, pods per plant, clusters per plant and pod density.

Cluster III comprised of 1 genotypes which was characterized as having above average values for duration of reproductive phase, days to maturity, plant height, primary branches per plant, pod length, grains per pod, 100 seed weight and yield per plot. Cluster IV consisting of 1 genotype showed above average values for days to 75% flowering, secondary branches per plant, pods per plant, clusters per plant, grains per plant, yield per planting and yield per plot.

Table.1 Source of 12 genotypes of green gram

S.NO.	Name of Variety/Inbred line	Source	Characteristics
1	HUM-1	BHU, Varanasi	Spring and Kharif season , Days to Maturity 60-65, Yield 9.4-16.0 q/ha
2	Gold	IIPR	unknown
3	Moongi	PAU, Punjab	unknown
4	HUM-1L	BHU, Varanasi	Summer season, Days to Maturity 60-62, Yield11.2 q/ha
5	PUSA-460	IARI, New Delhi	unknown
6	MLA 720	PAU, Ludhiana	unknown
7	Kopergane	BHU, Varanasi	Solid and Green bold seeds, Days to maturity 60-65, Yield 8-10q/ha
8	LM-5	BHU, Varanasi	Unknown
9	PUSA-Vishal	IARI, New Delhi	Summer season, bold seed, Days to Maturity 62, Yield 11.0 q/ha
10	LG-420	BHU, Varanasi	Unknown
11	IPM-2	IARI, New Delhi	Large seed suitable for rainy season, Days to Maturity 62-68, Yield 11-12 q/ha
12	SML-668	PAU, Ludhiana	Spring-Summer season , Tolerance to MYMV, Days to Maturity 60-63,Yield 11.3 q/ha

Table.2 ANOVA and Percent contribution of characters toward divergence in 12 Green gram genotypes

Sr. No.	Characters	Source of variation				Percent contribution	Rank
		Replication	Treatments	Error	CV		
	degree of freedom	2	11	18			
1	Days to 75% Flowering	5.0833	15.8864**	3.5379	4.55	0.00	
2	Days to Reproductive phase	12.1111	85.1793***	11.3838	13.07	0.00	
3	Days to maturity	2.5278	51.6263***	5.4975	3.49	15.15	III
4	Plant height (cm)	4.1657	96.3916***	11.2960	7.66	0.00	
5	Primary branches/plant	0.0166	0.7068*	0.2361	13.52	0.00	
6	Secondary branches/ Plant	0.5508	0.6028*	0.1696	6.07	0.00	
7	Cluster/plant	28.2138	176.7407***	9.5085	11.03	3.03	IV
8	Pods/plant	0.0958	1.4580***	0.1972	15.06	0.00	
9	Pod length (cm)	0.0155	0.7186***	0.1453	5.20	0.00	
10	No. of grain/pod	0.3278	3.0955**	0.7809	9.77	0.00	
11	Pod density	0.0038	0.0169**	0.0047	8.33	0.00	
12	100-Seed weight(g)	0.2002	2.1299***	0.1497	8.40	34.85	II
13	Yield/plant (g)	0.9164	3.5980***	0.4115	9.59	43.94	I
14	Yield/Plot (g)	122.93	854.19**	222.71	14.40	3.03	IV

*** Significant at 0.1% level, ** Significant at 1% level and * significant at level.

Table.3 Cluster profile of 12 genotypes of Green gram

Sr. No.	Cluster	No. of genotypes	Name of genotypes
1	I	5	Gold, LG-420, MLA-720, Pusa Vishal, IPM-2
2	II	5	HUM-1, Pusa-460, LM-5, HUM-1L, Kopergane
3	III	1	SML-668
4	IV	1	Moongi

Table.4 Estimation of intra (diagonal) and inter- cluster distances in 12 genotypes of Green gram

Cluster	I	II	III	IV
I	54.09	151.49	94.89	394.03
II		67.91	337.00	131.01
III			0.000	733.47
IV				0.000

*Diagonal value Intra-cluster distance

Table.5 Mean of fourteen characters in four clusters in Green gram genotypes

	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14
1 Cluster	**41.000**	24.867	65.867	**43.738**	**3.847**	6.823	24.973	2.604	7.342	8.771	**0.851**	**4.913**	6.319	104.783
2 Cluster	**42.333**	24.533	66.867	39.879	3.401	6.612	**31.323**	**3.371**	7.210	8.927	**0.812**	4.222	6.828	104.761
3 Cluster	36.667	**36.333**	**73.000**	**47.663**	**3.883**	6.997	15.027	1.940	**7.773**	**10.243**	0.763	**6.000**	**7.067**	109.970
4 Cluster	**41.667**	26.333	68.000	40.247	2.997	**7.140**	**38.887**	**4.550**	7.263	**9.797**	0.743	3.567	**7.440**	**121.153**
Mean	**40.416**	**28.016**	**68.433**	**42.881**	**3.532**	**6.892**	**27.552**	**3.116**	**7.397**	**9.434**	**0.792**	**4.675**	**6.913**	**110.17**

C1 =days to 50 % flowering**, C2** =days to reproductive phase**, C3** = days to maturity**, C4**= plant height (cm) **, C5** = primary branches plant^{-1}**, C6** = secondary branches plant^{-1}**, C7** = clusters plant^{-1}**, C8** = pods plant^{-1}**, C9** =pod length (cm), **C10** =grain pod^{-1}**, C11** =pod density**, C12** =100 seed weight (g),**C13** =yield plant^{-1} (%) and **C14**= yield per plot (g).

Fig.1 Clustering by Tocher Method

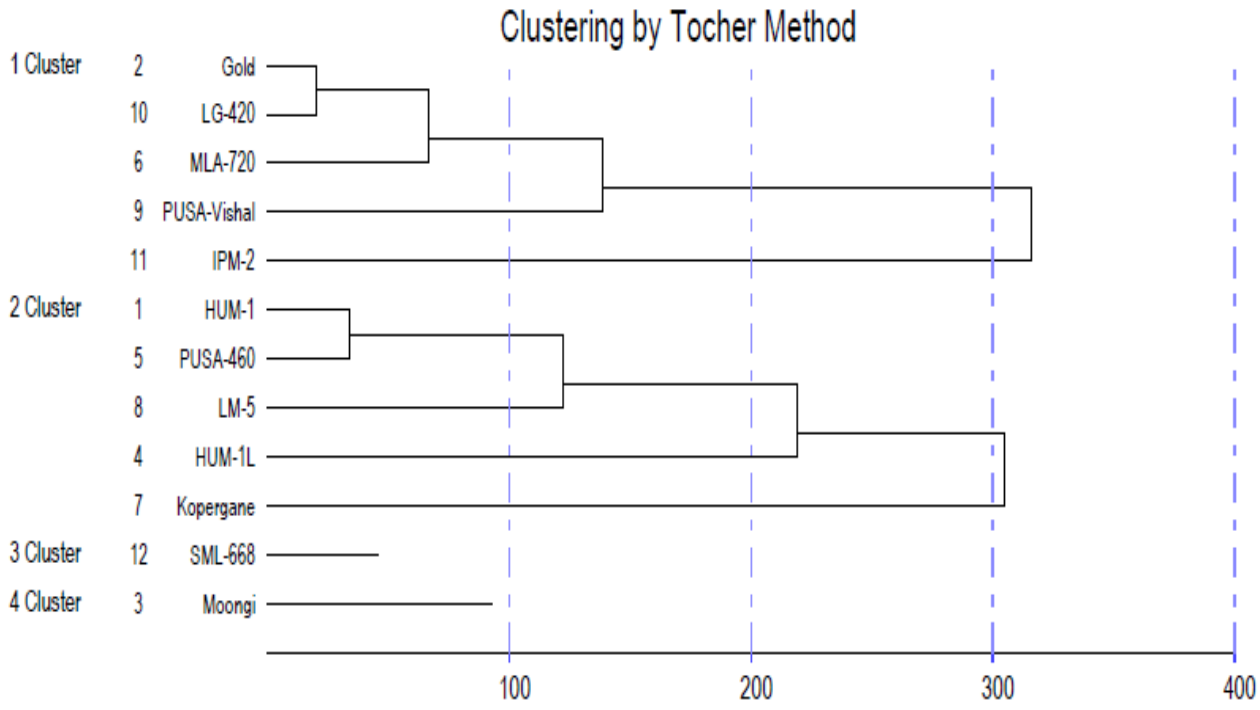
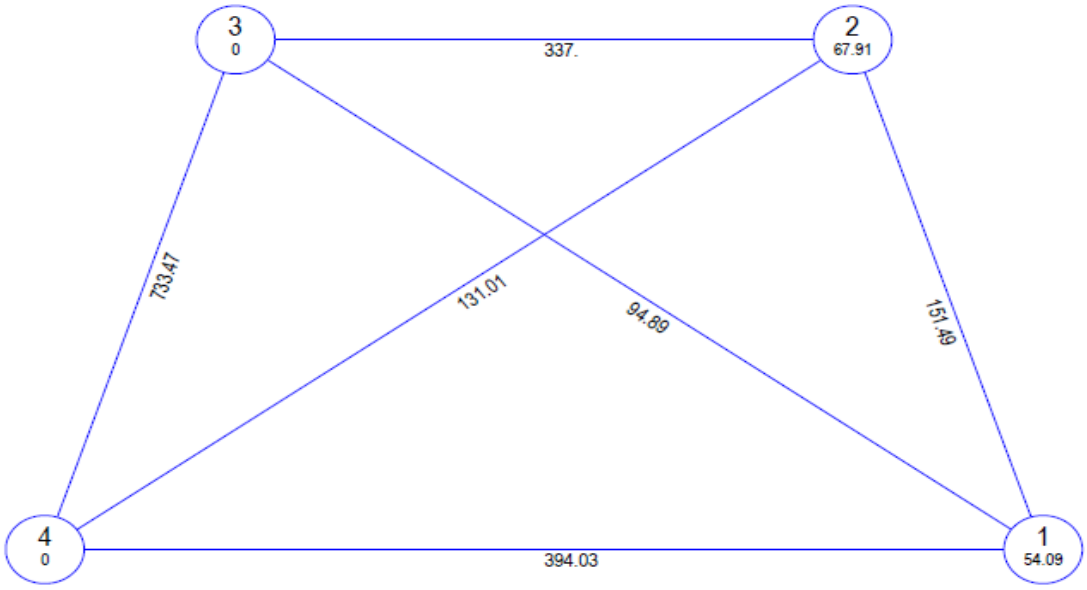


Fig.2 Intra and inter- cluster distance for 12 genotypes of Green gram



Similar finding was reported by Rasal *et al.*, (2017) and Ahmad *et al.*, (2013). The present study indicated that the distribution of genotypes into different clusters was at random and sufficient D^2 values among different cluster suggests that the genetic constitution of the promising lines in one cluster is in close proximity with the promising lines in other clusters of the pair may lead to desirable segregants having broad genetic base through hybridization between genotypes of two distant clusters. This finding will be helpful in planning future hybridization programme should involving diverse genotypes for crop improvement.

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