Original Research Article

STUDY OF GENETIC DIVERSITY IN GREENGRAM (*Vigna radiata* (L.) Wilczek) GERMPLASM IN PRAYAGRAJ REGION

ABSTRACT

The present study consists of 41 Greengram genotypes including one Check variety used to study the nature and magnitude of genetic divergence using Mahalanobsi's D^2 statistics. The data for 13 quantitative characters recorded from the genotypes raised in Randomized Block Design having three replications at Department of Genetics and Plant Breeding, SHUATS, Prayagraj, Uttar Pradesh, India during *Kharif*-2021. 13 quantitative characters *viz.*, Days to 50% flowering, Days to 50% pod setting, Days to maturity, Number of clusters per plant, Number of primary branches, Plant height(cm), Number of pods per plant, pod length (cm), Biological yield per plant (g), Number of seeds per pod, Harvest index (%), Seed yield per plant(g), Seed index to estimate the variability, heritability, genetic advance, genetic diversity among yield. SML-668 (14.96 g) has the highest Seed yield followed by IPM-205-7 (13.48 g), IPM-410-03913.21 g) showed the higher yield over the SM-20-29 (Check). Maximum (GCV), (PCV), Heritability was recorded for Number of primary branches. High Heritability coupled with high Genetic advance was recorded for Plant height (cm). Divergence analysis followed by Mahalanobis (1936) D^2 analysis has revealed the presence of a substantial amount of diversity among the genotypes. Clusters I contain 19 genotypes followed by Clusters II contain 18 genotypes while Clusters III, IV, V, VI are mono genotypic. The maximum inter-cluster distance was observed between Cluster IV and VI (290.82) followed by Cluster IV and V (238.70). Thus, genotypes present in these clusters suggest that the genetic architecture of the genotypes in one cluster differ from another cluster which provides a broad spectrum of variability in segregation and may be used as parents in the future hybridization programme to develop desirable genotypes.

Keywords: Greengram, GCV, PCV, Heritability, Variability, Cluster analysis, Divergence

Introduction

"Greengram (*Vigna radiata* (L.) Wilczek, 2n=22) belongs to genus Vigna of the Leguminose family and it is diploid. Greengram is one of the most important edible foods of Asia widely cultivated and consumed in India" **(*Datta et al.*, 2012).** "Greengram is a predominantly self-pollinated crop; considerable variation exists among greengram cultivars and its wild species" **(*Bisht et al.*, 2005).** "One of the constraints listed for lack of breakthrough in greengram production has been the deficit of genetic variability for high yielding potential" **(Ramanujam, 1978)** Greengram is also known as Mung. Greengram is an important pulse crop which comes up well under humid tropics, semi-arid and arid regions. In the Global scenario India is contributing about 25 to 28 percent of total production in pulses. Greengram is an excellent source of protein which can be consumed as whole grains, sprouted form as well as dal in a variety of ways in homes. In *kharif* season Greengram is cultivated about 70% and remaining 30% in summer or rabi season.

Greengram is one of the most widely adapted drought tolerant versatile green manuring and nutritious legumes. It is harvested in two months after sowing, which makes an ideal fit for fallow crop in wheat and rice production system. It can improve soil fertility by fixing atmospheric nitrogen through their root nodule. Greengram is highly nutritive and it constitutes an important source of protein (23.6 %) with carbohydrate (58 %).

"Genetic improvement mainly depends on genetic variability present in the population and serves as a source for providing wide variability. Genetic variability between traits is essential for breeding and choosing the desired qualities. Study of Genetic diversity in genetic resources is a critical factor for breeders to better understand the evolutionary and genetic relationships among populations, to select germplasm in a more systematic and efficient way to perform and develop strategies to incorporate useful diversity in their breeding programs" **(*Lavanya et al.*, 2008)**. The Genetic diversity was estimated by using Mahalanobis D^2 statistics tool. Considering these points the present investigation was designed to screen the greengram germplasm to study available genetic variability, heritability, divergence which will help to find the divergent parent for selection.

The Research Gap :

The increase in population and malnutrition implies there is a need for high yield of greengram varieties. Therefore, the present study is conducted to identify and evaluate the diversity among the Greengram by collecting and studying Greengram genotypes.

Aims and Objectives of this study :

1. To evaluate Greengram genotypes for Yield and Yield contributing traits.
2. To estimate genetic diversity in available Greengram genotypes using D^2 analysis.
3. To identify the divergent parent for future hybridization program.

The main object of this work was to classify the Greengram germplasm into distinct groups on the basis of genetic diversity and to identify diverse genotypes useful in hybridization programmes for the development of better recombinants.

Materials and Methods

The experimental materials for present investigation was consist of forty-one greengram genotypes including one check variety obtained from Department of Genetics and Plant Breeding, Naini Agriculture Institute, SHUATS, Prayagraj, Uttar Pradesh, India was evaluated at Field Experimentation Centre, SHUATS, Prayagraj, Uttar Pradesh, India during *Kharif*-2021 in Randomized Block Design with three replications. Data were recorded for five randomly tagged plants for characters *viz.*, Days to 50% flowering, Days to 50% pod setting, Days to maturity, Number of clusters per plant, Number of primary branches, Plant height(cm), Number of pods per plant, pod length (cm), Biological yield per plant (g), Number of seeds per pod, Harvest index (%), Seed yield per plant(g), Seed index. The experimental data was analysed statistically by the method of analysis of variance and different genetic parameters are estimated. **Mahalanobis (1936)** defined the distance between two populations as D^2 which was obtained by Tochers method described by **Rao (1952).** Contribution of individuals of characters towards divergence is determined by the method described by **Singh and Choudhary (1985).**

Statistical analysis :

The data recorded for 13 characters in 41 Greengram genotypes (Vigna radiata (L.) Wilczek) in three replications will be subjected to the following analysis. The data was analyzed using computer software programmed by the method of variance outlined by **Panse and Sukhatam (1985).**

1. Analysis of variance **(Fisher, 1918)**
2. Coefficient of variation **(Burton, 1952)**
    a. Phenotypic coefficient of variation(PCV)
    b. Genotypic coefficient of variation (GCV)
3. Heritability (broad sense) **(Burton and Devane, 1953)**
4. Genetic advance **(Johnson *et al.*, 1955)**
5. D^2 analysis **(Mahalanobsis, 1936)**

Results and Discussion

Among 41 genotypes, SML-668 (14.96 g), IPM-205-7 (13.48 g), IPM-410-03 (13.21 g) was found to be superior in seed yield per plant.

The analysis of variance revealed significant variance among genotypes for all character's studies, indicating the existence of wide genetic divergence among them. Environment plays an important role in the expression of Phenotype and Genotype, in present investigation Phenotypic coefficient of variance is higher than Genotypic coefficient of variance indicating that characters are influenced by Environment. Hence, variability can be observed through parameters like GCV, PCV, Heritability (broad sense), genetic advance**. Sivasubramanian and Madhava Menon (1973)** classified variability as Low (0 – 10%) and Moderate (10 – 20%) and High (>20%). High magnitude of GCV, PCV recorded for number of primary branches, number of pods per plant, seed yield per plant, plant height, biological yield, suggesting sufficient variability. ***Johnson et al. (*1955)** classified Heritability as Low (<30%) and Moderate (30 to 60%) and High (>60%). High heritability was recorded for number of primary branches, seed yield per plant, number of pods per plant, number of clusters per plant, plant height, indicating that these traits are likely to be controlled by additive gene components. ***Johnson et al.* (1955)** classified "Genetic advance as % mean Low (<10%) and Moderate (10 to 20%) and High (>20%). High GCV along with high Heritability coupled with high GAM for number of primary branches, number of pods per plant, seed yield per plant, plant height, biological yield. Low GCV along with Low Heritability coupled with Low GAM recorded for days to 50% pod setting".

Based on D^2 values 41 genotypes were grouped into six clusters based on the genotypes within the cluster having similar D^2 values among themselves. Cluster I is the largest cluster with nineteen genotypes followed by Cluster II with eighteen genotypes, followed by clusters III, IV, V, VI with single genotype. ***Das et al.* 2010** "grouped 23 genotypes into eight clusters; the clustering pattern of genotypes showed that genetic diversity was not related to geographic diversity".

The average intra cluster distance ranged from 16.18 to 22.62. Maximum intra cluster distance was recorded for cluster I (16.18) followed by cluster II (22.62). The inter cluster distance recorded higher between cluster IV and VI (290.82) followed by cluster IV and V (238.70), followed by cluster III and IV (232.87) followed by cluster II and IV (226.48), suggesting that the genotypes present in these clusters may be used as parents for hybridization programme to produce the better yield.

Mean performance of a cluster is the mean of overall values of individual correlated variables of all genotypes including in that cluster. Higher cluster mean for seed yield per plant was recorded for cluster IV (12.80) followed by cluster I (12.28) followed by cluster V (7.90) followed by cluster II (5.77) followed by cluster III (4.19) followed by cluster VI (3.92).

The percent contribution of 13 characters towards the genetic divergence, in present study maximum contribution towards the total divergence was exhibited by seed yield per plant (31.59) followed by biological yield (20.37) followed by number of seeds per pod (11.95) followed by harvest index (10.37) followed by number of pods per plant (10.12) selection of these characters for future hybridization may be rewarding. The contribution followed by plant height (5.00) followed by seed index (3.41) followed by (2.56) followed by days to 50% flowering (2.2) followed by pod length (1.59) followed by days to 50% pod setting (0.37) followed by number of clusters per plant (0.35) followed by days to maturity (0.12) was least to genetic diversity among 13 characters.

Conclusion

Among 41 genotypes of Greengram on the basis of mean performance SML-668(14.68 g) was found superior in seed yield per plant followed by IPM-205-7 (13.48 g), IPM-410-03 (13.21 g). The magnitude of GCV and PCV and Heritability recorded highest for number of primary branches (48.529%, 49.35%, 96.702%) and lowest for days to 50% pod setting (7.667%, 10.504%, 53.271%). Cluster IV and VI (290.82) and IV and V (238.70) had high inter cluster distance, were most diverse from each other and genotypes present in these clusters provide wide variability in segregation and used as parents for future hybridization programmes.

Table 1: Analysis of variance of 13 quantitative characters of 42 Greengram genotypes during *kharif*-2021

S.No.	Source	Replication	Treatment	Error
	Degrees of freedom	**2**	**40**	**80**
1	**Days to fifty percent flowering**	**7.2850**	**57.808****	**10.109**
2	**Days to fifty percent pod setting**	**3.6980**	**51.483****	**11.648**
3	**Days to maturity**	**12.2530**	**119.082****	**22.04**
4	**Plant height(cm)**	**3.0030**	**522.676****	**9.11**
5	**Number of clusters per plant**	**0.2990**	**5.68****	**0.099**
6	**Number of pods per plant**	**2.5030**	**150.377****	**2.385**
7	**Pod length (cm)**	**0.0080**	**1.742****	**0.324**
8	**Number of primary branches**	**0.0560**	**4.177****	**0.047**
9	**Seed Index (g)**	**0.270**	**0.78****	**0.135**
10	**Number of seeds per pod**	**1.4840**	**6.398****	**0.744**
11	**Biological yield**	**1.0910**	**210.966****	**4.093**
12	**Seed yield per plant (g)**	**0.4730**	**36.477****	**0.481**
13	**Harvest Index (%)**	**14.3020**	**63.814****	**12.839**

**** and * significant at 1% and 5% level of significance**

Table 2: Estimation of variability and Genetic parameters for 13 quantitative characters of 41 Greengram genotypes

S.No.	Parameters	GCV	PCV	h^2 (Broad Sense)	Genetic Advance	Gen.Adv as % of Mean
1	Days to fifty percent flowering	10.332	13.214	61.133	6.422	16.641
2	Days to fifty percent pod setting	7.667	10.504	53.271	5.479	11.527
3	Days to maturity	8.567	11.108	59.475	9.036	13.61
4	Plant height(cm)	33.028	33.895	94.947	26.263	66.296
5	Number of clusters per plant	29.44	30.21	94.968	2.738	59.1
6	Number of pods per plant	47.854	48.997	95.389	14.131	96.279
7	Pod length (cm)	9.104	11.823	59.299	1.091	14.442
8	Number of primary branches	48.529	49.35	96.702	2.377	98.308
9	Seed Index (g)	12.457	15.9	61.382	0.748	20.104
10	Number of seeds per pod	13.633	16.099	71.71	2.395	23.782
11	Biological yield	32.825	33.785	94.397	16.62	65.698
12	Seed yield per plant (g)	38.807	39.577	96.146	6.997	78.387
13	Harvest Index (%)	11.84	15.687	56.961	6.409	18.407

GCV = Genetic coefficient of variation, PCV = Phenotypic coefficient of variation, h^2 = Heritability

Table 3: Grouping of 41 greengram genotypes into clusters

Cluster Group	No. of Genotypes	List of Genotypes
Cluster 1	19	BM-2003-2, BM-2002-1, MGG-351, CO-08, BPMR-145, PANT MOONG-5, PUSA-105, GAM-5, IPM-02-03, ML-131, VBN-2, SML-832, IPM-205-7, IPM-02-14, CO-7, GM-3, IPM-410-03, MH-421 & SML-668
Cluster 2	18	PHULE MOONG 9339, SM-20-29 (CHECK), SPM-20-47, ML-337, PUSA BAISAKHI, PDM-139, TM 96-2, S.P.M.2040, SM-2029, SML-1638, LGG-450, JALGAON 781, TYPE-51, LGG-460, PHULE G-94418, SM-20-103, SHWETA & PS-16
Cluster 3	1	IPM-2-3
Cluster 4	1	MGG-295
Cluster 5	1	LGG-407
Cluster 6	1	T-44

Table 4: Inter and Intra cluster distance using Tochers method among 41 genotypes of Greengram

Clusters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	**16.18**	158.18	144.78	33.99	**149.54**	**188.35**
Cluster 2		**22.62**	35.03	**226.48**	42.09	59.47
Cluster 3			0.00	**232.87**	49.59	26.92
Cluster 4				0.00	**238.70**	**290.82**
Cluster 5					0.00	**104.61**
Cluster 6						0.00

Table 5: Cluster mean using Tochers method among 13 characters of Greengram

Clusters	Days to 50% flowering	Days to 50% pod setting	Days to maturity	Plant Height	Number of clusters per plant	Number of pods per plant	Pod Length	Number of Primary branches	Seed Index	Number of seeds per pod	Biological yield	Seed yield per plant	Harvest Index
Clusters 1	41.02	48.02	61.58	52.42	3.36	8.01	7.64	3.38	3.77	9.45	32.92	12.28	37.74
Clusters 2	36.56	47.19	71.17	26.95	5.97	21.72	7.38	1.52	3.62	10.59	17.96	5.77	32.27
Clusters 3	35.67	47.33	68.00	33.03	4.72	16.50	7.88	0.97	4.53	11.16	16.35	4.19	25.96
Clusters 4	41.67	49.00	63.00	52.80	3.73	9.20	7.47	4.93	4.33	8.27	38.70	12.80	33.14
Clusters 5	40.00	53.00	76.67	36.38	6.17	18.62	10.00	0.98	3.19	15.11	22.22	7.90	35.61
Clusters 6	29.67	38.00	63.00	20.97	3.98	14.37	6.17	0.52	3.73	8.11	11.25	3.92	34.84

Table 6: Percent contribution towards Genetic divergence among the 13 characters of Greengram genotypes

	Source	Contribution %	Times ranked 1st
1	**Days to fifty percent flowering**	2.2	18
2	**Days to fifty percent pod setting**	0.37	3
3	**Days to maturity**	0.12	1
4	**Plant height(cm)**	5	41
5	**Number of clusters per plant**	0.35	3
6	**Number of pods per plant**	10.12	83
7	**Pod length (cm)**	1.59	13
8	**Number of primary branches**	2.56	21
9	**Seed Index (g)**	3.41	28
10	**Number of seeds per pod**	11.95	98
11	**Biological yield**	20.37	167
12	**Seed yield per plant (g)**	31.59	259
13	**Harvest Index (%)**	10.37	85
	Total	100%	

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