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The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(12): 4490-4493

www.thepharmajournal.com
Received: 26-09-2022
Accepted: 29-10-2022

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Genetic diversity studies in greengram (*Vigna radiata* (L.) Wilczek)

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Abstract
The present investigation entitled, "Genetic Diversity Studies in Greengram (*Vigna radiata* (L.) Wilczek)" was undertaken to study the nature and extent of variability present among the genotypes for quantitative characters in greengram and grouping genotypes into various clusters. The knowledge of genetic diversity helps in identification of germplasm, gene stock and establishment of core collection. Genetic diversity is one of the basis of parent selection for breeding programme. Genetic diversity among parent, which is heritable, is a prerequisite for any successful breeding programme. The proper choice of parents in breeding programme is of paramount importance. Generally, plant breeder selects the parents on the basis of phenotypic divergence but for effective breeding knowledge of genetic diversity amongst the parents with respect to characters which are to be improved is essential. All the forty genotypes of greengram were grouped into eight clusters. Cluster II had maximum number of 20 genotypes, Cluster I, Cluster IV and Cluster V had 5 genotypes, Cluster VII had 2, while Cluster II, VI and VIII had single genotype each respectively.

Keywords: Greengram, genetic diversity and cluster analysis

Introduction
Greengram is a short duration plant. The recently developed high yielding varieties have dwarf plants of 45-75 cm, mature in 60-75 days and are determinate. It is erect or sub erect twinning herb annual with plant deeply hairy. The tap root is well branched and fairly extensive, smooth and round nodules carrying grove on the root. The stem is defuse, furrowed and much branched from the base. It is green or purple and is covered with dense brown hair pointing downward. The leaves are alternate, trifoliate with pointed leaflets subtended by small stipules. There are two stipules at the base of the petiole. The trifoliate leaves have long petioles. The leaflets are ovate to lanceolate with entire margin and sometime trilobed. The inflorescence is axillary. The flowers are light yellow, are born in clusters of 10-30 on long pedicels. The calyx bracts are oblong to ovate. It comprises five gamosepalous, imbricate and calyx lobs are linear. The corolla consists of five petals (one standard, two wings and two keels united) pale yellow. Flowers are cleistogamous and modeled on leguminous pattern. Stamens are diadelphous (9+1). Each stamen is a pollen sac and generally opens to release its mature pollens during the night before 5 AM to cause pollination of the enclosed stigma. The flowers open 4-8 hours after pollination by which time the fertilization is generally complete. The matured pods are 5-18 cm long, round slender and have short pubescence. The seeds are globular or sometimes drum shaped and generally green shining or green dull in colour, but sometimes are yellow, purple brown or a mosaic of black with green, yellow or brown dots. The seed surface has many fine and undulating ridges, which are mostly invisible to the naked eye. The hylum of the seed is white in colour and flat, in level with the seed surface. Germination is epigeal. The plants are fully self-fertile and self-pollinated.

The knowledge of genetic diversity helps in identification of germplasm, gene stock and establishment of core collection. Genetic diversity is one of the basis of parent selection for breeding programme. Genetic diversity among parent, which is heritable, is a prerequisite for any successful breeding programme. The proper choice of parents in breeding programme is of paramount importance. Generally, plant breeder selects the parents on the basis of phenotypic divergence but for effective breeding knowledge of genetic diversity amongst the parents with respect to characters which are to be improved is essential.

Mahalanobis (1936) [10] D^2 recognized as a powerful tool for estimating the divergence between two populations. Choice of divergent parent can be made for hybridization purposes on the basis of D^2 values between two genotypes or two clusters.

Genotypes from most divergent clusters can be chosen taking into account their desirable characters.

Materials and Methods

The present investigation entitled, "Genetic Diversity Studies in Greengram (*Vigna radiata* (L.) Wilczek) was conducted at farm of College of Agriculture, Badnapur, during *kharif* season of 2021-22. The experimental materials used for study consisted of thirty-six genotypes of Greengram, out of which 26 genotypes were obtained from the germplasm of National Bureau of Plant Genetic Resources, New Delhi, available at Agricultural Research Station, Badnapur, 10 stable interspecific recombinants from Agricultural Research Station, Badnapur and 4 standard checks *viz.*, BPMR 145, BM 2002-1, BM 4, BM 2003-2 were evaluated in a randomized block design with two replications during *kharif* season of 2021-22. Each genotype was sown in two rows of 4 m length with spacing of 45 cm between rows and 10 cm between plants.

Genotypes details

1. **EC:** Exotic collection
2. **IC:** Indigenous collection
3. **BMG-75:**
   Badnapur Mungbean Germplasm explored from the triable areas of Maharashtra
4. **BWU-9:** Badnapur Wild Urdbean (*Vigna sylvestris) Vigna sylvestris* is one of progenitor of urdbean
5. **BWM-29:** Badnapur Wild Mung (*Vigna sublobata-29*)
6. **SPS:** Interspecific recombinant (four way crosses) [(BM 4× BWM-29) ×BM 2002-1] × BM 2003-1]
7. **BMG-75-1 × BWU-9:** Single crosses (stable material)

The data were recorded on five randomly selected plants of each replication for all characters such as plant stand, days to 50% of flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight, seed yield and harvest index. The analysis of divergence was carried out by D^2 statistics proposed by Mahalanobis (1928, 1936) [10] as described by Rao (1952) [15].

Results and Discussion

All the forty genotypes of greengram were grouped into eight clusters using the method (Singh and Chaudhary, 1977) [16]. The distribution of the genotypes into clusters along with the geographical area of adaptation is presented in Table 1 and Fig.1. Cluster II had maximum number of 20 genotypes, Cluster I, Cluster IV and Cluster V had 5 genotypes, Cluster VII had 2, while Cluster II, VI and VIII had single genotype each respectively. The genotypes were distributed randomly in all the clusters. There was relationship between geographic diversity and genetic diversity as the genotypes from different geographic region were included in the same cluster.

With the help of D^2 values (Table 2), a cluster diagram was constructed showing the relationship between the different genotypes. The greatest distance between two clusters was existed between cluster IV and III (367.08) indicating greatest divergence, followed by cluster VII and IV (300.13), VI and IV (287.06), V and IV (276.22), IV and I (265.06), V and III (233.38), VII and III (225.68). Whereas the least distance was recorded between cluster VII and VII (26.81) followed by cluster I and I (27.84), cluster II and II (41.12) and cluster IV and IV (44.23) indicating least genetic divergence among genotypes.

The average intra cluster distance D^2 values of clusters were furnished in Table 2 and Fig. 1. The intra cluster values varied from 0.00 to 56.91. The maximum intra cluster distance of 56.91 was noticed in cluster V. It was 44.23 in cluster IV and 41.12 in cluster II. The genotypes belong to these clusters can be considered as parents for hybridization programme since genotypes within these clusters with a high degree of divergence would produce more desirable breeding material for achieving maximum genetic advance with regards to *per se*.

The cluster mean for the ten characters are presented in Table 3. A considerable inter cluster variation was observed among the cluster means for the characters studied *viz.*, days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g), seed yield per plant (g) and harvest index (%). The cluster mean for days to 50 per cent flowering varied from 31.50 (III) to 39.70 (V). The cluster mean for days to maturity ranged between 59.50 (III) to 69.10 days (VI). The cluster mean for plant height (cm) was 47.68 cm, which was observed in cluster (IV) and lowest for (cluster V) 68.77. The cluster mean for the number of primary branches per plant ranged from 6.10 (cluster VI) to 11.94 (cluster VI). The cluster mean for secondary branches per plant ranged between 5.10 (cluster VI) and 11.52 (cluster IV). The cluster mean for number of pods per plant was maximum in cluster III (14.30) and it was minimum in cluster VIII (32.00). The cluster mean for number of seeds per pod was maximum in cluster III (13.85) and it was minimum in cluster VI (11.10). The cluster mean for 100 seed weight was minimum in cluster I (3.24) and it was maximum in cluster III (6.75). The cluster mean for seed yield per plant ranged between (9.86) cluster V and (14.80) cluster VIII. The mean for harvest index was minimum in cluster I (39.15%) and maximum in cluster VIII (49.82%).

Table 1: Composition of forty greengram genotypes into different cluster by Tocher's method:

Cluster No.	No. of genotypes	Genotype included in the cluster
I	5	SPS-6-5-20-4-2, SPS-6-5-23-4-1, SPS-6-5-20-4-3, EC520010, SPS-6-5-22-5-1
		BM 2002-1, EC398898, C538134, BM 2003-2, EC260610, EC396128,
II	20	EC528087, EC396155, IC621812, BPMR 145, EC396529, EC398856, IC607181, EC538122, EC396530, EC398901, EC396113, EC396135, EC396147,
		EC251967-1
III	1	EC398885
		BMG-75-1×BWU-9 SPS-17-1-10-1-3-1-1, BMG-75-1×BWU-9 SPS-23-1-2-1-2-
IV	5	2, BMG-75-1×BWU-9 SPS-21-1-4-1-2-1-3, BMG-75-1×BWU-9 SPS-25-1-4-1-
		2-1-4, BMG-75-1×BWU-9 SPS 7-1-11-1-1-1-1

V	5	IC623693, IC548271, IC388916, SPS-6-5-22-5-2, EC13077-2,
VI	1	EC396129
VII	2	BM 4, IC76425
VIII	1	IC548271

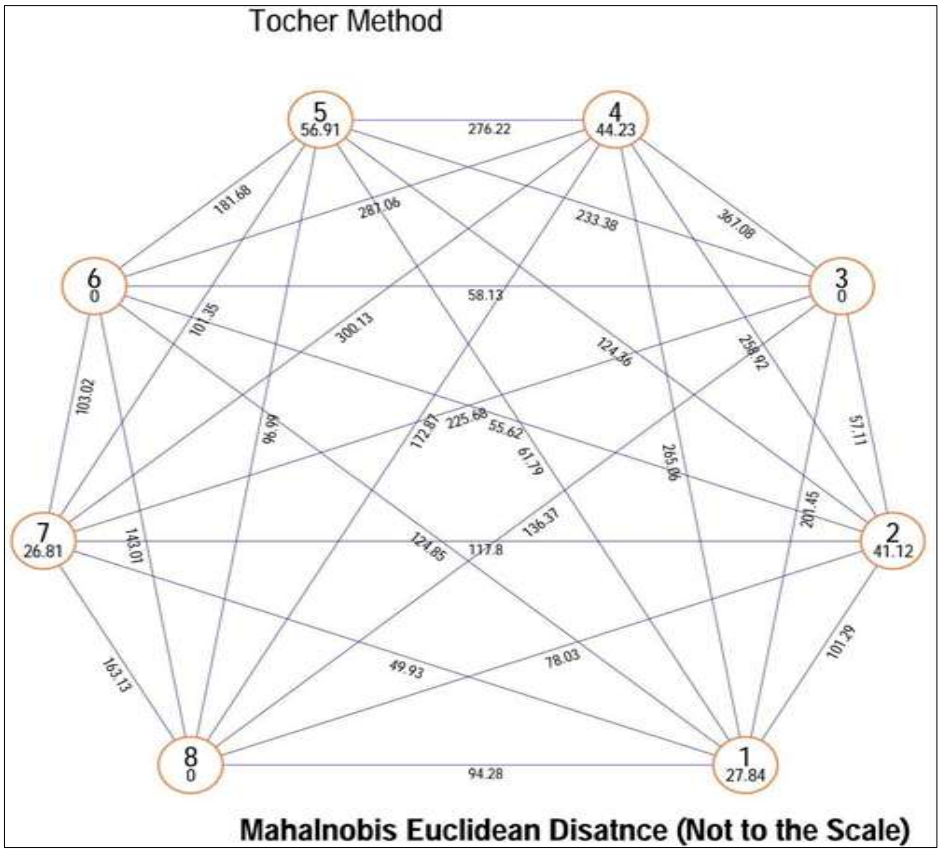

Fig 1: Distances among cluster by Tocher's method

Table 2: Average intra and inter cluster distance D^2 values in greengram:

Clusters	I	II	III	IV	V	VI	VII	VIII
I	27.84	101.29	201.45	265.06	61.79	124.85	49.93	94.28
II		41.12	57.11	258.92	124.36	55.62	117.8	78.03
III			00	367.08	233.38	58.13	225.68	136.37
IV				44.23	276.22	287.06	300.13	172.87
V					56.91	181.68	101.35	96.99
VI						00	103.02	143.01
VII							26.81	163.13
VIII								00

Table 3: Cluster mean of different characters for genetic diversity in greengram:

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of secondary branches per plant	No. of pods per plant	No. of Seeds per pod	100 seed weight (gm)	Seed yield per plant (gm)	Harvest index
Cluster I	33.20	66.20	54.42	7.26	6.92	21.80	13.81	3.24	11.05	39.15
Cluster II	35.55	63.40	56.63	7.52	6.36	17.71	13.00	5.52	13.35	46.31
Cluster III	31.50	59.50	57.00	6.90	5.35	14.30	13.85	6.75	14.30	48.19
Cluster IV	34.10	69.10	47.68	11.94	11.52	28.52	6.99	4.44	11.04	42.65
Cluster V	39.70	7.00	68.77	8.30	7.16	21.52	12.81	3.40	9.86	40.01
Cluster VI	32.00	65.00	50.25	6.10	5.10	16.00	11.10	5.50	10.90	39.63
Cluster VII	35.00	62.00	48.05	6.70	5.75	16.18	11.65	3.35	10.05	43.75
Cluster VIII	36.00	66.50	58.20	8.30	6.40	32.00	13.45	4.70	14.80	49.82

Table 4: Percent contribution of different characters to genetic diversity in greengram:

Sr. no.	Characters	Percent contribution	No. of time appearing 1st in ranking
1.	Days to 50% flowering	5.38%	42
2.	Days to maturity	0.00.%	00
3.	Plant height	8.08%	63
4.	Number of primary branches per plant	0.77%	6
5.	Number of secondary branches per plant	0.13%	1
6.	Number of pods per plant	15.51%	121
7.	Number of seed per pod	16.54%	129
8.	100 seed weight	42.05%	328
9.	Seed yield per plant	9.62%	75
10.	Harvest index	1.79%	14
	Total	100.00	780.00

The utility of D^2analysis was enhanced by its application to estimate the relative contribution of the various plant characters to genetic divergence. The per cent contribution of ten characters studied, towards total divergence is presented in Table 4.

It was observed that, 100 seed weight (42.05%) contributed highest for divergence. It was followed by number of seeds per pod (16.54%), number of pods per plant (15.51%), seed yield per plant (g) (9.62%), plant height (cm) (8.08%), days to 50 per cent flowering (5.38%), harvest index (1.79%), number of primary branches per plant (0.77%) and number of secondary branches per plant (0.13%).

The maximum contribution towards divergence was observed by 100 seed weight, number of seeds per pod, number of pods per plant, seed yield per plant, plant height and days to 50% flowering. The genotypes EC 398885, BMG-75-1× BWU-9 (SPS-17-1-10-1-3-1-1), BMG-75-1× BWU-9 (SPS-23-1-2-1-2-2), BMG-75-1× BWU- 9 (SPS-21-1-4-1-2-1-3), BMG-75-1× BWU-9 (SPS-25-1-4-1-2-1-4), BMG-75-1×BWU-9 (SPS-7-1-11-1-1-1-1), BM 4, EC 296129 was found to be diverse and superior for 100 seed weight, number of seeds per pod, number of pods per plant, number of secondary branches per plant, plant height and most of the yield attributing characters.

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