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Assessment of genetic divergence of 40 greengram genotypes (*Vigna radiata* (L.) Wilczek)

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Abstract
The present study entitled "Assessment of Genetic Divergence of 40 Greengram genotypes (*Vigna radiata* (L.) Wilczek)" was conducted to investigate the nature and extent of genetic divergence of forty Greengram genotypes using Mahalanobis D2 statistics. Data for eleven key quantitative traits collected from genotypes obtained in a two-replication randomized block design. Seed yield per plant was characterized by maximum phenotypic and genotypic coefficient of variation (PCV and GCV) followed by 100 seed weight. High heritability (broad sense) was found for days when flowering reached 50%.High heritability combined with high genetic advance was observed for plant height and number of pods per plant, suggesting the role of additive genetic advance and the possibility of achieving high genetic advance through selection. Forty Greengram genotypes were divided into eight clusters. Cluster I had the largest number of genotypes (12), then Cluster III and Cluster IV, each with the same number of genotypes (9 genotypes per cluster), Cluster V genotypes (4), and Cluster VI (3) genotypes, suggesting that the genetic composition of the genotypes in one cluster is completely different from that of other clusters. Number of pods per plant contribute most to the expression of genetic divergence.

Keywords: Greengram, D^2 analysis and cluster analysis

Introduction
Greengram [*Vigna radiata* (L.) Wilczek] is one of the most important legumes due to its short growing season, adaptation to low water requirements and soil fertility. It is widely grown and consumed in India. Greengram, commonly known as Moong, Greengram or Golden Gram, belongs to the family Leguminosae or Fabaceae and the subfamily Papilionaceae with a diploid chromosome number of 2n=2x=22.
The economically most important plant of the "*Vigna*" cluster.There are three subclusters of *Vigna radiata*: cultivated (*Vigna radiata* subsp. *radiata*) and two wild (*Vigna radiata* subsp. *sublobata* and *Vigna radiata* subsp. glabara) (Asari *et al*. 2019) [1]. Greengram (*Vigna radiata* var. *radiata*) is native to the Indian subcontinent (Vavilov, 1926; Zukovskij, 1962) [26, 16]. Since India is characterized by a large genetic diversity of cultivated and wild herb species, it is considered the region of its first domestication (Baudon and Maréchal, 1988) [2]. Greengram is a highly nutritious product and an important source of proteins (24%) and carbohydrates (58%). Among the various legumes, Greengram stands out for its high content of B vitamins. India is the largest producer and consumer of Greengram in the world.
Because grass is a self-pollinating species, there are significant differences between grass species and related species. Genetic improvement mainly depends on the degree of genetic variation in the base population and is a valuable source of the base population ensuring high variability. The main objectives of this study were to classify the available Greengram germplasm into different clusters based on its genetic diversity and to identify several useful genotypes in a breeding program aimed at developing improved recombinants to develop cultivars with improved plant characteristics.

Materials and Methods
In the present investigation "Genetic Diversity Studies in Grengram (*Vigna radiata* (L.) Wilczek)" The forty genotypes of greengram including 4 checks namely BPMR-145, BM2002-1, BM-4, BM-2003-2 were grown in a randomized block design with two replications during Kharif 2021-22 at College of Agriculture Badnapur. Each genotype is sown in single row of 4m length with spacing 45cm between rows and 10 cm between plants. The material used in the present study consisted of 40 greengram genotypes including 4 checks received from Agriculture Research Station, Badnapur.

Table 1: List of 40 greengram genotypes included in the study

Sr. No.	Genotypes	Sr. No.	Genotypes
1.	BPMR- 145 (C)	21.	EC-398942
2.	BM-2002-1 (C)	22.	EC-511380
3.	BM-4 (C)	23.	EC-397138
4.	BM-2003-2 (C)	24.	IC-76416
5.	PS-7	25.	IC-548266
6.	EC-396143	26.	EC-548271
7.	EC-538119	27.	IC-621812
8.	EC-398917	28.	IC-623193
9.	IC-102954	29.	IC-546591
10.	EC-520041	30.	EC-398929
11.	EC-520032	31.	EC-245963
12.	EC-396137	32.	EC-245947
13.	EC-538117	33.	IC-607332
14.	EC-520010	34.	EC-346115
15.	EC-396140	35.	IC-607185
16.	EC-538121	36.	EC-396417
17.	IC-607130	37.	MH-421
18.	IC-607174	38.	EC-338875
19.	EC-398924	39.	EC-528088
20.	IC-338814	40.	EC-249668-A

The data were recorded for five randomly selected plants for each genotype in each replicate, leaving the first two edge plants on either side of the row to avoid sampling error. Stand characteristics, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, weight of 100 seeds, seed yield per plant plant. Seeding and yield rates per plot were recorded. Based on these plants, an average genotypic value of was calculated for 11 different traits for each trait. The experimental data were subjected to statistical analysis. Mahalanobis (1936) [9] defined the distance between two populations as D2, determined using the Tochers method described by Rao (1952) [13].

Results and Discussion

The composition of the clusters was determined based on the relative size of the D^2 values according to the Tocher method (Rao, 1952) [13] as described by Singh and Chaudhary (1977), assuming that the genotype within the cluster is D^2 -Values had between them, i.e. belonging to different clusters. Using the D2 value, the 40 Greengram genotypes were divided into eight clusters and are listed in Table 1.

Cluster I had the highest number of genotypes (12), followed by Cluster III and Cluster IV, each having the same number of genotypes (9 genotypes in each cluster), Cluster V with (4) genotypes and Cluster VI with (3). genotypes. Clusters II, VII and VIII each had a single genotype.

The average intra- and inter-cluster and D2 values are shown in Table 2. The intra- cluster distance (D2) ranges from 48.76 to 45.30.The maximum distance between clusters (D2 = 278.17) was between cluster IV and cluster II, then cluster VII and II (D2 = 270.03), cluster II and cluster III (D2 = 224.92), cluster VII and cluster V (D2 = 164.81) observed). The minimum cluster distance (D2 = 32.49) was between clusters VII and IV. At the inter-cluster level, clusters IV and II achieved the highest value, followed by clusters VII and II.

The cluster means for the 10 characters are shown in Table 3. Significant differences were observed between clusters in the cluster means for the characteristics. The cluster mean Wfor all 10 characteristics showed significant differences between clusters. The feature had i ntervals, i.e. Days to 50% flowering, in the range of 12.From 20 (Cluster I) to 45.63 (Cluster V), days to maturity had an average value of 59.50 (Cluster II) to 73.25 (Cluster V), plant height ranged from 37.55 (Cluster VIII) to 66.37 (Cluster V) for the number of primary branches per plant was between 3.95 (Cluster II) and 4.80 (Cluster VIII), the number of secondary branches per plant was between 6.77 (Cluster VI) and 8.50 (Cluster VIII), the no. of pods on the plant ranged from 21.20 (Cluster VI) to 40.70 (Cluster II), the number of seeds in a pod ranged from 12.03 (Cluster VI) to 15.70 (Cluster II), the weight of 100 seeds ranged from 2.25 (Cluster VIII) and 6.97 (cluster VIII) seed yield per plant ranged from 9.47 (cluster VI) to 21.50 (cluster II) and harvest index had 22.40 (cluster VII) to 30.79 (cluster I).

Cluster I showed the highest cluster mean for harvest index (30.79) and the lowest mean for days to 50% flowering (12.20). Cluster II was characterized by the highest average value of pods per plant (40.70) and the highest seed yield per plant (15.7).7) while the average value of the lowest cluster is that of primary branches per plant (3.95). Clusters III and IV had moderate cluster means for all characteristics. Cluster V showed the highest cluster means for more than two characters i.e. Days up to 50% flowering (45.63), days maturity (73.25) and plant height (66.37). Cluster VI had a moderate to low mean cluster value for all traits and a l ow mean cluster value for the number of secondary branches per plant (6.77) and the number of pods per plant (21).20) also for the number of seeds in a pod (12.03) and the weight of 100 seeds (3.60). Cluster VII showed the highest mean clustering value for 100 seed weights (6.9 7).Cluster VIII showed the lowest cluster mean for plant height (37.55) and 100 seed weight (2.25), while the highest cluster mean for number of main branches per plant (4.80) and number of secondary branches per plant (8.50).The maximum degree of heterosis is expected from crosses with accessions that belong to the most divergent clusters.

Table 2: Clustering of forty greengram genotypes into different cluster by Tocher's method

Cluster No.	No. of genotypes		Genotypes included in cluster
I		12	EC-398917, EC-398929, EC-346115, EC-520032, EC-396417, EC-396137, EC-396143, EC-538117, IC-607174, EC-528088, EC-397138, BPMR-145
II	1		BM-2002-1
III	9		IC-607130, EC-398942, IC-621812, IC-548266, EC-396140, EC-511380, IC- 338814, EC-538119, EC-245963
IV	9		BM-4, EC-243668, EC-520010, MH-421, EC-398924, IC-607181, BM-2003- 2, EC- 245947, IC-607332
V	4		ID-623193, IC-546591, EC-538121, EC-548271
VI	3		IC-102954, EC-520041, PS-7
VII	1		EC-338875
VIII	1		IC-74416

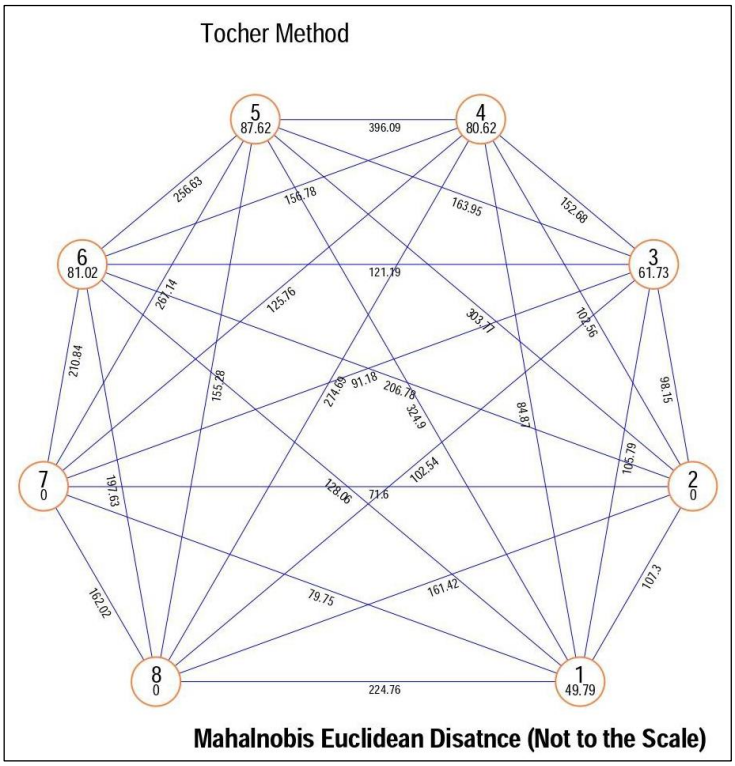

Fig 1: Distances among cluster by Tocher's method

Table 3: Average intra and inter cluster distance D2 values in greengram

Cluster No.	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	49.79	107.30	105.79	84.87	324.90	128.06	79.75	224.76
Cluster II		0.00	98.15	102.56	303.77	206.78	71.60	161.42
Cluster III			61.73	152.68	163.95	121.19	91.18	102.54
Cluster IV				80.62	396.09	156.78	125.76	274.69
Cluster V					87.62	256.63	267.14	155.28
Cluster VI						81.02	210.84	197.63
Cluster VII							0.00	162.02
Cluster VIII								0.00

Table 4: Cluster mean of different characters for genetic diversity in greengram

Character	Days to 50% Flowering (Days)	Days to maturity (Days)	Plant height (cm)	No of primary branches	No of secondary branches	No of pods per plant	No of seeds per pod	100 seed weight (gm)	Seed yield per plant (gm)	Harvest index (%)
Cluster I	12.20	60.83	50.39	4.37	7.95	25.11	12.13	5.68	14.22	30.79
Cluster II	40.00	59.50	46.30	3.95	7.70	40.70	15.70	5.05	21.50	29.25
Cluster III	41.39	64.72	51.37	4.00	7.37	25.35	12.37	5.11	15.86	27.81
Cluster IV	35.44	61.11	45.97	4.01	7.84	34.81	12.80	4.65	17.97	29.73
Cluster V	45.63	73.25	66.37	4.68	8.06	22.88	12.48	3.67	12.48	25.86
Cluster VI	37.17	62.00	49.20	4.23	6.77	21.20	12.03	3.60	9.47	27.22
Cluster VII	40.00	64.00	44.30	4.70	8.30	24.50	12.10	6.97	20.90	22.40
Cluster VIII	44.50	63.50	37.55	4.80	8.50	21.80	12.80	2.25	18.75	23.90

Table 4: Contribution of different characters to genetic diversity in greengram

Sr. No.	Characters	Percent contribution	No. of time appearing 1st
1.	Days to 50% flowering	44.74%	349
2.	Days to maturity	3.97%	31
3.	Plant height	4.87%	38
4.	Number of primary branches per plant	6.67%	52
5.	Number of branches per plant	0.00%	0
6.	Number of pod per plant	15.13%	118
7.	Number of seed per pod	0.26%	2
8.	100 seed weight	10.26%	80
9.	Seed yield per plant	7.82%	61
10	Harvest index	5.13%	40
	Total	100.00	781.00

The utility of D^2 analysis was enhanced by its use to estimate the relative contributions of different plant traits to genetic divergence. The percentage contribution of the eleven examined c haracteristics to the overall divergence is shown in Table 4. It was observed that the days up to 50% of flowering (44.74%) had the greatest influence on divergence, followed by the number of pods per plant (15.13%), the weight of 100 seeds (10.26%), seed yield per plant (7.82%), number of primary branches per plant (6.67%), harvest rate (5.13%), plant height (4.87%) in days to maturity (3.97%) Plant stand (1.15%), number of seeds per pod (0.26%).

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