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Genetic divergence in green gram [*Vigna radiata* (L.) R. Wilczek]

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Abstract
The current empirical study on "Genetic divergence in green gram (*Vigna radiata* (L.) R. Wilczek)" was conceded to assess genetic divergence in 72 genotypes of green gram. The experiment was conducted in RBD with 3 replications at the Pluses Research Station, J.A.U., Junagadh, during *kharif* 2021-22. On 11 traits, observations were recorded. Genetic diversity studies, using Mahalanobis's D^2 statistics, indicated existence of significant diversity among 72 green gram genotypes that were grouped into 12 clusters. Among 12 clusters formed, cluster II having highest number of genotypes (20) followed by cluster I (18) and cluster VI (12). On the other hand, cluster III, cluster IV, cluster VII, cluster VIII, cluster IX, cluster XI and cluster XII are solitary clusters. The intra-cluster distance was highest in cluster X (7.81) and lowest in cluster I (5.55). The maximum inter-cluster distance was found between cluster IV and XII (D = 19.16) followed by cluster XI and XII (D = 18.01), cluster III and XII (D = 16.59), cluster II and XII (D = 16.22), cluster IV and V (D = 15.89) and cluster VI and XII (D = 15.81). It was also revealed that the grain yield per plant (26.49%) contributed maximum towards the total divergence followed by 100-seeds weight (25.82%), number of pods per plant (11.15%), length of pod (9.04%), plant height (8.33%) and number of clusters per plant (7.71%).

Keywords: Green gram, genetic divergence and *Vigna radiata* (L.) R. Wilczek

1. Introduction
In Indian agriculture, pulse crops play an important role. The main source of protein for vegetarian diets is pulses. In fact, lysine is very well supplemented by the pulse protein, which is the most limiting essential amino acid in cereals. The soil fertility is enrich by them in terms of addition of organic matter and nitrogen through biological nitrogen fixation through *Rhizobium*.

Green gram [*Vigna radiata* (L.) R. Wilczek] is a legume cultivated for its edible seeds and sprouts across Asia. It has a diploid chromosome number of 2n=2x=22 and is a member of the Fabaceae family and subfamily Papilionaceae. According to Vavilov (1939) [6] green gram is native to India and Central Asia. Green gram contains about 24% protein, this is being about 2/3 of the protein content of soybean, twice that of wheat and thrice that of rice. This protein is comparatively rich in an amino acid and lysine that is deficient in cereal grains.

Green gram is rich in protein, fibre and less in fat that's why ayurveda suggests green gram is the right choice in a condition wherein obesity and extra fat pose a problem in day-to-day life. It has also been proven that green gram can enhance heart health with its nutritional content of flavonoids, an antioxidant which improves heart protection capacity especially in the case of women. The phosphorus and calcium content in green gram make beneficial for bones. The manganese content in it helps in improving brain activity as well. Green gram also has zinc content which also helps skin protection and ayurveda proposes that it can be smeared on the skin after transforming it into cream form. Regular intake of green gram will also help protect the skin.

2. Materials and Methods
The experimental material consisted of 72 genotypes of green gram from different origins were obtained from the Pulses Research Station, J.A.U., Junagadh were sown in a RBD with 3 replications during *kharif* 2021 at Pulses Research Station, J.A.U., Junagadh. Each genotype was accommodated in a single row of 4 m length with a spacing of 45 cm × 10 cm.

The observations were recorded for 11 traits *viz.*, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, length of pod (cm), 100-seeds weight (g) and grain yield per plant (g).

Genetic divergence analysis was performed using the procedure suggested by Mahalanobis (1936) [2].

Table 1: List of genotypes used in the experiment

Sr. No.	Genotype	Origin	Sr. No.	Genotype	Origin
1	GM 4	S. K. Nagar	37	EC 314286	IARI, New Delhi
2	K 851	Kanpur	38	EC 396523	IARI, New Delhi
3	BPMR 145	Kanpur	39	EC 450446	IARI, New Delhi
4	AKM 6802	Kanpur	40	EC 450450	IARI, New Delhi
5	Kopergaon	Kanpur	41	EC 482907	IARI, New Delhi
6	TARM 18	Akola / BARC	42	EC 482908	IARI, New Delhi
7	PM 2	Akola	43	EC 482909	IARI, New Delhi
8	Vaibhav	Rahuri	44	EC 486839	IARI, New Delhi
9	J 781	Akola	45	EC 496841	IARI, New Delhi
10	GM 1918	S. K. Nagar	46	EC 501566	IARI, New Delhi
11	GM 1924	S. K. Nagar	47	EC 501569	IARI, New Delhi
12	GM 1925	S. K. Nagar	48	IC 615-5	IARI, New Delhi
13	GM 1926	S. K. Nagar	49	IC 8917	IARI, New Delhi
14	GM 02-12	S. K. Nagar	50	IC 8961-5	IARI, New Delhi
15	GM 02-13	S. K. Nagar	51	IC 12434	IARI, New Delhi
16	GM 02-15	S. K. Nagar	52	IC 24789	IARI, New Delhi
17	GM 02-16	S. K. Nagar	53	IC 73536	IARI, New Delhi
18	GM 2K-3	S. K. Nagar	54	Local Collection 1	Junagadh
19	GM 2K-5	S. K. Nagar	55	Local Collection 2	Junagadh
20	RMG 62	Durgapur	56	Local Collection 3	Junagadh
21	RMG 268	Durgapur	57	GM 04-02	S. K. Nagar
22	OUM 11-5	Berhampur	58	GM 04-04	S. K. Nagar
23	GM 3	S. K. Nagar	59	GM 05-05	S. K. Nagar
24	CO 5	TNAU Coimbatore	60	GM 05-08	S. K. Nagar
25	CO 6	TNAU Coimbatore	61	GM 06-08	S. K. Nagar
26	COGG 912	TNAU Coimbatore	62	GM 02-16	S. K. Nagar
27	AKM 8803	Akola	63	GJM 1001	Junagadh
28	TARM 1	Akola	64	GJM 1002	Junagadh
29	TARM 2	Akola	65	GJM 1003	Junagadh
30	Asha	Haryana	66	GJM 1004	Junagadh
31	Pant M-2	Pantnagar	67	GJM 1005	Junagadh
32	Pant M-3	Pantnagar	68	GJM 1006	Junagadh
33	Pant M-4	Pantnagar	69	GJM 1007	Junagadh
34	Pant M-5	Pantnagar	70	GJM 1008	Junagadh
35	EC 251557-A	IARI, New Delhi	71	GJM 1009	Junagadh
36	EC 251810	IARI, New Delhi	72	GJM 1010	Junagadh

3. Result and Discussion

A single character has less significance to a plant breeder than the sum of several desired features and it gets more significant when they are thinking about a complicated trait like grain yield. In order to increase grain production, it is necessary to choose parents based on the number of characters having quantitative divergence, which may be determined using Mahalanobis' D^2 statistics (1936) [2].

With the help of Tocher's method, 12 clusters were formed from 72 genotypes of green gram. The composition of clusters is given in Table 2. The result revealed that cluster II having highest number of genotypes (20) followed by cluster I (18) and cluster VI (12). On the other hand, cluster III, cluster IV, cluster VII, cluster VIII, cluster IX, cluster XI and cluster XII are solitary clusters.

Table 2: Grouping of 72 green gram genotypes with clustering pattern in various clusters on the basis of D^2 statistics

Cluster	Total number of genotypes	Name of the genotypes
I	18	GM 4, AKM 6802, Kopergaon, TARM 18, VAIBHAV, GM 1918, GM 1925, GM 1926, GM 02-13, GM 2K-5, RMG 268, GM 3, EC 450446, EC 501566, IC 8961-5, LOCAL COLLECTION-3, GJM 1007 and GJM 1009
II	20	K 851, BPMR 145, TARM 1, GM 1924, GM 02-16, GM 2K-3, RMG 62, OUM 11-5, CO 5, CO 6, PANT M-2, EC 314286, EC 450450, IC 24789, LOCAL COLLECTION-1, LOCAL COLLECTION - 2, GM 04-02, GM 04-04, GM 05-08 and GJM 1003
III	1	GM 02-16
IV	1	ASHA
V	11	J 781, GM 02-12, GM 02-15, TARM 2, EC 396523, EC 482907, EC 482908, EC 486839, IC8917, GJM 1004 and GJM 1010
VI	12	COGG 912, AKM 8803, PANT M-3, EC 251810, EC 496841, EC 501569, IC 12434, IC 73536, GM 05-05, GM 06-08, GJM 1001 and GJM 1002
VII	1	PM 2
VIII	1	GJM 1006
IX	1	GJM 1008
X	4	PANT M-5, EC 251557-A, EC 482909 and IC 615-5
XI	1	PANT M-4
XII	1	GJM 1005

Fig. 1 shows that the intra-cluster distance (D) varied from 5.55 (cluster I) to 7.81. (cluster X). The intra-cluster distance for the clusters III, IV, VII, VIIII, IX, XI, and XII was 0 because they all had a single genotype. High intra-cluster distance suggested that the genotypes were more genetically diverse, which may be used to increase green gram yield. Thus, the genotypes included within a cluster tended to less diverse from one another. The maximum inter-cluster distance was found between cluster IV and XII (D = 19.16) followed by cluster XI and XII (D = 18.01), cluster III and XII (D = 16.59), cluster II and XII (D = 16.22), cluster IV and V (D = 15.89) and cluster VI and XII (D = 15.81). The minimum inter-cluster distance was observed between cluster VIII and IX (D = 4.36). To obtain a wide range of diversity among the segregates or to achieve maximum hybrid vigour in green gram, the genotypes from clusters that are statistically far apart might be employed in hybridization programmes. (Arunachalam, 1981) [1].

The clustering pattern might be used to choose the parents for a crossing and choose the best cross combinations that could produce the most variability for different attributes. The genotypes with high values in any cluster can be employed for hybridization to take advantage of heterosis breeding or for direct adoption as improved varieties. In the current study, cluster III received a favourable rating for earliness in terms of days to 50% flowering and days to maturity. The number of clusters per plant reached a maximum mean value in Cluster VI. Cluster XII had maximum mean value for number of pods per cluster, number of seeds per pod and grain yield per plant. Cluster III had maximum mean value for number of pods per plant. Cluster V had maximum mean value for 100-seeds weight.

A wide range of variation for several characters among multi-genotypic clusters was observed. However, the most important trait causing maximum genetic divergence was observed in grain yield per plant (26.49%) and was responsible for differentiating the genotypes studied. 100-seeds weight (25.82%), number of pods per plant (11.15%), length of pod (9.04%), plant height (8.33%) and number of clusters per plant (7.71%) were the next important traits contributed to total genetic divergence. A considerable diversity of 88.54% was observed due to these six characters. Grain yield per plant contributed maximum to genetic divergence and comparable outcome was noted by Rasal and Parhe (2017) [5] and Nagda *et al.* (2020) [4].

On the other hand, characters like days to 50% flowering, days to maturity, number of primary branches per plant, number of pods per cluster and number of seeds per pod contributed negligible genetic divergence towards total divergence. Low genetic diversity for these traits in such diverse group of genotypes may also suggest high degree of consistency and moderate to low heritability of these traits. Similar result was reported by Rasal and Parhe (2017) [5] for days to 50% flowering, days to maturity, number of primary branches per plant and number of seeds per pod. Nagda *et al.* (2020) [4] for days to 50% flowering, number of primary branches per plant and number of seeds per pod. Manthankumar *et al.* (2020) [3] for number of pods per cluster and number of seeds per pod.

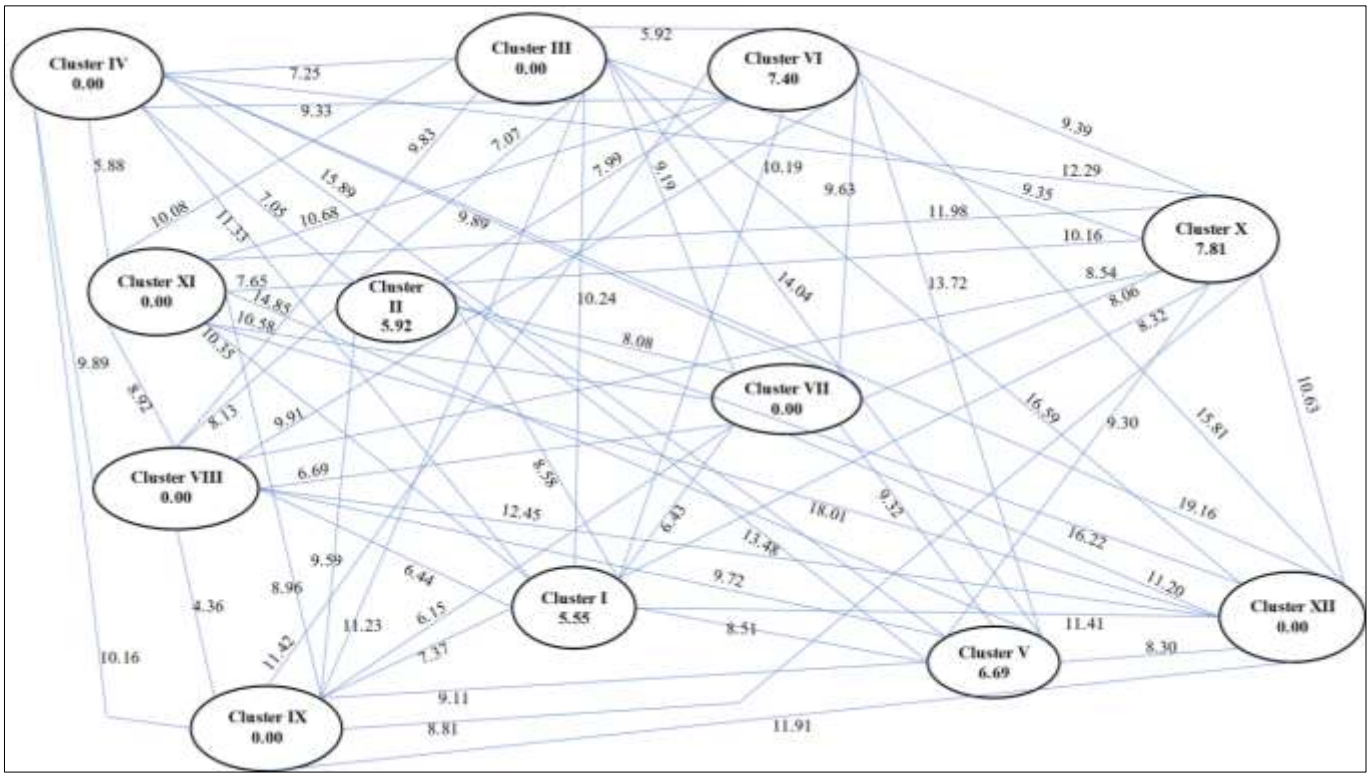

Fig 1: Cluster diagram showing inter and intra cluster distance in green gram

Table 3: Cluster mean for 11 different characters in 72 genotypes of green gram

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Number of seeds per pod	Length of pod (cm)	100-seeds weight (g)	Grain yield per plant (g)
I	38.57	71.63	56.10	2.71	2.66	3.32	16.14	9.59	7.18	4.75	7.28
II	38.18	70.68	56.85	2.56	2.87	3.62	17.48	9.68	7.50	3.92	6.75
III	35.33	67.00	64.00	2.67	3.93	3.87	22.73	9.60	7.63	3.99	8.68
IV	37.00	73.00	60.83	2.27	3.07	2.87	15.87	9.20	8.40	3.64	5.45
V	38.85	72.33	60.52	2.79	2.78	3.35	16.45	9.76	7.64	5.57	8.67
VI	38.03	70.31	63.40	2.96	3.54	4.16	22.42	9.86	7.61	4.09	8.83
VII	37.67	72.67	54.23	2.00	3.00	3.47	15.60	12.53	7.73	4.51	8.79
VIII	39.33	74.00	71.90	2.20	2.13	2.80	15.07	10.67	7.23	4.55	7.32
IX	39.67	73.67	67.60	2.13	2.07	2.53	13.47	11.60	8.27	4.87	7.61
X	38.75	71.17	63.10	2.97	2.97	3.78	21.67	10.72	7.98	4.78	10.40
XI	41.00	71.67	59.63	3.13	2.13	2.73	13.20	9.00	8.40	3.80	4.90
XII	36.00	72.67	61.47	3.07	2.33	4.47	16.87	12.60	7.73	5.45	11.44
Mean	38.37	71.27	59.24	2.72	2.90	3.56	17.99	9.86	7.52	4.50	7.82
S.Em ±	0.88	1.24	2.17	0.19	0.17	0.19	0.98	0.49	0.17	0.12	0.48
CV %	4.00	3.01	6.36	12.38	9.89	9.05	9.44	8.59	3.98	4.48	10.70
Percent contribution of characters towards total genetic divergence											
No. of times ranked first	10	3	213	84	197	99	285	97	231	660	677
Contribution (%)	0.39	0.12	8.33	3.29	7.71	3.87	11.15	3.79	9.04	25.82	26.49

4. Conclusion

From the current investigation, it can be suggested that genotype from cluster V (EC 396523, TARM-2, EC 482907 and GJM 1004); cluster VI (GM 05-05, GJM 1002 and EC 251810); cluster X (EC 251557-A, PANT M-5 and IC 615-5) and cluster XII (GJM 1005) should be selected as parent in hybridization programme for grain yield improvement in green gram, while for developing early maturing variety of green gram, parents will be selected from cluster I (GM 4); cluster II (RMG 62); cluster III (GM 02-16) and cluster VI (GJM 1002 and GJM 1001). The traits *viz*., grain yield per plant, 100-seeds weight, number of pods per plant, length of pod, plant height and number of clusters per plant had highest contribution towards total genetic divergence. Hence, emphasis must be given on the above-mentioned traits while imposing selection for genetic improvement in green gram.

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