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RESEARCH PAPER

Assessement of genetic diversity in green gram [*Vigna radiata* L. (Wilczek.)]

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Abstract: The presence of genetic diversity in a cultivated and wild crop species is a pre-requisite for any crop improvement programme. Utilization of diverse parents in hybridization programme could leads to production of potential transgressive segregants for yield and its attributing traits. Genetic diversity was studied in 78 green gram germplasm accessions, which included both indigenous and exotic origin using Mahalanobis's D^2 statistics. In the present investigation with non-hierarchical Euclidean cluster analysis, 78 genotypes of green gram were grouped into eighteen clusters. Out of these 18 clusters, XIV and XVIII clusters had single genotype (Coll.no NR/18-37 and Coll.no NR/18-06) revealed higher seed yield per plant, number of pods per plant and also observed to be early in maturity. Cluster XI and XIII were also had lowest number of days to flowering and days to maturity respectively could be regarded as good sources for earliness. Cluster II with twenty-three and cluster VIII with eight genotype were good source for number of seed per plant and number of cluster per plant. The accessions from these clusters could be utilized as parents for future breeding programmes to incorporate these characters for which they have shown superiority. Hence, these accessions will be used as source of divergent parents in breeding programme

Keywords: D^2 statistics, Genetic divergence, Germplasm, Mungbean

Introduction

Green gram is the major pulse crop after chickpea and pigeonpea in India. Green gram is the short duration crop and mainly grown in an arid and semi-arid condition across the country during *kharif* and *summer* season and it contributes nearly 15 per cent to the total pulse production. Nutritionally, mungbean contains about 20-25 percent protein along with good amount of amino acids particularly lysine, minerals and vitamins, those help to fulfill the dietary needs of the vegetarian population of the country. Due to its short duration nature, nitrogen fixing capability, ability to prevent soil erosion and it is grown as part of intercropping or mixed cropping system. Besides its importance in food and nutrition, it is also used as green fodder for cattle. (Kanatt *et al*., 2011).

The first step in any breeding programme is the evaluation and characterization of the available germplasm for 'genetic variability and identification of diverse and potential genotypes, disease resistant line from the given accessions. Success of high yield development programme mainly focused on the nature and vastness of genetic variability and genetic diversity available in the germplasm. Hence, the present study was carried out to assess the genetic diversity in greengram germplasm (landraces and advanced breeding lines) and to identify the potential greengram genotypes for their utilization in future breeding programme.

Material and methods

The experimental material was comprised of 78 green gram genotypes involving indigenous and exotic lines. They were evaluated using Randomized Block Design with two replication during *kharif* 2019 at ICAR-Indian Institute of Pulse Research-Regional Research Centre, UAS, Dharwad. Each genotype was sown in a row of 4m length with spacing 30 cm between row and 10 cm between the plants. All other cultural management practices were followed to raise successful crop. The observations were recorded on five randomly selected plants for characters *viz.,* days to 50% flowering, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, days to maturity, number of seeds per pod, pod length (cm), test weight (g) and seed yield per plant (g). The data generated on above traits were subjected to statistical analysis using (Mahalanobis, 1936) D^2 statistics and Tochers method as described by Rao (1952) for determining group constellation. The average inter and intra-cluster distances were estimated as per the procedure outlined by Singh and Choudhary (1977).

Results and discussion

The D^2 statistic helps in the selection of genetically divergent parents for their exploitation in hybridization programs. The technique measures the degree of diversity and determines the relative proportion of each component character to the total divergence. It measures the forces of differentiation at two levels *i.e*. intra cluster and inter-cluster levels. It provides reliable estimates of genetic divergence and a large number of genotypes can be evaluated at a time. In the present investigation, 78 genotypes were grouped into eighteen clusters using tochers methods. The intra and inter-cluster distance was calculated by using D^2 values.

The percentage contributions of different characters towards total genetic divergence in 78 green gram genotypes are depicted in Table 1. Test weight (36.03%) contributed maximum towards genetic divergence followed by days to

Table 1. Relative contribution of yield contributing characters towards genetic divergence in green gram

Characters	Times ranked first	% Contribution
Days to 50 % flowering	206	6.88
Days to maturity	611	20.35
Plant height (cm)	64	2.13
Number of pods per plant	123	4.1
Number of seeds per pod	3	1
Number of clusters per plant	55	1.83
Pod length (cm)	506	16.85
Seed yield per plant (g)	292	9.72
Test weight (g)	980	36.03
Number of branches per plant	61	2.03

maturity (20.35%), pod length (16.85%), seed yield per plant (9.72%). days to 50 % flowering (6.88%) and number of pods per plant (4.1%). The character *viz*., test weight, days to maturity, seed yield per plant and pod length was to be considered for selecting diverse parents. The characters contributing maximum to the D^2 values are to be given a greater emphasis for deciding on the cluster for further selection and choice of parents for hybridization. The earlier studies conducted by Pandiyan *et al*. (2012) also found the seed yield per plot contributing highest towards the total divergence.

Based on the D^2 results, seventy-eight accessions were categorized in to eighteen clusters. Cluster II consist of twenty three genotypes *viz.,*HUM-16, Sona mung, Kopergaon mung, V1003958B-BLM, CO-4, IPM-604-1-8, Vamban-2, Bari mung-2, IPM-14-24, IPM-410-3, EC-501566, EC-520034-1, Pant mung-2, Pant mung-6, IPM-312-934-3, IPM-604-1-7, IPM-430-4EC-550831, EC-520034, EC-398886, EC-520029, Pusa vishal and Bari mung-3. This represents a largest cluster having more number of accessions in it. Cluster I has fourteen genotype *viz.,* IPM-205-7, OUM-11-5, CO-5, HUM-12, CO-9, V1001654BG, HUM-1, V1003235AG, DGGS-4, IPM-9901-6-1, IPM-312-319-2, V1001974BG, Bari mung-5 and Bari mung-9. Cluster III with elven genotype *viz.,* Coll.no NR/18-35, Coll.no NR/18-36, Coll.no NR/18-14, Coll.no NR/18-23, Coll.no NR/18-89, DGGV-2, Coll.no NR/18-95, V1002195AG, Coll.no NR/18-27, Coll.no NR/18-67, and Coll.no NR/18-40. Custer IV has nine genotype *viz.,* EC-362096, V1003490AG, SML-668, IPM-14-49-5, IPM-14-49-5, IPM-312-394-1, IC-296672, EC-520024, and EC-319049. Custer VIII has eight genotype *viz.,* EC-398891, EC-591388, EC-319019, EC-398885, IPM-2-14, Coll.no NR/18-61, Coll.no NR/18-79 and Coll.no NR/18-8. Clusters V, VI, VII, XI, X, XI, XII, XIII, XIV, XV, XVI, XVII and XVIII were having single accession in it *i.e.,* TARM-1, V1003664AG, Bari mung-8, CO-6, COGG-912, Bari mung-4, EC-520022, Bari mung-6, Coll.no NR/18-37, VBN (Gg)-3, Bari mung-7, Coll.no NR/18-57 and Coll.no NR/18-06 respectively, indicating wide diversity from the rest and also from each other and this may be due to total isolation preventing the gene flow or intensive natural or human selection for diverse adaptive complexes. Inter-cluster value was found to be lowest between cluster V and VIII, it showing the same genetic makeup of the genotype and highest between cluster XIV and XVIII, it indicate

Table 2. Average intra cluster and inter cluster D^2 values of different clusters in greengram

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII
I	50.36	113.12	161.86	237.27	94.40	87.47	99.63	157.70	119.81	87.61	180.30	193.90	192.06	250.02	106.65	103.30	213.69	368.99
II		65.16	171.21	114.52	99.91	201.31	78.79	158.67	83.38	102.73	87.12	116.68	99.01	242.45	178.64	204.54	407.62	291.46
III			73.64	290.20	208.95	115.44	110.85	180.28	195.06	137.00	135.91	172.69	148.04	128.05	261.30	195.07	206.20	139.44
IV				79.22	123.34	401.74	203.76	231.79	182.55	262.07	142.26	154.04	174.29	354.67	295.31	402.88	670.97	410.32
V					00.00	226.28	177.57	111.46	181.27	196.76	166.22	158.58	236.50	281.30	110.66	233.05	394.41	434.84
VI						00.00	95.24	204.47	176.66	91.41	225.44	266.25	213.54	213.05	174.78	56.75	59.73	279.72
VII							00.00	172.22	66.58	43.42	83.66	101.66	51.95	220.94	158.28	96.69	264.44	192.44
VIII								91.39	165.51	214.51	167.85	182.59	275..09	291.10	166.19	222.55	305.34	371.54
XI									00.00	35.29	97.08	181.70	46.76	193.63	244.88	194.06	415.87	245.90
X										00.00	104.86	184.32	78.84	167.04	200.38	112.22	249.39	212.12
XI											00.00	176.59	69.44	134.36	300.28	277.67	415.68	149.99
XII												00.00	117.07	330.26	163.25	222.64	472.34	277.73
XIII													00.00	179.02	300.98	277.67	415.68	149.99
XIV														00.00	473.89	386.03	325.79	81.41
XV															00.00	77.45	304.77	411.05
XVI																00.00	155.20	422.79
XVII																	00.00	415.79
XVIII																		00.00

Table 3. Cluster arrangement based on the superiority of clusters for quantitative traits (mean value)

Cluster No	Days to 50 % flowering	Days to maturity	Plant height (cm)	Number of pods per plant	Number of seeds per pod	Number of clusters per plant	Pod length (cm)	Seed yield per plant (g)	Test weight (g)	Number of branches per plant
Cluster 14	36.00	63.00	27.20	27.00	11.00	3.50	10.50	11.25	5.25	6.00
Cluster 18	38.50	59.00	33.60	14.00	13.00	3.00	11.45	10.75	5.40	4.50
Cluster 8	43.94	68.06	37.48	24.75	11.88	6.00	8.21	10.59	4.26	4.13
Cluster 11	39.50	61.00	26.00	24.50	13.00	5.00	7.75	9.75	4.35	5.00
Cluster 9	42.50	61.00	19.25	11.00	10.50	6.00	6.85	8.80	4.65	5.00
Cluster 7	44.50	62.00	31.00	19.50	12.50	4.50	7.70	8.50	4.90	3.50
Cluster 5	41.50	69.50	26.75	16.50	11.00	3.50	7.40	8.25	3.70	4.00
Cluster 3	41.32	64.73	35.68	18.95	11.91	3.59	10.65	8.00	5.13	4.64
Cluster 10	44.50	62.00	25.00	14.50	10.00	4.50	7.25	7.95	5.20	6.00
Cluster 12	48.50	64.50	37.05	13.50	11.00	3.50	9.40	7.80	3.95	3.00
Cluster 17	42.50	69.00	39.50	21.50	12.50	3.50	9.85	7.25	6.45	5.00
Cluster 2	43.02	63.87	30.12	18.48	11.48	5.00	7.25	7.25	4.11	4.37
Cluster 4	41.17	64.17	32.05	19.22	10.89	5.50	7.44	6.88	3.19	3.56
Cluster 13	40.50	59.00	23.50	15.00	10.50	5.00	8.65	6.85	4.60	4.00
Cluster 15	49.50	70.00	21.00	17.00	12.50	4.00	7.25	6.75	4.35	3.50
Cluster 1	43.25	67.36	29.05	15.75	11.14	3.93	7.30	6.42	4.78	4.75
Cluster 6	42.50	66.00	30.50	18.00	10.50	5.00	8.90	6.25	5.80	4.00
Cluster 16	48.50	66.00	21.00	20.00	10.00	5.50	8.00	5.50	5.45	4.00

the high diversity between genotypes (Table 2). Cluster XIV has one genotype (Coll.no NR/18-37) and cluster XVIII also had one genotype (Coll.no NR/18-06) are the most diverse parents to be used for hybridization programs to obtain better recombinants. Grouping of genotypes evolved from the same location into different clusters indicated that geographical diversity and genetic diversity were not related. This is also in agreement with earlier reports indicating substantial diversity in green gram by Chauhan *et al*. (2008), Artibashisha *et al*. (2015) in blackgram. Similar type of study was done by Elangaimannan *et al.* (2009), Niranjan *et al.* (2009) in blackgram, Akhil *et al*. (2019) in green gram.

The mean values of each of the traits for 18 clusters exhibited that, various clusters were superior in respect to different quantitative traits. Cluster XIV having only one genotype (Coll.no NR/18-37) shows high seed yield per plant (11.25) g, number of pods per plant (27) and the genotypes were early maturing. Also cluster XVIII with a single genotype (Coll.no NR/18-06) represented high seed yield per plant (10.75) g and high number of clusters and pods per plant with lowest number of days to flowering and days to maturity respectively could be regarded as good sources for earliness along with useful source of alleles for yield and yield related traits. Cluster XI and XIII were also had lowest number of days to flowering and days to maturity respectively could be regarded as good sources for earliness these type of genotype were helpful in breeding programme. Cluster XVII with single genotype is a good source for higher seed weight. Cluster II with twenty three and cluster VIII with eight genotype were good source for number of seed per plantand number of cluster per plant. Similar, observations made by Sri Vidya *et al*. (2018) in blackgram.

Highest intra-cluster distance (91.39) was displayed by cluster VIII and cluster IV (79.22). It shows the presence of diverse accessions within these two clusters, minimum intra cluster distance was observed between clusters I (50.36) and lowest intra-cluster distance (0.0) were shown by cluster V, VI ,VII, IX, X, XI, XII, XIII, XIV, XV, XVI, XVII and XVIII. This solitary clustering indicates that these genotypes are diverse from remaining genotypes. It is desirable to select accessions from cluster showing higher inter cluster distance and also with highest grain yield as parents in recombination breeding programmes for obtaining desirable segregates. Hence, it would be logical to include these genotypes as parents in hybridization programme. The hybridization between two genotypes falling in the most distance clusters could result in maximum hybrid vigour and eventually desirable segregates or combinations leading to the development of improved varieties (Artibashisha *et al*., 2015).

Conclusion

Based on D^2 value and mean value of quantitative traits which are contributed most to greengram diversity genotypes where Coll.No.NR-18-37, Coll.No.NR-18-6, Coll.No.NR/18-57, Bari-mung-6, DGGV-2 and IPM-2-14 identified as genetically most diverse and could be utilized as potential parents for future breeding programme of greengram.

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