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RESEARCH PAPER

Genetic diversity studies in blackgram (*Vigna mungo* L. Hepper) germplasm

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Abstract: In the present study, 75 genotypes of blackgram comprises advance breeding lines, selections from local land races and released cultivars were evaluated for different traits during *kharif* 2017 at the IIPR Regional Research Centre, UAS Dharwad to assess the genetic diversity among the genotypes using Mahalanobis D2 statistics. The analysis of variance revealed highly significant differences among the genotypes of blackgram for the traits studied. The genotypes were grouped into twelve clusters. The cluster I with 48 genotypes was the largest cluster followed by cluster II with 9 genotypes and cluster VII with 5 genotypes. The intra-cluster distance was maximum (28.48) in cluster X followed by cluster II (13.68). The maximum inter-cluster distance was observed between cluster VI and VIII. The traits like 100 seed weight, clusters per plant, pods per plant and seed yield per plant contributed maximum towards diversity, while, traits like pod length, number of branches per plant and plant height contributed minimum to the genetic divergence. The present study revealed that genotypes belongs to cluster VI and VIII are most diverse in nature could be utilised in hybridization programme for the genetic improvement of blackgram.

Key words: Blackgram, Cluster analysis, D^2 analysis, Genetic diversity

Introduction

Pulses are the essential source of dietary protein in vegetarian population. Nutritionally they contain two to three times higher protein than cereals and the amino acid profile of pulses protein is supplementary to cereal protein. They are cheaper source to overcome protein malnutrition among human beings.

Among pulses, blackgram (*Vigna mungo* L. Hepper), belongs to the family leguminoseae with chromosome number 2n = 2x = 22 occupies a prominent place in India as it is the fourth important pulse crop in India, covering an area of about 3.24 million hectares with the production of 1.96 million tones (Anonymous, 2016). The major blackgram producing states are Andhra Pradesh, Madhya Pradesh, Maharastra, Tamil-Nadu and Karnataka. In Karnataka, blackgram covers an area of about 1.10 lakh hectares with production of 0.53 lakh tonnes and productivity of 506 kg ha^{-1} (Anon., 2016). Although it was grown in large area and important pulse crop of the southern zone, the average productivity is very low as compared to other pulses. Improving productivity is the major objective of blackgram breeding programme (Konda *et al*., 2017; Sarkar, 2014; Srimathy *et al*., 2012).

Blackgram being a pulse crop, it is endowed with many desirable characters *viz.*, short in duration, drought tolerant and highly suitable to grow in mixed/ intercropping system and also scavenge the residual soil moisture and soil fertility restoration by incorporating the crop residue after pod harvest and hence act as a green manure crop.

Genetic improvement of crop yield of any crop primarily depends on extent of genetic diversity present in the population and knowledge of the genetic diversity among the genetic resources is crucial for breeder to better understanding of evolutionary and genetic relationships among the genotypes. Selection of the genetically diverse parents helps to increase the heterosis in the progenies and also provide information about variability in the segregating generations. Such diverse crosses also provide new recombination of genes in the gene pool. Therefore, an attempt has been made in the present study to analyze the genetic divergence among the 75 genotypes of blackgram for different quantitative traits.

Material and methods

The 75 genotypes of blackgram was sown during *kharif* 2017 at ICAR-Indian Institute of Pulse Research, Regional Research Centre, Dharwad. The crop was sown using Randomized Block Design with two replication. Each genotype was sown in a row of 4m length. Each genotype was planted 30 cm row spacing and 10 cm between the plants. All the recommended package of practices was followed to raise a healthy crop. The data were recorded on five randomly selected plants of each replication for all the traits such as 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). Mean values were computed and data were analyzed for analysis of variance and analyzed genetic diversity using the method given by Mahalanobis D2 analysis (1936). The genotypes were grouped into different clusters following Tochers method as described by Rao (1952).

Results and discussion

Genetic divergence analysis is the important tool in the hands of plant breeder for assessment of diversity available in the germplasm. For a successful breeding programme, the diversity of parents is of utmost important, since the crosses made between the parents with maximum genetic divergence

are more likely to yield novel/desirable gene combinations in the progenies. The presence of low genetic diversity remains one of the major drawbacks for improving productivity in blackgram (Sarkar, 2014). In the present study, 75 genotypes of blackgram were evaluated for different quantitative traits during *kharif* 2017 to assess the genetic diversity using Mahalanobis D2 statistics.

The data collected on quantitative characters *viz.*, days to 50 per cent flowering, days to maturity, plant height (cm), number branches per plant, number of clusters per plant, pod length (cm), number of pods per plant, number of seeds per pod, 100-seed weight (g) and seed yield per plant (g) of blackgram were subjected to multivariate analysis and genetic divergence was estimated using Mahalanobis D^2 statistic. The magnitude of D^2 values suggested that there was considerable variability in the material studied, which led to genetic diversity.

Based on the D^2 values, the 75 genotypes were grouped into twelve clusters indicating large amount of genetic diversity among the genotypes (Table 1). Srimathy *et al.* (2012) also reported grouping of 46 genotypes of blackgram into twelve clusters. Among the twelve clusters, cluster I was the largest with forty eight genotypes followed by cluster II with 9 genotypes, cluster VII with five genotypes and cluster X with four genotypes. Cluster III, IV, V, VIII, IX, XI and XII were solitary comprised of single genotype. Clustering pattern indicated considerable differences among the genotypes of different clusters. It was observed that some of the genotypes collected from similar geographical region fall into same cluster like DU-1 and DBGV-5 in cluster-VI. However, some of the genotypes within cluster were also from different geographical origin indicating that the geographical diversity is not necessarily related to genetic diversity (cluster-VII and X). The similar finding on diversity has been previously reported in blackgram and other crops (Sarkar, 2014).

The intra and inter cluster distances (D^2) are presented in the Table 2. The inter cluster distance ranged from 6.36 to143.20. The inter cluster D^2 value was found to be lowest between cluster III and VIII (6.36) indicating similar genetic constitution of the genotypes included in these clusters and highest between cluster VI and VIII (143.20). This indicated high diversity among the genotypes, the cluster VIII has only one genotype (IPU-91-7) and the cluster VI has two (DU-1, DBGV-5) genotypes. The hybridization between genotypes belongs to diverse clusters could leads to better recombinants.

Maximum intra cluster distance (28.48) was observed for cluster X followed by cluster VII (28.21). This reveals the presence of divergent genotypes within these two clusters, minimum intra cluster distance was observed between cluster VI (4.36), zero intra cluster distance was shown by cluster III, IV, V,VIII, IX, XI and XII. This solitary clustering indicates that these genotypes are diverse from the remaining genotypes. Similar findings were made earlier in balckgram (Srimathy *et al.*, 2012; Sarkar, 2014). 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 recombinants (Srividya, *et al.,* 2018).

The mean value of each of the characters for 12 clusters showed that the different clusters were superior in respect of different characters (Table 3). Cluster VIII having only one genotype (IPU-91-7) showed high seed yield per plant (10.83), number of pods per plant (30) and the genotype was late maturing. The Cluster X with four genotypes (UH-99-149, Lam-Urd-2, NO-5131 and IPU-90-32-1) represented high seed yield per plant (8.10 g) and high number of clusters and pods per plant. These two clusters could be regarded as useful source of genes for yield and yield related traits. Cluster II and VI with low mean value for days to flowering and days to maturity respectively can be regarded as good sources for earliness. Clusters III with single genotype and VII with five genotypes are good source for high test weight. The genotypes from these two clusters could be selected as parents in crossing programmes to incorporate the characters for which they have shown superiority.

Table 1. Clustering pattern of 75 blackgram genotypes based on D^2 analysis

Cluster number	Number of accessions	Accessions
I	48	STY-2287, Uttara, LBG-20, PantU-3, STY-2868, IC-21001, PGRU-95-18, WBU-1372, PPU-8, UG-14-14, NG-2119, PU-30, MASH-391, IC-16511, BGP-28, TU-9910293, IPU-90-32, PGRU-95-16-2, Barbanki local, MASH-1-1, DVST-34, PantU-40, PU-19A, IPU-99-88, IPU-99-123, IPU-99-147, NAU-1, BIG-0067-1, UH-32-3, UPM-02-18, IPU-99-31, UH-80-26, PGRU-95- 16-1, BPG-0067-1, IPU-99-79, BG-369, UPU-97-10, IPU-94-2, MASH-479, URD-8831, MASH-1008, T-9/43, IC-10766, PLU-1, IPU-99-23, PGRU-1, IPU-99-40, IPU-96-6
II	9	MASH-114, MASH-218, IPU-94, DGG-5, MASH-338, SPS-5, IPU-2-43, TU-91—2, NO-7668-413
III	1	UBG-04-003
IV	1	IPU-95-13
V	1	U-3108
VI	2	DU-1, DBGV-5
VII	5	IPU-94-1, PU-19, PU-99-2, IPU-99-95, Lam-Urd-1
VIII	1	IPU-91-7
IX	1	PLU-28
X	4	UH-99-149, Lam-Urd-2, NO-5131, IPU-90-32-1
XI	1	IPU-98-36
XII	1	UH-85-15

Table 2. Average intra cluster and inter cluster D^2 values of 12 clusters of blackgram genotypes

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	12.31	23.23	21.31	19.83	19.95	76.26	23.85	39.55	31.30	40.64	44.62	38.24
II		13.68	31.55	46.99	26.33	56.65	37.69	55.42	40.85	50.95	68.80	25.70
III			0.00	23.03	4.58	109.45	38.65	6.36	43.14	31.19	83.02	45.47
IV				0.00	19.95	117.47	33.07	35.96	22.36	58.73	65.29	72.00
V					0.00	95.32	40.28	20.16	23.14	47.66	85.48	35.83
VI						4.36	63.22	143.20	100.58	128.04	87.25	43.24
VII							28.21	52.84	56.18	52.02	44.50	51.41
VIII								0.00	76.84	31.77	104.62	74.18
IX									0.00	92.22	79.94	55.83
X										28.48	62.46	71.97
XI											0.00	70.29
XII												0.00

Table 3. Cluster means for quantitative characters in 75 blackgram genotypes

	Plant heigh t (cm)	Days to 50 % flowering	Number of branches per plant	Number of clusters per plant	Days to maturit y	Number of pods per plant	Pod length (cm)	Number of seeds per pod	Seed yield per plant (g)	Test weight (g)
Cluster 1	37.32	43.71	4.96	4.50	78.71	19.70	4.67	6.65	5.64	4.70
Cluster 2	28.84	38.00	4.94	4.17	73.00	21.17	4.72	6.53	6.08	4.65
Cluster 3	40.20	42.50	5.00	4.50	77.50	25.50	4.73	6.65	8.97	5.32
Cluster 4	38.11	47.00	5.50	4.00	82.00	14.50	4.77	6.67	5.60	4.34
Cluster 5	41.60	40.40	4.50	3.50	75.40	21.00	4.72	6.83	7.92	4.59
Cluster 6	50.80	38.00	6.25	5.25	73.50	20.00	5.01	6.92	6.89	4.77
Cluster 7	42.63	43.50	6.00	5.60	76.50	20.50	5.04	7.23	6.55	5.22
Cluster 8	40.10	48.00	6.00	5.50	83.00	30.00	4.65	6.75	10.83	4.44
Cluster 9	38.60	41.50	4.00	2.00	79.00	11.00	4.78	7.00	3.02	5.10
Cluster 10	34.30	45.00	6.13	5.63	80.00	34.63	4.75	6.65	8.10	4.93
Cluster 11	51.30	43.00	6.00	5.00	81.00	27.00	5.22	6.67	3.57	4.92
Cluster 12	47.60	39.00	4.50	4.50	77.50	24.00	4.53	6.58	6.83	4.80

Among the quantitative characters studied, the most important character contributing to the divergence was 100 seed weight (24.51); followed by number of clusters per plant (22.07), yield per plant (15.28) and number of pods per plant (14.56). Whereas days to 50 % flowering, plant height, number of branches per plant, number of seeds per pod and days to maturity had least contribution towards divergence. Hence, the characters, 100 seed weight, number of clusters per plant, yield per plant, number of pods per plant, can be considered for selecting diverse parents. Major contribution of seed yield per plant and 100 seed weight towards genetic diversity in blackgram was also reported earlier in blackgram (Elangaimannan *et al.*, 2008 ; Sannarangaiah and Ramakrishna, 2016).

Conclusion

The use of genetically diverse parents in the breeding programme will be helpful in generating better transgressive segregants. The present study revealed that genotypes belongs to cluster VI and VIII are had maximum inter-cluster distances are most diverse in nature could be utilized in hybridization programme to produce desirable recombinants in blackgram.

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