

Original Research Article

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Assessment of Genetic Diversity in Blackgram [*Vigna mungo* (L.) Hepper] Genotypes Evaluated under Different Seasons

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ABSTRACT

Blackgram is an important *kharif* pulse crop in Karnataka and popularization of its cultivation during summer in command areas is very crucial for horizontal expansion of the crop for increasing production. There is need of systematic studies for identification of diverse genotypes for utilization in breeding for varieties for *kharif* as well as summer season. Twenty five genotypes were evaluated in six environments for 11 quantitative characters for quantifying genetic diversity using Mahalanobis' generalized distance (D^2). The analysis was performed over pooled data. The genotypes were grouped into nine distinct clusters indicating the existence of high degree of genetic diversity among the genotypes evaluated in the present study and hence these genotypes could serve as source for selecting diverse parents for use in hybridization programme to get transgressive segregants. The relative contribution of reproductive period was maximum (80.67 %) to the divergence of genotypes followed by 100-seed weight (10.67 %). The cluster pattern revealed that, cluster I was the largest, consisting of 11 genotypes followed by cluster II (7) and remaining seven clusters were solitary. The inter-cluster distance ranged from 0.42 to 20.57 indicating magnitude of diversity is not that high. Based on inter-cluster distance and cluster mean values, genotypes *viz.*, PU-31, TRCRU-22, LBG-685, BDU-20 were identified as diverse genotypes. They possess desirable traits like earliness, tall plants, more number of pods, clusters and high single plant yield which could be involved in recombination breeding programme for the improvement of blackgram.

Keywords

Blackgram,
Summer season,
Genotype,
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Introduction

Pulses occupy a unique position not only in Indian agricultural system but also in Indian dietaries. The pulses bring about a formidable solution to the alarming problem of protein scarcity of the world as they contain 20 to 25 per cent protein. They are also important for sustainable agriculture as they improve

physical, chemical and biological properties of soil. Blackgram [*Vigna mungo* (L.) Hepper] is an important pulse crop in India popularly known as urdbean. In India, it is grown over an area of 4.49 million ha with an annual production of 2.93 million tonnes (Anon., 2017). It is cultivated in almost all parts of India and is third most important pulse crop both in acreage and production.

However, it is mainly grown in the states of Madhya Pradesh, Maharashtra, Uttar Pradesh, Rajasthan, Karnataka and Bihar. During the post green revolution period, the production of pulses recorded a negative growth rate. This disturbing trend in the production of pulses has adversely affected the per capita availability of pulses which has declined from 60.7 g per day in 1950 to 43.0 g in 2016 (Anon., 2017). This situation is due to stagnation in expansion of pulse growing area and very slow progress in the improvement of productivity of all pulses. Therefore, there is urgent need to increase the area under pulse crops by promoting them into new areas and seasons for cultivation. Cultivating the crop in new area and season requires the availability of new varieties suitable for the new area and season. It is possible to popularize blackgram cultivation during summer after harvesting paddy, pigeonpea and Bt cotton in Tungabhadra and Upper Krishna project command areas and is very crucial for the horizontal expansion of the blackgram crop leading to increased production. However, the availability of dual season cultivars is limited. Therefore, we need systematic studies leading to the identification of diverse genotypes for utilization in breeding of blackgram varieties for *kharif* as well as summer. Therefore, present investigation was undertaken to measure the genetic diversity among blackgram genotypes and also for selection of divergent parents for hybridization programme using Mahalanobis' generalized distance (D^2) statistic.

Materials and Methods

The experiment material for the present investigation consisted of 25 blackgram genotypes collected from different sources *viz.*, Agricultural Research Station, Bidar; Nuclear Agriculture and Biotechnology Division, Bhabha Atomic Research Centre, Trombay, Mumbai; Indian Institute of Pulse

research, regional station, Dharwad and Regional Agricultural Research Station, LAM, Guntur. These were evaluated during *kharif*-2018 and summer-2019 across three locations *viz.*, Agricultural Research Station, Bidar, Agricultural Research Station, Kalaburagi and Agricultural Research Station, Bheemaranagudi. At each location, the experimental trial was laid out in Randomized Block Design with two replications. Each genotype in each replication was represented by a plot of 4 rows of 4 meter length with a spacing of 30 cm between rows and 10 cm between plants within a row. All the recommended agronomic practices were followed to raise a good crop. Observations on plant height, branches per plant, clusters per plant, pods per plant, seeds per pod, pod length, 100-seed weight and seed yield per plant were recorded on five competitive plants selected at random per genotype in each replication. Whereas, observations on days to 50 per cent flowering, days to maturity, reproductive period and seed yield (kg/plot) were recorded on plot basis. Days to 50 per cent flowering was recorded as number of days from sowing to the opening of the flower in 50 per cent of the plants, days to maturity was recorded as number of days from sowing to 50 per cent pod maturity, reproductive period was recorded as number of days from flowering to maturity and the seed yield per plot was recorded and weighed in kilograms (kg) and converted into seed yield kg/ha for each of the genotype. The pooled data obtained from six environments was subjected to analysis for estimation of genetic divergence using Mahalanobis' generalized distance (D^2) (Mahalanobis, 1936) and clustering of genotypes was done by using by Tocher's method (Rao, 1952).

Results and Discussion

D^2 statistic developed by Mahalanobis's (1936) provides a measure of magnitude of

divergence between biological population and the relative contribution of each component character to the total divergence. It is more reliable in selection of potential parents for hybridization programme. The pooled analysis of variance revealed highly significant differences among the genotypes for all the characters studied except for pod length and number of seeds per pod, indicating existence of sufficient variability among genotypes (Table-1).

The relative contribution of each character to the total diversity was different (Table-2). Among the traits recorded, relative contribution of reproductive period was maximum (80.67%) to the divergence of genotypes followed by 100-seed weight (10.67 %), whereas, remaining characters had very negligible contributions towards divergence. Similar results were also reported by Konda *et al.*, (2007) for relative contribution of 100-seed weight and reproductive period; Geetanjali *et al.*, (2015) for relative contribution of days to flowering, days to maturity and 100-seed weight to the total divergence in blackgram.

The genotypes under study were grouped into nine clusters based on D^2 values worked out on pooled data (Table-3). The cluster pattern revealed that, cluster I was the largest, consisting of 11 genotypes followed by cluster II (7) and remaining seven were solitary. The genotypes *viz.*, DU-1, LBG 685, PU-31, BDU-18, BDU-17, BDU-20, TRCRU-22 formed different solitary clusters by virtue of their diversity.

The majority of the genotypes in the present study were grouped in two cluster (I and II) indicating the presence of low magnitude of diversity among those test genotypes. The presence of limited degree of diversity might be attributed to their selection on the basis of seed yield in the previous generations and

derivation of these lines from progenies involving different mating and selection schemes with few selected parents.

The maximum intra-cluster distance was observed for cluster II (1.07) followed by cluster I (0.66) and remaining clusters had zero intra-cluster distance as they contained single genotype (solitary clusters) (Table-4). The formation of solitary clusters might be due to intensive artificial selection for seed yield.

The maximum inter-cluster distance was observed between cluster V and IX (20.57) followed by between cluster IV and IX (15.65). The lowest inter-cluster distance value was observed between cluster III and VI (0.42) followed by between cluster II and VI (0.43), indicating that genotypes were very close to each other.

These genotypes belonging to the clusters with maximum inter-cluster distance are genetically more divergent and hybridization between the genotypes of divergent clusters is likely to produce wide variability with desirable segregants. Hence, it would be logical to include genotypes like PU-31, TRCRU-22 and LBG-685 as parents in hybridization programme. Similarly, Gantait and Das (2009) identified WBU-105, LBG-731 and LBG-708 as diverse parents; Kumar *et al.*, (2018) identified NP 16, PU 99, UH86-4 and No.13/11 as diverse parents from their diversity studies in blackgram.

The cluster mean values for all traits were presented in Table-5. The cluster means generally indicate the characteristic features of the clusters and help in identifying potential clusters for different characters based on the mean values. Based on the mean values of different clusters, BDU-18 and TRCRU-22 were identified as good source for earliness (71.33 days).

Table.1 Pooled ANOVA for 12 quantitative traits in selected 25 genotypes of blackgram

Source of Variations	df	Days to 50% flowering	Days to maturity	Reproductive period	Plant height (cm)	Number of branches per plant	Number of pods per plant	Number of clusters per plant	Number of seeds per pod	Pod length (cm)	100- seed weight (g)	Seed yield per plant (g)	Seed yield (kg/ha)
Varieties	24	3.38 **	15.73 **	13.42 **	44.69**	0.46 **	48.38**	2.07*	0.18	0.07	0.67 **	4.52**	5.23 **
Environments	5	24.12 **	121.01 **	123.77 **	242.35**	27.46 **	322.08**	84.36**	11.71**	2.89**	2.40 **	42.59**	103.53 **
Env.+ (Var. x Env.)	125	2.76 **	12.60 **	13.24 **	30.77*	1.31 **	25.44**	4.39**	0.59**	0.19**	0.17 **	2.67**	5.83 **
Pooled Error	144	0.00	0.00	0.00	3.28	0.09	2.60	0.16	0.09	0.03	0.01	0.20	0.31

* Significant at 5% probability ** Significant at 1% probability

Table.2 Per cent contribution of different traits towards total diversity in blackgram

Sl.No.	Character	Per cent contribution
1	Days to 50% flowering	0.67
2	Days to maturity	3.00
3	Reproductive period	80.67
4	Plant height (cm)	1.33
5	Number of branches per plant	1.00
6	Number of pods per plant	2.00
7	Number of clusters per plant	0.00
8	Number of seeds per pod	0.00
9	Pod length (cm)	0.67
10	Hundred seed weight (g)	10.67
11	Seed yield per plant (g)	0.00
12	Seed yield (kg/ha)	0.00

Table.3 Clustering pattern of 25 blackgram genotypes

Cluster Number	Number of genotypes	Name of the genotypes
I	11	TRCRU-134, AKU-15, RU-16-9, COBG-657, TRCRU-43-1, BG-17-10, TRCRU-136, TRCRU-262, TU-94-2, RU-16-05, RU-16-10
II	07	LBG-465, LBG-20, IC-436516, IC-436778, TRCRU-18, TRCRU-339, TAU-1
III	01	DU-1
IV	01	LBG 685
V	01	PU-31
VI	01	BDU-18
VII	01	BDU-17
VIII	01	BDU-20
IX	01	TRCRU-22

Table.4 Intra (diagonal) and inter-cluster distances in blackgram

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	0.66	1.26	1.24	5.29	7.69	1.20	1.69	2.02	3.83
II		1.07	0.79	2.26	4.00	0.43	3.86	0.60	7.51
III			0.00	2.86	3.66	0.42	4.11	0.85	7.41
IV				0.00	1.48	2.40	10.82	1.81	15.65
V					0.00	3.42	14.46	2.78	20.57
VI						0.00	3.99	0.67	7.43
VII							0.00	5.77	1.07
VIII								0.00	9.96
IX									0.00

Table.5 Cluster means for 12 characters in blackgram

Characters/ Clusters	Days to 50% flowering	Days to maturity	Reproductive period	Plant height (cm)	Number of branches per plant	Number of pods per plant	Number of clusters per plant	Number of seeds per pod	Pod length (cm)	100- seed weight (g)	Seed yield per plant (g)	Seed yield (kg/ha)
I	38.85	74.00	35.15	32.91	3.12	21.41	5.78	5.85	4.23	4.55	4.86	850.00
II	39.83	75.67	35.83	33.07	3.03	21.50	5.57	5.60	4.04	4.87	4.85	837.00
III	37.50	74.50	37.00	31.48	3.07	19.77	5.35	5.88	4.06	4.26	4.28	763.00
IV	38.77	73.67	34.90	36.98	3.46	25.19	6.31	5.84	4.29	4.76	5.83	962.00
V	38.50	72.50	34.00	32.80	2.97	18.43	4.71	5.74	4.03	4.26	4.19	727.00
VI	39.00	71.33	32.33	31.50	2.97	19.90	5.18	5.52	4.09	4.44	4.36	790.00
VII	39.17	74.17	35.00	30.20	3.27	19.60	5.48	5.38	4.12	4.84	4.26	737.00
VIII	40.67	76.83	36.17	35.38	3.22	22.18	5.80	5.97	4.38	4.34	5.03	867.00
IX	37.33	71.33	34.00	32.02	3.15	25.28	6.52	5.57	4.15	4.74	5.72	941.00

Similarly, the cluster IV and VIII for plant height, cluster IX was good source for more number of pods, clusters per plant, single plant yield and seed yield (kg/ha) and clusters II and VII were good source of bold seeds. On the basis of inter-cluster distance and mean values, genotypes *viz.*, PU-31, TRCRU-22, LBG-685, BDU-20 were identified as diverse genotypes and also source of desirable traits like earliness, tall plants, more number of pods, clusters and high single plant yield which could be involved in recombination breeding programme for the improvement of blackgram.

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