Genetic Diversity Studies on Yield and Yield Contributing Characters in Blackgram (*Vigna mungo* (L.) Hepper)

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Abstract

In the present study, a total of twenty five blackgram genotypes were subjected to genetic diversity analysis based on nine different yield and yield contributing characters. Theplant height (cm) contributed maximum 33.90 per cent towards total genetic divergence followed by seed yield *per* hectare (27.66%). All the 25 genotypes were grouped into nine clusters. The cluster I had highest number of genotypes (12) followed by clusters II, III, IV, V and VIII with two genotypes each. The intra cluster distance was highest in cluster VIII (6.94), followed by cluster I (6.92). Highest inter cluster distance was noticed between clusters IV and VI (54.35) followed by clusters VI and IX (38.06). From this study it can be concluded that sufficient amount of genetic variability was observed among the genotypes for yield contributing characters. Based on genetic diversity study hybridization programme can be effected between the genotypes of cluster IV (KU 96-3, LBG 752) and VI (KPU 128-105) in order to get transgressive segregants for yield and yield contributing characters, since these genotypes showed maximum diversity.

Blackgram [*Vigna mungo* (L.) Hepper], popularly called as *urdbean* in India, It is a self pollinated crop with the chromosome number 2n (2x) = 22. Blackgram belongs to legume group contains high protein (20.8 to 30.5 per cent), carbohydrate (56.5 to 63.7 per cent). It is also popular for its fermented foods. In India, blackgram is cultivated in 4.01 million ha backing with a production of 2.89 million tonnes with productivity of 547 kg/ha. In Tamil Nadu, blackgram is being cultivated in about 4.16 lakh ha with a production of 2.80 lakh tonnes and productivity of 673 kg/ha (Anonymous, 2017). At present productivity level of pulses is very low which leads to requirement of pulses more than 80 g/day (per capita) as recommended by the FAO / WHO. The current per capita availability of pulses is below 40 g at national level. ICMR has recommended a minimum consumption of 47 g/day. The requirement of protein in Indian diet has to be met through pulses especially for the vegetarians. Genetic diversity assessment in pulses is the foremost important step in a crop improvement programme to improve the crop yield. Estimation of the nature and magnitude of diversity in a crop is essential to predict the extent of variation available for yield and its component traits. The selection of highly genetically divergent parents is expected to evolve superior and desirable segregants by crossing (Baisakh, 2014). It is also known that the germplasm is the source of pest and disease tolerance. Hence, its characterization and diversity analysis is needed for the selection of elite genotypes from the germplasm to be used in hybridization programme for crop improvement. Genetic diversity is one of the criteria of parent selection for hybridization programme. Multivariate analysis by means of the Mahalanobis generalized distance (D^2) statistic is a

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powerful tool in quantifying the degree of divergence at the genotypic level and might be an efficient tool in the quantitative estimation of genetic diversity (Mahalanobis, 1936). Therefore, the present investigation was aimed at ascertaining the nature and magnitude of genetic diversity among twenty five black gram genotypes for morphological, yield and yield attributing traits to identify suitable parents for hybridization program.

MATERIAL AND METHODS

The experimental materials for the present investigation consisted of twenty five genotypes were evaluated at JSA College of Agriculture and Technology, Tholudur, Cuddalore district, Tamilnadu during February 2021. The seeds were sown in ridges with a spacing 30 x 10 cm in one row with a length of four metre. The seeds were sown in RBD with three replication. The package of practices recommended in the crop production guide were judiciously followed. The observations were recorded in five randomly selected plants in each of the genotypes per replication on the following nine quantitative traits *viz.,* plant height (cm), number of branches per plant, number of pods per clusters, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight and seed yield per plant. The experimental data was analyzed statistically by testing the presence of variability among the traits is subjected to diversity analysis (Mahalanobis, 1936).

RESULTS AND DISCUSSION

Mohammadi (2003) suggested that, the evaluation, maintenance and the effective utilization of germplasm are important to investigate the extent of genetic diversity. Abna *et al*. (2012) suggested that the selection of parents is playing a vital role in a successful plant breeding program. Parents with more genetic distance can generate progenies with higher variation which can increase of genetic gain in selection. So depending upon the breeding objective the result of cluster analysis can be applied for crossing programme for blackgram improvement.

The analysis of variance revealed the presence of significant amount of variability among the twenty five

genotypes for all the characters studied. D^2 statistics was performed after ascertaining the presence of significant amount of variability among the genotypes as described by Rao (1952). Based on the relative magnitude of D^2 values all the twenty five genotypes of blackgram were grouped into nine clusters (Table 1). Cluster I has twelve genotypes followed by cluster

TABLE 1
Clustering pattern of genotypes based on D^2 analysis

Clusters	No of genotypes Clusters	Genotypes
I	12	GJU 1509, KPU 1720-140, AKU 1608, KPU 52-87, IPU 17-1, DKU 90, KPU 514-75, IPU 94-1, NUL 7, KUG 479, KU 17-04, MBG 1070.
II	2	DBGV 16, Pant U 31
III	2	MU 52, IPU 12-5
IV	2	KU 96-3, LBG 752
V	2	OBG 41, KUG 818
VI	1	KPU 128-105
VII	1	LBG 623
VIII	2	IPU 02-43, KUG 791
IX	1	KUG 818

II, III, IV, V, VIII with two genotypes and cluster VI, VII and IX consists of one genotype. Cluster I exhibited a genetic similarity among which is evidently in Table 2.

The cluster mean values of nine biometrical traits were represented inTable 3. The data indicated that the cluster mean for plant height was highest in cluster IX (45.33) and lowest in cluster VI (23.67). Number of primary branches per plant was highest in cluster II (3.17) and lowest in cluster VI (1.67). Number of clusters per plant was highest in cluster IV (12.00) and lowest in cluster VIII (5.33). Number of pods per cluster was highest in cluster VI (4.67) and lowest in cluster IV (3.50). Number of pods per plant was highest in cluster VII (44.67) and lowest in cluster

TABLE 2

Intra and inter cluster (diagonal) cluster values for nine biometrical traits twenty five black gram genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	6.92	13.75	13.55	31.71	15.48	11.27	13.74	19.44	29.26
II		3.01	14.53	35.80	29.31	23.32	26.08	17.26	38.05
III			3.81	12.45	12.24	26.89	10.72	11.75	12.88
IV				4.90	24.36	54.35	11.79	27.24	17.88
V					6.65	19.60	10.70	17.25	8.75
VI						0.00	27.11	24.14	38.06
VII							0.00	22.51	15.26
VIII								6.94	14.61
IX									0.00

VIII (22.50). Pod length was highest in cluster VII (5.43) and lowest in cluster II (4.52). Number of seeds per pod was highest in cluster V (7.17) and lowest in cluster II (5.67). 100-seed weight was highest in cluster VI (4.88) and lowest in cluster II (3.83). Seed yield per plant was highest in cluster VII (11.17) and lowest in cluster VIII (5.63). A critical appraisal of the observations indicated that none of the clusters contained genotypes with all the desirable traits, which could be directly selected and utilized. The maximum and minimum cluster mean values were distributed in different clusters and hybridization between genotypes of different clusters is necessary for the development of desirable genotypes. Hence, depending on the per se performance, the best genotypes within the clusters may be directly used as parents in future hybridization programme.

The selection of parents mainly depends upon contribution of characters towards divergence is represented in Table 4. Among the traits that contributed to genetic divergence plant height

TABLE 3

Cluster mean value for the nine biometrical traits of the twenty five black gram genotypes

Characters / clusters	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seed weight (g)	Seed yield per plant (g)
I	26.11	2.33	7.69	3.89	29.56	5.18	6.78	4.20	7.39
II	25.17	3.17	5.67	4.33	25.00	4.52	5.67	3.83	6.25
III	36.00	2.00	8.50	3.67	31.67	4.72	6.17	4.18	7.92
IV	41.50	2.50	12.00	3.50	41.50	4.80	6.17	3.96	10.38
V	39.00	2.67	8.50	3.67	30.83	5.37	7.17	4.71	7.71
VI	23.67	1.67	5.67	4.67	25.33	5.10	7.00	4.88	6.33
VII	35.00	3.00	10.67	4.33	44.67	5.43	7.00	4.22	11.17
VIII	34.33	2.33	5.33	4.33	22.50	5.02	5.83	4.39	5.63
IX	45.33	2.33	7.67	4.33	32.67	5.40	7.00	4.50	8.17

TABLE 4

Relative contribution of nine traits towards the genetic divergence in twenty five blackgram genotypes

Characters	Per cent contribution
Plant height (cm)	33.90
Number of primary branches per plant	3.66
Number of clusters per plant	13.66
Number of pods per cluster	2.33
Number of pods per plant	1.00
Pod length(cm)	8.33
Number of seeds per pod	7.33
100-seed weight(g)	2.10
Seed yield per plant(g)	27.66

contributed maximum (33.90 %) followed by seed yield per plant (27.66%).

The maximum inter cluster distance was recorded between cluster IV and VI (54.35) followed by cluster VI and IX (38.06) indicated more diversity among other clusters. The genotypes present in these clusters can be used as parents in hybridization programme for blackgram improvement by trait manipulation and to obtain the transgressive segregants in early segregating generation. The minimum inter cluster distance (8.75) was between clusters V and IX revealed the close relationship between them.

Further, the maximum intra cluster distance (6.94) was observed in cluster VIII followed by cluster I (6.92). Hence, selection of cluster I and VIII may be exercised based on improvement through inter varietal hybridization programme. Whereas, the clusters VI, VII and IX exhibited zero value for intra-cluster distance indicating the presence of single genotype in these clusters. Lal *et al.* (2001) suggested that the maximum inter-cluster value indicated that the genotypes included in these different clusters may give high heterotic response and there by better segregants. Natarajan *et al.* (1988) have also opined that selection of parents for hybridization should be done based on the inter-cluster distance to get maximum variability.

From the present investigations, it can be concluded that, the genotypes of cluster IV and VI are having desirable cluster mean values for important yield contributing traits. Similarly the inter cluster distance was also more between cluster IV and VI. Hence, these genotypes may be used as diverse parents in intervarietal hybridization programme to generate transgressive segregants with higher heterotic effect for yield improvement in blackgram.

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