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Genetic Divergence Studies in Blackgram (*Vigna mungo* (L.) Hepper)

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ABSTRACT

Divergence analysis among thirty blackgram genotypes for yield, yield contributing and water use efficiency traits was carried out using Mahalanobis D^2 statistics. Thirty genotypes were grouped into eight clusters. The contribution of relative water content was the maximum towards genetic divergence followed by SLA at 50 DAS. The maximum intercluster distance was observed between cluster III and VI. The maximum intracluster distance was reported in cluster V. Based on cluster means and divergence, it was concluded that the crosses PU-31 × KU-10-1169, UG-708 × KU-14-01 and WBG-26 × LOP-1070 could be successfully utilized in hybridization programmes to get desirable transgressive segregants for yield and water use efficiency.

Key words: *Black gram, D^2 analysis, Cluster distance.*

INTRODUCTION

Black gram (*Vigna mungo* L.) with chromosome number of 2n = 22 belonging to the family *Fabaceae*, is a self-pollinating and widely cultivated grain legume[5]. Assessment of extent of genetic diversity among the available blackgram genetic resources is essential for planning of an effective breeding programme. Inclusion of diverse parents in hybridization programme saves the purpose of combining desirable recombination[3]. Among the various techniques proposed for this purpose, the Mahalanobis's D^2 statistics is a powerful device for quantifying the degree of divergence among the genotypes. Therefore, an attempt has been made in the present investigation with a view to estimate genetic divergence among a set of 30 blackgram genotypes for yield, yield contributing and water use efficiency characteristics.

MATERIAL AND METHODS

The present investigation was carried out among 30 blackgram genotypes during *Kharif*, 2017 at dry land farm of Sri Venkateswara Agricultural College, Tirupati using a Randomized Block Design with three replications.

Recommended dose of chemical fertilizers (20 kg N, 50 kg P_2O_5 per hectare) in the form of urea and single super phosphate were broadcasted before sowing. Seed treatment was done with Bavistin @ of 3 g kg^{-1}.

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For the control of leaf eating caterpillars, chlorpyriphos @ of 2.5 ml L^{-1} and for the control of sucking pests monocrotophos @ of 1.6 ml L^{-1} was applied. Cultural practices like weeding and irrigation were followed to maintain good crop growth.

Observations were recorded on five randomly selected plants in each genotype for plant height, number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, harvest index, SPAD chlorophyll meter reading at 35 DAS, SPAD chlorophyll meter reading at 50 DAS, Specific leaf area 35 DAS, Specific leaf area 50 DAS, relative water content and seed yield per plant, whereas for days to 50 % flowering and days to maturity observations were recorded on plot basis.

The genetic divergence was estimated using mahalanobis'D^2 statistic[4] and genotypes were grouped into clusters following the Tochers' method as described by Rao[7].

RESULTS AND DISCUSSION

The 30 genotypes were grouped into eight clusters by using Tocher's method[7] and the distribution of genotypes in various clusters was presented in Table 1 and Fig 1. Among eight clusters, cluster II, III and V were largest with seven genotypes each followed by cluster I with five genotypes. Remaining four clusters were monogenotypic.

The average inter and intra cluster D^2 and D values were presented in the Table 2 and cluster diagram was furnished in Fig. 2. Intra cluster distance ranged from 0.00 to 6.09. Among all the clusters, cluster V had maximum intra cluster distance (6.09), followed by cluster III (5.21), cluster II (4.59) and cluster I (4.20). The clusters IV, VI, VII and VIII were monogenotypic.

Maximum inter cluster distance was observed between cluster III and VII (9.78) followed by cluster IV and VIII (8.97), cluster VI and VII (8.93), cluster VIII and V (8.85). The minimum inter cluster distance was observed between cluster IV and I (5.10) followed by cluster V and IV (5.35), cluster VII and II (5.77).

Intra and inter cluster D^2 values worked out from the above divergence analysis indicated that the inter-cluster distances were greater than intracluster distances, revealing that considerable amount of genetic diversity existed among the accessions. Similar results were also reported by Ali *et al.*[1], Srimathy *et al*[9], Singh *et al.*[8], Jayamani and Sathya[3], Panigrahi *et al.*[6], Geethanjali *et al.*[2], and Vinod *et al.*[10].

The results of cluster means for 17 traits in blackgram under inorganic fertilizer management are presented in Table 3. Analysis of data indicated considerable differences between clusters for most of the characters studied.

The cluster means for seed yield per plant ranged from 3.75 g (VI) to 5.62 g (V) with a general mean of 4.85 g. The superior clusters were V, VIII, III and IV.

Number of clusters per plant differed from 5.33 (VI) to 10.47 (IV) and superior clusters that exceeded the general mean (8.34) were IV, III, V and VIII. Number of pods per cluster exhibited an overall mean value of 2.86 with cluster means ranging from 2.33 (VIII) to 3.13 (VII) and the superior clusters that crossed general mean value were VII, V, VI and II.

Number of pods per plant was highest in V (31.53) and lowest in VI (16.13). Higher cluster means than the average (24.38) were recorded in the clusters V, III, IV and II.The superior clusters for number of seeds per pod over the general mean (5.98) were VIII, III, II and V. Their values were distributed between 5.47 (VI) and 6.87 (VIII).

Cluster means for 100 seed weight ranged from 4.00 g (IV) to 4.65 g (VI) and the clusters VI, II, III and VIII were superior with higher values than the general mean of 4.36 g. The cluster means for harvest index ranged between 17.19 per cent (VI) to 26.93 per cent (VIII) and higher values than the general mean (22.46%) were recorded in clusters VIII, VII and IV.

The cluster means for SCMR at 35 DAS was high in cluster I (43.67) and low in cluster VI (39.33). Higher values than the general mean (40.74) were observed in clusters I, V and IV. The maximum and minimum values were observed for SCMR at 50 DAS in cluster VII (49.20) and III (45.47) respectively.

SLA at 35 DAS recorded cluster means ranging from 249.27 (IV) to 321.74 (VI) and the desirable clusters with lower values than the general mean (284.97) were IV, VIII, I and III. The cluster means for SLA at 50 DAS ranged from 144.91 (VII) to 206.62 (VI) and the clusters VIII, VII, V and II were desirable clusters with lower values than the general mean (183.78).

The mean values for relative water content ranged between 63.57 per cent (VIII) and 80.98 per cent (I). The superior clusters that recorded higher values than the general mean (75.12%) were I, IV, VI, V and VII.

The number of times that each of the 17 characters appeared first in ranking and its respective per cent contribution towards genetic divergence is presented in Table 4**.** Among the seventeen characters, maximum contributor towards genetic divergence was relative water content (36.78%) followed by SLA at 50 DAS (33.56%). Whereas, lowest contribution has been noticed from days to maturity (0.23%).

Based on mean performance and genetic divergence, crosses PU-31 × KU-10-1169, UG-708 × KU-14-01 and WBG-26 × LOP-1070 could be successfully utilized in hybridization programmes to get desirable transgressive segregants for yield and water use efficiency.

Table 1. Clustering pattern of 30 blackgram genotypes by Tocher's method

Cluster no.	No. of genotypes	Name of the genotypes
I	5	LOP-1070, MBG-1045, P-1032, P-728, RFU-13-04
II	7	KU-11-685, KU-14-47, LBG-787, MBG-1050, SU-13-509, VBG-09-005, VBG-11031
III	7	KDRS-136, KU-10-1170, KU-12-56, NDU-11-201, PU-205, TBG-104, WBG-26
IV	1	VBN-4
V	7	PU-31, VBN-7, KU-14-39, UG-708, SU-13-08, P-112, TU-94-02
VI	1	LBG-752
VII	1	KU-14-01
VIII	1	KU-10-1169

Table 2. Average intra and inter cluster distances formed by Tocher's method in blackgram

	Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**	**Cluster 7**	**Cluster 8**
Cluster 1	**17.61 (4.20)**	42.80 (6.54)	65.14 (8.07)	26.06 (5.10)	46.38 (6.81)	47.57 (6.90)	48.60 (6.97)	73.39 (8.57)
Cluster 2		**21.03 (4.59)**	40.63 (6.37)	39.83 (6.31)	43.43 (6.59)	46.13 (6.79)	33.31 (5.77)	33.91 (5.82)
Cluster 3			**27.16 (5.21)**	39.55 (6.29)	58.82 (7.67)	44.32 (6.66)	95.61 (9.78)	50.34 (7.10)
Cluster 4				**0.00 (0.00)**	28.60 (5.35)	44.43 (6.67)	69.86 (8.36)	80.46 (8.97)
Cluster 5					**37.03 (6.09)**	64.12 (8.01)	60.82 (7.80)	78.40 (8.85)
Cluster 6						**0.00 (0.00)**	79.79 (8.93)	76.18 (8.73)
Cluster 7							**0.00 (0.00)**	51.99 (7.21)
Cluster 8								**0.00 (0.00)**

Figures in parenthesis indicate D values

Table 3. Cluster means for 17 characters in blackgram

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of clusters per plant	No. of pods per cluster	No. of pods per plant	Pod length (cm)	No.of seeds per pod	100seed weight (g)	Harvest index (%)	Seed yield per plant (g)	SPAD chlorophyll meter reading at 35DAS	SPAD chlorophyll meter reading at 50 DAS	Specific leaf area at 35 DAS ($cm^2 g^{-1}$)	Specific leaf area at 50 DAS ($cm^2 g^{-1}$)	Relative water content (%)
Cluster 1	42.33	70.80	41.11	1.89	7.84	2.81	23.91	4.20	5.51	4.11	20.77	4.39	43.67	47.38	266.96	188.30	80.98
Cluster 2	40.71	70.52	41.61	1.72	8.17	2.90	24.92	4.58	6.14	4.58	21.76	4.58	40.46	49.01	296.35	173.42	73.48
Cluster 3	40.86	69.86	45.23	1.92	10.26	2.84	28.98	4.62	6.32	4.55	21.27	5.38	40.40	45.47	282.79	203.20	70.49
Cluster 4	38.00	72.67	43.40	2.53	10.47	2.80	27.67	4.32	5.87	4.00	24.55	5.27	41.03	46.90	249.27	199.15	80.04
Cluster 5	38.95	69.10	39.89	2.27	10.05	3.08	31.53	4.40	6.09	4.19	20.96	5.62	42.10	49.14	289.79	179.24	77.56
Cluster 6	41.00	65.67	41.80	2.00	5.33	3.00	16.13	3.97	5.47	4.65	17.19	3.75	39.33	43.49	321.74	206.62	78.01
Cluster 7	41.00	72.67	35.33	1.60	5.73	3.13	18.20	4.21	5.60	4.33	26.21	4.23	39.43	49.20	312.09	144.91	76.79
Cluster 8	44.33	70.00	37.40	1.53	8.87	2.33	23.73	4.42	6.87	4.49	26.93	5.54	39.50	46.37	260.78	175.36	63.57
General mean	40.90	70.16	40.72	1.93	8.34	2.86	24.38	4.34	5.98	4.36	22.46	4.85	40.74	47.12	284.97	183.78	75.12

Table 4. Percent contribution of different characters towards divergence in blackgram genotypes

S. No.	Characters	Times ranked first	Contribution (%)
1.	Days to 50 % flowering	5	1.15
2.	Days to maturity	1	0.23
3.	Plant height (cm)	9	2.07
4.	No. of primary branches per plant	4	0.92
5.	No. of clusters per plant	3	0.69
6.	No. of pods per cluster	7	1.61
7.	No. of pods per plant	48	11.03
8.	Pod length (cm)	5	1.15
9.	No. of seeds per pod	-	-
10.	100 seed weight (g)	5	1.15
11.	Harvest index (%)	-	-
12.	Seed yield per plant (g)	7	1.61
13.	SPAD chlorophyll meter reading at 35 DAS	5	1.15
14.	SPAD chlorophyll meter reading at 50 DAS	15	3.45
15.	Specific leaf area at 35 DAS ($cm^2 g^{-1}$)	15	3.45
16.	Specific leaf area at 50 DAS ($cm^2 g^{-1}$)	146	33.56
17.	Relative water content (%)	160	36.78

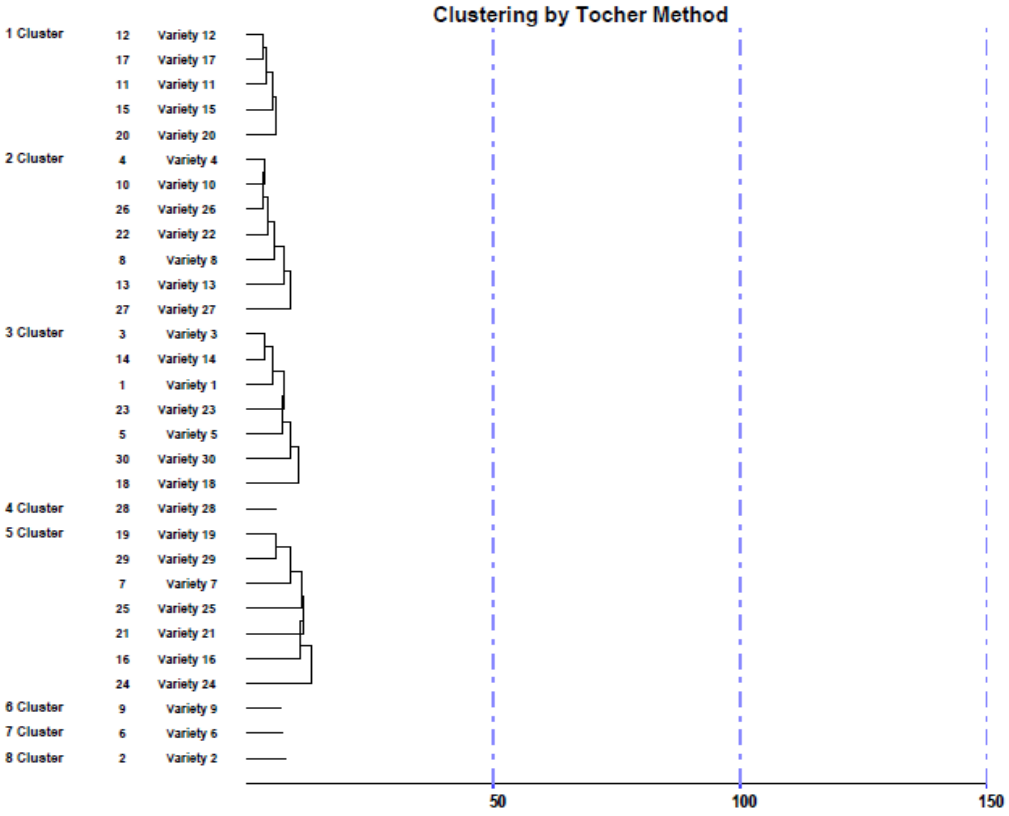

Fig. 1: Grouping of genotypes into clusters using Tocher's method

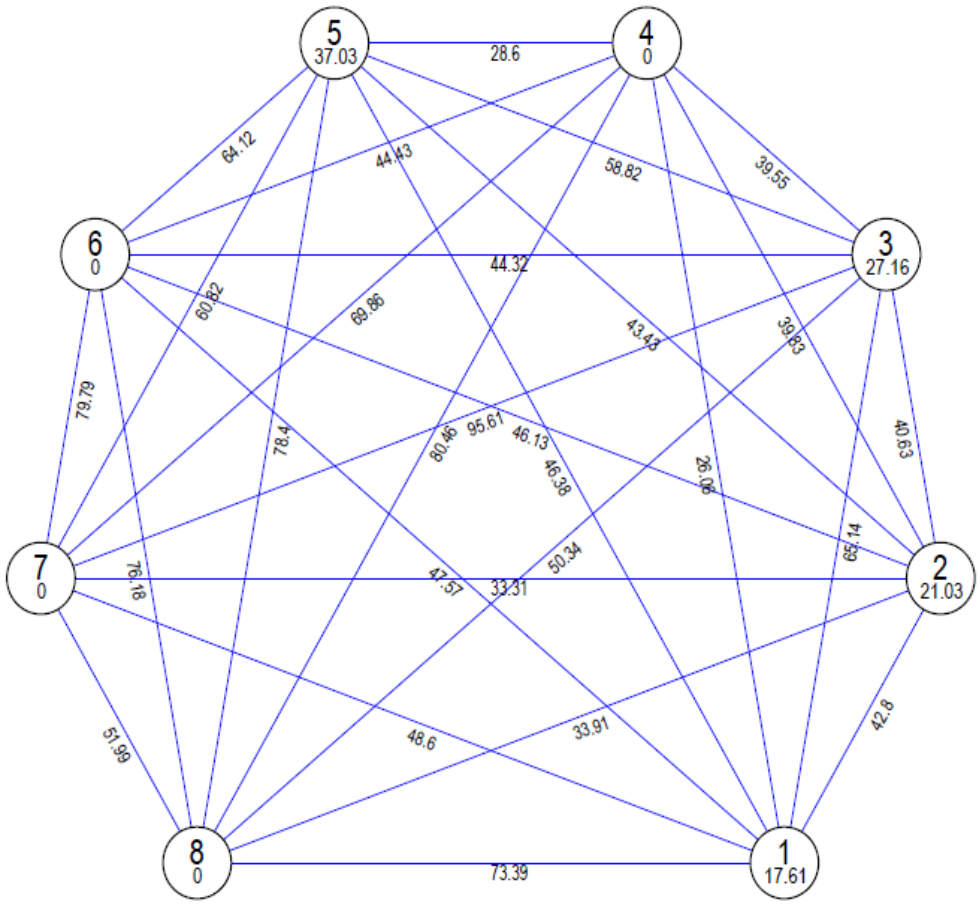

Fig. 2: Average inter and intra cluster distances

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