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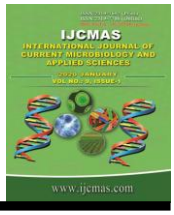

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Genetic Divergence Studies for Yield Components in Blackgram (*Vigna mungo L.*) Genotypes

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A B S T R A C T

The investigation consisting of thirty five blackgram genotypes along with four check varieties *viz.*, MBG-207, LBG-752, PU-31 and IPU-2-43 was carried out during rabi 2016 at Agricultural Research Station, Madhira. Three principal components viz PC I, PC II and PC III contributed about 86.61% of total variance for the genotypes studied. The genotypes were grouped into nine distinct clusters of which cluster 1 is the largest with a maximum number (22) of genotypes followed by cluster 5 with 7 genotypes, cluster 3 with 4 genotypes. Highest intra cluster distance of 32.38 was recorded for cluster 5. Data on cluster means for various traits showed that the highest mean value for number of clusters per plant and number of pods per plant was recorded by cluster VII. Cluster VIII recorded the highest mean for 100 seed weight followed by cluster III and cluster IV. Percent contribution revealed that days to maturity contributed the most (26.58%) followed by number of cluster per plant (18.08%), seed yield per plant (17.40%), 100 seed weight (14.84%) for total genetic divergence.

Introduction

Vigna is an expansive leguminous taxon containing 104 portrayed species conveyed in tropical and subtropical locales of Africa, Asia, America, and Australia. It is a widely cultivated legume in all over the world. Blackgram is an important food legume with excellent source of good quality protein and having ability to restore fertility of soil though symbiotic nitrogen fixation. Though India is the larger producer of blackgram, the productivity is still low. D^2 statistic is one of the potent techniques of measuring genetic diversity in plant breeding. Knowledge about genetic diversity is an invaluable aid in crop improvement strategies. The selection of genetically diverged parents is expected to throw superior and desirable segregants following crossing. The hybrids between genetically diverse parents yielded greater heterosis than those between more closely related parents a total of twenty one germplasm accessions of blackgram were subjected to divergence studies by D^2 statistic.

Materials and Methods

The investigation, which consisted of thirty five blackgram genotypes along with four check varieties *viz.*, MBG-207, LBG-752, PU-31 and IPU-2-43 was carried out during rabi 2016 at Agricultural Research Station, Madhira. Eight quantitative traits *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of clusters per plant, number of pods per plant, 100 seed weight (g), seed yield per plant (g) and seed yield (kg/ha) were recorded following standard procedures. Assessment of genetic divergence was done using Mahalanobis D^2 statistic and the genotypes were grouped into different clusters following Tochers method as described using Genres statistical package.

The germplasm lines were evaluated in a randomized block design with two replications at ARS, Madhira during *rabi* 2016. Each entry was planted in 2 rows of 5m length with 30 and 10 cm spacing between and within rows. Observations on agro morphological traits were recorded on randomly selected five plants per replication. Data on days to 50% flowering and days to maturity was noted on plot basis and the data was subjected to statistical analysis.

Divergence was estimated by the multivariate analysis using Mahalanobis's (1936) and D^2 statistic as described by Rao (1952). On the basis of D^2 values obtained, the variables were grouped into different clusters by employing Tocher's method (Rao, 1952). The percent contribution of each character to the total divergence was calculated by ranking each character on the basis of transformed uncorrelated values. Finally, the percent contribution for each character was calculated by taking total number of ranks of all the characters to hundred. The data were analyzed statistically using the software WINDOSTAT, developed by INDOSTAT services Ltd. Hyderabad, India.

Results and Discussion

The analysis of variance showed highly significant differences among the accessions for all the characters studied indicating the presence of considerable variability in the experimental material.

Principal component analysis

Partitioning of total variance through principle component analysis showed that three principal components viz PC I, PC II and PC III contributed about 86.61% of total variance for the germplasm lines studied (Fig 1). These three PCs i.e. PC I, PC II and PC III contributed 55.36, 20.29 and 10.96 % of total variance (Table 1). The results obtained from PCA were further corroborated by cluster analysis using UPGMC (Unweighted Paired Group Method using Centroids). The thirty nine blackgram genotypes lines were grouped into nine distinct clusters. Cluster 1 is the largest with a maximum number (22) of genotypes followed by cluster 5 with 7 genotypes, cluster 3 with 4 genotypes and cluster 2, cluster 4, cluster 6, cluster 7, cluster 8 and cluster 9 with single genotype each (Fig 2). The results of D^2 analysis helped to identify diverse accessions from the available germplasm lines for use in crop improvement programmes.

Cluster distances and cluster means

The genetic divergence among the genotypes as indicated by intra and inter cluster distances for nine different clusters are presented in Table 2 (Fig 3). Highest intra cluster distance of 32.38 was recorded for cluster 5 followed by cluster 1 (20.92) and cluster 3 (13.90), thus suggesting that different genotypes included in these clusters might have different genetic architecture. The clusters with lowest intra cluster distance indicated that the genotypes resembled one

another genetically and appeared to have evolved from a common gene pool. The inter cluster distance ranged from a minimum of 8.50 (between cluster 2 and 6) to a maximum of 187.13 (between cluster 3 and 5). The values of other inter cluster distances which are on the higher side are 180.17 (between cluster 5 and 9), 146.59 (between cluster 3 and 6), 134.63 (between cluster 5 and 8), 124.43 (between cluster 3 and 4), 114.22 (between cluster 7 and 9) and 107.29 (between cluster 4 and 9). Clusters 2, 4, 6, 7, 8 and 9 are solitary clusters with inter cluster distance of 0.00. The maximum amount of heterosis is expected from the crosses with parents belonging to the most divergent clusters i.e., between cluster 3 and 5 followed by parents in clusters of 5 and 9. These results are in agreement with earlier reports of Chauhan *et al*., (2008), Elangaimannan *et al.*, (2008), Mandal *et al.*, (2014) and Arya Gopinath *et al.*, (2018). The progenies derived from such crosses are expected to show wide variability, providing greater scope for isolating transgressive segregants in the advanced generations which can be used for selecting desirable genotypes for seed yield improvement in blackgram.

The cluster means for eight traits included in the present study are shown in Table 3. The lowest mean value for days to first flowering and days to maturity was recorded by cluster 5. The highest mean value for number of clusters per plant and number of pods per plant was recorded by cluster VII. Cluster VIII recorded the highest mean for 100 seed weight followed by cluster III and cluster IV. Hence crossing these genotypes would result in getting transgressive segregants for better seed weight.

Table.1 Principal component analysis for yield component traits in blackgram genotypes

		1 Vector	2 Vector	3 Vector
	Eigene value (Root)	**628.74570**	**230.48140**	**124.54900**
	% Var. Exp.	**55.36529**	**20.29544**	**10.96738**
	Cum. Var. Exp.	**55.36529**	**75.66072**	**86.62809**
1	**Days to 50% flowering**	0.37672	0.57644	0.14256
2	**Days to maturity**	0.62191	0.31043	0.18117
3	**Plant height**	0.16181	-0.11817	-0.70182
4	**Number of clusters per plant**	0.36107	-0.19444	-0.02115
5	**Number of pods per plant**	0.01326	-0.07559	-0.06036
6	**100 seed weight**	0.33216	-0.03557	-0.57148
7	**Seed yield per plant**	-0.32899	0.64634	-0.33136
8	**Seed yield per plot**	-0.30987	0.30798	-0.11755

Table.2 Intra and inter cluster distances for yield component traits in blackgram genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9
Cluster 1	20.92	36.47	77.57	43.95	91.70	38.79	42.94	34.17	48.34
Cluster 2	36.47	0.00	122.45	32.45	51.95	8.50	41.98	77.90	95.06
Cluster 3	77.57	122.45	13.90	124.43	187.13	146.59	73.83	70.17	76.33
Cluster 4	43.95	32.45	124.43	0.00	24.16	50.97	34.46	66.02	107.29
Cluster 5	91.70	51.95	187.13	24.16	32.38	73.66	62.36	134.63	180.17
Cluster 6	38.79	8.50	146.59	50.97	73.68	0.00	53.97	87.51	95.55
Cluster 7	42.94	41.98	73.83	34.46	62.36	53.97	0.00	93.91	114.22
Cluster 8	34.17	77.90	70.17	66.02	134.63	87.51	93.91	0.00	19.57
Cluster 9	48.34	95.06	76.33	107.29	180.17	95.55	114.22	19.57	0.00

Table.3 Cluster means for yield component traits in blackgram genotypes

	Days to 50% flowering	Days to maturity	Plant height	Number of clusters per plant	Number of pods per plant	100 seed weight	Seed yield per plant	Seed yield per plot
Cluster 1	43.73	73.70	28.34	7.70	27.33	3.87	5.29	1323.39
Cluster 2	42.50	72.00	15.50	5.15	18.20	3.55	3.25	808.00
Cluster 3	41.75	75.63	28.38	8.94	31.70	4.46	5.70	1428.13
Cluster 4	40.50	68.00	30.00	8.10	28.75	4.24	6.10	1523.00
Cluster 5	38.86	66.93	26.57	6.71	23.83	3.71	4.51	1126.79
Cluster 6	44.50	73.00	17.00	5.25	18.60	3.06	2.80	711.50
Cluster 7	42.00	69.50	28.00	10.50	37.05	3.01	5.60	1403.50
Cluster 8	43.50	75.00	32.50	6.95	24.75	5.40	6.65	1663.50
Cluster 9	47.00	76.00	34.50	4.25	15.00	4.66	3.50	869.00

Table.4 Percent contribution of yield component traits in blackgram genotypes

Source	Times ranked 1st	Contribution %
Days to 50% flowering	83	11.20
Days to maturity	197	26.58
Plant height	83	11.20
Number of clusters per plant	134	18.08
Number of pods per plant	110	14.84
100 seed weight	129	17.40
Seed yield per plant	5	0.67

Table.5 Clustering pattern in blackgram genotypes based on yield component traits

Cluster	No. of accessions	Genotypes
I	22	**IC-398973 IC-436559 IC-343962 IC-398970 IC-436524 IC-398958 IC-426768 IC-436512 IC-436536 IC-436535 IC-426769 IC-436517 IC-436545 IC-436518 IC-398998 IC-426766 IC-398380 IC-398989 IC-343812 IC-382811 IC-343943 IC-384812**
II	1	**IC-343936**
III	4	**MBG-207 LBG-752 IPU-2-43 PU-31**
IV	1	**IC-343967**
V	7	**IC-398956 IC-426759 IC-426459 IC-426760 IC-343947 IC-343942 IC-626763**
VI	1	**IC-260992**
VII	1	**IC-426761**
VIII	1	**IC-436508**
IX	1	**IC-436547**

Fig.1 Principal component analysis diagram for blackgram germplasm lines

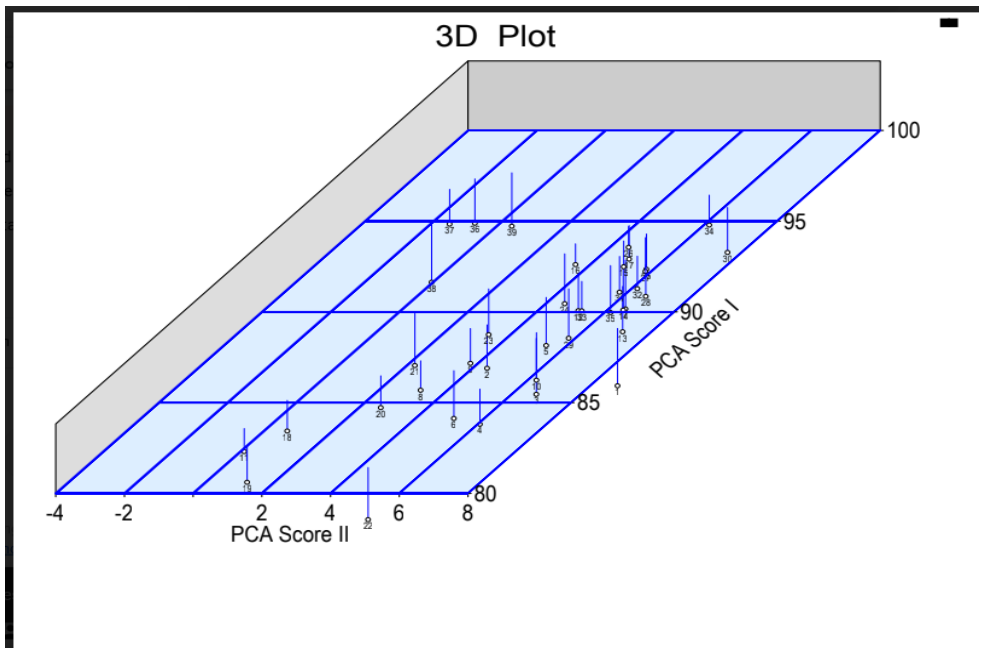


Fig.2 Dendrogram showing clustering of blackgram germplasm lines

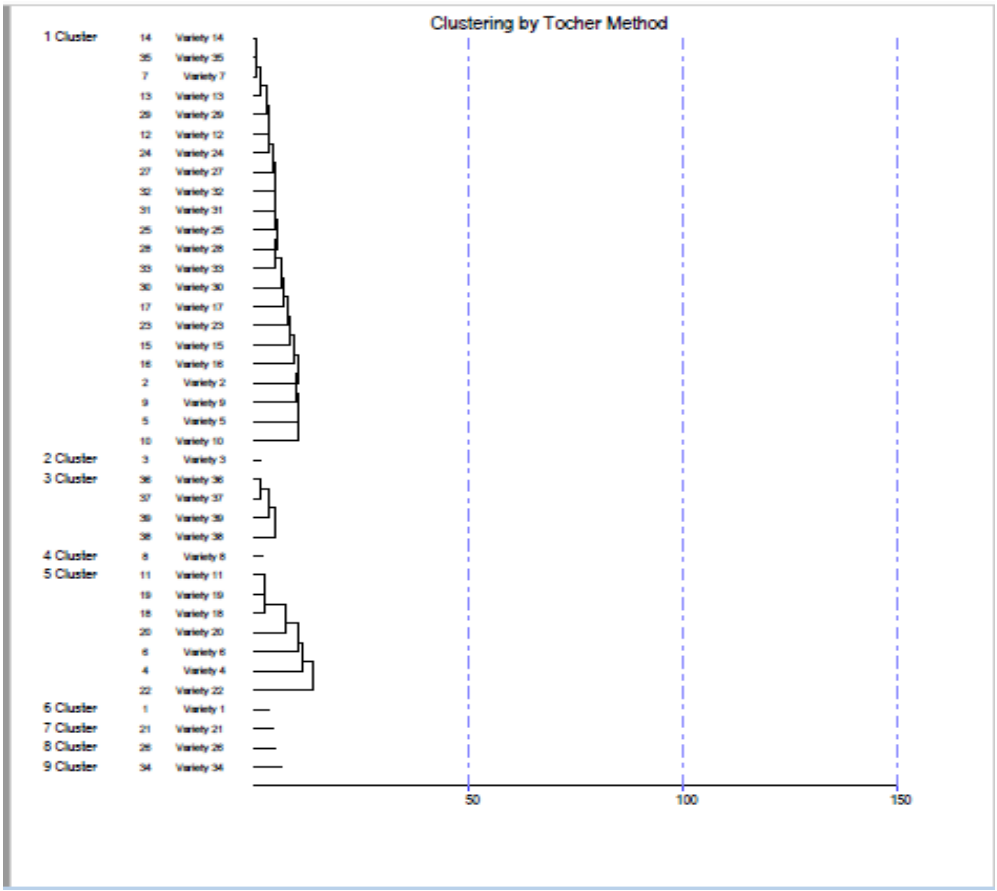
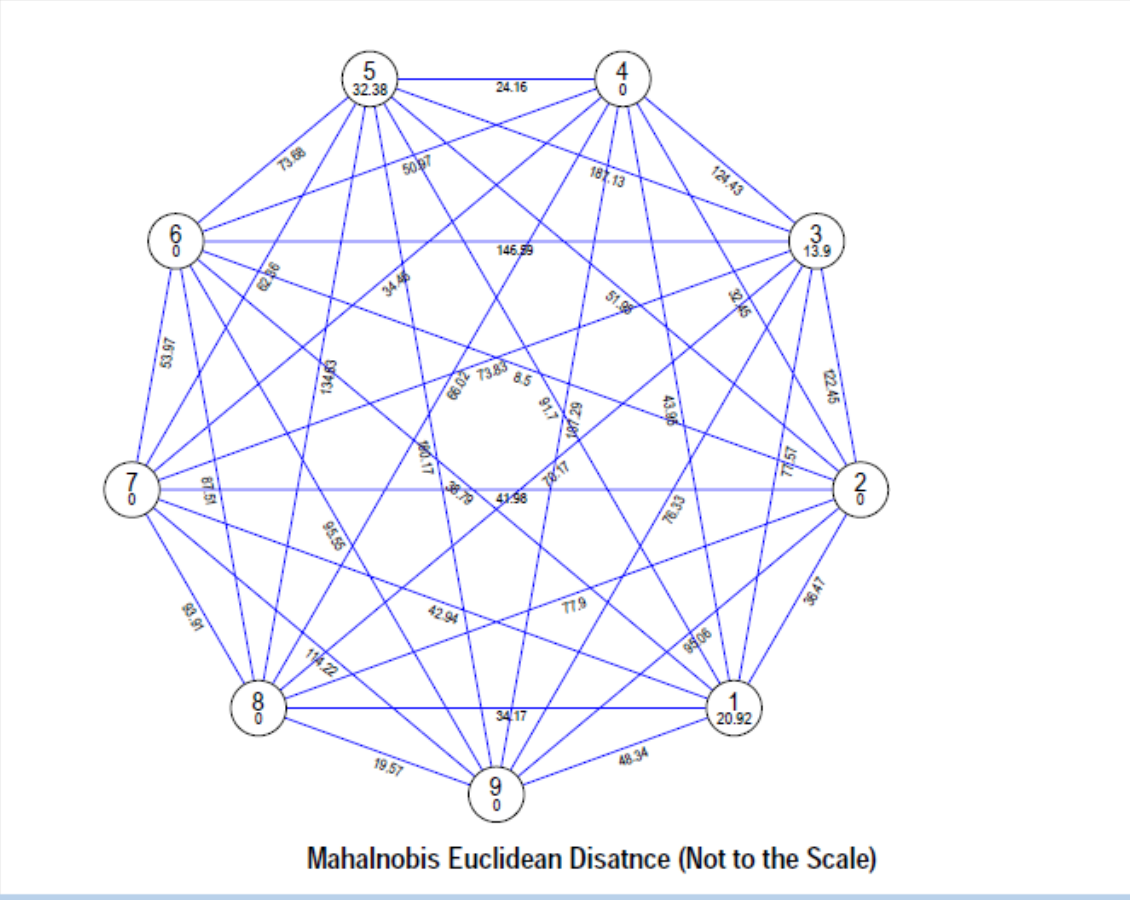


Fig.3 Mahalnobis Euclidean distances for blackgram germplasm lines



Percent contribution towards genetic divergence

The relative contribution of different traits included in the present study towards genetic divergence is shown in Table 4. Days to maturity contributed the most (26.58%) followed by number of cluster per plant (18.08%), seed yield per plant (17.40%), 100 seed weight (14.84%), days to 50% flowering (11.20%), plant height (11.20%) and seed yield (kg/ha) (0.67%). The grouping of blackgram genotypes based upon their genetic divergence into different clusters is shown in Table 5. The genotypes belonging to divergent clusters may be selected as parents for breeding varieties with good yield potential. Similar results were earlier reported by Chauhan *et al.,* (2008), Mandal *et al.,* (2014) and Srividya *et al.,* (2018). This information can also be used to assess the genetic divergence among the genotypes for framing an effective breeding programme for selection of parents for yield gain in blackgram genotypes under study.

References

Mahalanobis, P.C. (1936). On the generalized distance in statistics. Proceedings of National Institute of Sciences, India. 2:49-55

Rao, C.R. (1952). Advanced statistical methods in biometrical research. New York, USA. John Wiley and Sons Inc.

Chauhan, M. P., Mishra, A. C. and Singh, A. K. (2008). Genetic divergence studies in urd bean (*Vigna mungo* (L.) Hepper).

Legume Res, 31(1): 63-67.

Elangaimannan, R., Anbuselvam Y. and Karthikeyan P. (2008). Genetic diversity in black gram (*Vigna mungo* (L.) Hepper). *Legume Res*, 31 (1): 57 – 59.

Mandal. B. Asit., and N. D. Majumder. 2014. Genetic divergence, heritability and genetic advance in blackgram (*Vigna mungo* [L] Hepper). J. Andaman Science Association. 19:9-13.

Srividya.S, Sabesan. T, Saravanan.K. 2018. Genetic divergence studies in blackgram (*Vigna mungo* l.) for yield and quantitative traits. Journal of Phytology 10: 24-26.

Arya Gopinath, M.P, Desai S.S., Palshetkar M.G., Hawaldar Ayyajahmad Harun and Raje Mahadik V.A. 2018 Evaluation of genetic divergence in black gram [*Vigna mungo* (L.) Hepper] *Int.J.Curr.Microbiol.App.Sci* (2018) *7*(8): 472-479

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