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Evaluation of genetic divergence in blackgram (*Vigna mungo* L.) genotypes by D² statistic

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Abstract
Thirty nine genotypes were evaluated in a randomized block design with two replications at ARS, Madhira during *rabi* 2016 for genetic divergence studies. Partitioning of total variance through principle component analysis showed that five principal components viz PC I, PC II, PC III, PC IV and PC V contributed about 95.16% of total variance for the material studied. The blackgram genotypes were grouped into six distinct clusters of which cluster 1 is the largest with a maximum number (34) of genotypes. Percent contribution of the traits towards genetic divergence showed that 100 seed weight contributed the most (22.80%) followed by days to 50% flowering (21.32%), number of clusters per plant (21.18%), plant height (16.46%), seed yield per plant (8.50%), seed yield (kg/ha) (5.53%) and days to maturity (4.18%).

Keywords: Blackgram, genetic divergence, yield

Introduction
Vigna mungo (L.) Hepper] (2n = 22) belongs to Leguminosae (Fabaceae) family, is an important pulse crop in India. Blackgram [*Vigna mungo* (L.) Hepper] is one of the most ancient and important legume crop of India and contributes 70% of world's total production. It is suitable for cultivation under different farming situations. Urd bean occupies an important position due to its high seed protein (25-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins and ability to restore the soil fertility through symbiotic nitrogen fixation. Among pulses, black gram is an important pulse crop, which is widely cultivated and consumed throughout India. The low productivity of black gram attributed to excessive vegetative growth, high rate of flower and fruit drop, non-synchronous maturity, pod shattering and susceptibility to diseases and Pests etc. Lack of good quality seeds and crop management, extremely limited use of rhizobial sources, phosphatic fertilizers, fungicides and pesticides also contribute to lower productivity. Improvement of urdbean being an important pulse crop of India is an important task for pulses breeders. Many breeding efforts have been carried out to improve the yield of this crop and to break the yield plateau. Genetic diversity is an important factor and also a prerequisite in any hybridization programme. Analysis of genetic diversity in germplasm collections can facilitate reliable classification of genotypes and identification of subsets of core accessions with possible utility for specific breeding purposes. Also assessment of divergence or similarity among the genotypes would help in identification of genotypes that may be used in crossing programme to produce transgressive segregants. Genetic diversity arises due to either geographical separation, crossability barriers or due to different patterns of evolution.

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. The genotypes 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

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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) [1] and D^2 statistic as described by Rao (1952) [2].

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 five principal components viz PC I, PC II, PC III, PC IV and PC V contributed about 95.16% of total variance for the germplasm lines studied. These five PCs i.e. PC I, PC II,PC III, PC IV and PC V contributed 33.78, 26.53, 15.13, 13.14 and 6.58 % of total variance (Fig 1). The thirty nine blackgram genotypes were grouped into six distinct clusters (Fig.2).Cluster 1 is the largest with a maximum number (34) of genotypes. The remaining five genotypes were grouped as five different clusters indicating them to be diverse from the other genotypes under study. The results of D^2 analysis helped to identify diverse genotypes for use in crop improvement programmes as the lines belonging to diverse clusters are expected to give better transgressive segregants for desirable traits. Similar results were reported by Chauhan *et al* (2008), Srividya *et al.,* (2018) and Arya Gopinath *et al.,* (2018) [3, 6, 7].
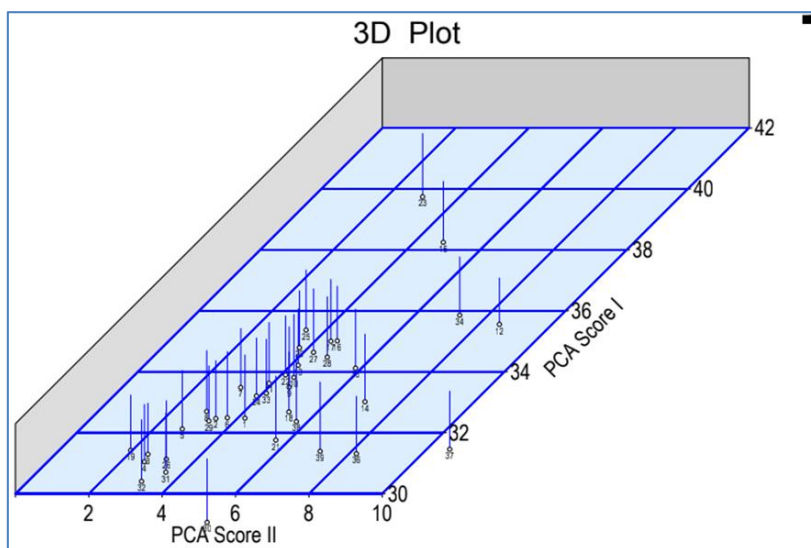

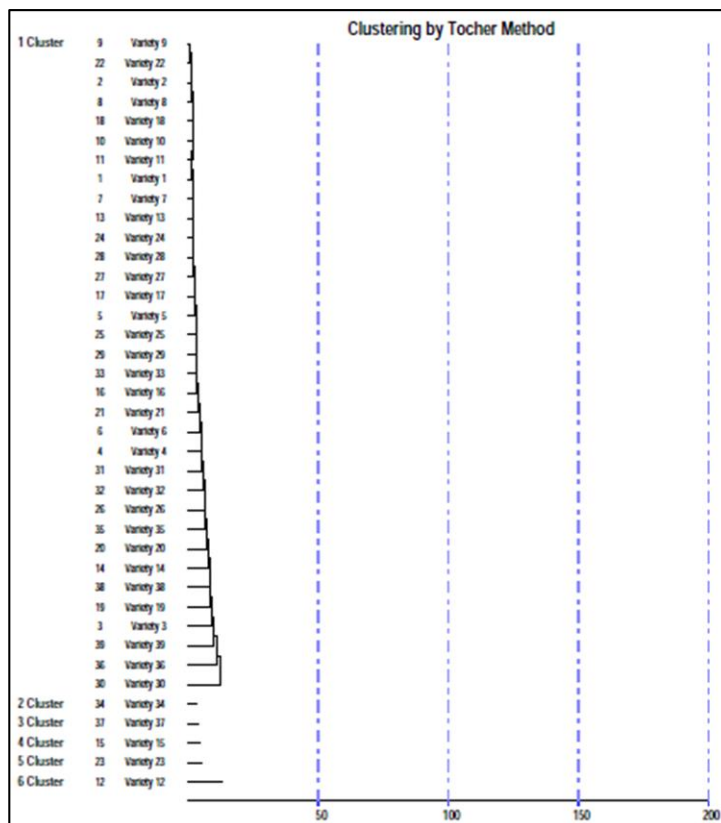**Fig. 1:** Principal component analysis diagram for blackgram germplasm lines

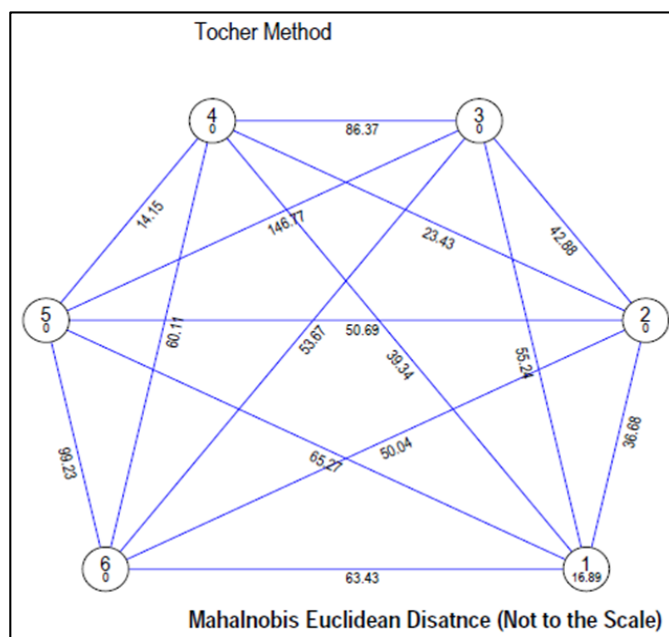**Fig 2:** Dendrogram showing clustering of blackgram germplasm lines

Fig 3: Mahalnobis Euclidean distances for blackgram germplasm lines

Cluster distances and cluster means

The intra and inter cluster distances for eight traits for the genotypes grouped into six different clusters are presented in Table 2. Only the cluster I had the highest intra cluster distance of 16.89. Remaining clusters are solitary clusters with single genotype and hence with 0.00 intra cluster distance. The inter cluster distance of cluster I with the remaining clusters viz., II, III, IV, V and VI is 36.68, 55.24, 39.34, 65.27 and 63.43, respectively. 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 yield improvement in blackgram. The cluster means for various traits included in the present study are shown in Table 3.

Percent contribution towards genetic divergence

The relative contribution of different traits included in the present study towards genetic divergence is shown in Table 4. 100 seed weight contributed the most (22.80%) followed by days to 50% flowering (21.32%), number of clusters per plant (21.18%), plant height (16.46%), seed yield per plant (8.50%), seed yield (kg/ha) (5.53%) and days to maturity (4.18%). The character number of pods per plant did not contribute anything towards genetic divergence in the present material.The grouping of germplasm lines based upon their genetic divergence into different clusters is shown in Table 5. 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. 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) [3,4, 5, 7].

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

		1 Vector	2 Vector	3 Vector	4 Vector	5 Vector
	Eigene value (Root)	164.09420	128.90460	73.53811	63.84252	31.97109
	% Var. Exp.	33.78363	26.53881	15.13999	13.14387	6.58219
	Cum. Var. Exp.	33.78363	60.32244	75.46245	88.60631	95.18851
1	Days to 50% flowering	0.62148	0.04941	0.03596	0.50236	0.57515
2	Days to maturity	0.06383	0.15478	0.09773	-0.04249	0.13071
3	Plant height	0.10970	0.72585	-0.56407	0.09491	-0.27615
4	Number of clusters per plant	0.51042	0.34614	0.54199	-0.33053	-0.32252
5	Number of pods per plant	-0.14980	-0.03481	-0.15172	0.02278	0.06475
6	100 seed weight	-0.44970	0.32944	0.59169	0.44457	-0.05150
7	Seed yield per plant	-0.31367	0.45646	0.02267	-0.37058	0.65689
8	Seed yield (kg/ha)	-0.11861	0.09363	-0.06001	0.54044	-0.18303

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 1	16.89	36.68	55.24	39.34	65.27	63.43
Cluster 2	36.68	0.00	42.88	23.43	50.69	50.04
Cluster 3	55.24	42.88	0.00	86.37	146.77	53.67
Cluster 4	39.34	23.43	86.37	0.00	14.15	60.11
Cluster 5	65.27	50.69	146.77	14.15	0.00	99.23
Cluster 6	63.43	50.04	53.67	60.11	99.23	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 (kg/ha)
Cluster 1	42.69	72.21	21.74	5.98	20.35	3.92	4.07	1018.71
Cluster 2	42.50	72.50	34.00	11.05	37.50	3.71	7.05	1757.00
Cluster 3	41.50	76.00	37.50	9.75	33.25	4.62	7.80	1953.50
Cluster 4	47.50	77.00	25.50	7.55	25.60	3.26	4.25	1057.50
Cluster 5	47.50	77.00	21.00	8.60	29.30	2.95	4.35	1098.00
Cluster 6	47.00	76.00	46.00	5.40	18.50	4.36	4.10	1030.00

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

Source	Times ranked 1st	Contribution %
Days to 50% flowering	158	21.32
Days to maturity	31	4.18
Plant height	122	16.46
Number of clusters per plant	157	21.18
Number of pods per plant	169	22.80
100 seed weight	63	8.50
Seed yield (kg/ha)	41	5.53

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

Cluster	No. of accessions	Genotypes
I	34	IC-436626 IC-436780 IC-436565 IC-436621 IC-436758 IC-436627 IC-436635 IC-436560 IC-436612 IC-436652 IC-436792 IC-436882 IC-436869 IC-436753 IC-436609 IC-436811 IC-436922 IC-282009 IC-436720 IC-436774 IC-436610 IC-436606 IC-519742 IC-282008 IC-436852 IC-436910 IC-436772 IC-436656 PU-31 IC-436765 IC-436604 IPU-2-43 MBG-207 IC-523949
II	1	IC-281993
III	1	LBG-752
IV	1	IC-436667
V	1	IC-436789
VI	1	IC-436638

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