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Genetic diversity analysis of black gram (*Vigna mungo* L.)

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Abstract
Twenty two genotypes of black gram were used to study the nature and magnitude of genetic divergence using Mahalanobis's D^2 Statistics. The data for ten important quantitative traits were recorded. D^2 analysis grouped 22 genotypes into five clusters. Cluster IV was largest with 10 followed by cluster V with 6 genotypes. The average intra-cluster distance between the genotypes was maximum for the cluster IV (49.2) and minimum for clusters I and II (1.00), respectively. The highest inter-cluster distance was noted between clusters I and II (16.77). The genotypes grouped in these clusters indicate their diverse nature. Number of branches per plant followed by biological yield per plant and plant height showed maximum per cent contribution towards total divergence among the genotypes. Ward cluster analysis grouped genotypes into two clusters, cluster I and II that were found apart at 25 rescaled values. The study provides scope for selection, further subsequent utility of the genotypes in future crop improvement programmes.

Keywords: black gram, diversity, D-square analysis, morphological traits, ward's cluster analysis

Introduction
Black gram {*Vigna mungo* (L.) Hepper} is one of the important pulse crops of India contributing 12 per cent of the total pulse production of the country. Inspite of its importance, the productivity of this crop is relatively low. The development of new varieties depends largely on the availability of genetic variability in the base material and the extent of variability for the desired character. The development of cultivated species and breeding of new varieties typically relies on the available biological diversity in existing genotypes [1]. Thus, the utility of techniques like Mahalonobis D^2 analysis to detect divergence in a group of genotypes and to identify genotypes which can effectively be used in crossing programme has often been stressed. Potential sources of genes for different characters can be identified by taking into consideration the clusters of genotypes which excel in each trait and diversity between the genotypes. Several workers studied the genetic diversity, clustering pattern, relative contribution of different characters toward divergence and effectiveness of selection [2, 3, 4, 5]. In the present study, genetic divergence and clustering pattern of the black gram genotypes for selection of suitable parents so as to utilize them in hybridization programme, extended to study the genetic parameters attributing to yield.

Materials and Methods
Seeds of 22 genotypes of black gram were procured from Agriculture Research Station (ARS), Durgapura, Jobner Agriculture University, Jaipur. Source details of the genotypes used are given in Table: 1. Jaipur has hot semi-arid steppe weather. Under this climatic condition, crop was raised during *zaid* of 2012 at ARS, Durgapura. Jaipur, located at an elevation of 431 meter above mean sea level on latitude of $26^0$59' North and longitude of $75^0$52' east. Twenty two genotypes were planted on Randomised Block Design in three replications. Observations were recorded on five randomly selected plants for ten quantitative traits *viz*, days to 50% flowering, plant height, number of branches per plant, number of pods per plant, pod length, seeds per pod, test weight, days to maturity, biological yield per plant (g), harvest index (%) and seed yield per plant. Mean data was used based on ANOVA [6]. The data were subjected to Mahalanobis's D^2 statistics as described by Rao (1952) and the genotypes could be grouped into different clusters by following Tocher's method [7]. In this study, the morphological and quality characters data based grouping of 22 genotypes of black gram was done using Ward's minimum variance method [8] using the IBM SPSS statistics software.

Table 1: Details of the genotypes used for present studied

S. No.	Genotype Code	Genotype	Source Centre
1.	G1	U-9	IIPR, Kanpur
2.	G2	UTTARA	IIPR, Kanpur
3.	G3	IPU2K-21	IIPR, Kanpur
4.	G4	UH-86-5	HAU, Hisar
5.	G5	PLU-144	IARI, Delhi
6.	G6	RUG-8	RAU, Durgapura
7.	G7	SPS-29	IIPR, Kanpur
8.	G8	UL-23	Uttar Pradesh
9.	G9	NHKD-31	IIPR, Breeding line
10.	G10	PANT-U30	GBPAU&T, Pant Nagar
11.	G11	IC-16511	NBPGR, New Delhi
12.	G12	UH-177	HAU, Hisar
13.	G13	PLU-1	IARI, Delhi
14.	G14	IPU99-233	IIPR, Kanpur
15.	G15	SHEKHAR-2	CSAUAT, Kanpur
16.	G16	PLU-446	IIPR, Kanpur
17.	G17	BG-369	Andhra Pradesh
18.	G18	U-17	IIPR, Kanpur
19.	G19	HPU-180	Himachal Pradesh
20.	G20	STY-2289	IIPR, Breeding line
21.	G21	IPU99-176	IIPR, Kanpur
22.	G22	STY-2834	IIPR, Breeding line

Result and Discussion

The average mean square values from the ANOVA for different characters revealed that the mean squares due to genotypes were highly significant for all the characters in the environments except for days to maturity. This indicated the presence of significant genetic variability in the material. On the basis of D^2 analysis the 22 genotypes could be grouped into V clusters. The clustering of genotypes are presented in Table: 2. It has been found that Cluster IV was the largest comprising 10 genotypes or 45% of the 22 genotypes belonged to this cluster followed by cluster V and III which contained 6 and 4 genotypes, respectively. The clusters I and II had only one genotype each.

Table 2: Cluster profile of 22 genotypes of *V. mungo* L.

Cluster	No. of genotypes	Genotypes
I	1	UH-177
II	1	PANT-U30
III	4	RUG-8, SPS-29, UL-23 and U-17
IV	10	IPU2K-21, UH-86-5, NHKD-31, IC-16511, PLU-1, IPU99-233, PLU-446, BG-369, HPU-180 and STY-2289
V	6	U-9, UTTARA, PLU-144, SHEKHAR-2, IPU99-176 and STY-2834

The average intra-cluster distance between the genotypes was found maximum in the cluster IV (49.2) followed, in descending order, by cluster V (23.98), III (17.86), I and II (1.00), respectively (Fig. 1). The highest inter-cluster distance was noted between clusters I and II (16.77) followed by clusters II and V (15.74), I and III (14.54), II and III (13.49) and so on. The genotypes grouped in these clusters indicated their diverse nature. The least (7.95) inter-cluster distance was observed for clusters IV and V indicated their genetic relatedness. Multivariate analysis is a potent biometrical tool for quantifying the degree of divergence in the germplasm [9, 10].

Based on mean values, (Table 3) cluster I (PANT-U30) had showed early flowering, early maturity and having above average values for all the characters. The per cent contribution towards total genetic divergence was maximum for the number of branches per plant followed by biological yield per plant and plant height. Mahalanobis distances ranged from 1.75 to 3.68 and maximum distance was found in PANT-U 30.

Table 3: Cluster means and overall average values for various characters in 22 genotypes of *V. mungo* L.

Cluster	No. of Genotype	Days to 50% maturity (days)	Days to maturity (days)	Plant height (cm)	Number of branches/plant	Number of pods/plant	Pod length (cm)	1000 seed weight (g)	Seed yield/ plant (g)	Biological yield/plant (g)	Harvest Index (%):
I	1	39.8	79	26.65	1	22	5.66	40	4.75	15.20	31.06
II	1	36.8	77	20.37	1	9	3.00	38.8	2.90	11.50	25.29
III	4	43.8	85	16.27	1	15.6	3.8	38.5	3.66	12.61	29.18
IV	10	39.3	79	18.76	1	17.6	3.99	36.5	3.90	13.18	29.65
V	6	40.7	80	18.22	1	19.5	4.02	41.7	4.74	13.69	34.90
Mean	4.4	40.08	80	20.05	1	16.74	4.09	39.1	3.98	13.23	30.01
Treat MSS		18.09	28.95	22.66	0.013	33.22	0.97	26.14	1.36	2.41	38.80
Err MSS		3.08	3.67	5.03	0.07	5.22	0.16	4.23	0.11	1.02	4.25
F Ratio		5.86	7.88	4.5	0.18	6.35	6.04	6.17	12.38	2.35	9.12
Percent contribution towards variability		0.004	0.001	0.012	0.945	0.003	0.003	0.003	0.000	0.095	0.00

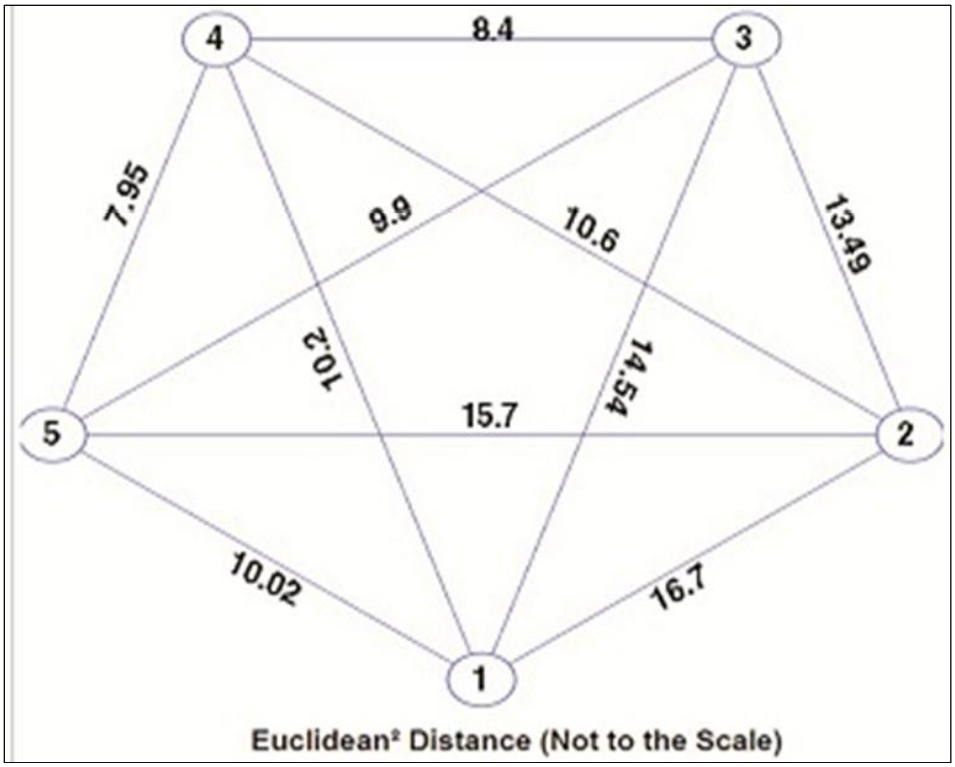

Fig 1: Intra and inter-cluster distance for 5 groups of 22 genotypes of *V. mungo L*.

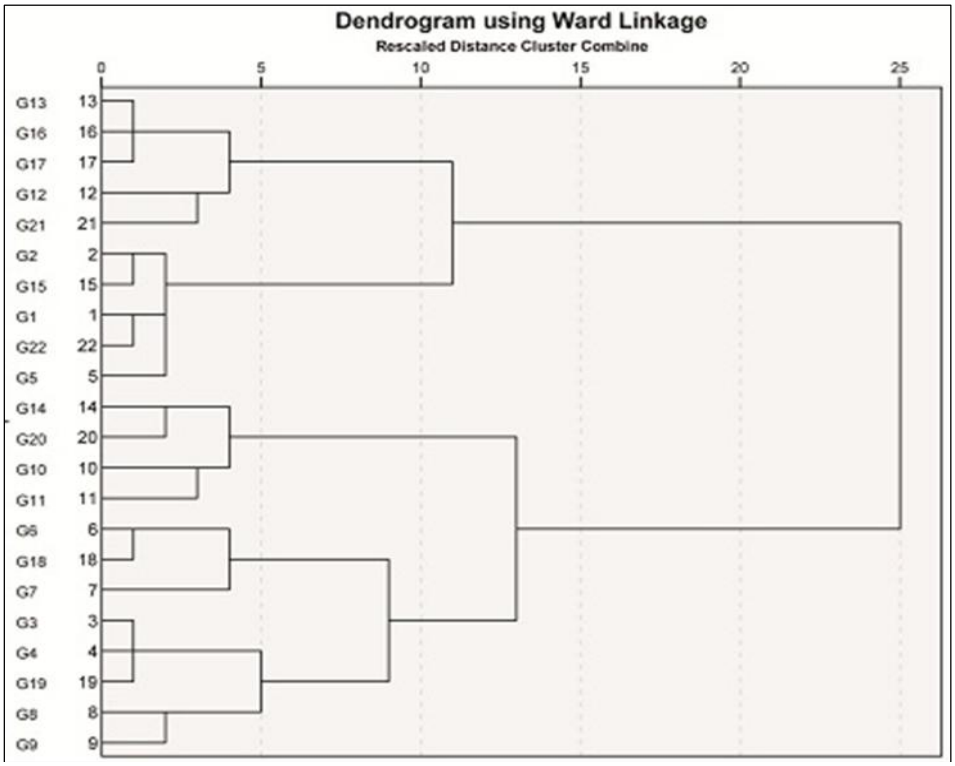

Fig 2: Dendrogram based on Ward's minimum variance cluster analysis for 22 genotypes of *V. mungo L*.

Ward's hierarchical cluster analysis was carried out on the basis of 10 morphological characters, used in order to measure genetic distance between the 22 *V. mungo* L. genotypes (Fig. 2). Cluster analysis resulted in grouping the genotypes into two clusters, cluster I consisted of 10 genotypes and II cluster consisted of 12 genotypes they were found at 25 rescaled values apart. Cluster analysis has been projected to be useful by Kumar *et al.* (2010) in grouping groundnut genotypes [11].

Conclusion

Among 22 genotypes PANT-U30 genotype had showed early flowering, early maturity and having above average value for all the characters that are potential processes for better crop productivity. The per cent contribution towards total genetic divergence was maximum for the number of branches per plant followed by biological yield per plant and plant height.

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