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Research Article

Genetic divergence among blackgram (*Vigna mungo*(L.) Hepper) genotypes using Mahalanobis D^2 statistic

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Abstract
The present study was conducted to evaluate the genetic divergence among 32 black gram genotypes using Mahalanobis D^2 statistic for ten biometric characters. The genotypes were grouped into nine discrete clusters. Among them cluster I grouped with a maximum of 11 genotypes, followed by cluster IV with 7 genotypes, clusters II and III each with 4 genotypes and cluster VIII with 2 genotypes, while the remaining clusters were solitary. The inter-cluster distance was higher than intracluster distance, confirming the presence of high genetic variability among the genotypes. Based on the inter-cluster distance, cluster V and IX and clusters V and VI were identified as the most diverse clusters and hence the genotypes from these clusters can be used in the hybridization programme for further genetic improvement. The maximum contribution to genetic divergence was by the number of branches per plant followed by plant height and hundred seed weight. Hence selection and utilization of genotypes based on these traits would be more effective in the selection for hybridization programme.

Keywords
black gram, D^2 statistic, divergence, cluster analysis

INTRODUCTION

Black gram (*Vigna mungo* (L.) Hepper), an important self-pollinating pulse crop contributes to 8.4 per cent of the total production of pulses in India(Naga *et al*., 2006; Swathi *et al*., 2013). It is highly proteinaceous containing about thrice the amount of protein when compared with cereals. Despite being cultivated in12.7 per cent of the total area under pulses, the productivity of this crop is relatively low. Improvement of crop yield largely depends upon the magnitude of genetic variability in the base population. Mahalanobis D^2greatly helps in gaining knowledge on genetic divergence of the genotypes under study and facilitates in further utilization of them in breeding programmes according to breeding objectives. In the present study, the genetic divergence of 32 black gram genotypes was studied so as to utilize them in the hybridization programme aimed for yield improvement.

MATERIAL AND METHODS

In the present study, 32 blackgram genotypes including checks were raised in randomized complete block design with two replications during *Kharif* 2019at National Pulses Research Centre, Vamban. Each entry was evaluated in the row of 4m length with 30x30 spacing. Recommended package of practices and need based crop protection measures were followed. Observations were recorded on five randomly selected plants in each replication for ten quantitative traits *viz*., days to 50% flowering, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, the total number of pods per plant, pod length (cm), number of seeds per pod, hundred seed weight (g) and seed yield per plant (g). The data were analyzed according to Mahalanobis D^2statistic (Mahalanobis, 1936). Based on this, clustering was done using Tocher's method as suggested by Rao (1952). The data were analyzed using the software, TNAU STAT (Manivannan, 2014).

RESULTS AND DISCUSSION

Analysis of variance for different characters also revealed high significant variations among the genotypes taken understudy, ensuring a high degree of genetic variability among the genotypes taken under study. Similar results have been reported by Manivannan *et al.* (1999), Ali *et al.* (2008), Chauhan *et al*. (2008) and Singh *et al*. (2012). The multivariate analysis indicated significant differences in all traits and Wilk's criteria were also found to be

significant. In the present study, 32 black gram genotypes were grouped into 9 clusters which indicate the presence of maximum divergence for further crop improvement programme (**Table 1**). Among the clusters, cluster I had a maximum number of genotypes(11), followed by cluster IV with 7 genotypes. The clusters II and III had 4 genotypes each whereas, cluster VIII was digenotypic and the remaining clusters; IV, V, VI, VII, IX were solitary. The pattern of distribution of the experimental genotypes into non-overlapping discrete clusters suggests the presence of a high magnitude of genetic diversity among the genotypes. Similar reports have been reported by Shanthi *et al.* (2006) and Katiyar and Dixit (2010).

Table 1. Clustering pattern in black gram genotypes

Cluster Number	Number of Genotypes	Constituent Genotypes
I	11	ACM BG 16-011, ACM BG 16-015, ACM BG 16-017, ACM BG 16-025, ACM BG 17-0 ACM BG 18-001, ACM BG 18-004, ACM BG 18-005, ACM BG 18-009, ACM BG 19-00 ACM BG 19-002
II	4	ADT 5, ADT 6, CO 5, ACM BG 17-003
III	4	MDU 1, ACM BG 18-003, ACM BG 18-006, ACM BG 18-007
IV	7	KKM 1, VBN (Bg) 4, VBN 8, ACM BG 14-001, ACM BG 17-001, ACM BG 17-006, ACM BG 18-010
V	1	ACM BG 17-005
VI	1	ACM BG 18-002
VII	1	ACM BG 18-008
VIII	2	ACM BG 17-002, ACM BG 17-004
IX	1	VBN 6

The average intra and inter-cluster D^2 distances are presented in **Table 2**. On comparing inter and intra-cluster distance, inter-cluster distance, proved to be higher denoting the fact, greater genetic divergence existed in the experimental material (Ali *et al.*, 2008; Chauhan *et al.*, 2008; Jayamani and Sathya., 2013; Panigrahi*et al.*, 2014; Geethanjali*et al.,* 2015; Reddy *et al.*, 2018). The maximum intracluster distance was noted in cluster VIII (33.03), followed by cluster I (24.5) and cluster IV (24.29); indicating that considerable genetic variability was present within these clusters. Minimum intracluster distance was observed in clusters II (18.38). This indicates that the genotypes within these clusters are genetically similar to narrow variability. Regarding the inter-cluster distances, maximum inter-cluster distance was noted between cluster V and IX (266.34) followed by cluster V and VI (257.02) suggesting that the genotypes belonging to these clusters are diverse, hence the selection of parents between these clusters for hybridization programmes generate a wide range of variability in the segregating population. Minimum inter-cluster distance was observed between clusters VI and IX (33.97), followed by clusters I and VII (38.86) and clusters V and VIII (41.88) indicating that the genotypes belonging them are less diverse and constitute similar genotypic makeup.

Table 2. Average intra (bold) and inter-cluster distances (D^2) in black gram

Cluster number	I	II	III	IV	V	VI	VII	VIII	IX
I	**24.50**	50.66	50.14	52.95	114.59	89.79	38.86	104.94	95.39
II		**18.38**	63.60	94.36	150.63	54.66	58.95	86.68	70.19
III			**21.12**	56.89	113.03	59.67	43.33	108.09	91.84
IV				**24.29**	50.93	160.79	65.35	73.71	194.37
V					**0.00**	257.02	124.56	41.88	266.34
VI						**0.00**	58.20	182.89	33.97
VII							**0.00**	99.29	89.20
VIII								**33.03**	210.95
IX									**0.00**

***figures given in diagonal are intra-cluster distance**

Table 3. Cluster mean values for various clusters

	Days to 50% flowering	Plant height (cm)	No. of branches per plant	No. of clusters per plant	No. of pods per cluster	Total number of pods	Pod length (cm)	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
I	41.73	49.38	1.84	11.13	2.33	**28.97**	5.44	6.73	4.03	5.16
II	**42.38**	50.18	1.58	7.48	2.18	17.54	5.38	6.50	*3.51*	2.44
III	*41.00*	49.40	1.48	9.58	2.08	20.98	5.79	7.05	4.29	4.24
IV	41.14	57.49	2.13	**11.44**	2.24	27.94	5.59	7.03	4.34	**5.49**
V	41.50	**57.70**	**3.60**	10.20	1.90	23.40	**5.90**	**7.20**	4.35	5.05
VI	*41.00*	41.50	*0.90*	*6.60*	1.90	14.00	5.00	6.60	3.95	*2.20*
VII	*41.00*	47.00	1.80	10.00	2.10	22.40	*4.80*	*6.30*	**4.85**	4.05
VIII	42.00	57.10	3.00	7.50	*1.45*	*13.75*	5.48	6.70	3.90	2.28
IX	41.50	*34.30*	1.90	8.40	**2.60**	19.20	5.50	6.60	3.70	3.40

Maximum and minimum values of each character are printed in bold and italics, respectively

The mean value of different clusters for each character is presented in **Table 3.** Cluster I shows the highest mean value for the total number of pods (28.97), whereas cluster II showed the highest mean value for days to 50% flowering (42.38). Cluster IV possessed the highest mean value for the character number of clusters per plant (11.44) and seed yield per plant (5.49). Cluster V showed the highest mean value for the characters, plant height (57.7) and the number of branches per plant (3.60), pod length (5.9), the number of seeds per pod (7.2). Cluster VII showed the highest mean value for hundred seed weight (4.85) whereas, cluster IX showed the highest mean value for the number of pods per cluster (2.60). Therefore crosses between members of clusters having high inter-cluster distance along with high mean value for important characters are likely to be highly rewarding. Best donor for hybridization may be chosen from an appropriate cluster and can be utilized in breeding programmes for improving any particular trait (Chauhan *et al.,* 2008; Elangaimannan *et al.,* 2008). The genotype ACM BG 17-005 of cluster V can be selected for hybridization programmes since it contains the highest mean for important yield attributing traits like plant height, the number of branches per plant, pod length and the number of seeds per pod. Similarly, VBN 6 of cluster IX can also be considered for inclusion in breeding programmes, as it contains the highest cluster mean for the character, the number of pods.

Table 4. Contribution of various quantitative traits towards genetic divergence

S.No	Characters	Times ranked first	Per cent contribution
1	Days to 50 % flowering	5	1.01
2	Plant height (cm)	93	18.75
3	No. of branches per plant	134	27.02
4	No. of clusters per plant	16	3.23
5	No. of pods per cluster	2	0.40
6	Total number of pods	66	13.31
7	Pod length (cm)	7	1.41
8	Number of seeds per pod	42	8.47
9	Hundred seed weight (g)	87	17.54
10	Seed yield per plant (g)	44	8.87

The characters contributing to maximum divergence are to be given greater emphasis on deciding the clusters for the purpose of selection of parents for further hybridization. The contribution of the various biometrical traits towards the genetic variation is presented in **table 4**. Among the various traits, the number of branches per plant (27.02%) contributed towards the maximum towards genetic diversity followed by plant height (18.75%) and hundred seed weight (17.54%), whereas the lowest contributor was the number of pods per cluster (0.40%). Hence selection of parents based on the number of branches per plant will generate more variability in the breeding programme.

To conclude, the present study revealed that the number of branches per plant followed by hundred seed weight recorded a higher level of contribution towards total divergence. Based on diversity, crosses may be made between cluster V (ACM BG 17005) and cluster IX (VBN 6) and between cluster V (ACM BG 17005) and cluster VI (ACM BG 18002) to create more variation in segregating population and to develop superior high yielding black gram varieties.

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