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Understanding the Genetic Distances among various Genotypes of Black Gram (*Vigna mungo* (L.) Hepper) using D^2 Statistics

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ABSTRACT: Fifty black gram genotypes were evaluated to assess the genetic diversity and to identify desired cross combinations for development of superior hybrids or transgressive segregants. Based on Mahalanobis D^2 statistics, the fifty black gram genotypes were grouped into twelve clusters. High range of variation was observed for trait contribution to the total diversity and pods per plant contributed maximum followed by seeds per pod and plant height. The fifty genotypes were grouped into twelve discrete clusters, among which cluster II was the largest with twenty genotypes followed by cluster I with fifteen genotypes and cluster III with six genotypes and remaining clusters *viz.,* IV, V, VI, VII, VIII, IX, X, XI and XII were all solitary. The maximum *per se* performance for grain yield was recorded in cluster III followed by cluster IX, XI and XII and the Mahalanobis D^2 distances between clusters III and clusters XI, XII & IX are 87.04, 72.94 and 43.24, respectively, indicating that these three monogenotypic clusters (XI, XII & IX) with high *per se* were having considerable divergence with cluster III.

Keywords: Black gram, Genetic distance, Genetic divergence, D^2, *Vigna mungo.*

INTRODUCTION

Black gram (*Vigna mungo* (L.) Hepper) also called as urdbean, extensively grown in India as well as in South East Asia. It is an annual, self-pollinated grain legume crop belonging to family Fabaceae and sub family Papilionacea with diploid chromosome number 2n = 2x= 22. It is suitable for cultivation under different agro- climatic regions. It is the third most important pulse crop grown in India in an area of 41.42 lakh hectares with an annual production and productivity of 7.22 lakh tonnes and 538 kg ha^{-1}, while in Andhra Pradesh it is grown in 3.93 lakh hectares with production and productivity of 3.64 lakh tonnes and 929 kg ha^{-1}(Ministry of Agriculture, 2020-21). Urdbean occupies an important source to vegetarians as it is highest source of seed proteins (24%), carbohydrates (60%), fat (1.5%), minerals, vitamins and amino acids and enriches soil fertility through symbiotic nitrogen fixation.

The failure of breeding programmes in legumes is due to availability of limited amount of variability to identify potential cultivars with high productivity (Jain, 1975). Diversity of parents is considered as one of the most important criteria for selecting parents for hybridization.

Genetic diversity studies helps in identification of parents with high diversity to obtain desired cross combinations in segregating generations. Among different biometrical approaches proposed by different research workers, Mahalanobis' D^2 has proven to be the most efficient method for classifying parental lines for production of high yielding genotypes in black gram (Dasgupta and Das 1984; Elangaimannan *et al*., 2008; Neelavathi and Govindarasu 2010; Rao *et al*., 2019; Rajalakshmi *et al*., 2020; Chippy *et al*., 2021).

Therefore, the present investigation was carried out to assess the genetic divergence among 50 genotypes of black gram for identification of diverse genotypes for their utilization in breeding programme.

MATERIALS AND METHODS

Fifty black gram genotypes collected from various sources *viz.,* RARS Lam, ARS Gantasala, CSAU Kanpur, Trombay, Uttarakhand, Karnataka, Jabalpur and Vamban, were evaluated during *Kharif*, 2021 in Augmented Randomized Complete Block Design at RARS, Lam, Guntur. Each genotype was sown in two rows with four meters row length, 30 cm between rows and 10 cm between plants within a row. All the recommended agronomic practices were followed to

raise a good crop. Observations on eight quantitative traits *viz.,* plant height, branches per plant, clusters per plant, pods per plant, pod length, seeds per pod, test weight and grain yield per plant were recorded on five competitive plants selected at random per genotypes. Whereas, data on days to 50% flowering and days to maturity were recorded on plot basis. Data on days to 50% flowering was recorded as number of days from sowing to opening of the flower in 50% of plants and days to maturity was recorded as number of days from sowing to 50 % of pod maturity.

The genetic divergence for ten characters was assessed by Mahalanobis D^2 statistic (Mahalanobis, 1936) and clustering pattern of genotypes by Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences for majority of characters under study indicating presence of required amount of variability among the genotypes under study.

D^2 values calculated from the means of 50 black gram genotypes for 10 quantitative characters was used to conduct genetic divergence analysis. The 50 genotypes were grouped into twelve clusters indicating that the extent of diversity is high. The dendrogram representing the clustering pattern was presented in Fig. 1. The clustering pattern revealed that, cluster II was largest with 20 genotypes followed by cluster I with 15 genotypes, cluster III with 6 genotypes and remaining clusters *viz.,* IV, V, VI, VII, VIII, IX, X, XI and XII were solitary clusters. Monogenotypic clusters obtained may be due to the geographical barriers preventing gene flow or intense natural and human selection for diverse and adaptable gene complexes (Arunachalam and Ram 1967).

The intra-cluster and inter-cluster distances were presented in Table 2. Intra cluster distances varied from 0.00 (Cluster IV, V, VI, VII, VIII, IX, X, XI and XII) to 34.09 (cluster III). The maximum intra cluster distance was observed in cluster III (34.09) whereas, the minimum intra cluster distance was found in cluster I (20.52), followed by cluster II (23.91), indicating that within these clusters, there exist considerable amount of variability.

The inter cluster distance ranged from 21.50 (clusters XI and XII) to 188.21 (cluster VI and XII), followed by clusters III and VI (184.06), clusters VI and IX (169.76), clusters III and VIII (151.69), clusters III and V (139.13), clusters VI and XI (136.37) and clusters IV and VI (135.39) indicating that the genotypes are diverse (Fig. 2) thus the progenies produced from such crosses are expected to show wide variability and superior transgressive segregants depending upon the gene action governing the trait of interest.

In the present investigation the cluster mean values revealed existence of sufficient variation among clusters for majority of traits (Table 3). Number of days taken to attain 50% flowering ranged from 39.50 days for genotypes in cluster V, XI, XII to 46.50 days for genotypes in cluster IV. The number of days taken to attain days maturity ranged from 75.50 days for genotypes in cluster XI to 90.50 days for genotypes in cluster IV. Cluster XII recorded highest mean (46.80) for plant height, while cluster VI recorded the lowest mean (20.50). Number of branches per plant ranged from 1.15 in cluster VIII to 5.86 in cluster III, number of clusters per plant ranged from 2.50 in cluster VI to 8.50 in cluster IX and XII. The highest mean for pods per plant was recorded by cluster III (36.18) and the lowest by cluster VIII (10.50). Pod length had a range of 3.90 cm (cluster VI) to 6.60cm (cluster X), number of seeds per pod ranged from 3.80 (cluster VI) to 6.10 (cluster XI), test weight varied from 3.25 g (cluster VI) to 4.95 g (cluster IX) and grain yield per plant ranged from 1.46 g (cluster VI) to 6.91 g (cluster III). Therefore, selection of genotypes for these characters can be made from these clusters. The best donor for hybridization can be picked from a suitable cluster and be used in breeding programmes to improve any specific trait (Chauhan *et al*., 2008; Elangaimannan *et al*., 2008). Cluster III has the maximum mean values for traits *viz.,* branches per plant, pods per plant and grain yield per plant.

The relative contribution of each character was presented in table 4. Character pods per plant (28.73%) contributed maximum to the divergence of the genotypes followed by seeds per pod (19.59%), plant height (14.61%), test weight (10.10%), days to maturity (7.67%), clusters per plant (7.27%), branches per plant (4.57%), days to 50% flowering (3.35%), pod length (2.29%) and grain yield per plant (1.71%) contributed least towards divergence. It is not necessary to choose genotypes only from more diverse clusters; rather, genotypes from any two different clusters may be diverse and have a significant genetic distance between them and such genotypes can also be preferred for conducting crosses because they have a reasonable chance of producing heterotic hybrids or transgressive segregants, provided that they report maximum per se values for the majority of yield-contributing traits.

Taking the above into consideration, maximum divergence was present between clusters VI & XII followed by clusters III & VI and clusters VI & IX. However, cluster VI recorded least mean values for all the characters, hence it is not wise to select genotypes from these three pairs of clusters. The maximum *per se* performance for grain yield was recorded in cluster III (LBG 932 & LBG 904) followed by monogenotypic clusters IX (PU 1504), XI (PU 31) and XII (VBG 17-012). These solitary clusters were also having considerable divergence with cluster III. Hence there is a great chance for cross combination *viz.,* LBG 932 × PU 1504, LBG 932 × PU 31, LBG 932 × VBG 17-012, LBG 904 × PU 1504, LBG 904 × PU 31 and LBG 904 × VBG 17-012 may result in superior hybrids or

transgressive segregants depending upon the gene action governing the trait of interest.

Similar usage of genetic distance analysis through Mahalanobis' D^2 statistics (Tocher's method) in obtaining the respective cluster diagram and dendrogram to understand the genetic diversity was earlier employed in various crops (Naik *et al*., 2016) in American cotton; Gowsalya *et al*. (2017) in black gram; Shivani *et al*. (2018) in rice; Ayesha and Babu (2019) in foxtail millet and Mohan *et al*. (2019) in greengram to indicate the successful hybrid combination to obtain superior hybrids or transgressive segregants depending on the gene action guiding for inheritance of different traits.

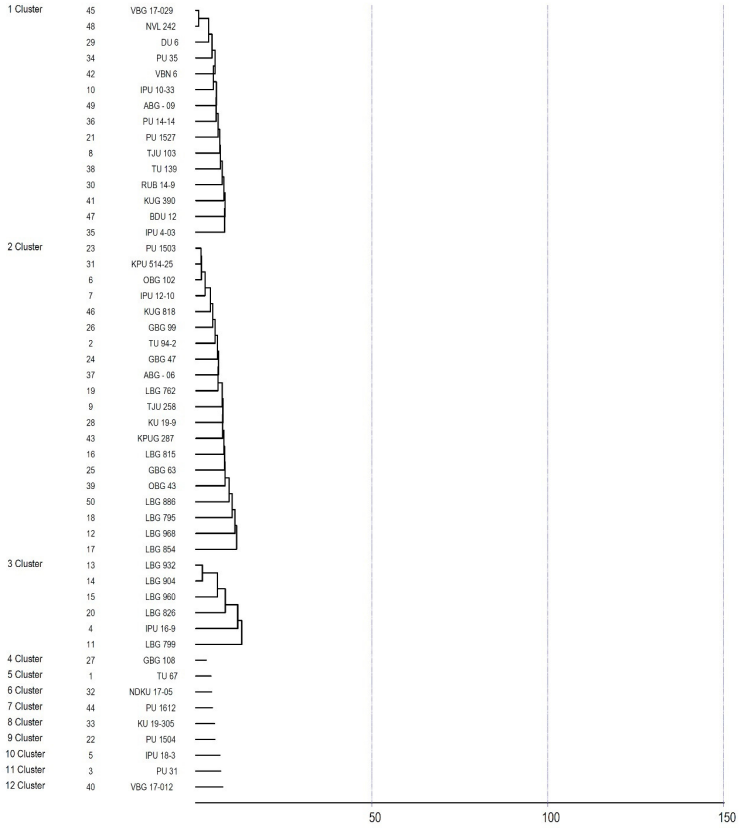

Fig. 1. Dendrogram exhibiting relationship among 50 blackgram genotypes in twelve clusters based on Mahalanobis' D^2 values.

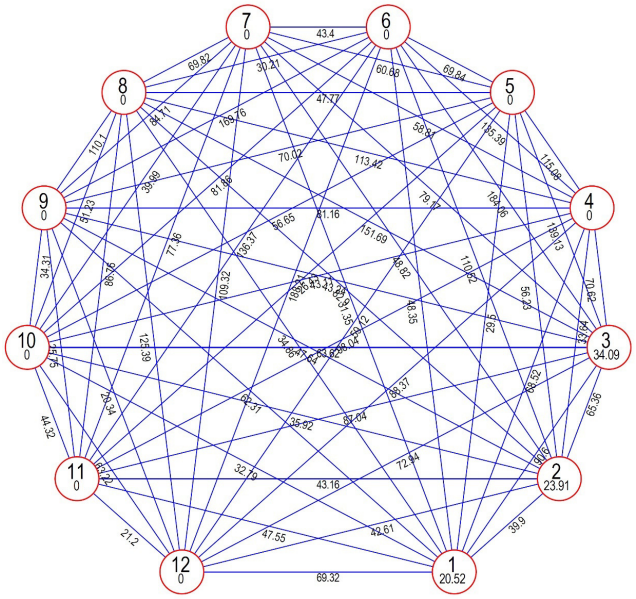

Fig. 2. Intra and Inter-cluster distance of 50 blackgram genotypes in twelve clusters based on Tocher's method.

Table 1: Clustering pattern of 50 black gramgenotypes by Tocher's method.

Cluster No.	No. of genotypes	Name of genotype (S)
I	15	VBG 17-029, NVL 242, DU 6, PU 35, VBN 6, IPU 10-33, ABG 09, PU 14-14, PU 1527, TJU 103, TU 139, RUB 14-9, KUG 390, BDU 12, IPU 4-03
II	20	OBG 102, PU 1503, KPU 514-25, IPU 12-10, KUG 818, GBG 99, TU 94-2, ABG-06, GBG 47, KU 19-9, LBG 762, KPUG 287, TJU 258, LBG 815, GBG 63, OBG 43, LBG 886, LBG 854, LBG 795, LBG 968
III	06	LBG 932, LBG 904, LBG 960, LBG 826, IPU 16-9, LBG 799
IV	01	GBG 108
V	01	TU 67
VI	01	NDKU 1705
VII	01	PU 1612
VIII	01	KU 19-305
IX	01	PU 1504
X	01	IPU 18-3
XI	01	PU 31
XII	01	VBG 17-012

Table 2: Average intra and inter-cluster distances (D^2 values) among twelve clusters (obtained by Tocher's method) of 50 blackgram.

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**20.52**	39.90	90.60	68.52	29.50	48.35	31.35	34.86	62.31	32.79	47.55	69.32
II		**23.91**	65.36	33.64	56.23	110.52	48.82	82.90	47.64	35.92	43.16	42.61
III			**34.09**	70.62	139.13	184.06	79.17	151.69	43.24	63.62	87.04	72.94
IV				**0.00**	115.08	135.39	58.81	113.42	81.16	43.11	98.04	88.37
V					**0.00**	69.84	60.68	47.77	70.02	56.65	26.43	59.12
VI						**0.00**	43.40	30.21	169.76	81.86	136.37	188.21
VII							**0.00**	69.82	84.71	39.99	77.36	109.32
VIII								**0.00**	110.10	51.23	86.76	125.39
IX									**0.00**	34.31	25.75	20.34
X										**0.00**	44.32	63.22
XI											**0.00**	21.20
XII												**0.00**

Table 3: Mean values of twelve clusters estimated by Tocher's method in 50 blackgram genotypes.

Cluster Number	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length	Seeds per pod	Test weight	Grain yield per plant (g)
I	41.47	83.03	29.19	3.53	4.33	17.09	4.42	4.86	4.02	3.19
II	43.20	85.35	38.34	4.39	4.65	23.78	4.69	5.02	4.39	4.03
III	43.50	86.25	29.23	5.86	7.99	36.18	5.09	5.44	4.57	6.91
IV	46.50	90.50	37.10	4.14	3.50	27.14	5.25	4.37	4.60	2.92
V	39.50	77.00	34.85	3.11	4.00	11.50	4.50	5.20	4.29	2.60
VI	41.00	81.50	20.50	1.98	2.50	11.20	3.90	3.80	3.25	1.46
VII	42.00	80.00	24.60	4.01	3.50	25.69	4.35	4.05	4.35	3.45
VIII	42.00	84.50	23.35	1.15	3.50	10.50	4.10	5.11	3.42	2.07
IX	40.00	81.50	34.40	4.29	8.50	27.50	5.99	5.96	4.95	5.67
X	41.00	81.50	31.30	2.15	5.00	24.69	6.60	4.96	4.27	4.70
XI	39.50	75.50	38.80	3.45	5.50	25.63	4.90	6.10	4.47	4.89
XII	39.50	84.00	46.80	5.14	8.50	22.50	5.00	6.00	4.64	5.07

Table 4: Contribution of different characters towards genetic divergence in 50 black gram genotypes.

Sr. No.	Source	No. of times ranked first	Per cent contribution
1.	Days to 50% flowering	41	3.35%
2.	Days to maturity	94	7.67%
3.	Plant height (cm)	179	14.61%
4.	Branches per plant	56	4.57%
5.	Clusters per plant	89	7.27%
6.	Pods per plant	352	28.73%
7.	Pod length (cm)	28	2.29%
8.	Seeds per pod	240	19.59%
9.	Test weight (g)	125	10.20%
10.	Grain yield per plant (g)	21	1.71%

CONCLUSIONS

The current investigation on genetic diversity study in 50 black gram genotypes revealed that there was ample variation in the material under study. The fifty genotypes were grouped in twelve clusters based on D^2 statistics implying high degree of genetic diversity among them. Highest inter-cluster distance was observed between cluster VI and XII, where as lowest in between cluster XI and XII. So, selection of genotypes from diversely related clusters with respect to maximum inter-cluster distance can give rise to better transgressive segregants in following generations.

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Conflict of Interest. The authors declare that there is no conflict of interests.

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