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Genetic divergence, variability and correlation studies in black gram [*Vigna mungo* (L.) Hepper]

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ABSTRACT

A field experiment was conducted to estimate genetic divergence, variability and correlation in 104 black gram genotypes for nine quantitative characters. Genetic diversity using Mahalanobis D^2 technique was studied for yield and yield contributing traits. Out of eight clusters, high inter cluster distance was recorded between clusters VI and VIII. Cluster V had low mean value for days to 50% flowering and cluster VII had high mean value for plant height, number of primary branches per plant and number of seeds per plant. The genotypes present in these clusters could be utilized for hybridization programmes. High heritability coupled with GAM was observed for plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant and single plant yield. From the association analysis, single plant yield had positive and significant association with plant height and number of primary branches per plant. Hence, simultaneous selection of the above traits would be more rewarding to bring genetic improvement in black gram breeding programmes.

Key words: Black gram, Correlation, Genetic divergence, Variability.

INTRODUCTION

Pulses are the major source of dietary protein in the vegetarian diet. Black gram [*Vigna mungo* (L.) Hepper] known as urd bean in India is a short duration, self-pollinating, diploid (2n=2x=22) grain legume crop belonging to the family Leguminosae with a small genome size estimated to be 0.56 g/PC (Gupta *et al*. 2008). Black gram has high protein content (20.8 to 30.5 per cent) with total carbohydrates ranging from 56.5 to 63.7 per cent and it is also a good source for phosphoric acid and calcium. Black gram is popular for its fermenting action and for making fermented foods. In India, the average productivity of black gram was 535 kg/ha, with a production of 1.75 million tonnes in 3.26 million hectares during 2010-11 (Gupta *et al.,* 2013). The major constraints in black gram genetic improvement are lack of exploitable genetic variability, absence of suitable ideotype for different cropping systems, poor harvest index, susceptibility to biotic and abiotic stresses and non-availability of quality seeds of improved varieties. It occurs due to repeated usage of few parents with high degree of relatedness in crossing programmes (Jayamani and Sathya, 2013). Evaluation of genetic diversity would promote efficient use of genetic variations in black gram breeding programmes (Ghafoor *et al*., 2001). D^2 statistic is a potent technique for measuring genetic divergence in plant breeding. The selection of genetically diverged parents is expected to throw superior and desirable segregants following crossing (Bhatt, 1973). Success of yield improvement in crops largely depends upon the magnitude and nature of genetic variability present in yield contributing traits (Johnson *et al*. 1955). Association analysis measures the mutual relationship between various plant characters and determines component characters on which selection can be based on improvement in the economically important characters (Hemalatha *et al.,* 2017).

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Hence, the present study was planned to investigate genetic divergence, genetic variability and correlation coefficients to identify superior black gram genotypes for future exploitation in breeding programmes.

MATERIALS AND METHODS

The present investigation involved in the study of genetic divergence in 104 black gram germplasm lines collected from National Bureau of Plant Genetic and Resources (NBPGR), New Delhi, Agricultural College and Research Institute, Madurai and Agricultural College and Research Institute, Killikulam. The field experiment was conducted at Department of Plant Breeding and Genetics in Agricultural College and Research Institute, Killikulam during 2017-18. The collected germplasm lines were sown in randomized block design (RBD) with two replications. Each genotype was planted in 3 meter row to accommodate 20 plants per row with a spacing of 30 x 10 cm. Observations were recorded on five randomly selected plants in each replication

for nine quantitative characters *viz.*, days to 50 % flowering, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per plant, hundred seed weight (g), pod length (cm) and single plant yield (g).

The genetic divergence was estimated using Mahalanobis D^2 statistic (Mahalanobis, 1936) and the genotypes were grouped into different clusters following Tocher's method as described by Rao (1952). The various genetic parameters *viz.,* Genotypic Coefficient of Variance (GCV), Phenotypic Coefficient of Variance (PCV), heritability (h^2) and Genetic Advance as percentage of Mean (GAM) were calculated by adopting the formulae given by Johnson *et al.* (1955). Genotypic correlation coefficient was calculated based on the formulae given by Al-Jibouri *et al.* (1958).

RESULTS AND DISCUSSION

Genetic divergence analysis separated the studied black gram 104 genotypes into eight clusters (Table 1 and Fig 1). Among the eight clusters, cluster I had maximum number of genotypes (87 No.), followed by cluster II (11 No.) and clusters *viz.,* III, I, V, VI, VII and VIII had one genotype each respectively. The intra and inter cluster D^2 values are presented in Table 2. The intra-cluster distance value ranged from 0.00 to 10.75. The maximum intra cluster D^2value was observed in cluster II (10.75) followed by cluster I (10.4). The inter cluster distance values ranged from 7.70 to 36.65. The maximum inter cluster D^2 value was observed in between clusters VI and VIII (36.65) followed by clusters VII and VIII (36.04) and clusters V and VIII (31.6) that indicated wide divergence among the genotypes of these clusters. From the studies, inter cluster distance was more than the intra cluster distances. Similar results were reported by Chauhan *et al*. (2008). Least value of inter-cluster D^2 value was observed in between clusters III and V (7.70) suggested that genotype in one cluster is close proximity with the genotype in the other cluster of pair. Hence, genotype from both clusters may not be useful in breeding programmes. This is in agreement with Konda *et al*. (2007).

The relative contribution of characters for genetic divergence in black gram is represented in Table 3. The maximum percentage of genetic divergence was contributed by number of pods per plant (38.27%) followed by single plant yield (16.08%), plant height (15.48%) and number of cluster per plant (14.30%). The cluster mean for the nine characters studied in black gram is given in Table 4. It revealed that cluster V with one genotype (VBG11018) had the lowest mean value for days to 50 % flowering and hence this genotype could be used as source for earliness. The highest mean value for plant height was recorded in cluster VII (52.3 cm). The highest mean values were recorded by the cluster VIII for number of clusters per plant (33.5); cluster VI for single plant yield (29.1 g); cluster VII for number of seeds per plant (7.80); cluster VII for number of primary branches per plant (6.60) and cluster V for hundred seed weight (5.70 g). Clusters *viz.,* V, VI and III recorded highest mean values for pod length (5.25 cm) and cluster VIII registered highest mean value for number of pods per plant

Table 1: Clustering pattern of studied genotypes in black gram.

Clusters	Number of genotypes	Genotypes
I	87	IC 343812, IC 343942, IC 343967, IC 436518, IC 436565, IC 436720, KKB 14009, KKB 14020, KKB 14038, KKM 1, KU 12668, KKB 14005, VBG 14003, IC 436811, VBN 4, IC 343856, IC 436508, IC 436524, IC 436560, IC 436597, IC 436606, IC 436774, KKB 14042, ADT 6, ADT 5, VBG 12042, VBG 12034, VBG 10027, VBG 11042, IC 343885, IC 436512, IC 436609, IC 436610, IC 436627, IC 436659, IC 436780, IC 436792, IC 436922, KKB 14004, KKB 140034, KKB 14002,KKB 14004,KKB 14044, KKB 14046,KKB 14051,VBG 10053, VBG 11040, ADT 3, IC 343936, IC 436604, IC 436612, IC 436753, IC 436910, KKB 14003, KKB 14033, KKB 14022, KKB 14001, KKB 14053, KKB 14052, VBG 10010, VBG 10024, IC 343939, IC 436517, IC 436535, IC 436536, IC 436545, IC 436762, KKB 14015, KKB 14041, KKB 14049, ABG 11030, IC 34394, IC 436869, IC 436547, IC 436621, IC 436626, IC 436635, IC 436652, IC 436656, IC 436758, IC 436882, KKB 14045, ABG 11032, VBG 12039, IC 36724, IC 281992 and ABG 11015.
II	11	IC 436811, KKB 14048, IC 436676, IC 436535, KKB 14043, IC 436852, IC 343943, IC 436869, KKB 14047, KU 11680 and IC 335331.
III	1	IC 282004
IV	1	IC 343962
V	1	VBG11018
VI	1	IC343962
VII	1	IC282002
VIII	1	IC43772

Source of origin of genotypes: National Bureau of Plant Genetic Resources (NBPGR), New Delhi, National Pulses Research Centre (NPRC), Vamban, Tamil Nadu Rice Research Institute (TRRI), Aduthurai and Agricultural College and Research Institute, Killikulam (AC&RI, Killikulam).

(5.15). Hence the genotypes present in the above said clusters would be utilized for hybridization programmes and that would result in getting transgressive segregants and exploiting genetic variation in future breeding programmes.

The success of any breeding programme depends largely on the extent of genetic variability present in base population. The variability parameters *viz*., GCV, PCV, heritability (h^2) and GAM for different characters are presented in Table 5. The highest genetic variation was observed in number of primary branches per plant (GCV 29.1% and PCV 32.9%); number of clusters per plant (GCV 36.8% and PCV 38.3%); number of pods per plant (GCV 37.2% and PCV 38.0%) and single plant yield (GCV 33.9% and PCV 35.4%). Moderate PCV (16.4%) and GCV (17.3%) were observed in plant height. Similar results of high GCV and PCV were recorded for number of primary branches per plant, number of pods per plant in black gram by Mehra *et al.* (2016). Moderate PCV and GCV values for plant height were reported by Priyanga *et al.* (2016). In the present study, high heritability estimates were observed for all the characters except pod length. High heritability was recorded for number of pods per plant (96.1%), number of clusters per plant (92.3%) single plant yield (91.1%) and plant height (89.7%). High GAM was recorded for number of pods per plant (75.2%) followed by number of clusters per plant (73.0%), single plant yield (67.0%), number of primary branches per plant (53.0%) and plant height (32.1%). In the present investigation high heritability coupled with high GAM was recorded for number of primary branches per plant, number of pods per plant, number of clusters per plant and single plant yield indicating that additive gene action is involved in the genetic control of these traits. It is in agreement with the findings of Veeramani *et al*. (2005) and Reddy *et al.* (2011).

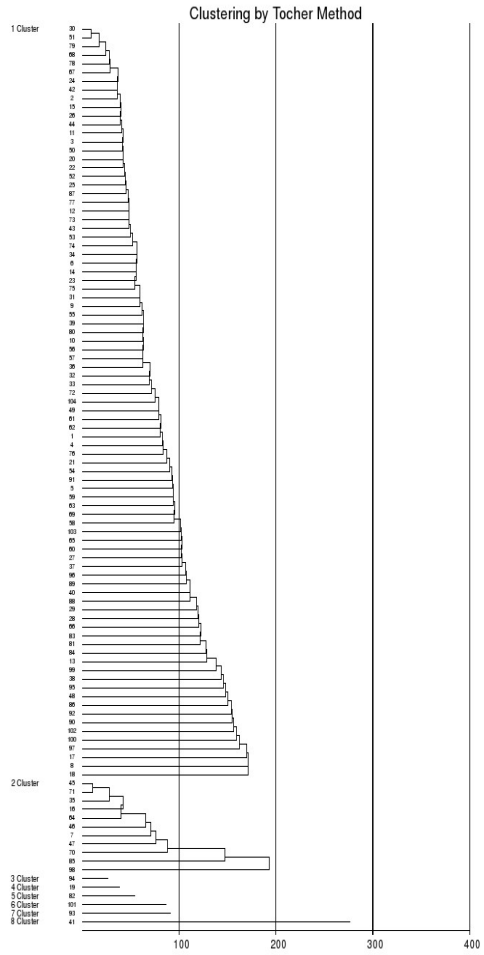


Fig 1: Clustering pattern of the studied genotypes in black gram by Tocher's method.

The genotypic correlation coefficient between different characters studied is presented in Table 6. From the intra correlation studies, seed yield per plant had significant and positive association with plant height (0.26) and number of primary branches per plant (0.16). Similar positive association of plant height with number of primary branches per plant was reported by Mehra *et al.* (2016) and Leninkumar *et al.* (2015). Days to 50% flowering had positive and significant association with pod length (0.349); plant height had positive and significant association with number of primary branches per plant (0.263); number of primary branches per plant had positive and significant association with number of seeds per pod (0.247) and number of clusters per plant had positive and significant association with number of pods per plant (0.665). Similar findings of association were reported by Rahim *et al.* (2010) and Zubair *et al.* (2007) in green gram.

It is, therefore, concluded that the genotypes belonging to different clusters having high means for desired characters and with maximum inter cluster distances (clusters *viz.,* VI & VIII; VII & VIII and V & VIII, respectively) could be successfully utilized in hybridization programmes. The traits

Table 2: Average intra (diagonal) and inter cluster (between) distance of black gram genotypes.

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**10.40**	15.36	13.74	13.48	15.71	20.95	16.96	24.86
II		**10.75**	18.52	23.20	21.67	24.58	23.83	22.03
III			**0**	13.36	7.700	9.750	9.670	30.93
IV				**0**	11.79	18.44	11.84	31.54
V					**0**	9.290	12.27	31.60
VI						**0**	14.25	36.65
VII							**0**	36.04
VIII								**0**

Table 3: Contribution of characters to genetic divergence in black gram.

Characters	Number of times ranked first	% contribution
Days to 50% flowering	265	4.95%
Plant height (cm)	829	15.48%
Number of primary branches per plant	236	4.41%
Number of clusters per plant	766	14.30%
Number of pods per plant	2050	38.27%
Number of seeds per pod	77	1.44%
100 seed weight (g)	233	4.35%
Pod length (cm)	39	0.73%
Single plant yield (g)	861	16.08%

Table 4: Cluster wise mean performance for different quantitative characters in black gram.

Traits / Cluster	Days to 50 % flowering	Plant height (cm)	Number of primary branches/plant	Number of clusters/ plant	Number of pods/ plant	Number of seeds/ pod	100 seed weight (g)	Pod length (cm)	Single plant yield (g)
I	36.5	38.3	3.53	10.0	27.9	6.26	4.65	4.66	10.1
II	37.7	39.1	4.45	14.3	52.1	6.39	4.62	4.60	11.8
III	34.5	44.0	6.45	8.80	26.4	6.20	4.74	5.25	19.8
IV	38.0	44.5	2.50	5.50	8.16	6.15	4.99	5.23	11.6
V	34.0	46.8	3.65	9.60	19.2	6.50	5.70	5.25	22.7
VI	37.0	46.4	5.60	8.40	25.2	6.00	4.53	5.25	29.1
VII	38.5	52.3	6.60	3.20	16.0	7.80	4.44	4.70	15.9
VIII	41.5	44.6	3.80	33.5	51.5	6.30	4.60	4.25	7.90
Mean	**37.2**	**44.5**	**4.57**	**11.6**	**28.3**	**6.45**	**4.78**	**4.89**	**16.1**

Table 5: Variability parameters in black gram.

Traits	GCV (%)	PCV (%)	Heritability (%)	GAM (%)
Days to 50 % flowering	7.43	8.37	78	13.6
Plant height	16.4	17.3	89	32.1
Number of primary branches per plant	29.1	32.9	78	53.0
Number of clusters per plant	36.8	38.3	92	73.0
Number of pods per cluster	37.2	38.0	96	75.2
Number of seeds per pod	7.45	10.0	55	11.3
100 seed weight	10.5	12.3	73	18.7
Pod length	6.57	9.91	44	8.98
Single plant yield	33.9	35.4	91	67.0

Table 6: Genotypic correlation coefficients in black gram.

Traits	Days to 50% flowering	Plant height	Number of primary branches per plant	Number of clusters per plant	Number of pods per plant	Number of seeds per pod	100 seed weight	Pod length	Single plant yield
Days to 50% flowering	**1.000**	0.019	-0.060	0.123	0.006	-0.022	0.143	0.349*	-0.020
Plant height		**1.000**	0.263*	0.035	0.013	0.167	0.071	-0.145	0.226*
Number of primary branches per plant			**1.000**	-0.108	0.147	0.247*	-0.226*	-0.086	0.316*
Number of clusters per plant				**1.000**	0.665 *	-0.084	-0.012	-0.177	0.047
Number of pods per plant					**1.000**	-0.004	-0.042	-0.253*	0.097
Number of seeds per plant						**1.000**	0.059	-0.039	-0.061
100 seed weight							**1.000**	0.006	0.116
Pod length								**1.000**	0.133
Single plant yield									**1.000**

*Significance at 5% level.

viz., plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant and single plant yield registered high heritability coupled with high GAM showed that the selection efficiency is high and it is due to the presence of additive gene action. Since the trait single plant yield had positive and significant association with plant height and number of primary branches per plant, selection of these traits would be more valuable to bring desired improvement in black gram breeding program.

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