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Research Article

Genetic divergence of black gram genotypes (*Vigna mungo* (L.) Hepper)

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Abstract

Divergence analysis was carried out among hundred black gram genotypes using Mahalanobis D^2 analysis. Among ten characters studied, seed yield per plant (g) contributes maximum to the genetic diversity (33.31%). Black gram genotypes were grouped into 14 clusters. Among this, cluster I had maximum number of genotypes. Maximum intra-cluster distance was found in cluster II and the maximum inter-cluster distance was observed between cluster IV and XI. Cluster XI (VBG 19-002) showed the highest cluster mean for seed yield per plant (g), the number of branches per plant and the total number of pods. Cluster IV (VBG 18-076) had superior mean for days to 50% flowering, plant height (cm) and pod length (cm). Hence, hybridization of genotypes VBG 18-076 (Cluster IV) and Mash 114 (Cluster XII) with VBG 19-002 (Cluster XI) could give wide range of variability in segregating population.

Keywords

Black gram, genetic diversity, intra and inter-cluster distance, cluster mean

INTRODUCTION

Black gram (*Vigna mungo* (L). Hepper), 2n = 22, belongs to the Fabaceae family, self pollinated and widely cultivated grain legume throughout India (Chandel *et al.,* 1984; Chatterjee and Bhattacharya, 1986; Manivannan *et al.,* 1999; Naga *et al.,* 2006; Shanthi *et al.,* 2006). It contributes about 12 per cent of total pulse production of the country (Vyas *et al.,* 2018). Black gram has high calorific value (350 cal/100g), carbohydrate (56.6%), protein (26.2%) and fat (1.2%) (Vyas *et al,* 2016). It is also rich in vitamins, minerals and phosphoric acid (Panigrahi and Baisakh, 2014). Due to short duration and ability to restore the soil fertility through symbiotic nitrogen fixation, it is being grown as rice fallow, catch crop and inter-crop. Though it has high production, but productivity level is very low (Vidya *et al.,* 2018), poor harvest index, lack of genetic variability, susceptible to biotic and abiotic stresses (Sarobol, 1997; Souframanien and Gopalakrishna, 2004; Srinives, 2006). Assessment of genetic diversity is essential for the planning an effective breeding programme (Reddy *et al.,* 2018). Crossing of genetically diverse parents exploits not only heterosis but also desirable transgressive segregants (Kumar *et al.,* 2014). Therefore, here an attempt has been made to assess genetic divergence among blackgram genotypes.

MATERIAL AND METHODS

One hundred black gram genotypes were evaluated at National Pulses Research Station, Vamban during *Kharif* 2019 in an Alpha-Lattice Design with two replications. All recommended package of practices was followed to raise a healthy crop. Observations were recorded on basis of five randomly selected plants for ten quantitative traits *viz.,* days to 50% flowering, plant height (cm), the number of branches per plant, the number of clusters per plant, the number of pods per cluster, the total number of pods, pod length (cm), the number of seeds per pod, 100-seed weight (g) and seed yield per plant (g). The analysis of divergence was carried out by Mahalanobis D^2 statistic (1936). Based on this, clustering was done using Tocher's method as suggested by Rao (1952). The statistical analyses were carried out using INDOSTAT software.

RESULTS AND DISCUSSION

A basic pre-requisite in multivariate analysis and grouping of genotypes is the presence of significant difference among the genotypes for multivariate traits. The analysis of multivariate indicated that all traits had significant differences and Wilk's criterion is also significant. The genetic divergence was studied by Mahalanobis D^2 analysis. Based on the analysis, 100 genotypes were grouped into 14 clusters by using Tocher's method (Table 1). Among these 14 clusters, cluster I was largest with 61 genotypes followed by cluster II with 27 genotypes. The clusters from III to XIV were solitary cluster consisting of only one genotype.

Table 1. Distribution of genotypes into clusters

Cluster Number	Number of Genotypes	Name of the Genotypes
I	61	ADT 3, ADT 5 , APK 1, CO 6, KKM 1, LBG 752, Mash 1008, PU 11-25, PU 14-28, SPS 5, TMV 1, TU 94-2, Vamban 1, Vamban 2, Vamban 3, VBN (Bg) 5, VBN 6, VBN (Bg)7, VBN 8, VBN 9, ACM BG 18-009, VBG 12-110, VBG 13-003, VBG 14-016, VBG 17-019, VBG 17-029, VBG 18-043, VBG 18-044, VBG 18-045, VBG 18-046, VBG 18-050, VBG 18-051, VBG 18-054, VBG 18-055, VBG 18-056, VBG 18-057, VBG 18-058, VBG 18-059, VBG 18-060, VBG 18-061, VBG 18-062, VBG 18-063, VBG 18-064, VBG 18-067, VBG 18-068, VBG 18-069, VBG 18-071, VBG 18-072, VBG 18-073, VBG 18-074, VBG 18-075, VBG 18-077, VBG 18-079, VBG 18-080, VBG 19-001, VBG 19-004, VBG 19-005, VBG 19-006, VBG 19-009, VBG 19-015, VBG 19-021
II	27	LBG 787, TU 68, SUG 1137, VBN (Bg) 4, VBN 10, ACM BG 14-001, ACM BG 16-017, VBG 17-012, VBG 17-026, VBG 18-040, VBG 18-041, VBG 18-042, VBG 18-047, VBG 18-048, VBG 18-070, VBG 19-003, VBG 19-007, VBG 19-008, VBG 19-011, VBG 19-012, VBG 19-013, VBG 19-014, VBG 19-016, VBG 19-017, VBG 19-018, VBG 19-019, VBG 19-020
III	1	VBG 17-007
IV	1	VBG 18-076
V	1	VBN 11
VI	1	VBG 18-065
VII	1	VBG 18-052
VIII	1	VBG 18-066
IX	1	CO 5
X	1	ADT 6
XI	1	VBG 19-002
XII	1	Mash 114
XIII	1	MDU 1
XIV	1	VBG 19-010

The average intra and inter-cluster distance (D) for various clusters was given in Table 2. Cluster II (6.23) had maximum intra-cluster distance followed by cluster I (5.65). Genotypes present within these clusters are more diverse than other clusters that had only one genotype. Maximum inter-cluster distance (16.51) was observed between cluster IV and XI followed by cluster XI and XII (13.96). The lowest inter-cluster distance was found between cluster III and VIII (4.45). Genotypes of clusters with high inter-cluster distance are more divergent. Hence, the hybridization between genotypes of these clusters may create more variability in segregating population. Based on the clustering pattern, VBG 18-076 (cluster IV) and Mash 114 (cluster XII) are divergent from VBG 19-002 (cluster XI). Hence, crossing between these genotypes will give a wide range of variability in segregating populations.

Mean performance of various clusters was presented in Table 3. Among clusters, the highest mean for seed yield per plant (8.55g) and the number of branches per plant (3.00) was observed in cluster XI. Genotypes present in cluster IV and VI (38 days) were early for days to 50% flowering followed by cluster VII (39 days). The genotype in cluster IV was dwarf (31.70cm) followed by cluster VI (32.50cm). Cluster IV had highest mean value of pod length (5.98cm). Cluster XI and XII had maximum number of pods (41.00) followed by cluster XIV (39.80). Cluster mean for 100-seed weight (g) ranged from 3.40 (cluster X) to 5.53 (cluster VII). The number of seeds per pod had highest cluster mean value of 7.50 was observed in cluster XIII followed by cluster V (7.20). The number of clusters per plant and the number of pods per cluster had maximum cluster mean in cluster XIV (18.50) and cluster XII (3.00) respectively. Hence, based on mean performance genotype of cluster XI (VBG 19-002) was useful to improve the seed yield per plant (g), the number of branches per plant and maximum number of pods whereas cluster IV (VBG 18-076) was useful to develop earliness, dwarf type plants with lengthy pod.

Table 2. Intra (diagonal) and inter-cluster distance (D) of black gram genotypes

Cluster Number	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	**5.65**	7.70	6.64	6.54	7.26	6.56	6.88	6.52	6.80	6.59	12.50	7.64	11.29	8.51
II		**6.23**	7.68	10.18	7.52	7.67	7.49	9.24	9.08	9.00	8.60	9.61	7.92	8.87
III			**0.00**	9.86	5.35	8.97	7.55	4.45	5.83	4.92	10.41	7.86	11.14	7.10
IV				**0.00**	9.77	7.67	7.29	8.67	7.38	8.61	16.51	9.03	13.94	10.64
V					**0.00**	9.95	7.68	5.71	8.25	6.55	10.08	10.57	9.10	9.89
VI						**0.00**	8.59	9.02	9.62	9.02	12.25	7.14	10.87	9.81
VII							**0.00**	8.82	7.72	9.70	12.37	10.01	10.74	9.38
VIII								**0.00**	6.96	4.59	12.80	8.82	13.21	9.51
IX									**0.00**	5.48	13.81	6.70	13.22	5.43
X										**0.00**	12.53	7.39	12.28	7.18
XI											**0.00**	13.96	7.02	11.95
XII												**0.00**	13.42	5.21
XIII													**0.00**	12.16
XIV														**0.00**

Table 3. Cluster Mean for Different Quantitative Traits in Black gram

Cluster No.	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)	No. of Seeds per Pod	100-Seed Weight (g)	Seed Yield per Plant (g)
I	39.99	41.22	1.32	9.44	2.33	22.67	5.25	6.47	4.30	3.73
II	41.30	49.51	2.07	11.82	2.50	30.94	5.47	6.72	4.55	5.86
III	43.50	59.70	1.50	11.40	2.00	27.60	4.52	6.40	4.23	4.17
IV	**38.00**	**31.70**	0.80	6.10	2.20	13.40	**5.98**	6.50	4.35	1.94
V	44.50	44.70	1.10	8.60	2.40	22.70	4.87	7.20	4.51	4.40
VI	**38.00**	32.50	1.40	11.10	2.60	30.40	5.39	6.00	4.09	5.43
VII	39.00	62.70	1.50	9.60	2.50	26.20	5.82	6.70	**5.53**	4.38
VIII	42.50	36.90	1.20	7.90	2.10	19.30	4.16	6.40	4.31	3.07
IX	43.00	56.30	1.85	11.40	1.88	23.10	5.49	6.35	3.95	2.03
X	41.50	38.90	1.30	10.00	1.80	18.80	4.55	6.80	3.40	2.44
XI	43.50	57.00	**3.00**	14.90	2.50	**41.00**	4.72	7.10	4.59	**8.55**
XII	40.50	50.80	1.70	17.60	**3.00**	**41.00**	5.33	6.00	3.61	3.42
XIII	43.00	45.30	1.60	13.70	2.30	31.70	5.89	**7.50**	4.66	7.89
XIV	41.00	64.40	2.50	**18.50**	2.60	39.80	5.44	6.60	3.88	3.29

The traits with highest mean values are indicated in **bold**, except for days to 50% flowering and plant height (cm)

Table 4. Contribution of different quantitative characters towards genetic divergence (D)

S. No.	Character	Times Ranked 1st	Contribution (%)
1.	Days to 50% flowering	332	6.71
2.	Plant height (cm)	167	3.37
3.	No. of branches per plant	863	17.43
4.	No. of clusters per plant	303	6.12
5.	No. of pods per cluster	118	2.38
6.	Total number of pods	68	1.37
7.	Pod length (cm)	595	12.02
8.	No. of seeds per pod	643	12.99
9.	100-seed weight (g)	212	4.28
10.	Seed yield per plant (g)	1649	33.31

Contribution towards genetic divergence was presented in Table 4. Among the ten characters, seed yield per plant (33.31%) was observed maximum contribution towards genetic divergence followed by the number of branches per plant (17.43%), the number of seeds per pod (12.99%) and pod length (12.02%) whereas the lowest contribution towards genetic divergence was observed for the total number of pods (1.37%). Similar findings were reported by Panigrahi and Baisakh (2014) and Vidya *et al.* (2018).

To conclude that selection of parents, based on seed yield per plant (g) will be effective as it contributed more to divergence. Cluster XI (VBG 19-002) can be used to improve seed yield per plant (g), the number of branches per plant and the total number of pods. Genotype VBG 18-076 is a desirable parent with earliness, dwarf plant height and long pods. Genotypes in cluster IV (VBG 18-076) and XI (VBG 19-002) had more genetic diversity followed by cluster XI (VBG 19-002) and XII (Mash 114). Hence, crossing between these genotypes will create more variability in segregating population which can be useful for improve the black gram.

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