

Genetic divergence studies in blackgram (*Vigna mungo* (L.) Hepper

V. Jayashree, A. Muthuswamy, P. Jayamani and K. K. Kumar



ISSN: 0975-928X

Volume: 10

Number: 2

EJPB (2019) 10(2):742-747

DOI:10.5958/0975-928X.2019.00097.8

<https://ejplantbreeding.org>



Research Article

Genetic divergence studies in blackgram (*Vigna mungo* (L.) Hepper

V. Jayashree^{1*}, A. Muthuswamy¹, P. Jayamani¹ and K. K. Kumar²

¹Department of Pulses, Centre for Plant Breeding and Genetics, TNAU, Coimbatore-03.

²Centre for Plant Molecular Biology and Bioinformatics, TNAU, Coimbatore-03.

*E-Mail: swami2k2002@yahoo.co.in

(Received: 07 May 2019; Revised: 29 May 2019; Accepted: 31 May 2019)

Abstract

Divergence analysis among fifty genotypes for yield and yield contributing traits was carried out by using mahalanobis D² statistics. The maximum intercluster distance was observed between cluster XI and XIII (16.03). The maximum intracluster distance was reported in cluster XII (9.75). Based on cluster mean performance and intercluster divergence, it was concluded that the genotypes from cluster XI and XII, cluster XI and XIII could produce desirable segregants through hybridization programme.

Keywords

Blackgram, D² analysis, Quantitative traits, Cluster analysis

Introduction

Blackgram (*Vigna mungo*) popularly known as urd bean or mash, is a grain legume domesticated from *Vigna mungo* var. *silvestris* (Lukoki *et al.*, 1980) it is one of the most ancient and important legume crop of India which contributes 70% of world's total production. It is grown over an area of around 3.26 million ha with annual production of 1.76 million tonnes. Urd bean occupies an important position due to its high seed protein (25-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins with additional ability to restore the soil fertility through symbiotic nitrogen fixation. The major constraints for achieving higher yield of this crop are lack of genetic variability, absence of suitable ideotypes for different cropping system, poor harvest index and susceptibility to biotic and abiotic diseases. It is mainly due to the repeated usage of few parents with high degree of relatedness in crossing programmes (Jayamani and Sathya, 2013). Yield improvement of pulse crop, highly depends upon the magnitude and nature of genetic variability present in the yield contributing characters (Johnson *et al.* 1955). The main objective of this study is to investigate the genetic diversity in blackgram accessions using multivariate techniques on the basis of biometrical traits, and to identify divergent genotypes for further breeding programme.

Materials and Method

In the present investigation 50 black gram genotypes collected from Ramiah Gene Bank, Department of Plant Genetic Resources, TNAU, Coimbatore were sown in RBD with two replications at Department of Pulses, Centre for Plant Breeding and Genetics, TNAU, Coimbatore

during *Rabi* season in the year 2018. Each genotype was sown in a row of 4m length to accommodate 40 plants per row with a spacing of 30 x 10 cm. Observations were recorded for 12 traits *viz.*, petiole length (cm), peduncle length (cm), plant height (cm), days to 50% flowering, number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pods, pod length (cm), 100 seed weight (g), and single plant yield (g). The genetic divergence was estimated using Mahalanobis' D² statistic (Mahalanobis 1936) and genotypes were grouped into various clusters and average intra and inter cluster distances were determined using GENRES version 3.1

Results and discussion

The study was conducted to assess the extent of genetic diversity and relationship among the 50 blackgram genotypes. The multivariate analysis (D²) is a powerful tool to measure the genetic divergence within a set of genotypes (Murthy and Arunachalam, 1996). On the basis of D² analysis, genotypes were grouped into thirteen clusters.

The cluster I was formed with sixteen genotypes followed by eight genotypes present in the cluster VII, 5 genotypes were formed in the cluster VIII, 3 genotypes in cluster VI and X, cluster XIII were mono genotypic and the remaining seven clusters were formed with two genotypes (Table 1). Among the characters studied, seed yield per plant showed maximum contribution (42.78%) for genetic divergence followed by days to fifty percent flowering (20.25%) (Table 2).

The average intra and inter cluster D^2 values were presented in the Table 3. From the inter cluster D^2 values of thirteen clusters, it was found that the highest divergence occurred between cluster XI and XIII (16.03), cluster II and XIII (15.64), cluster III and XIII (15.49), cluster V and XIII (15.35), cluster IV and XIII (15.28). The parents from these clusters can be used in the crossing program and based on the performance of the hybrids they can be either used in heterosis breeding or for development of good segregants.

Minimum inter cluster distance was observed between cluster III and V (4.78) followed by cluster II and III (5.24), cluster II and IV (5.62) and cluster II and XI (5.62). This indicated that genotypes of these clusters were not genetically much diverse. The maximum intra cluster distance was observed in cluster XII (9.75) and minimum intra cluster distance was observed in cluster II (3.50).

The inter cluster distance were greater than intra cluster distances, revealing that considerable amount of genetic diversity existed among the genotypes. Similar findings were earlier reported by Chauhan *et al.* (2008), Srimathy *et al.* (2012), Singh *et al.* (2011), Jayamani and Sathya (2013) and Kumar *et al.* (2014).

The clusters mean values for 12 characters are given in Table 4. Cluster XIII recorded maximum mean value for petiole length (13.59 cm), peduncle length (10.87 cm) and plant height (43.83 cm). For the traits, days to 50 per cent flowering (45.75 days) and number of primary branches (2.41), highest mean were observed in cluster IV (45.75 days and 2.41). Cluster VI was found to have highest mean value for number of clusters per plant (18.77). Cluster XII was found to be maximum for mean number of pods per plant (40.11). Cluster XI recorded highest mean value for number of seeds per pod (5.14). Maximum pod length was found in the cluster VI (5.83 cm). In case of shelling per cent, highest mean value was recorded in cluster IX (71.13%). Hundred seed weight was found to be maximum in cluster VI (5.90 g). In case of single plant yield maximum mean value was found in cluster XII (14.02 g). Based on the mean

performance and genetic divergence, it was concluded that the hybridization between cluster XI and XIII for petiole length (cm), peduncle length (cm), plant height (cm), Cluster XI and XII for number of pods per plant, single yield per plant (g) could be successfully utilized for breeding programmes to get desirable transgressive segregants.

References

- Chauhan, M. P., Mishra, A. C., and Singh, A. K. 2008. Genetic divergence studies in urd bean (*Vigna mungo* L.). *Legume Res* **31**(1): 63-67.
- Jayamani, P., and Sathya, M. 2013. Genetic diversity in pod characters of blackgram (*Vigna mungo* L. Hepper). *Legume Res.* **36**(3): 220-223.
- Johnson, H. W., Robinson, H. F., and Comstock, R. 1955. Estimates of genetic and environmental variability in soybeans 1. *Agronomy J.*, **47**(7): 314-318.
- Kumar, Y. L., Anuradha, C. H., Reddy, S. S., and Subbaiah, K. V. 2014. Genetic divergence and Variability Studies in Blackgram (*Vigna mungo* L. Hepper). *J. Agric Sci*, **5**(6): 1299-1303.
- Lukoki, L., Marechal, R., and Otoul, E. 1980. The wild ancestors of the cultivated beans *Vigna radiata* (L.) Wilczek and *V. mungo* (L.) Hepper. *Bull. Jard. Bot. Nat. Belg.* **50**(3/4): 385-391.
- Mahalanobis, P. C. 1936. On the generalized distance in statistics. *National Institute of Science of India.* 49-50.
- Murty, B. R., and Arunachalam, V. 1966. Nature of genetic diversity in relation to breeding system in some crop plants. *Indian J. Genet*, **26**, 188-198.
- Singh, P. B. D. P., and Khulbe, R. K. 2011. Genetic diversity, correlation coefficient, genetic advance and heritability analysis in black gram. *Crop Imp*, **38**, 1-67.
- Srimathy, M., Sathya, M., and Jayamani, P. 2012. Genetic diversity studies in blackgram [*Vigna mungo* (L.) Hepper]. *J. Food Leg*, **25**(4): 279-28.



Table1. Distribution of 50 blackgram genotypes into different clusters

Cluster number	Number of genotypes	Genotype name
I	16	P-3, P-20, P-30, P-33, P-37, P-38, P-47, P-64, P-69, TN Palayam, AC-43, AC-143, LU-134, LU-160, LU-162, Palladam
II	2	DU-3, PHM-7
III	2	JLU-5, CJM-2
IV	2	M-1, Jalagon
V	2	Nagpur, Uridujjam
VI	3	Kamuthi, CKM-2, LAM BG-226
VII	8	Guntur Local, Anaipiranthan-1, Trichy, Pant-U-19, Pant-U-26, M-2, Cudalore Local, LBG-402
VIII	5	M-4, NCB-P-6, NCB-P-7, KB-63, Krishna
IX	2	CJM-1, Masli-48
X	3	KCB-M-2, CKM-2, Mash (PDU-1)
XI	2	NM-5, Mangala
XII	2	LBG-17, Veppur Local
XIII	1	LAM BG-295



Table 2. Contribution of different characters towards genetic divergence in blackgram

Character	Contribution	
	No. of first rank	% contribution
Petiole length	13	1.06
Peduncle length	9	0.73
Plant height	59	4.82
Days to fifty percent flowering	248	20.25
Number of primary branches per plant	22	1.80
Number of clusters per plant	37	3.02
Number of pods per plant	26	2.12
Number of seeds per pod	24	1.96
Pod length	53	4.33
Shelling percentage	70	5.71
Hundred seed weight	140	11.43
Single plant yield	524	42.78
Total	1225	100



Table 3. Average inter and intra distances in blackgram genotype

Cluster	Average intra (diagonal) and intra- cluster distances												
	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	7.33	6.47	6.57	7.31	7.22	11.23	7.64	9.48	10.13	8.94	7.95	11.84	14.22
II		3.50	5.24	5.62	5.77	11.32	6.93	10.05	9.98	7.39	5.62	12.94	15.64
III			3.51	6.81	4.78	11.84	7.98	9.96	11.28	8.33	8.08	12.98	15.49
IV				3.84	5.87	10.28	6.51	9.87	10.43	8.52	7.16	11.71	15.28
V					4.25	12.09	7.77	9.85	11.06	9.37	8.47	11.59	15.35
VI						8.18	10.24	10.27	7.95	10.00	11.79	14.13	11.54
VII							7.43	9.30	9.36	9.36	7.55	11.17	13.51
VIII								9.13	8.86	10.71	11.13	10.96	9.87
XI									6.42	9.89	10.44	12.71	9.77
X										9.04	9.28	14.56	15.12
XI											8.28	13.16	16.03
XII												9.75	12.97
XIII													0.00



Table 4. Cluster means for 12 characters

Cluster no	Petiole length	Peduncle length	Plant height	Days to 50% flowering	Number of primary branches per plant	Number of clusters per plant	Number of pods per plant	Number of seeds per pod	Pod length	Shelling percentage	100 seed weight	Seed yield per plant
Cluster 1	9.32	8.06	33.18	43.69	1.53	9.98	23.42	4.57	5.37	58.73	5.17	6.35
Cluster 2	8.06	7.88	29.84	43.75	1.48	8.62	25.25	4.76	4.93	65.22	5.13	4.71
Cluster 3	9.60	7.69	29.50	44.25	1.78	9.83	25.50	4.16	4.80	54.42	4.69	4.81
Cluster 4	9.70	9.74	34.42	45.75	2.41	14.59	27.84	4.67	4.89	64.92	5.64	6.60
Cluster 5	10.92	9.28	32.50	45.25	1.78	11.64	25.67	4.31	4.28	63.19	4.68	5.49
Cluster 6	9.08	7.71	35.00	37.67	1.82	18.77	30.19	4.50	5.83	63.99	5.90	6.60
Cluster 7	9.70	8.70	37.74	44.06	1.91	13.25	30.89	4.92	5.58	64.34	5.60	6.98
Cluster 8	11.04	9.41	36.03	39.60	1.71	10.93	28.42	4.59	4.98	57.36	5.33	8.33
Cluster 9	9.04	7.62	39.98	37.00	1.21	11.86	20.73	4.72	5.21	71.13	5.54	6.00
Cluster 10	7.39	6.63	23.24	39.67	1.31	10.36	20.26	4.32	5.12	61.59	5.32	5.27
Cluster 11	8.04	7.19	36.08	45.00	1.71	10.24	29.58	5.14	5.77	69.11	5.70	5.37
Cluster 12	11.38	8.20	41.06	44.75	1.50	15.50	40.11	4.60	5.59	66.81	5.73	14.02
Cluster 13	13.59	10.87	43.83	34.00	1.70	12.15	36.67	5.06	5.36	53.79	5.55	9.80

