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

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ABSTRACT

Divergence analysis of 46 genotypes including 20 genotypes of blackgram and 26 accessions of *V. mungo var. silvestris*, a wild progenitor species for eleven biometrical traits was carried out using Mahalanobis D^2 statistics. The genotypes were grouped into twelve clusters. The cluster I was the largest with 25 accessions of *V. mungo var. silvestris* while, other clusters consisted of two cultivated genotypes. Cluster XII had only one accession *viz., V. mungo. var. silvestris* acc 10. This study showed clear grouping of *V. mungo var. silvestris* accessions from the cultivated blackgram (*V. mungo*) genotypes. Cluster XI recorded the maximum intra cluster distance of 12.58 followed by cluster X with a distance of 11.39. The highest inter cluster distance was found between cluster IX and cluster XII (28.71) followed by cluster XI and XII (23.79) and cluster V and XII (23.30). Based on cluster mean and divergence, it was concluded that the hybridization between accessions of *V. mungo var. silvestris* in clusters I and XII and cultivated genotypes in the other clusters could produce desirable recombinants for plant type, important economic traits and grain yield.

Key words: Blackgram, Cluster analysis, D^2 analysis, Genetic divergence, *V.mungo var. silvestris*

Blackgram (*Vigna mungo* (L.) Hepper) popularly known as urdbean or mash, is a grain legume domesticated from *V. mungo var silvestris* (Chandel, 1984). This wild progenitor is resistant to bruchid infestation and also tolerant against abiotic stresses. Blackgram is a rich source of protein (20.8 to 30.5 per cent) with total carbohydrates ranging from 56.5 to 63.7 per cent. It is also a good source of phosphoric acid and calcium. India is the largest producer and consumer of blackgram in the world. It is the fourth important pulse crop in India, cultivated as a sole crop and intercrop covering an area of about 3.24 million hectares and producing 1.46 million tons. However, the productivity is very low with 526 kg/ha (Anonymous, 2010). Many breeding efforts have been carried out to improve the yield level of this crop and to break the yield plateau, but it could not be done because of narrow genetic base of parents used in hybridization.

Genetic diversity is an important factor and also a prerequisite in any hybridization programme. Inclusion of diverse parents in hybridization programme serves the purpose of producing desirable recombinants. Multivariate analysis by means of Mahalanobis D^2 statistic is a powerful tool in quantifying the degree of divergence at genotypic level. Therefore, an attempt has been made in the present investigation with a view to estimate genetic divergence among a set of 46 genotypes including cultivated genotypes of blackgram and its wild progenitor accessions for eleven biometrical traits.

MATERIALS AND METHODS

Forty six genotypes of cultivated blackgram and its wild progenitor, collected two decades ago, were evaluated at Department of Pulses, Tamil Nadu Agricultural University, Coimbatore in a randomized block design (RBD) with two replications. Each genotype was sown in paired rows of four meter length with a spacing of 30 x 10 cm. Recommended package of practices were followed to raise a healthy crop. Five randomly taken plants were considered to record data for days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g) and yield per plant (g). The mean values of five plants were taken for the analysis of genetic divergence following Mahalanobis (1936). The genotypes were grouped into different clusters following Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

Genetic diversity is the basic requirement for successful breeding programme. Collection and evaluation of germplasm lines and genotypes of any crop is a pre-requisite for any programme, which provides a greater scope for exploiting genetic diversity. The multivariate analysis (D^2) is a powerful tool to measure the genetic divergence within a set of genotypes (Murthy and Arunachalam, 1966). The present study was planned to examine the trend of genetic divergence in 20 genotypes of cultivated blackgram and 26 accessions of *V.mungo var. silvestris*, a wild progenitor species. The genotypes were grouped into twelve clusters indicating large amount of genetic diversity among the genotypes (Table 1). Elangaimannan *et al.* (2008) also reported grouping of 55 blackgram genotypes into seven clusters, where cluster I was the largest (34 genotypes) followed by clusters IV (eight genotypes), II (six genotypes), V (four genotypes), while rest of the clusters had one genotype each. Grouping of accessions by multivariate method in the present study is of practical

value to the breeders. Representative accessions may be chosen from particular cluster for hybridization programme.

In the present study, cluster I was the largest with 25 accessions of *V. mungo var silvestris* while, other clusters consisted of two genotypes each except cluster XII which had only one accession *viz.*, *V. mungo var silvestris* acc. 10. High level of variability was observed for several morphological and biometrical traits among the accessions of *V. mungo var silvestris* in cluster I. Even though all the accessions of *V. mungo var silvestris* formed a single cluster, a good level of variability was also observed in the mean values of different traits. Similar kind of separate grouping of cultivated genotypes and *V. mungo var silvestris* accessions was observed in a dendrogram based on SSR analysis (data not shown). Contribution of various biometrical characters towards genetic divergence is presented in Table 3. Among the characters studied, yield per plant contributed maximum towards divergence, followed by number of pods per cluster, 100 seed weight and days to 50 per cent flowering. Similar results were also reported earlier by Ghafoor and Ahmed (2005), Konda *et al.* (2007), Shanthi *et al.* (2006). Plant height and number of branches per plant contributed minimum to the genetic divergence leading to the inference that in general, the variability for these characters are low in blackgram genotypes used in this study.

The intra and inter cluster D^2 values among the clusters are presented in the Table 2. Cluster XI recorded the maximum intra cluster distance of 12.58 followed by cluster X with a distance of 11.39. There was one solitary cluster (cluster XII) possessing no intra cluster value. This accession had smaller seed size and found to be resistant to bruchid infestation. The highest inter cluster distance was found between cluster IX and cluster XII (28.71) followed by cluster XI and XII (23.79), cluster VII and XII (23.35) and cluster V and XII (23.30). The inter cluster distance of all other clusters with cluster XII showed higher values when compared to the inter cluster distance between other clusters. The least inter cluster distance was found between cluster II and IV (6.19).

The mean values of 11 characters for twelve clusters are presented in the Table 3. Cluster IV recorded the highest mean value (38.00) for days to 50 % flowering followed by cluster XII (37.50) and clusters VII and X (37.00), whereas cluster XI recorded the lowest mean value for days to 50 % flowering (31.50). Cluster IV recorded the highest mean value for days to maturity (68.00) followed by cluster XII (67.50) and clusters VII and X (67.00), while Cluster XI recorded the minimum days to maturity (61).

Cluster IV recorded the maximum plant height of 30.88 cm followed by cluster XII (29.77 cm), while cluster XI recorded the minimum plant height of 20.22 cm. The highest mean value for number of branches per plant was recorded by cluster VI and XII (1.84) and the lowest was recorded by cluster XI (1.42). The highest mean for number of clusters per plant was recorded by cluster V (13.00) followed by cluster VII (12.00)

Table 1. Constitution of D^2 clusters of 46 genotypes of blackgram

Cluster number	Number of genotypes	Name of the genotype
I	25	*Vigna mungo var. silvestris* acc 1, acc 2, acc 3, acc 4, acc 5, acc 6, acc 7, acc 8, acc 9, acc 11, acc 12, acc 13, acc 14, acc 15, acc 16, acc 17, acc 18, acc 19, acc 20, acc 21, acc 22, acc 23, acc 24, acc 25, acc 26,
II	2	AC-305, PLS-44
III	2	Cotton leaf – 32, K 951
IV	2	P-169, Co 5
V	2	P-226, PLS 364/92
VI	2	P-123, T9
VII	2	P-153, VBN (Bg) 4
VIII	2	P-307/1-1/, VBN 3
IX	2	P-202, Co-02/103
X	2	AC-43, VBN (Bg) 5
XI	2	P 133/13, CoBG 653
XII	1	*V. mungo var. silvestris* acc 10

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

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**8.95**	12.86	11.18	12.18	14.86	10.24	15.45	11.56	17.53	12.71	11.90	17.71
II		**3.21**	6.31	6.19	9.85	9.49	6.87	6.23	9.21	9.44	12.33	23.16
III			**4.24**	6.98	8.42	7.97	9.37	6.99	11.55	7.75	11.69	20.63
IV				**4.35**	9.49	9.31	6.63	8.63	10.79	8.42	13.58	20.16
V					**4.82**	10.55	8.27	9.83	10.45	11.68	12.67	23.30
VI						**5.73**	12.04	8.59	11.60	10.04	9.36	22.77
VII							**5.81**	9.38	9.19	11.73	14.62	23.35
VIII								**8.16**	10.86	10.17	10.67	22.88
IX									**9.94**	13.80	14.31	28.71
X										**11.39**	14.60	21.42
XI											**12.58**	23.79
XII												0.00

Table 3. Cluster mean values for 11 biometrical characters in blackgram

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches/ plant	Number of clusters/ plant	Number of pods/ cluster	Number of pods/ plant	Pod length (cm)	Number of seeds/pod	100 seed weight (g)	Single plant yield (g)
I	34.16	63.96	27.47	1.62	7.72	4.51	34.99	4.04	5.66	3.96	6.88
II	36.25	66.25	23.33	1.42	8.50	3.46	29.50	4.86	6.00	5.13	5.16
III	35.50	65.50	23.00	1.67	6.42	2.84	18.77	4.64	5.78	4.68	5.92
IV	38.00	68.00	30.88	1.58	9.50	3.59	34.52	4.44	5.98	4.80	6.71
V	34.25	64.25	22.43	1.67	13.00	2.59	28.67	4.58	5.88	4.90	8.53
VI	34.50	64.50	29.20	1.84	8.50	4.22	36.50	4.54	6.10	4.88	8.91
VII	37.00	67.00	29.67	1.67	12.00	2.90	34.50	4.54	6.08	5.18	6.09
VIII	34.00	64.00	26.96	1.57	8.84	3.70	26.00	4.46	5.78	4.98	5.51
IX	35.75	65.75	23.58	1.83	11.50	3.35	39.50	4.72	5.80	5.80	8.14
X	37.00	67.00	27.71	1.59	8.09	4.21	23.25	4.55	5.85	4.75	7.24
XI	31.50	61.50	20.22	1.42	10.67	4.14	41.80	4.59	5.63	4.58	8.43
XII	37.50	67.50	29.77	1.84	5.73	2.50	26.00	3.15	5.30	2.00	4.32
Contribution of traits toward divergence	4.54	0.39	0.10	0.19	1.06	17.10	5.80	0.48	0.68	17.29	52.37

and maximum mean of number of pods per cluster was recorded by cluster I (4.51) while, the lowest mean for number of pods per cluster was recorded by cluster XII (2.50). The highest mean value for number of pods per plant was recorded by cluster XI (41.80) and cluster III recorded the lowest mean (18.77).

Cluster II recorded the maximum mean value for pod length (4.86 cm) followed by cluster IX (4.72 cm) and the lowest pod length was recorded by cluster XII (3.15 cm). Cluster VI recorded the maximum value for number of seeds per pod (6.10) followed by cluster VII (6.08) while, cluster XII recorded the lowest mean value for number of seeds per pod (5.30). Cluster IX recorded the maximum hundred seed weight (5.80 g) and cluster VI recorded maximum single plant yield (8.91 g) while, Cluster XII recorded lowest mean value for hundred seed weight (2.0 g) and single plant yield (4.32 g). The accession *V. mungo var silvestris* acc 10 recorded lowest mean value for most of the traits *viz*., number of clusters/plant, number of pods/cluster, pod length, 100 seed weight and yield/plant. The uniqueness of the accession could be the reason for the formation of separate cluster XII, when compared to all other accessions of *V. mungo var silvestris* in the cluster I.

From the present investigation, it was concluded that blackgram displayed a wide range of diversity for few traits and there were few accessions with unique characters. *Vigna mungo var silvestris* accessions were distinctly separated from the other blackgram genotypes. Hence, the accessions of *V. mungo var silvestris* can be used in inter sub-specific hybridization program to transfer genes for resistance to biotic and tolerance to abiotic stresses, improved plant type and also to broaden the genetic base in blackgram.

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