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Assessment of Genetic Divergence in Blackgram (*Vigna mungo* (L.) Hepper) Genotypes

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ABSTRACT: *Blackgram (*Vigna mungo *(L.) Hepper) commonly known as urdbean in India, is a self-pollinating diploid crop with a rich source of protein and carbohydrate. Blackgram germplsm accessions (144) were evaluated for genetic diversity which grouped into eight clusters depending upon their divergence following Mahalanobis' D^2 statistics. The cluster II had more number of genotypes (71), followed by cluster I with forty nine genotypes, cluster IV with thirteen genotypes, cluster VIII with two genotypes and remaining clusters were solitary in nature. The maximum intra cluster distance was observed in cluster IV followed by cluster I indicating the higher genetic diversity exists among the genotypes of these clusters. The inter cluster distance was high between the clusters VIII and II indicating the larger variation among these clusters. The cluster means for six characters revealed that pods/plant recorded highest mean value in cluster VIII, for seeds per pod was recorded by cluster VI and for pod length by cluster III. Pods per plant (42.5%) followed by plant height (27.5%) and pod length (10.5%) contributed maximum towards genetic diversity. Based on the cluster means and inter-cluster distance promising genotypes were selected for the hybridization programme for further improvement of blackgram .*

Key words: *Blackgram, Germplasm, Diversity, Cluster distance.*

INTRODUCTION

Blackgram (*Vigna mungo* (L.) Hepper) is an important grain legume crop which occupies unique position in Indian agriculture and besides forming a sustainable component of Indian agriculture. It is a major source of vegetable protein to large masses of the country, who are basically vegetarian in their food habit. Blackgram, commonly known as urdbean is a cheap source of dietary protein (24%), carbohydrate (67%), fibre(3-5%) fat 1.74% and lysine in the human diet (1).

The productivity of pulse crop is very low when compared to cereals, which have been selected for high grain yield under high input conditions, while the selection pressure in case of pulses have been focused on the adaptation to both biotic and abiotic stresses. Hence, a large part of the genetic variability for yield contributing characters was lost during the course of evolution. Therefore, for increasing the productivity of pulses, collection and characterization of germplasm from different regions of cultivation need specific emphasis (2). The concept of genetic distance is very important while differentiating well defined population. Several measures of genetic distances have been proposed over the past two decades to suit various objectives in which Mahalanobis generalized distance occupied a unique place, several plant breeders used this technique of D^2 for selection of divergent parents and their further exploitation in hybridization programmes which helps breeders in genetic interpretation of the material under investigation. In the present study, attempt has been made to utilize this useful technique D^2 statistic to know the genetic diversity among the genotypes of blackgram.

MATERIALS AND METHODS

The present study was conducted in *kharif,* 2011, at college of agriculture, Dharwad to know the divergence among the different genotypes of blackgram based on the morphological traits. The genotypes of blackgram were sown in two rows of 4 m with inter and intra spacing of 30 cm and 10 cm, respectively. All standard agronomic practices were followed to raise a good crop. At the time of harvest,

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observations were recorded on 5 randomly selected plants for plant height (cm), number of branches/ plant, number of pods/plant, seeds/pod, pod length (cm), and 100-Seed Weight (g). The estimates of diversity study were done through Mahalanobis (1936) D^2 analysis. Clustering of genotypes was done following the Tocher's method as described by Rao (3).

RESULTS AND DISCUSSION

On the basis of D^2 analysis 144 genotypes of blackgram were grouped into eight clusters indicating large amount of variation exist among the genotypes studied. Cluster II was found to be the largest with 71 genotypes collected from diversified source, followed by clusters, I, IV and VIII with 49, 13 and 2 respectively. The remaining clusters were solitary in nature, from the cluster grouping it was noticed that there was no direct relationship of genotypes collected from different sources and their genetic origin and can be used for hybridization and selection these results are similar with the findings of Elangaimannan (1) and Srimathy (2). Murthy and Arunachalam (4) reported that geodistribution and genetic diversity as estimated by D^2 statistics need not be directly related. Our findings confirmed this view and similar observations were also made by konda *et al.,*(5) and Srimathy *et al.*, (2).

It was reported that intercrossing parents selected from the same geographic origin which are genetically divergent among themselves are desirable than choosing parents from other regions because of their better adaptation (1, 2). Accordingly, the strains of same origin falling under different clusters have been used in breeding programme for hybridization programme for selecting the lines with high yielding, disease resistant and high protein content.

The D^2 values were ranging from 23.86 to 151.62 (Table 1), intra D^2 value were higher than the inter D^2 values indicating larger variation among the material studied. The highest intra cluster value was observed in cluster IV followed by cluster I. The inter cluster distance was high between the clusters VIII and II followed by the cluster VI and II, VI and III, VII and VI and IV and II indicating the larger variation among the genotypes belonging to these clusters.

On the contrary the lowest inter cluster distance was observed between the clusters VII and I revealing that genotypes belonging to these clusters are very close to each other, hence inter cluster distance helps in selecting the diverse genotypes for hybridization and isolation of superior segregants. The above results are well supported by the findings of Srimathy *et al.*, (2) and Konda *et al.*, (5). It was also suggested that the importance of identifying "stable-diverse varieties" which would provide best breeding material from the stand point of achieving the maximum genetic advance with regard to yield per se provided other factors do not operate to limit the realization of this potential (2, 6).

It was observed that cluster VIII was recorded highest mean values for number of pods per plant and 100 seed weight (Table 2). Cluster III was recorded highest mean values for pod length and number of seeds per pod where as cluster II recorded highest mean value for number of branches per plant.. Cluster VII recorded highest mean value for plant height. Based on these results, the hybridization between the genotypes belonging to clusters showing maximum divergence and complimentary traits of interest will lead to accumulation of genes in a single variety. The genotypes selected for hybridization are diverse and at the same time show complementary for the traits of interest (5). Among the traits studied pods per plant contributed more towards the divergence followed by plant height hence these characters should be considered while choosing the genotypes for hybridization for further improvement.

Table 1
Average intra - and inter-cluster distances in different blackgram accessions

Clusters	*Group 1*	*Group 2*	*Group 3*	*Group 4*	*Group 5*	*Group 6*	*Group 7*	*Group 8*
I	**31.59**	55.59	51.14	59.51	42.2	94.70	39.89	107.08
II		**23.86**	46.35	101.12	68.40	137.47	62.39	151.62
III			**25.00**	89.10	76.91	131.48	57.75	133.90
IV				**37.15**	54.32	54.37	69.20	62.23
V					**0**	73.74	59.26	98.71
VI						**0**	104.97	45.11
VII							**0**	119.08
VIII								**0**

Table 2
Cluster means and per cent contribution of different characters in blackgram

Clusters	*Plant height (cm)*	*Number of branches per plant*	*Number of pods per plant*	*Pod length (cm)*	*No.of seeds*	*100 seed weight (gm)*
I	46.50	2.95	36.28	5.44	7.20	4.21
II	32.27	3.89	29.87	5.19	6.61	4.31
III	51.67	3.67	62.83	6.57	8.17	4.13
IV	48.54	3.69	45.15	5.27	7.08	4.41
V	22.00	2.00	18.00	5.10	6.00	4.02
VI	34.00	3.00	28.00	6.50	9.00	4.57
VII	76.00	2.00	22.00	5.10	8.00	4.07
VIII	45.00	3.00	71.00	5.50	8.00	4.74
Percent contribution(%)	27.5	7.5	42.5	10.5	9.0	3.0

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