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GENETIC DIVERSITY FOR YIELD AND ITS COMPONENTS IN BLACKGRAM

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ABSTRACT

Multivariate analysis by D^2 statistic is a powerful tool in quantifying the degree of divergence among all possible pairs of population at genotypic level. The availability of genetically diverse germplasm is the basic need for the progress in plant breeding. Choice of parents for hybridization is one of the important considerations for creating new variability. Several biometrical approaches have been shown to be useful in selecting parents for successful hybridization programmes. D^2 analysis has been found most effective and, therefore, widely used for the classification of parental lines. The present study was therefore, undertaken to estimate the amount of genetic diversity in twenty five genotypes of black gram (Vigna mungo L.) and to identify genetic diverse parents for hybridization programme aimed at yield improvement in this crop. Twenty five genotypes of blackgram (Vigna mungo (L.) comprising released varieties and landraces were analysed during rabi 2015 for genetic diversity using Mahalanobis D^2 stastistic based on six characters. The genotypes were grouped into 6 clusters. Group IV had maximum number of genotypes (6) followed by III and V with 5 genotypes each. Maximum intercluster divergence was found between V and VI. The intercluster distances were greater than intra cluster distances revealing that considerable amount of genetic diversity existed among the accessions. Pods per plant, days to 50% flowering and branches per plant were major traits causing genetic divergence among accessions. Cluster IV has more number of pods per plant and has more number of days to 50% flowering. Cluster I has highest plant height, more number

of branches per plant and more number of pods per plant. The genotypes belong to cluster V and VI has highest intercluster distance and can be used for hybridization programme.

INTRODUCTION :

Blackgram (*Vigna mungo* L.Hepper, 2n=22) is one of the nutritious pulse crop. Popularly known as urdbean. It is important short duration pulse crop and self pollinated grain legume grown in many parts of India. This crop is grown in cropping systems as mixed crop, catch crop, sequential crop besides growing as sole crop under residual moisture conditions after the harvest of rice and also before and after the harvest of other summer crops under semi irrigated and dryland conditions. Its seeds are highly nutritious with protein (25-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins. Like other pulses it also enriches the soil fertility, improves the soil structure and used as green fodder for cattle. Blackgram is one of the important pulse crops of India contributing 12 per cent of the total pulse production of the country.Inspite of its importance, the productivity of the crop is relatively low. The development of new varieties depends largely on the availability of genetic variability in the base material and the extend of variability for the desired character. The information about the nature and magnitude of genetic divergence is essential for selection of diverse parents which upon hybridization lead to a wide spectrum of recombinations. Mahalanobis's D^2 statistics is very sensitive tool for measuring genetic divergence based on quantitative traits and also widely used by many breeders for section of divergent parents for hybridization programme. The importance of genetic diversity of parents in hybridization programme has been much emphasized (Joshi and Dhawan,1960 and Murthy and Arunachalam,1966). Genetically diverse parents are likely to produce not only high heterotic effect but also desirable segregants. Therefore , the present investigation to study the genetic divergence in blackgram is to suggest suitable genotypes for use in future breeding programme.

MATERIALS AND METHODS

The material under investigation consisted of twenty five genotypes of blackgram (*Vigna mungo* L.Hepper) were grown in *Rabi* 2014-15 and evaluated in a randomized block design with three replications at Regional Agricultural Research Station, Lam, Guntur , Andhrapradesh. The spacing adopted between rows was 30cm and 10cm within the row. About 1-2 seeds per hill

were sown and later, thinned out to a single seedling per hill. All the recommended package of practices were followed for raising healthy crop. Five plants were tagged randomly for recording observations in each replication for the characters , plant height, days to 50% flowering, number of branches per plant, number of pods per plant, hundred seed weight and seed yield per hectare were used for stastistical analysis. Mahalanobis's D^2 (Mahalanobis,1936) statistics and grouped into different clusters following Tocher's method as described by Rao (1952).Average intra and inter cluster distances were determined Using GENRES version 3.11,1994 Pascal Intl. Software as suggested by Singh and Chaudhary (1977).

RESULTS AND DISCUS SIONS

The analysis of variance for randomized block design revealed highly significant differences among accessions for all the characters under investigation thereby indicating the presence of a presence of a considerable magnitude of genetic variability among 25 accessions of blackgram for these characters (Table-1)

The multivariate analysis giving the D^2 values between 25 accessions, all these entries can be grouped into six clusters (Table-2). On the basis of divergence 25 genotypes under investigation have been grouped into six distinct clusters (Table 2), indicating wide diversity in the experimental materials for majority of the characters. Distance between all pairs of genotypes was calculated using squared Euclidean distance method and the genotypes were clustered based on Tocher's method. Cluster IV had maximum 6 genotypes (6) followed by cluster III and V1 which has 5 each, followed by cluster II which has 4 genotypes followed by cluster I which has 3 genotypes and cluster VI has digenotypic. The pattern of clustering proved the existences of significant amount of variability. It is obvious that the genotypes have grouped into different cluster irrespective of their geographical origins. It means that the genetic constitution of the varieties was more important than their origin and origin and distribution (Rai et al., 2009). The divergence within the cluster indicates the divergence among the genotypes in the same cluster. On the other hand inter cluster divergence suggests the distance (divergence) between the genotypes of different 2 clusters. Inter and intra cluster D^2 values were worked out from divergence analysis. Critical assessment of clusters showed that clusters were heterogeneous within themselves and between each other based on major character relation.

The lower D^2 value between their characters suggested that the genetic constituents of these genotypes in one cluster were in close proximity with those genotypes in other cluster. Similar result was reported earlier by Gadakh *et.al.*(2013).

The composition of cluster and values of inter and intra cluster distances are given in Table 3 and Fig.1. The inter cluster distance were greater than the intra cluster distance revealing that significant amount of diversity existed among the accession. The intra cluster distance ranged from 0.000 to 14.343 and the inter cluster distance ranged from 10.145 to 113.676 indicating that the land races were divergent (Table 3). The minimum intra cluster distance was recorded in cluster I (4.705) followed by cluster II (10.210). Cluster V had highest (14.343) intra cluster distance. The genotypes within the cluster were less divergent. The maximum inter cluster distance was observed between cluster V and VI (113.676) followed by cluster III and V (86.881). The inter cluster distance between cluster VI with rest of the cluster were more, suggesting that the land race LBG 752 belonging to this cluster may be used as a parent for further hybridization programme to develop desirable type because divergent parents results in transgressive segregants. Least inter cluster distance was recorded between cluster I and IV(10.145) followed by clusters I and II (19.536).

The cluster mean values were estimated over genotypes for 6 yield attributing characters in black gram related to yield, which revealed that a wide range of variation (Table 4). Minimum days to 50% flowering was observed in genotype of cluster V followed by cluster I. A maximum day to 50% flowering was recorded in cluster IV. Highest mean value for plant height was recorded with cluster I. Cluster VI had lowest mean value for plant height. Number of primary branches plant was was more with the genotypes of cluster I. The maximum number of pods per plant was observed in cluster IV followed by cluster I. The maximum 100 seed weight was observed in cluster V and yield were more in genotypes of recorded in cluster I. The characters contributing maximum divergence needs greater emphasis for deciding on the clusters for the purpose of selection of parents in the respective cluster for hybridization. The number of times each of the yield component characters appeared first in rank and its respective percent contribution towards genetic divergence was presented in Table 5. Among the yield attributing traits the maximum contribution towards divergence was made by pods per plant (63%) followed by yield (17.33%) and days to 50% flowering (10.33%). Genotypes belonging to different

clusters having high means for desired characters and with maximum divergence may be successfully used in hybridization programmes.

Promising genotypes from each cluster for specific traits which can be further utilized in breeding programme are presented in Table 5. From the above study it can be concluded the diversity in blackgram genotypes for yield and yield attributing characters may be due to early maturity, number of cluster/plant, pod/plant, seed/pod, pod length and 100 seed weight results are similar with the reports of Pariya *et al.*, 1997, Singh et al. 2012 and Ali et al. 2008. The pattern of distribution of genotypes into various clusters indicates that geographical diversity having no parallelism with clustering pattern which was in agreement with earlier reports in black gram (Ganesh Ram *et al.* 1997; Sagar. *et al.* 2001). The genotypes belonging to different clusters having maximum divergence can be successfully utilized in hybridization programmes to get desirable transgressive segregants. It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters (Panigrahi *et al*. 2014). However, for a practical plant breeder, the objective is not only high heterosis but also to achieve high level of production. To improve any particular trait donor for hybridization could be chosen from an appropriate cluster and that should be utilized in breeding programme.

Table :1 Analysis of variance for yield and yield attributing characters of 25 blackgram genotypes during *rabi* 2015.

Source Variation	**Replication**	**Accessions**	**Error**
df	**2**	**24**	**48**
character	**Mean sum of square**		
Days to 50% flowering	0.280	2.614 ***	0.224
Plant height (cm)	3.64	222.513 ***	39.14
Branches/plant	0.026	1.3655 ***	0.121
Pods/plant	0.777	355.95 ***	4.686
100 seed weight (g)	0.003	0.074 ***	0.015
Yield (Kg/ha)	35670.45	257909.83 ***	12657.38

Table 2 : Distribution of blackgram genotypes in 6 clusters

Cluster Number	No.of consisting genotypes	Name of Genotypes
I	3	IPU2-43,Vamban 7,TU 94-2
II	4	TU 67,DKU 11,NDUK 13-4,NDUK 13-6
III	5	PU-11-14,IU02-13,NUL 244,AKU-11-8,AK 10-6
IV	6	MU 44, LBG 791,KU 13-01,MU 06,VBG 11-31,VBG 11-016
V	5	COBG 10-6,SBC 47,KUG 715,PU 0937,KU 96-7
VI	2	LBG 752,LBG 623

Table 3: Intra and inter cluster average divergence (D^2 values) among eight clusters involving of 25 blackgram genotypes (Tocher Method)

Clustert	I	II	III	IV	V	VI
I	4.705	19.536	38.414	10.145	19.917	67.85
II		10.210	30.963	18.667	38.285	44.378
III			12.834	36.081	86.881	21.026
IV				0.000	24.752	49.518
V					14.343	113.676
VI						0.000

Table 4: Cluster means involving 25 blackgram genotypes in respect of 6 clusters (Tocher Method)

Cluster	Days to 50% flowering	Plant height (cm)	Branches/plant	Pods/plant	100 seed weight (g)	Yield (kg/ha)
I	41.0	40.3	3.26	38.45	4.03	1133.5
II	48.74	39.9	1.80	33.20	4.06	655.8
III	44.90	40.14	2.67	36.33	3.96	1009.3
IV	61.0	38.33	2.66	49.07	4.24	1028.3
V	40.1	39.22	2.88	19.28	4.33	949.8
VI	59.6	38.0	2.33	11.93	3.96	598.6

Table 5: Percent Contribution of different characters towards diversity in blackgram genotypes

Name characters	No.of time ranked 1st	Percent contribution
Days to 50% flowering	31	10.33
Plant height (cm)	9	3.00
Branches/plant	16	5.33
Pods/plant	189	63.00
100 seed weight (g)	3	1.00
Yield (Kg/ha)	52	17.33

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