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Studies on Genetic Diversity Analysis in Black gram (*Vigna mungo* L. Hepper) Genotypes under western U.P. conditions

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Abstract

The present investigation was carried out with 40 diverse genotypes of Black gram at Crop Research Centre of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, U.P. Observations were recorded on various characters viz. *days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, pod length, number of seeds per pod, biological yield per plant, test weight, harvest index, and grain yield per plant. Analysis of variance revealed substantial amount of variability for all eleven characters. Mahalanobis (D^2) static revealed considerable genetic diversity among the genotypes. Genotypes were grouped into 5 clusters. Cluster I was the largest including 14 genotypes. The intra cluster distance among various clusters exhibited maximum intra cluster distance for cluster III and lowest intra cluster distance was reported for cluster II. The maximum intra cluster distance was because of wide genetic diversity among its genotypes. The highest inter cluster distance was revealed between cluster IV and V. The clearly indicates that the genotypes included in this cluster are having broad spectrum of genetic diversity and could very well be used in hybridization programme of black gram for improving grain yield. The minimum inter cluster distance was revealed between clusters I and VII. It is suggested that, crosses among the parents belonging to most divergent clusters would be expected to manifest maximum heterosis and also wide variability of genetic architecture.*

key word: Primary branches, genotypes, heterosis, biological yield, Black gram

Introduction

Blackgram [*Vigna mungo* (L) Hepper] is predominantly a self-pollinated crop with low percentage of natural out crossing and widely cultivated grain legume. It belongs to family fabaceae. Center of genetic diversity for black gram is found in India (Zeven et al., 1982). The major portion of blackgram is utilized in making dal, curries, soup, sweets and snacks. Its seeds contain approximately protein (24-26%), carbohydrates (60%), fat (1.5%), fiber (3.5-4.5%), ash (4.5-5.5%), minerals, amino acids and vitamins. It is the richest sources of phosphoric acid being 5-10 times richer than other crops. Besides, being used as food for inexpensive source of dietary protein it is better to use for bean sprouts than mung bean for its longer shelf life (Mishra and Khan, 2001). It also enriches the soil fertility, improves the soil structure and used as green fodder for cattle. Black gram is still cultivated on marginal lands under rain fed conditions and faces terminal drought which affects its productivity to a great extent. Low and uneven rainfall pattern of the state since last few years have urged the need to develop early maturing varieties of black gram to avoid yield losses due to long dry span during maturity. India is the largest producer and consumer of black gram in the world. Black gram has been distributed mainly in tropical to sub-tropical countries where it is mainly grown in India, Pakistan, Sri-Lanka, Burma, and some countries of South East Asia. It produces about 1.5 to 1.9 million tons of black gram annually from about 3.5 million hectares of area, with an average productivity of 500 kg per hectare. Black gram output accounts for about 10% of India's total pulse production (*Ministry of Agriculture, Govt. of India, 2015*). In 2014-2015, 1.61 million tonnes Urd production in the country is largely concentrated in five states *viz,* Uttar Pradesh (UP), Maharashtra,

Madhya Pradesh, Andhra Pradesh and Tamil Nadu. These five states together contribute for about 70% of total Urd production in the country (*Ministry of Agriculture, Govt. of India, 2015*). In U.P. Blackgram is grown in about 3.91 lakh hectares with a total production of 1.72 lakh tones (Annual Report 2014-2015). Among the states of India, Orissa ranks first in area 777 thousand hectares and production 396 thousand tones. However, Bihar is a leading state in productivity with 898 kg/hectare (Pulses in India, Ministry of Agriculture and Farmer welfare, Govt. of India, 2015). Per capita availability of pulses per day is only 47g as against the minimum requirement of 104g as recommended by nutritional experts of World Health Organization/Food and Agriculture Organization (Hariprasanna and Bhatt, 2002). 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 in the adaptation to both biotic and abiotic stresses. The reason for low yield is; i) adaption of crop to marginal lands of rain fed nature. The crop has been traditionally cultivated under less fertile soils with least inputs, ii) unavailability of cultivars with high potential, iii) stress to disease insects and environmental fluctuations, etc. The breeding progress has been slow and uneven because several desirable traits need to be combined for developing appropriate plant type for a particular growing region and cropping system. Development of high yielding varieties of crops requires information on nature and magnitude of genetic variability present in the available population. Seed yield in black gram is a complex character like other crops, and is determined by various components. The assessment of variation provides us a correct picture of the extent of variation, further helping us to improve the genotypes. Genetic diversity is one of the criteria of parent selection in the hybridization program. The availability of transgressive segregant in any breeding program depends upon the diversity between the parents involves. The quantification of genetic diversity through biometrical procedures such as Mahalanobis's D2-statistic has made possible to choose genetically diverged parents. Recent works indicated that the Mahalanobis generalized distance (D^2-statistic) may be an efficient tool in the quantitative estimation of genetic diversity (Mahalanobis, 1936). The divergence analysis has a definite role to play in an efficient choice of divergent parents for hybridization to exploit maximum heterosis.

Materials and Methods

The material under investigation consisted of forty genotypes of black gram (Vigna mungo L. Hepper) were grown in *Zaid* 2017 at Crop Research Centre of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U.P.), situated at an elevation of about 297 meters above mean sea level with 29.01 º'N latitude and 77.75 º'E longitudes, representing the North western plain zone. Experiment was done according to randomized block design with three replications, All the recommended package of practices was followed for raising healthy crop. Each plot consisted of a three row of 5.0 m length with a spacing of 30 cm between rows and 10 cm between plants was maintained by proper thinning. Observations were recorded on, plot as well as on single plant basis. Observations on plot basis were recorded for days to 50% flowering and days to maturity. For recording single plant observations, five competitive plants from each plot were randomly selected. Average of these five plants in respect of plant height, number of primary branches per plant, number of pods per plant, number of seeds per plant, number of seeds per pod, 1000-seed weight, biological yield per plant harvest index and seed yield per plant was used for statistical analysis. Mahalanobi's D2 statistic was employed to assess the genetic diversity.

Results and Discussion

The mean sums of squares of 11 different traits are presented in (Table 1). High significant differences for all characters under study among the 40 black gram genotypes were found in analysis of variance, at 1 % level of significance indicating the presence of sufficient considerable genetic variability among different genotype. These results were in agreement with the findings of Balachandran *et al.* (2010), Kumar *et al.* (2015), Priyanka et al. (2016), Rolaniya *et al*. (2017) and Nagmi and Lal (2017).

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 distribution (Mehandi *et al.*2013). Genetic divergence analysis was widely

Table 1: Analysis of variance (ANOVA) for eleven characters of forty genotypes in Blackgram (*Vigna mungo* (L.) Hepper)

Source of variations	d. f.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/plant	No. of pods/plant	Pod length (cm)	No. of Seeds/pod	Biological yield/plant	Harvest (100 seed)	Test weight index (%)	Grain yield/ plant
Replication	2	1.34	1.76	9.52	0.09	6.78	0.29	0.13	0.03	0.089	0.11	0.07
Treatments	39	275.50**	193.01**	524.02**	1.19**	259.14**	1.11**	1.05**	98.89**	13.99**	0.63**	1.57**
Error	78	1.20	1.48	5.11	0.01	1.47	0.07	0.03	1.53	1.06	0.04	0.07

** Significant at 1% level

used to determine the genetic relationship among the genotypes and find out the suitable genotypes for future breeding programme. Genetic diversity analysis also helps in tagging and elimination of the duplicate accessions from genetic stock. On the basis of divergence 40 genotypes under investigation have been grouped into five distinct clusters (Table 2), indicating a wide range of diversity in the experimental materials.

Among the five clusters, cluster I was the largest including 14 genotypes followed by cluster IV had ten genotypes, cluster III had eight genotypes and cluster II and cluster V had four genotypes each. These results revealed that geographic diversity might not be an important factor in determining genetic divergence. The genotypes included in a cluster were diverse geographical origin; it shows that geographic divergence need not important related to genetic diversity. 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 two clusters. Critical assessment of clusters showed that clusters were heterogeneous within them 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. These finding are supported with the results obtained by Manikannan *et al.* (2000), Lad *et al.* (2005), Konda *et al.* (2007), Majumdar *et al.* (2011) and Panigrahi *et al.* (2014) in black gram.

Table 3 revealed that the intra cluster distances were found higher than the inter cluster distance revealing a considerable amount of genetic diversity among the genotypes studied. The highest inter cluster distance was revealed between cluster IV and V (6.54) followed by cluster II and cluster V (6.26), cluster I and cluster V (5.33), cluster III and cluster V (4.40), cluster III and cluster IV (3.63), cluster II and cluster III (3.53), cluster I and cluster II (3.23), cluster I and cluster III (2.95), cluster II and cluster IV (2.93) and. The genotypes grouped in these clusters can be used in breeding programme in order to get a wide spectrum of variability and transgressive segregates. The minimum distance between clusters I and IV (2.39) indicated that they were genetically closure clusters. Selection of parents from such clusters may be avoided because it may result in narrow genetic base. This result is supported by findings of Venkatesan *et al.* (2003), Lad *et al.* (2005), Konda *et al.* (2007), Umadevi and Ganesan (2007) and Katna and Verma (2003) in black gram.

The intra cluster distance among various clusters exhibited maximum intra cluster distance for cluster III (2.96) and lowest intra cluster distance was reported for cluster II (1.68). The maximum intra cluster distance was because of wide genetic diversity among its genotypes. The chance of developing good segregates by crossing the genotypes of the same cluster showing low value for intra cluster distance are very low. Therefore, it would be logical to attempt crosses between the genotypes of clusters separated by larger inter cluster distance. The little diversity and selection of parents within the clusters having higher mean for a particular character may also be useful for further developing high yielding black gram varieties.

The cluster mean for each eleven characters are presented in Table 4. The genotypes of cluster III were higher for test weight (5.28) and pod

Table 2: Grouping of forty genotypes of Blackgram (*Vigna mungo* (L.)) in seven clusters

Cluster	No. of genotypes	Genotypes
I	14	PLU-1287, IC-570274, IC-616494, IC-296266, IC-530650, IC-330889, IC-250252, IC-393556, IC-399642, IC-38599, IC-530657, IPU2-43, WBU-108, UTTARA
II	4	PLU-1029, IC-471989, IC-616491, IC-600664
III	8	IC-530656, IC-616488, IC-258965, IC-530639, IC-393593, IC-570263, Barabanki Local
IV	10	PLU-694, PLU-89, NG-2119, IC-530658, IC-530637, IC-471999, IC-395559, IC-570268, Pant U-49, IC-121645
V	4	IC-447534, IC-436508, IC-305233, IC-447790

Table 3: Average intra and inter cluster distance (D^2 value) among seven clusters of forty five genotypes in rice (*Oryza sativa* L.)

Clusters	I	II	III	IV	V
	2.25				
	3.23	1.68			
	2.95	3.53	2.96		
	2.39	2.93	3.63	2.01	
	5.33	6.26	4.40	6.54	2.16

length (4.55) followed by cluster V (3.83) and (4.88) respectively. The genotypes of cluster IV had highest harvest index (21.12) followed by cluster I (18.55). The genotypes fall in the cluster V were having the desirable direction of characters i.e. days to 50% flowering (43.25), days to maturity (68.00), plant height (54.250), number of primary branches per plant (3.57), number of pods per plant (49.51), number of seeds per pod (5.52), biological yield per plant (40.25) and grain yield per plant (6.67). Cluster I for days to 50% flowering and days to maturity, cluster III for plant height, number of primary branches per plant, number of pods per plant, biological yield per plant and grain yield per plant, cluster IV for seeds per pod (Table 4).

It is suggested that, crosses among the parents belonging to most divergent cluster would be expected to noticeable maximum heterosis and also wide variability of genetic architecture. Thus the crosses between the genetically diverse genotypes of cluster IV and V characterized by days to 50% flowering, days to maturity, plant height, number of seeds per pod, number of primary branches per plant, harvest index and grain yield per plant with the genotypes IC- 530658, IC- 447534, IC- 305233, IC- 436508 and Pant U-49 are expected to exhibit high heterosis and are also likely to produced new combinations with desired characters to get desirable segregates with higher yield for developing superior varieties of black gram.

The number of times that each of eleven characters appeared first rank and its percentage contributed highest divergence presented in Table 5. The results showed that the contribution of pod length was highest (12.70), followed by harvest index (11.06), number of pods per plant (10.81), test weight (10.68), days to maturity (10.56), grain yield per plant (9.86), plant height (8.86), biological yield per plant (6.80), number of seeds per pod (6.60), number of primary

Table 4: Cluster mean values for eleven characters of forty genotypes in Blackgram (*Vigna mungo* (L.)

Clusters	Characters										
	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of pods/ plant	Pod length (cm)	No. of Seeds/ pod	Biological yield/ plant	Harvest index (%)	Test weight (100 seed)	Grain yield/ plant
I	58.80	74.95	27.32	3.10	31.01	3.70	4.15	27.35	18.55	4.80	5.03
II	75.97	92.58	33.69	3.08	35.48	3.81	4.00	31.85	16.56	4.57	5.27
III	60.96	77.19	31.04	3.25	42.66	4.55	4.00	34.46	17.74	5.28	6.07
IV	69.73	85.80	23.93	2.57	32.43	3.79	4.20	25.46	21.12	4.82	5.37
V	43.25	68.00	54.25	3.57	49.51	3.83	5.52	40.25	16.68	4.88	6.67

branches per plant (6.49) and lower contribution was made by days to 50% flowering (5.58) towards the genetic divergence.

Table 5: Contribution (%) of eleven characters towards genetic divergence in Black gram (*Vigna mungo* (L.) Hepper)

S. No.	Characters	Contribution (%)
1	Days to 50% flowering	5.58
2	Days to maturity	10.56
3	Plant height (cm)	8.86
4	Number of primary branches per plant	6.49
5	Number of pods per plant	10.81
6	Pod length (cm)	12.70
7	Number of Seeds per pod	6.60
8	Biological yield per plant	6.80
9	Harvest index (%)	11.06
10	Test weight (100 seed)	10.68
11	Grain yield per plant	9.86

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