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Genetic diversity in yield and yield component in Blackgram [*Vigna mungo* (L) Hepper]

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Abstract
34 genotypes collected from various sources were grouped into six clusters following Mahalanobis D^2 statistics. Cluster III was the largest (12 genotypes) followed by clusters II (eight), VI (Six) and VI (four). The maximum intra-cluster distance was observed in cluster III, II and V suggesting that genotypes are having diverse genetic architecture. The inter-cluster distance was high between clusters V and VI there by indicating wide range of variation among the clusters. The per cent contribution towards genetic diversity was high in 100 seed weight (59.00%), days to 50 % flowering (15.15%) and days to maturity (11.94%), Selection pressure on these traits may lead to an overall increase in grain yield per plant. The inter-cluster representatives of distant clusters would be more useful for choosing the parents in hybridization programme.

Keywords: Mahalanobis D^2 statistics, cluster distance, genetic diversity, hybridization

Introduction
Blackgram, commonly known as urdbean (*Vigna mungo* (L.) Hepper) is one of the important pulse crop grown in India for its nutritional quality and the suitability to cropping system. Blackgram is native to India. (Vavilov, 1926) [11]. The progenitor of blackgram is believed to be *Vigna mungo* var. silvestris, which grows wild in India. (Lukoki *et al.* 1980) [6]. It is an important source of dietary proteins, carbohydrates, vitamins, minerals as well as of dietary fibers. Like other pulses, it also enriches the soil fertility, improves the soil structure and used as green fodder for cattle. It is often used as dry season intercrop in rice or wheat as it has a beneficial effect on soil nutrient status (Parashar, 2006) [8]. Center of genetic diversity for black gram is found in India (Zeven *et al*. 1982) [12]. It is a staple crop in the Central and South East Asia; however it is extensively used only in India and now grown in the Southern United States, West Indies, Japan and other tropics and subtropics (Delic *et al*. 2009) [1]. Blackgram is grown in varying agro- ecological conditions and cropping systems with diverse cultural practices, so it needs appropriate plant type for each growing situation. India is the world's largest producer of blackgram. However its productivity is lower (469 kg/ha) than the world average and it imports a large amount to meet the growing domestic needs. Major constraints in achieving higher yield in black gram are absence of suitable ide type for different cropping system, poor harvest index and lack of stable cultivars. Therefore, for increasing the productivity of blackgram, collection and characterization of germplasm from different regions of cultivation need specific emphasis for further exploitation in breeding programs. Selection of suitable parents and promising F_1 hybrids is important. Yield is a complex trait determined by several component traits, hence selection for yield should take into account. The knowledge of genetic divergence is of paramount importance for any breeding programme. Information on genetic diversity analysis helps to identify the genetically diverse genotypes for their use in breeding programmes. Of the several methods available Mahalanobis's generalized distance estimated by D^2 statistic (Rao, 1952) [9] is a unique tool for discriminating population. It has been followed by several workers on a wide range of crop species, including blackgram, to measure the genetic distance among the breeding lines and to identify characters responsible for such divergence. The replicated data were subjected to genetic divergence analysis using Mahalanobis D^2 statistic (Mahalanobis, 1936) [7] as suggested by Rao (1952) [9]. All the genotypes were grouped into respective clusters on the basis of D^2 values following Tocher's method. The objective of present investigation was to determine the magnitude of genetic divergence among the blackgram and mungbean germplasm for yield and component traits and to identify genetically diverse and agronomically desirable genotypes for their further exploitation in blackgram and mungbean improvement programme.

Materials and methods

The experimental materials consisted of 34 blackgram including 2 mungbean genotypes obtained from the Department of Genetics and Plant Breeding, GB Pant University of Agriculture and Technology, Pantnagar, raised in Randomized Block Design with three replications in the spacing of 30 cm x 10 cm at the Norman E Borlaugh Crop Research Centre Pantnagar, and the recommended cultural practices were followed. Observations were recorded on five randomly taken plants from each replication for eight quantitative traits viz., days to 50% flowering, days to maturity, plant height, number of pods per plant, pod length, number of seeds per pod, 100 seed weight and grain yield per plant. The data collected on different characters were analysed through Mahalanobis (1936) [7] D^2 analysis. Clustering of genotypes was done following the Tocher's method as described by Rao (1952) [9].

Results and discussion

The cluster III was the largest which consisted of 12 genotypes (PU 08-2, Pant U 31, PU 08-3, PU 08-4, PU 08-6, PU 08-10, PU 08-11, PU 08-12, PU 08-13, PU 08-15, PU 06-15 and PU 06-17), followed by clusters II, V and VI with eight (PU 08-5, PU 08-8, PU 08-9, PU 08-14, Pant U 40, PU 08-7, DPU 88-31 and PU 06-18), six (PMU-02, PMU-03, Local 60, PU 06-14, PU 06-16 and PU 06-19) and four (PU 06- 21, PU 06-22, PU 06-23 and PU 06- 24) genotypes respectively. The clusters I (PU 08-1 and PU 07-7) and IV (PMU -01 and BDYR-1) consisted only 2 genotypes (Table 1). From the clustering pattern, it was found that the genotypes collected from different regions were independent of their genetic origin. Hence, the genotypes studied are reliable enough for hybridization and selection. Gupta and Singh (1970) [2] have 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. In the present investigation, intra cluster D^2 values between all 34 genotypes ranged from 0.00 to 10.355 (Table 2), which indicated the presence of adequate amount of genetic diversity in the materials studied. The maximum intra–cluster distance was observed in cluster III (D^2 = 10.355), cluster II (D^2 = 6.52) and in cluster V (D^2 =6.41), thus suggesting that different genotypes included in this cluster might have different genetic architecture. However, the lowest intra–cluster distance found in cluster IV and VI (D^2 = 0.00) and in cluster I (D^2 = 4.40) indicated that the genotypes resembled one another genetically and appeared to have evolved from a common gene pool, which is in accordance with the findings of Shanmugam and Sreerangaswamy (1982) [10]. This kind of clustering of genotypes from different eco-geographic locations into one cluster was attributed to free exchange of genotypes from one region to another and also be due to the character constellation that might be practiced in several regions resulting in segregation of genotypes irrespective of their geographic region. The inter–cluster distance (Table 2) was high between cluster V and VI (D^2 = 117.464) followed by cluster III and VI (D^2 =85.390) and clusters I and V (D^2=55.875), there by indicated wide range of variation among the clusters formed. Hence, the genotypes underlying in these clusters could be selected for hybridization to obtain potential segregants. Whereas lowest inter-cluster distance was observed between cluster I and II (D^2= 9.995) followed by cluster II and IV (D^2= 10.660) and cluster I and III (D^2= 11.189), indicated that they were genetically closure clusters. (Figure 1) Selection of parents from such clusters may be avoided because it may result in narrow genetic base. This result is supported by findings of Lad *et al.* (2005) [5], Konda *et al*. (2007) [4] and Katna and Verma (2003) [3] in black gram.

It was observed that cluster I recorded high mean values (Table 3) for days to maturity (88.33), and plant height (49.848) and days to 50 % flowering (34.788) and lowest mean value for 100 seed weight (3.769), pod length (4.406) and seeds/pod (5.585). Cluster II recorded high mean values for days to maturity (87.98) and plant height (54.08) and days to 50 % flowering (35.929) and lowest mean value for 100 seed weight (4.275), pod length (4.472) and seeds/pod (5.329). Cluster III recorded high mean values for days to maturity (88.47), and plant height (55.17) and days to 50 % flowering (36.53) and lowest mean value for 100 seed weight (3.45), pod length (4.43) and grain yield/plant (5.14). Cluster IV recorded high mean values for days to maturity (89.00) and plant height (45.47) and days to 50 % flowering (40.00) and lowest mean value for pod length (4.11), grain yield/plant (4.23) and 100 seed weight (4.37). Cluster V recorded high mean values for days to maturity (89.33) and plant height (52.90) and days to 50 % flowering (35.83) and lowest mean value for pod length (4.48), seeds/pod (5.28) and 100 seed weight (5.46). Cluster VI recorded high mean values for days to maturity (84.33) and plant height (48.60) and days to 50 % flowering (33.67) and lowest mean value for 100 seed weight (3.08), grain yield/plant (3.98) and seeds/pod (5.37). Therefore, the genotypes among these clusters might result in simultaneous improvement of these traits. Among the eight characters studied, 100 seed weight contributed maximum (59.00%) (Figure 2) followed days to 50 % flowering (15.15), days to maturity (11.94), pod length (3.92), grain yield/plant (3.39), pods/plant (2.85), plant height (2.32) and seeds/pod (1.43) towards genetic diversity (Table 4). Hence, these characters may be considered during selection of genotypes and in order to generate more heterotic F_1s and desirable segregants.

Table 1: Distribution of 34 black gram and mungbean genotypes to different clusters on the basis of D^2 statistics

Clusters	No. of genotypes	Genotypes
I	2	PU 08-1 and PU 07-7
II	8	PU 08-5, PU 08-8, PU 08-9, PU 08-14, Pant U 40, PU 08-7, DPU 88-31 and PU 06-18
III	12	PU 08-2, Pant U 31, PU 08-3, PU 08-4, PU 08-6, PU 08-10, PU 08-11, PU 08-12, PU 08-13, PU 08-15, PU 06-15 and PU 06-17
IV	2	PMU -01 and BDYR-1(Mungbean)
V	6	PMU-02, PMU-03, Local 60, PU 06-14, PU 06-16 and PU 06-19
VI	4	PU 06- 21, PU 06-22, PU 06-23 and PU 06- 24

Table 2: Intra and inter-cluster (D) values for 34 black gram and mungbean genotypes

Cluster	I	II	III	IV	V	VI
I	4.401	9.995	11.189	18.323	55.875	22.221
II		6.523	20.982	10.660	32.505	38.122
III			10.355	23.182	85.390	20.923
IV				0.000	36.691	53.817
V					6.412	117.464
VI						0.000

Table 3: Cluster means for eight characters in 34 black gram and mungbean genotypes

Clusters	Days to 50 % Flowering	Days to Maturity	Plant Height (cm)	Pods/ Plant	Pod Length (cm)	Seeds/ Pod	100 Seed Weight (g)	Grain Yield/ Plant (g)
I	34.788	88.333	49.848	19.458	4.406	5.585	3.769	6.609
II	35.929	87.976	54.081	18.952	4.472	5.329	4.275	5.982
III	36.533	88.467	55.173	19.240	4.431	5.573	3.454	5.139
IV	40.000	89.000	45.467	16.467	4.113	5.400	4.370	4.227
V	35.833	89.333	52.900	18.467	4.475	5.283	5.455	6.827
VI	33.667	84.333	48.600	17.533	6.190	5.367	3.080	3.980

Table 4: Contribution of different characters towards diversity in black gram and mungbean

S. No.	Characters Contribution (%)	Number of times ranked first	Contribution %
1	Days to 50 % Flowering	85	15.15
2	Days to Maturity	67	11.94
3	Plant Height (cm)	13	2.32
4	Pods/ Plant	16	2.85
5	Pod Length (cm)	22	3.92
6	Seeds/ Pod	8	1.43
7	100 Seed Weight (g)	331	59.00
8	Grain Yield/ Plant (g)	19	3.39

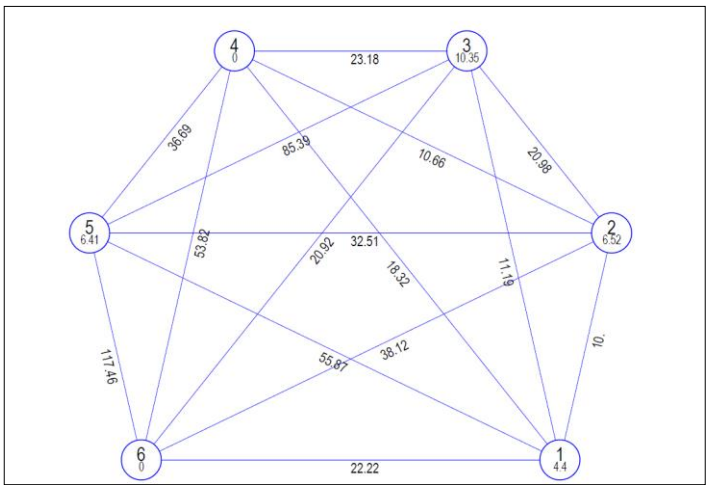

Fig 1: Mahalanobis Euclidean Distance of 6 clusters through inter and intra-clusters distribution in 34 genotypes of black gram and mungbean

Mahalnobis Euclidean Distance (Not to the Scale)

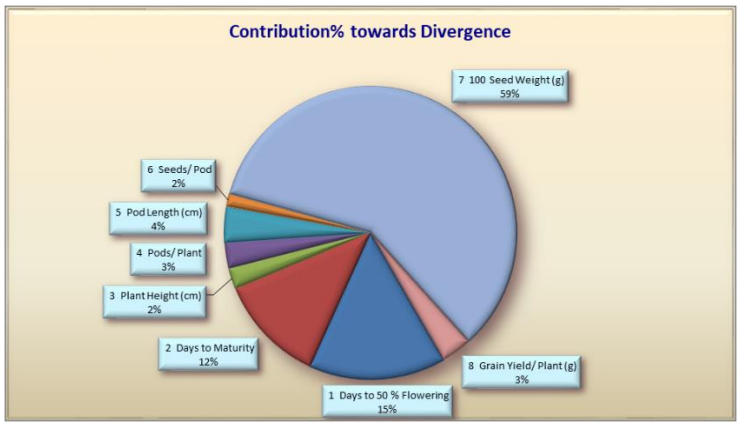

Fig 2: Contribution of different characters towards diversity in blackgram and mungbean

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