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Study of genetic divergences using mahalanobis d^2 analysis in black gram (*Vigna mungo* L. Hepper) germplasm

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Abstract
The present experiment was conducted at Research cum Instructional Farm of SGCARS Kumhrawand, Jagdalpur, Bastar (C.G.). The experiment was conducted in Randomized Complete Block Design (RCBD) with two replications. Crop was grown proper spacing 30×10cm during *Kharif* 2019. The study was undertaken on the 82 black gram genotypes along with two checks (Indira Urd Pratham and T.U. 94-2) to study the D^2 analysis. Eighty two genotypes of black gram were used to study the nature and magnitude of genetic divergence using Mahalanobis's D^2 Statistics. The data for thirteen important quantitative traits were recorded. D^2 analysis grouped genotypes into eight clusters. Among the eight clusters formed, cluster I was found to be largest group consisting of 19 genotypes followed by cluster IV having 18 genotypes, cluster V 11 genotypes, cluster II 9 genotypes, both cluster VII and VIII have 7 genotypes, cluster III 6 genotypes and cluster VI have 5 genotypes respectively. The average intra-cluster distance between the genotypes was maximum for the cluster VII (2.898) and minimum for clusters VIII (2.331), have been recorded. The highest inter-cluster distance was noted between clusters VIII and cluster II (6.706). The genotypes was eight different grouped in these clusters indicate their diverse nature. Number of pods per plant followed by Days to 50 per cent flowering and Pod length maximum per cent contribution towards total divergence among the genotypes. The study provides scope for selection, further subsequent utility of the genotypes in future crop improvement programmes.

Keywords: Genetic, divergences, gram, programmes, germplasm

Introduction
Pulses are important commodity group of food crops that can play a vital role of national food and food security. Those provide high quality proteins, vitamins and minerals complementing cereal proteins for pre-dominantly feasible vegetation population of the world. In India, pulses have been described as a "poor man's meat and rich man's vegetable". Besides improving soil fertility and physical structure, pulses fit well in mixed or intercropping systems, crop rotation and dry farming, pulses provide green vegetable (pods/beans) and nutritious fodder for cattle as well thereby contributing to a sustainable food and cropping system. India is larger producer (25% of global production), consumer (27% of word consumption) and importer (14%) of pulses in the world. Pulses can be produced with a minimum use of recourses and hence, it becomes less costly even than animal protein. Important states growing black gram in India total area (lakh ha) and production (lakh tonnes) of black gram is 44.78, 28.32 respectively in which Madhya Pradesh (12.03)(8.17), Utter Pradesh (6.44)(3.57), Andhra Pradesh (5.00)(3.29), Rajasthan (4.77)(3.05), Tamilnadu (4.30)(2.74), Maharashtra (3.38)(1.83), Gujarat, (1.97)(1.19), Jharkhand (1.57)(1.39), Orissa (1.09)(0.49) and Other states (3.29)(2.06) respectively. (Anon. 2016) [1]. In the year 2018–19 during rabi and 2019-20 during kharif in India area (lack ha) and production (lack tonnes) is 7.629, 26.5, 37.52 and 25.6, respectively (Anon. 2019) [2]. In Chhattisgarh black gram area (000 ha) and production (kg/ha) according to the year wise in 2015-16(154.51) (305), 2016-17(144.94) (320), 2017-18(164.44) (332) occupies respectively. (Anon. 2019) [2]. D^2 statistic is one of the potent techniques of measuring genetic diversity in plant breeding. Knowledge about genetic diversity is an invaluable aid in crop improvement strategies. The selection of genetically diverged parents is expected to throw superior and desirable segregates following crossing**.**

Materials and Method
Seeds of 80 genotypes of black gram were collected from Bastar region and two check variety seeds from Shaheed Gundadhur College of Agriculture and research Station, Jagdalpur.

The present experiment entitled "Diversity analysis in black gram [*Vigna mungo* (L.) Hepper] was conducted at "Research cum Instructional Farm, Shaheed Gundadhoor College of Agriculture and Research Station, Kumhrawand, (Jagdalpur), Indira Gandhi Krishi Vishwa vidyalaya, Raipur (Chhattisgarh)" located at N 19°5'39'' longitude E 81°59'33'' latitude and at an altitude 553.400 meters above mean sea level (MSL) with an annual rainfall 14.39 mm. The experimental material comprised of eighty two black gram genotypes along with two check varieties Indira Urd Pratham and T.U. 94-2. The experimental material was planted in a Randomized Complete Block Design with two replications during *kharif* 2019. Each genotype was planted in two rows of 3 m length × 1 m width having 30 ×10 cm spacing between rows and plants. The observations were recorded on five randomly selected plants per replication for each accession.

Genetic Divergence Analysis or Cluster Analysis

"Cluster analysis or clustering is the task of grouping a set of objects in such a way that objects in the same group (called a cluster) is more similar to each other than to those in other groups (clusters). Cluster analysis has no mechanism for differentiating between relevant and irrelevant variables. Therefore, the choice of variables included in a cluster analysis must be underpinned by conceptual considerations. This is very important because the clusters formed can be very dependent on the variables included. In the present study, Euclidian distance between genotypes was calculated from the standardized data matrix by Unweighted Pair Group Method using Arithmetic Averages (UPGMA) method and clustering was done by Agglomerative Hierarchical method using XLSTAT 2017 software". Mahalanobis (1936) [9] D^2 - statistic was used for assessing of the genetic divergence between genotypes. The generalized distance between any two populations is defined as,

$$D = \sum y\, ij\beta i\, \beta j$$

Where

Yij = the reciprocal matrix to the common dispersion matrix

βi = The difference between the two mean values of the two populations for ith character (μi1 -μi 2)

βj = The difference between the mean values of the two populations for the jth character (μj1 - μ j2)

μ = Vector mean values for all the characters. The formula for the estimation of distance, D^2 from samples

$$D^2 p = d1\ (S - 1)\ d$$

Where

D^2 p = Square of the distance considering P values.

$d1 = (Xi_1 - Xi_2)$

X = Vector for mean values of all the characters

S -1 = inverse of variance covariance matrix

The original correlated unstandardized variables (Xi) were transformed to standardized uncorrelated variables (Yi) so that the computation of D^2 values reduce to simple summation of squares of the differences between values of transformed variables of the two population i.e., D^2 i.

From the newly transformed uncorrelated variables, the square of the distance was computed using the following formula,

$$D^2 = \sum (Yi_1 - Yi_2)\ 2$$

Where

Yi_1 = Vector of transformed mean values, for first genotype

Yi_2 = vector of transformed mean values, for second genotype

Results and Discussion

Multivariate analysis was done utilizing Mahalanobis D^2 statistic. Rao (1952) [12] used D^2 statistics technique for the estimation of genetic diversity among germplasm lines. It is used to measure the degree of diversification and also determines relative portion of each component trait to total divergence. This technique says that, if distance between clusters of genotypes is large, there will be more genetically diversity and if small distance exists then genotypes are less divergent from each other. So, genotypes falling under different cluster will be more divergent from each other corresponding to those falling in the same cluster. Genotypes belonging to different clusters can be used for the hybridization programme.

Grouping of genotypes into clusters

Experimental material consisting of eighty two genotypes had been clustered into eight, different clusters on the basis of assessed values of D^2 statistics. Clustering pattern of germplasm lines of black gram are depicted in table 1. and through dendogram in Fig 1. Among the eight clusters formed, cluster I was found to be largest group consisting of nineteen genotypes followed by cluster IV having eighteen genotypes, cluster V eleventh genotypes, cluster II nine genotypes, both cluster VII and VIII have seventh genotypes, cluster III six genotypes and cluster VI have five genotypes respectively.

Inter cluster distances

"The basic theme behind formation of clusters is to get the intra and inter cluster distances. These distances are used as index for parents with diverse origin. The intra and inter cluster values are means derived from D^2 values of cluster elements. It is assumed that the statistical distance (D) is the index of genetic diversity. Table 2 represents the average D^2 values of intra and inters cluster distances of black gram germplasm under study" Among the eight clusters formed from the eighty two black gram genotypes, the uppermost intra cluster distance was found in cluster VII (2.89) trailed by IV (2.679), VI (2.665), IV (28.870), II (2.608), V (2.501), III (2.480), I (2.336) and VIII (2.331) have recorded intra cluster distance. The distances between two clusters are the measure of the degree of diversification. The grater the distances between two cluster the grater the divergences and lower the distances lower divergences. Large cluster distance specified that the genotypes present under these clusters have substantial genetic distance among them while lower intra-cluster distance indicates relative genetic closeness of genotypes (Suryanarayna *et al*. 2014) [16]. The intra cluster distance ranged from 0.000 to 5.350 and their inter cluster distances ranged from 4.719 to 15.070 (Panigrahi *et al*. 2014) [11]. It is indicated that the inter cluster distances were greater than intra cluster distances which shows considerable amount of genetic 105 diversity existed among the genotypes. Similar reports were given by Singh (2001) [15]. Among the eight clusters formed inter cluster distance ranged from 2.293 to 6.706. Maximum inter cluster distance was noticed between cluster VIII and II (6.706), cluster VIII and V (6.565), cluster VIII and I (5.769), cluster VIII and III (5.597) and at last between cluster VIII and IV (5.319) whereas least inter cluster

distance was found between cluster V and I (2.293), cluster II and I (2.756), cluster IV and I (2.899) and last one is cluster IV and IV (2.981) suggested that the genetic constitution of genotype in one cluster were in close proximity with the genotype in the other cluster of the pair. Hence, genotypes from these clusters may not be useful. This result supported by findings of Kanta and Verma (2003) [6], Lad *et al*. (2005) [8] and Konda *et al*. (2008) [7].

Cluster mean value for thirteen characters in Black Gram

Table 3 represents the comparison of cluster means for various traits. The results obtained from cluster means for different characters showed frequent variation present among clusters categorized according to D^2 analysis. Range of means made it conceivable to know the characters effecting divergence. Highest cluster mean recorded for the trait days to maturity (80.14) and lowest for days to 50% flowering (2.4).

Contribution of characters towards genetic divergence

The contribution of the characters towards the genetic divergence is presented in table 4 and Fig. 2 Out of the thirteen traits assessed, Number of pods per plant (10.47), days to 50 per cent flowering (9.75), pod length (9.63), 1000 seed weight (9.24), petiole length (9.02), seed yield per plant (8.50), number of seeds per pod (8.46), number of primary branches per plant (7.75), days to maturity (6.52), days to first mature pod (5.59), number of pods cluster (5.47), harvest index (5.07) and plant height (4.76) showed least contribution toward genetic divergences. The above discussed results on cluster analysis of black gram genotypes are in confirmation with finding of earlier workers *viz*., Chowdhury *et al.* (2020) [3], Rao *et al.* (2018) [13], Reddy *et al.* (2018) [14], Mahesha and Gabriel (2017) [10], Reddy *et al.* (2018) [14], Gupta *et al.* (2016) [5] Geethanjali *et al.* (2015) [4].

Table 1: Clustering arrays of genotypes of black gram based on D^2 analysis

Clusters	No of genotypes	Genotypes
I	19	4,9,10,11,18,21,26,27,28,29,30,34,35,42,44,46,57,61,70
II	9	15,36,40,43,45,51,56,67,71
III	6	13,24,41,47,50,59
IV	18	3,8,12,14,16,19,20,22,23,25,33,39,49,58,63,65,73,78
V	11	17,31,32,37,38,48,52,53,54,55,77
VI	5	1,2,7,74,76
VII	7	60,62,66,72,75,79,80
VIII	7	5,6,64,68,69, Indira urd pratam, T.U. 94-2

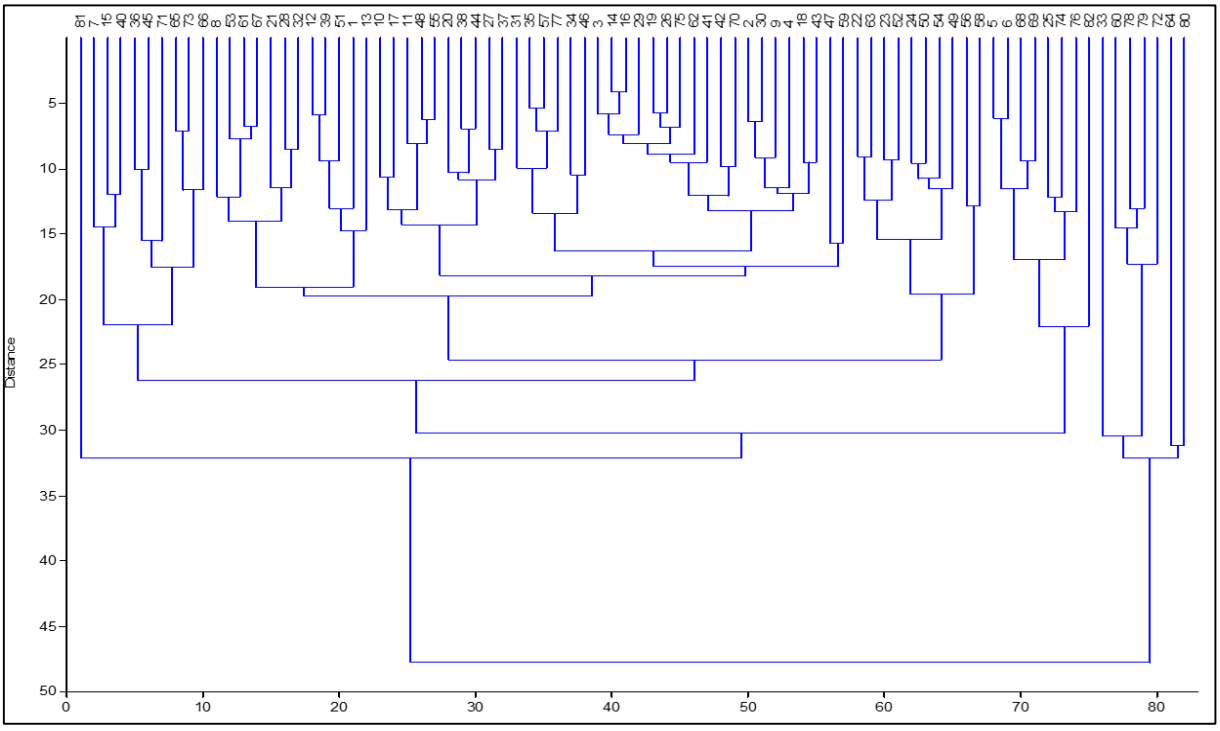

Fig 1: Dendogram describing the distribution of black gram genotype

Table 2: Average intra and inter cluster distances among black gram Germplasm for yield and yield related component traits

Clusters	I	II	III	IV	V	VI	VII	VIII
I	2.336							
II	2.756	2.608						
III	3.110	3.229	2.480					
IV	2.899	3.004	2.981	2.679				
V	2.293	3.022	3.284	3.380	2.501			
VI	3.349	3.868	4.508	3.769	4.976	2.665		
VII	3.854	4.272	3.640	3.292	4.879	3.514	2.898	
VIII	5.769	6.706	5.597	5.319	6.565	4.433	4.576	2.331

Table 3: Cluster means for seed yield and its component traits in black gram Germplasm

Characters	Days to 50% flowering	No. of pri branches / plant	Pods per plant	Pod length (cm)	Plant height (cm)	No. of seed per pod	Days to First Mature Pod	Days to maturity	Petiole length (cm)	No of Pods per Cluster	Harvesting Index	1000 Seed weight (g)	Seed yield per plant (g)
I	39.92	1.93	44.97	4.75	39.89	6.55	61.24	74.18	10.67	3.75	55.16	25.26	20.33
II	39.50	1.78	43.71	4.99	41.10	6.28	62.06	75.78	9.01	3.21	38.29	25.43	24.52
III	37.42	2.25	50.05	4.67	50.63	6.79	64.75	77.25	8.06	3.42	52.54	25.85	21.57
IV	40.61	2.27	44.03	4.65	52.07	6.36	66.42	78.92	10.91	3.38	48.92	26.44	19.75
V	40.18	1.33	45.59	4.39	41.75	6.24	62.64	75.27	8.91	3.38	59.34	23.89	20.15
VI	41.60	2.40	48.78	5.29	47.35	6.41	61.20	75.90	11.95	4.16	42.43	33.05	29.65
VII	41.71	2.39	50.97	5.53	66.27	7.01	64.29	77.36	10.94	3.37	50.30	30.14	16.10
VIII	42.36	2.20	54.83	5.07	52.60	7.24	68.07	80.14	12.21	4.25	60.62	40.83	36.12

Table 4: Contribution of characters towards genetic divergence

Characters Contribution	Characters Contribution
Number of pods per plant	10.47
Days to 50 per cent flowering	9.75
Pod length	9.63
Test weight 1000 seeds	9.24
Petiole length	9.02
Seed yield per plant	8.50
Number of seeds per pod	8.46
Number of primary branches per plant	7.52
Days to maturity	6.52
Days to first mature pod	5.59
Number of pods cluster	5.47
Harvest index	5.07
Plant height	4.76

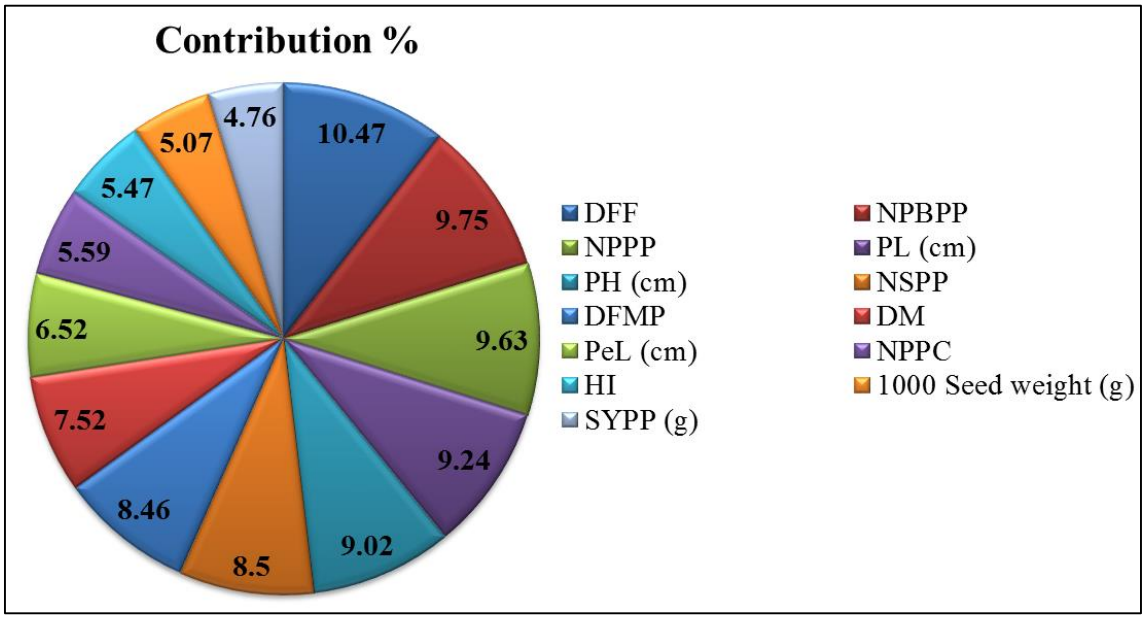

Fig 2: Percent contribution of characters towards genetic divergence

DFF= Days to 50 percent flowering, DM= Days to maturity, PH= Plant height, NPBPP= Number of primary branches per plant, NPPP= Number of pods per plant, PeL= Petiole length, PL= Pod length, NSPP= Number of seeds per pod, NPPC=Number of pods per cluster, DFMP=Days to first mature pod, HI= Harvest index, SYPP= Seed yield per plant, TW= Test weight of 1000seeds.

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