Studies on Genetic Divergence ~~analysis~~ Analysis in Black gram ~~genotypes~~ (*Vigna mungo* L. Hepper) genotypes

Abstract

The present investigation on Genetic Divergence and clustering pattern was carried out with twenty-eight diverse genotypes of Black gram using Mahalanobis's D^2 Statistics. The experiment was conducted in Randomized Block Design with three replications at Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Chidambaram. Observations were recorded on nine various Biometrical characters viz. Plant height at maturity (PH), length of the pods (LP), number of branches per plant (NBPP), number of clusters per plant (NCPP), number of pods per cluster (NPPC), number of pods per plant (NPPP), number of seeds per pod (NSPP), 100 seed weight (SW), and seed yield per plant (SY). Analysis of variance revealed a substantial amount of variability for all eleven characters. Mahalanobis (D^2) static revealed considerable genetic diversity among the genotypes. Genotypes were grouped into 6 clusters. Cluster VI was the largest including 11 genotypes. The intra cluster distance for cluster IV is the maximum and the lowest intra cluster distance was reported for cluster II. The highest inter cluster distance was revealed between cluster I and III then between cluster II and III. This 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 yield. The minimum inter cluster distance was revealed between clusters I and II. The percentage contributed to total divergence by various characters are seed yield was higher (50.997) followed by 100 seed weight (29.456) and number of pods per plant (8.121). 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.

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Introduction

Black gram (*Vigna mungo* L. Hepper), also called urd bean is a member of the Asian Vigna crop species (Delic *et al.*, 2009). Black gram is also known as Mash in India and is a grain

legume domesticated from *V. mungo var. silvestris*. The major portion of black gram 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 source~~s~~ of phosphoric acid being 5-10 times richer than other crops. It belongs to the family ~~fabaceae~~Fabaceae. ~~Center~~ The center of genetic diversity for black gram is found in India (Zeven *et al*., 1982). It is grown in an area of about 5.44 million hectares in India with production of 3.56 million tonnes and productivity of 653 kg/ha (Anonymous, 2017-18). In spite of its importance, the productivity of this crop is relatively low. 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. The development of new varieties depends largely on the availability of genetic variability in the base material and the extent of variability for the desired character. The development of cultivated species and breeding of new varieties typically relies on the available biological diversity in existing genotypes (Datta and Lal, 2011). Limited variability has been exploited in varietal development program~~me~~s in black gram (Jayamani and Sathya, 2013). The breeding progress has been slow and uneven because several desirable traits need to be combined ~~for~~ to develop~~ing~~ appropriate plant type for a particular growing region and cropping system in black gram. Genetic diversity is a pre-requisite for any crop improvement program as it helps in estimating and establishing genetic relationships in germplasm collection, identifying diverse parental combinations to create segregating progenies with maximum genetic variability and superior recombinations for further selection and ~~introgressing~~introgression desirable genes from diverse germplasm. The D^2 analysis proposed by Mahalanobis (1936) is an effective tool ~~in~~ for quantifying the degree of genetic divergence among the genotypes. Keeping the above in view, the present study was undertaken to identify the best performing germplasm of black gram based on quantitative traits using Mahalanobis D^2 statistics and Tocher's method. In the present study, genetic divergence and clustering patterns of the black gram genotypes for selection of suitable parents so as to utilize them in the hybridization program~~me~~, extended to study the genetic parameters attributing to yield.

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Materials and Methods

The material under investigation consisted of twenty-six genotypes of black gram (Vigna mungo L. Hepper) that were grown in ~~kharif~~ Kharif 2022 at the Plant Breeding Farm,

Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University ~~is~~ situated in 11.39° North latitude 79.71° East longitude and 12 km away from Bay of Bengal with an altitude of 6 m above sea level. The climate is relatively warm and humid. The genotypes used are listed ~~at~~ in ~~table~~Table 1. ~~Experiment~~ The experiment was done according to a randomized block design with three replications~~,~~. All the recommended packages of practices ~~was~~ were followed for raising healthy and productive crop with proper agronomic measures. Each plot consisted of ~~a~~ three rows ~~of~~ 5 m in length with a spacing of 25 cm between rows and 15 cm between plants it the row, which was maintained by proper thinning. Observations were recorded on single plant basis. For recording single plant observations, five competitive plants from each replication were randomly selected. ~~Average~~ The average of these five plants in respect of plant height at maturity, length of the pods, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, 100 seed weight, and seed yield per plant was used for statistical analysis. Mahalanobi's D^2 statistic was employed to assess the genetic diversity. The genotypes were collected from Tamil Nadu Agriculture University (Coimbatore), the National Pulses Research Centre (Vamban), and some local regions of Tamilnadu.

Comment [D3]: in which phenophase of plant development the analyzes were done

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Table 1. List of Black gram Germplasms used for Genetic diversity analysis

Accession No.	Genotypes	Accession No.	Genotypes
G1	K 1	G15	Omalur local
G2	Erode local	G16	Mettur local
G3	ADT 3	G17	Madurai local
G4	Shankari local	G18	VBN 5
G5	Chidambaram local	G19	PAIYUR 1
G6	Sirkali local	G20	TMV 1
G7	Salem local	G21	CO 1
G8	ADT 5	G22	CO 2
G9	VBN 3	G23	CO 5
G10	T 9	G24	CO 6
G11	APK 1	G25	VBN 1
G12	VBN 4	G26	VBN 2

G13	VBN 6	G27	Aatur local
G14	VBN 7	G28	Sethiyathoppu local

Results and Discussion

The mean sums of squares of nine different traits are analysed using ANOVA. High significant differences for all characters under study among the twenty-eight black gram genotypes were found in analysis of variance, at 5 % level of significance indicating the presence of sufficient considerable genetic variability among different genotypes. 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 a significant amount of variability. It is obvious that the genotypes have grouped into different clusters 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 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 eliminating of the duplicate accessions from genetic stock. On the basis ofBased of divergence 28 genotypes under investigation have been grouped into six distinct clusters given at Table 2, indicating a wide range of diversity in the experimental materials.

Comment [D5]: move this to material and method

Table 2. Composition of D^2 clusters for 28 Black gram Germplasms

Clusters	List of Genotypes of Black gram under each clusters	Total number of genotypes
I	G1, G2, G4, G10	4
II	G7, G16, G27	3
III	G3, G8, G11	3
IV	G5, G6, G15, G17, G28	5
V	G19, G20	2
VI	G9, G12, G13, G14, G18, G21, G22, G23, G24, G25, G26	11

Among the five clusters, cluster VI was the largest including 11 genotypes followed by cluster IV had 5 genotypes, cluster I had 4 genotypes, cluster II and cluster III had 3 genotypes each and cluster V had 2 genotypes. These findings suggested that genetic divergence may not be strongly influenced by geographic diversification. The genotypes in a cluster came from a variety of geographic origins, demonstrating that genetic diversity is not necessarily correlated with geographic divergence. The divergence among the genotypes in the same cluster is indicated by the divergence within the cluster. Inter cluster divergence, one on either hand, denotes the divergence between the genotypes of various two groups. Based on main character relations, a critical analysis of clusters revealed that they were heterogeneous within and between one another. The lower D^2 value between their characters indicated a close genetic relationship between these genotypes in one cluster and those in the other cluster. These findings are supported ~~with~~ by 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. Average inter and intra cluster D^2 values for 28 Black gram genotypes

Clusters	I	II	III	IV	V	VI
I	8.923	5.865	80.791	22.35	52.134	20.86
II		1.994	80.438	18.315	44.364	16.342
III			4.487	51.231	20.003	50.762
IV				22.85	28.199	20.21
V					6.491	25.223
VI						16.596

It is revealed in ~~table~~Table ~~-~~3, that the intra cluster distances were found Lower than the inter cluster distance revealing a considerable amount of genetic diversity among the genotypes under various clusters. The highest inter cluster distance was revealed between cluster I and III (80.791) followed by cluster II and cluster III (80.438), cluster I and cluster V (52.134), cluster III and cluster IV (51.231), cluster III and cluster VI (50.762), cluster II and cluster V (44.364), cluster IV and cluster V (28.199), cluster V and cluster VI (25.223) and between cluster I and cluster IV (23.383). The genotypes grouped in these clusters can be used in a breeding program~~me~~s in order to get a wide spectrum of variability and transgressive segregates. The

minimum distance between clusters I and II (5.865) indicated that they were genetically ~~closure~~ closed clusters. Selection of parents from such clusters may be avoided because it may result in a narrow genetic base. This result is supported by the findings of 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 IV (22.85) and the lowest intra cluster distance was reported for cluster II (1.994). 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~~ is 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.

Table 4. cluster mean of 28 black gram genotypes for observed traits

Clusters	PH	NBPP	NCPP	NPPC	NPPP	NSPP	LP	SW	SY
I	30.12	2.56	7.90	4.21	32.67	4.56	4.60	3.99	6.86
II	28.52	2.51	8.12	4.43	33.31	4.74	4.64	4.21	6.31
III	31.32	3.01	6.87	5.90	36.21	6.27	4.98	5.28	9.07
IV	28.90	2.53	7.95	4.64	34.61	4.62	4.50	4.52	6.65
V	27.86	2.33	5.91	5.17	29.97	4.83	4.86	5.11	6.71
VI	29.33	2.78	7.21	5.03	33.44	4.73	4.72	4,41	6.70

(Plant height at maturity (PH), length of the pods (LP), number of branches per plant (NBPP), number of clusters per plant (NCPP), number of pods per cluster (NPPC), number of pods per plant (NPPP), number of seeds per pod (NSPP), 100 seed weight (SW), and seed yield per plant (SY))

The cluster mean for each eleven characters ~~are~~ is presented in Table 4. The genotypes of cluster III were higher for 100 seed weight (5.28) and pod length (4.98) followed by cluster V (5.11) and (4.86) respectively. The genotypes fall in the cluster III were having the desirable direction of characters *i.e.*, plant height (31.32), number of branches per plant (3.01), number of pods per plant (36.21), number of pods per cluster (5.90), number of seeds per pod (6.27) and seed yield per plant (9.07). ~~followed~~Followed by cluster I for plant height, number of branches

per plant, number of clusters per plant, and number of pods per plant are high. 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 I and III, I and II, I and V, III and IV, III and VI, II and III, III and V, IV and V, V and VI, I and VI 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.

Table 5. contribution of different characters for genetic diversity of Black gram

Sl.No	Observed Characters	Percentage of contribution
1	Plant Height at Maturity	2.988
2	Number of Branches	1.005
3	Number of clusters per plant	2.220
4	Number of pods per cluster	0.782
5	Number of pods per plant	8.121
6	Number of seeds per plant	0.754
7	Length of the pod	3.661
8	100 seed weight	29.456
9	Seed yield	50.997

The percentage contributed toshare of the total divergence of the various characters are presentedis shown in Table 5. The results showed that the contribution of seed yield was higher (50.997) followed by 100 seed weight (29.456) and number of pods per plant (8.121) then than other characters contribution is pod length was (3.661), plant height (2.988), number of clusters per plant (2.220), number of branches per plant (1.005) and lower contribution was made by number of seeds per pod (0.754) and number of pods per cluster (0.782) towards the genetic divergence.

Conclusion

The 28 black gram germplasms used for the genetic diversity assessment demonstrated a significant range of variance. The 28 black gram germplasms were divided into 6 clusters, which

was consistent with the Mahalanobis D^2 clustering pattern. The parents for the hybridization programme should be chosen based on the genetic distance, the contribution of various characters to the total divergence, and the magnitude of the cluster means for various characters performing with the greatest heterosis. Thus the crosses between the genetically diverse genotypes of cluster I and III, I and II, I and V, III and IV, III and VI, II and III, III and V, IV and V, V and VI, I and VI 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.

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