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Studies on Genetic Divergence Analysis in Black Gram (*Vigna mungo* L. Hepper) Genotypes

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

In order to select superior genotypes for the creation of genetic stock for hybridization program or the introduction of a crop variety, plant breeders can assist from genetic diversity both within and between plant species. Mahalanobis D2 Statistics was used to conduct the current study on Genetic Divergence and clustering pattern utilizing twenty eight different genotypes of Black gram. 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, Tamil Nadu, India. Nine different biometrical characteristics were observed and documented viz., plant height at maturity (PH), pod length (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

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seed yield per plant (SY). All of these characters have a significant degree of variability, according to an analysis of variance. Mahalanobis (D2) 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 and then between cluster II and III. This demonstrates unambiguously that the genotypes in this cluster exhibit a wide range of genetic variation and may be useful in a black gramme hybridization scheme to increase production. Between clusters I and II, the minimal inter-cluster distance was discovered. The percentage that each character contributed to the overall divergence was as follows: the number of pods per plant (50.997), the greater seed output (50.997), and the 100 seed weight (29.456). (8.121). It is proposed that crossings between parents from the most divergent clusters should show the highest level of heterosis as well as the greatest degree of genetic architectural variability.

Keywords: Genetic diversity; genotypes; plant breeding; seed yield; black gram; seedling growth.

1. INTRODUCTION

"Black gram (*Vigna mungo* L. Hepper), also called urd bean is a member of the Asian *Vigna* crop species" [1]. "Black gram is also known as Mash in India and is a grain legume domesticated from *V. mungo var. silvestris*. The majority of black gram produced is used to make soup, dal, curries, snacks, and desserts. About 24 – 26% protein, 60% carbs, 1.5% fat, 3.5 – 4.5% fibre, 4.5 – 5.5% ash, and several minerals, vitamins, and amino acids are included in its seeds. Compared to other pulse crops, it is five to ten times more abundant in phosphoric acid, making it the most abundant source. It is a member of the Fabaceae family. India is the location of the black gram's center of genetic diversity" [2]. "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). "Inspite of its importance, the productivity of this crop is relatively low. The world's major supplier and consumer of black gram is India. Black gram is mostly grown in India, Pakistan, Sri Lanka, Burma, and some South East Asian nations. It is primarily distributed in tropical and subtropical regions. 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" [3]. "Limited variability has been exploited in varietal development programs in black gram" [4]. The breeding progress has been slow and uneven because several desirable traits need to be combined to develop appropriate plant type for a particular growing region and cropping system in black gram. In order to generate segregating progenies with maximum genetic variability, identify diverse parental combinations, and identify outstanding recombinations for further selection and introgression of desirable genes from wide and varied germplasm, genetic diversity analysis is a prerequisite for any crop improvement program. Mahalanobis (1936) developed "the D^2 analysis, which is a useful method for estimating the level of genetic divergence between genotypes. In light of the aforementioned, the current study used Mahalanobis D^2 statistics and Tocher's technique to determine the best-performing black gram germplasm based on quantitative traits". In the present study, genetic divergence and clustering pattern of the black gram genotypes for selection of suitable parents so as to utilize them in the hybridization program, extended to study the genetic parameters attributing to yield.

2. MATERIALS AND METHODS

The material under investigation consisted of twenty eight genotypes of black gram (*Vigna mungo* L. Hepper) that were grown in *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 6m above sea level. The climate is relatively warm with an average temperature of about 29 – 30^{o}C, and humid of about 65 – 70%. The genotypes used are listed in Table - 1. The research field adopted in a randomised block design (RBD) fashion with three replications and all prescribed cultivation approaches for

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

establishing a robust and productive crop with appropriate agronomic measures were maintained. Each plot separated by 25 cm between rows and 15 cm between plants, all of which were kept under check by appropriate thinning. Five competing plants from each replication were chosen at random to be the subjects of single plant observations. Observations were recorded on individual plant basis. For statistical analysis, the average of these five plants was utilised, considering factors such as plant height at maturity, pod length, number of branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, 100 seed weight, and seed yield per plant. The genetic diversity was evaluated using Mahalanobi's D2 statistic. The National Pulses Research Centre (Vamban), Tamil Nadu Agriculture University (Coimbatore) and some local regions of Tamil Nadu are the source of collection for genotypes under study.

3. RESULTS AND DISCUSSION

ANOVA is used to analyze the mean sums of squares of nine various characters. Analysis of variance revealed high significant differences for all traits under investigation among the twenty-eight black gram genotypes, at the five percent significance level, suggesting the existence of adequate substantial genetic diversity among various genotype. These outcomes coincided with the conclusions of Kumar et al. [5], Priyanka et al. [6], Balachandran et al. [7], Rolaniya et al. [8] and Nagmi and Lal [9]. The clustering pattern demonstrated the presence of a considerable degree of diversity. It is clear that the genotypes, regardless of where they originated, have clustered into distinct groups. This indicates that the genetic makeup of the cultivars played a greater role than their origin and geographic range (Mehandi et al., 2013). To assess the phylogenetic relationship between the genotypes and identify the appropriate genotypes for subsequent breeding programmes, genetic divergence assessment was employed extensively. The process of identifying and removing duplicate accessions from gene pools is aided by genetic diversity analysis. Table 2 presents six unique clusters that were formed based on the genetic divergence of 28 genotypes under consideration.

Out of the five clusters, cluster VI had the most genotypes (11 genotypes) followed by cluster IV with five genotypes, cluster I with four genotypes, cluster II and III with three genotypes, and cluster V with two. According to these results, regional diversification may not have a significant impact on genetic divergence. The genotypes originated from different geographical locations found under same cluster, proving that genetic diversity and geographic divergence are not always connected. Within the cluster, the divergence reflects the divergence between genotypes in the same cluster. On the other hand, inter-cluster divergence indicates the differences in genotype between two dissimilar clusters. A rigorous investigation of the clusters showed that they were diverse both within and between one another based on nine key character relations. These genotypes in one cluster and those in the other cluster had a tight genetic link, as evidenced by the reduced D^2 value between their characters. These findings are supported by the results obtained by Manikannan et al. (2000), Lad et al. [10], Konda et al. [11], Majumdar et al. (2011) and Panigrahi et al. (2014), Partap et al. [12], Rolaniya et al. [8], Mallikarjuna et al. [13] in black gram.

Table 2. Composition of D^2 clusters for twenty eight black gram germplasms

Clusters	List of Genotypes of Black gram under each cluster	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, G24, G12, G18, G21, G14, G22, G23, G25, G13, G26	11

Table 3. Average inter and intra-cluster D^2 values for twenty eight 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

Table 4. Cluster mean of twenty eight 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

Note: 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)

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 Table 3 displays that there is a considerable effect and significant degree of genetic variety among the genotypes under the different clusters, with the intra-cluster distances being found to be lower than the inter-cluster distances. 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 were found to have the highest inter-cluster distances (23.383). These clusters of genotypes can be employed in a breeding program to obtain transgressive segregates and a broad range of diversity. These clusters of genotypes can be employed in a breeding program to obtain transgressive segregates and a broad range of diversity. The minimal separation distance of 5.865 between clusters I and II suggested a tight

genetic relationship between these clusters. It may be best to avoid selecting parents from these clusters since this might lead to a restricted narrow genetic basis. This result is supported by the findings of Jayamani and Sathya [4], Lad et al. [10], Konda et al. [11], Umadevi and Ganesan [14] and Katna and Verma [15] in black gram. The results indicate that cluster IV had the highest intra-cluster distance (22.85) among the clusters, whereas cluster II had the lowest intra-cluster distance (1.994). Because of the great genetic variety among its genotypes, the intra-cluster distance was greater. By crossing the genotypes of the same cluster that exhibit a low value for intra-cluster distance, there is very little possibility of delivering exceptional segregates. Therefore, it would be logical to attempt crosses between the genotypes of clusters separated by larger inter-cluster distance. The limited variation and choice of parents in the clusters with higher means for a selected characters could also be helpful in the future development of high-yielding black gram cultivars.

The Table 4, illustrates the cluster mean for each of the nine characters. For 100 seed weight (5.28) and pod length (4.98), the genotypes of cluster III were greater than those of cluster V (5.11) and (4.86), respectively. The traits 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) are among the desired direction of traits possessed by the genotypes that belong to cluster III. The cluster I is stands next in terms of plant height, branches per plant, clusters per plant, and large quantity of pods per plant. It is proposed that greatest heterosis and broad genetic architectural diversity would be predicted in crossings between parents from the most divergent cluster. In order to produce desirable segregates with higher yield for developing superior varieties of black gram, it is therefore expected that 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 will exhibit high heterosis.

The Table 5, depicts the percentage impact to the total divergence of the different traits. The results indicated that the seed yield was higher (50.997) followed by number of pods per plant (8.121), 100 seed weight (29.456), and seed yield (50.997) contributed more to the genetic divergence than the other characters such as pod length (3.661), plant height (2.988), number of clusters per plant (2.220), number of branches per plant (1.005), and number of seeds per pod (0.754) and number of pods per cluster (0.782) towards total divergence [16].

4. CONCLUSION

There was a greater height of variation among the twenty eight black gram germplasms that were employed in the genetic diversity evaluation. Six clusters were formed from the twenty eight black gram germplasms, which was in accordance with the Mahalanobis D^2 clustering pattern. The genetic distance, the contribution of individual characteristics to the overall divergence, and the size of the cluster means for individual characters exhibiting the highest heterosis should all be taken into consideration when selecting the parents for the hybridization procedure. 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 probable to generate novel associations with the desired traits to gain the appropriate segregates with increased yield for creating better black gram cultivars.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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