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GENETIC DIVERSITY STUDIES IN BLACKGRAM [*VIGNA MUNGO* (L.) HEPPER] GENOTYPES USING D^2 STATISTICS

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ABSTRACT

Genetic divergence analysis is very helpful to compute the nature and extent of genetic diversity in a group of germplasm and also for the identification of genetically diverse genotypes for hybridization programme. Mahalanobis D^2 statistics was used to conduct the study on genetic divergence and clustering pattern utilizing thirty genotypes of blackgram for eight quantitative traits. The genotypes studied were grouped into five clusters. Cluster-I was the largest comprising of 22 genotypes followed by cluster II with 5 genotypes and cluster III, cluster IV and cluster V with one genotype each. The distribution of genotypes was random and genotypes from different geographic regions were grouped in the same cluster, while genotypes from the same geographic region were scattered in different clusters. Results on inter cluster distance revealed highest divergence was observed between cluster III and cluster V (507.93) followed by cluster II and III (396.44), cluster III and IV (371.15) and cluster I and V (313.96) while intra cluster distances was noticed to be maximum for cluster I (51.25). On comparing inter and intra cluster distance, inter cluster distances proved to be higher denoting the fact that, greater genetic divergence existed in the experimental material. Cluster I (51.25) had the highest intra cluster distance among the five clusters indicated the presence of some amount of genetic divergence in the genotypes belonging to this cluster. The genotypes carefully selected from this cluster may be used in future recombination breeding programme. The remaining four clusters had zero intra cluster distances as they each had a single genotype except cluster II indicated that by crossing the genotypes of the same clusters that exhibited a low value for intra cluster distance, there is very little possibility of delivering exceptional segregates. Maximum per se performance for seed yield per plant was recorded in cluster III followed by cluster V and cluster I. Cluster III has recorded less cluster mean for days to flowering, days to maturity and plant height in desired direction for earliness and dwarf plant type and also no. of seeds per pod and 100 seed weight. Cluster V recorded high cluster mean for plant height (64.80), no. of pods per plant, while high cluster mean for no. of clusters per plant was recorded by cluster I. Greatest heterosis and broad genetic architectural diversity would be predicted in crossings between parents from the most divergent cluster along with high mean value for important characters are likely to be highly rewarding. The genotype MBG-1070 belongs to cluster III may be utilized in hybridization programme aimed at improvement of the traits. Seed yield per plant (48.04) was noticed to contribute maximum for genetic divergence followed by 100 seed weight, days to 50% flowering, no. of pods per plant and plant height. In order to produce desirable segregants with higher yields for developing superior varieties of blackgram, it is therefore expected that crosses between the genetically divergent genotypes of cluster III and cluster I, cluster IV and I, cluster III and V will exhibit high heterosis.

Key words : Blackgram, D^2 analysis, Diversity, Yield.

Introduction

Blackgram [*Vigna mungo* (L.) Hepper] is popularly known as urdbean or mash is a grain legume domesticated from *Vigna mungo* var. Silverstris. It is one of the most important ancient and important legume crop of India which contributes 70% of worlds total production. Urdbean occupies an important position due to its high seed protein (25-26%), carbohydrates (60%), fat (15%), minerals, amino acids and vitamins with additional ability to restore the soil fertility through symbiotic nitrogen fixation. The crop is a potential component of various cropping systems, especially in rice and wheat fallows owing its short life cycle (70-90 days), capacity to fix nitrogen and drought tolerance. India produces approximately 2.7 million tonnes from an approximately 4.4 m ha area with an average yield of 598 kg/ha. (Directorate of Economics and Statistics, 2021). Approximately 60 % of the crop area is cultivated during the *kharif* season, however the *rabi* season cultivation increases due to adoption of early maturing (75-80 days) varieties in rice fallows. Blackgram is a highly nutritious grown legume crop, mainly grown in South and South East Asia with largest area in India, where the crop is challenged by several biotic and abiotic stresses leading to significant yield losses. Improving genetic gains to increase on farm yields is the primary goal of blackgram breeding programmes. Blackgram breeding programmes rely upon a limited number of parental lines, leading to narrow genetic base of the developed varieties. For accelerating genetic gain, there is an urgent need to include more diverse genetic material for improving traits for better adaptability and stress resistance in breeding populations (Nair *et al.*, 2024). Yield improvement of pulse crop highly depends upon the magnitude and nature of genetic variability present in the yield contributing characters (Johnson *et al.*, 1955). Assessment of genetic divergence helps in recognition of genotypes with diverse gene complexes and hybridization between them will be responsive for genetic improvement (Arunachalam, 1981). In this context, the present study was undertaken to assess the nature and magnitude of genetic divergence in 30 blackgram genotypes for seed yield and yield components using D^2 statistics for identification of suitable parents for use in hybridization programme for improvement of seed yield in blackgram.

Materials and Methods

In the present study, 30 blackgram genotypes were raised in Randamized Complete Block design with two replications during *Rabi* 2021-22 at Agricultural Research Station, Madhira, Telangana. Each entry was sown in the two rows of 4m length with 30 × 10 cm spacing. Recommended package of practices and need based crop protective measures were followed. Observations were recorded on five randomly selected plants in each replication for plant height (cm), no. of clusters per plant, no. of pods per plant, no. of seeds per pod, seed yield per plant (g) and 100 seed weight (g), whereas, on whole plot basis for days to 50% flowering and days to maturity. The data was subjected to analysis of variance and Mahalonobis D^2 statistics (Mahalonobis, 1936) were used for genetic divergence analysis. Analysis of variance was performed as per the method suggested by Panse and Sukhatme (1978). The genotypes were clustered by using Tocher's method as suggested by Rao (1952). The intra and inter cluster distances were calculated and were used to describe the genotypic relationship with the help of the formula given by Singh and Chaudhary (1977).

Results and Discussion

The basic pre-requisite for clustering of genotypes through multivariate analysis is existence of significant differences among the genotypes for multivariate traits (Punithavathy *et al.*, 2020). The analysis of variance for different characters also revealed significant variation among the genotypes taken under study ensuring a high degree of genetic variability among the blackgram genotypes in Table 1. Similar results has been reported by Rajalakshmi *et al*. (2020).

In the present study, 30 blackgram genotypes were grouped into 5 clusters, which indicates the presence of divergence for further crop improvement programme in Table 2. It is clear that the genotypes regardless of where they originated have clustered into distinct groups. Among the clusters, cluster I had a maximum number of genotypes (22) followed by Cluster II with 5 genotypes, whereas, cluster III, cluster IV and cluster V had one genotype each. According to the results, regional diversification may not have a significant impact on genetic divergence. The genotypes originated from different geographical locations found under same clusters proving that genetic diversity and geographical divergence are not always connected. The pattern of distribution of the experimental genotypes into non overlapping discrete clusters suggests the presence of high magnitude of genetic diversity among the genotypes. Similar results reported by Shanti *et al*. (2006), Katiyar and Dixit (2010), Jayashree *et al*. (2019), Rajalakshmi *et al*. (2020) and Prasanna *et al*. (2024).

The average intra and inter cluster D^2 distances are pretended in Table- 3. Within the clusters, the divergence reflects the diversified genotypes in the same cluster. On the other hand, inter cluster divergence indicates the difference in genotypes between two dissimilar clusters. A rigorous investigation of the clusters showed that they were diverse both within and between one another based on the eight key character relations. These genotypes in one cluster and those in the other cluster had a tight genetic link as evidence by the reduced D^2 values between their characters. On comparing inter and intra cluster distance, inter cluster distances proved to be higher denoting the

Table 1 : Analysis of Variance in Blackgram genotypes [*Vigna mungo* (L.)] Hepper.

Source of variations	Degree of freedom	DFF	DM	PH	NC	NP	SPP	SYP	100SW
Replication	1	81.66	56.06	34.80	13.06	48.60	8.06	7.07	0.06
Treatment	29	16.37	12.97	129.69	8.43	88.05	5.81	4.32	0.46
Error	29	0.80	1.89	10.17	1.92	11.66	0.61	0.06	0.01

DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, NC: No. of clusters per plant, NP: No. of pods per plant, SPP: No. of seeds per pod, SYP: Seed yield per plant and 100SW: 100 seed weight.

Table 2 : Grouping of accessions into different clusters based on D^2 values in Blackgram genotypes [*Vigna mungo* (L.)] Hepper.

S. no.	Cluster	Names of genotypes	Total
1	Cluster I	MBG-1069, ABFBG-23 RS, GBG-1, TBG-104, MASH-114, IPU-2-43, MBG-1047, NBG-207, DHARMA, LBG-787, RU-18-33, PU-31, TU-94-2,TU-50, MBG-1034, MBG-1066, GBG-45, MBG-1071, MBG-1045, ABFBG-26 RD, MBG-1046, LBG-752	22
2	Cluster II	MBG-1044, RU-13-113, IC-398958, IC-398956, LBG-685	5
3	Cluster III	MBG-1070	1
4	Cluster IV	IC-436658	1
5	Cluster V	IC-436638	1

Table 3 : Average inter and intra-cluster distances (D^2) values in Blackgram genotypes [*Vigna mungo* (L.)] Hepper.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	**51.25**	134.01	143.15	188.22	313.96
Cluster 2		**0.00**	396.44	135.33	196.46
Cluster 3			**0.00**	371.15	507.93
Cluster 4				**0.00**	91.98
Cluster 5					**0.00**

fact, greater genetic divergence existed in the experimental material. These findings were supported by the results obtained by Panigrahi *et al*. (2014), Geetanjali *et al*. (2015) and Reddy *et al*. (2018). The intra cluster values ranged from zero to 51.25. Cluster I (51.25) had the highest intra cluster distances among the five clusters and rest of the clusters have found to be zero gaps indicating the presence of some amount of genetic divergence in the genotypes belonging to this cluster. The genotypes carefully selected from this cluster may be used in future recombination breeding programme. The remaining four clusters had zero intra cluster distances as they each had a single genotype except cluster II. This indicated that by crossing the genotypes of the same clusters that exhibit a low value for intra cluster distance, there is very little possibility of delivering exceptional segregates.

From the inter cluster D^2 values of five clusters it was found that inter cluster distances ranged from 91.98 to 507.93 and highest divergence was observed between Cluster III and cluster V (507.93) followed by cluster II and III (396.44), cluster III and IV (371.15) and cluster I and V (313.96). The minimal separation distance of 91.98 between clusters IV and V suggested a tight genetic relationship between the clusters. It might be best to avoid selecting parents from these clusters since this might lead to a restricted narrow genetic base.

Similarly, the relatively short inter cluster distances were obtained between cluster II and V (196.46) followed by cluster I and IV (188.22), cluster I and III (143.15), cluster II and IV (135.33), cluster I and II (134.01) and cluster IV and V (91.98). The greater the distance (D^2) between clusters, the greater will be genetic divergence between accessions belonging to that cluster (Ramyashree *et al*., 2016) and crossing between genotypes from different clusters increases the variability of the gene pool. Blackgram germplasm lines from cluster III (MBG-1070) and V (IC 436638) were found to be most divergent and they may be used in the recombinant breeding programme to get good segregants. The limited variation and choice of parents in the clusters with higher means for a selected character could also be helpful in the future development of high yielding blackgram varieties.

Considerable difference was noticed among the cluster means for all the characters depicted in Table 4. The genotypes in cluster V had maximum mean performance for days to 50% flowering (55.50), plant

Table 4 : Cluster means for eight characters in Blackgram genotypes [*Vigna mungo* (L.)] Hepper.

Clusters	DFF	DM	PH	NC	NP	SPP	SYP	100SW
Cluster 1	43.52	73.48	33.44	10.45	22.80	6.84	5.74	5.23
Cluster 2	44.00	73.80	36.24	9.80	21.60	6.60	3.55	4.35
Cluster 3	43.50	73.50	26.20	6.00	11.50	7.50	8.85	5.60
Cluster 4	51.50	84.50	47.60	8.00	18.50	13.00	4.75	5.10
Cluster 5	55.50	79.50	64.80	9.00	27.50	13.00	5.85	4.45

DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, NC: No. of clusters per plant, NP: No. of pods per plant, SPP: No. of seeds per pod, SYP: Seed yield per plant and 100SW: 100 seed weight

Table 5 : Relative contribution of different characters towards total genetic diversity in Blackgram genotypes [*Vigna mungo* (L.)] Hepper.

S. no.	Character	No. of times ranked first	Contribution (%)
1	Days to 50% flowering	28	6.44
2	Days to maturity	2	0.46
3	Plant height	11	2.53
4	No. of clusters per plant	2	0.46
5	Number of pods	21	4.83
6	Number of seeds in pod	5	1.15
7	Seed yield/plant	209	48.04
8	100 seed weight	157	36.09

height (64.80) and number of pods per plant (27.5). Cluster I had maximum no. of clusters per plant (10.45) and cluster IV had maximum mean performance for days to maturity (84.50). The genotypes in cluster III showed highest 100 seed weight (5.60) and seed yield per plant (8.85). Cluster IV and V had maximum number of seeds per pod (13.00). The genotypes in cluster III had minimum mean performance for days to 50% flowering (43.50), plant height (26.20), no. of clusters per plant (6.00) and number of pods per plant (11.50). Cluster II had shown minimum values for number of seeds per pod (6.60), 100 seed weight (4.35) and seed yield per plant (3.55). Cluster I recorded minimum mean performance value for days to maturity (73.48). It is proposed that greatest heterosis and broad genetic architectural diversity would be predicted in crossings between parents from the most divergent cluster along with high mean value for important characters are likely to be highly rewarding. Best donor for hybridization may be choosen from an appropriate clusters and can be utilized in breeding programme for improving any particular trait. (Chauhan *et al.*, 2008 and Prasanna *et al*., 2024). However genotypes selection made in the more divergent clusters is not mandatory instead genotypes grouped under ant two clusters will have ample amount of genetic diversity (Ayesha *et al.*, 2021). Hence, grouping between genotypes with high performance grouped under any two different clusters may have a fair chance of generating heterotic hybrids or transgressive segregants.

The characters contributing to maximum divergence are to be given greater emphasis on deciding the clusters for the purpose of selection of parents for further hybridization. The contribution of the various traits towards total diversity is calculated based on the number of times the characters appear in the first rank. Seed yield per plant appeared 209 times in the first rank, indicating the greatest contribution to total diversity. Days to maturity and no. of clusters per plant on the other hand appeared twice in the first rank, indicating a lower contribution to total diversity. The relative contribution of each trait towards total divergence is mentioned in Table 5. The results revealed the highest contribution of seed yield per plant (48.04%) towards total diversity, followed by 100 seed weight (36.09%), days to 50% flowering (6.43%), number of pods per plant (4.82%) and plant height (2.52%) while other traits like days to maturity (0.45%) and number of seeds per pod (1.14%) were noticed as the lowest contribution towards diversity. Hence, selection of the parents based on seed yield per plant and days to 50% flowering will create more variability in the breeding programme.

The results suggested that the blackgram accessions selected for the present study are mostly divergent for seed yield per plant, 100 seed weight, days to 50% flowering and number of pods per plant as these four characters contributed 95.38 % to the total diversity. The present findings were in agreement with the results obtained by Bhareti *et al*. (2019), Jayashree *et al*. (2020) for days to 50% flowering, 100 seed weight and seed yield per plant, Devi *et al*. (2020) for seed yield per plant and no. of pods per plant, Reni *et al*. (2022) for 100 seed weight and Prasanna *et al*. (2024) for seed yield per plant, no. of pods per plant and 100 seed weight.

Conclusion

The current investigation findings shows that the selected blackgram lines were highly diverse and formed into a total of 5 clusters from the thirty blackgram genotypes, which was in accordance with the Mahalanobis D^2 clustering pattern. The genetic distance contribution of individual characterization to the overall divergence, the size of the cluster means for individual characters exhibiting the highest heterosis should all be taken into consideration while selecting the parents for the hybridization. Based on mean performance and genetic divergence the accessions belong to the most distant clusters namely cluster (III and V), cluster (II and III), cluster (III and IV) and cluster (I and V) and cluster II and cluster III (MBG-1070) and cluster V (IC 436638) in all possible combinations. These might be used directly or as parents in blackgram hybridization programme and are also probable to generate novel associations with the desirable traits to create more variability in segregating material for the development of high yielding blackgram varieties.

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