Nature and Magnitude of Genetic Divergence among Blackgram [Vigna mungo (L.) Hepper] Genotypes

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ABSTRACT

Background: The choice of parents is a very crucial step which decides the success or failure of any plant breeding programme. Using the diversity analysis, parents with high diversity can be chosen to generate high magnitude of useful variability. Therefore, the present investigation was planned to assess the genetic divergence among 100 genotypes of blackgram for identification of diverse genotypes for their utilization in breeding programme.

Methods: The material for study consisted of 100 blackgram genotypes collected from different sources and were evaluated at ARS, Bidar during kharif-2018. The experimental trial was laid out in lattice design (10×10) with two replications. Observations on 12 quantitative characters. The genetic divergence was assessed by using Mahalanobis’ generalized distance (D²) and clustering of genotypes by Tocher’s method.

Result: The relative contribution of each character to the total diversity was different and contribution of days to maturity was maximum (66.04%) followed by reproductive period (15.86%). The genotypes were grouped into nine clusters by Tocher’s method. The cluster pattern revealed that, cluster II was the largest with 28 genotypes followed by cluster I (26), V (19), III (11), IV (10) and VII (3) and remaining viz., VI, VIII and IX were solitary clusters. The inter-cluster distance ranged from 15.50 to 514.44 indicating high magnitude of diversity. The genotypes belonging to cluster III viz., BDU-20, BDU-3-20, BDU-68, TRCRU-22 possessed desirable traits like earliness and higher seed size and genotypes of cluster IV viz., BDU-9, BDU-10, LBG-752 possessed traits like higher reproductive period, maturity and high seed yield were identified as diverse. These genotypes could be involved in recombination breeding programme for the improvement productivity in blackgram.

Key words: Blackgram, Character/trait, Cluster, Diversity, Genotype.

INTRODUCTION

Pulses occupy a unique position not only in Indian agricultural system but also in Indian dietaries. The pulses bring about a formidable solution to the alarming problem of protein scarcity of the world as they contain 20 to 25 per cent protein. They are also important for sustainable agriculture as they improve physical, chemical and biological properties of soil. Blackgram [Vigna mungo (L.) Hepper] is third most important pulse crop both in acreage and production in India. In India, it is grown over an area of 3.64 million ha with an annual production of 1.72 million tonnes (Anonymous, 2020). It is cultivated in almost all parts of India. However, it is mainly grown in the states of Madhya Pradesh, Maharashtra, Uttar Pradesh, Rajasthan, Karnataka and Bihar. During the post green revolution period, the production of pulses recorded a negative growth rate. This disturbing trend in the production of pulses has adversely affected the per capita availability of pulses which has declined from 60.7 g per day in 1950 to 43.0 g in 2016 (Anonymous, 2017). This situation is due to stagnation in expansion of pulse growing area and very slow progress in the improvement of productivity of all pulses. Limited variability has always been suggested as one of the reasons for the failure of the current breeding programmes in legumes to identify potential cultivars with high productivity (Jain, 1975). Plant breeders consider different criteria for selecting parents for hybridization programme and one of the criteria is the diversity of the parents. Therefore, it necessitates the identification of parents with high diversity so as to generate productive / desirable segregating plants in F₂ population. Several methods have been advocated by various workers to estimate the genetic divergence in crop plants. However, Mahalanobis’ generalized distance estimated by D² statistic (Rao, 1952) is a unique tool for...
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discriminating genotypes considering a set of parameters together rather than inferring from indices based upon morphological similarities, eco-geographical diversity. Therefore, the present investigation was planned to assess the genetic divergence among 100 genotypes of blackgram for identification of diverse genotypes for their utilization in blackgram breeding programme.

MATERIALS AND METHODS

The material for study consisted of 100 blackgram genotypes collected from different sources viz., Agricultural Research Station, Bidar, Karnataka; Nuclear Agriculture and Biotechnology Division (NABD), BARC, Trombay, Mumbai, Maharashtra; Indian Institute of Pulse Research, Regional station, Dharwad, Karnataka and Regional Agricultural Research Station, LAM, Guntur, Andhra Pradesh. These were evaluated at Agricultural Research Station, Bidar during kharif-2018. The experimental trial was laid out in lattice design (10×10) with two replications. Each genotype in each replication was represented by a plot size of 4 rows of 4 meter length with a spacing of 30 cm between rows and 10 cm between plants within the row. All the recommended agronomic practices were followed to raise a good crop. Observations on 12 quantitative characters viz., plant height, branches per plant, clusters per plant, pods per plant, seeds per pod, pod length, 100-seed weight and seed yield per plant were recorded on five competitive plants selected at random per genotype in each replication. Whereas, observations on days to 50 per cent flowering, days to maturity, reproductive period and seed yield (kg/plot) were recorded on plot basis. Days to 50 per cent flowering was recorded as number of days from sowing to the opening of the flower in 50 per cent of the plants, days to maturity was recorded as number of days from sowing to 50 per cent pod maturity, reproductive period was recorded as number of days from flowering to maturity and the seed yield per plot was recorded and weighed in kilograms (kg) and converted into seed yield kg/ha for each of the genotype. The genetic divergence was assessed by using Mahalanobis’ generalized distance (D²) (Mahalanobis, 1936) and clustering of genotypes by Tocher’s method (Rao, 1952).

RESULTS AND DISCUSSION

It is believed that the choice of parents is a very crucial step which decides the success or failure of the plant breeding programme. Using the diversity analysis, parents with high diversity can be chosen to generate high magnitude of useful variability. In the present study, 12 quantitative characters were considered for quantifying diversity among 100 blackgram genotypes using Mahalanobis’ generalized distance (D²).

Analysis of variance

The analysis of variance revealed significant differences among blackgram genotypes for all the characters studied, indicating presence of sufficient genetic variability among

| Source of Variation | df | Days to 50% flowering | Days to 100% flowering | Days to maturity | Reproductive period | Pods per plant | Number of clusters per plant | Number of branches per plant | Number of pods per plant | Seed length per pod (cm) | Seed weight per pod (g) | Pod number per plant | Seed yield per plot (kg) | Seed yield per ha (kg/ha) |
|---------------------|----|-----------------------|------------------------|-----------------|---------------------|------------------|----------------------------|----------------------------|------------------------|------------------------|------------------------|------------------------|-------------------------|------------------------|
| Replications        | 1  | 1.519                 | 25.947                 | 19.43           | 0.005               | 0.006           | 0.006                     | 0.006                     | 0.006                  | 0.005                  | 0.006                  | 0.006                  | 0.005                   | 0.006                  |
| Genotypes           | 99 | 681.05**              | 188.37**               | 197.60**        | 197.60**            | 197.60**        | 197.60**                  | 197.60**                  | 197.60**               | 197.60**               | 197.60**               | 197.60**               | 197.60**                | 197.60**               |
| Blocks              | 18 | 2.927                 | 15.838                 | 12.637          | 21.315              | 5.915**         | 3.73                      | 0.015                     | 0.015                  | 0.015                  | 0.015                  | 0.015                  | 0.015                   | 0.015                  |
| Error (Intrablock)  | 81 | 7.719                 | 11.473                 | 15.173          | 26.084              | 0.12            | 0.016                     | 0.016                     | 0.016                  | 0.016                  | 0.016                  | 0.016                  | 0.016                   | 0.016                  |
genotypes used for assessing the diversity (Table 1). Similar studies were carried out by Anu et al. (2017) and Senapati and Misra (2010) in blackgram and identified desirable genotypes for different traits.

**Contribution of different characters towards divergence**

The relative contribution of each character to the total diversity was different (Table 2). Character days to maturity (66.04%) contributed maximum to the divergence of genotypes followed by reproductive period (15.86 %), days to 50 per cent flowering (9.31 %) and 100-seed weight (4.26%). However, remaining characters had very negligible contributions towards divergence. Plant height, 100-seed weight, days to maturity and reproductive period contributed much for diversity (Konda et al., 2007); Geetanjali et al. (2015) reported that days to 50 per cent flowering, days to maturity and plant height contributed much for the diversity. While, Kumar et al. (2018) reported that plant height, days to 50 per cent flowering and single plant yield contributed much for the diversity in blackgram.

**Group constellation**

The estimates of genetic divergence ($D^2$) were used to classify genotypes into clusters by Tocher’s method (Table 3). In the present study, the genotypes were grouped into nine clusters indicating the extent of diversity observed was high. The clustering pattern revealed that, cluster II was the largest with 28 genotypes followed by cluster I (26), V (19), III (11), IV (10) and VII (3) and remaining clusters viz., VI, VIII and IX were solitary clusters. Geographic origin is one of the primary factors which contribute to the level of genetic diversity. The genotypes involved in the present study represented diversified geographic regions of their adaptation. Maximum number of genotypes (28) were grouped in the same cluster even though their area of adaptation was different. The results suggested that the geographic distribution would not exclusively determine cluster compositions which support the earlier observation of Dasgupta and Das (1991) and Gantait and Das (2009) in blackgram. The grouping of varieties of different geographic origin in the same cluster could also be expected because of the free exchange of material from one region to another. Another reason attributed for coming together of entries from different geographical regions in the same cluster is unidirectional selection practiced by plant breeders of different locations (Singh and Bains, 1968). Nevertheless, few entries from ARS, Bidar (BDU-11, BDU-12, BDU-18 in cluster VII), few entries from Lam, Guntur, Andhra Pradesh (LBB-465, LBB-645, LBB-757, LBB-685 in cluster II) remained together and entered different clusters, indicating that the geographic distribution continued to play an important role in determining the genetic affinity. Thus, the importance of geographic distribution cannot be over ruled altogether.

**Intra-cluster and inter-cluster distances**

The intra-cluster and inter-cluster distances are presented in the Table 4. The maximum difference among the genotypes

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**Table 2:** Per cent contribution of different traits towards total diversity in blackgram genotypes.

| Character                          | Kharif  |
|-----------------------------------|---------|
| Days to 50% flowering             | 9.31    |
| Days to maturity                  | 66.04   |
| Reproductive period               | 15.86   |
| Plant height (cm)                 | 1.27    |
| Number of branches per plant      | 0.02    |
| Number of pods per plant          | 0.48    |
| Number of clusters per plant      | 0.30    |
| Number of seeds per pod           | 0.10    |
| Pod length (cm)                   | 0.24    |
| Hundred seed weight (g)           | 4.26    |
| Seed yield per plant (g)          | 0.65    |
| Seed yield (kg/ha)                | 1.45    |

**Table 3:** Clustering pattern of 100 blackgram genotypes.

| Cluster Number | Number of genotype/Cluster | Name of the genotypes                              |
|----------------|-----------------------------|----------------------------------------------------|
| I              | 26                          | Manikya, PANT-U-40, TRCRU-103, TRCRU-136, Vamsan-3, TRCRU-134, TRCRU-24, TU-91-2, IPU-2-43, GP-728 RU 1605, VBG-04, RU-16-02, DBG-11, RU-16-14, DBGV-5, Shekhar, MASH-1, 2KU-63, BG-17-10, LBG-20, TU-98-1-18, BG-17-06, PU-19, Uttar9 and IC-436516. |
| II             | 28                          | KU-537, DU-7-638, IC-436778, TAU-1-12, AKU-15, BDU-3-3, DU-2, VBG-5, 488-15-16, TRCRU-18, COBG-657, LBB-685, TRCRU-67, LBB-757, BDU-6, LBG-645, RU-16-12, TU-98-10-5, LBG-645, RU-16-07, OBG-33, TU-94-04, DU-1, TAU-1, BDU-17, GP-BDU-3-01, RU-16-10 and BDU-3-23. |
| III            | 11                          | BDU-3-20, I-447-2, 2KU-64, GP-553, BDU-1, T-200-6, LBG-17, BDU-68, TRCRU-22, TRCRU-339, BDU-20. |
| IV             | 10                          | BDU-58, DU-3-2, BDU-10, BDU-9, T-9, LBG-752, RU-16-9, BDU-3-21, GPS-53-1, TU-94-2. |
| V              | 19                          | PMS-2, RU-16-15, LBB-623, KU-5-527, LBB-3-4, 2KU-15, BDU-5, VBN-4, KML-8, TRCRU-262, RU-16-8, OBG-647, TU-99-852, K-3, BDU-3-22, TRCRU-26, TRCRU-43-1, BG-17-03, PU-31. |
| VI             | 01                          | PU-30                                             |
| VII            | 03                          | BDU-11, BDU-12, BDU-18                            |
| VIII           | 01                          | TRCRU-111                                         |
| IX             | 01                          | WBU-1372                                          |
within same cluster was seen in cluster VII as it exhibited maximum intra-cluster $D^2$ value (47.34) whereas, the minimum intra-cluster distance was observed in cluster I (19.95). The inter-cluster distance ranged from 15.50 to 514.44 and considering the upper limit of the $D^2$ values, the extent of diversity was high. Similar studies were also carried out in blackgram by Konda et al. (2007) and Gantait and Das (2009).

**Cluster means**

The cluster means generally indicate the characteristic features of the clusters and help in identifying potential clusters for different characters based on the mean values. In the present investigation, the cluster mean values revealed existence of sufficient variation among clusters for all most all traits (Table 5). Cluster VI may be regarded as a good source for earliness as it recorded lowest mean for days to 50 per cent flowering. Plant height is one of the important component traits of yield (Ram and Singh, 1993 and Mahto and Mahto 1997) and taller plants are best suited for mechanical harvesting. Cluster VII was regarded as good source for taller plants as it recorded higher mean values. Cluster IV was good source of genotypes having higher mean for reproductive period, an important phenological trait influencing yield through its positive association with main components of yield. Cluster VII was superior with respect to seed yield per plant as well as seed yield (kg/ha) and also recorded high number of clusters, number of pods.

**CONCLUSION**

Development of varieties with high yield potential is the ultimate goal of plant breeders in a crop improvement programme. Earliness, seed size and seed yield are most important traits in blackgram. Hundred seed weight is an important character deciding consumer preference and market acceptability. Usually, a variety with larger seed size is preferred by farmers, consumers as well as trades. In order to bring about improvement either for the earliness or for improvement of yield or seed size, the genotypes from diverse cluster should be chosen to effect hybridization so that desirable variability with high magnitude is created for these characters. From this point of view, the genotypes of cluster III are early maturing with higher seed size (BDU-20, BDU-3-20, BDU-68, TRCRU-22) whereas, genotypes of cluster III are early maturing with higher seed size (BDU-9, BDU-10, LBG-752). Cluster III is more diverse to cluster IV compared to other clusters on basis of inter-cluster $D^2$ values. Therefore, selected genotypes of cluster III may be crossed to selected genotypes of clusters of IV for recombining the desirable features viz., earliness, productivity and larger seed size. The same strategy may be adapted for improvement other traits.

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