



Genetic Divergence Studies in Blackgram

Key words : Genetic Divergence, Blackgram

Blackgram (*Vigna mungo* (L.) Hepper) is an important pulse crop of India. This crop is a major source of dietary protein, minerals and vitamins for Indian vegetarians. Blackgram root also fix approximately 38 kg nitrogen in the soil from atmosphere and thus adds to the soil nitrogen wherever it is grown. In breeding programmes selection of parents for hybridization is largely based on wide adoption. Progenies derived from a set of diverse crosses are expected to throw a broad spectrum of genetic variability providing larger scope for isolating high yielding segregants. For this, precise information about the extent of genetic divergence is very crucial. D^2 statistic developed by Mahalanobis (1936) is a powerful tool in quantifying the degree of genetic divergence among the biological populations and accessing the relative contribution of different components to the total divergence at intra and inter cluster levels. In the present investigation, an attempt was made to ascertain the nature and magnitude of genetic divergence in 70 germplasm accessions of blackgram. Seventy diverse germplasm accessions of blackgram obtained from Regional Agricultural Research Station, Lam Farm, Guntur were evaluated in Randomised Block Design with three replications during *rabi*, 2009-10 at Agricultural Research Station, Podalakur representing Southern Zone of Andhra Pradesh. Each accession was sown in a three rows of 4.0 m length with a spacing of 30 cm x 10 cm. The recommended cultural practices were followed to raise a good crop. Observations were recorded on ten randomly chosen plants in each accession and replication for seven traits *viz.*, plant height, number of clusters/plant, number of pods/plant, pod length, number of seeds/pod, 100-seed weight and seed yield/plant. The data was subjected to the D^2 statistical analysis as suggested by Mahalanobis (1936). Group constellations were determined as per the Tocher's method (Rao, 1952).

The analysis of variance revealed significant differences among the genotypes for all the traits studied. Based on D^2 statistics, the 70 accessions

were grouped into six clusters with variable number of accessions revealing the presence of considerable amount of genetic diversity in the material. Cluster I had the maximum number of genotypes (57) followed by cluster II with 8 genotypes and cluster IV with two genotypes (Table 1). The clusters I and II together had 65 genotypes reflecting a narrow genetic diversity among them. Further, clusters III, IV and VI had one genotype each demonstrating the impact of selection pressure in increasing the genetic diversity. The germplasm accessions included in a cluster were from diverse geographical origin indicating that the geographic diversity need not be necessarily related to genetic diversity. The absence of correlation between genetic diversity and geographical diversity has also been reported by Elangaimannan *et al.* (2008) and Revanappa *et al.* (2004). The random pattern of distribution of genotypes into various clusters from different eco-geographic regions suggests that forces other than geographic influence such as exchange of breeding material, common parentage, genetic drift, natural and artificial selection are responsible for diversity (Murthy and Arunachalam, 1966).

Contribution of different characters towards genetic divergence is represented in Table 2. It was observed that among all the characters, the seed yield/plant contributed towards genetic divergence maximum (47.49%) followed by 100-seed weight (40.95 %) and plant height (8.24 %). These characters together accounted for more than 96 % of the total divergence. This was also confirmed by Abdul Ghafoor and Muhammad Arshad (2008) and Chauhan *et al.*, (2008). The inter cluster D^2 values ranged from 6.52 to 17.73 (Table 3). The maximum inter cluster distance was observed between the cluster II and V (18.55) followed by II and VI (17.73) and II and III (15.73) which indicated that the crosses among the genotypes included in these clusters may give high heterotic response and thus better segregants. The minimum inter cluster distance was observed between cluster III and IV (6.52) indicating the close relationship among the genotypes of these

Table 1. Distribution of 70 blackgram germplasm lines in different clusters.

| Cluster | No. of genotypes | Name of the genotypes |
|---------|------------------|--|
| I | 57 | UBGP 45, UBGP 55, UBGP 63, LBG 17, UBGP 52, UBGP 46, UBGP 3, UBGP 68, UBGP 19, UBGP 48, UBGP 2, UBGP 43, UBGP 16, UBGP 43, UBGP 45, UBGP 56, UBGP 44, UBGP 60, UBGP 23, UBGP 70, PBG 201, LBG 709, UBGP 32, UBGP 53, LBG 752, UBGP 11, LBG 623, UBGP 11, UBGP 13, UBGP 47, UBGP 26, UBGP 36, UBGP 33, UBGP 57, UBGP 12, UBGP 20, UBGP 27, PBG 107, UBGP 49, PBG 201, UBGP 40, UBGP 14, UBGP 8, UBGP 39, UBGP 59, UBGP 61, ADILABAD LOCAL, LBG 645, UBGP 1, UBGP 17, UBGP 18, UBGP 48, UBGP 65, UBGP 38, PBG 32, UBGP 41, UBGP 69 |
| II | 8 | LBG 20, UBGP 66, UBGP 32, UBGP 51, UBGP 50, UBGP 25, UBGP 24, UBGP 37, |
| III | 1 | PBG 1 |
| IV | 1 | UBGP 42 |
| V | 2 | UBGP 9, UBGP 34 |
| VI | 1 | UBGP 10 |

Table 2. Cluster means and contribution of each character towards total divergence in blackgram.

| Character | Cluster means | | | | | | Contribution to diversity (%) |
|-----------------------|---------------|-------|-------|-------|-------|-------|-------------------------------|
| | I | II | III | IV | V | VI | |
| Plant height(cm) | 19.31 | 22.92 | 27.00 | 27.00 | 17.83 | 31.67 | 8.24 % |
| No. of clusters/plant | 3.80 | 5.75 | 11.00 | 7.33 | 2.50 | 12.00 | 1.78 % |
| No. of pods/plant | 8.88 | 13.88 | 13.00 | 14.33 | 6.33 | 21.67 | 0.58 % |
| No of seeds/pod | 5.84 | 6.29 | 6.67 | 7.00 | 6.33 | 8.00 | 0.66 % |
| pod length (cm) | 4.32 | 4.33 | 4.87 | 5.33 | 4.33 | 4.57 | 0.29 % |
| 100-seed weight(g) | 3.88 | 4.03 | 5.10 | 5.30 | 5.92 | 5.27 | 40.95 % |
| Seed yield /plant(g) | 5.27 | 32.57 | 7.20 | 18.67 | 9.22 | 12.47 | 47.49 % |

clusters. The maximum intra-cluster distance was reported in cluster II (7.16) followed by cluster V (6.40). The data on the character means for six clusters (Table 2) indicated that the cluster VI showed the highest cluster mean for three characters viz., no. of clusters/plant, no. of pods/plant and no. of seeds/pod. The Cluster II showed the highest mean

values for seed yield/plant, cluster V for 100-seed weight and cluster IV for pod length. Therefore, on the basis of D^2 value and high mean values it is suggested that hybridization between the genotypes of clusters II (UBGP 37), V (UBGP 9) and VI (UBGP 10) would produce wide array of variability in the segregating generations and useful in making the new gene pool for selection.

Table 3. Average intra and inter-cluster distance for the six clusters in blackgram.

| Cluster | I | II | III | IV | V | VI |
|---------|-----------------------|-----------------------|-------------------------|-----------------------|-----------------------|-----------------------|
| I | 6.62 (2.57) | 13.53 (3.67) | 9.67 (3.11) | 10.64 (3.26) | 13.39 (3.66) | 15.57 (3.95) |
| II | | 7.16 (2.68) | 15.73 (3.97) | 11.66 (3.41) | 18.55 (4.31) | 17.73 (4.21) |
| III | | | (0.00) (0.00) | 6.52 (2.55) | 8.79 (2.97) | 10.75 (3.28) |
| IV | | | | 0.00 (0.00) | 8.87 (2.98) | 11.07 (3.33) |
| V | | | | | 6.40 (2.53) | 15.26 (3.91) |
| VI | | | | | | 0.00 (0.00) |

D values in parenthesis

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