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# Genetic Diversity for Yield and its Components in Blackgram(*Vigna mungo* L.)

Biotechnology

**KEYWORDS :** Genetic Divergence, Vigna-mungo, yield attributes.

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## ABSTRACT

*Fifty two genotypes of blackgram were subjected to genetic divergence by using D2 statistic. The genotypes were grouped into ten clusters by D2 analysis. Cluster Iconsisted maximum accessions (24) followed by cluster II and III (8) and cluster IV with (6) and cluster V,VI,VII,VIII,IX and X consisted only 1 accession. The inter-cluster distances were greater than intra-cluster distances, revealing that considerable amount of genetic diversity existed among the accessions. Maximum intra cluster distance was observed in cluster IV (6.91), followed by cluster III (6.32), cluster II (6.28) and cluster I (5.42) indicating that some genetic divergence still existed among the genotypes. This could be made use of in the yield improvement through recombination breeding. Highest mean values exhibited plant height in cluster X (68.33) and No. of branches per plant, No.of clusters per plant in cluster V (17.00) and No. of pods per plant (30.33). No.of seeds per pod in cluster VI (8.00),100 seed weight in cluster X (5.43) and Days to full maturity recorded (54.67) and seed yield per plant in cluster III (68.94). The characters contributing maximum towards diversity among the accessions are Days to initial flowering (22.85%) followed by % disease incidence (21.64%), days to full maturity (19.23%), plant height (17.27%), 100 seed weight (5.58%).These characters combining with early maturity are the major traits causing genetic divergence among the accessions. It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters.*

## I.INTRODUCTION

It has been postulated that lack of genetics diversity is one of the basic causes for relatively poor success achieved in raising yield level in urdbean (*Vigna mungo* L. Wilczek).An assessment of the genetic diversity is an important first step in a program to improve crop yield. The proper estimate of nature and magnitude of diversity in a crop is essential to infer about extent of variation available for yield and its component traits. The selection of genetically divergent parents is expected to produce superior and desirable segregants following crossing (Bhatt, 1973). The availability of genetically diverse germplasm is the basic need for the progress in plant breeding. Choice of parents for hybridization is one of the important considerations for creating new variability. Several biometrical approaches have been shown to be useful in selecting parents for successful hybridization program me. D2 analysis has been found most effective and, therefore, widely used for the classification of parental lines for developing high yielding genotypes in blackgram. The present study was therefore, undertaken to estimate the amount of genetic diversity in Seventy five genotypes of black gram Gram (*Vigna mungo* L. Hepper) and to identify genetic diverse parents for hybridization programmed at yield improvement in this crop.

## 2. METHODOLOGY

Fifty two blackgram genotypes collected from diverse geographical origin were evaluated during rabi season 2014-2015 at experimental field of college form in Professor Jayashankar Telangana state Agriculture university,(PJTSAU), Rajendranagar, Hyderabad. All the 52 genotypes were sown in rondomised block design with three replications each genotype was grown in row of 2m length with 30cm row to row and 10cm plant to plant distance. ten competitive plants from each entry were randomly chosen to record the observations on plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod,100 seed weight, days to initial flowering, days to full maturity and seed yield per plant. The genetic divergence was estimated using mahalanobis'$D^2$ statistic(Mahalanobis,1936) and genotypes were grouped into clusters following the Tochers' method as described by Rao,1952.

## 3.Results and Discussion

Fifty two genotype were found to be distributed in 10 clusters (Table. 1). Out of ten clusters, cluster I was the largest comprising of twenty four genotypes followed by cluster II and cluster III with eight genotypes, cluster IV with six genotypes and cluster V,VI,VII,VIII,IX and X with one genotype each. The cluster V, VI,VII,VIII, IX and X were represented by single genotype indicating high degree of heterogeneity among the genotypes. Maximum intra cluster distance was observed in cluster IV (6.91), followed by cluster III (6.32), cluster II (6.28) and cluster I (5.42) indicating that some genetic divergence still existed among the genotypes. This could be made use of in the yield improvement through recombination breeding. From the inter cluster $D^2$ values of the ten clusters, it can be seen that the highest divergence occurred between IX and X (15.02) followed by cluster III and IV (14.07),cluster IV and VII (13.07),cluster III and IX (12.96),cluster II and X (12.71) that the crosses involving varieties from these clusters would give wider and desirable recombination. While the lowest was noticed between cluster VI and VII (5.64) followed by cluster VIII and IX (5.99), cluster VI and VIII (6.03), cluster V and VII (6.24), cluster V and VI (7.10), cluster V and VIII (7.54), cluster I and II (7.58). Minimum inter cluster distance indicate that genotypes of these clusters had maximum number of gene complexes. The genotypes of these clusters may be used as parents in the crossing program to generate breeding material with high diversity. The results are in accordance with Solomon *et al.* (2012). The cluster means for each of 11 characters are presented in Table 4.6. From data it can be seen that considerable differences existed for all the characters under study. The data indicated that the cluster mean for plant height was highest in cluster X (68.33) and lowest in cluster IX (23.00). No. of branches per plant was highest in cluster X (14.00) and lowest in cluster V (7.00). No.of clusters per plant was highest in cluster V (17.00) and lowest in cluster IX (5.33). No. of pods per plant was highest in cluster V (30.33) and lowest in cluster II (14.88). cluster VII were recorded lower (4.40) pod length and highest in cluster XI (5.03). 100 seed weight was highest in cluster X (5.43) and lower in cluster VI (3.17). Days to initial flowering was highest in cluster X (8.28) and lower in cluster II (3.46). Days to 50% flowering was highest in cluster X (49.00) and lower in cluster IX (32.00). Days to full maturity recorded highest in cluster X (54.67) and lower in cluster IX (36.00). seed yield per

plant was highest in cluster III (68.94) and lower in cluster VIII (27.20). The results indicate that selection of genotypes having high values for particular trait could be used in the hybridization programme for improvement of that character. The characters contributing maximum divergence needs greater emphasis for deciding on the clusters for the purpose of selection of parents in the respective cluster for hybridization. The number of times each of the yield component characters appeared first in rank and its respective percent contribution towards genetic divergence was presented in Table 4. Among the yield attributing traits the maximum contribution towards divergence was made by Days to initial flowering (22.85%) by taking 303 times ranking first, followed by days to full maturity (19.23%) by 255 times, plant height (17.27%) by 299 times. Vohra and beniwal (1979) reported that MYMV infection affect seed yield when the plants have infection up to 50 days after planting and reduction in yield contributing characters such as pods per plant, seeds per pod, 100 seed weight.The pattern of distribution of genotypes into various clusters indicates that geographical diversity having no parallelism with clustering pattern which was in agreement with earlier reports in black gram (Ganesh Ram *et al.* 1997; Sagar. *et al.* 2001). The genotypes belonging to different clusters having maximum divergence can be successfully utilized in hybridization programmes to get desirable transgressive segregants. It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters (Panigrahi *et al.* 2014). However, for a practical plant breeder, the objective is not only high heterosis but also to achieve high level of production. To improve any particular trait donor for hybridization could be chosen from an appropriate cluster and that should be utilized in breeding Programme.

**Table 3.1. Clustering pattern in black gram genotypes in Mohalanobis $D^2$ analysis.**

| Cluster no | No.of genotypes | Names of genotypes |
|---|---|---|
| I | 24 | CO.BG-653,MASH-1114,MBG-1041,MBG-1055,KDRS-254,MBG-207,MBG-217,MBG-220,KU-551,WBG-26,MBG-1048,KU-12-18,RU-10-628,CN-9062,CN-8072,RFU-1301,RFU-1309,MBG-1050,MBG-1052,MBG-223,LBG-20,LBG-645,PU-31, |
| II | 8 | KU-11-662,KU-08-668,RU-10-632,KU-08-155,SU-509,RFU-1310,KU-11-652,SU-505, |
| III | 8 | LBG-17,LBG-402,LBG-685,MBG-226,RU-13-114,MBG-1058,MBG-1034,BG-7 |
| IV | 6 | KU-12-56,KU-8-551,KU-12-06,KU-12-37,KU-08-235,T9 |
| V | 1 | RU-12-05 |
| VI | 1 | KDRS82/B |
| VII | 1 | RU-13-108 |
| VIII | 1 | MBG-1054 |
| IX | 1 | RU-10-625 |
| X | 1 | LBG-752 |

**Table 3.2. Mean values of 10 clusters obtained by Tocher's method in 52 Black gram genotypes.**

| Cluster No | Plant height (cm) | No.of Branches/ plant | No. of clusters/ plant | No of pods/ plant | No of seeds/pod | pod length | 100 seed weight | Days to initial flowering | Days to 50% flowering | Days to full maturity | Seed yield / plant |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Cluster I | 37.75 | 9.10 | 12.31 | 16.89 | 5.78 | 4.86 | 4.13 | 4.02 | 36.49 | 41.19 | 66.34 |
| Cluster II | 32.83 | 7.25 | 7.00 | 14.88 | 5.63 | 4.40 | 4.19 | 3.46 | 34.46 | 39.25 | 66.91 |
| Cluster III | 35.08 | 11.42 | 12.33 | 19.42 | 5.58 | 4.67 | 4.69 | 5.12 | 43.92 | 49.63 | 68.94 |
| Cluster IV | 61.17 | 9.44 | 11.39 | 22.39 | 5.44 | 4.92 | 4.26 | 5.25 | 36.39 | 40.83 | 49.22 |
| Cluster V | 29.67 | 7.00 | 17.00 | 30.33 | 5.33 | 4.50 | 4.20 | 6.77 | 40.33 | 43.33 | 40.40 |
| Cluster VI | 41.33 | 10.33 | 15.00 | 18.33 | 8.00 | 4.83 | 3.17 | 4.65 | 39.67 | 45.00 | 28.60 |
| Cluster VII | 27.00 | 7.33 | 12.67 | 23.33 | 7.00 | 5.03 | 3.83 | 6.25 | 43.67 | 46.67 | 33.17 |
| Cluster VIII | 30.33 | 8.67 | 10.67 | 15.33 | 6.00 | 4.83 | 3.87 | 3.60 | 35.33 | 41.00 | 27.20 |
| Cluster IX | 23.00 | 8.00 | 5.33 | 18.67 | 5.00 | 4.40 | 4.23 | 4.01 | 32.00 | 36.00 | 34.00 |
| Cluster X | 68.33 | 14.00 | 14.00 | 23.00 | 6.67 | 4.97 | 5.43 | 8.28 | 49.00 | 54.67 | 66.60 |

**Table 3.3. Average intra (bold)and inter cluster distances formed by Tocher's method in black gram genotypes.**

| Cluster | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI | Cluster VII | Cluster VIII | Cluster IX | Cluster X |
|---|---|---|---|---|---|---|---|---|---|---|
| Cluster I | **5.42** | 7.58 | 8.47 | 9.84 | 8.47 | 8.29 | 9.95 | 8.29 | 9.72 | 10.21 |
| Cluster II | | **6.28** | 11.08 | 10.19 | 10.43 | 9.74 | 10.42 | 10.02 | 8.81 | 12.71 |
| Cluster III | | | **6.32** | 14.07 | 9.41 | 9.67 | 9.30 | 10.19 | 12.96 | 9.19 |
| Cluster IV | | | | **6.91** | 11.76 | 9.72 | 13.07 | 10.60 | 10.42 | 11.51 |
| Cluster V | | | | | **0.00** | 7.10 | 6.24 | 7.54 | 8.96 | 12.26 |
| Cluster VI | | | | | | **0.00** | 5.64 | 6.03 | 9.25 | 9.72 |
| Cluster VII | | | | | | | **0.00** | 8.26 | 10.06 | 11.63 |
| Cluster VIII | | | | | | | | **0.00** | 5.99 | 12.04 |
| Cluster IX | | | | | | | | | **0.00** | 15.02 |
| Cluster X | | | | | | | | | | **0.00** |

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**Table 3.4. Percent contribution of different characters towards divergence in Black gram genotypes.**

| S. No | Characters | Contribution (%) | Times ranked first |
|---|---|---|---|
| 1 | Plant height(cm) | 17.27% | 229 |
| 2 | No.of Branches/ plant | 0.83% | 11 |
| 3 | No. of clusters/ plant | 2.79% | 37 |
| 4 | No of pods/plant | 4.90% | 65 |
| 5 | No of seeds/pod | 0.00% | 0 |
| 6 | Pod length | 0.30% | 4 |
| 7 | 100 seed weight | 5.58% | 74 |
| 8 | Days to initial flowering | 22.85% | 303 |
| 9 | Days to 50% flowering | 4.45% | 59 |
| 10 | Days to full maturity | 19.23% | 255 |
| 11 | Seed yield /plant | 0.15% | 2 |

**Conclusion**

The following conclusions are drawn from this present work. The pooled divergence for all the characters within the accessions was significant. Fifty two accessions of black gram were grouped into ten clusters by D2 analysis. The accessions IU-65-2-1 and IU-73-2-1 may serve as potential parents for hybridization programme in the improvement of yield. The accessions, IU-67-2-1 and IU-83-3 for early in days to 50% flowering; IU-77-5 for early in maturity; IU-62-3, IU-62-3-1 and IU-67-2-1 for dwarf; IU-77-5 for number of primary branches per plant; IU-73-2 and IU-73-2-1 for number of pods per plant; IU-73-2, IU-73-2-1, IU-78-2 and IU-83-3 for number of seeds per plant; IU-83-3 for number of seeds per pod; IU-73-2, IU-73-2-1 and IU-83-3 for 1000-seed weight; and 99-V-42, IU-73-2, IU-73-2-1, IU-78-2 and IU-83-3 for seed yield per plant may be used as suitable parent.

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