

PARENTAL SELECTION FOR BREEDING PROGRAMS IN GREEN GRAM (*Vigna radiata* (L.) Wilczek)

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Received: January 25, 2019

Accepted: March 10, 2019

ABSTRACT: Success of any plant breeding depends on the choice of parents being selected. Diversified genotypes exhibits more variability so that they can be selected for further hybridization programme. The present investigation was carried out using twenty eight genotypes of green gram to estimate the magnitude of genetic divergence for eight morphological characters viz, days to first flower, plant height, number of branches, number of clusters per plant, number of pods per plant, number of seeds per pod, hundreded seed weight, seed yield per plant. Twenty eight genotypes fell into ten clusters by the application of D² clustering technique. Cluster I comprises thirteen genotypes of diversified origin. Maximum number of genotypes were included in this cluster followed by clusters IV and VI each with three genotypes. Clusters V and VIII possessed two genotypes each and the clusters II, III, VII, IX and X had only one genotype each. Cluster I showed minimum intra cluster distance (8.38) and maximum intra cluster distance (9.59) was exhibited by cluster VI. Maximum inter cluster distance was found to exist between the clusters IV and X (53.71) and least inter cluster distance was recorded between the clusters II and III (5.28). D² analysis revealed the absence parallelism between geographic and genetic diversity. Characters such hundreded seed weight, days to first flower, number of pods per cluster and number of seeds per pod contributed much to divergence. The possibility of heterotic expression for yield components by intercrossing two divergent clusters would maintain variability in the natural population.

Key Words: genetic divergence, inter cluster, intra cluster, variability.

INTRODUCTION

Vigna radiata (L.) Wilczek is commonly known as green gram or mungbean, it is the most widely distributed pulse crop. The current breeding approaches to yield improvement in green gram are based on the recognition that this crop has lost a large part of their genetic variability in the process of adaptation to stress environment. The foremost need for this purpose is the collection of germplasm from different parts of the world and the organisation of a very intensive hybridization programme, using diverse genetic stocks as parental lines. Selection of parents for hybridization based merely on geographic diversity can no more be a suitable criterion. The importance of genetic diversity has long been appreciated by crop specialists. Such an analysis will eventually help to choose desirable parents for hybridization and evolve superior genotypes. Taking this rationale into consideration, the present investigation was carried out in green gram for certain morphological characters, to estimate the genetic diversity for the selected genotypes to assess the amount of homogeneity and heterogeneity existing among them, using Mahalanobis D² technique.

MATERIALS AND METHODS

Twenty eight genotypes of green gram (*Vigna radiata* (L.) Wilczek) of diversified origin were collected. The present investigation was conducted at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University. The experiment was laid out in a randomized block design with three replications. Two to three seeds were dibbled on one side of the ridge. In each replication, the genotypes were raised in single row of three meters length, spaced 20 cm within row and 45 cm between rows. Thinning was done leaving one sturdy and healthy seedling per hill. Cultural and agronomic practices were followed as per standard recommendations and need based protection measures were taken. Observations were recorded from five randomly selected plants for each genotype in each replication for all the characters studied. The individual plant observations were utilised for statistical analysis. The following were the morphological characters studied. They were days to first flower, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of seeds per pod, hundreded seed weight, seed yield per plant.

EXPERIMENTAL RESULTS

Twenty eight genotypes of green gram (*Vigna radiata*) of diversified origin were subjected to biometrical analysis for eight yield attributing characters. The results of analysis of variance are presented in the table 1. The variance due to genotypes for different characters studied was significant at one per cent level, indicating that the genotypes were selected for the present study were genetically divergent. Similar results were recorded by Suganthi *et al*, (2007) and Veeramani (2005).

D² analysis:

Utilizing Mahalanobis (1936) generalized distance, the divergence in twenty eight genotypes of green gram were assessed for eight morphological characters and the results were presented.

Understanding the magnitude of genetic divergence for yield components is very important in planning breeding program of crop plants. It helps both in choosing parental combinations to get maximum recombinations and also in understanding the pattern of evolution for different characters. Singh and Gupta (1968), using D² statistic in cotton found that the progenies derived from diverse crosses gave divergent and useful progenies. Similar results were recorded by Suganthi *et al*, (2007), Venkatesan *et al*, (2004) and Veeramani (2005).

Group constellations: The twenty eight genotypes were grouped into ten clusters by the application of clustering technique. The composition of different cluster and their origin are presented in the table 2. Cluster I comprises thirteen genotypes of diversified origin. Maximum number of genotypes were included in this cluster followed by clusters IV and VI each with three genotypes. Clusters V and VIII possessed two genotypes each and the clusters II, III, VII, IX and X had only one genotype each.

The intra cluster distance ranged from 8.38 to 9.59 (table 3). Cluster I showed minimum intra cluster distance and maximum intra cluster distance was exhibited by cluster VI. Maximum inter cluster distance was found to exist between the clusters IV and X (53.71) followed by the clusters IV and V1 (49.18) and a least inter cluster distance was recorded between the clusters II and III (5.28).

The results suggests that the geographic isolation is not the factor causing genetic diversity and this point should be considered in selecting parents for hybridization program. To explain the lack of relationship between geographic and genetic diversity, many interpretations were made by different authors.

Murthy and Arunachalam (1966) and Upadhy and Murthy (1970) than geographic isolation can do Das and Borthakur (1973) and Dhagat and Singh (1983), however, that if similar selection criteria are exercised in different geographic areas, it may result in genetic similarity of the cultivars of different geographic regions. All these factors can be considered to support the current finding. Similar results were recorded by Suganthi *et al*, (2007) and Veeramani (2005)

The cluster mean values for the eight characters are presented in the table 4. Maximum mean value for this character days to first flower was recorded by the cluster X (45.62). While minimum value was found in the cluster VI (36.11). The character plant height, cluster X recorded a maximum mean value of 32.41 cm for this character. While minimum value of 23.33 cm was recorded by the cluster IX.

Maximum and minimum mean values for number of branches per plant of 3.89 and 3.31 were registered by the clusters III and VII & VI respectively. The number of clusters per plant, clusters II and IX recorded maximum and minimum mean values of 8.10 and 3.91 respectively. Number of pods per cluster, least mean value of 2.74 was recorded by the cluster I. While cluster II registered the maximum mean value for number of pods per cluster (5.12). Number of seeds per pod maximum mean value of 10.68 was seen in the cluster IV. In contrast, cluster VII showed minimum value of 9.30. Hundred seed weight, least and peak mean values were accounted by the clusters X and IV (2.81 and 7.41) respectively. Seed yield per plant had cluster IV had maximum mean value (15.10) while cluster I possessed minimum mean value (3.99).

An assessment of the contributions of the different characters revealed that hundred seed weight shows the total maximum contribution to divergence followed by days to flower, number of pods per cluster, number of seeds per pod, number of branches per plant, number of clusters per plant, seed yield per plant and plant height in that order of these eight characters. The same was recorded by Natarajan *et al*, (1988). Similar results were recorded by Suganthi *et al*, (2007) and Veeramani (2005). The genetic divergence offered by these characters will offer scope for improving yield through rationale selection.

Twenty eight genotypes fell into ten clusters by the application of D² clustering technique. It was observed that there is absence of parallelism between geographic and genetic diversity as the genotypes from different geographic sources fell in the same cluster and also genotypes from similar geographic sources had a tendency to spread over different clusters. This gives stress on the fact that in breeding

programs, geographic diversity need not be considered as an index of diversity for the selection of parents.

Intercrossing among the genotypes of the divergent clusters may result in heterotic expression for yield components owing to the possession of greater intercluster distance. It was observed that the characters hundred seed weight, days to first flower, number of pods per cluster, number of seeds per pods contributed about 77 per cent to the total divergence, indicating their major role in maintaining variability in the natural population.

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Table 1 : Analysis of variance for various morphological characters in green gram

| Source | Df | Days to first flower | Plant Height | Number Of branches per plant | Number of clusters per plant | Number of pods per cluster | Number of seeds per pod | Hundred seed weight | Seed yield per plant |
|-------------|----|----------------------|--------------|------------------------------|------------------------------|----------------------------|-------------------------|---------------------|----------------------|
| | | MSS | MSS | MSS | MSS | MSS | MSS | MSS | MSS |
| Replication | 2 | 0.91 | 8.38 | 0.29** | 0.31 | 0.014 | 0.31 | 0.03 | 0.09 |
| Genotypes | 27 | 18.342** | 41.69** | 0.78** | 5.16" | 1.58** | 1.71 | 5.89** | 51.44** |
| Error | 54 | 0.51 | 4.17 | 0.09 | 0.14 | 0.03 | 0.10 | 0.03 | 0.42 |

Table 2: Composition of D² clusters in green gram

| Cluster Number | Number of Genotypes | Name of the Genotypes |
|----------------|---------------------|--|
| I | 13 | EC 16 70 88, WGG 48, GPLM 139, PDM 89 226, PUSA 90 21, AVRDC 54 6, AUGG 8, PLM 214, GPLM 163, EC 30 94 69, VGG 4, PLM 404, EC 31 42 92 |
| II | 1 | AUGG 4 |
| III | 1 | AUGG 7 |
| IV | 3 | EC 31 02 77, EC 31 22 82, LM 608 |
| V | 2 | VGG 7, KM 4 |
| VI | 3 | VGG 8, AUGG 5, ADT 3 |

| | | |
|------|---|----------------------|
| VII | 1 | GPLM 84 |
| VIII | 2 | PLS 265, EC 31 42 95 |
| IX | 1 | CO 4 |
| X | 1 | PDM 89 226 |

Table 3 : Average intra (diagonal) and inter cluster D2 and D (bold values) in green gram

| Cluster | I | II | III | IV | V | VI | VII | VIII | IX | X |
|---------|---------------|-----------------|-----------------|------------------|------------------|------------------|------------------|-----------------|------------------|------------------|
| I | 69.83 8.35 | 382.59 19.56 | 291.41 17.08 | 1927.13 43.92 | 234.39 15.31 | 153.97 12.43 | 163.27 12.77 | 654.34 25.59 | 179.29 13.38 | 292.52 17.11 |
| II | | 0.00 0.00 | 27.78 5.28 | 1745.73 41.79 | 256.38 16.02 | 295.11 17.19 | 170.56 13.07 | 828.36 28.79 | 218.82 14.78 | 454.61 21.34 |
| III | | | 0.00 0.00 | 1611.53 40.13 | 159.36 12.64 | 241.72 15.57 | 171.2 13.09 | 677.11 26.03 | 217.12 14.72 | 446.22 21.13 |
| IV | | | | 87.37 9.37 | 1102.18 33.21 | 2420.14 49.18 | 2261.41 47.57 | 455.31 21.32 | 1654.23 40.68 | 2883.66 53.71 |
| V | | | | | 48.28 6.97 | 344.76 18.59 | 323.93 17.98 | 271.49 16.49 | 237.78 15.42 | 699.14 26.43 |
| VI | | | | | | 91.69 9.59 | 137.19 11.72 | 991.78 31.48 | 208.19 14.43 | 294.32 17.17 |
| VII | | | | | | | 0.00 0.00 | 952.92 30.89 | 160.37 12.68 | 126.42 11.22 |
| VIII | | | | | | | | 86.87 9.34 | 596.83 24.44 | 1388.12 37.27 |
| IX | | | | | | | | | 0.00 0.00 | 361.61 19.01 |
| X | | | | | | | | | | 0.00 0.00 |

Table 4 : Cluster means for yield attributing characters in green gram

| Cluster | Days to first flower | Plant height | Number of branches per plant | Number of clusters per plant | Number of pods per cluster | Number of seeds per pod | Hundred seed weight(g) | Seed yield per plant (g) |
|--------------------------|----------------------|--------------|------------------------------|------------------------------|----------------------------|-------------------------|------------------------|--------------------------|
| I | 40.19 | 24.78 | 3.39 | 4.41 | 2.74 | 9.62 | 3.49 | 3.99 |
| II | 37.31 | 25.59 | 3.31 | 8.10 | 5.12 | 10.10 | 3.48 | 14.61 |
| III | 36.31 | 27.89 | 3.89 | 7.79 | 4.50 | 10.58 | 3.49 | 13.10 |
| IV | 40.10 | 31.81 | 3.31 | 5.38 | 3.50 | 10.68 | 7.41 | 15.10 |
| V | 36.39 | 27.41 | 3.81 | 6.01 | 3.31 | 9.48 | 4.30 | 8.51 |
| VI | 36.11 | 23.70 | 3.31 | 4.97 | 3.61 | 10.20 | 2.94 | 5.20 |
| VII | 41.32 | 27.32 | 3.31 | 6.94 | 3.10 | 9.30 | 3.31 | 8.51 |
| VIII | 39.11 | 28.21 | 3.79 | 4.41 | 2.94 | 10.10 | 5.93 | 7.80 |
| IX | 40.11 | 23.33 | 3.31 | 3.91 | 4.82 | 9.71 | 4.14 | 7.40 |
| X | 45.68 | 32.41 | 3.70 | 6.31 | 3.73 | 10.63 | 2.81 | 7.52 |
| Character contribution % | 18.26 | 2.94 | 9.83 | 6.64 | 18.27 | 11.14 | 29.90 | 3.19 |