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# Genetic divergence studies in clusterbean [*Cyamopsis tetragonoloba* (L.) Taub]

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**ABSTRACT :** Thirty one genotypes of clusterbean collected from various sources were assessed for genetic divergence using Mahalanobis $D^2$ technique. The genetic material exhibited wide range of genetic diversity for all the characters investigated and grouped into 3 different clusters. The maximum intra cluster distance was observed in cluster I indicated that genotypes are having diverse genetic architecture. The intercluster distance was high between cluster II and cluster III, this indicated wide range of variability among clusters. The per cent contribution towards genetic diversity was high for pod yield per hectare (26.02) followed by pod length (18.06) and plant height (14.62). On the basis of intercluster distance and per se performance observed in the present study a hybridization programme involving genotypes for a specific character has been chosen using cluster mean.

**KEY WORDS :** Genetic diversity, Clusterbean, Tocher's method, Cluster distance

**C**lusterbean or guar [*Cyamopsis tetragonoloba* (L.) Taub] (2n = 14) is a drought tolerant annual legume crop. It is an important legume whose cultivation is mainly concentrated in marginal and submarginal soils receiving low rainfall. In India, it is an important legume crop and about three- forth of the global clusterbean cultivation since ancient times (Vavilov, 1951). In India, clusterbean occupies an area of 2.20 million hectares with a production of 0.60 million tons (Singh *et al.,* 2009). In North Indian states like Rajasthan, Haryana, Gujarat and Punjab it is mainly cultivated for guar gum production and for forage, whereas in South India it is being cultivated for vegetable purpose. In Karnataka it is being grown in limited area and is cultivated mainly in northern districts like Dharwad, Belgaum, Bijapur, Haveri etc. for tender vegetable pods and it is cultivated year round.

Guar is mainly cultivated for food, feed and fodder. Its young pods are used as vegetables, which also known for cheap source of energy (16 Kcal), moisture (8 g), protein (3.2 g), fat (1.4 g), carbohydrate(10.8 g), vitamin A (65.3 IU), vitamin C (49 mg), calcium (57 mg) and iron (4.5 mg) for every 100 g of edible portion (Kumar and Singh, 2006). Guar being leguminous crop, it improves fertility of soil by fixing considerable amount of atmospheric nitrogen and adding organic matter. Guar meal and seeds are the source of high protein and nutritious feed

to the cattle. Its seed is also used for extraction of gum; hence it has emerged as a new industrial crop with high export value. Because of high absorbent capacity of guar gum it has diversified uses in paper, textiles, cosmetics, mining, explosives, oil industry, paints and bakery products. India occupies top position in guar gum and it has earned Rs. 1275 crores of foreign exchange (Kumar and Singh, 2002). Despite the importance of this crop, only limited breeding work has been done and very little attention has been given for its genetic improvement in the past in order to enhance the productivity level.

Information on the nature and magnitude of genetic diversity present in the genotype is pre-requisite. Parents should be selected on the basis of combining ability and $F_1$ heterosis for selecting high yielding varieties through hybridization (Arunachalam, 1989). Literature available on the nature and magnitude of diversity in clusterbean indicates that the studies of this kind are scanty and not properly documented. Therefore, an attempt in the present investigation was made to study degree of genetic diversity in a set of 31 genotypes of clusterbean collected from different location.

## RESEARCH METHODS

The material consisted of 31 phenotypically superior and

| Table A : Source and place of collection used in the study of clusterbean genotypes | | |
|---|---|---|
| Source | Number of genotypes | Genotypes |
| Dharwad | 1 | Pusa Navbahar |
| UAS Dharwad | 14 | BJ-1, RB-1, JKD-1, Line15, Line16, Line17, Line18, Line19, Line20, Line21, Line22, Line23, Line24, Line25. |
| KRCCH Arabhavi | 10 | Line1, Line2, Line3, Line4, Line5, Line6, Line7, Line8, Line9, Line10, Line 11, Line 12, Line 13, Line 14, Line 15. |
| Sarphan seeds Ltd | 1 | Sarphan |
| Mahyco | 1 | Varsha |

diverse genotypes of clusterbean from different sources (Table A). All these genotypes were evaluated in Randomised Complete Block Design with two replications at Main agricultural research station, University of Agricultural sciences, Dharwad, during *Kharif* 2009. Each genotype was sown in a single row of 10 m long as experiment plot, spacing followed was 45 cm between rows and 20 cm between plants within row. Optimum cultural practices were followed as per University recommendations. For recording various observations five plants in each experimental plot were selected randomly by avoiding border plants. Observations recorded in the present investigation were plant height (cm), number of branches per plant, days to 50% flowering, number of pod clusters per plant, number of pods per plant, number of pods per cluster, pod length (cm), pod width (mm), seeds per pod, total yield per plant (g) and pod yield per hectare (t).

The average data were subjected for statistical analysis and Mahalanobis $D^2$ (1928) statistics was used to study genetic divergence. Group constellation was performed according to the method suggested by Tocher, contribution of individual trait towards genetic divergence was quantified on the basis of co-efficient of variation at genotypic and inter-cluster levels (Vavilov, 1951).

## RESEARCH FINDINGS AND DISCUSSION

Analysis of variance showed highly significant difference among the genotypes for all the eleven characters studied. This suggested the presence of appreciable amount of diversity among the genotypes under study. The 31

genotypes were grouped into 3 clusters (Table 1). Cluster I included maximum of 29 genotypes, followed by cluster II and cluster III had single genotype.

The clusterbean accessions from different origin were accommodated in same cluster indicating their close affinity. These results suggested that the accessions within the cluster might have some degree of ancestral relationship; on the other hand the accession collected from the same district was distributed in different clusters indicating geographical diversity may not be necessarily related with genetic diversity. Therefore, the selection of accessions for hybridization to generate new gene combination should be based on genetic diversity rather than geographical diversity. Similar findings of Henry and Krishna(1990), Raghu *et al.*(2008) and Singh *et al.* (2003) collaborated that the distribution of genotypes from different agro-ecological locations into cluster was random indicating geographical distribution doesn't necessarily exhibit genetic divergence.

Among the clusters, cluster I had maximum intracluster distance (15.28). Minimum intra cluster distance was recorded by cluster II and cluster III as included single genotype in each cluster (Table 2). The maximum inter cluster $D^2$ values (Table 3) was recorded between cluster I and cluster III ( 50.31) followed by cluster II and cluster III (44.21) suggested wide diversity among the genotypes between the group and crossing between the genotypes of clusters would result in heterotic combinations as reported by Singh *et al.*(2003) and Mathur and Henry (2001). Minimum $D^2$ value between cluster I and cluster II indicates close relationship among the

| Table 1 : Grouping of clusterbean genotypes based on $D^2$ Values | | |
|---|---|---|
| Cluster | Name of genotypes | Number of genotypes |
| I | Line 1, line 2, line 3, line 4, line 5, line 6, line 7, line 8, line 9, line 10, line 11, line 12, line 13, line 14, line 15, line 16, line 17, line 18, line 19, line 20, line 21, line 22, line 23, line 4, line 25, BJ-1, JKD-1, Sarphan, Varsha | 29 |
| II | RB-1 | 1 |
| III | Pusa Navbahar | 1 |

| Table 2 : Average intra and inter cluster $D^2$ values of clusterbean genotypes | | | |
|---|---|---|---|
| Cluster distances | Cluster I | Cluster II | Cluster III |
| Cluster I | 15.28 | 34.13 | 50.31 |
| Cluster II | | 0 | 44.21 |
| Cluster III | | | 0 |

**Table 3 : Per cent contribution of 11 characters towards diversity in clusterbean genotypes**

| Characters | Per cent contribution | Order of contribution |
|---|---|---|
| 50% flowering | 9.68 | IV |
| Plant height | 14.62 | III |
| Number of branches | 5.81 | VII |
| Clusters per plant | 3.23 | VIII |
| Pods per cluster | 7.74 | V |
| Pods per plant | 6.88 | VI |
| Pod length | 18.06 | II |
| Pod width | 2.37 | IX |
| Number of seeds per pod | 3.23 | VIII |
| Pod yield per plant | 2.37 | IX |
| Pod yield per hectare | 26.02 | I |

**Table 4 : Cluster means for 11 characters in clusterbean genotypes**

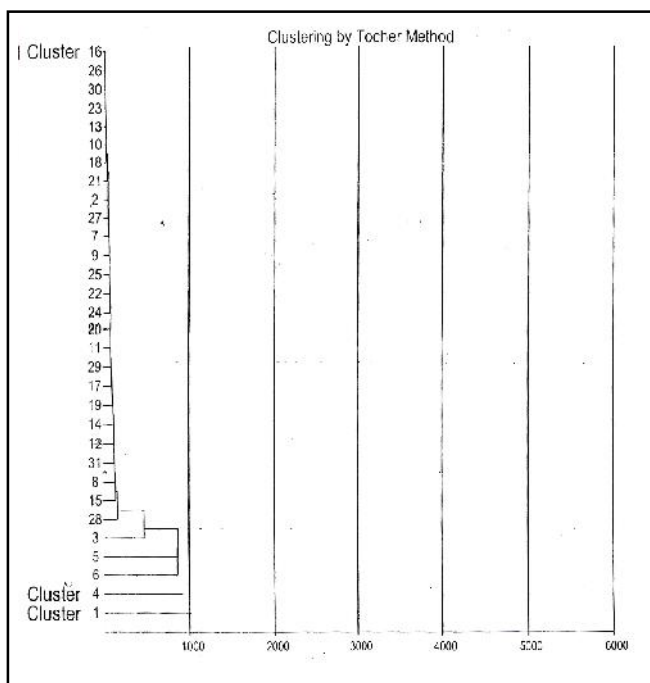| Cluster means | Cluster I | Cluster II | Cluster III |
|---|---|---|---|
| 50% flowering | 35.26 | 42.5 | 30.5 |
| Plant height | 39.07 | 94.75 | 100.85 |
| Number of branches | 5.79 | 6.75 | 0 |
| Clusters per plant | 28.53 | 32.5 | 14 |
| Pods per cluster | 6.97 | 14.1 | 7.97 |
| Pods per plant | 119.1 | 113.9 | 75.5 |
| Pod length | 5.44 | 6.23 | 10.1 |
| Pod width | 7.08 | 7.24 | 10.17 |
| Number of seeds per pod | 6.34 | 6 | 7.6 |
| Pod yield per plant | 120.1 | 173.35 | 155.59 |
| Pod yield per hectare | 13.62 | 18.74 | 16.8 |



**Fig. 1 : Cluster pattern of 31 clusterbean genotypes**

genotypes of these clusters and had maximum of similar gene complexes among them.

Apart from genetic divergence due importance should be given to the performance of genotypes and character with maximum contribution towards divergence (Table 4). The contribution of various traits was worked out from their rank and maximum contribution (26.02%) was from yield per hectare followed by pod length (18.06), plant height (14.62%), days to 50% flowering (9.68%), pods per plant (6.88%), number of branches (5.81%), clusters per plant and number of seeds per pod (3.23%).

The mean value of cluster (Table 4) for all the characters was calculated which indicated that cluster III had desirable mean values for early flowering, plant height, number of branches, pod length, pod width and number of seeds per pod. High mean value indicated by cluster I for clusters per plant, pods per cluster and pods per plant. Whereas cluster II had highest mean value for pod yield per plant and yield per hectare. Hence, these characters may be considered during selection of genotypes for further improvement.

As such based on intercluster distance and character with higher contribution to $D^2$ values there is scope for varietal

improvement through hybridization programme involving genotypes of cluster III with genotypes possessing desirable characters of cluster II (50% flowering, clusters per plant, pods per cluster, pod yield per plant and yield per hectare) and cluster I (Number of pods per cluster and pods per plant).

It was evident from the study that there was considerable degree of variability for vegetable pod yield and its component characters. A few of the most promising genotypes for vegetable pod yield were line 22, line 25, line16, RB-1, JKD-1 and Pusa Navbahar. The genotypes like Sarphan, Pusa Navbahar, line 22 and line 23 were early flowering. The genotype line 22 (185) and line 14 (165.67) produced more number of pods per plant, pod breadth was found highest in Pusa Navbahar, Varsha and Sarphan. Apart from these characters there are other desirable characters like pod length found highest in Pusa Navbahar.

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