Full Length Research Paper

Studies on genetic diversity in Snake Gourd (*Trichosanthes anguina* L.)

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Genetic diversity among 50 genotypes was worked out using Mahalanobis D^2 statistic. Based on D^2 analysis, the genotypes were grouped into four different clusters, where the cluster I possessed higher number (32) of genotypes followed by the cluster II (2), III (15) and IV (1). Clustering pattern revealed that geographical diversity was not associated with genetic diversity that is, genotypes collected from same location were grouped into different clusters. The maximum inter-cluster distance was observed between the clusters III and cluster IV and that of minimum in between the Clusters I and Cluster II. In case of intra-cluster distance, the maximum distance was observed in the cluster III and that of minimum was observed in the cluster IV. Among the nine traits studied, maximum contribution was made by average fruit weight (31.84%) followed by days to first male flower appearance (25.96%), yield per hectare (23.59%) and fruit length (17.31%). Considering cluster mean, the genotypes of cluster I and cluster III could be selected for yield and yield attributing characters. The wider genetic diversity was observed in cluster II, III and IV which indicate the potentiality of this diverse genotype collection for providing basic material for future breeding programmes.

Key words: Snake gourd, *Trichosanthes anguina* L., genetic diversity, cluster, D^2 analysis.
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INTRODUCTION

Snake gourd (*Trichosanthes anguina* L.) belongs to the family Cucurbitaceae and it is an important summer vegetable but it may grow throughout the year except extreme winter. It is important as a good sources of minerals, fiber and nutrients to make the food wholesome and healthy (Ahmed et al., 2000). Its medicinal value is also high. It is one of the few vegetables which fetches more yield per unit area but the average yield of the crop is low. A large number of local lines are cultivated in the country but there is no recommended cultivar. No serious attempts have so far been made to upgrade the productivity of vegetable can be increased to a greater extent through varietal improvement. In crop improvement programme, genetic diversity has been considered as an important factor which is also essential pre-requisite for hybridization programme for obtained progenies with important desirable characters like disease resistance, earliness, quality or even perfor-mance of a particular character for the yield improvement and future utilization of local germplasm (Choudhury et al., 1975). Such study also selects the genetically divergent parents to obtain desirable combinations in the segregating generations. Information on nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding programme. Keeping this in view, the present study was focused to assess the genetic diversity of fifty promising snake gourd genotypes using Mahalanobis D^2 statistics.

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Table 1. Distribution of 50 genotypes of snake gourd in different cluster.

Cluster	Number of genotypes with percent in each cluster	Genotypes with collection site
I	32	IC202157, IC202158, IC202159, IC212465, IC212474, IC212475, IC212483, IC212484, IC546083, IC212509, IC212512, IC212513, IC212517, IC212527, IC212416, IC265646, IC427743, IC410146, IC321016, IC426984, IC410160, IC411877, IC413027, IC413589, IC308557, IC284875, IC321019, IC410159, IC284753, IC410142, IC347377 and IC277390.
II	2	Co2 and Kumbamonam Local Short
III	15	IC333314, IC539825, IC418478, IC411878, IC433526, IC470907, Coimbatore Local, P.K.M.1 MDU.1, Madurai Local Long, Madurai Local Short, Kulithalai Local, Kumbamonam Local Long, Palayajeyamkondam Local and Jeyamkondam local.
IV	1	Nagapatinum Local

MATERIALS AND METHODS

The present investigation was conducted in the Department of Horticulture, Agricultural College and Research Institute, Madurai during 2011 to 2012. Totally 50 genotypes were collected from different geographical location and utilized for study. Among 50 genotypes, 38 genotypes were collected from NBPGR, New Delhi, three varieties were collected from Tamil Nadu Agricultural University *viz.*, PKM1, MDU1 and Co2 and nine local types were collected from in and around Tamil Nadu *viz.*, Kulithalai, Kumbakonam, Palayajeyamkondam, Nagappattinam, Jeyamkondam, Madurai and Coimbatore. The experiment was laid out in Randomized Block Design with three replications. The seeds were sown at a spacing of 2 x 2 m. The plants were supported by trellis and other intercultural operations such as weeding, irrigation, plant protection measures etc, were done as and when needed. Each treatment comprised of ten hills, two plants were allowed to grow per hill, and finally one plant was kept for final observation. The observations of five randomly selected plants were recorded. Observation was taken for yield and yield contributing characters. The characters were vine
  length, days to first female flower appearance, days to first male flower appearance, fruit length, fruit girth, average fruit weight, number of fruit per vine, number of seeds per fruit and yield (tonnes/ha). The analysis of variance and covariance were done for selected characters for divergent studies. Genetic diversity was worked out following Mahalanobis (1936) genetic distance (D^2) extended by Rao (1952) to clustering in Tocher's method.

RESULTS AND DISCUSSION

Clustering of genotypes

Analysis of variance showed significant difference for all the nine characters studied among the genotypes. Based on D^2 value 50 genotypes were grouped into four clusters (Table 1). Maximum number of genotypes (32 genotypes) was grouped in Cluster I. Cluster III consists of 15 genotypes followed by cluster II with two genotypes. Cluster IV had only one genotype. The overall composition of the clustering pattern showed that

genotypes collected from the same geographic origin were distributed in different clusters. Similar findings of non-correspondance of geographic origin with genetic diversity were also reported by Khatun et al. (2010); they are agreement with Rashid (2000) in pumpkin, Banik (2003) and Rahman (2004) in snake gourd.

In crop improvement, genetic diversity has been considered as an important factor, which is an essential pre-requisite for any breeding programme as to obtaining high yielding progenies. Quantitative measurement of genetic divergence among individuals have enabled the plant breeders to understand the racial affinities and evolutionary pattern in various crop species or cultivated plants as well as, in decision making for selection of desirable parents in hybridization programme.

The intra and inter cluster distance are presented in Table 2. Inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among the genotypes. The maximum inter cluster distance was observed between Cluster III and cluster IV (922.896) followed by between Cluster I and cluster IV (673.272). The genotypes grouped in the Cluster III and IV showed that maximum inter cluster distance are expected to obtain high heterosis in hybridization and to show wide variability in genetic make-up. The hybrids developed from the selected members of these clusters would produce highly variable population in the segregating generation. The lowest inter cluster distance observed in the Cluster I and Cluster II suggests that genotypes of these cluster had closeness among themselves. The maximum intra cluster distance was highest in cluster III followed by cluster I. Hence, selection within these cluster may be exercised based on the highest areas for the desirable traits, which would be made use of improvement through intervarietal hybridization (Joshi et al., 2008; Dora et al. (2001) in pointed gourd). The minimum intra cluster distance was observed in the Cluster IV and II. However, the wider genetic diversity was observed

Table 2. Average intra (bold) and inter cluster distance (D^2) for 50 snake gourd genotypes.

Clusters	I	II	III	IV
I	444.794	347.867	582.901	673.272
II		60.375	535.189	641.737
III			630.285	922.896
IV				0.000

Table 3. Cluster means for nine characters in 50 genotypes of snake gourd.

Cluster	I	II	III	IV
Vine length (cm)	520.09	455.00	508.33	455.00
Days to first female flower appearance	43.297	43.500	43.400	46.500
Days to first male flower appearance	40.453	41.000	40.300	43.500
Fruit length (cm)	58.510	38.923	53.380	99.000
Fruit girth (cm)	17.241	21.507	17.936	19.880
Fruit weight (g)	53.111	49.975	50.266	46.475
Number of fruits per plant	21.406	19.500	25.533	16.000
Number of seeds per fruit	77.998	75.603	65.223	68.100
Yield (t/ha)	14.626	13.025	19.537	11.520

in cluster II, III and IV suggests that genotypes of these clusters could be selected for yield and other yield contributing characters.

Cluster mean

A perusal of results of cluster mean (Table 3) revealed the cluster I with 32 genotypes exhibited highest vine length (570.09), number of seeds per fruit (77.998), average fruit weight (53.111) and lowest mean value for days to first female flower appearance (43.297), yield per hectare (14.626), number of fruits per vine (21.406), fruit length (58.510), fruit girth (17.241) and days first male flower appearance (4.453). Cluster II had two genotypes, which exhibited highest fruit girth (21.507). Cluster III was characterized by highest in yield (19.537), number of fruits per vine (29.537) and lowest number of seeds per fruit (25.533), while the cluster IV had maximum in days to first female flower appearance (46.500), fruit length (99.00) and days to first male flower appearance (43.50). None of the cluster contained genotypes with all the desirable traits, which could be directly selected and utilized. All the minimum and maximum cluster mean value were distributed in relatively distant clusters.

However the cluster I recorded desirable mean for highest vine length, days to first female flower appea-rance, fruit length and average fruit weight. The Cluster III recorded desirable mean for number of fruits per vine, yield per hectare and minimum number of seeds per fruit.

Similar results were also reported by Khatum et al., 2010 in snake gourd. While studying the divergence in snake gourd genotypes thereby underlining the fact that the hybridization between genotypes of different cluster is necessary for the development of desirable genotypes (Figure 1). Based on the per se performance of the best genotypes within the clusters, there may be directly selected or may be used as potential parents in hybridization programme.

Contribution of individual character towards total divergent

The contribution of each trait to total divergence is pre-sented in Table 4. Among the traits studied average fruit weight contributed maximum divergence 31.84% followed by days to first male flower appearance (25.96%), yield per hectare (23.59%), fruit length (17.31%), fruit girth (0.73%), number of seeds per fruit (0.49%) and number of fruits per vine (0.082%). The traits *viz.*, average fruit weight, days to first female flower appearance, yield per hectare, fruit length contributed 98.70% towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population.

Conclusion

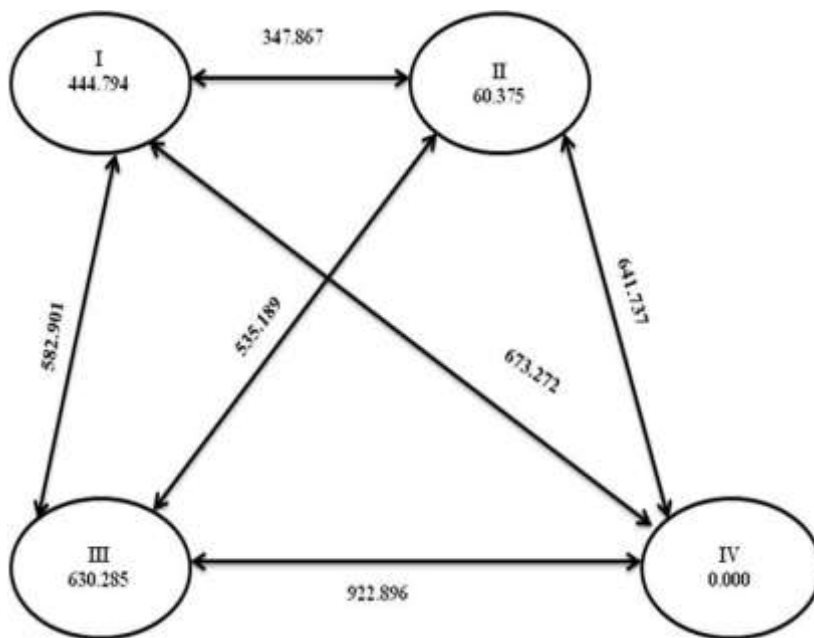The result indicate that the wider genetic diversity was

Figure 1. Cluster diagram showing the average intra and inter cluster distances ($D = D^2$) of snake gourd genotypes Inter and intra-cluster distance.

Table 4. Percentage of contribution of each character towards total divergence.

Character	Number of first rank	Per cent contribution
Vine length	0	0.0
Days to first female flower appearance	0	0.0
Days to first male flower appearance	318	25.9592
Fruit length	212	17.3061
Fruit girth	9	0.7347
Average fruit weight	390	31.8367
Number of fruits per vine	1	0.0816
Number of seeds per fruit	6	0.4898
Yield (t/ha)	289	23.5918
Total	**1225**	**100**

observed in II, III and IV clusters, suggests that genotypes of these clusters could be selected for yield and other yield contributing characters. The characters such as yield per hectare, average fruit weight, fruit length, days to first female flower appearance and number of seeds per fruit should also be considered while selecting parents for hybridization as they are important contributors of genetic divergence.

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