



RESEARCH ARTICLE

BREEDING POTENTIAL OF SNAKE GOURD (*Trichosanthes Anguina* L.) GENOTYPES USING D² ANALYSIS

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ABSTRACT

“An inve“Breeding potential of snake gourd (*Trichosanthes anguina* L.) genotypes using D² analysis” was carried out in the Department of Horticulture, Faculty of Agriculture, Annamalai University, Tamil Nadu. The parents from diversified genotypes in snake gourd were evaluated for fruit yield per plant, yield attributing characters and quality traits with the objective of selecting superior genotypes for heterosis breeding. The characters observed were days to first male and female flower opening, number of fruits per plant, fruit length, fruit girth, flesh thickness, single fruit weight, fruit yield per plant, number of seeds per fruit, Vitamin C and acidity content of fruit. The degree of divergence among 40 genotypes was computed using D² analysis. The results revealed that the genotype G27 followed by G2, G29, G5 and G12 expressed the maximum fruit yield per plant. High PCV, GCV and genetic advance as per cent of mean were observed among the genotypes for most of the traits studied except days to first male flower opening and acidity content of fruit. Among the 40 genotypes studied, the genotypes were grouped into eight clusters. Among 40 diversified genotypes, the cluster I consists the maximum number of 23 genotypes. The traits namely single fruit weight, fruit length, number of fruits per plant, number of seeds per fruit and fruit girth contributed more to the fruit yield per plant.

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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 a popular vegetable with moderately high nutritive value. It is important as a good source of minerals, fiber and nutrients to make the food wholesome and healthy (Ahmed et al., 2004). It is also one of the important vegetables which fetch more yield per unit area but the average yield of the crop is low. For developing superior varieties, it is necessary to improve the earliness and yield in snake gourd. This can be achieved through effective utilization of germplasm resources and integration of genomic tools to impart efficiency and pace of breeding processes (Banga, 2012). Knowledge of genetic diversity among existing cultivars of any crop is essential for long-term success in breeding programme and to maximize the exploitation of the germplasm resources (Belaj et al., 2002). Because, it provides us about the relationship among elite breeding population and helps in selecting desirable parents for establishing new breeding population. In the present study, an attempt has been made to assess the genetic divergence in a set of 40 genotypes of snake gourd.

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MATERIALS AND METHODS

The study was carried out at Annamalai university, Department of Horticulture, Chidambaram. Seeds of all 40 genotypes were sown separately with a spacing of 2 × 2 m. Experiment was laid in Randomized Block Design, replicated thrice. Twenty plants per genotype were maintained in each replication. Recommended agronomic practices and need based plant protection measures were given. Data on five randomly selected plants from each genotype from each replication were collected for fruit yield and its component traits. The mean of replications was used for D² statistical analysis. The following observations were recorded days to first male and female flower anthesis, node number for first male and female flowers, days to first fruit harvest, total number of fruits per plant, maturity period, length and diameter of fruit, fruit index, fruit weight, flesh thickness, vine length, total soluble solids and yield per plant.

RESULTS AND DISCUSSION

In the present study, the 40 genotypes were grouped into eight different clusters, based on relative magnitude of D² values. Cluster I was the largest comprising of 23 genotypes, followed by cluster II with six genotypes. The cluster IV and VII comprised three genotypes each.

Intra and Inter cluster distances (D^2 values) of snake gourd genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII
I	35.04 (5.92)	62.73 (7.92)	60.14 (7.75)	81.93 (9.05)	46.61 (6.83)	46.01 (6.78)	50.28 (7.09)	75.31 (8.68)
II		35.72 (5.98)	43.96 (6.63)	78.99 (8.89)	77.96 (8.83)	63.17 (7.95)	55.79 (7.47)	57.72 (7.60)
III			0.00 (0.00)	76.59 (8.75)	66.16 (8.13)	59.30 (7.70)	66.46 (8.15)	58.59 (7.65)
IV				28.69 (5.36)	107.03 (10.35)	101.40 (10.07)	56.31 (7.50)	48.09 (6.93)
V					0.00 (0.00)	30.39 (5.51)	79.22 (8.90)	101.34 (10.07)
VI						26.27 (5.13)	71.44 (8.45)	94.14 (9.70)
VII							31.38 (5.60)	51.44 (7.17)
VIII								0.00 (0.00)

Composition of D^2 clusters for 40 snakegourd genotypes

S.No	Clusters	Number of genotypes	Genotypes	Source of collection
1.	I	23	G2, G11, G3, G40, G5, G1, G6, G9, G4, G13, G17, G10, G21, G39, G38, G28, G14, G19, G15, G22, G20, G26, G23	Hessaraghatta Local, Karnataka MDU1 (F1 hybrid), Tamil Nadu Pappanipara Local, Kerala Vridachalam Local, Tamil Nadu Trichy Local, Tamil Nadu Viralipatti Local, Tamil Nadu Mayiladuthurai Local, Tamil Nadu
2.	II	6	G27, G29, G30, G16, G25, G31	Michaelpalayam Local, Tamil Nadu Nadupatti Local, Tamil Nadu Bhuvanagiri Local, Tamil Nadu Vedasandur Local, Tamil Nadu Thiruvananthapuram Farm, Kerala
3.	III	1	G12	Ottanchattiram Local, Tamil Nadu
4.	IV	3	G32, G34, G36	Co-1, Tamil Nadu PKM-1, Tamil Nadu Chinnupatti Local, Tamil Nadu
5.	V	1	G35	Vellayani Local, Kerala
6.	VI	2	G33, G37	Co-1, Tamil Nadu Tittagudi Local, Tamil Nadu
7.	VII	3	G7, G8, G18	Palur Local, Tamil Nadu IC-212464, NBPGR, Trichur, Kerala IC-212465, NBPGR, Trichur, Kerala
8.	VIII	1	G24	IC-212484, NBPGR, Trichur, Kerala

The cluster VI had two genotypes. The remaining clusters namely III, V and VIII were monogenotypic clusters. The clustering pattern in the present study revealed that the genotypes from different sources clustered together showing that there was no association between ecogeographical distribution of genotypes and genetic divergence. Similar findings were also reported by Karuppaiah *et al.*, 2005 in ridge gourd. This indicated that selection has been towards the same goal in the different centres of origin of those genotypes and yet, there is sufficient genetic variability that distinctly differentiates them into eight clusters. Hence, the genotypes used in the present study could be considered as a valid material. The intracluster distance varied from 0.00 to 2.98. The intercluster distance ranged from 5.51 (between V and VII) to 10.35 (between IV and V). The cluster I contained the maximum of 23 genotypes. Among 23 genotypes, the G2 (10.01 kg) recorded the maximum fruit yield per plant coupled with more number of fruits per plant.

The cluster II comprised of six genotypes. Among the six genotypes, the G27 (10.49 kg) registered the highest fruit yield per plant, high fruit girth, high flesh thickness coupled with less number of seeds per fruit. The cluster III had monogenotypic with G12 which exhibited less number of days to first male and female flower opening, high flesh thickness with single fruit weight and high fruit yield per plant (9.62 kg). The cluster IV had three genotypes. Among the three genotypes, the G34 recorded the highest fruit length (175.79 cm) with average fruit yield per plant. The cluster V had only one genotype namely G35 which exhibited the minimum fruit length (34.73 cm) with more fruit girth and flesh thickness, low acidity content of fruit coupled with average fruit yield per plant. The clusters VI had two genotypes which were poor yielder. The cluster VII had three genotypes which were also showed poor performance for most of the traits. The cluster VIII had only one genotype namely G24 which registered the least number of days to first male and female flower opening

among the genotypes with more single fruit weight and moderate fruit length coupled with more fruit yield per plant (7.36 kg) than the population mean of 6.90 kg. Based on the *per se* performance of different yield component traits and cluster distance (diversity). Six genotypes had been selected namely G2, G27, G12, G34, G35 and G24 from the clusters I, II, III, IV, V and VIII for the further study respectively. These six genotypes had been utilized as the parents for the hybridization programme to exploit the heterosis for commercial cultivation of hybrids. The genotype G11 (MDU 1) was considered as a standard parent. The parent MDU 1 is a hybrid between Thaniamangalam, Tamil Nadu selection and a local short fruited striped snake gourd. It is also a short duration variety with a stable fruit yield. It is also resistant to fruit fly with marketable fruit length.

Summary

Genetic divergence using Mahalanobi's D^2 statistic was studied in a population of 40 snake gourd genotypes. The genotypes differ significantly and were grouped into 8 clusters based on similarities of D^2 values.

The pattern of distribution of genotypes from different regions into various clusters was at random, demonstrating that the geographical isolation may not be the only factor for causing biological or genetic diversity.

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