Vegetable Science (2015) 42 (2) : 104-106

Short Communication

Genetic diversity studies in snake gourd (*Trichosanthes anguina* L.)

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Received: August, 2014 / Accepted: September, 2015

Snake gourd (*Trichosanthes anguina* L.) is an annual climber belongs to the family Cucurbitaceae. It is important as a good sources of minerals, fiber and nutrients to make the food wholesome and healthy (Ahmed *et al.,* 2000). A large number of local strains/ lines are cultivated in the country but there is hardly few recommended cultivar. No serious attempts have so far been made to improve the productivity and acceptability of this crop. In crop improvement programme, genetic diversity has been considered as an important factor which is also essential pre-requisite for hybridization programme for obtaining progenies with important desirable characters like disease resistance, earliness, quality or even performance of a particular character (Chowdhury et al., 1975).

The present investigation was carried out in the Department of Horticulture, Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal during 2014**.** Totally 41 genotypes were collected from different geographical locations and utilized for study. Among 41 genotypes, 20 genotypes were procured from NBPGR, New Delhi. Varieties namely PLR-1 and PLR-2 were collected from Vegetable Research Station, Palur; CO-2 variety from Tamil Nadu Agricultural University; KAU-1 from Kerala Agricultural University; 11 local genotypes from Nagapattinam, Dindugul, Coimbatore, Trichy, Salem and Villupuram districts of Tamil Nadu; two genotypes from Karaikal district, U.T of Pudhucherry; four genotypes from Kozhikode, Idukki and Thrissur districts of Kerala; and one genotype from Chittore district of Andhra Pradesh. The experiment was laid out in a Randomized Block Design with three replications in the pandal system. Two seeds were sown in the pits on the long channels of 60 cm width with a spacing of 1.5 m between the beds. The plants were supported with the jute threads and usual intercultural operations are carried out as and when needed. The observations of five randomly selected plants were recorded. Observation was taken for yield and yield contributing characters. The characters were vine length, node at first male and female flower appearance, days to first male and female flower anthesis, sex ratio, fruit length, fruit girth, fruit weight, number of fruit per vine, number of seeds per fruit and yield per plant, protein content, total soluble solids and total sugar content. The recorded data was subjected to statistical analysis and genetic diversity was worked out following Mahalanobis (1936) genetic distance (D^2) extended by Rao (1952) to clustering in Tocher's method.

The analysis of variance exhibited significant difference among the genotypes for all the characters except for node at first male flower appearance. The genotypes were clustered based on diversity analysis. The D^2 values were worked out. By the application of clustering technique, the 41 genotypes were grouped into seventeen different clusters (Table 1). Sanwal *et al.* (2008) opined that the geographical distribution need not directly be related to genetic diversity as estimated by D^2 statistics. A similar finding was reported by Wahab and Gopalakrishanan (1993). In contrast, cluster I had 13 genotypes each coming from different geographical origin (New Delhi, Tamil Nadu and Kerala). Cluster II to XIII had two genotypes of different locations.

Among the seventeen clusters it was observed that cluster I was the largest with 13 genotypes followed by two genotypes were formed in the cluster's II, III, IV, V, VI, VII, VIII, IX, X, XI, XII, XIII Clusters XIV, XV, XVI and XVII had only one genotype (Table 1). Inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among the genotypes. The values showed that the cluster XIII had the maximum intra D value (12.92) followed by the cluster XII (11.11). This is indicative of the fact that the

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Table 1: Clustering pattern of 41 genotypes of snake gourd

Cluster	Number of genotypes	Genotypes	Source
I	13	T.A-1 (Dindugul local) T.A-2 (Coimbatore local) T.A-3(Trichy local) T.A-4 (IC 202155) T.A-5 (White short-salem) T.A-6 (PLR -2),T.A-7 (PLR -1) T.A-8 (Mannuthy local) T.A-9 (KAU-1) T.A-10 (CO- 2) T.A-11 (Kumaly local) T.A-25 (IC 212465), T.A-28 (IC 212513)	Dindugul- Tamilnadu Coimbatore- Tamilnadu Trichy- Tamilnadu NBPGR, New Delhi Rasi seeds-salem, VRS,Palur Kerala KAU, Kerala TNAU, Coimbatore Kerala NBPGR, New Delhi
II	2	T.A-37 (IC 539812) T.A-39 (Vadakara local-long)	NBPGR, New Delhi Vadakara, Kerala
III	2	T.A-21 (IC 202158), T.A-33 (IC 539825)	NBPGR, New Delhi
IV	2	T.A-29 (IC 212517), T.A-34 (IC 536671)	NBPGR, New Delhi
V	2	T.A-14 (Paravai local-short) T.A-35 (IC 433526)	Paravai, Tamilnadu NBPGR, New Delhi
VI	2	T.A-20 (IC 212509), T.A-26 (IC 546082)	NBPGR, New Delhi
VII	2	T.A-16 (Tindivanam local-long) T.A-18 (Mayiladuthurai local-short)	Tindivanam, Tamilnadu Mayiladuthurai, Tamilnadu
VIII	2	T.A-17 (Mayiladuthurai local-long) T.A-30 (IC 212416)	Mayiladuthurai, Tamilnadu NBPGR, New Delhi
IX	2	T.A-15 (Tindivanam local-short) T.A-22 (IC 212475)	Tindivanam, Tamilnadu NBPGR, New Delhi
X	2	T.A-24 (IC 212474), T.A-38 (IC 410159)	NBPGR, New Delhi
XI	2	T.A-23 (Salem local) T.A-32 (IC 410146)	Salem, Tamilnadu NBPGR, New Delhi
XII	2	T.A-27 (IC 212483) T.A-41 (Paravai local-long)	NBPGR, New Delhi Paravai, Tamilnadu
XIII	2	T.A-31 (IC 212512) T.A-40 (Vadakara local-baby)	NBPGR, New Delhi Vadakara, Kerala
XIV	1	T.A-13 (Agalankannu local short)	Karaikal, Pudhucherry
XV	1	T.A-36 (IC 970907)	NBPGR, New Delhi
XVI	1	T.A-12 (Agalankannu local long)	Karaikal, Pudhucherry
XVII	1	T.A-19 (Chittore local)	Andhra Pradesh
Total = 17 clusters	Total = 41		

Table 2: Mean intra-cluster (diagonal) and inter-cluster D^2 and D values of snake gourd genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII
I	210.761 (14.518)	162.368 (12.742)	276.334 (16.623)	165.228 (12.854)	158.375 (12.585)	217.201 (14.738)	145.853 (12.077)	238.331 (15.438)	216.307 (14.707)	175.294 (13.240)	226.744 (15.058)	204.460 (14.299)	185.894 (13.634)	309.832 (17.602)	238.563 (15.445)	867.672 (29.456)	362.984 (19.052)
II		32.933 (5.739)	153.888 (12.405)	85.571 (9.250)	150.509 (12.268)	180.574 (13.438)	117.364 (10.833)	164.042 (12.808)	183.194 (13.535)	136.015 (11.663)	186.146 (13.644)	171.060 (13.079)	108.845 (10.433)	304.630 (17.454)	154.470 (12.429)	708.257 (26.613)	288.213 (16.977)
III			56.622 (7.525)	179.362 (13.393)	246.668 (15.706)	173.479 (13.171)	219.349 (14.810)	212.606 (14.581)	194.435 (13.944)	159.082 (12.613)	378.309 (19.450)	287.157 (16.946)	214.933 (14.661)	469.045 (21.657)	386.974 (19.672)	997.987 (31.591)	255.767 (15.993)
IV				56.624 (7.525)	149.893 (12.243)	157.019 (12.531)	137.475 (11.725)	218.602 (14.785)	232.668 (15.253)	93.557 (9.672)	199.681 (14.131)	142.271 (11.928)	125.059 (11.183)	355.816 (18.863)	148.171 (12.173)	723.518 (26.898)	337.629 (18.375)
V					57.952 (7.613)	188.097 (13.715)	103.439 (10.171)	279.938 (16.731)	171.736 (13.105)	136.258 (11.673)	167.594 (12.946)	183.250 (13.537)	141.767 (11.907)	334.953 (18.302)	260.680 (16.146)	783.898 (27.998)	231.790 (15.225)
VI						66.795 (8.173)	117.617 (10.845)	185.539 (13.621)	270.222 (16.438)	166.485 (12.903)	367.538 (19.171)	201.160 (14.183)	132.626 (11.516)	298.128 (17.266)	345.746 (18.594)	1062.734 (32.600)	301.823 (17.373)
VII							76.127 (8.725)	141.862 (12.911)	145.496 (12.062)	131.943 (11.487)	244.018 (15.621)	108.728 (10.427)	121.717 (11.033)	185.192 (13.609)	266.101 (16.313)	1042.014 (32.280)	214.004 (14.269)
VIII								89.497 (9.460)	210.019 (14.492)	218.037 (14.766)	402.190 (20.055)	198.930 (14.104)	196.476 (14.017)	286.816 (16.936)	319.988 (18.888)	1251.243 (35.373)	369.658 (19.226)
IX									101.304 (10.065)	184.427 (13.580)	225.738 (15.025)	227.342 (15.078)	250.990 (15.843)	307.416 (17.533)	318.533 (17.847)	1067.796 (32.677)	269.815 (16.426)
X										103.967 (10.196)	254.304 (15.947)	145.725 (12.072)	154.357 (12.424)	341.588 (18.482)	247.639 (15.737)	914.767 (30.245)	290.743 (17.051)
XI											112.856 (10.623)	311.401 (17.647)	256.375 (16.012)	461.883 (21.491)	155.537 (12.471)	543.562 (23.314)	476.145 (21.821)
XII												123.420 (11.109)	167.295 (12.934)	270.169 (16.437)	286.973 (16.940)	1193.348 (34.545)	272.519 (16.508)
XIII													166.941 (12.921)	371.664 (19.279)	230.092 (15.169)	866.023 (29.428)	293.408 (17.129)
XIV														0.000	464.137 (21.544)	1314.433 (36.255)	507.828 (22.535)
XV															0.000	570.190 (23.879)	649.642 (25.488)
XVI																0.000	1375.777 (37.091)
XVII																	0.000 (0.000)

Table 3: Relative contribution of different characters to genetic diversity in snake gourd

S. No	Characters	Number of first rank	Percentage of contribution
1	Vine length	75	9.15
2	Number of primary branches	0	0.00
3	Node at first female flower appearance	0	0.00
4	Days to first male flower anthesis	1	0.12
5	Days to first female flower anthesis	13	1.59
6	Sex ratio	5	0.61
7	Days to first fruit harvest	4	0.49
8	Fruit length	92	11.22
9	Fruit girth	10	1.22
10	Fruit cavity	126	15.37
11	Fruit flesh thickness	58	7.07
12	Fruit weight	6	0.73
13	Number of fruits per vine	16	1.95
14	Number of seeds per fruit	60	7.32
15	Protein	10	1.22
16	Total soluble solids	114	13.90
17	Total sugar	45	5.49
18	Yield per vine	185	22.56
	Total	820	100

genotypes included in these cluster are very diverse.

At inter cluster level (Table 2), minimum D value was observed between cluster II and cluster IV (9.25) revealing closer relation among the genotypes included in the clusters. The inter cluster D value was found to be maximum between cluster XVI and XVII (37.09) followed by cluster XIV and XVI (36.25). The relative contribution for each character towards genetic divergence was estimated by the individual characters. Yield per vine contributed the maximum i.e. 22.56 per cent towards the genetic divergence (Table 1) followed by fruit cavity (15.37 per cent), total soluble solids (13.90 per cent), fruit length (11.22 per cent), vine length (9.15 per cent), number of seeds per fruit (7.32) and fruit flesh thickness (7.07) (Table 3).

Wide range of genetic divergence was noticed among the studied 41 genotypes of snake gourd, and this divergence of the genotypes may be taken into account for selecting the parents for hybridization and future breeding program. The characters such as yield per vine, fruit cavity, total soluble solid, fruit length, vine length and fruit flesh thickness should also be considered while selecting parents for hybridization as they are important contributors of genetic divergence.

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