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RESEARCH ARTICLE

STUDIES ON GENETIC DIVERSITYIN SNAKE GOURD (*TRICHOSANTHESANGUINA* L.)

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An investigation entitled "Genetic divesityin snake gourd (*Trichosanthesanguina* L.)" was carried out in the Department of Horticulture, Faculty of Agriculture, Annamalai University, Tamil Nadu, India during 2004. 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 D^2 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 diversed 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. Based on the *per se* performance with specific trait and genetic divergence from different clusters, six genotypes namely P_1–Hessaraghatta local (Bangalore, Karnataka), P_2–Ottanchathiram local (Dindigul district, Tamil Nadu), P_3–IC-212484, NBPGR, Trichur, P4–Michaelpalayam local (Dindigul district, Tamil Nadu), P_5–PKM–1 (mutant variety, HC&RI, TNAU, Periyakulam), P_6–Vellayani local (Kerala) were selected for crossing in full diallel programme.

Key words: Fruit Length, Fruit Girth, Flesh Thickness, Single Fruit Weight, Fruit Yield Per Plant.

INTRODUCTION

We must increase the vegetable production in India to meet the requirements of our growing population (Dwivedi *et al.,* 2003). So it is necessary to increase the production and productivity to meet the self sufficiency of our daily requirements. A further increase in snake gourd productivity needs intensive research in genetics and crop breeding. Greater genetic diversity in the germplasm enhances the breeding potential and scope for crop improvement. The *per se* performance of the parents always give a correct indication of their breeding potentialities.

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Crosses between genetically diverse parents are likely to produce high heterotic effects and also produce a wide spectrum of variability in segregating generations. In the present investigation, Mahalonobis D^2 statistics analysis was adopted to find out the genetic divergence and genetic variability for fruit yield and their component characters among snake gourdgermplasm.

MATERIALS AND METHODS

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 D^2 statistical analysis.

RESULTS AND DISCUSSION

Variability studies

Estimates of variance components obtained for the eleven traits in the present study have shown that the high PCV and GCV (>20per cent) were observed for almost all the traits except the traits days to first female flower opening and acidity content of fruit. However these traits recorded moderate PCV and GCV. Snake gourd being a cross pollinated crop, there exists much variation and therefore the present observation is quite rational and reported earlier by Karuppaiah *et al*., (2002) in ridge gourd. The very low ECV observed for almost all the traits except the fruit yield per plant. Fruit yield per plant is the complex and polygenic trait which was slightly influenced by the environment. Burton (1952) had suggested that high GCV with heritability would give the best picture on the amount of progress to be expected by selection. The estimates of heritability were very high for all the eleven traits. Genetic advance as percent of mean was also high for almost all the traits except the traits days to first female flower opening and acidity content of fruit. A character can be improved only if it's highly heritable. The magnitude of heritability indicates the effectiveness with which the selection of genotypes can be made based on phenotypic performance (Johnson *et al*., 1955). In the present investigation, almost all the characters exhibited high heritability with high genetic gain. This indicates predominant of additive gene action in these traits and highly heritable suggesting the possibility of improvement through selection (Burton, 1952). Similar observations were made by Sheepujan Singh *et al*., (1996) in bitter gourd. The high heritability with low genetic gain indicates non-additive gene action in the traits such as days to first female flower opening and acidity content of fruit. Similar observations are also made by Nisha, 1999 in pumpkin.

Divergence analysis

Genetic divergence as measured by Mahalanobis (1936) in terms of generalized distance (D^2) has been one of the important statistical tools to estimate the genetic distance between genotypes. It provides rational basis for selection of parents for hybridization programme. Crosses among divergent parents are likely to yield desirable combinations. Therefore, a crossing programme can be initiated between the genotypes belonging to different characters. In this context, two important points are to be considered as i) choice of the particular cluster from which genotypes are to be used as parent in crossing programme and ii) selection of genotype from selected clusters. The greater the distance between two clusters, wider is the genetic diversity among the parents, to be included in hybridization programme. In the present study, the 40 genotypes were grouped into eight different clusters, based on relative magnitude of D^2 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. 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 byKaruppaiah *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

Table 1. Analysis of variance of snake gourd genotypes

Source	Mean sum of squares (MSS)											
	df	Days to first male flower opening	Days to first female flower opening	Number of fruits per plant	Fruit length (cm)	Fruit girth (cm)	Flesh thickness (cm)	Fruit weight (g)	Fruit yield (Kg)	Number of seeds per fruit	Vitamin C content (mg per 100g)	Acidity content (percent)
Replication	2	0.64	7.58	1.79	2.25	0.52	0.01	355.22	6.98	13.18	4.06*	0.0004
Genotype	39	146.03**	148.95**	70.30**	2964.64**	59.27**	0.11**	110236.60**	13.24**	816.27**	35.22**	0.002**
Error	78	1.76	1.67	0.40	2.46	0.18	0.01	88.52	0.55	2.40	0.24	0.0001

** Significant at 1% level; * Significant at 5% level

Table.2. Genetic variability for eleven traits of snake gourd genotypes

Traits	PCV (%)	GCV (%)	ECV (%)	H^2 (BS)	GA	GA as % of mean
Days to first male flower opening	20.47	20.35	3.89	98.80	14.20	41.66
Days to first female flower opening	15.84	15.75	2.90	98.89	14.35	32.27
Number of fruits per plant	36.63	36.53	4.81	99.42	9.91	75.03
Fruit length (cm)	42.38	42.36	2.16	99.92	64.70	87.22
Fruit girth (cm)	23.82	23.78	2.28	99.70	9.13	48.93
Flesh thickness (cm)	25.05	24.91	4.60	98.88	0.38	51.03
Single fruit weight (g)	33.85	33.84	1.66	99.92	394.57	69.68
Fruit yield per plant	30.61	29.97	10.79	95.86	4.15	60.44
Number of seeds per fruit	31.26	31.21	2.93	99.71	33.88	64.20
Vitamin C Content (mg per 100 g)	25.35	25.27	3.63	99.32	7.01	51.87
Acidity content (per cent)	16.97	16.54	6.55	95.03	0.05	33.22

Table.3 Composition of D^2 clusters for 40 snake gourd genotypes

S.No	Clusters	Number of genotypes	Genotypes
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
2.	II	6	G27, G29, G30, G16, G25, G31
3.	III	1	G12
4.	IV	3	G32, G34, G36
5.	V	1	G35
6.	VI	2	G33, G37
7.	VII	3	G7, G8, G18
8.	VIII	1	G24

Table.4. 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)

Table 5. Cluster mean of 40 snake gourd genotypes for various characters

Clusters	I	II	III	IV	V	VI	VII
Traits							
Days to first male flower opening	33.60	30.05	21.75	43.94	36.17	45.84	36.83
Days to first female flower opening	42.49	47.52	32.50	50.67	41.33	55.58	50.33
Number of fruits per plant	14.54	11.03	12.85	7.72	16.17	12.00	14.05
Fruit length (cm)	63.80	75.44	63.67	153.82	34.73	36.64	103.18
Fruit girth (cm)	18.22	22.47	20.13	10.93	25.89	27.89	14.77
Flesh thickness (cm)	0.67	1.00	0.95	0.72	1.02	0.98	0.61
Single fruit weight (g)	452.40	888.01	847.83	673.72	392.67	515.68	586.78
Fruit yield per plant	6.41	9.61	9.62	5.40	6.38	6.09	6.77
Number of seeds per fruit	50.13	55.86	90.75	66.76	61.00	56.92	37.32
Vitamin C Content (mg per 100 g)	14.53	12.72	9.50	10.33	9.23	10.87	15.44
Acidity content (per cent)	0.16	0.16	0.16	0.12	0.10	0.20	0.13

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 Thaniyamangalam, 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.

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