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Evaluation of snap melon (*Cucumis melo* var. *momordica* Duth. & Full) genotypes for growth, yield and quality parameters

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Abstract

The present study was carried out to evaluate the performance of snap melon genotypes for growth, yield and quality related attributes at Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore. Among the genotypes used for investigation, early harvest was obtained from T₁₈ (Melur local) (55.26) followed by T₃ (Amaravathi) (56.58) and T₂ (Tanjore) (58.04). The genotype T₃ (Amaravathi) (13.80) excelled in highest fruit yield per plant followed by the genotypes T₁₃ (Gujarat local) (13.70) and T₆ (Kariapatti) (12.70). The genotype T₁₆ (Thirumangalam long) (7.4°Brix) recorded highest TSS followed by the genotype T₈ (6.30 °Brix) and T₇ (6.20 °Brix). High amount of ascorbic acid content was observed in the genotype T₁₂ (Ranne bannur) (11.25 mg/100g) followed by T₁₃ (Gujarat local) (10.23 mg/100g) and the lowest amount of ascorbic acid content was recorded in T₃ (Amaravathi) (4.42 mg/100g). Regarding carbohydrate content highest amount was observed in T₁ (Virudhunagar) (21.23 mg/100 g) followed by T₃ (Amaravathi) (19.86 mg/100 g) and T₂ (Tanjore) (18.52 mg/100 g).

Keywords: Snap melon, ascorbic acid, genotype, harvest, evaluation

Introduction

India has witnessed a voluminous increase in horticulture production over the last few years. Significant progress has been made in the area expansion resulting in higher production. Over the last decade, the area under horticulture grew by about 3% per annum and annual production increased by 5.4%. During 2016-17, the production of horticulture crops was about 295.2 million tonnes from an area of 24.9 million hectares. India is the second largest producer of vegetable next to China. The production of vegetables has increased from 58.5 million tonnes to 175 million tonnes since 1991-92 to 2016-17. During 2016-17, the area under vegetables is estimated at 10.3 million hectares with a production of 175 million tones and productivity of 17.01 tonnes/ha in India. For this period the total vegetable production was highest in case of Uttar Pradesh followed by West Bengal. (Horticulture statistics in India, GOI).

The per capita consumption of vegetables in India must be 300 g per day as per ICMR recommendation. However, the per capita intake of vegetable is only 145 g. Therefore, there is a need for increasing the production of vegetables by growing high yielding genotypes/varieties/hybrids with high nutritive value by adopting improved production technologies.

Melons are important horticultural crops belong to cucurbitaceae family. India is being one of the secondary centre of origin of *Cucumis melo* in which the cultivated forms comprises of 40 species (Whitaker and Davis, 2008). There are several local varieties of melon grown in different regions of India. Mostly the crop is confined to Gujarat in the west and West Bengal in the east. In North India snap melon is otherwise called as "Phoot" which is known as to split and in Kerala locally it is called as "Pottuvellari". There are numerous uses of melons depending on the type and maturity of the fruit. Sweet types are consumed as dessert, non sweet types are used as vegetable and immature fruits are eaten as raw, pickled or cooked. The fruits contain vitamin C, sugars, minerals and fibre.

The fruits also contains 3 percent carbohydrate, 0.3 per cent protein, 95.7 per cent moisture, 0.1 per cent fat, 10 mg vitamin C 100g⁻¹ and 265 IU vitamin A 100 g⁻¹ (Peter and Hazra, 2012). Seed contains 12.5 to 39.1 per cent edible oil. Therefore a systematic study of variability and heritability in the available germplasm is the only way to increase the yield

potential and also to improve the quality traits, pest and disease incidence. The present study was carried out for collection and characterization of genotypes of snap melon in different parts of India and also to assess the variability existing in the germplasm for morphological, yield and quality traits. Being a cross pollinated crop, there is a tremendous variation exists among the crop. Therefore, identification of quantitatively inherited characters from available germplasm can be efficient way to obtain greater genetic variation in melons.

Materials and Methods

The experiment was carried out in the year 2016-2017 at the college orchard, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore. A total of 23 accessions were collected from different regions in India like Kerala, Gujarat, Karnataka in and around Tamil Nadu and a released variety from IARI, New Delhi. The experiment was laid out in Randomized Block Design with three replications. Three pits were raised separately for each accessions at a spacing of 1.5m x 2m under each replication. The 23 genotypes under each replication were raised in the three pits and two to three seeds were sown in each pit. The cultural and management practices were adopted according to the package of practices recommended by Tamil Nadu Agricultural University, Coimbatore.

The observations were recorded from five randomly selected plants in each genotype. Morphological characters like number of primary branches, node at which first male flower appearance, node at which first female flower appearance, days to first male flower, days to first female flower, internodal length, stem thickness, peduncle length, number of male flowers per vine, number of female flowers per vine, length of the fruit (cm), girth of the fruit (cm), weight of the fruit (cm), days to first harvest, number of fruits per plant, yield per plant (kg), vine length (m), flesh thickness (cm), and quality characters like total soluble solids ($^{\circ}$ Brix), ascorbic acid and carbohydrate content were analyzed in this study. Analysis of variance of the data from each attribute was computed using AGRES computer programme. The least significant differences test at 5 per cent of probability was used to test the significance among the mean values.

Results and Discussion

Significant differences among the genotypes were observed for all the characters. Earliness is one of the main attribute which is measured in terms of node at which first male and female flower appearance. The genotype T₂₃ (Kulasekaranatham) and T₆ (Kariapatti) produced male flowers at lowest node (1.22) followed by T₄ (Vizhavayal) (Table 2). The genotype T₈ (Pattukottai) produced female flower at lowest node (3.11) followed by T₅ (Sathyamangalam) (3.15) and T₁₈ (Melur local) (3.16). Similar trend of earliness was reported by Rakhi and Rajamony (2005) [10], Venkatesan *et al.* (2016) [16] in musk melon and Priya (2012) [8] in snap melon. Early harvest is also one of the important desirable trait for any crop improvement programme. The present study was also brought out certain genotypes with significant early harvest. The genotypes T₁₈ (Melur local) (55.26) recorded early harvest followed by T₃

(Amaravathi) (56.58) and T₂ (Tanjore) (58.04). This is in accordance with the findings of Ahmed *et al.* 2005 [1] and Rakhi and Rajamony (2005) [10].

Fruit length indirectly increases the yield in any type of the crop. Therefore, it is considered to be an important trait in selecting the melon genotypes. Longer fruits were observed in the genotype T₁₂ (Ranne bannur) (34.90 cm) followed by T₃ (Amaravathi) (33.06 cm) and T₂ (Tanjore) (32.87 cm). Studies conducted by Priya (2012) [8]; Rakhi and Rajamony (2005) [10], Pandey *et al.* (2010) [6] also recorded the similar trend of results in fruit length. Greater fruit girth was observed in the genotype T₃ (Amaravathi) (16.76 cm) followed by T₇ (Thirumangalam - short) and T₁₆ (Thirumangalam long) (13.90 cm). Similar trend of results were reported by Venkatesan *et al.* 2016 [12] in musk melon. The highest average fruit weight was observed in the genotype T₃ (Amaravathi) (2.24 kg) followed by T₁₆ (Thirumangalam long) (1.71 kg) and T₂₃ (1.35 kg). Smaller size of fruits were observed in T₁₉ (PAU) (0.70 kg) followed by T₂₁ (Pusa Shandar) (0.74kg). Similar pattern of results were found by Rad *et al.* (2010) [9], Priya (2012) [8]. With respect to number of fruits per plant the genotypes T₃ (Amaravathi) (14.20) and T₆ (Kariapatti) (12.70) were the best performing genotypes among the twenty three genotypes. Maximum flesh thickness was observed in the genotype T₆ (Kariapatti) (2.23 cm) followed by T₁₇ (Kothayapatti local) (1.64 cm) and T₁₄ (Namanasamuthiram) (1.62 cm). This is in corroboration with the findings of Priya (2012) [8] and Rakhi & Rajamony (2005) [10].

Peduncle length is another important character which is relatively contributes to yield. The peduncle length was highest in the genotype T₁ (Virudhunagar) (4.60 cm) followed by T₃ (Amaravathi) (4.50 cm) and T₇ (Thirumangalam short) (4.30 cm). Similar pattern of results was reported by Dhillon *et al.* (2007) [3]. In respect of fruit yield per plant, the genotypes, T₃ (Amaravathi) (13.80) and Gujarat local excelled in fruit yield per plant when compared to other genotypes. Highest marketable fruit yield per plant recorded by these genotypes might have been due to the presence of maximum number of fruits per plant and average fruit weight. These two characters directly influenced the marketable fruit yield per plant. The similar trend of result of high marketable fruit yield per plant was obtained by Sidhu (2013) in bitter gourd, Priya (2012) [8] in snap melon.

Generally, higher TSS and CHO content would increase the nutritive value and sweetness of the fruits respectively. In the present study, the genotypes T₁₆ (Thirumangalam long) (7.4 $^{\circ}$ Brix) recorded highest TSS followed by the genotypes T₈ (Pattukottai) (6.3 $^{\circ}$ Brix) and T₇ (Thirumangalam short) (6.2 $^{\circ}$ Brix). With respect to carbohydrate content in plant the highest CHO content was observed in T₁ (Virudhunagar) (21.23 mg/100 g) followed by T₃ (Amaravathi) (19.86 mg/100 g) and T₂ (Tanjore) (18.52 mg/100 g). Ascorbic acid in plant has immense medicinal value mainly due to its hypoglycemic properties (Behera, 2004) [2]. High amount of ascorbic acid content was observed in the genotype T₁₂ (Ranne bannur) (11.25 mg/100g) followed by T₁₃ (Gujarat local) (10.23 mg/100g). Whereas low ascorbic acid content was observed in T₃ (Amaravathi) (4.42 mg/100g). This result was in accordance with Okiei *et al.* (2009) [5] in cucumber.

Table 1: Sources of various snap melon genotypes used in the study

Treatments	Name of the genotypes/varieties	Source
T ₁	Virudhunagar	Virudhunagar Dt.
T ₂	Tanjore	Tanjore Dt.
T ₃	Amaravathi	Sivagangai Dt.

T ₄	Vilavayal	Pudukottai Dt.
T ₅	Sathyamangalam	Erode Dt.
T ₆	Kariapatti	Virudhunagar Dt.
T ₇	Thirumangalam short	Madurai Dt.
T ₈	Pattukottai	Tanjore Dt.
T ₉	Kalacherry	Cuddalore Dt.
T ₁₀	Kodikulam	Virudhunagar Dt.
T ₁₁	Vizhupuram	Vizhupuram Dt.
T ₁₂	Ranne bannur	Haveri Dt, Karnataka
T ₁₃	Gujarat local	Gujarat
T ₁₄	Namanasamuthiram	Pudukottai Dt.
T ₁₅	Watrap local	Virudhunagar Dt.
T ₁₆	Thirumangalam long	Madurai Dt.
T ₁₇	Kothayapatti local	Pudukottai Dt.
T ₁₈	Melur local	Pudukottai Dt.
T ₁₉	PAU	Punjab Agricultural University, Punjab.
T ₂₀	Kodungalur	Mala Block, Kerala
T ₂₁	Pusa Shandar	IARI, New Delhi
T ₂₂	Thambipatti	Virudhunagar Dt.
T ₂₃	Kulasekaranatham	Tuticorin Dt.

Table 2: Mean values for growth, yield and quality characters in snap melon

Characters/Treatments	Number of primary branches	Node at which first male flower appearance	Node at which first female flower appearance	Days to 1st male flower appearance	Days to 1st female flower appearance	Internodal length (cm)	Stem thickness (cm)	Peduncle length (cm)	Flesh thickness (cm)
T ₁	4.80	1.27	3.20	21.80	30.80	9.35	2.05	4.60	1.44
T ₂	5.20	1.44	3.62	22.40	40.80	11.58	3.56	3.10	1.26
T ₃	6.60	2.32	5.40	21.80	26.30	10.80	3.28	4.50	1.42
T ₄	4.40	1.24	3.25	25.00	31.80	7.52	3.22	3.90	1.36
T ₅	4.00	1.23	3.15	22.60	35.00	8.65	2.85	3.20	1.34
T ₆	5.80	1.22	3.20	20.80	28.90	7.57	3.39	4.20	2.23
T ₇	5.60	1.34	3.35	22.40	34.00	6.54	2.72	4.30	1.15
T ₈	6.00	1.35	3.11	22.80	33.10	6.79	2.30	3.90	1.23
T ₉	5.80	1.34	3.25	22.80	29.00	10.12	3.11	3.20	1.10
T ₁₀	5.30	3.41	3.54	21.20	32.80	9.46	2.65	4.10	1.25
T ₁₁	5.20	1.33	3.43	22.60	32.00	9.35	2.27	3.80	1.22
T ₁₂	6.30	1.42	3.56	19.40	31.40	10.57	3.06	3.50	1.45
T ₁₃	4.60	1.25	5.45	22.40	31.00	7.45	3.15	4.10	1.57
T ₁₄	2.50	1.23	3.23	21.40	29.80	8.10	2.98	3.40	1.62
T ₁₅	6.40	2.31	3.46	22.40	33.60	6.77	2.84	3.00	1.50
T ₁₆	4.80	1.35	3.51	21.80	30.70	9.91	3.07	3.20	1.42
T ₁₇	3.60	1.36	4.24	23.40	35.70	8.20	2.45	3.70	1.64
T ₁₈	3.40	1.35	3.27	25.20	29.20	9.15	2.98	4.00	1.23
T ₁₉	3.00	1.34	3.16	26.20	32.50	7.63	3.02	3.20	1.36
T ₂₀	3.00	1.40	3.23	26.20	34.00	8.77	4.97	3.40	0.87
T ₂₁	2.80	1.42	3.30	21.40	31.90	7.63	2.68	3.20	0.92
T ₂₂	3.20	1.26	4.62	21.40	33.80	6.58	2.74	4.10	1.48
T ₂₃	3.20	1.22	3.54	23.00	38.83	6.02	2.06	3.80	1.52
Grand mean	4.58	1.49	3.61	22.62	32.47	8.45	2.93	3.71	1.37
S.Ed	0.06	0.02	0.06	0.45	0.85	0.18	0.13	0.05	0.02
CD at 0.05%	0.13	0.05	0.13	0.92	1.71	0.36	0.27	0.11	0.05

Table 2: Cont....

Characters/Treatments	Number of male flowers per vine	Number of female flowers per vine	Length of the fruit (cm)	Girth of the fruit (cm)	Weight of the fruit (kg)	Days to 1st harvest	Number of fruits/plant	Yield /plant (kg)	Vine length (m)	TSS (° Brix)	Ascorbic acid	CHO
T ₁	123.57	19.24	31.38	11.79	1.30	61.23	6.50	7.30	1.05	4.50	8.26	21.23
T ₂	128.42	17.96	32.87	12.10	1.30	58.04	7.60	6.50	1.47	3.90	7.52	18.52
T ₃	133.74	23.32	33.06	16.76	2.24	56.58	14.20	13.80	2.11	5.00	4.42	19.86
T ₄	121.07	14.24	30.89	12.11	0.96	59.24	6.70	5.20	1.78	4.10	4.95	11.85
T ₅	105.27	17.75	29.23	12.17	0.82	64.71	8.30	4.30	1.54	3.70	5.02	10.27
T ₆	112.69	21.22	30.54	12.19	0.87	63.95	12.70	6.50	1.77	5.20	5.13	13.25
T ₇	138.50	12.71	12.75	13.90	0.83	63.04	9.40	7.20	1.43	6.20	6.25	12.58
T ₈	146.30	18.95	16.68	11.29	0.96	58.82	11.90	5.60	1.67	6.30	6.03	13.69
T ₉	109.78	13.58	23.54	13.11	1.18	61.08	11.50	5.00	1.90	5.10	4.56	15.22
T ₁₀	127.89	19.64	24.32	11.50	1.32	62.89	11.10	7.50	1.32	5.30	7.32	17.02
T ₁₁	130.02	18.14	31.09	12.97	1.10	58.52	7.30	4.90	1.10	4.50	6.47	12.58
T ₁₂	117.23	20.58	34.90	13.90	1.10	60.25	12.20	8.20	1.22	4.90	11.25	13.20

T ₁₃	129.09	14.52	31.20	14.17	1.25	58.23	13.70	11.90	1.54	4.90	10.23	13.78
T ₁₄	108.67	20.61	30.87	14.15	0.87	60.28	9.20	9.20	1.33	5.60	5.06	11.25
T ₁₅	98.31	13.58	31.86	13.20	1.20	62.75	9.00	9.00	1.29	4.80	7.36	17.56
T ₁₆	127.54	21.08	30.07	13.90	1.30	55.26	11.90	6.90	2.10	7.40	5.18	16.68
T ₁₇	118.20	17.93	28.24	11.23	0.85	60.57	8.20	4.20	1.86	4.70	6.61	16.58
T ₁₈	120.11	18.25	30.11	11.47	0.98	59.26	8.50	8.20	1.79	5.30	5.28	15.58
T ₁₉	78.32	20.97	12.26	11.58	0.70	61.25	4.90	4.90	0.85	5.80	7.23	14.36
T ₂₀	134.52	17.04	16.08	12.69	0.82	62.36	4.20	8.51	1.29	5.60	6.58	14.36
T ₂₁	100.23	19.50	23.22	11.23	0.74	63.03	5.30	11.32	1.01	6.80	8.32	13.52
T ₂₂	121.04	22.00	24.09	13.52	1.24	58.42	10.50	5.30	1.89	5.00	6.58	17.56
T ₂₃	111.28	20.00	13.05	12.52	1.35	64.04	11.30	10.50	1.85	5.90	6.22	16.89
Grand mean	119.20	18.38	26.18	12.75	1.11	60.60	9.37	7.47	1.52	5.23	6.60	15.10
S.Ed	2.75	0.38	0.64	0.28	0.02	1.26	0.20	0.16	0.09	0.11	0.16	0.35
CD at 0.05%	0.36	0.76	1.29	0.57	0.04	2.55	0.41	0.33	0.18	0.23	0.33	0.70

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