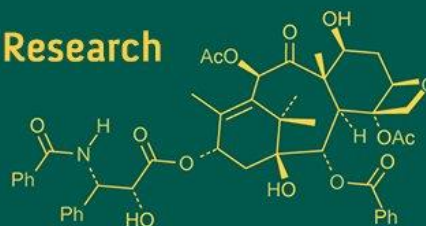
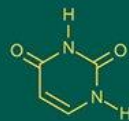
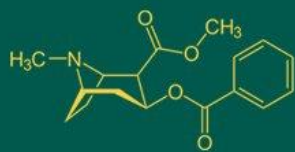


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Evaluation of different genotypes of snapmelon (*Cucumis melo* var. *momordica* Duth. and Full.) grown under agro-climatic conditions of Konkan region

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Abstract

The present investigation was carried out with the objective to evaluate different genotypes of snapmelon (*Cucumis melo* var. *momordica*) grown under Konkan Agro-climatic conditions, at College of Horticulture, Dapoli (MS), Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth Dapoli, Dist. Ratnagiri, 415712 in *kharif* season during 2023-2024. The experiment was laid out in Randomized Block Design (RBD) with fifteen treatments as genotypes replicated thrice. Analysis of variance revealed that the genotypes differed significantly for all the growth, yield and yield attributing characters under study. Among the genotypes studied, T₁₁ (DPL-SM-11) was found superior with respect to fruit yield per plant (3.91 Kg) and yield per ha (32.87 t/ha) followed by T₁₄ (Konkan Madhur) T₁ (DPL-SM-1) and T₁₅ (Pusa Shandar) has performed better for fruit yield per plant and per hectare. The genotype T₃ (DPL-SM-3) recorded significantly best performance with respect to precocity like days to first female flowering (40.21 days) and crop duration (84.85 days). The better performance was observed for yield attributing traits like fruit length (27.25 cm), average fruit weight (1.50 Kg) in T₁ (DPL-SM-1), number of fruits (5.09) was found higher in T₁₁ (DPL-SM-11). In the current study superior genotypes namely T₁₁ (DPL-SM-11), T₁ (DPL-SM-1), T₁₄ (Konkan Madhur), T₃ (DPL-SM-3), T₁₂ (DPL-SM-12) and T₁₅ (Pusa Shandar) identified for yield parameters. Therefore, these genotypes with high yield may be employed directly either for commercial cultivation or in breeding programmes to develop new cultivars of snapmelon having improved characters. The genotypes differed significantly in most of the parameters and offer a good scope for selection of parent for crop improvement programme.

Keywords: Snapmelon genotypes, *Chibud*, *Phoot*, vegetative characters and yield

Introduction

Melons are important horticultural crops belong to the family cucurbitaceae. India is being one of the secondary centres of origin of *Cucumis melo* in which the cultivated forms comprise of 40 species (Whitaker and Davis, 2008) [24]. There are several local genotypes of melons grown in different regions of India. Snap melon (*Cucumis melo* var. *momordica* Duth. and Full.) is an underutilized vegetable crop belonging to the family cucurbitaceae, with a chromosome number 2n = 24. Snap melon is commonly known as 'Phoot' which means to 'split'. Snap melon is a locally cultivated dessert melon known as 'Chibud' in Goa and coastal Maharashtra, in areas of Karnataka as 'Hibadihannu' or 'Phoottikai' and in Kerala locally it is known as 'Pottuvellari'. Snapmelon is originated in India and is commercially grown in the states namely Tamil Nadu, Maharashtra, Kerala, Karnataka, Haryana, Punjab, Rajasthan and Bihar. It is very popular in arid and semi-arid regions (Hazra *et al.*, 2011) [10]. The use of snap melon depends on the type of fruits. Sweet or ripe fruits are consumed as dessert, while non-sweet or immature fruits are used as vegetable in some of the regions. Ripe fruits are commonly consumed fresh, whereas immature fruits are used in curries and pickles. It is rich in sugar, vitamin C, minerals and dietary fibres. The fruit of snapmelon contains carbohydrate (3%), protein (0.3%), fat (0.1%), vitamin A (265 IU /100gm), moisture (95.7%) and vitamin C (10 mg /100 gm) (Peter and Hazra, 2012) [17]. Besides nutritional factor, snap melon embraces many medicinal uses. Fruit is commonly used as cooling and intestine cleanser and moisturizer for skin. Fruits are also used for treating burns and abrasions. Fruits improve appetite, cure stomach pain and help in relieving constipation

and vomiting. Seeds are antitussive, digestive, febrifuge and vermifuge. Roots are diuretic and emetic.

Snapmelon is an annual vine crop. Snapmelon plants have short taproots and a fragile woody stem. The leaves are simple to palmately lobed, placed alternately. Flowers are solitary, with male and female flowers produced on separate nodes of the same plant. Male flowers are produced in clusters, while female flowers often born single. The plant is cross-pollinated in nature, and the fruit is pepo. Snapmelon is grown in well drained, light to sandy loam soil and is sensitive to acidic conditions. Snap melon is warm season crop cultivated in tropical and subtropical climates. It can be grown at optimum temperature of 22 °C. It is a resilient crop which is cultivated as a sole crop in summer season and as mixed crop along with field crops like maize, sorghum and pearl millet in rainy season (Seshadri and More, 2009) [20].

In Maharashtra, it is popularly grown in Konkan region especially Raigad, Ratnagiri and Sindhudurg districts during *kharif* season. However, it shows variation in growth and yield characters in relation to fruit traits like size, shape, colour, taste texture and biochemical composition. Snapmelon is grown in kitchen garden but recently gaining popularity as commercial crop especially during *kharif* season due to its wider adaptability, short duration, and preference among consumers.

Snapmelon is one of the most important underexploited vegetable crop capable of producing high yields per unit area. A large number of local genotypes are grown in traditional but there are only few improved and cultivars are recommended for commercial cultivation. Despite economic and medicinal importance of the crop, due attention was not given towards a crop improvement programme as well as on production protocol. Creating variability by crossing available local genotype will widen the scope for further selection to develop new variety.

Snapmelon is highly cross pollinated crop which exhibit considerable variation for different traits in the Konkan

region. Evaluating locally adopted snapmelon genotypes for commercial cultivation is priority research area for improving the productivity, uniformity, fruit quality and market acceptance. Assessment of nutraceutical properties is also necessary while identifying the superior genotypes. Hence, there is a need of focused research to evaluate the available variability to select promising high yielding genotypes for commercial cultivation. Hence, it is proposed to conduct experiment entitled “Evaluation of different genotypes of snapmelon (*Cucumis melo* var. *momordica* Duth. & Full.) Grown under Konkan agro-climatic conditions”.

Materials and methods

The field experiment was carried out in 2023-24 during the *kharif* season at the Department of Vegetable Science, College of Horticulture, Dapoli. Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli (Maharashtra). A total of 15 locally grown genotypes were collected from Ratnagiri, Sindhudurg, Raigad and Thane district of Konkan region for investigation based on their variation in morphological character as well as flowering and fruiting habit. These types were evaluated along with the variety Konkan Madhur released by Dr. B. S. K. K. V, Dapoli as Local Check under field conditions and a released variety Pusa Shandar from IARI, New Delhi.

The experiment was laid out in Randomized Block Design with three replications. Each genotypes were grown at a spacing of 2 m x 0.6 m with sowing of two to three seeds in each pit. The cultural and management practices were adopted according to the package of practices recommended by Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli. The data on growth and yield attributing characters for snapmelon were recorded on five randomly selected equally competitive plants in each genotype and replication. The mean values of recorded observations was computed for each trait and statistically analyzed (Panse and Sukhatme, 1995) [16].

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

Sr. No.	Genotypes	Source
1.	T ₁ - DPL-SM-1	Phondaghat, Kankavali, Sindhudurg 16.3841° N, 73.8068° E
2.	T ₂ - DPL-SM-2	Nandivase, Chiplun, Ratnagiri 17.5422° N, 73.6879° E
3.	T ₃ - DPL-SM-3	Palavani, Mandangad, Ratnagiri 17.9251° N, 73.2268° E
4.	T ₄ - DPL-SM-4	Tulsuli, Kudal, Sindhudurg 16.0171° N, 73.6965° E
5.	T ₅ - DPL-SM-5	Ghave, Dapoli, Ratnagiri 17.7212° N 73.1735 ° E
6.	T ₆ - DPL-SM-6	Alibaug, Raigad 18.6624° N 72.8871 ° E
7.	T ₇ - DPL-SM-7	Tondavali, Kankavali, Sindhudurg 16.3939° N 73.7129 ° E
8.	T ₈ - DPL-SM-8	Kasal, Kudal, Sindhudurg 16.1549° N 73.6789 ° E
9.	T ₉ - DPL-SM-9	Latawan, Mandangad, Ratnagiri 17.9312° N 73.3462 ° E
10.	T ₁₀ - DPL-SM-10	Ponda, South Goa 15.3865° N 74.0012 ° E
11.	T ₁₁ - DPL-SM-11	Kalavande, Chiplun, Ratnagiri 17.4664° N 73.4973 ° E
12.	T ₁₂ - DPL-SM-12	Adavali, Lanja, Ratnagiri 16.9060° N, 73.5987 ° E
13.	T ₁₃ - DPL-SM-13	Bandhatiware, Dapoli, Ratnagiri 17.8083° N 73.2054 ° E
14.	T ₁₄ - Konkan Madhur (check)	Dr. B. S. K. K. V., Dapoli
15.	T ₁₅ - Pusa Shandar	IARI, New Delhi

Result and discussion

The data pertaining to comparative performance of various snapmelon genotypes grown under Konkan agro-climatic condition are presented in Table 2 and Table 3. The results revealed significant differences among the genotypes for all the characters.

Vegetative parameters

Magnitude of various growth parameters is strongly associated with life span, maturity as well as yield. Longest vine length was registered in genotype T₁₄ -Konkan Madhur (2.40 m) and which was at par with genotypes T₁₁ (2.30 m), T₁₂ (2.29 m), and T₃ (2.13 m), whereas lowest was recorded in the genotype T₁₃ (1.29 m). Variation in vine length among the genotypes might be due to genetic make-up of genotype as well as environmental factors, which ultimately responsible for increasing the photosynthetic activities. Similar trend of vine length was reported by Priya (2012) [18], Shirke *et al.* (2013) [9], Muthuselvi *et al.* (2019) [14], Rizvi *et al.* (2023) [19] in Snapmelon and Venkatesan *et al.* (2016) [23] in muskmelon.

The highest number of nodes (38.88) was recorded in genotype T₁₁ which was significantly superior over the rest of genotypes. The lowest number of nodes was recorded by T₂ (23.47). The number of nodes per plant is directly proportional to the production of fruits, which ultimately lead to higher fruit yield. Trends in results were also reported by Bhagwat *et al.* (2018) in cucumber, Shrestha *et al.* (2021) [21] in zucchini and Akhter *et al.* (2023) [2, 4].

The highest number of primary branches was observed in genotype T₁₁ (6.00) which was significantly superior over other genotypes, whereas lowest number of primary branches (3.35) was recorded in genotype T₂. Similar trend of results were reported by Dhillon *et al.* (2007) [7], Muthuselvi *et al.* (2019) [14] in snapmelon, Ganiger *et al.* (2017) [8] in wild melon, Pal *et al.* (2017) [15] in cucumber and Deshmukh *et al.* (2024) [6] in pumpkin.

Flowering behaviour

Earliness is one of the main attribute which is measured in terms of days at which first female flower appearance. The genotype T₃ was observed early (40.21 days) for the first appearance of female flower which was at par with T₁₁ (41.05 days), T₁₄ (41.10 days) and T₁ (42.34 days), whereas the highest number of days (46.20 days) was observed in the genotype T₁. Differences in days to appearance of 1st female flowering among the genotypes, is usually governed by the genetic makeup of the plant as well as internodal length, number of internodes, environmental factor and vigour of the crop. Trends in results were also reported by Muthuselvi *et al.* (2019) [14] and Rizvi *et al.* (2023) [19] in snapmelon and Deshmukh *et al.* (2024) [6] in pumpkin.

The lowest male: female ratio was noticed in genotype T₁₀ (11.72) which was at par with the genotype T₁₁ (12.02), T₁₂ (12.21), T₁₄ (12.42), and T₁ (12.60). Significantly the highest sex ratio was recorded in T₆ (14.60). Low sex ratio (male to female) is a favourable trait in cucurbits and is advantageous as lower sex ratio is obtained when number of female flowers is more. This is in corroboration with the findings of Venkatesan *et al.* (2016) [23], Shivakumara (2019) [30], Omprasad *et al.* (2021) [29], Kalaiselvan and Lenin (2023) [32] in muskmelon, Tamilselvi and Jansirani (2017) [31], Dahatonde *et al.* (2024) [5] in pumpkin and Aiswarya *et al.* (2023) [1] in watermelon.

The genotype T₁₂ produced first fruit at lowest node (7.60) which was at par with the treatment T₁₁ (7.98), T₁ (8.21) and T₅ (8.25). However the genotype T₁₃ produced first fruit at highest node (11.24). Earliness in fruit set is primarily governed by the genetic makeup of the cultivar. Similar pattern of results was reported by Yogananda (2018) [25] in bottle gourd, Shivakumara (2019) [30] in muskmelon and Pavithra (2021) [28] in watermelon.

Fruit parameters

Variation in various fruit parameters was also observed. Longer fruits were exhibited in the genotype T₁ (27.25 cm) which was at par with T₁₁ (26.50 cm), T₁₅ (26.34 cm) and T₈ (26.02 cm). The genotype T₁₃ recorded shortest length of fruit (20.26 cm). Increase in fruit yield is mostly influenced by fruit length. Studies conducted by Priya (2012) [18], Muthuselvi *et al.* (2019) [14] and Rizvi *et al.* (2023) [19] in snapmelon, Venkatesan *et al.* (2016) [23] in muskmelon, Joy *et al.* (2020) [12] in watermelon and Deshmukh *et al.* (2024) [6] in pumpkin also recorded the similar trend of results in fruit length.

Greater fruit width (20.77 cm) was recorded in the round fruited genotype T₉ which was at par with T₁₂ (20.31 cm), whereas it was lowest in genotype T₈ (11.65 cm). The higher fruit width and higher fruit length result in to higher fruit weight. Similar trend was reported by Priya (2012) [18], Muthuselvi *et al.* (2019) [14] and Rizvi *et al.* (2023) [19] in snapmelon, Venkatesan *et al.* (2016) [23] in muskmelon and Joy *et al.* (2020) [12] in watermelon.

The highest length to width ratio (2.06 cm) was observed in the genotype T₁ followed by T₁₁ (2.04 cm), T₂ (1.89 cm) and T₈ (1.86 cm). However, the lowest length to width ratio was observed in the genotype T₁₃ (1.07 cm). The variation in fruit length to width ratio might have been due to genotypic differences among the genotypes. A similar pattern was discovered by Mishra and Singh (2017) [13] in bitter gourd, Pouyesh *et al.* (2017) [26] in cantaloupe and Prabhu (2024) [27] in snapmelon.

Table 2: Growth and yield attributing characters of snapmelon genotypes under Konkan agro-climatic conditions

Genotypes	Vine length (m)	Number of nodes	Number of primary branches	Appearance of 1 st female flowers (days)	Sex ratio (M: F)	Nodal position of 1 st fruit	Fruit length (cm)	Fruit width (cm)	Length to width ratio
T ₁ - DPL-SM-1	1.94	31.14	5.02	42.34	12.60	8.21	27.25	12.51	2.06
T ₂ - DPL-SM-2	1.34	23.47	3.35	45.98	13.98	9.45	23.28	12.09	1.89

T ₃ - DPL-SM-3	2.13	29.79	5.12	40.21	13.18	9.02	22.30	15.75	1.58
T ₄ - DPL-SM-4	1.55	27.68	4.57	46.14	13.68	9.56	24.77	15.91	1.54
T ₅ - DPL-SM-5	1.60	25.20	5.49	43.12	13.20	8.25	23.42	12.42	1.60
T ₆ - DPL-SM-6	2.02	31.46	5.15	45.02	14.60	9.41	24.70	13.26	1.71
T ₇ - DPL-SM-7	1.84	34.46	4.20	44.16	13.51	10.26	24.23	12.91	1.75
T ₈ - DPL-SM-8	1.80	24.97	5.13	43.25	13.21	9.52	26.02	11.65	1.86
T ₉ - DPL-SM-9	1.54	30.68	4.02	45.84	14.21	10.12	22.23	20.77	1.68
T ₁₀ - DPL-SM-10	1.88	26.40	5.61	43.89	11.72	9.21	22.30	14.50	1.78
T ₁₁ - DPL-SM-11	2.30	38.88	6.00	41.05	12.02	7.98	26.50	12.28	2.04
T ₁₂ - DPL-SM-12	2.29	28.40	5.45	45.60	12.21	7.60	23.12	20.31	1.18
T ₁₃ - DPL-SM-13	1.29	24.39	4.45	46.20	14.25	11.24	20.26	12.14	1.07
T ₁₄ - Konkan Madhur (Check)	2.40	34.24	5.60	41.10	12.42	9.00	23.00	18.13	1.10
T ₁₅ - Pusa Shandar	2.05	32.59	5.20	43.89	13.96	9.35	26.34	15.31	1.66
Range	1.29-2.40	23.47-38.88	3.35-6.00	40.21-46.20	11.72-14.60	7.60-11.24	20.26-27.25	11.65-20.77	1.07-2.06
Mean	1.86	29.58	4.96	44.51	13.17	9.12	24.04	15.61	1.63
Result	SIG	SIG	SIG	SIG	SIG	SIG	SIG	SIG	SIG
S.Em±	0.15	1.21	0.15	1.01	0.45	0.40	0.81	0.77	0.10
CD@5%	0.43	3.60	0.45	3.00	1.35	1.14	2.34	2.23	0.28

Table 3: Yield attributing characters of snapmelon genotypes under Konkan agro-climatic conditions

Genotypes	Flesh index (%)	Maturation period (days)	Crop duration (days)	100 seed weight (g)	Number of fruit per plant	Fruit weight (Kg)	Yield per plant (Kg)	Yield per hectare (t/ ha)
T ₁ - DPL-SM-1	56.00	36.45	87.12	10.25	2.30	1.50	3.53	29.65
T ₂ - DPL-SM-2	53.98	38.15	92.10	10.14	1.85	1.23	2.26	19.11
T ₃ - DPL-SM-3	62.14	35.12	84.85	11.18	2.54	1.32	3.33	28.04
T ₄ - DPL-SM-4	61.97	36.62	93.01	9.50	1.90	1.18	2.19	18.52
T ₅ - DPL-SM-5	67.21	32.15	88.02	10.79	2.39	1.25	2.96	24.93
T ₆ - DPL-SM-6	55.62	35.44	86.12	9.63	2.20	1.37	2.99	25.16
T ₇ - DPL-SM-7	52.41	36.32	91.26	11.46	1.99	1.21	2.38	20.12
T ₈ - DPL-SM-8	62.12	33.61	85.00	9.52	2.30	1.31	2.98	25.08
T ₉ - DPL-SM-9	55.20	38.80	90.54	13.09	1.95	1.26	2.42	20.47
T ₁₀ - DPL-SM-10	60.12	35.20	88.40	11.65	2.16	1.37	2.93	24.69
T ₁₁ - DPL-SM-11	72.56	31.15	85.20	13.52	2.71	1.46	3.91	32.87
T ₁₂ - DPL-SM-12	62.74	34.12	87.82	11.75	2.54	1.32	3.30	27.77
T ₁₃ - DPL-SM-13	52.21	36.68	90.12	11.50	1.92	1.17	2.21	18.73
T ₁₄ - Konkan Madhur (Check)	63.10	32.16	86.50	12.34	2.65	1.44	3.78	31.80
T ₁₅ - Pusa Shandar	62.41	32.47	89.10	9.00	2.61	1.37	3.39	28.55
Range	52.21-72.56	31.15-38.80	84.85-93.01	9.00-13.52	1.85-2.71	1.17-1.50	2.19-3.91	18.52-32.87
Mean	65.32	34.96	88.35	11.02	2.27	1.32	2.97	25.03
Result	SIG	SIG	SIG	SIG	SIG	SIG	SIG	SIG
S.Em±	0.97	1.01	1.56	0.45	0.18	0.07	0.14	1.73
CD@5%	2.81	2.94	4.52	1.31	0.53	0.20	0.41	5.01

Yield and Yield attributing characters

- The data regarding yield and yield attributing characters of different snapmelon genotypes are summarized in Table 3.
- The maximum flesh index (72.56%) was observed with genotype T₁₁ which was at par with the genotype T₅ (67.21%) only. The minimum flesh index (52.21%) was observed in the genotype T₁₃. The difference may be due to the inherent character and genetic makeup.
- Data in relation to maturation period and crop duration are presented in Table 3 and graphically depicted in

Fig.1. The earliest fruit maturity (31.15 days) from flowering to fruit maturity was noticed in genotype T₁₁ which was at par with the genotype T₅ (32.15 days) and T₈ (33.61 days), whereas the highest days to maturity were observed in genotype T₉ (38.80 days). This variation might be due to the genetic makeup of the plant as well as the prevailing environmental conditions. The variation in maturation period of snapmelon was also noticed by Priya (2012) ^[18].

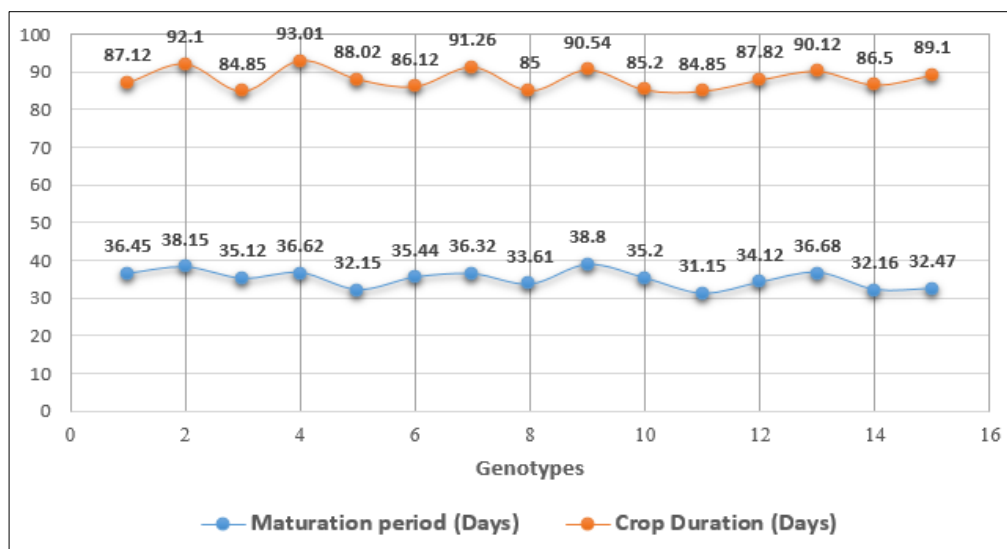


Fig 1: Variation in maturation period and crop duration (days) of snapmelon genotypes

The number of days required for crop duration is usually determined by the genetic makeup of the plant and the environmental conditions in which the crop is being grown. The earliest days for crop duration (84.85 days) was noticed in genotype T₃ which was at par with the genotype T₈ (85.00 days), T₁₁ (85.20 days), T₆ (86.12 days), T₁₄ (86.50 days), T₁₂ (87.82 days) and T₅ (88.02 days). The genotype T₄ recorded highest number of days (93.01 days) for days to crop duration. Similar results were reported by Priya (2012) [18], Muthuselvi *et al.* (2019) [14] in snapmelon, Venkatesan *et al.* (2016) [23], Omprasad *et al.* [29], (2021), Akhter *et al.* (2023) [2] in muskmelon and Bairwa *et al.* (2018) [3] in ash gourd.

The highest seed weight of 100 seed was recorded in genotype T₁₁ (13.52 g) which was at par with the genotype T₉ (13.09%). The lowest seed weight of 100 seed (9.00 g) was recorded in genotype T₁₃. The results obtained are in lines with those of Priya (2012) [18], Shrilatha (2021) in snapmelon, Pal *et al.* (2017) [15] in cucumber, Bairwa *et al.* (2018) [3] in ash gourd and Dahatonde *et al.* (2024) [5] in pumpkin.

Yield characters

In respect of number of fruits per plant, the genotypes T₁₁ (2.71) followed by T₁₄ (2.65) and T₁₅ (2.61) were the best performing genotypes among fifteen genotypes. The lowest number of fruit per plant was recorded in genotype T₂ (1.85). The number of fruits per plant is dependent on number of

flowers produced per plant and per cent fruit set which in turn are dependent on the genetic makeup. This is in corroboration with the findings of Shirke *et al.* (2013) [9], Rizvi *et al.* (2023) [19] in snapmelon, Omprasad *et al.* (2021 and Akhter *et al.* (2023) [2, 29] in muskmelon.

The highest fruit weight (1.50 Kg) was observed in the genotype T₁ followed by T₁₁ (1.46 Kg) and T₁₄ (1.44 Kg), whereas the lowest weight of fruit (1.17 Kg) was recorded in genotype T₁₃. Average fruit weight along with number of fruits per plant ultimately decides the yield potential of that variety. Similar type of variations related to fruit weight was also reported in snapmelon by Rizvi *et al.* (2023) [19], Shruti *et al.* (2015) [22] in oriental pickling melon, Ganiger *et al.* (2017) [8] in wild melon.

The genotypes, T₁₁ (3.91 Kg), T₁₄ (3.78 Kg) and T₄ (3.53 Kg) 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 which is ultimately governed by genetic makeup of the plant. These two characters directly influenced the marketable fruit yield per plant. The similar trend in marketable fruit yield was obtained by Muthuselvi *et al.* (2019) [14], Rizvi *et al.* (2023) [19] in snapmelon, Venkatesan *et al.* (2016) [23], Shivakumara (2019) [30], Omprasad *et al.* (2021), Akhter *et al.* (2023) [2] in muskmelon [29].

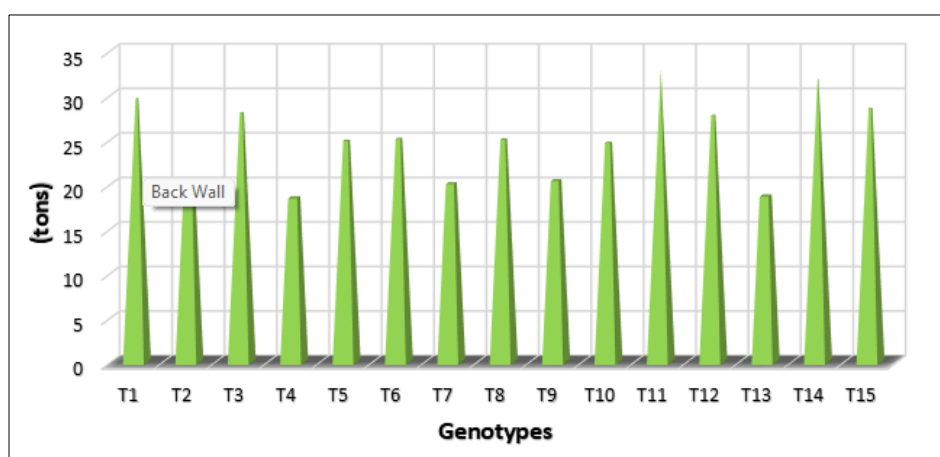


Fig 2: Variation in fruit yield per hectare (t/ha)

Data in relation to fruit yield per hectare are presented in Table 3 and graphically depicted in Fig.2. The highest fruit yield (t/ha) were recorded in the genotype T₁₁ (32.87 t/ha), T₁₄ (31.80 t/ha) and T₁ (29.65 t/ha) when compared to other genotypes. The lowest fruit yield per ha was recorded in genotype T₄ (18.52 t/ha). The similar trend of fruit yield was obtained by Shirke *et al.* (2013)^[9] in snapmelon, Ingle *et al.* (2025)^[11] in muskmelon and Mishra and Singh (2017)^[13] in bitter gourd.

Conclusion

It can be concluded from present investigation that wide variation exist in various growth, yield and yield attributing characters. Significant variation were observed in all the characters. Among the fifteen evaluated genotypes, T₁₁ (DPL-SM-11), T₁₄ (Konkan Madhur), T₁ (DPL-SM-1) and T₁₅ (Pusa Shandar) demonstrated significantly superior performance in terms of the number of fruits per vine, average fruit weight and total fruit yield compared to the other genotypes. Additionally, T₃ (DPL-SM-3) and T₁₂ (DPL-SM-12) exhibited outstanding performance for earliness traits, including days to first female flowering, number of nodes to the 1st fruit and days to harvest. The study revealed substantial genetic diversity within the germplasm for traits related to earliness and yield. Such wide variation in growth, earliness and yield parameters among the genotypes provides a effective basis for selecting promising candidates for the development of new high-yielding snapmelon hybrid.

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