Stability Analysis of Yield and ~~its~~ ItsComponents in ~~snap~~ Snap ~~melon~~ Melon(*Cucumismelo*var*momordica)*

Abstract

Comment [RN1]: Add a brief introduction to the abstract.

This study was carried out to assess the nature and magnitude of genotype-environment interaction and stability among some parameters in snap melon genotypes. Twentyfivelocal cultivars along with three standard checks were evaluated in randomized block design with three replications at three environments during summer 2023 at Navsari.Eberhart and Russell model of stability analysis was employed which has been proved to be a reliable model.The study revealed that the mean sum of squares due to genotypes when tested against pooled deviation were highly significant for all the traits studied. Environment ×~~x~~ Genotype (linear) showed significant differences for all characteristics except fruit weight and yield per vine, indicating that prediction could be possible by considering individual genotypes for these traits. A significant non-linear component (pooled deviation) was observed for fruit weight and fruit yield per vine, suggesting that genotypes varied considerably in terms of stable performance for these traits. The G x E interaction was only significant for flesh thickness and yield per vine, with all other traits being non-significant.The genotypes T 14 (HUB 18) and T 17 (HUB 21) were relatively stable and can be further used as parents to develop a more robust stable genotype. These identified genotypes could pave way introducing high performing snap melon varieties.

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Introduction

Snap melon, scientifically known as *Cucumismelo* L. var. *momordica* (Roxb.), is a crop native to India and belonging toCucurbitaceae family. The snap melon has a chromosome number of 2n=2x=24 and is a tropical old world species of cucurbit that is cultivated in various regions, including arid and semi-arid areas[1].It is commonly referred to as '*Phoot*' due to its tendency to split either in the middle or longitudinally. In India, it is grown in Gujarat, Rajasthan, Haryana, Punjab, West Bengal, Uttar Pradesh, Kerala and some parts of the North Eastern states[2].Snap melon is one of thedesert cucurbit, the low sugared mature fruits are eaten as raw, whereas,immature fruits cooked or pickled. Fruit is rich in quality and its juice is gaining popularity as squash, due to its wide application of medicinal values used as a good summer drink since it reduces heat from the body and rich source of vitamin C, sugars, minerals and dietary fibre [3].

Precise knowledge of the nature and magnitude of genotype x environment interaction is very important in understanding the stability of different traits of a particular genotype, before it has recommended for commercial cultivation. The different sources of variation including genotype x environment interaction are of great importance to the plant breeders for deciding appropriate testing and selection procedure for planning an efficient plant-breeding programme.The main goal of plant breeders is to develop high-yielding cultivars that perform consistently well in different environments. Snap melons are particularly sensitive to environmental changes, and the interaction between genotype and environment may responsible for lack of widely adapted cultivars [4]. This study aimed to identify and isolate snap

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melon genotypes that show stable performance across different environmental conditions.

Material methods

The present investigation was conducted during summer, 2023in three different environments *i.e.*, three different sowingdates *viz.*,1st march, 15th march and 30th marchat Regional Horticultural Research Station (RHRS), ASPEE College of Horticulture, NavsariAgricultural University, Navsari. The experimental materials for this study comprised of twenty-eight genotypes obtained from the different geographical locations of India. Among them twenty-five are land races and three are released varieties (Table 1). The nursery raised14 days old seedlings were used for transplanting in 2x1 m spacing. The experiment was carried out in randomized block design with three replications.Recommended agronomic practices and need based plant protection measures were carried out. The observations were recorded on six traits *viz.*, flesh thickness, number of fruits per vine, fruit weight, fruit length, fruit diameter and fruit yield per plant. The data was subjected to Eberhart and Russell [5] model of stability analysis. The statistical analysis was carried out using IndoStat software.

Comment [RN6]: It would be good if done in two planting seasons; summer and early monsoon.

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Table1: Details of the snap melon genotypes used in the present study

SL.NO.	LINES	SOURCE
1	T 1(HUB - 1)	Lakhamapura, Badami taluk, Bagalkote district
2	T 2(HUB - 2)	Sattari, Goa
3	T 3(HUB - 3)	S. D. Patak, Ramdurg Belgaum district
4	T 4(HUB - 4)	Salcete, Goa
5	T 5(HUB - 5)	Dapoli, Maharashtra
6	T 6(HUB - 6)	Hireshellikeri, Bagalkote
7	T 7 (HUB - 8)	Dodamarg, Maharashtra
8	T 8 (HUB - 9)	Santhosh awti, SathihalaBasavanaBagevadi
9	T 9 (HUB - 10)	Katageri, Badami taluk
10	T 10 (HUB - 11)	Kundargi,Bagalkote
11	T 11(HUB - 14)	Rampur, Bagalkote
12	T 12 (HUB - 15)	Haveli, Bagalkote
13	T 13 (HUB - 16)	Kallapur, Nargunda
14	T 14 (HUB - 18)	Bailhongal, Belgaum
15	T 15 (HUB - 19)	Cancona, Goa
16	T 16 (HUB - 20)	Murnal, Bagalkote
17	T 17 (HUB - 21)	Mankani, Bagalkote
18	T 18 (HUB - 22)	Gokak, Belgaum
19	T 19 (HUB - 24)	Mudhol, Bagalkote
20	T 20 (HUB - 25)	Mannur, Sindagi
21	T 21 (HUB - 31)	Belgaum

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22	T 22 (HUB - 35)	Gadag
23	T 23 (HUB - 42)	Ramdurga
24	T 24 (HUB - 46)	Haveli, Bagalkote
25	T 25 (HUB - 49)	Bagalkote
26	T 26(AHS - 10)	CIAH, Bikaner
27	T 27 (AHS - 82)	CIAH, Bikaner
28	T 28 (PusaShandar))	IARI, New Delhi

Result and discussion

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Analysis of variance

The analysis of variance representing the mean sum of square due to different sources of variation as per Eberhart and Russel [5] for the 18 characters are presented in Table 2. Pooled analysis of variance over three different environments showed that, the variances due to genotypes were highly significant when tested against pooled error for all the characters studied showed that these genotypes were found suitable with a sufficient range of variation under the various sowing conditions for these characters in present investigation.Environment linear component was showed significant differences among the test genotypes forall the characters studied,indicating that prediction could not be made easily for these traits in this study. Environment x Genotype (linear) was showed significant differencesfor all the characters studied except fruit weight and yield per vine, reflecting that prediction could be possible by considering individual genotype for these traits. The significant non-linear component (pooled deviation) was observed for fruit weight and fruit yield per vine, suggested that the genotypes differed considerably with respect to stable performance for the traits. The G x E interaction wasdetected significant only for the traits flesh thickness and yield per vine and all other traits found non-significant. These results were also in similar with the finding of [6, 7, 8 & 9]

Stability parameters

The estimate of stability parameters for yield and quality contributing characters presented in Table 3. According to Eberhart and Russel [5] model, stability judged

Table.2: Analysis of variance (mean sum of square) for yield and its components in 28 genotypes of snap melon ~~as per Eberhart and Russell's Model, 1966.~~

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Source of variation	**d.f.**	**Fleshthickness (mm)**	**Number of fruits per vine**	**Fruit weight (g)**	**Fruit length (cm)**	**Fruit diameter (cm)**	**Fruit yield per vine (kg)**
Variety	27	8.62**	0.25**	27034.35**	16.13**	3.89**	0.91**
Environment	2	8.72	4.22**	105541.34**	8.972	17.18**	3.29**
Var.X Environ.	54	3.65**	0.09	8541.27	3.24	1.96	0.17*
Env+VarXEnv	56	3.83	0.24	12005.56	3.44	2.50	0.28
Env (Linear)	1	17.50**	8.44**	211082.69**	17.94**	34.36**	6.58**
Env X Var (Lin)	27	4.95**	0.12**	7579.78	6.48**	3.23**	0.12
Pooled Deviation	28	2.26	0.06	9163.38**	0	0.66	0.21**
Pooled Error	162	5.37	0.14	6650.77	6.75	3.03	0.18

*and ** indicate significant at 5 and 1 *per cent* probability

Table 3: Estimates of stability parameters for fruit yield and its components in snap melon as per Eberhart and Russell'sModel, 1966

S.L.	Genotype	FT			NF/V			FW		
		Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
1	**T 1**	17.18	-0.12	-1.76	3.83	0.94	0.28*	433.13	-0.16	-1498.08
2	**T 2**	22.66	-2.47	1.00	4.22	1.22	-0.03	628.72	1.05	2908
3	**T 3**	21.06	2.55	-1.78	4.35	1.38	0.01	619.00	0.16	-1072.33
4	**T 4**	21.93	0.98	-1.69	4.46	2.02	0.02*	628.80	0.59	10380.51*
5	**T 5**	25.12	5.67*	-1.77	3.91	2.94	-0.02	746.25	1.69	-1484.43
6	**T 6**	23.25	2.65	-1.72	4.31	1.25	0.20	630.87	0.48	3258.20
7	**T 7**	24.62	6.55	-1.09	3.66	0.28	0.04	703.41	1.26	-310.54
8	**T 8**	25.43	3.51	0.82	4.31	0.92	-0.03	772.17	2.30	23681.05**
9	**T 9**	24.61	1.71	-1.75	3.87	0.36	0.02	686.51	1.69	32865.39**
10	**T 10**	19.69	-0.88	-1.54	4.37	0.71*	-0.04	642.09	1.5	461.61
11	**T 11**	23.31	0.54	-1.76	4.1	0.16	-0.01	801.50	2.62*	-2203.04
12	**T 12**	23.32	1.28	1.86	4.02	0.31	0.13	711.24	1.55	387.96
13	**T 13**	21.92	-2.08	1.89	4.02	0.72	-0.02	628.25	1.15	2721.61
14	**T 14**	22.60	-2.52	-0.34	4.16	1.4	0.002	746.42	2.86	2495.58
15	**T 15**	22.62	1.74	1.82	4.35	0.19*	-0.04	793.58	0.86	7203.97*
16	**T 16**	20.09	-4.62	-1.51	3.97	0.92	-0.03	468.57	-0.24	-1689.89
17	**T 17**	21.89	1.6	-1.58	4.82	1.71	-0.04	720.16	0.37	34662.99**
18	**T 18**	20.94	-0.37	11.61**	4.53	0.78	-0.04	703.49	0.10	-1714.21
19	**T 19**	23.02	3.78	5.76*	4.45	1.82	0.05	906.96	1.23	21920.17**
20	**T 20**	21.85	0.04	-0.32	4.5	1.07	-0.02	602.19	-0.03	2159.721
21	**T 21**	23.23	-0.66	-1.73	4.82	1.30	0.02	652.77	-1.21	-1947.42
22	**T 22**	21.60	-1.54	2.46	4.57	1.04	-0.04	625.82	0.63*	20847.84**
23	**T 23**	22.14	-1.87	-0.78	4.44	0.67	0.01	718.78	2.48	-2024.26
24	**T 24**	22.42	1.22	2.46	4.07	0.09	-0.02	690.92	1.69	44021.4**
25	**T 25**	21.8	3.41	-0.79	4.44	1.66	0.02	740.65	0.60	-2211.14
26	**T 26**	21.96	3.38	4.82	4.62	0.97	-0.04	598.50	-0.55	-2014.42
27	**T 27**	22.08	-1.91	-0.76	4.28	0.43	-0.01	672.30	1.27	4643.91
28	**T 28**	23.60	6.42	1.53	4.56	0.62	-0.02	699.66	1.98	-1949.4
	Pooled mean	22.36			4.29			677.60		
	S.E. (mean)	1.06	1.90		0.17	0.44		67.69	1.10	

*, ** =Significant at 5 % and 1 % level of significance, respectively, FT = Flesh thickness (mm), NF/V = No. of fruits per vine, FW = Fruit weight

Cont..

S.L.	Genotype	FL			FD			FY/V		
		Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
1	T 1	20.14	-4.05*	-2.25	24.247	-0.48	-0.98	1.63	0.24	-0.05
2	T 2	21.68	-1.78*	-2.25	26.80	1.69	-0.79	2.86	0.61	0.03
3	T 3	18.57	1.87*	-2.25	26.11	-0.87	-0.93	2.67	0.08	-0.06
4	T 4	22.23	0.81	-2.25	26.75	1.14	-0.99	2.87	1.50	0.55
5	T 5	25.62	8.39*	-2.25	28.02	3.74	-1.00	3.72	0.39	-0.05
6	T 6	22.49	4.71*	-2.25	27.83	0.71	-0.96	2.88	0.12	0.01
7	T 7	23.73	-0.57*	-2.25	25.21	-0.33	-0.66	2.54	1.18	-0.05
8	T 8	24.43	3.51*	-2.25	27.64	2.77	0.17	3.43	2.46	0.52
9	T 9	24.83	1.28	-2.25	28.42	1.67	-0.50	2.68	1.30	0.86
10	T 10	22.76	-1.72*	-2.25	26.02	-0.97	-0.92	2.88	0.88	0.01
11	T 11	26.11	7.16*	-2.25	26.3	1.20	-0.87	3.52	1.35	-0.05
12	T 12	25.21	2.24*	-2.25	26.19	3.21	-0.04	2.97	0.80	0.22
13	T 13	24.36	1.31	-2.25	25.74	-0.86	-0.94	2.62	1.46	0.13
14	T 14	24.38	4.05*	-2.25	28.07	2.39	0.48	3.66	0.84	0.52
15	T 15	19.51	-1.88*	-2.25	27.15	2.48	-0.43	3.54	0.42	0.15
16	T 16	19.05	-1.66*	-2.25	26.61	-0.63	-0.97	1.91	0.30	-0.03
17	T 17	19.71	-0.25*	-2.25	25.68	0.62	-0.92	3.70	1.18	0.48
18	T 18	24.76	3.56	-2.25	24.73	-1.85	-0.98	3.17	0.72	-0.05
19	T 19	19.02	-4.27*	-2.25	29.19	3.89	0.40	4.30	2.15	0.07
20	T 20	22.45	0.27*	-2.25	26.35	-1.563	-0.78	2.85	0.03	-0.04
21	T 21	22.72	0.73	-2.25	26.74	0.23	-1.00	3.27	-0.46	-0.03
22	T 22	25.94	0.23*	-2.25	25.73	1.17	-0.88	2.97	1.64	0.12
23	T 23	24.67	1.53	-2.25	27.06	1.02	-0.91	3.39	1.45	0.03
24	T 24	23.49	3.12*	-2.25	27.83	2.91	-0.56	2.74	1.70	0.87
25	T 25	20.77	-5.33*	-2.25	28.00	2.18	-0.56	3.29	1.76	0.01
26	T 26	23.36	0.28*	-2.25	26.72	1.71	-0.73	2.64	0.38	-0.02
27	T 27	25.99	3.70*	-2.25	26.63	-0.77	-0.95	2.90	1.35	0.13
28	T 28	22.22	0.68	-2.25	27.39	1.54	8.55	3.35	2.06	0.07
	Pooled mean	22.87			26.76			3.40		
	S.E.	0.00	0.00		0.58	0.73		0.33	0.96	

*,**_Significant at 5 % and 1 % level of significance, respectively, FL = Fruit length (cm),FC = Fruit diameter (cm), FY/V = Fruit yield per vine

by four criteria *i.e.*, variety is general adaptable or stable if mean is high than population mean, bi=l or non-significant and S^2d_i =0 (least or non- significant); variety is adaptable under poor environment or above average stability if mean is high, b_i<l andsignificant and S^2d_i=0 (least or non-significant); variety is adaptable under favourable environment or below average stability if mean is high, b_i> I and significant and S^2d_i =0 (least or non-significant) and variety is unstable if mean is high or low, bi is significant or non-significant and S^2d_i is significant or $S^2d_i \neq 0$. Genotypes with high b_i values have low stability and are specifically adapted to high yielding environments and conversely low b_i values indicate a high stability and adaptation to low yielding environments [10].

The deviation from regression coefficient (bi) values were higher or lower than unity and non-significant S^2di, with higher mean values than population mean (22.36), were recorded in genotypes T 2, T 5, T 6, T 7, T 8, T 9, T 11, T 12, T 14, T 15, T 21, T 24 and T 28 which shows these genotypes will be more stable in favourable conditions or other for flesh thickness. Higher the mean value from the population mean is desirable for number of fruits per vine to select high yielding genotypes. The coefficient values (bi) near to one along with higher mean values as compared to population mean (4.29) and non-significant S^2di estimates deviated from zero observed from the genotypes T 8, T 10, T 18, T 20, T 22 and T 26 indicated their grater suitability to all sowing conditions. For fruit weight the genotypes T 2, T 13 and T 15 showed regression coefficient near to unity, indicates stable performance over different environment. Higher mean values for fruit length than population mean values (22.87) coupled with regression coefficient values (bi) lower to unity and non-significant S^2di values were showed by the genotype T 7, T 22 and T 26 indicating its stability for poor environment *i.e.*, above average stability.

Genotype T 4, T 8, T 9, T 11, T 12, T 13, T 14, T 18, T 23, T 24 and T 27 showedhigher mean values than population mean values (22.87) coupled with regression coefficient values (bi) higher to unity and non- significant S^2di values indicating its stability for favourable environment *i.e.*, below average stability for fruit length. For fruit diameter genotype T 6 and T 23 showed their average stability due to higher population mean values (26.76) coupled with regression coefficient values (bi) near to unity and non- significant S^2di values. Genotypes T 5, T 8, T 9, T 14, T 15, T 24 and T 25 showed higher mean values than population mean values coupled with higher regression coefficient values (bi) and non- significant S^2di values, which indicating its stability for favourable environment. For fruit yield per vine the coefficient values (bi) near to one along with higher mean values as compared to population mean (3.40) and non-significant S^2di estimates deviated from zero observed from the genotypes T 14 and T 17, indicated their grater suitability to all sowing conditions. Genotypes T 5 and T 15 exhibited non-significant deviation from regression and regression coefficient were found to be lesser than unity indicating above average stability or stable poor environment. Whereas, T 8, T 11 and T 19 which shows their suitability to favourable sowing condition. Similar results earlier were also reported by [11, 12, 8 & 6].

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Conclusion

The genotype T 19 (HUB 24)were found to be high yielding with respect to fruit yield and its component traits with highest *per se* performance. Analysis of variance for stability also indicated that both predictable (linear) and non-predictable (non-linear) components contributed towards significant differences in stability among the genotypes for the characters studied. The Genotype × Environment analysis indicated that the genotypes T 14 (HUB 18) and T 17 (HUB 21) to be comparatively stable for fruit yield per plant with better yield. Hence, these genotypes can be used as parent in breeding programmes and also for general cultivation after testing over a wide range of environments.

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