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STABILITY ANALYSIS IN SNAPMELON (*CUCUMIS MELO VAR. MOMORDICA*) GENOTYPES USING EBERHERT RUSSEL MODEL FOR GROWTH, FLOWERING AND EARLINESS PARAMETERS

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ABSTRACT

An experiment was conducted during *Rabi* 2024 across four locations COH, Bagalkot (E1), COH, Munirabad (E2), KRCCH, Arabhavi (E3) and AICRP on vegetable crops, Dharawad (E4) using 10 snapmelon (*Cucumis melo var momordica*) genotypes in three replications with objective to identify stable snapmelon genotype across environments for growth, flowering and earliness parameters. The Eberhart and Russel model was implied for stability analysis. The pooled analysis revealed significant effect due to genotypes showing considerable variation among genotypes and G× E interactions were significant for all characters except node bearing first male flower and number of primary branches per vine. The pooled deviation was non-significant for all characters showing their performance is consistent and predictable. The genotype T2 (HUB-8) was found stable for many characters like vine length (m) at final harvest, number of primary branches per vine, sex ratio and node bearing first female flower. T6 was stable for sex ratio, T8 and T1 were stable for days to first female flower and T10 was stable for node bearing first male flower. The genotype T2 (HUB-8) genotype can be used as parent in breeding programmes and for general cultivation after testing over a wide range of environments.

Keywords : Stability, snapmelon, G× E interaction

Introduction

Snapmelon (*Cucumis melo* var. *momordica*) is a cucurbit family vegetable crop with diploid chromosome number 2n=22, considered as underexploited melon. Unlike muskmelon, the fruits of snap melon are prone to splitting or cracking when they ripen hence commonly referred as *Phoot*. The usage of snap melon is quite diverse and varies with the fruit type. Sweet varieties are typically consumed as dessert fruits, while the non-sweet types, when harvested at the immature stage, are eaten raw, pickled or cooked as vegetables. Snapmelon accessions from India are known to possess significant resistance to diseases and insect pests and many of these are internationally acknowledged and used as standard reference accessions (Cohen *et al.*, 2003). Snapmelon has numerous health benefits as it is a cooling ingredient and due to its fibre content, it is a natural gut cleanser and appetite improver. In Karnataka it is grown in districts Vijayapura, Bagalkot, Gadag, Dharawad and Belgaum, to increase its production and productivity in Karnataka and India, Snapmelon breeding for development of superior and high yielding varieties is needed. However, a significant barrier to the development of improved variety for cultivation is the instability and uncertainty of yield caused by genotype-environment interactions (Raffi *et al.*, 2004).

Genotypic performance across varying environments is equally crucial as its yield potential. Since yield is a complex quantitative trait influenced by multiple genes, it is highly sensitive to the interaction between genetic makeup and environmental factors. The environment includes a wide range of physical, chemical and biological components that collectively shape plant growth conditions. Genotypes do not always exhibit consistent phenotypic expression under diverse environmental situations; their performance may vary significantly depending on the surroundings. While some genotypes thrive in particular environments, others perform better under different conditions, this variability is referred to as genotype × environment (G×E) interaction. Stability refers to the consistent expression of agronomic traits across diverse environments, as defined by Allard and Bradshaw (1964). Stability, in this context, denotes a genotype's capacity to produce uniform growth and yield despite environmental fluctuations. Over the years, various statistical models have been developed to assess genotypic adaptability and stability, among which the Eberhart and Russell (1966) model remains one of the most widely used and accepted for evaluating stable performance across environments. Considering this, the present study was undertaken with the objective of identifying stable snapmelon genotypes across diverse locations. To identify stable snap melon genotypes over environments for growth and earliness parameters.

Material and methods

The experiment was conducted in *Rabi* 2024, across four environments (locations) to evaluate the stability of 10 genotypes of snapmelon (*Cucumis melo*) belonging to Momordica group. The environments were E1- College of Horticulture, Bagalkot (Karnataka), E2- College of Horticulture, Munirabad (Karnataka), E3- Kittur Rani Channamma College of Horticulture, Arabhavi (Karnataka) and E4- AICRP on vegetable crops, RHREC, Dharwad (Karnataka). The experiment was carried out in Randomized complete block design with 3 replications in all locations. The observations related to growth and earliness parameters like vine length (m) at final harvest, number of primary branches per vine, sex ratio, days to first female flower, node bearing first male flower, node bearing first female flower and days to first harvest were collected at respective stages of growth. For estimation of stability parameters, Eberhart and Russell (1966) model was employed.

Table 1 : List of genotypes used in present study.

Sl. No.	Genotypes	Source
1	T1 (HUB-4)	Salcete, Goa
2	T2 (HUB-8)	Dodamarg, Maharashtra
3	T3 (HUB-9)	Sathihala, Basavana Bagevadi
4	T4 (HUB-19)	Cancona, Goa
5	T5 (HUB-21)	Mankani, Bagalkote
6	T6 (HUB-22)	Gokak, Belgaum
7	T7 (HUB-25)	Mannur, Sindagi
8	T8 (Pusa Shandar)	IARI New Delhi
9	T9 (AHS-10)	CIAH, Bikaner
10	T10 (AHS-82)	CIAH, Bikaner

Table 2 : Pooled analysis of variance (mean square) for various characters in snapmelon

Source of variation	df	VL	NPB	SR	DFFF	NFMF	NFFF	DFH
Genotype	9	0.192**	0.600**	70.682**	103.979**	0.063**	0.195*	116.762**
Environment	3	0.573**	0.867	184.804**	286.297**	0.258**	2.033**	18.567*
Genotype× Environment	27	0.057**	0.178	5.166**	12.893**	0.022	0.146*	9.592*
Environment+ (Genotype×Environment)	30	0.036**	0.082**	7.710**	13.411**	0.015**	0.111**	3.497**
Environment (linear)	1	0.573**	0.868**	184.804**	286.297**	0.258**	2.033**	18.157**
Genotype×Environment (linear)	9	0.037**	0.100**	2.542**	6.909**	0.009	0.097**	5.711**
Pooled deviation	20	0.009	0.046	1.181	2.693	0.005	0.022	1.746
Pooled error	72	0.009	0.037	0.712	2.019	0.002	0.028	1.655

VL-Vine length (m), NPB- Number of primary branches per vine, SR- Sex ratio, DFFF- Days to first female flower, NFMF- Node bearing first male flower, NFFF- Node bearing first female flower, DFH -Days to first harvest

Table 3 : Estimates of stability parameters for growth and earliness traits.

S. No.	**Geno types**	**VL**			**SR**			**DFFF**			**NFFF**			**DFH**		
		Mean	**bi**	**S^2di**	**Mean**	**bi**	**S^2di**	**Mean**	**bi**	**S^2di**	**Mean**	**bi**	**S^2di**	**Mean**	**bi**	**S^2di**
1	T1	1.56	1.53	0.02	15.25	1.54**	-0.24	41.77	1.00	-1.27	3.35	0.44	0.02	76.25	0.62*	-1.60
2	T2	1.90	0.90	-0.01	12.84	0.91	0.36	38.83	0.25*	1.05	3.33	1.01	-0.02	76.45	0.61	1.96
3	T3	1.70	0.19	0.01	18.97	1.44	1.50	43.85	1.89**	0.42	3.42	0.91	-0.03	76.53	2.03	-0.89
4	T4	1.59	1.77	0.01	20.90	1.13	1.35	44.17	0.44	7.00*	3.27	2.23**	-0.02	73.93	1.57	-0.75
5	T5	1.75	2.42**	0.00	15.13	1.33**	-0.53	38.08	1.41*	-1.25	3.33	1.38*	-0.02	73.56	-1.62**	0.01
6	T6	1.63	1.68	0.01	15.86	1.05	-0.61	43.91	1.31	-1.11	3.45	0.30**	-0.03	79.58	-2.17**	-0.07
7	T7	1.42	0.37**	-0.01	16.53	0.73*	-0.41	47.53	0.75	5.94	3.63	0.78	0.00	80.58	3.60**	-0.85
8	T8	1.67	0.83**	-0.01	13.39	0.82	1.89*	39.27	0.96	-0.18	3.23	1.95**	-0.02	74.07	2.35	4.23*
9	T9	1.66	0.21**	-0.01	16.79	0.69	1.35	43.94	0.71**	-1.91	3.53	0.91	0.01	79.56	1.48	0.32
10	T10	1.60	0.09**	-0.01	17.45	0.35**	0.04	42.80	1.27**	-1.92	3.22	0.09	0.05	82.62	1.54	-1.44
	Pooled mean	1.65			16.31			42.41			3.38			77.31		
	SE mean	0.07			0.66			1.04			0.11			0.89		

Table 4 : Mean values of snapmelon genotypes over environments for number of primary branches per vine and node bearing first male flower.

S. No.	**Genotypes**	**Number of primary branches per vine**	**Node bearing first male flower**
1	T1	3.83	1.51
2	T2	4.52	1.51
3	T3	4.03	1.59
4	T4	4.15	1.52
5	T5	4.00	1.51
6	T6	4.27	1.61
7	T7	3.83	1.56
8	T8	3.98	1.52
9	T9	3.93	1.56
10	T10	3.80	1.35
Population mean		4.04	1.52
SE mean		**0.10**	**0.04**

Results and Discussion

Analysis of variance

The findings revealed significant (at p=0.01) variability among the genotypes for all characters showed that these genotypes were found suitable with a sufficient range of variation under the different locations for these characters in present investigation. The variance attributed to the environment (linear) showed significant effects (p=0.01) on all traits under study indicating that prediction could not be made easily for these traits in this study. Variance due to genotype× environment (linear) was highly significant (at p=0.01) for except node bearing first male flower reflecting that prediction could be possible by considering individual genotype for these traits. The pooled deviation was found non-significant for all characters under study. Markedly significant genotype × environment interactions at the p=0.01 level was identified for all characters under study except number of primary branches per vine and node bearing first male flower.

Stability parameters

The regression coefficient (bi) serves as an indicator of the responsiveness of a genotype to environmental variation. Genotypes with bi > 1 exhibit above-average sensitivity, performing better under favourable environments. Those with bi = 1 demonstrate average responsiveness and are considered widely adaptable. Genotypes having bi < 1 are relatively insensitive to environmental variations and when associated with high mean yield, they are regarded as suitable for marginal or stress-prone environments. Conversely, genotypes with low mean performance, irrespective of regression behaviour, are classified as poorly adapted across environments.

The stability parameters for vine length (m) at final harvest are summarized in table 3. Genotypes T2 was identified as stable for vine length, given its higher mean value, regression coefficient tending toward unity and non-significant deviations from regression. Genotype T5 recorded higher mean values with a regression coefficient exceeding one and non-significant deviation from regression, suggesting its adaptability to favourable environments. In contrast, genotypes T3, T8 and T9, though possessing higher mean values, were categorized as better suited to less favourable environments, as indicated by regression coefficients below unity and non-significant deviations from regression. Comparable findings were reported earlier by Yadav and Ram (2010) in muskmelon, Balat *et al.* (2021) and Singh *et al. (*2023) in bottle gourd and Kumar *et al.* (2022) in pumpkin.

The G × E interaction for the number of primary branches per vine was statistically non-significant, therefore, only the mean values are reported in table 4. Genotype T2 had the greatest number of primary branches per vine, followed by T6 and T4, which were regarded as stable. Comparable observations were also documented by Koraddi *et al.* (2016) in soybean, Hanchinamani and Patil (2008) and Krishnaprasad and Pitchaimuthu (2004) in cucumber.

The parameters of stability for sex ratio are presented in table 3. Genotypes T2 and T6 were identified as stable, as they exhibited lower mean values (desirable for sex ratio) along with regression coefficients almost equal to one and non-significant deviations from regression. In T5 and T1 lower mean values combined and deviation from regression was not significant, while their regression coefficients exceeded unity, indicating suitability under favourable environments.

The parameters of stability for days to first female flower. Lower mean values, which are desirable, indicate earlier flowering. Genotypes T8 and T1 were classified as stable since they exhibited lower mean values accompanied by regression coefficients approximately equal to unity and non-significant deviations from regression. T5 also showed lower mean values; however, its regression coefficient was greater than one, suggesting suitability under favourable environments. T2, with lower mean values but a regression coefficient below one, was considered suitable for less favourable environments. The findings of the present study are consistent with those reported by Yadav and Ram (2010) in muskmelon, Acharya *et al.* (2019) and Khan and Sarolia (2019) in bitter gourd, Balat *et al.* (2021) in bottle gourd Dhakare and More (2008) in muskmelon and Thakur and Khattra (1996) in bitter gourd.

The stability parameters for node bearing the first female flower are shown in table 3. Genotype T2 was identified as stable, as it exhibited lower mean values (considered advantageous) along with regression coefficients close to unity and non-significant deviations from regression. T8, T4 and T5 were identified as suitable for rich environments, as they exhibited lower mean values along with regression coefficients exceeding unity and non-significant deviations from regression. The genotypes T1 and T10 were identified as suitable for poor environments, as they exhibited lower mean values along with regression coefficients below unity and non-significant deviations from regression. Similar variations in genotype response to changing environments for this trait have also been reported by Balat *et al.* (2021) in bottle gourd, Varalakshmi and Krishnamurthy (2017) in ridge gourd, Hanchinamani and Patil (2008) in cucumber and Dhakare and More (2008) in muskmelon.

As the interaction between genotype and environment for node bearing of the first male flower was non-significant, only the mean values are provided in table 4. Genotype T10 recorded the lowest mean value for this trait, followed by T1, T2 and T5, which were regarded as stable across environments. corresponding findings were recorded by Balat *et al.* (2021) in bottle gourd.

With respect to days to first harvest, genotypes T3 and T4 were identified as suitable to favourable environments, as they showed lower mean values (advantageous) along with regression coefficients exceeding unity and non-significant deviations from regression. Genotypes T1, T2 and T5 were considered appropriate for unfavourable environments, because they exhibited lower mean values with non-significant deviations from regression and regression coefficients below unity. Similar variations in cultivar responses to different environments for this trait were also noted by Acharya et al. (2019) and Khan and Sarolia (2019) in bitter gourd, Trivedi et al. (2024) in vegetable cowpea, Singh et al. (2023) and Balat et al. (2021) in bottle gourd, Thakur and Khattra (1996) in bitter gourd and Rai and Singh (1999) in cabbage.

Conclusion

The genotype T2 (HUB-8) was found stable for many characters like vine length (m) at final harvest, number of primary branches per vine, sex ratio and node bearing first female flower. T6 was stable for sex ratio, T8 and T1 were stable for days to first female flower and T10 was stable for node bearing first male flower. 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. This genotype can be used as parent in breeding programmes and for general cultivation after testing over a wide range of environments.

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