

Genetic Variability, Heritability and Genetic Advance for Yield and Yield Components in Snap Melon (*Cucumis melo* var. *momordica*)

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ABSTRACT

Genetic variability, heritability and genetic advance were studied in twenty eight snap melon genotypes. The variance analysis for twenty five quantitative characters showed that genotypes differ significantly among them for all the characters under study indicating great variability among the genotypes selected. High estimates of genotypic and phenotypic coefficient of variation were recorded for pulp placenta ratio, average fruit weight, node to first male flower appearance, vine length, length of fruit cavity, fruit yield vine⁻¹, 100 seed weight and number of seeds fruit⁻¹. High heritability and high genetic gain were observed for 100 seed weight, pulp placenta ration and average fruit weight, suggesting better scope for

improvement of these traits by effective selection of genotypes.

Keywords Genetic variability, Genetic advance, Heritability, Snap melon.

INTRODUCTION

Snap melon (*Cucumis melo* L. var. *momordica*) belonging to family Cucurbitaceae is a crop native to India and commonly known as ‘phut’ which means to split as the fruit tends to split either from the middle or longitudinally. Some other synonym is phootkakari. Melons are one of the important horticultural crops worldwide and India, being one of the secondary centers of origin of *Cucumis melo* has its various cultivated forms which comprises nearly 40 species (Whitaker and Davis 1962). The chromosome number of snapmelon is $2n=2x=24$ and it is a tropical old-world species of cucurbit and found to be cultivated in many parts of world including some of the arid and semi-arid regions. In India, it is widely cultivated in states of Gujarat, Rajasthan, Haryana, Punjab, West Bengal, Uttar Pradesh and few areas of North Eastern states (Hazara *et al.* 2011).

Snap melon is a monoecious crop and fruit color ranges from creamish yellow to orange, immature fruits are cooked or pickled, the low sugared mature fruits are eaten as raw. Fruit is rich in quality and its juice is gaining popularity as squash, due to its wide

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application of medicinal values it is used as a good summer drink since it reduces heat from the body. Snap melon germplasm has been found to be a very good source of disease and insect resistance. *Cucumis melo* L. is a diversified species has large number of botanical types and varieties or groups with great variation in various fruit traits, have reported rich diversity in cultivation and uses. The information on variability present in the material, extent of heritability and genetic gain for a particular trait and contributing effect of one character on the other is prerequisite for formulating a suitable breeding technique to bring out a high jump in yield of any crop. Since snap melon is an underutilized cucurbitaceous vegetable, very little attempts have been made to gather genetic information in this crop. The present study was undertaken to collect the accessions of different snap melon genotypes under different geographical regions of India and also to assess the variation present in the germplasm for various morphological characters, yield and its attributes with the collections.

MATERIALS AND METHODS

The experiment was carried out in vegetable science experimental block at University of Horticultural Sciences, College of Horticulture, Bagalkot, Karnataka during *rabi* 2020-21. It is located in the northern part of Karnataka. The geographical location lies at 16°12'N, 75°45'E the average elevation above mean sea level of this area reaches approximately 610 m. A total of 28 snap melon genotypes which are collected from different places of India (Table 1) were raised in a Randomized Complete Block Design (RCBD) with two replications. All recommended package of practices were followed during the crop production. Five plants were randomly selected from each genotype for recording observations viz., vine length (cm) at 50 DAS, internodal length (cm) at harvest, number of branches vine⁻¹ at 50 DAS, node of first male flower appearance, node of first female flower appearance, days to first male flower, days to first female flower, number of male flowers vine⁻¹, number of female flowers vine⁻¹, days to first fruit set, days to first harvest, sex ratio (male: female), number of fruits vine⁻¹, average fruit weight (g), fruit length (cm), fruit circumference (cm), fruit yield vine⁻¹ (kg), fruit color, flesh thickness (mm), fruit splitting or

Table 1. Details of 28 accessions of snap melons and their source.

Sl. No.	Lines	Source
1	L ₁ (HUB - 1)	Lakhamapura, Badami taluk, Bagalkote district
2	L ₂ (HUB - 2)	Sattari, Goa
3	L ₃ (HUB - 3)	S. D. Patak, Ramdurg Belgaum district
4	L ₄ (HUB - 4)	Salcete, Goa
5	L ₅ (HUB - 5)	Dapoli, Maharashtra
6	L ₆ (HUB - 6)	Hireshellikeri, Bagalkote
7	L ₇ (HUB - 8)	Dodamarg, Maharashtra
8	L ₈ (HUB - 9)	Santhosh awti, Sathihala Basavana Bagevadi
9	L ₉ (HUB - 10)	Katageri, Badami taluk
10	L ₁₀ (HUB - 11)	Kundargi, Bagalkote
11	L ₁₁ (HUB - 14)	Rampur, Bagalkote
12	L ₁₂ (HUB - 15)	Haveli, Bagalkote
13	L ₁₃ (HUB - 16)	Kallapur, Nargunda
14	L ₁₄ (HUB - 18)	Bailhongal, Belgaum
15	L ₁₅ (HUB - 19)	Cancona, Goa
16	L ₁₆ (HUB - 20)	Murnal, Bagalkote
17	L ₁₇ (HUB - 21)	Mankani, Bagalkote
18	L ₁₈ (HUB - 22)	Gokak, Belgaum
19	L ₁₉ (HUB - 24)	Mudhol, Bagalkote
20	L ₂₀ (HUB - 25)	Mannur, Sindagi
21	L ₂₁ (HUB - 31)	Belgaum
22	L ₂₂ (HUB - 35)	Gadag
23	L ₂₃ (HUB - 42)	Ramdurga
24	L ₂₄ (HUB - 46)	Haveli, Bagalkote
25	L ₂₅ (HUB - 49)	Bagalkote
26	L ₂₆ (AHS - 10)	CIAH, Bikaner
27	L ₂₇ (AHS - 82)	CIAH, Bikaner
28	L ₂₈ (Pusa Shandar)	IARI New Delhi

cracking habit, cavity diameter (mm), length of fruit cavity (cm), pulp placenta ratio, rind firmness (kg/cm²), seed size (mm), seed color, number of seeds per fruit and 100 seed weight (g) were analyzed in this study. The mean over replications for each trait was subjected to statistical analysis. The phenotypic and genotypic coefficients of variations (PCV and GCV) were estimated by using the formulae suggested by Burtone and Devane (1953). Heritability in broad sense was estimated by using the formulae suggested by Burtone and Devane (1953) and expected genetic advance was computed by using formulae suggested by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The population mean, range, phenotypic and genotypic coefficient of variation, heritability (h²), genetic

Table 2. Mean, GCV, PCV, heritability and genetic advance as per cent of mean for 32 characters in snap melon.

Sl.No.	Characters	Range	Mean	GCV (%)	PCV (%)	h ² (%)	GA (5%)	GAM (5%)
1	Vine length (cm)	50.5 – 171.2	103.4	25.21	26.98	87.32	50.18	48.53
2	Internodal length (cm)	5.2 – 10.8	8.3	11.15	16.46	45.94	1.30	15.57
3	No. of branches per vine	4.7 – 7	5.7	7.93	11.45	47.96	0.65	11.31
4	Node of first male flower	1.3 – 4.6	2.8	30.83	32.53	89.83	1.69	60.20
5	Node of first female flower	3.9 – 7.1	5.2	12.49	17.72	49.73	0.95	18.15
6	Days to first male flower	29.8 – 43.1	36.5	9.26	13.13	49.74	4.91	13.45
7	Days to first female flower	40.6 – 49.8	45.1	4.43	6.78	42.80	2.70	5.98
8	Number of male flowers	162.5 – 217.2	187.1	6.35	10.21	38.72	15.24	8.14
9	Number of female flowers	14.3 – 20.1	18.1	6.43	10.12	40.43	1.52	8.43
10	Days to first fruit set	42.4 – 50.3	46.1	4.13	6.31	42.80	2.57	5.57
11	Days to first harvest	69.4 – 86.9	76.0	4.10	6.13	44.67	4.29	5.64
12	Sex ratio	8.4 – 10.8	9.7	4.55	6.76	45.37	0.61	6.32
13	Number of fruits per vine	3.6 – 7.5	5.4	13.38	18.65	51.49	1.08	19.78
14	Average fruit weight (g)	382.6 – 1348.8	792.6	30.94	32.39	91.24	482.63	60.88
15	Fruit length (cm)	15.7 – 35.8	23.5	16.91	20.44	68.42	6.78	28.82
16	Fruit circumference (cm)	20.7 – 31.6	26.9	7.24	12.75	32.27	2.28	8.48
17	Fruit yield per vine (kg)	2.7 – 6.9	4.6	22.29	24.14	85.23	1.96	42.39
18	Flesh thickness (mm)	15.9 – 30.1	23.1	16.06	18.17	78.21	6.78	29.27
19	Cavity diameter (mm)	33.9 – 48.2	41.8	7.11	10.86	42.80	4.01	9.58
20	Length of cavity (cm)	8.7 – 21.9	14.5	23.43	25.57	83.93	6.42	44.22
21	Pulp placenta ratio	3.2 – 19.5	5.8	56.81	58.13	95.52	6.66	114.39
22	Rind firmness (kg/m ²)	2.8 – 4.9	4.0	8.31	12.71	42.80	0.45	11.21
23	Seed size (mm)	6.7 – 9.7	8.2	7.41	11.32	42.80	0.82	401.05
24	Number of seeds per fruit	401.0 – 1030.6	797.4	21.51	23.97	80.55	317.21	39.77
25	100 seed weight (g)	1.2 – 2.8	1.8	21.80	22.28	95.74	0.81	43.94

GCV = Genotypic coefficient of variation, h² = Heritability (Broad sense) GAM = Genetic advance as per cent mean, PCV = Phenotypic coefficient of variation, GA = Expected genetic advance.

advance (GA) and genetic advance as per cent mean (GAM) for 25 characters are presented in Table 2.

The success of any breeding program depends on the extent of variability existing in the germplasm. Variability may be defined as the amount of variation present among the member of population or species for one or more characters at genotypic or phenotypic levels. Phenotypic variability is noticeable and it includes both genotypic and environmental variation and hence called total variation. Genotypic variation refers to genetic or inherent variability, which remains unchanged by environmental conditions. It is in terms of genotypic variance and consist of additive, dominance and epistatic components. Environmental variance is measured in terms of error mean variance (Chaudhary *et al.* 1985). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are derived by mean and are used to assess the magnitude of variation.

In general, the genotypic variance and genotypic

coefficient of variation were lesser than the phenotypic variance and phenotypic coefficient of variation, respectively. The present study reported the extent of variability available in 28 genotypes collected from different sources and the scope of selection through heritability and genetic advance estimates was analyzed and the results obtained are discussed here under. The analysis of variance revealed significant differences among the 28 genotypes for all the traits studied (Fig.1). The results support the selection programme for high fruit yield.

Phenotypic and genotypic coefficients of variation

Estimates of genotypic and phenotypic coefficient of variation was high for pulp placenta ratio, average fruit weight, node to first male flower appearance, vine length, length of fruit cavity, fruit yield vine⁻¹, 100 seed weight and number of seeds fruit⁻¹ (Table 2), indicating traits having higher range of variation



Fig. 1. variability in fruit characters of snap melon.

have a better scope of improvement through selection. The results are in accordance with the reports of Muthuselvi *et al.* (2019) and Pasha *et al.* (2019) in snap melon. The moderate estimates of genotypic and phenotypic coefficient of variation were observed for internodal length, node at first female flower appearance, days to first male flower, number of fruits vine⁻¹, fruit length, flesh thickness and rind firmness, indicating presence of sufficient amount of variability for these traits (Table 2). The results are in conformity with those reported by Basavarajeshwari *et al.* (2012) in cucumber and Anburani *et al.* (2019) in watermelon. GCV and PCV were very low in magnitude for number of branches vine⁻¹, days to first female flower, number of male and female flowers, days to first fruit set, days to first harvest, sex ratio, fruit circumference, cavity diameter and seed size indicating lower amount of variability present in the population studied (Table 2). The results are in concurrence with Ullah *et al.* (2012) in cucumber.

The result from this study indicated that phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the traits in twenty eight genotypes under study, indicates the predominant effect of environment on the expression of traits. Even though PCV was more than GCV but the difference was very narrow in characters viz., vine length, node of first male flower, days to first

female flower, days to first set, days to first harvest, sex ratio, average fruit weight, fruit yield vine⁻¹, length of cavity, pulp placenta ratio, number of seeds fruit⁻¹ and 100 seed weight, suggesting that these traits were under the control of genetic system and low influence of environment. Hence, these characters can be relied upon and simple selection can be practiced for further improvement.

Heritability and genetic advance as percent mean

Heritability is a good index of the transmission of characters from parents to their offspring (Phundan and Narayanan 1993). The estimations of heritability help the breeder in selection of elite genotypes from diverse genetic population.

High heritability coupled with high genetic advance as per cent mean were recorded for the traits like 100 seed weight, pulp placenta ratio, average fruit weight, vine length, node at first male flower, fruit length, fruit yield vine⁻¹, flesh thickness, length of fruit cavity and number of seeds fruit⁻¹ (Table 1), indicating a predominance of additive gene effects and suggested that these traits may be improved by effective selection of genotypes. Jat *et al.* (2014) in kakri, Pasha *et al.* (2019) in snap melon and Anburani *et al.* (2019) in watermelon reported high estimates

of heritability with high GAM which supports the present results. However, the characters like days to first female flower, number of male flowers, number of female flowers vine⁻¹, days to first fruit set, days to first harvest, sex ratio, fruit circumference and cavity diameter showed moderate estimates of heritability but genetic advance as per cent of mean was low because of lower values of GCV and PCV, indicating the presence of lower amount of variability for these traits in the population studied (Table 2). Similar results were reported by Kandasamy (2017) in cucumber and Muthuselvi *et al.* (2019) in snap melon.

CONCLUSION

The findings of the present investigation led to the conclusion that the good amount of genetic variability existed in the snap melon collections and almost all the characters exhibited high heritability estimates and from this it was concluded that there was a greater number of additive genes were acting for these characters. Considering the diverse nature of the material, the genotypes under investigation in the present study had the greater quantity of heritable variation particularly for average fruit weight, number of fruits per vine, fruit length and flesh thickness and there is possibility for improvement of these traits by selection.

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