Plant Archives Vol. 25, Supplement 1, 2025 pp. 2201-2205 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.supplement-1.301

GENETIC VARIABILITY AND HERITABILITY STUDIES IN SNAP MELON (*CUCUMIS MELO* VAR. *MOMORDICA*) FOR YIELD AND QUALITY TRAITS

**Anand D. Jadhav[1]*, Jaiprakash Narayan, R.P.[2], Palthe Vasudev Naik[3], Ravi P.[1]
and Hanumanthappa Shrihari[4]**
[1]Department of Horticulture, College of Agriculture, University of Agricultural Sciences, Raichur, Karnataka, India
[2]ICAR-KVK, Kawadimatti, Department of Horticulture, College of Agriculture,
University of Agricultural Sciences, Raichur, Karnataka, India
[3]ICAR-KVK, Kalaburagi, Department of Horticulture, College of Agriculture,
University of Agricultural Sciences, Raichur, Karnataka, India
[4]ICAR-KVK, Raichur, Department of Entomology, College of Agriculture, University of Agricultural Sciences,
Raichur, Karnataka, India
*Corresponding author E-mail: Jadhav4128@gmail.com

(Date of Receiving : 07-11-2024; Date of Acceptance : 11-01-2025)

ABSTRACT

The present investigation was carried out at Herbal Garden, College of Agriculture, Raichur during, *summer* 2023-2024. The experimental material comprised of 16 snap melon genotypes collected from various locations in and around Karnataka and also from other states of India. The experiment was laid out in randomized block design with three replications. Analysis of variance revealed that there is a considerable variability exists among the genotypes for all the characters. High phenotypic and genotypic coefficients of variation were recorded for vine length, number of branches leaf area per vine, fruit length, fruit weight, fruit yield per vine, fruit yield per plot, ascorbic acid, carotene content, flesh thickness and pulp to seed ratio. High level of heritability with high genetic advance as percentage mean was recorded by vine length, number of branches, number of nodes per main vine, number of leaves per vine, leaf area per vine, node at which first male appeared, node at which first female flower appeared, fruit length, fruit diameter, fruit weight, fruit yield per vine, fruit yield per plot, TSS , ascorbic acid, carotene content, shelf life, rind thickness, flesh thickness, pulp to seed ratio, and fruit firmness indicating the involvement of additive gene effect and selection would be more effective.

***Keywords* :** Variability, Genetic advance, Heritability and Snap melon

Introduction

India is one of the primary centre of origin for many cucurbitaceous vegetables, where these plants thrive and grow well, even in the hot summer conditions. Like other crops such as legumes and cereals, cultivated cucurbits are not only economically significant but are also commonly grown in the tropics, subtropics, and some temperate regions. The Cucurbitaceae family includes the largest group of cultivated vegetables. Within this family, melons are among the most important commercial crops grown across India. Melons can be classified into several species and exhibit a diverse range of cultivation practices. Over the years, many scientists have studied and described melon and its various classifications.

A recent and widely adopted classification of melons, proposed by Robinson and Decker-Walters (1997), divides the species into six botanical groups: *C. melo* var. *cantaloupensis*, *inodorus*, *conomon*, *dudaim*, *flexuosus*, and *momordica*. Many of these groups are of significant economic value in developed countries, and their classification is largely based on culinary traits. These melon varieties exhibit considerable variation in characteristics such as fruit size, shape, colour, taste, texture, and biochemical composition. This diversity offers a valuable genetic resource for breeders and has led to growing interest in understanding their genetic variation.

Collected melon germplasm from the humid tropics of southern India and identified two main groups: *C. melo* var. *acidulus* and *C. melo* var. *momordica* (Roxb.) Duthie et Fuller. They suggested that additional melon collections from southern India could uncover genetic diversity not currently represented in global melon collections. The snap melon (*Cucumis melo* var. *momordica* L.), an underutilized but morphologically diverse and economically significant cucurbit, is widely grown in India. The fruit has many uses, and the Indian accessions of snap melon are known to be a valuable source of disease and pest resistance, often serving as reference varieties in global research (Pitrat *et al*., 2000; Cohen *et al*., 1996). In India, snap melon is commonly cultivated during the rainy season as an intercrop with maize and sorghum, primarily by resource-poor farmers for local consumption.

The understanding of genetic variability in breeding material plays a crucial role in the success or failure of breeding programs. Therefore, assessing genetic variability and understanding the inheritance patterns of both qualitative and quantitative traits are fundamental to any crop improvement effort. The effectiveness of selection for any traits depends not only on the amount of phenotypic and genotypic variability, but also on the magnitude of heritability. The magnitude of heritability indicates the effectiveness with which selection of genotypes can be made based on phenotypic performance (Johnson et al., 1955).This study aimed to evaluate the genetic variability in snap melon, categorize genotypes based on morphological and physiological characteristics, and examine the heritability and genetic advance for these characters .

Materials and Methods

The present investigation carried out at Herbal Garden, College of Agriculture, Raichur during, *summer* 2023-2024. A total of 16 genotypes of snap melon were raised in a randomized block design (RBD) with three replications. Observations were recorded on five randomly selected plants from each replication for yield and its associated traits viz., vine length (cm), number of branches, number of nodes per main vine, number of leaves per vine, leaf area per vine (cm^2), total chlorophyll content (mg/g), days to first male flower appearance, days to first female flower appearance, node at which first male flower appeared, node at which first female flower appeared, days to 50 per cent flowering, fruit length, fruit diameter (cm), fruit weight (kg), number of fruits per plant, fruit yield per vine (kg), fruit yield per plot (kg), TSS (^{0}Brix), ascorbic acid (mg/100g), shelf life (days), rind thickness (cm), flesh thickness (cm), pulp to seed ratio and fruit firmness. The phenotypic and genotypic coefficients of variations (PCV, GCV) were estimated by using the formulae suggested by Burton and Devane (1953). Heritability in broad sense was estimated by using the formulae suggested by Lush (1940) and expected genetic advance was computed by using formulae suggested by Johnson *et al*., 1955.

Results and Discussion

The results in the current study showed that the phenotypic coefficient of variation (PCV) values are higher than the genotypic coefficient of variation (GCV), suggesting that environmental factors have a significant impact on the performance of genotypes. The findings related to genetic variability, heritability and genetic advance for various traits are discussed in this study are presented in Table 1. Higher estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for vine length, number of branches, leaf area per vine, fruit length, fruit weight, fruit yield per vine, fruit yield per plot, ascorbic acid, carotene content, flesh thickness and pulp to seed ratio. The similar results were also observed by Srikanth *et al.* (2017), Rani *et al.* (2015), Khan *et al.* (2015), Bhimappa (2015) in musk melon; Muthuselvi *et al.* (2019) in snap melon, Pasha *et al.* (2019) in snap melon, Poteker *et al.* (2014) in musk melon, Kumbar *et al.* (2021) in pickiling melon; Karadi *et al.* (2016a) in wild melon and Kumbar *et al.* (2021) in mangalore melon.

Moderate GCV and PCV values were reported for the traits *viz*., number of nodes per main vine, number of leaves per vine, node at which first female flower appeared, fruit diameter, TSS, shelf life, rind thickness, and fruit firmness. These observations are in line with the findings of Indraja *et al.* (2021) in musk melon, Sulochana *et al.* (2021) in snap melon, Joseph (2012) in snap melon, Srikanth *et al.* (2017).

Low GCV and PCV values were reported for the traits *viz*., chlorophyll content, days to first male flower appearance, days to first female flower appearance, days to 50 per cent flowering and number of fruits per vine. Babu and Rao (2018) in oriental pickling, Khomphet *et al.* (2022) in thai melon, Singh *et al.* (2017), Kalgudi *et al.* (2021). This indicates the low variability for these parameters in the germplasm and preponderance of nonadditive gene action. This offers very limited opportunity for improving these traits by selection. This suggests the narrow genetic base and hence the variability has to be generated for these characters through hybridization to recover transgressive segregants or through mutation breeding.

The difference between GCV and PCV values were more for the trait *viz.*, node at which first male flower appeared, internodal length and fruit diameter indicating that influence of environment was more, while, the values of GCV and PCV for other traits under study were very close to each other indicating the influence of environment and selection based upon phenotypic expression for these characters would be effective for the improvement of this crop. These results are same as the results of Lakshmi *et al.* (2017), Silpa *et al.* (2020) and Kalgudi *et al.* (2021).

High heritability accompanied by high genetic advance over mean was observed for vine length, number of branches, number of nodes per main vine, number of leaves per vine, leaf area per vine, node at which first male appeared, node at which first female flower appeared, fruit length, fruit diameter, fruit weight, fruit yield per vine, fruit yield per plot, TSS, ascorbic acid, carotene content, shelf life, rind thickness, flesh thickness, pulp to seed ratio, and fruit firmness indicating the involvement of additive gene effect and selection would be more effective. These, results are accordance with Reddy *et al.* (2013) in musk melon, Poteker *et al.* (2014) in musk melon, Janghel *et al.* (2018), Joseph (2012) in snap melon.

High heritability accompanied by moderate genetic advance over mean was observed for days to first male flower appearance, days to first female flower appearance and days to 50 per cent flowering, indicating that the trait was entirely determined by the additive and non-additive gene effect. This may not be effective for selection. These results are accordance with findings of Mali *et al.* (2020), Bhimappa (2015) and Indraja *et al.* (2021) in musk melon, Tomar *et al.* (2008).

Moderate heritability accompanied by low genetic advance over mean was observed for number of fruits per vine indicating the involvement of additive gene effect and non-additive gene action therefore, selection would not be more effective. These results are accordance with days to first male flower days to first male flower. Pandey *et al.* (2005) in musk melon, Janghel *et al.* (2018), Indraja *et al.* (2021) in musk melon, Kamgoud (2018) in oriental pickling melon.

Table 1 : Genetic variability estimates for growth, yield and quality parameters in snap melon genotypes

Sl. No	Traits	Mean	Range	PCV(%)	GCV (%)	h^2bs (%)	GAM (%)
1	Vine length (cm) (60 DAS)	91.45	49.23-134.38	23.62	22.31	89.21	43.41
2	Number of branches (60 DAS)	9.13	5.53-15.73	31.32	30.36	93.96	60.62
3	Number of nodes per main vine (60 DAS)	23.98	16.93-31.67	17.04	15.91	87.26	30.63
4	Number of leaves per vine (60 DAS)	104.25	82.53-141.07	15.79	14.47	84.00	27.32
5	Leaf area per vine (cm^2) (60 DAS)	10308.93	6604.74-14610.86	55.18	54.53	82.59	97.45
6	Total chlorophyll content (SPAD reading) (60 DAS)	77.60	70.14-82.18	6.49	3.31	26.00	3.47
7	Days to first male flower appearance	28.40	25.93-33.53	7.49	7.11	90.25	13.92
8	Days to first female flower appearance	33.22	29.07-38.73	8.27	7.72	87.22	14.86
9	Node at which first male flower appeared	1.64	1.33-2.47	23.24	19.90	73.34	35.11
10	Node at which first female flower appeared	5.46	4.00-6.87	17.56	15.12	74.11	26.81
11	Days to 50 per cent flowering	39.33	35.67-44.67	6.99	6.30	81.22	11.69
12	Fruit length (cm)	10.08	4.81-19.23	39.51	39.17	98.27	79.99
13	Fruit diameter (cm)	7.87	6.07-10.41	16.53	15.27	85.35	29.06
14	Fruit weight (kg)	0.37	0.15-0.74	50.06	49.36	97.23	75.67
15	Number of fruits per vine	6.17	5.33-7.13	8.92	6.70	56.45	10.37
16	Fruit yield per vine (kg)	2.36	0.88-5.39	55.18	54.53	97.65	97.45
17	Fruit yield per plot (kg)	27.81	9.18-54.38	51.73	51.44	98.90	97.26
18	TSS (^{0}Brix)	5.10	4.33-5.78	12.90	11.71	82.37	21.90
19	Ascorbic acid (mg/100g)	5.73	4.18-9.44	28.54	27.87	95.36	56.07
20	Carotene content	1.02	0.80-1.80	28.61	27.62	93.20	54.92
21	Shelf life (days)	4.04	3.00-5.00	19.91	16.21	66.31	27.19
22	Rind thickness (cm)	0.09	0.05-0.11	16.78	14.72	76.88	26.58
23	Flesh thickness (cm)	1.30	0.69-1.85	29.36	28.78	96.07	58.11
24	Pulp to seed ratio	304.83	124.70-596.68	49.69	49.07	97.49	99.80
25	Fruit firmness	1.40	0.95-1.73	17.03	16.16	90.04	31.59

GCV- Genotypic coefficient of variation; h^2bs- Heritability (Broad sense)

PCV- Phenotypic coefficient of variation; GAM- Genetic advance over mean; S. Em- Standard Error

Conclusion

In the current study, the majority of the traits exhibited high heritability estimates, indicating the presence of a larger number of additive genes influencing these traits. Considering the diverse nature of the material, the genotypes studied showed a greater amount of heritable variation, especially for fruit weight, fruit length, fruit diameter, number of fruits per vine, and yield per vine. This suggests that these traits can be improved through selection.

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