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**Shaik Thaher Ahmed**  
 Department of Vegetable  
 Science, College of  
 Horticulture, Bagalkot,  
 Karnataka, India

**Hadimani HP**  
 Assistant Professor,  
 Department of Vegetable  
 Science, College of  
 Horticulture, Bagalkot,  
 Karnataka, India

**Yashavanth Kumar KH**  
 Assistant Professor,  
 Department of Vegetable  
 Science, College of  
 Horticulture, Bagalkot,  
 Karnataka, India

**Mulla SR**  
 Assistant Professor,  
 Department of Biotechnology  
 and crop improvement, COH,  
 Bagalkot, Karnataka, India

**Ramanagouda H**  
 Assistant professor,  
 Department of Entomology,  
 College of Horticulture,  
 Bagalkot, Karnataka, India

**Norulla H**  
 Assistant Professor,  
 Department of Plant  
 pathology, College of  
 Horticulture, Bagalkot,  
 Karnataka, India

**Corresponding Author:**  
**Shaik Thaher Ahmed**  
 Department of Vegetable  
 Science, College of  
 Horticulture, Bagalkot,  
 Karnataka, India

## Assessment of genetic variability in F<sub>2</sub> population of snap melon (*Cucumis melo* var. *momordica* Duth. & Full) for productivity and quality traits

**Shaik Thaher Ahmed, Hadimani HP, Yashavanth Kumar KH, Mulla SR, Ramanagouda H and Norulla H**

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### Abstract

The Present investigation was carried out at Department of Vegetable Science, College of Horticulture, Bagalkot Dist. Karnataka, India during Dec – march 2023-2024. The experimental material consists of 231 F<sub>2</sub> seeds collected from the Dept. of Vegetable Science, COH, Bagalkot. The experimental design followed is Augmented Block Design with seven blocks and three checks. Analysis of variance exhibited considerable variability among all the F<sub>2</sub> plants of cross (HUB-25 x HUB-3) for all the characters studied. High range of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was recorded for Node at 1<sup>st</sup> staminate flowers appear (41.46 and 45.61), Node at 1<sup>st</sup> pistillate flowers appear (25.03 and 21.55), sex ratio (25.79 and 27.82), Internodal length at last harvest (21.16 and 22.42), no. of branches per vine at last harvest (28.69 and 31.61), average weight of fruit (25.63 and 28.90), number of fruit per vine (35.10 and 38.22), yield of fruit per vine (38.63 and 41.15), TSS (30.54 and 31.83), rind firmness (24.51 and 28.39) and shelf life (24.87 and 28.14). High heritability (h<sup>2</sup> bs) coupled with the high Genetic advance over mean (GAM) was observed for all the traits except, Day to 1<sup>st</sup> male flower appear, day to 1<sup>st</sup> female flowers appear, days to primary harvest and days to final harvest.

**Keywords:** Genetic variability, heritability, genotypic coefficient of variation, phenotypic coefficient of variation, F<sub>2</sub> population, snap melon

### Introduction

Cucurbits, comes under gourd family, also known as Cucurbitaceae, which includes 118 genera and 825 species predominantly found in tropical and subtropical regions. The most significant genera in this family are *Cucurbita*, *Cucumis*, *Citrullus*, *Lagenaria*, and *Luffa*. Cucurbits are crucial for providing humans with edible products and valuable fibers. Among these, melons hold a prominent place as commercially cultivated crops across India. Melons can be classified into various species, exhibiting diverse characteristics and cultivation practices (Muthuselvi *et al.*, 2019) [13]. Oriental pickling melon and snap melon stand out among melons for their uniqueness and display significant variability in the Western Ghats. Snap melon (*Cucumis melo* var. *momordica* L., 2n = 2x = 24) is an underutilized cucurbit crop with significant morphological diversity. This out-crossing horticultural species, part of the Cucurbitaceae family, holds considerable economic value. It is cultivated across India, and its fruit offers numerous benefits for people. Indian snap melon accessions are known to be valuable sources of resistance to diseases and insect pests, and many of them serve as reference accessions globally (Pitrat *et al.*, 2000) [14]. Snap melon is a hardy crop typically grown on its own during the summer season. In the rainy season, it is often cultivated as a mixed crop alongside field crops such as maize, sorghum, and pearl millet ((Seshadri and More, 2009) [18]).

Genetic variability is crucial for the success of any melon crop improvement program. Breeders need to have a wide range of diverse populations to initiate breeding efforts effectively. During the improvement process, desirable plants are consistently selected from a genetically diverse population. Fruit yield is the most important economic trait in any crop. Several other traits that influence yield, as well as yield itself, are controlled by multiple genes and follow a pattern of quantitative inheritance (Hayes *et al.*, 1955) [3].

The first and most crucial step in any plant breeding program is utilizing genetic variability. Understanding this variability is key to making effective selections for yield improvement. By measuring phenotypic and genotypic variation, breeders can assess the extent of diversity in essential traits within a breeding population. Heritability and genetic advance provide insight into the potential for improvement through selection (Hayes *et al.*, 1955) [3]. The segregating generation is ideal for selection, as it exhibits high levels of segregation and recombination. Genetic variability is essential for successfully identifying superior progenies from these segregating generations for further selection and breeding efforts (Thirugnanakumar *et al.*, 2011) [22]. Hence, the present study was conducted to assess the Genetic variability in F<sub>2</sub> population of HUB-25 x HUB-3 cross for growth, earliness, yield and fruit quality traits.

### Materials and Methods

The present study was conducted during *Late Rabi* 2023-2024 at the Department of Vegetable Science, College of Horticulture, Bagalkot, Karnataka, India. The material for present study consists of F<sub>2</sub> generation of cross HUB-25 x HUB-3 was grown along with their respective parents and Pusa Shandar as commercial check. The spacing followed was 2 x 1 m with total several blocks. All recommended practices were followed and plant protection measures were taken during growth of crop. Sufficient irrigation had been given and weeds had been removed at regular intervals. Observations were recorded on all the individual vines in segregating F<sub>2</sub> population and replicated parents in the blocks for the following productivity traits *viz.* Node at 1<sup>st</sup> male flower appearance, Node at 1<sup>st</sup> female flowers appearance, Days to initial male flower appear, Days to initial female flower appear, sex ratio, internodal length at last harvest, no. of branch at last harvest, fruits length, diameter of fruit, average weight of fruit, no. of fruit per vine, yield of fruit per vine, days to initial harvest, days to final harvest, TSS, rind firmness, cavity diameter, shelf life. Genetic variability parameters had been estimated using R-STUDIO software.

### Results and Discussion

#### Estimate of genetic variability parameters in F<sub>2</sub> population of HUB-25 x HUB-3 cross.

The present investigation results showed that PCV values are higher than GCV for the traits under study, which indicates the influence of environment was high. The estimates of variability based on genotypic variance (V<sub>g</sub>), phenotypic variance (V<sub>p</sub>), genotypic (GCV) and phenotypic coefficients of variation (PCV), heritability (h<sup>2</sup><sub>bs</sub>), and genetic advance as a percentage of the mean (GAM) are shown in Table (1).

ANOVA revealed significant difference among F<sub>2</sub> population of HUB-25 x HUB-3. Variability is a key characteristic of any population. Assessing genetic variability is a crucial step in predicting the response to selection, as the success of breeding efforts relies on the extent, type, and magnitude of this variability. Variability for the fruit traits in F<sub>2</sub> population shown in Fig.1. High PCV and GCV (more than 20%) were recorded for Node at 1<sup>st</sup> staminate flowers appear (41.46 and 45.61), Node at 1<sup>st</sup> pistillate flowers appear (25.03 and 21.55), sex ratio (25.79 and 27.82), Internodal length at last harvest (21.16 and 22.42), no. of branches per vine at last harvest (28.69 and 31.61), average weight of fruit (25.63 and 28.90), number of

fruit per vine (35.10 and 38.22), yield of fruit per vine (38.63 and 41.15), TSS (30.54 and 31.83), rind firmness (24.51 and 28.39) and shelf life (24.87 and 28.14). These results are consistent with the findings of previous researchers *viz.*, Muthuselvi *et al.* (2019) [13] in snap melon, Ahirwar and Singh, (2018) [11] for length of fruit and yield of fruit per vine. Shah *et al.* (2018) [19], Silpa *et al.* (2020) [20], Kalgudi *et al.* (2021) [6]. Ibrahim (2013) [5] for weight of fruit, fruits yield per plant and length of fruit. Reddy *et al.* (2013) [17] in muskmelon, for no. of branches per vine; Kamagoud *et al.* (2018) [7] in oriental pickling melon for length of fruit. Mehta *et al.* (2010) [12] in muskmelon for yield of fruit and Karthick *et al.* (2019) [8] in cucumber for number of fruit per vine. Sulochana *et al.* (2021) [21] for sex ratio. Pasha *et al.* (2019) [23] for node at 1<sup>st</sup> female appearance. Hiremata *et al.* (2022) [4] for TSS and shelf life. It is also in accordance with findings of Naroui Rad *et al.* (2010) [16] in cucumber.

Moderate GCV and PCV (between 10-20%) were observed for total no. of male flowers (Muthuselvi *et al.* 2019) [13], length of fruit (Lakshmi *et al.* 2017) [9] in oriental pickling melon, cavity diameter (Hiremata *et al.* 2022) [4]. These characters showed moderate PCV and GCV, indicating that the trait is influenced by both additive and non-additive gene actions. Therefore, recurrent selection can be used for its improvement. Moderate GCV and High PCV was recorded for fruit diameter (Lakshmi *et al.* 2017) [9]

Low GCV and PCV (less than 10%) were observed for days to 1<sup>st</sup> male flowers appear, days to 1<sup>st</sup> female flowers appear, days to initial harvest and final harvest. These results are in accordance with Sulochana *et al.* (2021) [21]; Choudhary *et al.* (2011) [2] for days to 1<sup>st</sup> male flowers appear, days to 1<sup>st</sup> female flowers appear. Pasha *et al.* (2019) [23]; Kalgudi *et al.* (2021) [6] for days to initial harvest. This provides minimal potential for enhancing these traits through selection, indicating a narrow genetic base. To increase variability for these traits, hybridization can be employed to produce transgressive segregants, or mutation breeding can be used. High heritability (more than 60%) coupled with high Genetic advance as percent over mean (more than 20%) was observed for node at 1<sup>st</sup> staminate flower appear, no. of staminate flower, total no. of pistillate flowers (Muthuselvi *et al.* 2019) [13], node at 1<sup>st</sup> pistillate flower appear (Pasha *et al.* 2019) [23], sex ratio (Mali *et al.* 2015 [10] in musk melon), internodal length at last harvest (musk melon), No. of branches per vine at last harvest (Muthuselvi *et al.* 2019; sulochana *et al.* 2021 [13, 21] in snap melon; Choudhary *et al.* 2011) [2]. Length of fruit, diameter of fruit (Hiremata *et al.* 2022 [4]; Pasha *et al.* 2019 [23]; shah *et al.* 2018) [19], Average weight of fruit and no. of fruits per vine (Sulochana *et al.* 2021; Muthuselvi *et al.* 2019) [21, 13], yield of fruit per vine (Mali *et al.* 2015 [10] in musk melon; Muthuselvi *et al.* 2019 [13] in snap melon; Hiremata *et al.* 2022) [4], TSS, rind firmness, cavity diameter, shelf life (Muthuselvi *et al.* 2019 [13] in snap melon; Pasha *et al.* 2019 [23]; sulochana *et al.* 2021) [21] shelf life (Hiremata *et al.* 2022) [4]. High heritability (more than 20%) but moderate genetic advance over mean (between 10-20%) was observed for days to 1<sup>st</sup> male and female flower appear (Muthuselvi *et al.* 2019 [13]; Choudhary *et al.* 2011 [2]; Pasha *et al.*, 2019) [23]. Days to initial harvest and days to final harvest. These results are same as findings of (Muthuselvi *et al.* 2019) [13]. This suggests that additive genetic factors play a dominant role in these traits, making direct selection a more effective approach for improving them.



**Fig:** Variability for the fruit traits in F<sub>2</sub> population obtained from the cross-I (HUB-25 x HUB-3)

**Table 1:** Estimation of genetic variability parameters for growth, earliness, yield and fruit quality traits of cross-I (HUB-25 x HUB-3)

Traits	Mean ± S. Em	MIN	MAX	PV	GV	GCV (%)	PCV (%)	h <sup>2</sup> bs (%)	GAM (%)
Node at 1 <sup>st</sup> staminate flower appearance	2.2 ± 0.07	1	6	1.03	0.85	41.46	45.61	82.62	77.74
Node of 1 <sup>st</sup> pistillate flower appearance	4.8 ± 0.08	3	9	1.45	1.08	21.55	25.03	74.11	38.27
Days to 1 <sup>st</sup> male appearance	32.6 ± 0.22	26	40	10.86	9.35	9.38	10.10	86.11	17.95
Days to 1 <sup>st</sup> female appearance	40.9 ± 0.22	33	47	11.33	9.07	7.36	8.22	80.07	13.58
No. of male flowers	178.9 ± 1.83	83	312	762.07	717.91	15.00	15.46	94.21	30.04
No. of female flowers	16.9 ± 0.23	6	22	12.81	10.90	19.58	21.25	85.10	37.26
sex ratio (M:F)	11.1 ± 0.20	7	21.44	9.53	8.19	25.79	27.82	85.98	49.34
Internodal length at last harvest (cm)	5.5 ± 0.09	3	8	1.55	1.38	21.16	22.42	89.11	41.21
No. of branches per vine at last harvest	5.6 ± 0.12	2	11	3.12	2.57	28.69	31.61	82.40	53.73
Length of fruit (cm)	17.38 ± 0.15	12	22.5	4.66	4.11	11.67	12.42	88.33	22.63
Diameter of fruit (cm)	7.6 ± 0.11	4.7	12.7	2.68	1.99	18.45	21.42	74.21	32.79
Average weight of fruit (g)	728.4 ± 13.77	200.58	1255.5	44174.67	34735.93	25.63	28.90	78.63	46.88
Days to initial harvest	73 ± 0.29	61	82	19.03	18.69	5.92	5.97	98.22	12.1
Days to final harvest	83.8 ± 0.28	70	92	17.67	17.44	4.98	5.01	98.67	10.21
No. of fruits per plant	4.7 ± 0.13	2	11	3.29	2.78	35.10	38.22	84.32	66.49
Fruit yield per vine (kg)	3.29 ± 0.09	1.03	9.41	1.83	1.61	38.63	41.15	88.13	74.81
TSS (°B)	5.2 ± 0.11	3.2	9.8	2.81	2.79	30.54	31.83	92.11	60.48
Rind firmness (kg/cm <sup>2</sup> )	3.5 ± 0.07	2.01	6.98	1.01	0.75	24.51	28.39	74.53	43.65
Cavity diameter (mm)	37.2 ± 0.36	24	62	29.19	27.64	14.08	14.47	94.68	28.26
Shelf life (days)	4.1 ± 0.08	3	10	1.35	1.05	24.87	28.14	78.08	45.33

PV- Phenotypic variance

GCV- Genotypic coefficient of variation

h<sup>2</sup> bs – Heritability (Broad sense)

GV-Genotypic variance

PCV- Phenotypic coefficient of variation

GAM- Genetic advance over mean

S. Em – Standard Error deviation from mean

## Conclusion

From the study, it was concluded that a larger number of additive genes influenced these traits. Considering diverse nature of the material, the segregating population examined in this study exhibited a significant amount of heritable variation, particularly in traits such as the node at which the first staminate flower appears, TSS, average weight of fruit, length of fruit, diameter of fruit, no. of fruits per vine, and yield of fruit per vine. This suggests that there is potential for improving these traits through selection.

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## Reference

- Ahirwar CS, Singh DK. Assessment of genetic variability in cucumber (*Cucumis sativus* L.). Int J Curr Microbiol App Sci. 2018;7(3):813-22.
- Choudhary H, Ram HH, Singh DK. Genetic variability study in muskmelon. Prog Hort. 2011;43(2):231-3.
- Hayes HK, Immer FR, Smith DC. Methods of plant breeding. New York: McGraw Hill Book Co.; c1955. p. 551.
- Hiremata V, Shet RM, Gunnaiah R, Prashantha A, Hongal S, Naika BN, et al. Assessment of genetic variability for fruit yield and quality traits in F<sub>2</sub> generation of intraspecific hybrids derived from muskmelon and Mangalore melon. J Pharm Innov. 2022;11(12):3121-3126.
- Ibrahim EA. Variability, heritability and genetic advance in Egyptian sweet melon under water stress conditions. Int J Plant Breed Genet. 2013;6(4):238-244.
- Kalgudi A, Shet RM, Shantappa T, Lakshmidamma TN, Hongal S, Rathod V. Assessment of heterosis in intraspecific hybrids derived from muskmelon (*Cucumis melo* L.) and Mangalore melon (*Cucumis melo* var. acidulous) for yield and quality traits including shelf life. Biol Forum Int J. 2021;13(3):423-428.

7. Kamagoud S, Shet RM, Nishani S, Hongal S, Hanchimani CN, Prashanta A. Assessment of genetic variability among oriental pickling melon (*Cucumis melo* var. *conomon*) genotypes. *Int J Chem Std.* 2018;6(4):2630-3.
8. Karthick K, Arumugam T, Rajasree V, Ganesan KN, Karthikeyan M. Evaluation and assessment of genetic variability of cucumber (*Cucumis sativus* L.) genotypes. *J Pharm Innov.* 2019;8(11):156-160.
9. Lakshmi LM, Lingaiah HB, Mohan AR, Puttaraju TB, Pitchaimuthu M, Gowda DM. Variability and genetic divergence studies for economic traits in indigenous oriental pickling melon (*Cucumis melo* var. *conomon*) genotypes. *Electron J Plant Breed.* 2017;8(1):365-70.
10. Mali MD, Musmade AM, Ranpise SA. Genetic variability and interrelationship among different traits in F<sub>3</sub> progenies of muskmelon (*Cucumis melo* L.). *Bioinfolet.* 2015;12(3b):733-8.
11. Marker S. Genetic variability, correlation and path analysis study on snap melon (*Cucumis melo* L. var. *momordica*) farmer's varieties. *Int J Bio-resour Stress Manag.* 2019;10(6):636-644.
12. Mehta R, Singh D, Bhalala MK. Genetic variability, heritability and genetic advance for fruit yield and components traits in muskmelon. *J Maharashtra Agri Univ.* 2010;66(35):464-466.
13. Muthuselvi R, Praneetha S, Kennedy ZJ, Uma D. Assessment of variability in snap melon (*Cucumis melo* var. *momordica* Duth. & Full.) genotypes. *J Pharmacogn Phytochem.* 2019;8(4):654-657.
14. Pitrat M, Hanelt P, Hammer K. Some comments on interspecific classification of cultivars of melon. *Acta Hort.* 2000;510:29-36.
15. Potekar SV, Nagre PK, Sawant SN. Genetic variability study in muskmelon (*Cucumis melo* L.). *Int J Trop Agric.* 2014;34(3-4):349-351.
16. Rad MRN, Allahdoo M, Fanaei HR. Study of some yield traits relationship in melon (*Cucumis melo* L.) germplasm gene bank of Iran by correlation and factor analysis. *Trakia J Sci.* 2010;8(1):27-32.
17. Reddy SAK, Shanthi A. Variability and genetic diversity studies of muskmelon accession in the coastal region of Karaikal. *Green Farming.* 2013;4(6):764-766.
18. Seshadri VS, More TA. Cucurbit vegetables - Botany, production and utilization. New Delhi: Stadium Press Pvt. Ltd.; c2009. p. 482.
19. Shah KN, Rana DK, Singh V. Evaluation of genetic variability, heritability and genetic advance in cucumber (*Cucumis sativus* L.) for various quantitative, qualitative and seed characters. *Int J Curr Microbiol App Sci.* 2018;7:3296-303.
20. Silpa R, George ST, Anitha P, Pradeepkumar TVSS, Bastian D, Pathrose B. Genetic divergence analysis in oriental pickling melon (*Cucumis melo* var. *conomon* Mak.). *Res J Agri Sci.* 2020;11(1):115-119.
21. Sulochana, Hadimani HP, Hachinamani CN, Kukanoor L, Lakshmiddevamma TN, Ashok. Assessment of genetic variability for yield and quality traits in snap melon (*Cucumis melo* var. *momordica* Duth. & Full.). *J Pharma Innov.* 2021;10(11):161-164.
22. Thirugnanakumar S, Narasimman R, Anandan A, Senthil Kumar N. Studies of genetics of yield and yield component characters in F<sub>2</sub> and F<sub>3</sub> generations of rice (*Oryza sativa* L.). *Afr J Biotechnol.* 2011;10(41):8797-8800.
23. Pasha A, Ramzan M. Asymmetric impact of economic value-added dynamics on market value of stocks in Pakistan stock exchange, a new evidence from panel co-integration, FMOLS and DOLS. *Cogent Business & Management.* 2019 Jan 1;6(1):1653544.