Society of Krishi Vigyan
www.iskv.in

J Krishi Vigyan 2025, 13(2) : 197-202

DOI: 10.5958/2349-4433.2025.00039.3

ISSN 2319-6432 (Print)
ISSN 2349-4433 (Online)

Analysis of Variance Components for Quantitative Traits in F_2 Population of *Cucumis melo* L. derived from the Cross *Cucumis melo* ssp. *agrestis* (local cultivar) X *Cucumis melo ssp. momordica* (Snap melon)

Afreen Mohammed Siraj B, Rekha B Chittapur, Satish D, Namita Raut and Shivayogi Rayavalad

University of Horticultural Sciences, Bagalkot-587104, Karnataka, India

www.IndianJournals.com
Not for Commercial Use
Downloaded From IP - 216.73.216.57 on dated 15-Nov-2026

ABSTRACT

An experiment was conducted during the *Kharif* season of 2023 at the College of Horticulture, Bagalkot, to evaluate the genetic variability of yield and quality traits in a 235-member F_2 population of *Cucumis melo* L. The study utilized an augmented block design with three checks. Analysis of variance revealed significant differences among the genotypes for nearly all traits, indicating substantial genetic variability. The range of variation was widest for individual fruit weight (110–930 g), yield per vine (480–5180 g), shelf life (5–16d), and total soluble solids (3.10–6.71°Brix). Genotypic coefficients of variation (GCV) were lower than phenotypic coefficients of variation (PCV) for all traits, suggesting environmental influence on trait expression. High heritability coupled with high genetic advance over mean (GAM) was observed for all traits except days to first male and female flower appearance. These findings suggest that selection for most traits can be effective, with the exception of flowering time traits.

Keywords: Coefficient of Variation, Genetic Advance, Genotype, Genotypic, Heritability, Phenotypic.

INTRODUCTION

Cucumis melo is an economically important plant belonging to the Cucurbitaceae family, widely cultivated in both temperate and tropical regions (Fernandez-Trujillo *et al*, 2011). It is a diploid species with a chromosome number of 2n = 24 (Dane, 1991) and has a relatively small genome size, estimated between 4.5 and 5.0 × 10^8 base pairs (Arumuganathan and Earle, 1991; Wang *et al*, 2006). In India, melons are cultivated over 54,100 ha, yielding 1,230,660 t with a productivity of 22.74 t/ha (Anonymous, 2021). Melons are highly valued for their rich *β*-carotene and Vitamin-C content while being low in fat, salts, and cholesterol, and they provide essential nutrients such as potassium. The nutritional profile per 100 grams of fresh melon includes protein (0.54 g), fat (0.14 g), carbohydrates (9.09 g), fibre (0.8 g), calcium (6 mg), iron (0.17 mg), magnesium (10 mg), phosphorus (11 mg), potassium (228 mg), sodium (18 mg), zinc (0.15 mg) and ascorbic acid (18 mg) (Rachmi *et al*, 2020).

The *Cucumis melo* germplasm collections in India have not been extensively characterized for their potential to enhance overall production and improve fruit quality. As a cross-pollinated crop, muskmelon exhibits significant variability in plant architecture and fruit traits, which can be harnessed for breeding purposes. The absence of improved varieties, coupled with production constraints, has resulted in low yields and poor fruit quality. Therefore, developing superior *Cucumis melo* varieties or hybrids tailored to specific agro-ecological conditions and end users is essential. Notably, the Indian *Cucumis melo* germplasm possesses genes associated with unique traits such as fruit quality and resistance to biotic and abiotic stresses, which can be introduced into existing cultivars through hybridization.

Conventional breeding's success hinges on the availability of genetic diversity for target traits (Ara *et al*, 2009). Plant breeders harness genetic resources to create novel gene combinations, developing crop varieties better suited to various agricultural systems (Glaszmann *et al*, 2010). However, direct selection for yield may not always lead to significant crop improvement, as yield is a complex quantitative trait. Therefore, assessing genetic parameters such as genotypic and phenotypic coefficients of variation, heritability, and genetic advance is essential to distinguish between heritable and non-heritable variations. Understanding genetic variability is a fundamental prerequisite for breeding programs. Considering these factors, this study aimed to estimate genetic variability, genetic advance, and heritability for

Corresponding Author's Email - afreen012018@gmail.com

fruit yield and its component traits to predict the selection response in the F_2 population of *Cucumis melo*.

MATERIALS AND METHODS

The study was conducted at the College of Horticulture, Bagalkot, during the *Kharif* season of 2023. The experiment was designed using an augmented block design with three checks. F_2 population seeds were directly sown in the field with a row-to-row spacing of 1.5 meters and a plant-to-plant spacing of 1 meter. Standard agronomic practices were followed to ensure healthy, disease-free plant growth. Observations were recorded on individual plants for various traits, including vine length at 45 days and at harvest, number of primary branches, internodal length, days to first male and female flower appearance, node number to first female flower, days to first fruit harvest, number of male and female flowers, sex ratio, fruit length and diameter, individual fruit weight, number of fruits per vine, fruit yield per vine, pulp thickness, seed cavity size, moisture content, shelf life, total soluble solids (TSS), and β-carotene content.

Analysis of variance was performed for each character using standard statistical methods based on the augmented block design, as outlined by Panse and Sukhatme (1985). Genotypic and phenotypic variances were calculated using standard formulas. Genotypic and phenotypic coefficients of variation (GCV and PCV) were computed following the methods suggested by Burton (1952) and Johnson *et al* (1955), and classified as low (<10%), moderate (10–20%), and high (>20%). Heritability estimates (broad sense) were calculated using the formula by Johnson *et al* (1955) and categorized as low (0–30%), medium (30–60%), and high (>60%). Expected genetic advance (GA) as a percentage of the mean was determined using the method by Johnson *et al* (1955) and classified as low (<10%), moderate (10–20%), and high (>20%). This approach provided a comprehensive analysis of genetic variability, heritability, and genetic advance, which are essential for effective selection in breeding programs aimed at improving muskmelon traits.

RESULTS AND DISCUSSION

The analysis of variance (Table 1) conducted on the F_2 population of *Cucumis melo* at the College of Horticulture, Bagalkot, during the *Kharif* season of 2023 revealed significant differences among genotypes for all traits studied. This indicates considerable genetic variability, suggesting ample potential for improvement through selective breeding. The range of variation was documented for the characters *viz.,* vine length at 45 days (0.40-2.40 m), vine length at harvest (0.80-3.50 m), inter nodal length (3.75-8.40 cm), number of primary branches (2-3), days to first male flower (30-38), days to first female flower (38-47), node at first female flower appears (5-7), number of male flowers (61-159), number of female flowers (5-14), sex ratio (6.8-14), days to first fruit harvest (64-84), fruit length (7-41.5 cm), fruit diameter (3.10-9.50 cm), pulp thickness (0.65-3.50 cm), seed cavity (1.20-5.10 cm), individual fruit weight (110 – 930g), number of fruits per vine (2-11), fruit yield per vine (480–5180 g), moisture content (82.50- 93.10%), shelf life (5-16), total soluble solids (3.10 – 6.71°Brix) and beta carotene content (0.13 – 0.28 mg/100g).

The observed variations in fruit weight can be attributed to the increased translocation of assimilates into the fruits during the post-reproductive growth phases. Additionally, the ratio of male to female flowers is influenced by maternal changes, which are in turn affected by various environmental factors. These findings suggested that environmental conditions play a significant role in determining fruit characteristics. Overall, no single accession demonstrated superior performance across all traits studied. This indicates that while some genotypes may excel in specific characteristics, a comprehensive selection approach is necessary to improve multiple traits simultaneously. Such an approach would involve identifying and selecting genotypes that collectively exhibit desirable attributes, thereby enhancing overall crop performance.

Potekar *et al* (2014), Reddy *et al* (2013), and Janghel *et al* (2013) have reported similar findings. The analysis of the coefficients of variation at both phenotypic and genotypic levels indicated that, for most traits, the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV). This suggests that environmental factors have a significant influence on the expression of these traits. However, the narrow difference between PCV and GCV implies that the environmental impact is relatively minor, allowing for effective selection based on phenotypic performance. Such findings are consistent with previous studies, which have observed similar patterns in various crops, indicating that while environmental factors do play a role, the genetic potential of the traits remains a crucial determinant of their expression (Table 2).

High magnitude of maximum GCV was recorded for number of primary branches (70.95%), fruit yield per vine (54.45%), Individual fruit weight

www.IndianJournals.com
Not for Commercial Use
Downloaded From IP - 216.73.216.57 on dated 15-Nov-2026

www.IndianJournals.com
Not for Commercial Use
Downloaded From IP - 216.73.216.57 on dated 15-Nov-2026

(46.41%), Vine length at 45 days (39.45%), Number of fruits per vine (32.80), Vine length at harvest (32.60), Pulp thickness (30.73%), Fruit length(28.00), Shelf life (23.90), Seed cavity (20.47%) and beta carotene content (132.14%). These high (>20 %) estimates of both GCV and PCV are showing a large range of variance and greater opportunity for selective improvement. The moderate GCV was recorded for traits *viz.,* Number of male flowers (19.69%), Fruit diameter (18.64%), Number of female flowers (16.74%) Internodal length (15.66 %), Total soluble solids (15.57%), Moisture content (13.61%), Sex ratio (12.30%), Node at first female flower appears (11.80%), Days to first female flower (10.71%) observed low genotypic coefficients of variation (GCV) for traits such as days to first fruit harvest (8.75%) and days to first male flower (2.62%) suggest that these characteristics exhibit limited genetic variability. Additionally, the low phenotypic coefficient of variation (PCV) for days to first male flower (4.21%) indicates that environmental factors have a minimal influence on the expression of this trait. However, relying solely on GCV and PCV may not provide a complete understanding of the heritable and non-heritable components of variation. Estimating heritability and genetic advance would offer more comprehensive insights into the genetic potential of these traits.

These findings aligned with previous studies in related crops. Kumar *et al* (2011) observed similar patterns of genetic variability in sponge gourd, highlighting the importance of considering both genetic and environmental factors in breeding programs. Similarly, Chaudhari *et al* (2011) reported comparable results in muskmelon, emphasizing the need for comprehensive genetic analyses to inform selection strategies. In conclusion, while certain traits may exhibit low genetic variability, understanding their heritability and potential for genetic improvement is crucial for effective breeding programs aimed at enhancing crop performance.

High value of heritability were observed in most of the traits, such as vine length at 45 days (98.05%), vine length at harvest (79.37%), inter nodal length (94.50%), number of primary branches (99.78%), node at first female flower appears (96.28%), number of male flowers (95.53%), sex ratio (84.86%), days to first fruit harvest (65.52%),fruit length (93.05%), fruit diameter (96.93%), pulp thickness (97.22%), seed cavity (90.88%), individual fruit weight (98.70%), number of fruits per vine (95.11%),moisture content (95.24%), shelf life (90.32%), total soluble solids (96.31 %) and β-carotene (98.88%). The findings indicated that these traits were genetically controlled and not influenced by environmental factors, suggesting that selection based on observable characteristics would be reliable. However, since broad-sense heritability includes total genetic variance comprising both additive (heritable) and non-additive (dominance and epistatic) effects such traits might not be ideal for further genetic improvement through selection. Moderate heritability was observed for days to first male flower (38.59%), days to first female flower (45.83%), and number of female flowers (59.50%), highlighting the role of non-additive gene actions like dominance and epistasis. None of the traits examined showed low heritability.

High GAM (above 20%) was observed for vine length at 45 days (79.79%), vine length at harvest (59.91%), number of primary branches (31.41%), internodal length (146.22%), node to first female flower appearance (23.96%), Days to first fruit harvest (39.71%), Number of male flowers (39.71%), number of female flowers (26.64%), sex ratio (23.45%), days to first fruit harvest (25.41%). fruit length (55.73 %), fruit diameter (37.84%), pulp thickness (61.63%), seed cavity (40.26%), individual fruit weight (95.61%), number of fruits per vine (66.00%), fruit yield per vine (109.55%), moisture content (26.70%), shelf life (46.90%), TSS (31.52%) and β-carotene (272.28%). Due to the influence of additive gene action, direct selection based on phenotypic expression of these traits could be effective. Similar observations were made in muskmelon by Janghel *et al* (2018). In contrast, moderate genetic advance as a percentage of mean (GAM) was recorded for days to first male flower (3.35%) and days to first female flower (3.78%), suggesting the involvement of non-additive genetic effects. Generally, traits exhibiting both high heritability and high genetic advance are predominantly controlled by additive genes, making phenotypic selection a reliable method for improvement. Traits with such a genetic pattern were observed in this study. These findings are consistent with those reported by Potekar *et al* (2014) and Janghel *et al* (2018) in muskmelon.

CONCLUSION

The results suggested that the analysis of variance revealed significant variability among the F2 population for most of the traits studied. Traits such as number of primary branches, fruit yield per vine, individual fruit weight, and beta carotene showed the highest values for both phenotypic and genotypic coefficients of variation (PCV and GCV). Moreover,

Table 1. Analysis of variance for yield and yield contributing traits in F_2 population derived from the cross UHSCS-12 X AHS-10.

Source of variation	Block (ignoring Treatments)	Treatment (eliminating Blocks)	Treatment: Check	Treatment: Test and Test vs. Check	Treatment (ignoring Blocks)	Treatment: Check	Treatment: Test	Treatment: Test vs. Check	Block (eliminating Treatments)	Residuals
d.f.	6	237	2	235	237	2	234	1	6	12
VL45	1.59 **	0.16 **	0.29 **	0.16 **	0.20 **	0.29 **	0.19 **	2.99 **	0.01	0
VLH	4.52 **	0.34 **	0.76 **	0.34 **	0.45 **	0.76 **	0.40 **	11.94 **	0.14	0.08
IL	2.116**	0.796**	5.59**	0.755**	0.849**	5.59**	0.791**	5.036**	0.023	0.043
NPB	1.942**	3.799**	0.003	3.832**	3.848**	0.003	3.893**	1.031**	0.003	0.009
DFMF	7.55 **	2.43	47.23 **	2.04	2.58	47.23 **	2.21	0.23	1.24	1.36
DFFF	7.36 *	3.16	40.87 **	2.83	3.28	40.87 **	2.86	28.58 **	2.28	1.55
NFFF	0.14 **	0.67 **	7.41 **	0.61 **	0.67 **	7.41 **	0.54 **	16.79 **	0.09 **	0.02
NMF	359.95 **	365.87 **	4956.62 **	326.80 **	374.73 **	4956.62 **	331.33 **	1367.87 **	9.74	14.82
NFF	2.93	3.99 *	85.14 **	3.30 *	4.01 *	85.14 **	3.11 *	51.99 **	2.25	1.26
SR	1.35 *	2.35 **	5.99 **	2.32 **	2.36 **	5.99 **	2.27 **	15.17 **	1.19 *	0.34
DFFH	14.38	15.87	455.12 **	12.13	15.9	455.12 **	8.39	895.03 **	13.23	8.33
FL	423.39 **	29.76 **	252.91 **	27.87 **	40.41 **	252.91 **	38.66 **	23.36 *	3.01	2.69
FD	5.08 **	1.56 **	50.34 **	1.15 **	1.69 **	50.34 **	1.27 **	2.90 **	0.06	0.04
PT	0.95 **	0.20 **	3.36 **	0.17 **	0.22 **	3.36 **	0.19 **	0.65 **	0	0.01
SC	1.49**	0.497**	12.21**	0.398**	0.534**	12.21**	0.436**	0.002	0.052	0.04
IFW	61748.08 **	21444.88 **	169633.33 **	20183.70 **	23004.49 **	169633.33 **	21840.90 **	2027.78 **	143.51	64.88
NFPV	9.84 **	2.40 **	37.76**	2.10 **	2.64 **	37.76**	2.19 **	39.46 **	0.12	0.11
FYPV	2181163.8**	548193.27 **	1681518.25**	538547.95 **	602797.10**	1681518.25**	588496.05 **	1791799.79**	24312.53	28761
MC	8.66*	2.66	19.75**	2.51	2.79	19.75**	2.6	12.30*	3.5	2.39
SL	0.77	4.29 **	57.33**	3.83 **	4.29 **	57.33**	3.84 **	3.20*	0.79	0.37
TSS	1.37**	1.01**	36.43**	0.71**	1.04**	36.43**	0.65**	22.81**	0.12**	0.02
BC	0.155**	0.099**	0.033**	0.100**	0.1039**	0.033**	0.104**	0.002**	0.00009	0.00012

**And ** indicates significance of values at P=0.05 and P=0.01, respectively*

traits including fruit yield per vine, individual fruit weight, number of fruits per vine, number of primary branches, *β*-carotene content, and vine length at 45 days exhibited high heritability along with a high genetic advance as a percentage of the mean. This indicates that these traits are largely influenced by additive genetic effects and should be prioritized during selection.

www.IndianJournals.com
Not for Commercial Use
Downloaded From IP - 216.73.216.57 on dated 15-Nov-2026

Analysis of Variance Components for Quantitative Traits in F2 Population

Table 2. Estimation of genetic variability parameters for yield and yield contributing traits in F_2 population derived from the cross UHSCS-12 X AHS-10.

Sr. No.	Trait	Mean ± S.Em	Range		PCV (%)	GCV (%)	h^2_{bs} (%)	GAM (%)
			Min	Max				
1	Vine length at 45 days (m)	1.10±0.03	0.40	2.30	39.45	39.06	98.05	79.79
2	Vine length at harvest (m)	1.72±0.04	0.80	3.50	36.59	32.60	79.37	59.91
3	Internodal length (cm)	5.51±0.06	3.75	8.40	16.11	15.66	94.50	31.41
4	Number of primary branches	2.65±0.03	2.00	3.00	71.03	70.95	99.78	146.22
5	Days to first male flower	35.31±0.10	30.00	38.00	4.21	2.62	38.59	3.35
6	Days to first female flower	42.23±0.11	38.00	47.00	14.00	10.71	45.83	3.78
7	Node at first female flower	6.12±0.05	5.00	7.00	12.00	11.80	96.28	23.96
8	Number of male flowers	90.24±1.19	61.00	159.00	20.50	19.69	95.53	39.71
9	Number of female flowers	8.11±0.12	5.00	14.00	21.70	16.74	59.50	26.64
10	Sex ratio	11.12±0.10	6.80	14.00	13.39	12.30	84.86	23.45
11	Days to first fruit harvest	78.71±0.19	64.00	84.00	12.30	8.75	65.52	25.41
12	Fruit length (cm)	21.42±0.41	7.00	41.50	29.03	28.00	93.05	55.73
13	Fruit diameter (cm)	5.95±0.07	3.10	9.50	18.92	18.63	96.93	37.84
14	Pulp thickness (cm)	1.43±0.03	0.65	3.50	30.73	30.30	97.22	61.63
15	Seed cavity (cm)	3.08±0.04	1.20	5.10	21.47	20.47	90.88	40.26
16	Individual fruit weight (g)	317.84±9.64	110.00	930.00	46.48	46.41	98.70	95.61
17	Number of fruits per vine	4.38±0.10	2.00	11.00	33.64	32.80	95.11	66.00
18	Fruit yield per vine (g)	1370.40±50.04	480.00	5180.00	55.83	54.45	95.11	109.55
19	Moisture content %	88.52±0.11	82.50	93.10	13.88	13.61	95.24	26.70
20	Shelf life (days)	7.78±0.13	5.00	16.00	25.17	23.92	90.32	46.90
21	Total soluble solids (°B)	5.04±0.05	3.10	6.71	15.86	15.57	96.31	31.52
22	Beta carotene (mg/100g)	0.24±.02	0.13	0.28	132.14	132.06	98.88	272.28

GCV-Genotypic coefficient of variation

PCV- Phenotypic coefficient of variation

S.Em-Standard Error deviation from mean

h^2bs-Heritability (Broad sense)

GAM- Genetic advance over mean

www.IndianJournals.com
Not for Commercial Use
Downloaded From IP - 216.73.216.57 on dated 15-Nov-2026

REFERENCES

Anonymous (2021). *Area and production of horticulture crops for 2021-2022.* (3rd Advance Estimates), Ministry of Agriculture and Farmers Welfare, Government of India.

Ara A, Narayan R, Ahmed N and Khan SH (2009). Genetic variability and selection parameters for yield and quality attributes in tomato. *Indian J Hort* **66**(1): 73-78.

Arumuganathan K and Earle ED (1991)., Nuclear DNA content of some important plant species. *Pl. Mol Biol Rep* **9**:211–215.

Burton GW (1952). Quantitative inheritance in grasses. In: *Proceeding of 6th International Grassland Congress* 1:277-283.

Choudhary H, Ram HH and Singh DK (2011)., Genetic variability studies in muskmelon *Prog Hort* **43**(2):231-233.

Dane F (1991). *Cytogenetics of the genus Cucumis.* In: Tsuchiya T, Gupta PK (eds) Chromosome engineering in plants: Genetics, breeding, evolution, Part B. Elsevier, Amsterdam.

Fernandez-Trujillo JP, Pico B, Garcia-Mas J, Alvarez JM and Monforte AJ (2011). *Breeding for fruit quality in melon*. In: Bebeli PJ (ed) Jenks MA. Breeding for fruit quality. John Wiley & Sons Inc, Hoboken.

Glaszmann JC, Kilian B, Upadhyaya HD and Varshney R K (2010). Accessing genetic diversity for cropimprovement. *Curr Opin Pl Biol* **13**: 167-173.

Janghel A K, Trivedi J, Sharma D, Kishore Y and Kumar L (2018). Geneticvariability in muskmelon (*Cucumis melo* L.) under protected condition. *Int J Curr Microbiol Appl Sci* **6**: 211-217.

Johanson H W, Robinson H F and Comstock R E (1955). Estimates of genetic and environmental variability of soybean. *Agron J* **47**: 314-318.

Kumar D, Kumar R, Thakur K S and Singh B D (2013). Estimation of genetic variability and divergence for fruit yield and quality traits in cucumber (*Cucumis sativus* L.) in North-Western Himalayas. *Univ J Pl Sci* **1**(2):27-36.

Panse V G and Sukhatme P V (1985). *Statistical Methods for Agricultural Workers*. 2nd Edition ICAR New Delhi.

Potekar S V, Nagre P K and Sawant S N (2014). Genetic variability study in muskmelon (*Cucumis melo* L.). *J Trop Agric* **32**(3-4): 349-351.

Rachmi D, Samanhudi and Purnomo D (2020). The effectiveness of fruit extract and temperature for in vitro culture of kepok banana (*Musa balbisiana*). *IOP Conf. Series*: *Earth Environ Sci* **466** (1): 012008.

Reddy B P K, Begum H, Suil N, Reddy M T, Babu J D, Reddy R V S K and Reddy B P (2013). Multivariateanalysis of morphological diversity in local landraces of muskmelon (*Cucumis melo* L.) in Andhra Pradesh. *J Agri Sci Technol* **9**(4):817-828.

Sebastian P, Schaefer H, Telford I R and Renner S S (2010). Cucumber (*Cucumis sativus*) and melon (*C. melo*) have numerous wild relatives in Asia and Australia, and the sister species of melon is from Australia. *Proceedings of the National Academy of Sciences* 107(32): 14269-14273.

Veena R, Amrik S S, Pitchaimuthu M and Souravi K (2012). Genetic evaluation of Cucumber (*Cucumis sativus* L.) genotypes for some yield and related traits. *Electronic J Pl Breed* **3**(3): 945-948.

Wang Y H, Dean R A and Joobeur T(2006), Genetic mapping and molecular breeding in cucurbits. *Pl Breeding Rev* 27:213–244.

Received on 20/2/2025 Accepted on 25/42025

www.IndianJournals.com
Not for Commercial Use
Downloaded From IP - 216.73.216.57 on dated 15-Nov-2026