



Study of Genetic Variability, Heritability and Genetic Advance for Yield- Related Traits in Inter-Botanical Cross of Melon Kashi Madhu (*Cucumis melo* var. *chandalak*) x IC231371 (*Cucumis melo* var. *indicus*)

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ABSTRACT: The study investigated genetic variability, heritability, and genetic advance as percent of mean (GAM) for yield and related traits across melon generations. In F₂, ovary length, ovary width, pistil scar size, seed cavity, yield per plant, and seed length showed high GCV, PCV, heritability, and GAM, indicating additive gene effects. Leaf traits, flesh thickness, fruit weight and TSS expressed moderate variability but high heritability with promising selection potential. In contrast, days to first female flowering and days to first fruit maturity revealed low variability and GAM. In BC₁P₁, ovary length, pistil scar size, fruits per plant, and yield per plant displayed high variability and GAM, whereas fruit length, width, seed cavity, flesh thickness, and fruit weight showed moderate variability with high heritability. Flowering and maturity traits had low variability. In BC₁P₂, ovary length, leaf length, pistil scar size, fruit weight, and TSS exhibited high variability with substantial GAM. Yield per plant and seed width showed moderate to high variability, while flowering and maturity were less variable. Overall, ovary length, pistil scar size, fruit weight, yield per plant, and TSS are identified as key selection targets due to their high variability, heritability and GAM.

Keywords: Melon, Genetic variability, Heritability, GCV, PCV.

INTRODUCTION

Melons (*Cucumis melo* L.) are one of the economically important horticultural crops grown extensively throughout India and other tropical and sub-tropical regions of the world (Dhaliwal, 2017). Melons are nutritious and vitamin-rich wholesome fruits. Majority of melon contain more than 90 per cent water and are rich in antioxidants, primary metabolites (protein, lipid, and carbohydrate), several vitamins (Vitamin A, Vitamin B1, Vitamin B2, Vitamin B6, etc.) and minerals notably Potassium, Calcium, Iron, Magnesium and Phosphorous. The fruits have approximately 45 kcal energy per 100 g (Salunkhe and Kadam 1998). The yellow and orange-fleshed melons contain carotene (Lester, 1997; Chakrabarti, 2001; Shivapriya *et al.*, 2021). Polyphenol content in fruits has health beneficial property (Shivapriya *et al.*, 2021). Seed kernels are edible, tasty, nutritious and rich in oil and energy. The entire melon fruit (including peel and seed) has anti-inflammatory, analgesic and anti-proliferative (supporting cancer prevention)

activity (Jackson *et al.*, 2007; Vayssade *et al.*, 2010; Huang and Ho 2010).

The significant genetic variability in any breeding material is a prerequisite as it does not only provide a basis for selection but also provide some valuable information regarding selection of diverse parent for use in hybridization programme (Meshram and Yadav 2022).

The increased demand for sweet melons by consumers, requires a thorough research on selection and breeding of hundreds of cultivars belonging to numerous market types (Paris *et al.*, 2012). The knowledge on genetic variability is a basic prerequisite to develop high yielding varieties for a systematic breeding programme in melons. Wider the genetic variability more will be the chances of improvement through selection. However, the yield being a complex quantitative trait direct selection for yield may not result in successful crop improvement. Information on character association, direct and indirect effects of component traits on yield would greatly help in formulating the selection criteria and using them effectively in the crop improvement

programme. Therefore, it is necessary to partition the observed variability into heritable and non-heritable components by calculating genetic parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic advance. Further, yield is a complex trait and depended on other associated traits.

MATERIAL AND METHODS

The present investigation was carried out by utilizing two representative melon lines, Kashi Madhu and IC321371, which belong to distinct botanical groups, *chandalak* and *indicus*, respectively. These contrasting parental lines were selected to generate genetic populations and to study inheritance of yield and related quantitative traits. The required hybrids and backcross generations were developed under polyhouse conditions at the *Regional Horticultural Research and Extension Centre*, University of Horticultural Sciences, GKVK campus, Bengaluru.

For ensuring reliability of results, the parental lines and F₁ hybrid were each replicated six times. Evaluation of the parental genotypes, F₁ hybrid, F₂ generation, and backcross progenies (BC₁P₁ and BC₁P₂) was subsequently undertaken under polyhouse conditions at a farmer's field in Pavagada taluk, Tumakuru District, during the summer season of 2021. The experiment was laid out following the Augmented Block Design (ABD), which permitted efficient evaluation of a large number of genotypes along with repeated checks.

Observations were systematically recorded for fifteen key quantitative traits that are critical to growth, reproductive biology, fruit development, and yield performance. These included:

- **Days to first female flowering (DFF)**, an indicator of earliness;
- **Ovary length (OL) and ovary width (OW)**, reflecting initial fruit dimensions;
- **Days to fruit maturity (DFM)**, denoting crop duration;
- **Fruit length (FL) and fruit width (FW)**, representing fruit shape and size;
- **Flesh thickness (FT) and seed cavity (SC)**, which influence consumer preference and edible portion;
- **Seed length (SL) and seed width (SW)**, indicators of seed morphology;
- **Average fruit weight (AFW)**, an important yield determinant;
- **Total number of fruits per plant (TNF) and yield per plant (YLD)**, the direct measures of productivity;
- **Total soluble solids (TSS)**, reflecting sweetness and fruit quality; and
- **pH of fruit juice**, associated with taste, storability, and consumer acceptability.

This comprehensive set of traits was chosen to capture both yield-contributing parameters and quality-related attributes, thereby facilitating a thorough understanding of genetic variability, heritability, and advance in the studied populations.

RESULTS

The details of the genetic variability and derived parameters are presented in Table 1. In F₂ generation, high per cent of GCV and high per cent of PCV along with high estimates of heritability and high GAM recorded for the characters ovary length (21.68 %, 22.02 %, 96.98 % and 44.06 %, respectively), ovary width (21.41 %, 23.00 %, 86.68 % and 41.12 %), size of pistil scar (38.19 %, 49.86 %, 58.42 % and 60.22 %), seed cavity (21.57 %, 21.60 %, 99.80 % and 44.46 %), yield per plant (21.30 %, 23.93 %, 79.27 % and 39.13 %) and seed length (22.10 %, 22.47 %, 96.75 % and 44.46 %), whereas, moderate per cent of GCV and moderate per cent of PCV combined with high estimates of heritability and high GAM for the traits like leaf length (17.57 %, 18.35 %, 91.66 % and 34.70 %), leaf width (13.45 %, 14.34 %, 87.98 % and 26.03 %), fruit length (16.76 %, 19.74 %, 72.15 % and 29.38 %), fruit width (15.06 %, 17.43 %, 74.57 % and 26.82 %) and seed width (16.52 %, 17.66 %, 87.55 % and 44.85 %). The parameters flesh thickness, average fruit weight and TSS expressed moderate GCV (17.98 %, 19.91 % and 19.67 %), high per cent of PCV (20.31 %, 19.91 % and 19.67 %) along with high heritability (78.32 %, 92.65 % and 92.21 %) and high GAM (32.82 %, 39.54 % and 38.96 %). Days to first female flowering expressed low per cent of GCV (9.38 %), moderate PCV (10.43 %), high heritability (80.82 %) and moderate GAM (17.40 %). Days to first fruit maturity showed low GCV (4.97 %) and low per cent of PCV (5.77 %) along with high heritability (74.31 %) and low GAM (8.85 %). Moderate per cent of GCV (11.33 %) and high PCV (20.55 %) along with moderate estimates of heritability (30.38 %) and moderate GAM (12.88 %) recorded for total number of fruits per plant. The trait PH recorded low per cent of GCV (4.25 %), moderate PCV (14.25 %) along with low heritability (8.91 %) and GAM (2.62 %) (Table 1).

In BC₁ (P₁) generation, high per cent of GCV and high per cent of PCV along with high estimates of heritability and high GAM recorded for the characters ovary length (23.20 %, 24.09 %, 92.77 % and 46.11 %, respectively), size of pistil scar (27.66 %, 29.04 %, 90.72 % and 54.36 %), total number of fruits per plant (22.28 %, 22.28 %, 100.00 % and 45.97 %) and yield per plant (23.96 %, 24.03 %, 99.45 % and 49.30 %). Moderate per cent of GCV and PCV combined with high heritability and high GAM expressed for the traits leaf length (14.54 %, 16.50 %, 77.36 % and 26.43 %), fruit length (11.82 %, 12.08 %, 95.72 % and 23.85 %), fruit width (11.33 %, 11.60 %, 95.47 % and 22.84 %), flesh thickness (15.86 %, 16.12 %, 96.79 % and 32.19 %), seed cavity (12.98 %, 13.55 %, 91.74 % and 25.65 %) and average fruit weight (18.28 %, 18.34 %, 99.35 % and 37.58 %), whereas days to female flowering and days to fruit maturity expressed low per cent of GCV (8.89 % and 7.07 %) and low per cent of PCV (9.75 % and 7.36 %) along with high heritability (83.14 % and 92.35 %) and moderate GAM (16.71 % and 14.02 %). Ovary width

recorded moderate GCV (10.31 %), PCV (17.55 %), heritability (34.46 %) and GAM (12.48 %). Leaf width showed low GCV (9.07 %), moderate PCV (13.54 %), moderate heritability (44.92 %) and moderate GAM (12.54 %). The trait TSS expressed moderate GCV (17.84 %), high PCV (20.61), high heritability (74.94 %) and high GAM (31.86 %). Low

GCV (9.70 %), moderate PCV (12.46 %) along with high heritability (60.58 %) and moderate GAM (15.58 %) observed for the trait pH. The trait seed length exhibited low per cent of GCV (3.72 %), PCV (8.43 %), heritability (19.52 %) and GAM (3.39 %) (Table 1, Plate 1).

Table 1: Estimates of variability, heritability and genetic advance as per cent mean for quantitative traits in F₂ and backcrosses derived from the inter-botanical cross Kashi Madhu x IC321371.

Characters	GCV (%)			PCV (%)			h ² (BS)			GA as % mean		
	F ₂	BC ₁ (P ₁)	BC ₁ (P ₂)	F ₂	BC ₁ (P ₁)	BC ₁ (P ₂)	F ₂	BC ₁ (P ₁)	BC ₁ (P ₂)	F ₂	BC ₁ (P ₁)	BC ₁ (P ₂)
Days to first female flowering	9.38	8.89	7.24	10.43	9.75	9.50	80.82	83.14	58.09	17.40	16.71	11.38
Ovary length	21.68	23.20	32.06	22.02	24.09	32.48	96.98	92.77	97.48	44.06	46.11	65.31
Ovary width	21.41	10.31	14.74	23.00	17.55	15.66	86.68	34.46	88.64	41.12	12.48	28.63
Days to first fruit maturity	4.97	7.07	3.93	5.77	7.36	5.20	74.31	92.35	57.00	8.85	14.02	6.12
Fruit length	16.76	11.82	15.55	19.74	12.08	16.00	72.15	95.72	94.39	29.38	23.85	31.16
Fruit width	15.06	11.33	14.07	17.43	11.60	14.28	74.57	95.47	97.15	26.82	22.84	28.61
Flesh thickness	17.98	15.86	13.45	20.31	16.12	20.77	78.32	96.79	41.93	32.82	32.19	17.97
Seed cavity	21.57	12.98	15.68	21.60	13.55	17.23	99.80	91.74	82.76	44.46	25.65	29.42
Average fruit weight	19.91	18.28	20.64	20.69	18.34	21.53	92.65	99.35	91.97	39.54	37.58	40.84
Total number of fruits per plant	11.33	22.28	12.04	20.55	22.28	21.24	30.38	100.00	32.12	12.88	45.97	14.07
Yield per plant	21.30	23.96	22.41	23.93	24.03	23.87	79.27	99.45	30.47	39.13	49.30	27.05
Total soluble solids	19.67	17.84	24.53	20.48	20.61	25.06	92.21	74.94	95.84	38.96	31.86	49.55
pH	4.25	9.70	14.30	14.25	12.46	16.22	8.91	60.58	77.63	2.62	15.58	25.98
Seed length	22.10	3.72	10.72	22.47	8.43	10.89	96.75	19.52	96.84	44.46	3.39	21.76
Seed width	16.52	5.10	16.86	17.66	16.83	20.32	87.55	9.19	68.89	44.85	3.19	28.87

Cross-I = IC321367 x Arka Sheetal	Cross-II = Kashi Madhu x IC321371	Cross- III = Kashi Madhu x IC632170
GCV = Genotypic coefficient of variation	PCV = Phenotypic coefficient of variation	h ² (BS) = Heritability broad sense
GAM = Genetic advance as per cent mean	F ₂ – F ₂ generation	BC ₁ (P ₁) – F ₁ backcross to parent 1
BC ₁ (P ₂) – F ₁ backcross to parent 2		

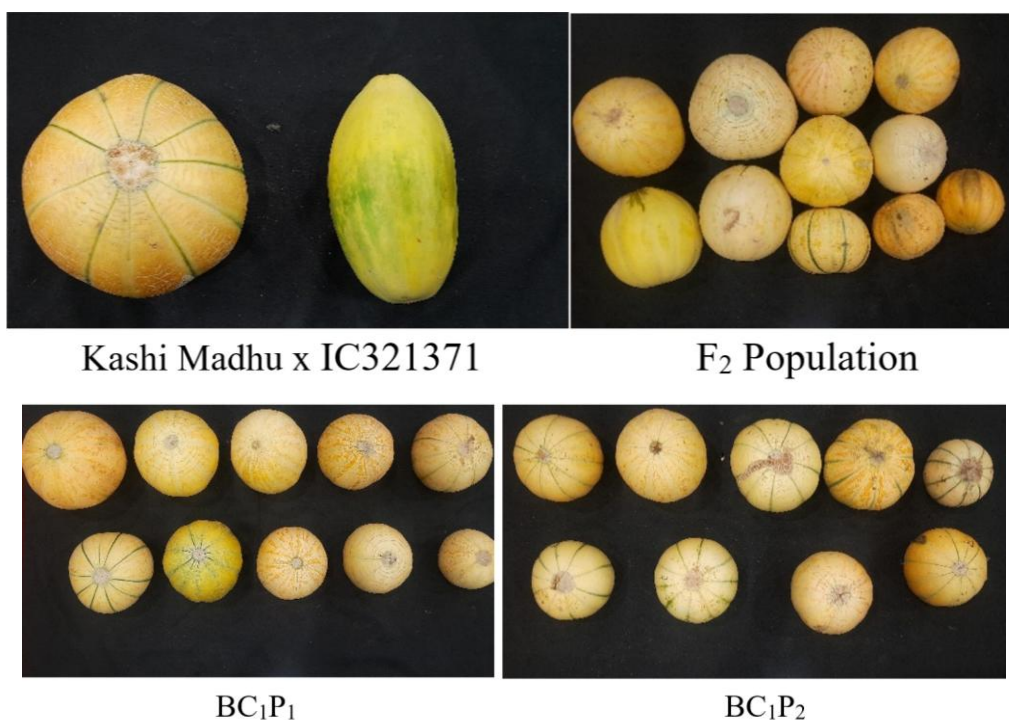


Plate 1: Genetic variability in F₂ and backcross generations of Kashi Madhu × IC321371.

In BC₁ (P₂) generation, high per cent of GCV and PCV along with high estimates of heritability and GAM recorded for the characters ovary length (32.06 %, 32.48 %, 97.48 % and 65.31 %, respectively), leaf length (21.64 %, 22.69 %, 90.98 % and 42.59 %), size of pistil scar (22.72 %, 28.84 %, 92.37 % and 54.96 %), fruit weight (20.64 %, 21.53 %, 91.97 % and 40.84 %) and TSS (24.53 %, 25.06 %, 95.84 % and 49.55 %). The moderate per cent of GCV, moderate per cent of PCV coupled with high heritability and high GAM recorded for the trait's ovary width (14.74 %, 15.66 %, 88.64 % and 28.63 %), leaf width (19.12 %, 19.83 %, 92.94 % and 38.02 %), fruit length (15.55 %, 16.00 %, 94.39 % and 31.16 %), fruit width (14.07 %, 14.28 %, 97.15 % and 28.61 %), seed cavity (15.68 %, 17.23 %, 82.76 % and 29.42 %), PH (14.30 %, 16.22 %, 77.63 % and 25.98 %) and seed length (10.72 %, 10.89 %, 96.84 % and 21.76 %). The traits flesh thickness and total number of fruits per plant expressed moderate GCV (13.45 % and 12.04 %), high PCV (20.77 % and 21.24 %), moderate heritability (41.93 % and 32.12 %) and moderate GAM (17.97 % and 14.07 %). The trait days to first female flowering expressed low per cent GCV (7.24 %), low per cent PCV (9.50 %), high heritability (94.25 %) and moderate GAM (15.85 %). Days to fruit maturity recorded low GCV (3.93 %), PCV (5.20 %), moderate Heritability (57.00 %) and low GAM (6.12 %). High per cent of GCV (22.41 %), PCV (23.87 %), moderate heritability (30.47 %) and high GAM (27.05 %) exhibited by yield per plant. Seed width showed moderate GCV (16.86 %), high PCV (20.32 %), high heritability (68.89 %) and high GAM (28.87 %).

DISCUSSION

In the present study high GCV and PCV recorded for ovary length and width, seed cavity and yield per plant in F₂ generation. In back cross generations *i.e.*, BC₁ (P₁) and in BC₁ (P₂) of inter-botanical cross Kashi Madhu x IC321371 for total number of fruits per plant and yield per plant recorded high GCV and PCV. In other studies, high PCV and GCV recorded for average fruit weight and fruit yield per plant (Torkadi *et al.*, 2007; Tomar *et al.*, 2008; Choudhary *et al.*, 2011; Bhimappa and Choudhry 2017; Kavya, 2017; Sachin, 2018; Chaitra, 2019; Indrajya *et al.*, 2021; Harsh and Pal 2022), number of fruits per plant, flesh thickness and TSS (Tomar *et al.*, 2008; Chaitra, 2019; Indrajya *et al.*, 2021), ovary length, ovary width, fruit length, size of pistil scar, number of fruits per vine and yield per vine (Kavya, 2017; Chaitra, 2019) and acidity (Janghel *et al.*, 2018). High heritability and high GAM recorded for majority of the traits in the present study. These results are in line with other studies for fruit and yield traits (Kalloo *et al.*, 1983; Hazem *et al.*, 2024), average fruit weight (Singh and Lal, 2005), fruit length, fruit girth, 1000 seed weight, average fruit weight, keeping quality of fruit, flesh-cavity ratio and yield per plant (Rakhi and Rajmony 2005), fruit length, average fruit weight, fruit

cavity length and TSS (Reddy *et al.*, 2013), total number of fruits and TSS (Potekar *et al.*, 2014; Janghel *et al.*, 2018; Harsh and Pal 2022) and flesh thickness (Kadi and Sambhaj 2003). Other studies reported moderate heritability coupled with high genetic advance as per cent mean for fruit yield per plant in muskmelon (Singh and Lal 2005). Low heritability and genetic advance were noticed for days to fruiting by Janghel *et al.* (2018). Moderate heritability coupled with low genetic advance as per cent mean for days to first pistillate flowering was recorded (Torkadi *et al.*, 2007; Bhimappa and Choudhary 2017; Indrajya *et al.*, 2021) in oriental picking melon (Ramana, 2000).

CONCLUSIONS

The present investigation revealed substantial genetic variability for yield and yield-related traits in the F₂ and backcross generations of the inter-botanical cross Kashi Madhu × IC321371. High GCV, PCV, heritability and GAM were consistently recorded for ovary length, pistil scar size, fruit weight, total number of fruits per plant and yield per plant across different generations, highlighting the predominance of additive gene action and the potential for effective selection. Traits such as TSS and flesh thickness also expressed high heritability with promising GAM, suggesting their usefulness as selection indices in melon improvement programs. Moderate variability with high heritability and GAM was observed for fruit length, fruit width and leaf traits indicating that improvement through phenotypic selection is feasible though progress may be relatively gradual. In contrast, flowering and maturity traits consistently exhibited low to moderate variability with comparatively low GAM, reflecting the influence of non-additive gene action and environmental factors, which may limit direct selection gains for earliness. The overall findings emphasize that traits directly contributing to yield and quality, such as ovary traits, fruit weight, number of fruits per plant, flesh thickness, and TSS offer the greatest promise for selection and genetic improvement in melon. Consequently, breeding programs focusing on these characters can achieve significant genetic gains, while traits with low variability and GAM may require alternative approaches such as heterosis breeding or multi-environment evaluation.

FUTURE SCOPE

Future studies should focus on advancing the segregating generations to stabilize superior lines and validate additive effects, while incorporating molecular tools such as QTL mapping and marker-assisted selection to accelerate improvement. Traits governed by non-additive gene action, particularly earliness, may be better exploited through heterosis breeding. Multi-environment trials are also needed to assess genotype × environment interactions and identify stable, high-yielding genotypes. Additionally, expanding the scope

to include quality and post-harvest attributes such as shelf-life, rind thickness, and aroma, along with the use of diverse germplasm, will strengthen breeding strategies and ensure market-oriented melon improvement.

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