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GENETICS OF QUANTITATIVE TRAITS IN INTER-BOTANICAL CROSS OF MELON (*CUCUMIS MELO* L.)

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ABSTRACT

In plant breeding, a thorough understanding of the gene action underlying yield and related traits is crucial for developing effective breeding strategies. To elucidate these genetic mechanisms in melon (*Cucumis melo* L.), a generation mean analysis was performed using an inter-botanical cross between Kashi Madhu (P_1) and IC321371 (P_2). Scaling tests and joint scaling revealed significant epistatic interactions for all the twelve traits except for total number of fruits, which fit an additive-dominance model. Additive genetic effects played the most significant role in governing days to fruit maturity. Conversely, dominance and epistatic genetic effects primarily controlled traits such as days to first female flowering, ovary length and width, and fruit length and width. Duplicate gene interaction was expressed by traits ovary length and width, days to fruit maturity, fruit length and width, Seed cavity, Seed length and width, average fruit weight, total number of fruits and yield per plant. Notably, significant and higher magnitude of additive genetic effect [d] observed for fruit length and fruit width, seed cavity and yield per plant. These findings offer valuable insights into the complex genetic architecture of quantitative traits in this melon cross, emphasizing the importance of considering epistatic interactions for effective breeding strategies aimed at developing improved melon cultivars.

Key words : Generation mean analysis, *Cucumis melo*, Additive, Dominance, Duplicate.

Introduction

Melons (*Cucumis melo* L., 2n = 24) are one of the important horticultural crops grown worldwide. Melon belongs to the family Cucurbitaceae. Although, East Africa was believed to be the centre of origin of melon, the recent literature suggests the Asiatic origin (Schaefer *et al*., 2009; Sebastian *et al*., 2010). The species, *Cucumis melo* L. is more diverse and polymorphic than other species in the genus (Pitrat *et al*., 2000). For instance, the parent lines used in this study, Kashi Madhu and IC321371, represent distinct botanical groups, *chandalak* and *indicus*, respectively. Melons are highly cross-pollinated crop due to different sex forms and crossability among different botanical groups has led to the emergence of numerous intermediate forms (Pitrait, 2016).

The core objective of any melon breeding program is to enhance yield while simultaneously ensuring superior fruit quality, encompassing desirable traits like flavor, texture, nutritional value and post-harvest shelf-life. The yield is a quantitative, composite trait influenced by the interplay genotype, environment and their interactions. Therefore, understanding the genetic components of variation and the inheritance patterns of yield-related traits

is paramount for selecting effective breeding procedures (Haymen, 1958; Jinks and Jones, 1958). Generation mean analysis, a powerful biometrical approach, allows for the estimation of various genetic effects, including additive (d), dominance (h), additive x additive (i) additive x dominance (j) and dominance x dominance (l) interactions involved in the expression of polygenic traits like yield and its components. Specifically, the combined estimates of dominance [h] and dominance × dominance [l] gene effects offer the most reliable representation of their individual magnitudes and directions, as they are independent of the degree of gene distribution. Consequently, these components are critical for discerning the type of epistasis influencing the phenotypic performance of different generations for quantitative traits. Opposite signs for [h] and [l] signify duplicate epistasis, whereas similar signs indicate complementary epistasis (Mather and Jinks, 1982; Kearsey and Pooni, 1996).

The understanding of gene action is fundamental to successful crop breeding for enhanced yield and related traits. Previous studies on melon (*Cucumis melo* L.) have yielded varied insights into the genetic control of these characteristics. Zalapa *et al*. (2006) observed significant additive gene effects governing primary branch number and fruit number per plant in the USDA 846-1 x TopMark cross. In contrast, Shashikumar *et al.* (2016) highlighted the prevalence of larger dominance x dominance (l) gene effects for average fruit weight, number of fruits per vine, and yield per vine in the RM 43 x IIHR 121 cross. Javanmard *et al.* (2018) reported significant additive and dominance effects influencing fruit diameter, fruit length/ diameter ratio, flesh thickness and skin thickness in the Tashkandi x Alien cross.

Despite these valuable contributions, research on the inheritance of yield-affecting traits in melon, particularly the comprehensive estimation of genetic components and the elucidation of gene action types, remains limited. The current study addresses this gap by aiming to estimate the genetic components of variation, including additive, dominance and epistatic effects and to determine the type of gene action controlling specific traits. This detailed genetic analysis will be instrumental in predicting the performance of crosses and in developing more effective and targeted breeding strategies for melon improvement.

Materials and Methods

The experiment of the present study was conducted under polyhouse conditions at farmer's field in the B. K. Halli village, Nagalamadike Hobli, Pavagada taluk, Tumkur district. The parents Kashi Madhu X IC321371 were used to generate progenies (F_1, F_2, BC_1 P_1 and BC_1 P_2) and were evaluated during summer 2021. The female parent, Kashi Madhu, produces fruits with dense netting, sutures on the surface, and orange-colored flesh. In contrast, the male parent, IC321371, has fruits without netting or sutures on the surface and green-colored flesh.

The experimental land was brought to a fine tilth by repeated ploughing and harrowing. Portrays were used to raise melon seedlings and 15 days old seedlings were transplanted to the soil. Plants were grown vertically with the help of poles. Gap filling was done one week after transplanting and regular irrigation was given to maintain a good plant population. Prophylactic sprays for the protection of plants against pests and diseases were taken up and regular weeding was done.

The data were recorded from each genotype for thirteen quantitative traits *viz*., Days to first female flowering (DFF), Ovary length (OL), Ovary width (OW), Days to fruit maturity (DFM), Fruit length (FL), Fruit width (FW), Flesh thickness (FT), Seed cavity (SC), Seed length (SL), Seed width (SW), Average fruit weight (AFW), Total number of fruits (TNF), Yield per plant (YLD).

GMA technique is based on six different generations of a cross, *viz*., parents (P_1, P_2), their (F_1, F_2) and back crosses, BC_1 (P_1) and BC_1 (P_2). Statistical analysis was carried out using 'Windostat' software programme. scaling test (A, B, C and D) determines the presence or absence of epistasis (Mather, 1949). Joint scaling test of Mather and Jinks (1982) check for adequacy of the simple additive-dominance model (mean, additive and dominance effects) was determined by χ^2 test. The three-parameter model was found inadequate therefore six parameter model was used to calculate various non allelic gene effects. To provide information on the nature of gene action governing the quantitative traits, estimates of mean (m), additive (d), dominance (h), additive x additive (i), additive x dominance (j) and dominance x dominance (l) gene effects were calculated using the means of six population *viz*., P_1, P_2, F_1, F_2, BC_1 and BC_2 according to six parameter model developed by Hayman (1958).

The dominance [h] and dominance × dominance [l] gene effects are independent of the degree of gene distribution due to which the combined estimates of [h] and [l] could be considered to be the best representative of sign and magnitude of individual h's and l's, respectively. Hence, practically [h] and [l] are the only components which can safely be used to determine the type of epistasis may have influence on the observed *per se* performance of generations for quantitative traits Opposite

sign of [h] and [l] determines duplicate epistasis whereas, same sign indicates complimentary epistasis (Mather and Jinks, 1982; Kearsey and Pooni, 1996).

Results and Discussion

The mean values, standard error and variance for quantitative traits in inter-botanical cross of melon is presented in Table 1. The male parent IC321371 recorded high mean value for ovary length (15.72 mm), days to first fruit maturity (76.87 days), fruit length (15.38 cm) and fruit width (13.45 cm). The F_1 generation recorded highest mean value for ovary width (8.02 mm) and flesh thickness (3.32 cm). The F_2 generation exhibited minimum mean value for days to first female flowering (44.56 days) and seed cavity (4.35 cm). The trait average fruit weight was on par in all the generations. The trait average fruit weight (0.89 kg), total number of fruits per plant (2.75) and yield per plant (2.21 kg) was highest in Kashi Madhu (P_1). The variation among F_2 and backcrosses of Kashi Madhu x IC321371 is presented in Plate 1.

Mather (1949) scaling tests and joint scaling revealed significance for all the parameters days to first female flowering, ovary length, ovary width, days to fruit maturity, fruit length, fruit width, flesh thickness, seed cavity, seed length, seed width, average fruit weight and yield per plant indicating the presence of epistatic interaction. But total number of fruits showed non-significance for all the four scales and failed to exhibit non-allelic interactions. Hence, the data holds good with additive-dominance model (Table 2).

Estimates of gene effects for thirteen quantitative characters in inter-botanical cross Kashi Madhu x IC321371 presented in Table 3. The additive (-2.07) and dominance (5.06) genetic effect along with the additive x dominance (-4.01) and dominance x dominance (10.60) digenic epistasis was significant for days to first female flowering. Ovary length showed significant values of dominance (-11.23), additive x additive (-8.57), additive x dominance (0.99) and dominance x dominance (31.95). for ovary width all the epistatic components were significant. the main genetic effect, additive (1.80) and dominance (10.22) along with the interaction effect additive x additive (6.53) were all found to be positively significant for days to fruit maturity. The fruit length exhibited significant values of dominance (-4.07), additive x additive (-6.08), additive x dominance (3.53) and dominance x dominance (11.17) estimates. The parameter fruit width revealed main genetic effect additive (0.66) and dominance (2.15) components were significant. Only additive x dominance (-0.48) and dominance x dominance (1.52) genetic interactions were significant along with complimentary type of epistasis for the trait flesh

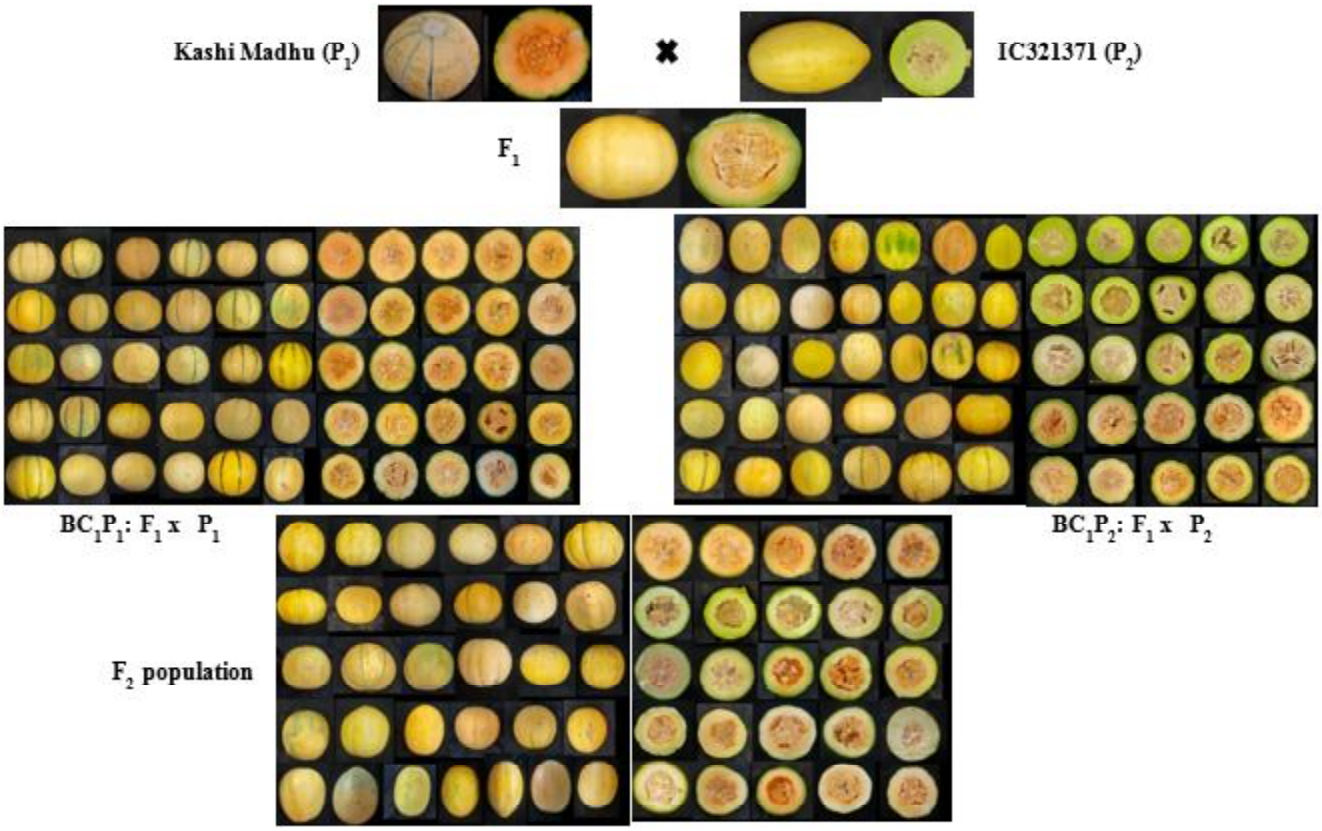

Plate 1 : Variation among F_2 and backcrosses of Kashi Madhu X IC321371.

Table 1 : Estimates of means, standard error and variance for fourteen quantitative characters for P_1 (Kashi Madhu), P_2 (IC321371) F_1, F_2, BC_1 (F_1 x P_1) and BC_2 (F_1 X P_2) derived from inter-botanical cross of melon.

Character	P_1	Var	P_2	Var	F_1	Var	F_2	Var	BC_1	Var	BC_1	Var
	Mean ± SE		Mean ± SE		Mean ± SE		Mean ± SE		Mean ± SE		Mean ± SE	
DFF[a]	48.28±0.29	0.70	46.00 ± 0.26	0.57	49.75 ± 0.97	7.64	44.56 ± 0.46	21.72	47.34 ± 0.46	18.77	46.41 ± 0.43	19.48
OL[b]	13.06±0.30	0.73	15.72± 0.16	0.20	14.73 ± 0.22	0.39	12.36 ± 0.20	4.35	10.05 ± 0.18	3.06	12.39 ± 0.24	6.02
OW[c]	7.68± 0.13	0.13	5.72 ± 0.06	0.03	8.02 ± 0.29	0.67	6.42 ± 0.14	2.18	6.53 ± 0.08	0.65	4.56 ± 0.07	0.52
DFM[d]	79.50 ± 0.26	0.57	76.87 ± 0.58	2.69	81.87 ± 0.97	7.55	77.69 ± 0.44	20.11	80.22 ± 0.62	34.84	77.42 ± 0.40	16.66
FL[e]	9.01 ± 0.38	1.18	15.38 ± 0.28	0.63	14.62 ± 0.31	0.81	13.86 ± 0.27	7.48	11.30 ± 0.15	2.22	15.23 ± 0.19	3.94
FW[f]	10.97 ± 0.44	1.57	13.45 ± 0.12	0.13	12.00 ± 0.20	0.33	12.85 ± 0.22	4.98	13.40± 0.16	2.38	12.74 ± 0.18	3.28
FT[g]	3.10 ± 0.05	0.02	2.37 ± 0.03	0.01	3.32 ± 0.13	0.14	2.77 ± 0.05	0.31	2.99 ± 0.04	0.18	2.35 ± 0.05	0.30
SC[h]	5.18 ± 0.13	0.14	5.07 ± 0.22	0.41	5.40 ± 0.12	0.11	4.35 ± 0.16	2.64	5.32 ± 0.11	1.08	5.12 ± 0.13	1.73
SL[i]	9.21±0.08	0.06	9.00±0.22	0.02	7.67±0.19	0.01	8.25±0.20	4.30	8.14±0.07	0.47	8.56±0.08	0.68
SW[j]	3.35±0.10	0.09	3.17±0.11	0.09	2.75±0.16	0.21	4.12±0.07	0.52	3.48±0.04	0.17	3.50±0.05	0.26
AFW[k]	0.89 ± 0.07	0.05	0.88 ± 0.02	0.01	0.86 ± 0.02	0.01	0.82 ± 0.02	0.02	0.85 ± 0.02	0.02	0.83 ± 0.02	0.03
TNF[l]	2.75 ± 0.12	0.28	2.50± 0.18	0.21	2.12 ± 0.12	0.12	2.38 ± 0.04	0.23	2.32 ± 0.05	0.26	2.33 ± 0.04	0.24
YLD[m]	2.21 ± 0.08	0.06	1.91 ± 0.09	0.07	1.92 ± 0.17	0.23	1.65±0.03	0.15	2.12 ± 0.04	0.15	1.56 ± 0.03	0.14

[a]Days to first female flowering; [b]Ovary length; [c]Ovary width; [d]Days to fruit maturity, [e]Fruit length, [f]Fruit width, [g]Flesh thickness, [h]Seed cavity, [i]Seed length, [j]Seed width, [k]Average fruit weight, [l]Total number of fruits, [m]Yield per plant.

thickness. as regards to seed cavity additive x dominance (-0.56) and dominance x dominance (-9.30) genetic components were significant. Only the interaction genetic effect, additive x dominance (-0.17) and dominance x dominance (0.41) were significant for average fruit weight. The parameter yield per plant exhibited significant dominance x dominance (1.86) effect.

Estimates of additive genetic effects [d] and their variances (σ^2_A) and dominant genetic effects [h] and their variances (σ^2_D) in the inheritance of quantitative traits in melon presented in Table 4. In the cross Kashi Madhu X IC321371 the estimates of σ^2_A were higher than the [d] for ovary width (3.19), days to fruit maturity (46.65), fruit length (8.80), fruit width (4.29), seed cavity (2.47), seed length (7.45). The σ^2_D were higher compare to [h] for the trait's days to first female flowering (12.39), ovary length (4.29) and days to fruit maturity (26.80).

Significant but lower magnitude of additive genetic effect and genetic variance were recorded to be important in the expression of days to first female flowering (1.56 and 5.19), ovary width (0.62 and 3.19), days to fruit maturity (1.45 and -11.28), fruit width (1.70 and 4.29) and yield per plant (0.10 and 0.02). significant but lower magnitude of additive genetic effect [d] coupled with small and non-significant additive genetic variance (σ^2 A) were noted to be important in for the traits ovary length (-2.37 and -0.37), leaf width (0.66 and -4.02), size of pistil scar (0.43 and 0.16), flesh thickness (0.42 and 0.14), average fruit weight (0.40 and 0.003) and TSS (1.40 and -0.69). Significant but lower magnitude of additive genetic effects coupled with large and significant additive genetic variance were observed for the traits fruit length (-2.15 and 8.80) and seed length (0.40 and 7.45).

Significant but negative estimates of dominance genetic effects [h] coupled with significant dominance genetic variance (σ^2_D) were found to be important for the expression of traits like days to first female flowering (-3.40 and 12.39), ovary length (-16.62 and 4.29), leaf length (-0.97 and 5.03), leaf width (-1.11 and 6.41) and size of pistil scar (-0.93 and 0.18). positive significant estimates of dominance genetic effects [h] coupled with significant dominance genetic variance (σ^2_D) were recorded for the trait's days to fruit maturity (2.00 and 26.80) and fruit length (1.05 and -2.18). Non-

Table 2 : Estimates of scaling tests and Joint scaling tests for fourteen quantitative in inter-botanical cross of melon.

Character	A	B	C	D	*m*	*d*	*h*	χ^2
DFF[a]	-10.94**±1.37	-2.91*±1.34	-17.11**±2.72	-1.62^{NS}±1.12	47.67**	1.56**	-3.40**	80.55**
OL[b]	-10.69**±0.53	-12.68**±0.56	-14.80**±1.00	4.28**±0.51	12.34**	-2.37**	-16.62**	810.40**
OW[c]	-6.64**±0.36	-4.62**±0.33	-3.76**±0.84	3.74**±0.31	6.32**	0.622**	-2.44**	56.30**
DFM[d]	-0.92^{NS}±1.61	-1.89^{NS}±1.39	-9.35**±2.71	-3.26**±1.16	77.97**	1.45**	2.00**	13.40**
FL[e]	0.99^{NS}±0.59	-6.07**±0.58	0.99^{NS}±1.82	3.04**±0.60	12.52**	-2.15**	1.05**	144.75**
FW[f]	2.84**±0.34	4.02**±0.43	6.00**±1.08	-0.43^{NS}±0.50	11.51**	1.70**	1.66**	102.95**
FT[g]	-1.04**±0.17	-0.08^{NS}±0.17	-0.72*±0.35	0.20^{NS}±0.13	2.55**	0.42**	0.37**	53.32**
SC[h]	3.79**±0.28	4.92**±0.36	8.13**±0.74	-0.29^{NS}±0.36	7.01**	0.10^{NS}	-0.43**	338.35*
SL[i]	0.59*±0.25	1.53**±0.33	3.46**±0.09	2.79**±0.42	8.80**	0.40**	-1.56**	58.38**
SW[j]	-1.12**±0.21	-0.91**±0.22	4.47**±0.46	3.25**±0.15	3.19**	-0.016ns	-0.76**	426.74**
AFW[k]	-0.39**±0.08	-0.05^{NS}±0.04	-0.47**±0.11	0.01^{NS}±0.04	0.83**	0.02^{NS}	0.09^{NS}	26.19**
TNF[l]	0.034^{NS}±0.25	0.04^{NS}±0.24	0.29^{NS}±0.41	0.10^{NS}±0.12	2.53**	-0.02^{NS}	-0.38*	0.92^{NS}
YLD[m]	-0.89**±0.21	-0.71**±0.21	-1.36**±0.40	0.12^{NS}±0.09	1.97**	0.10*	-0.68**	19.03**

*, ** = 0.05% & 0.01 % Level of significance, respectively.

[a] Days to first female flowering; [b] Ovary length; [c] Ovary width; [d] Days to fruit maturity, [e] Fruit length, [f] Fruit width, [g] Flesh thickness, [h] Seed cavity, [I] Seed length, [j] Seed width, [k] Average fruit weight, [l] Total number of fruits, [m] Yield per plant.

significant dominance genetic effects along with significant dominance genetic variance (σ^2_D) were observed for the trait TSS (0.48 and 4.91) and pH (0.27 and 0.29). Non-significant estimates of dominance genetic effects [h] along with non-significant dominance genetic variance (σ^2_D) noted for the trait average fruit weight (0.09 and 0.01). Significant but smaller magnitude of dominance genetic effects [h] coupled with non-significant dominance genetic variance (σ^2_D) were recorded for the trait ovary width (-2.44 and -1.38), fruit width (1.66 and 0.09), flesh thickness (0.37 and 0.09), seed cavity (-0.43 and -0.02), total number of fruits per plant (-0.38 and 0.07), yield per plant (-0.68 and -0.01), seed length (-1.56 and -3.41) and seed width (-0.76 and -0.23).

Comparison of means and variances in early segregating generations derived from the crosses is a commonly used method to assess the relative potential of cross combinations to identify superior lines (Suresh *et al.*, 2017). The parents *per se* performance were reflected in their progeny. The parameter fruit length, fruit width and flesh thickness of F_1 and F_2 has recorded its performance towards the highest mean parent. The fruit length and fruit width of the F_1 hybrid of oriental pickling melon was also reported to be towards the highest mean parent (Pornsuriya and Pornsuriya, 2009). The mean performance of BC_1P_1 and BC_1P_2 were intermediate between both the parents. The mean performance of BC_1 (P_1) generation of three intra-botanical crosses of muskmelon was better than F_1 generation for days to anthesis, vine length and number of fruits per vine (Shashikumar *et al.*, 2016). Slightly increased *per se* performance of melon backcross generation was noticed for yield components in two different locations (Zalapa *et al.*, 2006). The mean performance of backcross generations towards their respective parent for earliness, fruit and yield traits were noticed in intra-botanical crosses of muskmelon (Patil *et al.*, 2014).

Dominance, dominance x dominance gene effect for days to first female flowering and for ovary traits has been recorded in this cross. Dominance x dominance gene effect for days to first female flowering has been recorded for slicing cucumber and author inferred more dominance effects that reveal biparental mating or recurrent selection to generate heritable variation followed by conventional selection (Bommesh *et al.*, 2018). Duplicate type of epistasis in the expression of days to fruit maturity indicates predominantly dispersed alleles at the interacting loci (Jinks and Jones, 1958). Selection in later generation based on family (F_3 and onwards) performance maybe effective and this can be achieved by reciprocal recurrent selection (Zalapa *et al.*, 2008). Duplicate epistasis observed for fruit length and width and seed cavity hence, single seed descent for facilitating gene fixation and subsequent selection would be appropriate breeding method. Both additive and dominance effect govern fruit length in muskmelon (Torkadi *et al.*, 2007; Tomar *et al.*, 2008; Sakulphrom *et al.*, 2017). Greater dominant gene effect was noticed by Patil *et al.* (2014) in muskmelon.

Table 3 : Estimation of gene effects for fourteen quantitative characters in inter-botanical cross of melon.

Characters	*m*	*d*	*h*	*i*	*j*	*l*	Gene interaction
DFF[a]	44.56**±0.46	-2.07**±0.63	5.06*±2.46	3.25^{NS}±2.25	-4.01**±0.66	10.60**±3.73	Complimentary
OL[b]	9.365**±0.20	-0.33^{NS}±0.30	-11.23**±1.0	-8.57**±1.03	0.99**±0.35	31.95**±1.58	Duplicate
OW[c]	6.42**±0.14	-0.02^{NS}±0.11	-6.17**±0.69	-7.49**±0.63	-1.00**±0.13	18.75**±0.95	Duplicate
DFM[d]	77.69**±0.44	1.80*±0.74	10.22**±2.54	6.53**±2.33	0.48^{NS}±0.81	-3.71^{NS}±4.04	Duplicate
FL[e]	13.86**±0.27	-0.07^{NS}±0.25	-4.07**±1.26	-6.08**±1.20	3.53**±0.34	11.17**±1.68	Duplicate
FW[f]	12.85**±0.22	0.66**±0.24	2.15*±1.06	0.86^{NS}±1.01	-0.59^{NS}±0.33	-7.73**±1.45	Duplicate
FT[g]	2.77**±0.05	0.03^{NS}±0.07	0.33^{NS}±0.30	-0.40^{NS}±0.26	-0.48**±0.07	1.52**±0.45	Complimentary
SC[h]	7.58**±0.16	0.06^{NS}±0.17	0.29^{NS}±0.75	0.58^{NS}±0.73	-0.56**±0.21	-9.30**±1.01	Duplicate
SL[i]	9.25**±0.20	0.57**±0.11	-7.02±0.88	-5.59**±0.85	0.47**±0.16	7.72**±1.04	Duplicate
SW[j]	4.12**±0.07	-0.01NS±0.06	-7.02±0.36	-6.50**±0.31	-0.10NS±0.10	8.54**±0.53	Duplicate
AFW[k]	0.82**±0.01	-0.01^{NS}±0.02	-0.10^{NS}±0.09	0.02^{NS}±0.08	-0.17**±0.04	0.41**±0.14	Duplicate
TNF[l]	2.38**±0.04	-0.03^{NS}±0.07	-0.58^{NS}±0.30	-0.21^{NS}±0.24	-0.00^{NS}±0.15	0.13^{NS}±0.51	Duplicate
YLD[m]	1.65**±0.04	0.05^{NS}±0.05	-0.38^{NS}±0.26	-0.24^{NS}±0.19	-0.09^{NS}±0.08	1.86**±0.45	Duplicate

*, ** = 0.05% & 0.01 % Level of significance, respectively. m = Mean, d = Additive, h = Dominance

[a] Days to first female flowering; [b] Ovary length; [c] Ovary width; [d] Days to fruit maturity, [e] Fruit length, [f] Fruit width, [g] Flesh thickness, [h] Seed cavity, [I] Seed length, [j] Seed width, [k] Average fruit weight, [l] Total number of fruits, [m] Yield per plant.

Table 4 : Estimates of additive genetic effects and their variances (σ^2_A) and dominant genetic effects and their variances (σ^2_D) in the inheritance of quantitative traits in melon.

Characters	[d]	(σ^2_A)	[h]	(σ^2_D)	σ^2_D/σ^2_A
DFF[a]	1.56**	5.19**	-3.40**	12.39**	2.39
OL[b]	-2.37**	-0.37^{NS}	-16.62**	4.29*	-11.59
OW[c]	0.622**	3.19*	-2.44**	-1.38^{NS}	-0.43
DFM[d]	1.45**	-11.28*	2.00**	26.80**	-2.38
FL[e]	-2.15**	8.80**	1.05**	-2.18*	-0.25
FW[f]	1.70**	4.29**	1.66**	0.09^{NS}	0.02
FT[g]	0.42**	0.14^{NS}	0.37**	0.09^{NS}	0.64
SC[h]	0.10^{NS}	2.47*	-0.43**	-0.02^{NS}	-0.01
SL[i]	0.40**	7.45*	-1.56**	-3.41NS	-0.46
SW[j]	-0.016NS	0.60**	-0.76**	-0.23NS	-0.38
AFW[k]	0.40**	0.003^{NS}	0.09^{NS}	0.01^{NS}	3.33
TNF[l]	-0.02^{NS}	-0.03^{NS}	-0.38*	0.07^{NS}	-2.33
YLD[m]	-1.23**	-0.31^{NS}	-0.96**	0.25*	-0.81

*, ** = 0.05% & 0.01% level of significance, respectively.
m = Mean, d = Additive, h = Dominance

[a] Days to first female flowering; [b] Ovary length; [c] Ovary width; [d] Days to fruit maturity, [e] Fruit length, [f] Fruit width, [g] Flesh thickness, [h] Seed cavity, [I] Seed length, [j] Seed width, [k] Average fruit weight, [l] Total number of fruits, [m] Yield per plant.

Interallelic interactions were of greater importance than main effects for seed cavity for Kashi Madhu x IC321371, inferring that breeding plan based on restricted selection by way of intermating the most desirable segregants followed by selection and a diallele selective mating system to recover desirable transgressive segregants will facilitate favorably the interacting gene constellations. This will achieve perfect pyramiding of desirable genes (Pornsuriya and Pornsuriya, 2009; Bommesh *et al*., 2018).

Average fruit weight is a crucial component positively associated with yield. Higher magnitude of dominant genes along with duplicate epistasis observed in the present study. Dominance gene effect in the inheritance of fruit weight in intra-specific cross of melon was recorded (Metwally *et al*., 2015). The dominance gene effect in cucumber was recorded by Dineshkumar (2001) and Rai *et al*. (2018) and it was inferred that heterosis breeding or recurrent selection would be useful in improving the average fruit weight. The digenic epistasis, dominance x dominance (l) played a significant role in the expression of yield per plant along with duplicate epistasis in Kashi Madhu x IC321371. Except additive x dominance, all other genetic effects were significant in muskmelon (Shetty, 2010; Patil *et al*., 2014) and intra-specific cross of melon (Metwally *et al*., 2015). The author inferred that heterosis breeding or initial single seed descent till high level of gene fixation is attained followed by reciprocal recurrent selection in subsequent generation would improve this trait.

High magnitude of the estimates of σ^2_A in ovary width, fruit length and width, seed cavity, yield per plant, seed length and width indicate long-term genetic gains as they could be exploited through the constellation of desired genes. This is because σ^2_A is fixable by selection and hence it is possible to predict response to selection

(Shivakumar *et al*., 2017).

Both additive and dominance genetic effects were important for flesh thickness in the cross Kashi Madhu X IC321371, while for yield per plant, pH and seed width in all the three crosses. Simple selection may not be effective in improving these traits as dominance x dominance gene effects is not fixable. Perhaps one or two cycles of biparental mating followed by recurrent selection is advisable with twin objective of dissipating [h] and enhancing frequency of genes with increasing effects on the expression of these traits (Salimath and Bahl, 1985).

Significant positive dominance genetic effects [h] coupled with significant dominance genetic variance (σ^2_D) observed for the traits like fruit maturity and fruit length suggested the role of increasing allele with directional dominance. Non-significant dominance genetic effects and non-significant dominance genetic variance for few traits suggested absence of dominance for these traits.

Small but significant estimates of dominance genetic effect [h] and non-significant estimate of dominance genetic variance (σ^2_D) suggest simple selection is expected to be effective for genetic improvement of the traits (Shivakumar *et al*., 2017).

Conclusion

This study effectively characterizes the inheritance patterns of key quantitative traits in the inter-botanical melon cross involving Kashi Madhu and IC321371, highlighting significant differences between the parents and segregating generations. The male parent, IC321371, was identified as a valuable source for alleles conferring increased ovary length, days to first fruit maturity, fruit length and fruit width. Conversely, the F_1 generation showed advantages in ovary width and flesh thickness, while the F_2 exhibited traits like early female flowering and reduced seed cavity size. The consistent average fruit weight across all generations suggests its relative stability in this cross. The superior performance of Kashi Madhu (P_1) for average fruit weight, total fruit number and yield per plant emphasizes its potential as a breeding parent for these traits.

The significant results from Mather scaling tests and joint scaling for most traits indicate the presence of epistatic interactions (non-allelic interactions), which are crucial considerations for breeding strategies. This suggests that simple additive-dominance models may not fully explain the inheritance of these complex traits, highlighting the need to account for epistatic effects in further analysis and breeding efforts. However, the total number of fruits per plant, demonstrating non-significant scaling tests, suggests that this trait might be primarily governed by additive-dominance genetic effects.

The detailed analysis of gene effects revealed the involvement of both additive and dominance genetic components, alongside various forms of digenic epistasis (additive x additive, additive x dominance, dominance x dominance) for most traits, including days to first female flowering and ovary length. The significance of all epistatic components for ovary width further emphasizes the complexity of its genetic control. These findings underscore the importance of understanding the intricate genetic architecture of quantitative traits in melon, particularly the influence of epistatic interactions, to facilitate more targeted and efficient breeding programs. The identified variations within the F_2 and backcross populations (Plate 1) likely represent a rich source of genetic diversity that can be harnessed for developing improved melon cultivars.

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