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GENETIC VARIATION AND INHERITANCE OF QUALITATIVE FRUIT CHARACTERS IN MELON: EVIDENCE OF DUPLICATE, COMPLEMENTARY AND INHIBITORY GENE ACTIONS

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ABSTRACT

A comprehensive study was conducted to investigate the variation and inheritance of qualitative fruit traits in a cross between two contrasting melon genotypes, Kashi Madhu and IC321371. A wide variation observed for all the studied characters such as stigma colour, ovary pubescence, fruit shape at peduncle and blossom end, rind and flesh characteristics. Inheritance study revealed, the F_2s of melon fruits for fruit rind colour, fruit suture and strength of attachment of fruit segregated 13:3 ratio, further supporting inhibitory epistasis. Fruit grooves showed duplicate gene action. Netting on the fruit surface showed complementary gene action. Flesh colour segregated into orange, green, and orange-green classes, with F_2 conforming to a 1:2:1 ratio ($\chi^2 = 5.045$; P = 0.080), indicating monogenic incomplete dominance. Fruit shape in longitudinal section exhibited oblate, round, and oval types, fitting a 1:2:1 ratio ($\chi^2 = 3.495$; P = 0.174), suggesting incomplete dominance.

Keywords: Melon, qualitative traits, Inheritance, epistasis, incomplete dominance.

Introduction

Melons (*Cucumis melo* L., 2n = 24) are one of the important horticultural crops grown worldwide which belongs to the family Cucurbitaceae. The species, *Cucumis melo* L. is more diverse and polymorphic with respect to fruit related traits such as shape, size, colour, texture, taste and composition than other species in the genus (Pitrat *et al.*, 2000). The diversity observed in melon fruits has prompted researchers to unravel the genetic basis of their qualitative traits, many of which are controlled by simple genes or their interactions.

Genetic investigations in melons began in the late 1930s, leading to the identification of numerous genes associated with seed and seedling traits (Ganesan, 1988; Perin *et al.*, 2002), leaf and foliage (Ganesan and Sambandam, 1979), plant architecture (Gabillard and Pitrat, 1988; Ohara *et al.*, 2001), flower traits (Rosa, 1928; Poole and Grimball, 1939; Wall, 1967) and fruit characters (Rosa, 1928; Hughes, 1948; Kubicki, 1962; Bains and Kang, 1963; Wall ,1967; Davis 1970; Takada *et al.*, 1975; Ganesan, 1988; Herman *et al.*, 2008; Galperin *et al.*, 2003).

In melons, white rind (*Wi*) colour of immature fruit was dominant to green (Kubicki, 1962) whereas, in mature fruits white (*w*) was recessive to dark green fruit skin in a cross between Honeydew (*w*) and Smiths Perfect cantaloupe (*W*, dark green) (Hughes, 1948). A polygenic control of external fruit colour was recorded in the cross Piel de Sapo x PI 161375 (Whitaker and Davis, 1962; Monforte *et al.*, 2004; Eduardo *et al.*, 2007; Obando *et al.*, 2008). Single recessive gene (*s*) was reported to control vein tracts or sutures on fruits (Bains and Kang, 1963; Davis 1970). Ridge fruit surface was reported to be controlled by a single gene (*ri* in C68), recessive to ridge less (*Ri* in 'Pearl') (Takada *et al.*, 1975). Single dominant gene govern the development of net tissue regardless of the degree of netting (Lumsden, 1914; Herman *et al.*, 2008). Many genes influence the intensity of flesh colour, but individual major gene determines whether the flesh is orange (which is dominant), green or white. Recessive alleles of two genes govern green flesh (*gf*) and white flesh (*wf*) (Hughes, 1948; Iman *et al.,* 1972). Fruit quality is a polygenic trait, but several individual genes have a major effect. In wild melon populations, fruits may be bitter due to Bif allele (Ma *et al.,* 1997; Parthasarathy and Sambandam, 1981) and mealy flesh texture because of the *Me* allele (Ganesan 1988). Sour taste is dominant to sweet and a single dominant gene, *So-2* (Sour-2) govern the trait (Perin *et al.,* 1999; Burger *et al.,* 2003). A recessive allele (*jf*) for juicy flesh (Chadha *et al.*, 1972) and a dominant allele (*Mu*) for musky flavour (Ganesan, 1988) have been reported. Sweetness is reported to be controlled by single recessive gene (*suc*) in a cross between Faqqous (low sucrose) and Noy Yizre el (High sucrose) melons (Burger *et al.,* 2002). The cross between Hara Madhu x Japenese Cantaloupe and Hara Madhu x New Melon showed monogenic control with dominance of green rind over yellow, white flesh over green flesh and less juicy over juicy. Two dominant genes-controlled absence of sutures with complimentary and supplementary relationships (Chadha *et al.,* 1972). When green-fleshed Durgapura Madhu was crossed with white-fleshed Lucknow Safeda, F_2 showed 3:1 segregation showing that green flesh is governed by a recessive gene (Ramaswamy *et al.*,1977).

The present investigation was undertaken to assess the variation of some qualitative traits and to gain insights into the genetic basis and inheritance patterns of several economically important fruit traits. Specific focus was given to rind colour, fruit surface grooves, sutures, netting, flesh colour, fruit shape in longitudinal section and the strength of fruit attachment to the peduncle.

Materials and Methods

The experimental material consisted of parents of two different botanical groups *viz.,* Kashi Madhu (*Cucumis melo* var. *chandalak*) and IC231371 (*Cucumis melo* var. *indicus*). The F_1's, F_2 and backcross populations (BC_1 (P_1) and BC_1 (P_2)) to both the parents were produced. All these six generations were taken for variation and inheritance study during summer 2021 under polyhouse conditions at farmer's field in the Pavagada taluk, Tumkur District.

Observations were systematically recorded across all six generations, namely the parents, F_1, F_2, and backcrosses, following the PPV & FRA DUS guidelines. The characters evaluated included fruit rind colour, presence of grooves, fruit suture, surface netting, flesh colour, fruit shape in longitudinal section, and the strength of fruit attachment to the peduncle at maturity. To determine the inheritance patterns of these fruit traits, chi-square analysis was performed on the collected data. In addition to these primary descriptors, variation studies were conducted for a broader set of parameters. These included stigma colour, ovary pubescence, fruit shape at the peduncle and blossom ends, intensity of fruit skin colour, fruit suture and its pigmentation, density of surface netting, flesh firmness, fruit flavour, mildness of flavour, and seed coat colour. Collectively, these comprehensive evaluations provided deeper insights into the morphological diversity and inheritance of key fruit quality traits.

Chi square test was performed according to Gomez and Gomez, 1984.

$$\chi^2 = \frac{\sum(O-E)^2}{E}$$

O = Observed value; E = Expected value.

Results and Discussion

Stigma colour was visually observed and recorded as light green (11 F_2, one BC_1 (P_1) and 28 BC_1 (P_2)), medium green (50 F_2, 33 BC_1 (P_1), 49 BC_1 (P_2), including Kashi Madhu, IC321367 and F_1) and dark green (40 F_2s, 54 BC_1 (P_1) and 24 BC_1 (P_2)). Ovary pubescence was categorized as dense (76 F_2s, 77 BC_1 (P_1), 79 BC_1 (P_2) including parents and F_1), Medium (19 F_2, 11 BC_1 (P_1) and 21 BC_1 (P_2)) & sparse (6 F_2s and 1 BC_1 (P_2).

Strength of attachment of fruit to peduncle at maturity revealed that, fruits of 17 F_2s, 15 BC_1 (P_1), 0 BC_1 (P_2) including Kashi Madhu and F_1 detached easily during maturity (weak attachment) and fruits of 84 F_2s, 73 BC_1 (P_1), 101 BC_1 (P_2) including the parent IC321371 remained attached to peduncle during maturity (strong attachment). The F_2 population showed 84 non-slippable fruits and 17 slippable fruits. The chi square deviated from the hypothetical 3:1 ratio and fitted to 13:3 ($\chi^2 = 0.243$; P = 0.621) and exhibited inhibitory epistatic gene action. The BC_1 (P_1) generation supported this by segregating into 3:1 ratio with χ^2 of 2.969 (p value = 0.084). The BC_1 (P_2) exhibited 1:0 ratio (101 non-slippable: 0 slippable).

Fruit shape in longitudinal section exhibited a wide range of variation such as oblate (33 F_2s, 41 BC_1 (P_1) and 0 BC_1 (P_2), Kashi Madhu and F_1), round (43 F_2s, 46 BC_1 (P_1) and 45 BC_1 (P_2)) and oval (25 F_2s, 56 BC_1 (P_2) and IC321371). Fruit shape in F_2 generation was classified into oblate (33 lines), round (43 lines) and oval (25 lines). Test of goodness of fit was done to know the segregation pattern and it revealed significant fit to 1:2:1 (χ^2 = 3.495; P = 0.174) for F_2 generation. The BC_1 (P_1) generation exhibited 1:1 (41 oblate: 46 round) with the χ^2 of 0.295 (p value = 0.586) and BC_1 (P_2) revealed chi square value of 1.198 with a probability of 0.549 and showed a significant fit to 1:1 ratio (45 round: 56 oval).

Fruit shape at peduncle end was classified as round (27 F_2s, 8 BC_1 (P_1) and 25 BC_1 (P_2)), Pointed (22 F_2S, 1 BC_1 (P_1), 14 BC_1 (P_2) and IC321371) and truncate (52 F_2s, 79 BC_1, 62 BC_1 (P_2), Kashi Madhu and F_1) with respect to blossom end one fruit of BC_1 (P_1), was pointed, 16 F_2s, 4 BC_1 (P_1), 12 BC_1 (P_2) including IC321371 were intermediate and 85 F_2s, 83 BC_1 (P_1), 89 BC_1 (P_2), Kashi Madhu and IC321371 exhibited truncate type of fruit shape at blossom end.

As per the visual assessment, colour of fruit skin was recorded as dark yellow (61 BC_1 (P_1), 81F_2s) and 0 BC_1 (P_2) and lemon yellow (26 F_2s, 27 BC_1 (P_1) and 101 BC_1 (P_2)). In the present study F_1 exhibited lemon yellow fruit rind colour. The F_2 segregated in the ratio 13:3 with the chi square value 2.653 along with probability 0.103 exhibiting inhibitory epistatic. This was supported by BC_1 (P_1) population with the segregation ratio 3:1(χ^2 = 1.515; P = 0.218). the BC_1 (P_2) exhibited 0:1 ratio (0 dark yellow: 101 lemon-yellow). Intensity of fruit skin colour was visually observed and grouped as light (37 F_2s, 55 BC_1 (P_1) and 53 BC_1 (P_2)), medium (49 F_2s, 27 BC_1 (P_1), 44 BC_1 (P_2), IC321371 and F_1) and dark (15 F_2s, 6 BC_1 (P_1), 4 BC_1 (P_2) and Kashi Madhu).

Based on the visual observations 95 F_2s, 87 BC_1 (P_1), 82 BC_1 (P_2) including the parent Kashi Madhu and F_1 were found to have grooves on the surface of fruit. Whereas, 6 F_2s, 1 BC_1 (P_1), 19 BC_1 (P_2) and IC321371 did not exhibit grooves on fruit surface. In F_2s, grooves were present in 95 lines and absent in 6 lines. The chi square calculated (χ^2 = 0.016; P = 0.897) was not in agreement with Mendelian ratio of 3:1 and fitted into 15:1 ratio indicating the duplicate gene action. For the backcross to recessive parent, the segregation was 82 present: 19 absent and the χ^2 for the 3:1 expected ratio was 2.062 (p value = 0.150). The backcross to dominant parent exhibited 1:0 (87 present: 1 absent) ratio.

Fruit suture was observed on 80 F_2, 87 BC_1 (P_1), 94 BC_1 (P_2), Kashi Madhu and F_1 and rest of the F_2s, BC_1 (P_1), BC_1 (P_2) including IC321371 were suture less. Among fruits having sutures, 37 F_2s, 48 BC_1 (P_1), 53 BC_1 (P_2), Kashi Madhu and F_1 were having green-coloured sutures, 43 F_2s, 39 BC_1 (P_1) and 41 BC_1 (P_2) were having cream-coloured sutures. For the fruit suture, the F_1 generation indicated presence of suture. F_2 plants segregated 80: 21 (present: absent) (χ^2 = 0.276; P = 0.598) and exhibited inhibitory epistatic gene action. Plants in the BC_1 (P_1) generation (parent with fruit suture) segregates 1: 0 (88 present: 0 absent). The BC_1 (P_2) (parent without fruit suture) segregated as expected 3:1 ratio and a χ^2 of 3.594 (p value = 0.057).

Fruit surface netting was classified as absent (47 F_2s, 28 BC_1 (P_1), 65 BC_1 (P_2) and IC321371) and present (54 F_2s, 60 BC_1 (P_1), 36 BC_1 (P_2), Kashi Madhu and F_1). Presence or absence of netting on fruit surface segregated into 9: 7 ratio (54 present: 47 absent) with the chi square value 0.318 (p= 0.572) and exhibited complementary gene action. The back cross generation supported this by exhibiting 1:3 (33 present: 68 absent) ratio when crossed to recessive parent (BC_1 (P_2)) while the BC_1 (P_2) (parent with presence of netting) exhibited 1: 0 (85 present: 3 absent). Density of surface netting was classified as moderate (49 F_2s, 39 BC_1 (P_1), 35 BC_1 (P_2) and F_1), dense (5 F_2s, 21 BC_1 (P_1), 1 BC_1 (P_2) and Kashi Madhu).

As per the visual assessment, fruit flesh colour was recorded as green orange (24 F_2s, 38 BC_1 (P_1),46 BC_1 (P_2) and F_1), orange (58 F_2s, 50 BC_1 (P_1), 0 BC_1 (P_2) and Kashi Madhu) and green (19F_2s, 0 BC_1 (P_1) and 55 BC_1 (P_2) and IC321371. The calculated chi square (χ^2 = 5.045; P = 0.080) of F_2 fitted to 1:2:1 ratio exhibiting monogenic, incomplete dominance. The BC_1 (P_1) generation supported this by fitting to 1:1:0 ratio (38 green orange: 50 orange) with the χ^2 of 0.801 (p value = 0.441) and BC_1 (P_2) revealed chi square value of 0.801 with a probability of 0.669 and showed a significant fit to 1:1 ratio (46 green orange: 55 green).

For fruit flesh firmness, the fruits were divided into three states such as, firm flesh (66 F_2s, 65 BC_1 (P_1), 78 BC_1 (P_2) including parents and F_1) and intermediate firm (35 F_2s, 23 BC_1 (P_1) and 23 BC_1 (P_2)). None of the genotypes showed soft flesh.

Presence or absence of fruit flavor was observed organoleptically. All F_2s, BC_1 (P_1), BC_1 (P_2) including parents and F_1 were flavored. Fruit flavor was further subdivided as strong (17 F_2s, 3 BC_1 (P_1), 15 BC_1 (P_2) including parents and F_1), medium (57 F_2s, 72 BC_1 (P_1) and 67 BC_1 (P_2)) and mild (27 F_2s, 13 BC_1 (P_1) and 19 BC_1 (P_2)).

Based on the visual observation, seed colour was classified as white (5 F_2, 1 BC_1 (P_1), 2 BC_1 (P_2) and Kashi Madhu), cream (12 F_2s) and creamy white (84 F_2s, 87 BC_1 (P_1), 99 BC_1 (P_2), IC321371 and F_1).

Discussion

The ovary pubescence was polymorphic in F_2 and backcross *i.e.*, dense, medium and sparse (Table 1). The variation for ovary pubescence was noticed earlier in melons (Kirkbride, 1993; Stepansky *et al.,* 1999; Sudhakara, 2014; Kavya and Manchali, 2019; Chaitra, 2019). Stigma colour was classified as dark green, medium green and light green in the present study. Variation for stigma colour was also noticed in muskmelon segregating population (Kavya, 2017).

Hughes (1948) recorded that white colour of mature fruits was recessive to dark green fruit skin. Yellow reported to be inherited as a monogenic dominant trait when yellow rind crossed with dark green rind (Tadmor *et al.*, 2010). The variation in skin colour is due to amount of chlorophyll degradation and amount of carotenoids and others pigments exposure or accumulation (Flores *et al.*, 2001). The genes naringerin-chalcone (*Nca*), chlorophyll (*Chl*) and carotenoid (*Car*) control accumulation of pigment in rind of matured fruits. A polygenic control of the external fruit color was reported (Whitaker and Davis, 1962; Monforte *et al.,* 2004; Eduardo *et al.,* 2007; Obando *et al.*, 2008).

Table 1: Variation in F_2 and backcross population derived from the inter-botanical cross Kashi Madhu X IC321371 for qualitative characters

Sl. No.	Character	Classes	F_2	BC_1 (P_1)	BC_1 (P_2)	Parents and F_1
1	Sex expression	Andromonoecious	101	88	101	Kashi Madhu, IC321371 and F_1
		Monoecious	0	0	0	
2	Stigma color	Light green	11	1	28	
		Medium green	50	33	49	Kashi Madhu, IC321371 and F_1
		Dark green	40	54	24	
3	Ovary pubescence	Dense	76	77	79	Kashi Madhu, IC321371 and F_1
		Medium	19	11	21	
		Sparse	6	0	1	
4	Strength of attachment of fruit to peduncle at maturity	Strong	84	73	101	IC321371
		Weak	17	15	0	Kashi Madhu and F_1
5	Fruit shape in longitudinal section	Oblate	33	41	0	Kashi Madhu and F_1
		Round	43	46	45	
		Oval	25	0	56	IC321371
6	Fruit shape at peduncle end	Round	27	8	25	
		Pointed	22	1	14	IC321371
		Truncate	52	79	62	Kashi Madhu and F_1
7	Fruit shape at blossom end	Pointed	0	1	0	
		Intermediate	16	4	12	IC321371
		Truncate	85	83	89	Kashi Madhu and F_1
8	Color of fruit skin	Dark yellow	81	61	0	Kashi Madhu
		Lemon yellow	26	27	101	IC321371 and F_1
9	Intensity of fruit skin color	Light	37	55	53	
		Medium	49	27	44	IC321371 and F_1
		Dark	15	6	4	Kashi Madhu
10	Fruit groves	Absent	6	1	19	IC321371
		Present	95	87	82	Kashi Madhu and F_1
11	Fruit sutures	Absent	21	0	17	IC321371
		Present	80	88	84	Kashi Madhu and F_1
12	Fruit suture color	Green	37	48	53	Kashi Madhu and F_1
		Cream	43	39	41	
		Absent	21	1	7	IC321371
13	Fruit surface netting	Absent	47	3	68	IC321371
		Present	54	85	33	Kashi Madhu and F_1
14	Density of surface netting	Moderate	49	39	35	F_1

Sl. No.	Character	Classes	F_2	BC_1 (P_1)	BC_1 (P_2)	Parents and F_1
		Dense	5	21	1	Kashi Madhu
		Absent	47	28	65	IC321371
15	Colour of fruit flesh	Green orange	24	38	46	F_1
		Orange	58	50	0	Kashi Madhu
		Green	19	0	55	IC321371
16	Flesh firmness	Firm	66	65	78	Kashi Madhu, IC321371 and F_1
		Intermediate	35	23	23	
17	Fruit flavor	Absent	0	0	0	
		Present	101	88	101	Kashi Madhu, IC321371 and F_1
18	Mildness of fruit flavor	Absent	0	0	0	
		Strong	17	3	15	Kashi Madhu, IC321371 and F_1
		Medium	57	72	67	
		Mild	27	13	19	
19	Seed colour	White	5	1	2	Kashi Madhu
		Cream	12	0	0	
		Cream white	84	87	99	IC321371 and F_1

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

Table 2: Chi square analysis of F_2's and back cross populations derived from the inter-botanical cross Kashi Madhu x IC231371

Sl. No.	Characters	G	Categories	O	E	Ratio	χ^2	P	Gene action
1.	Fruit rind color	F_2	Dark yellow	81	82.03	13:3	2.653	0.103	Inhibitory epistatic
			Lemon yellow	26	18.93				
		BC_1 (P_1)	Dark yellow	61	66.00	3:1	1.515	0.218	
			Lemon yellow	27	22.00				
		BC_1 (P_2)	Dark yellow	0		0:1			
			Lemon yellow	101					
2.	Fruit grooves	F_2	Present	95	94.65	15:1	0.016	0.897	Duplicate
			Absent	6	6.31				
		BC_1 (P_1)	Present	87		1:0			
			Absent	1					
		BC_1 (P_2)	Present	82	75.75	3:1	2.062	0.150	
			Absent	19	25.25				
3.	Fruit suture	F_2	Present	80	82.03	13:3	0.276	0.598	Inhibitory epistatic
			Absent	21	18.93				
		BC_1 (P_1)	Present	88		1:0			
			Absent	0					
		BC_1 (P_2)	Present	84	75.75	3:1	3.594	0.057	
			Absent	17	25.25				
4.	Netting	F_2	Present	54	56.79	9:7	0.318	0.572	Complementary
			Absent	47	44.17				
		BC_1 (P_1)	Present	85		1:0			
			Absent	3					
		BC_1 (P_2)	Present	33	25.25	1:3	3.171	0.074	
			Absent	68	75.75				
5.	Flesh color	F_2	Green orange	24	22	1:2:1	5.045	0.080	Monogenic, Incomplete dominance
			Orange	58	44				
			Green	19	22				

Sl. No.	Characters	G	Categories	O	E	Ratio	χ^2	P	Gene action
		BC$_1$ (P$_1$)	Green orange	38	44.00	1:1	0.801	0.441	
			orange	50	44.00				
		BC$_1$ (P$_2$)	Green orange	46	50.50	1:1	0.801	0.669	
			Green	55	50.50				
6.	Fruit shape	F$_2$	Oblate	33	25.25	1:2:1	3.495	0.174	Monogenic, Incomplete dominance
			Round	43	50.50				
			Oval	25	25.25				
		BC$_1$ (P$_1$)	Oblate	41	44	1:1	0.295	0.586	
			Round	46	44				
		BC$_1$ (P$_2$)	Round	45	50.50	1:1	1.198	0.549	
			Oval	56	50.50				
7.	Strength of attachment of fruit	F$_2$	Non-slippable	84	82.06	13:3	0.243	0.621	Inhibitory epistatic
			Slippable	17	18.93				
		BC$_1$ (P$_1$)	Non-slippable	73	66	3:1	2.969	0.084	
			Slippable	15	22				
		BC$_1$ (P$_2$)	Non-slippable	101		1:0			
			Slippable	0					

G = Generations O - Observed value E – Expected value *P- Probability at 0.05%
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

In the present study, Kashi Madhu had non-prominent grooves/ ridges on fruit surface and IC321371 did not have any ridges. When the parent Kashi Madhu crossed with IC321371, the F$_1$ exhibited ridge fruit surface. Grooves in fruit was found to be recessive to ridge less (Takada *et al.*, 1975). Inheritance pattern of fruit grooves in muskmelon F$_2$s found to be controlled by more than one gene in a cross combination of Kashi Madhu x *acidulous* melon (Kavya and Manchali, 2019). The other studies reported variations for fruit grooves pattern in muskmelon (Stepansky *et al.,* 1999; Pitrat, 2013; Sudhakara, 2014) and also in other groups of melons (Chaitra, 2019).

Absence of sutures was reported as digenically dominant with supplementary relationship (Chadha *et al.,* 1972). But in other studies, it was found to be controlled by a single recessive gene, *s* (Bains and Kang, 1963; Davis 1970). Suture less was monogenically dominant over sutured (Hagiwara and Kamimura, 1936; Bains and Kang, 1963; Ramaswamy *et al.*, 1977; Sandhu, 1990; Perin *et al*., 1999; Kavya and Manchali, 2019). In fruits having suture, its colour varied including cream and green. The variation in suture colour was also observed in intra-specific classification of melons (Stepansky *et al.*, 1999), wild and cultivated melons (Pitrat, 2013), melon landraces (Sudhakara, 2014; Mamatha, 2016), F$_2$ population of muskmelon (Kavya and Manchali, 2019) and inter-botanical groups of melon (Chaitra, 2019).

Fruit surface netting is one of the important traits for shelf-life analysis in melons. Netted melons have less storage life, that may be a result of the presence of fissured epidermal tissue (netted), which is an elaborated system of lenticels as they are more prone to lose moisture and also the netted rind fruit melons produce higher amounts of ethylene at the stage of ripening (Pratt, 1971). In the present study, fruit surface netting was found to be controlled by more than one gene in the cross Kashi Madhu x IC321371. Control of netting by two dominant genes over smoothness was reported in muskmelon (Ramaswamy *et al.,* 1977). Digenic control of netting was recorded in muskmelon (Kavya, 2017). Netting in melon was reported as monogenic and partially dominant over smoothness (Sandhu, 1990). Single dominant gene governing the development of net tissue regardless of the degree of netting was observed by Herman *et al.* (2008).

In the present study, when oblate fruited plants crossed with oval fruited one, oblate shape was obtained. fruit shape in melon was found to be incompletely dominant. Fruit shape was reported to be controlled by a single gene *O* (Oval shape), dominant to round (Wall, 1967). Spherical fruit shape is controlled by a single gene (*sp*) recessive to an obtuse fruit shape (Lumsden, 1914; Bains and Kang, 1963). Fruit shape in F$_2$ melon was found to be incompletely dominant (Kavya and Manchali, 2019).

In the present study, Orange flesh-coloured parents crossed with green, double coloured (orange-green) fruits were observed in F$_1$ and showed monogenic. Co-dominance in the cross Kashi Madhu x IC321371. Melon fruit flesh color reported to be controlled by two genes, green flesh (*gf*), recessive to orange flesh (Hughes, 1948; Bains and Kang, 1963; Sandhu, 1990) and white flesh (*wf*) (Iman *et al.*,1972; Chadha *et al.*, 1972). The development of flesh colour is an ethylene-independent trait. Flesh colour is an important trait from the consumer point of view. The expression of colour in the fruit flesh is conditioned by the particular carotenoid type and concentrations, which are influenced by genetic and environmental factors. Variation in fruit flesh colour was also noticed in landraces (Bokashi *et al.*, 1992; Stepansky *et al.*, 1999; Fergany *et al.*, 2011; Aragao *et al.*, 2013; Malik *et al.*, 2014) and wild and cultivated melons (Pitrat, 2013).

In cross Kashi Madhu x IC321371 all the generations have only firm pulp textured fruits. The flesh texture at fruit maturity can be mealy (with no consistency) as in *flexuosus* or *momordica* type and it can also be crispy, firm, juicy, dry or fibrous (Pitrat, 2016). The variation in the flesh firmness from firm to soft flesh were recorded in muskmelon cultivars (Khokhar *et al.*, 1988), wild and cultivated melons (Pitrat, 2013) and muskmelon landraces (Sudhakara, 2014; Mamatha, 2016).

In the present investigation, strength of attachment of fruit to peduncle at maturity stage was recorded as slippable and non- slippable in parents as well as their progenies in different generations. Some melon fruits when ripe develop an abscission layer at the attachment zone between the fruit and the stem, whereas, others remain attached to the stem even after they are ripe (Kirkbride, 1993). Fruit abscission at maturity was reported to be controlled by two independent loci (Takada *et al.*, 1975). In the present study, non-slippabale was dominant and digenic in the cross Kashi Madhu x IC321371. A single dominant gene (*Al-5*) was reported to control fruit abscission layer formation in the climacteric western shipper type (Zheng *et al.*, 2002). A wide variation for fruit shape at peduncle and blossom end was reported in other studies (Stepansky *et al.*, 1999; Pitrat, 2013; Sudhakara, 2014; Kavya, 2018; Chaitra, 2019).

Fruit taste was sensory evaluated for its sweetness. Fruit taste categorized as sweet, less sweet and sour in the present study. All the three crosses exhibited sweet and less sweet, whereas Kashi Madhu x IC321371 did not exhibit sour type melons. Different categories of fruit taste recorded in muskmelon (Kavya, 2018). High value of total sugars is desirable because of consumer preferences but the sugar content varies depending upon the different fruit parts in melon (Chrost and Schmitz, 1996; Yativ *et al.*, 2010) and also variation in sucrose levels accounts for the genetic differences in total sugar content and for the natural variability within a particular cultivar due to environmental differences (Stepansky *et al.*, 1999).

Based on the visual observation, seed colour was classified as white, cream and creamy white. Earlier, Pitrat (2013) studied seed colour variation in melons and noted that seed colour can be white or brown in both wild and cultivated melons. Creamish yellow and white coloured seeds were noticed in local melon types of Karnataka (Sudhakara, 2014) and in muskmelon (Kavya, 2018).

Presence or absence of fruit flavour was sensory evaluated. All the crosses exhibited variation for fruit flavor and intensity of fruit flavor. Variation for fruit flavour recorded in muskmelon cultivars (Khokhar *et al.*, 1988), wild and cultivated melons (Pitrat, 2013), melon landraces (Sudhakara, 2014), muskmelon (Kavya, 2018). Variation in fruit flavour is a result of concentration of complex mixtures of volatile compounds in the fruits (Jordan *et al.*, 2001; Shalit *et al.*, 2001).

Conclusion

The present investigation on the cross Kashi Madhu × IC321371 revealed significant morphological variation and diverse patterns of inheritance for fruit- and plant-related traits in melon. Traits such as stigma colour and ovary pubescence were polymorphic, while fruit rind colour, grooves, sutures, and netting exhibited non-Mendelian ratios, confirming the role of epistatic and duplicate gene actions. Fruit shape in longitudinal section and flesh colour followed a 1:2:1 segregation ratio, indicating monogenic inheritance with incomplete dominance. Traits such as strength of attachment of fruit to peduncle (slippable vs. non-slippable) and fruit sutures showed evidence of inhibitory epistasis, while fruit netting segregated according to complementary gene action. Overall, the study demonstrated that the inheritance of key fruit traits in melon is governed by a combination of monogenic, polygenic, and epistatic interactions. These findings provide valuable insights into the genetic architecture of melon and will serve as a useful resource for breeders aiming to develop cultivars with desirable fruit quality, enhanced shelf life, and consumer-preferred characteristics.

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