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BIOLOGY

Genetic control of quality melon traits

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ABSTRACT: This research studied the genetic control of the traits related to melon fruit quality. The F_1, F_2, BC_1, BC_2 generations from the OL x A-16 and OL x PV crossings were evaluated in two separate trials conducted in randomized blocks with three replications. The evaluated traits were: average fruit weight, shape index, pulp thickness, pulp firmness, soluble solids content and cracking rate. The analyses were accomplished through a classic study of generations involving mixed models. The parameters on heritability and number of loci controlling the traits were evaluated in a broad and narrow sense. The inheritance of the evaluated traits is complex, presenting one gene of greater effect and polygenes with additive and dominant effects.

Key words: *Cucumis melo* L., greater effect genes, inheritance, mixed models, polygenes.

Controle genético de caracteres de qualidade do melão

RESUMO: Objetivou-se com este trabalho estudar o controle genético de caracteres relacionados à qualidade do fruto do melão. Foram avaliadas as gerações F_1, F_2, RC_1, RC_2 dos cruzamentos OL x A-16 e OL x PV em dois ensaios separados conduzidos em blocos casualizados com três repetições. Os caracteres avaliados foram: peso médio do fruto, índice de formato, espessura da polpa, firmeza da polpa, sólidos solúveis e porcentagem de rachadura. As análises foram feitas por meio de estudo clássico de gerações envolvendo modelos mistos. Foram estimados os parâmetros de herdabilidades nos sentidos amplo e restrito e número de loci que controlam o caráter. A herança dos caracteres estudados é complexa com a presença de gene de efeito maior e poligenes com efeitos aditivos e de dominância.

Palavras-chave: *Cucumis melo* L., genes de efeito maior, herança, modelos mistos, poligenes.

INTRODUCTION

The Northeast region is the main producer and exporter of melons in Brazil. The main production is carried out in the states of Rio Grande do Norte and Ceará. Most of the produced melons are exported to Europe and the United Kingdom (MDIC, 2021). Consumers such as these are highly selective regarding fruit quality. Currently, plant breeding programs around the world have been making efforts to produce high yielding and quality cultivars.

Defining quality on melons is highly complex, mainly regarding the melon types. The major types of melon produced in the Northeast region are the Yellow type, the Santa Claus melon, the Cantaloupe, the Galia melon and the Charentais melon (FIGUEIRÊDO et al., 2017). Therefore, fruit quality is easier to evaluate from a market viewpoint, which regards a wide range of external and internal traits.

Aiming international commercialization, the main evaluated trait is the soluble solids content (LI et al., 2019). Other traits highly regarded in plant breeding programs are the average fruit weight, the shape index, the pulp thickness and the pulp firmness. Due to European culture, small fruits and fruits that are firmer are likely to be sent abroad due to a longer shelf life. Regarding fruit shape, the Yellow and the Santa Claus are desirable for their elliptical shape, while Honeydew, Galia and Cantaloupe are popular for their round shape (NUNES et al., 2015).

The breeding feasibility of a trait depends on, among other things, its genetic control. Knowledge

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of the inheritance of traits assists the researcher on plant breeding strategies, assuring proper selection by recognizing major genotypic values to be identified and selected. Thereby, the aim of the study is accomplished with less time spent, saving labor and resources. Inheritance studies are important due to the type of information obtained therein: (1) gene action, (2) estimates of the components of variance and (3) estimates of the heritabilities in broad and narrow senses and the calculation of the number of genes of the trait (ZALAPA et al., 2006).

Traditionally, in many crops, the studies of inheritance are achieved using the generation analysis approach, through the evaluation of the genitors, the filial generations F_1, F_2 and the backcrossing with both genitors (PIEPHO & MÖHRING, 2010). However, studies to date concerning the inheritance of relevant traits to melon crops are still scarce. Moreover, no reports regarding studies in semiarid conditions were reported. Therefore, it is relevant to obtain information on genetic control in melon crops because the melon breeding programs have intensified recently in Brazil.

Due to the importance of this research, the aim was to study the genetic control of traits related to fruit quality in melon crops.

MATERIALS AND METHODS

Genitors

The strains used as genitors were A-16, PV and OL, which are in the germplasm bank of the Universidade Federal Rural do Semi-Árido (UFERSA). The A-16 strain composes the botanical group *acidulus*, has flattened fruits, white mesocarp with high firmness and low soluble solids content (< 5ºBrix). The PV strain has no botanical group defined, its fruits are long, have green mesocarp of low firmness and low soluble solids content (< 7ºBrix). The OL strain composes the botanical group *cantaloupensis*, whose fruits are flattened, with orange mesocarp, with flavor, firm and of high soluble solids content (≥ 9ºBrix).

Experiments

The experiments were carried out in the Vegetable Garden of the Department of Plant Sciences of the UFERSA, Mossoró, RN, at 18 m of altitude and geographic coordinates 5°11' S and 37°20' W. The soil preparation was held by plowing and harrowing, followed by one row, with the soil amendment based on soil chemical analysis. A drip system was used for irrigation. The spacing used in this process was 2.0 m wide, with plants spaced 0.3 m in the row.

The genitors, filial generations F_1, F_2 and the backcrossing with each genitor were evaluated in a block design with three replications. Due to the genetic variability in each generation, the plots were composed of the following number of plants: 15 plants (genitors and F_1), 120 plants (generation F_2) and 60 plants (each backcrossing).

The evaluated traits were: Average fruit weight (AFW), which was obtained by determining the ratio of all fruits in the plot to the number of harvested fruits, in kg; Pulp thickness (PT), obtained by cutting the fruit in equal halves and measuring the pulp in mm; Shape index (SI): length/diameter ratio measured in the center of the fruit; Pulp firmness (PF): the fruit was cut longitudinally, then each half was measured with a penetrometer with an 8 mm tip to test resistance in the median region in each half of the fruit. Pulp firmness was measured in lbs transformed to Newton (N), multiplying the value by 4.4482; Soluble solids content (SS) was determined by digital refractometer, PR-100 Paletti model, with automatic temperature compensation, obtained by removing some drops of juice from one slice of each fruit cut longitudinally, and factoring the average of the measurements in ºBrix.

Statistical analyses

In order to estimate the genetic parameters and adjust to the additive-dominant model, the PIEPHO & MÖHRING (2010) mixed model approach was used. The SAS code, PROC MIXED Proceeding, was adapted from PIEPHO & MÖHRING (2010) for the analyses of generations. Thus, the mean components related to the additive [a] and dominance [d] effects, the additive and dominance variances, as well as heritability, were estimated. The average degree of dominance (ADD) and the minimal number of genes (η) related to the trait expression were also estimated, according to WRIGHT (1934). Mean components were estimated and tested by Wald's F test ($P < 0.05$).

Genetic models were tested for maximum probability in mixing normal density functions according to SILVA (2003). The distributions of each population were the following:

P_1:N(μ-[a]-A,σ^2); P_2:N(μ-[a]+A,σ^2); F_1:N(μ-[d]-D,σ^2),

$$F_2: \frac{1}{4}N\left(\mu + \frac{[d]}{2} - A, \sigma^2 + V_A + V_D\right) + \frac{1}{2}N\left(\mu + \frac{[d]}{2} + D, \sigma^2 + V_A + V_D\right) + \frac{1}{4}N\left(\mu + \frac{[d]}{2} + A, \sigma^2 + V_A + V_D\right);$$

$$BC_{11}: \frac{1}{2}N\left(\mu + \frac{[a]}{2} + \frac{[d]}{2} - A, \sigma^2 + \frac{V_A}{2} + V_D - S_{AD}\right) + \frac{1}{2}N\left(\mu - \frac{[a]}{2} + \frac{[d]}{2} + D, \sigma^2 + \frac{V_A}{2} + V_D - S_{AD}\right);$$

$$BC_{12}: \frac{1}{2}N\left(\mu + \frac{[a]}{2} + \frac{[d]}{2} + A, \sigma^2 + \frac{V_A}{2} + V_D + S_{AD}\right) + \frac{1}{2}N\left(\mu + \frac{[a]}{2} + \frac{[d]}{2} + D, \sigma^2 + \frac{V_A}{2} + V_D + S_{AD}\right).$$

where, μ: constant of reference; A: additive effect of major gene effect; D: dominance effect of the major gene effect; [a]: additive polygenic component; [d]: dominance polygenic component; V_A: additive variance; V_D: variance attributed to deviances of the dominance polygenic effects; S_{AD}: component of variation relative to the products of the additive polygenic effect by the dominance polygenic effects; σ^2: environmental variance.

In the construction of the genetic model, the model considered most complete was the gene showing a major effect, polygenes with additive and dominance effects, and the same environmental variances in all generations (Table 1). Independent genes were also admitted (as polygenes as major gene effect).

Because of similarities in the functions of each provided model, it was possible to compose the most relevant tests taking into consideration different hypothesis. The tests for probability were performed by the LR statistics: $2ln\frac{L(M_i)}{L(M_j)}$, where $L(M_i)$ and $L(M_j)$ are the functions of probability of *i* and *j* models; where *i* model must be hierarchical in relation to *j* model. The tests were calculated by the statistical software named Monogen v.0.1 (SILVA, 2003).

RESULTS AND DISCUSSION

Mean components

According to the approach for generation analysis proposed by PIEPHO & MÖHRING (2010), the block, the additive and the dominance effects were observed for all significant differences in traits from the two crossings (Table 2). In each situation, the additive effect explained the major part of the variation about the dominance effect. The missing adjustments were not significant in these situations, pointing out that the additive dominant model without epistasis was adequate in the block design.

In the study of inheritance with genetic models using maximum probability for all traits, one gene of major effect with additive and dominance effects was identified by testing the hypothesis of comparison of models 1 (Major gene with additive and dominance effects + polygenes with additive and dominance effects) and 5 (Polygenes with additive and dominance effects) (Table 3). The test between the models 1 and 7 (Major gene with additive and dominance effects) showed that the confrontation involving one major gene plus polygenes and one gene of major effect was significant, thus proving that the polygenes were controlling the traits.

Studies of the inheritance of traits are still scarce in this field. In relation to the average fruit weight, SHASHIKUMAR & PITCHAIMUTHU (2016) and POUYESH et al. (2017) observed additive and non-additive effects, finding that additive effects were more prominent. However, ZALAPA et al. (2006), when studying the inheritance of the average fruit weight from the crossing between the strain of growth habits (Fractal) USDA 846-1 and the cantaloupe cultivar Top Mark, observed the inheritance of average fruit weight is due to dominance and the epistasis effects. Differing results among studies are mainly related to the group of genitors used in the experiments. In addition, the environmental effects also influenced the obtained information. MONFORTE

Table 1 - Models of inheritance used by the software Monogen v. 0.1 (SILVA, 2003).

Model	Parameter
1: Major gene with additive and dominance effects + polygenes with additive and dominance effects	μ, A, D, [a], [d], V_A, V_D, S_{AD}, σ^2
2: Major gene with additive and dominance effects + polygenes with additive effects	μ, A, D, [a], V_A, σ^2
3: Major gene with additive effect + polygenes with additive and dominance effects	μ, A, [a], [d], V_A, V_D, S_{AD}, σ^2
4: Major gene with additive effect + polygenes with additive effect	μ, A, [a], V_A, σ^2
5: Polygenes with additive and dominance effects	μ, [a], [d], V_A, V_D, S_{AD}, σ^2
6: Polygenes with additive effect	μ, [a], V_A, σ^2
7: Major gene with additive and dominance effects	μ, A, D, σ^2
8: Major gene with additive effect	μ, A, σ^2
9: Environmental effect	μ, σ^2

μ: General mean; A: Additive effect of the major gene effect; D: Dominance effect of the major gene effect; [a]: Additive polygenic component; [d]: Dominance polygenic component; V_A: Additive variance; V_D: Variance attributed to the dominance deviances of the polygenic effects; S_{AD}: Component of the variation related to the products of the additive polygenic effects by the polygenic effects of dominance; σ^2: Environmental variance.

Table 2 - Test F (Wald) of the additive dominant model for average fruit weight (AFW), shape index (SI), pulp thickness (PT), pulp firmness (PF), and soluble solids content (SS) of melons.

	Traits				
	AFW (g)	SI	PT (cm)	PF (N)	SS (ºBrix)
Crossing OL x A-16					
SV	F (Wald)				
Block	9.32**	8.98**	8.52**	29.28**	12.92**
[a]	142.80**	42.21**	210.86**	166.62**	174.79**
[d]	62.77**	10.40**	48.82**	35.85**	49.76**
No adjust	1.77	2.29	1.48	0.59	0.53
Parameters	Estimation (Additive Dominant Model)				
m	604.12	1.23	3.47	3.77	6.50
a	300.59**	0.25**	1.89**	2.38**	2.60**
d	174.55**	0.10**	0.71**	1.29**	1.20**
Crossing OL x PV					
SV	F (Wald)				
Block	14.43**	17.42**	6.34**	3.62**	4.12**
[a]	28.75**	228.45**	10.34**	26.53**	16.03**
[d]	22.43**	27.32**	10.22**	16.96**	10.91**
No adjust	0.16	0.02	1.61	0.34	0.20
Parameters	Estimation (Additive Dominant Model)				
m	1280.99	1.35	4.40	2.42	7.90
a	359.72**	0.32**	1.01**	1.10**	1.70**
d	218.48**	0.21**	0.12*	0.37**	0.45*

SV: Sources of variation; **, *: Significative by test F of Wald at 1 and 5% probability, respectively, or significative by test t at 1 and 5% probability, respectively; AFW: Average Fruit Weight; SI: Shape Index of the fruit; PT: Pulp Thickness; PF: Pulp Firmness; SS: Soluble Solids content; [a]: Additive polygenic component; [d]: Dominance polygenic component; m: Mean; a: Additive effect; d: Dominance effect.

et al. (2004) & PARIS et al. (2008), using molecular markers, verified polygenic control of the average fruit weight. In melons, the average weight of the fruit is an important trait because the destination of the fruit depends on it. Generally, for melon types like Yellow, Cantaloupe, Galia and Honeydew, fruits between 1.5 and 2.0 kg are intended for the international market, while larger fruits are marketed domestically. For Santa Claus melons intended for Spain, larger fruits (> 3.0 kg) are preferred.

Concerning the shape index, no information about inheritance of predominant gene actions were found. Studies by PARIS et al. (2008) and BALOCH et al. (2016) indicated polygenes controlled this trait. In Yellow melons, an oval shape is preferred, and round for Cantaloupe, Galia and Honeydew. Fruits with a long elliptical shape are preferred for Santa Claus melons.

Regarding pulp thickness, BARROS et al. (2011) concluded that it is controlled by additive effects, but MOHAMMADI et al. (2014) concluded that it is controlled by additive and dominance effects. These differing conclusions are due to different genitors used in the studies. The segregating population of each crossing is a function of the background of the genitors, and the constituent alleles of each genitor. In addition, environmental variations are noticeable when dealing with traits controlled by several genes (ARAGÃO et al., 2015). Fruits with larger pulp thickness are highly desirable because it is the edible part of the fruit. Indirectly this also relates to the lower internal cavity and, consequently, provides a longer post-harvest shelf life.

Regarding pulp firmness, the results obtained by BARROS et al. (2011) and SHASHIKUMAR & PITCHAIMUTHU (2016) are in line with the information of this work. These authors detected significant additive and non-additive effects for pulp firmness, which is a highly regarded trait for melon exportation. Softer fruits are not recommended for the foreign market due to the long journey to European supermarkets, thus causing the fruit to become flaccid and undesirable to consumers.

Table 3 - Tests of genetic models using the maximum probability function for average fruit weight (AFW), shape index (SI), pulp thickness (PT), pulp firmness (PF), and soluble solids content (SS) of melons.

Test	DF	---------------------------	---------------- χ^2_c	----------------	---------------------------
		AFW (g)	SI	PT (cm)	PF (N)	SS (ºBrix)
---Crossing OL x A-16---						
1 vs. 2	3	23.08^{**}	7.46^{**}	44.16^{**}	7.29^{**}	6.46^{**}
1 vs. 3	1	15.54^{**}	1.76	6.98^{**}	0.34	5.76^{*}
1 vs. 4	4	97.93^{**}	13.96^{**}	61.51^{**}	33.74^{**}	43.24^{**}
1 vs. 5	5	16.39^{**}	12.00^{**}	7.49^{**}	17.22^{**}	43.24^{**}
1 vs. 6	5	97.93^{**}	13.96^{*}	61.51^{**}	33.74^{**}	43.28^{**}
1 vs. 7	5	110.64^{**}	16.53^{**}	119.46^{**}	37.47^{**}	45.55^{**}
1 vs. 8	6	112.65^{**}	17.31^{**}	73.85^{**}	45.75^{**}	46.97^{**}
1 vs. 9	7	197.39^{**}	52.54^{**}	125.46^{**}	120.04^{**}	124.05^{**}
---Crossing OL x PV---						
1 vs. 2	3	33.43^{**}	12.43^{**}	41.24^{**}	15.87^{**}	12.34^{**}
1 vs. 3	1	23.23^{**}	17.23^{**}	18.34^{**}	32.23^{**}	12.54^{**}
1 vs. 4	4	11.23^{**}	18.70^{**}	29.32^{**}	17.98^{**}	13.76^{**}
1 vs. 5	5	12.32^{**}	13.43^{**}	11.43^{**}	16.32^{**}	21.23^{**}
1 vs. 6	5	3.27	0.70	9.49	18.64^{**}	1.47
1 vs. 7	5	8.75	14.76^{**}	9.22^{*}	10.65^{**}	9.81^{**}
1 vs. 8	6	8.90	70.04^{**}	9.69	21.42^{**}	1.51
1 vs. 9	7	9.39	0.42	26.75^{**}	25.88^{**}	3.09

DF: Degrees of freedom; **, *: Significant effect by Chi-square test at 1 and 5% probability, respectively.

Soluble solids content is the main quality trait (LI et al., 2019). Fruits of better quality, i.e. the fruits of higher soluble solids content (> 10°Brix), are marketed abroad, while lower quality fruits are destined for the national market or even for processing into fruit pulp. Therefore, much research has been done on pulp firmness. BARROS et al. (2011) and SHASHIKUMAR & PITCHAIMUTHU (2016) observed additive and non-additive effects with a predominance of additive effects. However, MONFORTE et al. (2005) detected a single significant additive effect.

Variance components

When studying inheritance from variance components, it was reported that additive variances were superior to the variances of dominance for all traits studied in the two crossings (Table 4). The additive variance is due to the average effects of the alleles that are inherited by offspring. Therefore, the presence of high genetic variability in a segregating population is very relevant because the gains from selection are directly proportional to heritability. The dominance variance is due to deviations in the dominate genes and is mainly exploited in vegetative propagation species. The additive dominant variance was virtually null in all situations, except for the shape index and pulp firmness for the OL x A-16 crossing, as well as soluble solids content for the OL x PV crossing.

Heritability can be expressed in broad and narrow senses. Broad sense indicates how much of the phenotypic variance is due to genetic (additive and non-additive) factors, whereas narrow sense heritability indicates how much of the phenotypic variance is due to inheritable additive genetic factors. Regarding the estimations of broad and narrow sense heritability for average fruit weight, pulp thickness, pulp firmness and soluble solids contents, it was observed that the values obtained for the OL x A-16 crossing were higher than those of the OL x PV crossing, with the exception of the shape index (Table 4). In general, heritability ranges in the narrow sense for the two crossings can be considered intermediate (0.37 to 0.65), except for the shape index of the OL x A-16 crossing and the pulp thickness of the OL x PV crossing. Heritability in the broad sense was intermediate to high (0.43 to 0.87), with a very low estimate for pulp thickness of the OL x PV crossing. Low heritability values make the selection process hard, as there is a greater chance of selecting superior genotypes the closer the heritability estimate is to 100% (CRUZ et al., 2014).

Table 4 - Variance components of the additive dominant model of average fruit weight (AFW), shape index (SI), pulp thickness (PT), pulp firmness (PF), and soluble solids content (SS) of melons.

Variance component	---Estimations – Traits---				
	AFW (g)	SI	PT (cm)	PF (N)	SS (ºBrix)
---Crossing OL x A-16---					
σ^2_A	28007	0.008	1.808	5.864	4.695
σ^2_D	16474	0.006	0.765	2.706	1.575
σ^2_{AD}	0	0.003	0	0.181	0
σ^2_p	1718.88	0.001	0.547	0.105	0
σ^2_e	9023.29	0.019	0.006	0.855	0.973
h^2_n (%)	0.51	0.22	0.58	0.6	0.65
h^2_b (%)	0.81	0.46	0.82	0.9	0.87
ADD	1.08	1.22	0.92	0.96	0.82
η	24.46	14.29	5.74	6.31	5.2
---Crossing OL x PV---					
σ^2_A	94935	0.013	0.073	0.507	1.65
σ^2_D	49518	0.008	0.044	0.217	1.006
σ^2_{AD}	0	0	0	0	0.238
σ^2_p	3468.74	0	0.028	0.317	0.166
σ^2_e	78836	0.011	0.346	0.389	1.408
h^2_n (%)	0.42	0.41	0.15	0.42	0.37
h^2_b (%)	0.64	0.66	0.24	0.43	0.65
ADD	1.02	1.11	1.1	0.93	1.1
η	9.35	13.28	21.21	8.01	7.76

σ^2_A: Additive variance; σ^2_D: Dominance variance; σ^2_{AD}: Additive dominance variance; σ^2_p: Plot variance; σ^2_e: Error variance; h^2_n: Heritability in narrow sense; h^2_b: Heritability in broad sense. ADD: Average degree of dominance; η: Number of loci.

In this research, heritability in broad and narrow senses for average fruit weight, pulp thickness, pulp firmness and soluble solids content are in the same range as heritability estimated under conditions of the Mossoró-Assu Agricultural Complex (MELO et al., 2011; ARAGÃO et al., 2015; GUIMARÃES et al., 2016). There are also estimates from research performed abroad for some traits evaluated in this study. ZALAPA et al. (2006) obtained higher estimates in both broad and narrow senses, while EDUARDO et al. (2007) obtained lower values in the broad sense. With regard to fruit shape, EDUARDO et al. (2007) obtained estimates in the broad sense similar to the current work, PARIS et al. (2008) also obtained similar estimates concerning pulp firmness. Regarding soluble solids content, PARIS et al. (2008) observed similar values to the OL x PV crossing, but inferior values for the OL x A-16 crossing, while PERPIÑÁ et al. (2016) reported very low estimates.

It should be emphasized that comparisons of heritability among different works should be done with caution, since heritability is intrinsic to the population and the environment in which the population was evaluated, in addition to the method used to estimate it. Nevertheless, estimates of heritability should not be overlooked because they are obviously relevant to the object of the study, as well as for guidance of future surveys.

Degree of dominance and number of loci

The average degree of dominance (ADD), obtained from additive and dominance variances, indicates the type of average gene action in the various loci of a polygenic trait. An ADD value that equals zero indicates an absence of dominance (additivity), an ADD value that equals 1 indicates complete dominance, ADD values between 0 and 1 mean incomplete dominance and ADD values greater than 1 indicates overdominance (RAMALHO et al., 2012).

In the current research, overdominance (ADD > 1.0) was verified for the average fruit weight and the shape index in the two crossings, as well as for the pulp thickness and soluble solids content for the OL x PV crossing (Table 4). For pulp thickness, pulp firmness and soluble solids content for the OL x A-16 crossing and pulp firmness for the OL x PV crossing, the ADD value indicates partial dominance ($0 < ADD < 1.0$).

The estimates of the average degree of dominance indicates the presence of dominance or overdominance (Table 2). In effect, heterosis can be exploited for the production of simple hybrids for all the traits studied in this work. The use of simple hybrids in Rio Grande do Norte and Ceará began in the 1980s. Currently, almost all of the cultivars planted in these Brazilian states are simple hybrids (NUNES et al., 2011). The greatest advantages of simple hybrids are their high productivity (> 25 t ha^{-1}), higher quality (> 11°Brix) and overall uniformity of the product, which is one of the main requirements to marketing internationally.

The number of loci estimated for each trait varied among the crossings (Table 4). Regarding average fruit weight, the data was discrepant with estimates of approximately 25 loci for the OL x A-16 crossing and 10 loci for the OL x PV crossing. ZALAPA et al. (2006) obtained negative estimates for the number of loci of the average fruit weight, thus differing from the present study. However, the average fruit weight is indicated as polygenic (MONFORTE et al., 2004; EDUARDO et al., 2007; WANG et al., 2016; AMANULLAH et al., 2018). MONFORTE et al. (2004) identified six QTLs from the F_2 and double-haploid generation of the Santa Claus strain x the PI accession 161375 crossing. From isogenic strains derived from the same Santa Claus strain x the PI 161375 crossing, EDUARDO et al. (2007) identified eleven QTLs controlling the average fruit weight.

For the shape index, 12 and 14 loci were estimated. No estimates were reported in the literature for the traits average fruit weight and fruit shape. However, the authors agree that both traits have polygenic inheritance (MONFORTE et al., 2004; EDUARDO et al., 2007). Four QTLs were identified in the same positions in study of MONFORTE et al. (2004), thus indicating that the effects of these QTLs can be consistent and therefore useful in breeding programs. It should be emphasized that environmental influence has little effect on shape index, even under polygenic control (EDUARDO et al., 2007). In this sense, the results observed in this study agree in part with other literature findings that suggested that several loci control the inheritance of fruit weight and fruit shape.

Different values for pulp thickness were observed. A higher estimate was observed at the OL x PV crossing (~ 22 loci) regarding the OL x A-16 crossing (~ 5.74 loci). There are no reports of the number of loci controlling this trait. The results of the current study indicated the improvement of melon crops is relatively difficult due to its oligo/polygenic nature, and to environmental effects.

Regarding pulp firmness, 6 and 8 loci were estimated at the OL x A-16 and OL x PV crossings, respectively (Table 4). No estimates of the number of genes for this trait were reported. However, the work conducted by PARIS et al. (2008) identified eight QTLs related to pulp firmness, only three being consistent in the two evaluated environments (mp7.2, mp10.3 and mplg7.5).

Concerning soluble solids content, 6 and 8 loci were estimated, respectively, for the OL x A-16 and OL x PV crossings (Table 4). MELO et al. (2011) evaluated the F_2 generation and the backcrossing of the population generated by a Honeydew inodorus strain, with high soluble solids content and an *acidulus* strain of low soluble solids content, which obtained an estimate of 28 loci. MONFORTE et al. (2004) identified five QTLs from a Santa Claus strain x a Korean access (PI 161375) crossing. EDUARDO et al. (2007) identified 15 QTLs from isogenic strains at the same crossing.

Verifying the additive and dominance effects in the traits studied is important information for the breeder. Because the non-additive effect controls the evaluated trait, it is preferable to exploit the hybrid's generation for that trait. Currently, in the Brazilian semi-arid environment, the productive sector has cultivated simple hybrids (NUNES et al., 2011). According to producers, the greatest advantages of simple hybrids are their high productivity (> 25 t ha^{-1}), higher quality (> 11°Brix) and overall uniformity of the product, which is one of the main requirements to marketing internationally. Based on the results, the inheritance of average fruit weight, shape index, pulp thickness, pulp firmness and soluble solids content is complex, with the presence of one gene of greater effect and the presence of polygenes with additive and dominance effects. From a pragmatic point of view, it is recommended to use recurrent selection for the gradual accumulation of favorable alleles (BERNARDO, 2014).

CONCLUSION

The inheritance of traits fruit weight, shape index, pulp thickness, pulp firmness and soluble solids is complex, with the presence of a major gene and polygenes with additive and dominance effects.

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DECLARATION OF CONFLICT OF INTEREST

The authors declare no conflict of interest. The founding sponsors had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, and in the decision to publish the results.

AUTHORS' CONTRIBUTIONS

All authors contributed equally for the conception and writing of the manuscript. All authors critically revised the manuscript and approved of the final version.

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