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Inheritance of hydrogen potential (pH) and titratable acidity in the melon[1]

Herança do potencial hidrogeniônico (pH) e da acidez titulável em melão

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ABSTRACT - Acidity is one of the main determinants of the taste and quality of melon fruit, together with sugars and volatile compounds. The aim of this study was to investigate the inheritance of hydrogen potential (pH) and titratable acidity in melon fruit. A randomized block design with three replications was used to evaluate the F_1 and F_2 generations and backcrosses (RC_1 and RC_2) of the Védrantais melon (*Cucumis melo* subsp. *melo* var. *reticulatus*) with high pH and low titratable acidity, and of the AC-16 melon (*C. melo* subsp. *melo* var *acidulus*), with low pH and high titratable acidity. Inheritance of pH and titratable acidity in the melon is complex, and each involves a major gene with additive and dominance effects associated with polygenes with additive effects.

Key words: *Cucumis melo*. Quality. Genetic control. Polygenes. Mixed models.

RESUMO - A acidez é um dos principais determinantes do sabor e qualidade dos frutos do meloeiro juntamente com açúcares e compostos voláteis. O objetivo deste trabalho foi estudar a herança do potencial hidrogeniônico (pH) e da acidez titulável dos frutos do meloeiro. Foram avaliadas em um delineamento em blocos casualizados com três repetições as gerações F_1, F_2 e os retrocruzamentos (RC_1 e RC_2) a partir dos genitores Védrantais (*Cucumis melo* subsp. *melo* var. *reticulatus*), com alto pH e baixo teor acidez total titulável, e AC-16 (*C. melo* subsp. *melo* var *acidulus*), com baixo pH e elevado teor de acidez titulável. A herança do pH e da acidez titulável em melão são complexas e cada uma envolve um gene maior com efeitos aditivos e de dominância associado a poligenes com efeitos aditivos.

Palavras-chave: *Cucumis melo*. Qualidade. Controle genético. Poligenes. Modelos mistos.

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INTRODUCTION

The taste and quality of edible fruits are determined by a combination of sugars, organic acids and volatile compounds (COHEN *et al*., 2012). Citric acid is the principal organic acid in the pulp of commercial melon fruit, followed by malic acid (BURGER *et al*., 2003). Other organic acids are also found, such as tartaric, ascorbic and oxalic (BURGER *et al*., 2003; COHEN *et al*., 2014; FALAH *et al*., 2015). The fruit pulp of current cultivars have a low organic-acid content and pH values close to neutral (> 6.0) (AYRES *et al*., 2019; COHEN *et al*., 2014).

The melon is the most polymorphic species of the genus *Cucumis*. The species is subdivided into two subspecies (*melo* and *agrestis*) comprising different botanical groups (PITRAT *et al*., 2016). The *conomon*, *flexuosus*, *momordica*, *dudaim*, *chate* and *acidulus* botanical groups have genotypes with greater acidity in the fruit (LEIDA *et al*., 2015). The fruit of these groups is consumed while still immature before accumulating acids, similar to the cucumber. Fruit with high acidity accumulate hardly any sugar (PITRAT *et al*., 2016).

The genetic diversity for acidity and pH found in the germplasm allows for genetic improvement programs aiming at melon cultivars with more-acidic fruit, so as to improve the flavour of the pulp, which is determined by the ratio of soluble solids to acidity. In order to obtain recombinants with high levels of sugars and organic acids, Burger *et al*. (2003) crossed the non-sweet and high-acidity line 'Faqquos' (*C. melo* botanical group *flexuosus*) with a high sugar line of low-acidity. The authors found inheritances in the F_2 generation that were independent of the sugar or acid content. The A6 recombinant genotype was obtained, with high levels of sugars and acids, especially citric acid. The above study therefore showed that it is possible to obtain melon genotypes with a high sugar and organic-acid content, generating cultivars of unique quality regarding the sugar to acidity ratio.

The acidity trait of the melon was initially described as being controlled by a locus termed *So*, with complete dominance of the allele that conditions acidity (KUBICKI, 1962). Subsequent studies involving other contrasting parents confirmed the monogenic inheritance of that trait (DANIN-POLEG *et al*., 2002). In addition, some studies have identified molecular markers linked to acidity and/or pH in the melon (DANIN-POLEG *et al*., 2002; OBANDO *et al*., 2008; SINCLAIR *et al*., 2006). Cohen *et al*. (2014) identified a gene family whose main effect was on fruit acidity. These authors identified the *PH* gene in a natural mutation of the melon. In the same study, it was found that the duplication of four amino acids in the gene distinguishes primitive genotypes with acidic fruit from current melons with sweet fruit.

Despite the achievements of several studies and advancements in the understanding of molecular genetics, the vast majority of authors agree that further studies should be carried out (KUBICKI, 1962; DANIN-POLEG *et al*., 2002; OBANDO *et al*., 2008; SINCLAIR *et al*., 2006; COHEN *et al*., 2014) covering the germplasm of different botanical groups to clarify the genetic control related to acidity in the melon. In view of the above, the aim of the present work was to investigate the inheritance of hydrogen potential and titratable acidity in melon fruit under the conditions of the semi-arid region of Brazil.

MATERIAL AND METHODS

Characterisation of the site

The experiment was carried out at the Rafael Fernandes Experimental Farm in the district of Lagoinha, located 20 km from the city of Mossoró in the western mesoregion of the State of Rio Grande do Norte, at 5°03"37" S and 37°23"50" W, at an approximate altitude of 72 metres. During the experiment, the maximum recorded temperature was 29 ºC with a minimum of 21 ºC. The mean relative humidity was 62%.

The soil in the experimental area is classified as a sandy-loam Argisolic Red-Yellow Latosol (EMBRAPA, 2006). Single soil samples were collected at a depth of 0 to 0.20 m and analysed at the Soil and Water Analysis Laboratory of UFERS, with the following mean results: pH (H_2O) = 7.34; Ca = 1.65 cmol dm^{-3}; Mg = 0.13 cmol dm^{-3}; K = 108.7 mg dm^{-3}; Al = 0.00 cmol dm^{-3}; P = 10.6 mg dm^{-3}.

Post-harvest analysis of the fruit was carried out at the Post-harvest Laboratory of the Centre for Research in Plant Sciences of the Semi-Arid Region (CPVSA) at the Federal Rural University of the Semi-arid Region (UFERSA).

Germplasm

The Védrantais line (low acid content and high pH) and AC-16 line (high acid content and low pH) were used as contrasting parents. Védrantais is a French cultivar with round Charentais-type fruit with orange-coloured mesocarp, belonging to the botanical group *cantaloupensis*, developed by the Vilmorin Seed Company. The AC-16 line belongs to the botanical group *acidulus*, and has a white mesocarp with a yellow exocarp. Both parents are andromonic and were crossed to obtain the F_1 generation, which was self-fertilized to obtain the F_2 generation and crossed with each parent to originate the RC_1 and RC_2 backcross generations respectively.

Conducting the experiment

The field experiment was conducted from 30 May to 4 July 2018. Based on the soil analysis, a 6-24-12 commercial formulation of 48.90 kg ha^{-1} N, 195 kg ha^{-1} P_2O_5 and 98.5 kg ha^{-1} K_2O was applied. The irrigation system consisted of hoses with self-compensating drippers spaced 0.30 m apart, with a mean flow of 1.5 L h^{-1}. The ridges were then covered with black plastic film.

Irrigation was carried out daily, with the water quantity determined based on the crop evapotranspiration. Throughout the crop cycle, a total depth of 387 mm was used. The cover fertiliser was applied two days after transplanting, in the following doses: 93.82 kg ha^{-1} N, 81.74 kg ha^{-1} P_2O_5 and 162.88 kg ha^{-1} K_2O, corresponding to 6.76 kg N, 5.89 kg P and 11.73 kg K, distributed daily via fertigation, with the doses varying according to the phenological stage of the crop. The sources used as fertiliser were urea, mono-ammonium phosphate (MAP) and potassium chloride.

Sowing was carried out in expanded polystyrene trays of 200 cells filled with Polifértil® commercial substrate. The seedlings were transplanted after the first expanded true leaf at 14 days. Phytosanitary control and other crop treatments were carried out based on the technical recommendations adopted in the region for the melon (NUNES *et al*., 2016). The fruit was harvested between 58 to 64 days after transplanting (DAT), depending on maturation.

The two parents (AC-16 and Védrantais), F_1, F_2, and the backcrosses (RC_1 and RC_2) were evaluated in an experimental design of randomised blocks with three replications. The plot size for each generation was defined based on their genetic composition: 5 plants for the parents and F_1, 60 plants for F_2, and 14 for each backcross.

Laboratory analysis

Hydrogen potential and titratable acidity were analysed in one fruit per plant for each generation under evaluation. The sample size for each generation was as follows: 15 for the parents (AC-16 and Védrantais) and F_1, 172 for F_2, and 42 for the backcrosses.

The pH was determined with the aid of a digital potentiometer (Model mPA-210, Tecnal®, Brazil), with automatic temperature adjustment, previously standardised with pH 4.0 and pH 7.0 buffer solution. Aliquots of 10 g of the pure homogenised pulp were used, diluted in 50 ml of deionised water. The electrode was inserted into the sample, and once the results had stabilised, the data were expressed as true pH values. The titratable acidity (TA) was determined in 10 g of the processed pulp titrated with NaOH 0.1 N, with phenolphthalein (1%) being used as an indicator of the change in the solution from acidic to basic (AOAC, 2002).

Statistical analysis

Generation analysis using Mixed Models

To estimate genetic parameters and adjust the additive-dominant model, the Mixed Model methodology was used (PIEPHO; MÖHRING, 2010). The test of the additive-dominant model was implemented by adding the lack of fit effect (λi) to the model, as per the following expression: $\mu_i = m + [a]x_{i1} + [d]x_{i2} + \lambda_i$ (KEARSEY; POONI, 1996), where: μ_i - value of the i-th generation under the additive-dominant model, with i=1, ..., g; m - intercept; [a] - additive effect; [d] - dominance effect; x_{i1}, x_{i2} - respective coefficients of the additive and dominance effect; λ_i - lack of fit effect.

The variance-covariance structure was adjusted by defining the effect of the Generation x Plant interaction and considering individual plants as independent units. To do this, the variance structure TYPE = LIN(3) was used in the PROC MIXED procedure (PIEPHO; MÖHRING, 2010). Heritability in the broad and narrow sense, number of genes, and average degree of dominance were also estimated (KEARSEY; POONI, 1996).

Liklihood testing of genetic models

The genetic models were tested using maximum likelihood in a mixture of normal density functions. The distributions for each generation were as follows:

$$p_1 : N(\mu - [\alpha] - A, \sigma^2), p_2 : N(\mu - [\alpha] + A, \sigma^2), F_1 : N(\mu - [d] - D, \sigma^2),$$

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

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

and,

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

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

In constructing the genetic model, the most general model was considered as having a gene of major effect plus polygenes with additive and dominance effects, and equal environmental variances in each generation.

Table 1 - Inheritance models and their respective parameters used by the Monogen v 0.1 software

Model	Parameters
1	Major gene with additive and dominance effects + polygenes with additive and dominance effects (∫, A, D, [a], [d], V_A, VD, S_{AD}, ∫²)
2	Major gene with additive and dominance effects + polygenes with an additive effect (∫, A, D, [a], V_A, ∫²)
3	Major gene with an additive effect + polygenes with additive and dominance effects (∫, A, [a], [d], V_A, V_D, S_{AD}, ∫²)
4	Major gene with an additive effect + polygenes with an additive effect (∫, A, [a], V_A, ∫²)
5	Polygenes with additive and dominance effects (∫, [a], [d], V_A, V_D, S_{AD}, ∫²)
6	Poligenes with an additive effect (∫, [a], V_A, ∫2)
7	Major gene with additive and dominance effects (∫, A, D, ∫²)
8	Major gene with an additive effect (∫, A, ∫²)
9	Environmental effect only (∫, ∫²)

A - additive effect of a gene of major effect; D - dominance effect of the gene of major effect; [a] - additive polygenic component; [d] - dominance polygenic component; VA - additive variance; VD - variance attributed to the dominance deviations of the polygenic effects; SAD - variation component relative to the products of the additive polygenic effects and the dominance polygenic effects; ∫² - environmental variance

Independent genes were also allowed (both polygenes and major effect) (Table 1). The tests of interest were composed considering different hypotheses. The tests were carried out using the Monogen v 0.1 software (SILVA, 2003), as specified by Batista *et al*. (2017).

RESULT AND DISCUSSION

In the present study, higher pH and lower titratable acidity was seen in fruit pulp from the parent Védrantais compared to the parent AC-16, respectively (Table 2), confirming the heterogeneity between the parents and the correct choice for obtaining the segregating generations. This was expected, since the Védrantais line, belonging to the subspecies *melo* and botanical group *cantaloupensis*, has sweet fruit (ºBrix > 10), less titratable acidity and a pH greater than 6.0, while the AC-16 line, belonging to subspecies *agrestis* and botanical group *acidulus*, has acidic fruit (pH < 3.0) with lower values for soluble solids (ºBrix < 10).

The components related to the additive effect of the genes [a] and the effect of the dominance deviation [d] of the additive-dominant model were significant by the Wald F-test ($p < 0.05$) for both pH and titratable acidity (Table 2), confirming the presence of additive and dominance effects in the inheritance of both traits. The estimate of the dominance component [d] was negative for both traits, indicating the presence of dominance as increasing the acidity of the fruit and, as a result, reducing the pH.

It should be noted that the negative sign of the dominance effect in both traits (Table 2), despite the negative association between the two traits under study (Figure 1), is explained by the use of the parent with the highest average as the first parent in the statistical analysis of inheritance carried out in the present study. Another result that reinforces the presence of dominance for acidity in melon fruit is the asymmetric frequency distribution to the left in the F_2 generation for both variables (Figure 1), and the average degrees of dominance close to 1.0, especially for titratable acidity (Table 2).

In a pioneering study, Kubicki (1962) identified that the inheritance of acidity in the melon is controlled by one gene, termed *So*, with the allele that gives the fruit an acid flavour being dominant. Later studies confirmed monogenic inheritance and complete dominance as increasing acidity in melon fruit (BURGER *et al*., 2003; DANIN-POLEG *et al*., 2002; HAREL-BEJA *et al*., 2010). The *So* gene was located on chromosome 8 (SHERMAN *et al*., 2013). This gene was later termed the *PH* gene (COHEN *et al*., 2014).

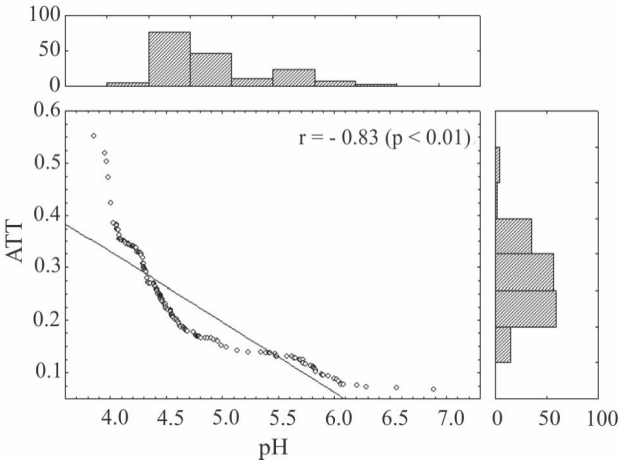
The estimate of the linear correlation coefficient between titratable acidity and pH was negative, high and significant ($r = -0.83$; $p < 0.01$). Quantification of the association between the two traits is relevant from a practical point of view, since measuring pH is easier, less onerous and immediate, the opposite to quantifying titratable acidity. In fact, for breeders, who evaluate many genotypes at the same time, and often in various experiments, it is more advisable to select genotypes for pH. Lee and Kim (2006) found negative correlations between pH and titratable acidity in melon fruit. Gur *et al*. (2017), argue that the genetic variability for acidity in the melon is unique, given the great difference between two genotypes with close pH values, which is reflected in differences in $[^+H]$ of the order of 10^2, for genotypes with acidic and non-acidic fruit. Lee and Kim (2006) found

Table 2 - Estimates of mean value and variance components, heritability, average degree of dominance and number of genes, obtained for titratable acidity (g/100 mL juice) and hydrogen potential (pH) evaluated in a study of generations from a cross between Védrantais and A-16 parents

Generation	Titratable acidity		pH	
	Mean	Variance	Mean	Variance
P_1 (Védrantais)	0.130	0.007	5.679	0.172
P_2 (A-16)	0.379	0.004	1.899	0.066
F_1	0.376	0.007	2.522	0.399
F_2	0.233	0.015	2.464	0.493
RC_1	0.236	0.011	4.907	0.370
RC_2	0.306	0.010	3.026	0.423
	---------- Mean-value components ----------			
SV	Estimate	F (Wald)	Estimate	F (Wald)
Block	-	1.23^{ns}	-	1.69^{ns}
[a]	0.119	6.67**	1.90	5.82**
[d]	-0.046	4.43*	-1.37	3.26*
	---------- Variance components ----------			
σ^2_A	0.0081		0.1935	
σ^2_D	0.0034		0.0411	
σ^2_{AD}	0.0000		0.0001	
σ^2_p	0.0003		0.0123	
σ^2_e	0.0098		0.2588	
h^2_r (%)	38.02		39.21	
h^2_a (%)	53.99		47.54	
ADD	0.92		0.65	
|	6.65		14.84	

**,*: Significant by F-test (Wald) at ($p < 0.01$) and ($p < 0.05$) respectively (PIEPHO; MÖHRING, 2010). [a] - Additive effect; [d] - Dominance effect; 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_r - Narrow-sense heritability; h^2_a - Broad-sense heritability. ADD – Average degree of dominance; e, | - number of genes

Figure 1 - Joint dispersion and frequency distribution of titratable acidity (TA) (g/100 mL juice) and hydrogen potential (pH) in the F_2 generation, resulting from the cross between the Védrantais and AC-16 parents



that the limit for pH value between plants with acidic and non-acidic fruit was approximately pH = 5.7. These authors also recommended pH as an indirect measure of acidity in melon fruit, as they considered it reliable.

According to the variance components, it was found that additive variance was superior to dominance variance in the two traits under study (Table 2). Genetic variance, in the absence of epistasis, consists of both additive and dominance variance. In sexual reproduction, additive variance is the most important as it is passed on to the filial generation, and is therefore determinant in estimating heritability in the narrow sense (NDUKAUBA *et al*., 2015; ENE *et al*., 2016). Heritability, whether in the narrow or broad sense, can take a value between 0.0 and 1.0 (100%) (SILVA *et al*., 2018); the closer to one, the greater the confidence that the phenotypic values represent the genetic values, and the lower the environmental effect. In this study, the estimates of heritability in the

narrow sense can be considered moderate ($0.2 < h^2_r < 0.4$) (BASTIAANSE *et al*., 2019), indicating a significant effect from the environment. Heritability estimates in the melon are rare. Obando *et al*. (2008) obtained heritability values of 12% and 33%, and Zhang *et al*. (2010), of 26%, for acidity, corroborating the results of the present work, and confirming strong environmental action on the two traits.

The estimates of broad heritability were greater than those in the narrow sense, as their determination includes all the genetic variance; however, the values were not significant. Furthermore, the estimates of the number of loci, based on the ratio between the additive variance and the dominance variance (Table 2), underline the fact that both variables are quantitative in nature, i.e. they are controlled by several genes of small effect and are greatly affected by the environment (ENE *et al*., 2016).

The methodology adopted by Kubicki (1962) and Danin-Poleg *et al*. (2002), was useful, but can be considered limited, since the authors treated the pH trait as qualitative when using a cut-off point to classify individuals into acidic and non-acidic. However, the variables investigated in the present work are quantitative and continuous, and should therefore be studied using statistical techniques that allow more genotypic and phenotypic information to be gained. In addition to the classic methodology for studying generations suggested by Kearsey and Pooni (1996), new models that detect the presence of one or more genes of major effect and polygenes have been developed in studies of the genetic control of quantitative traits (BATISTA *et al*., 2017; WEI *et al*., 2020; ZHANG *et al*., 2010).

In the study of inheritance using maximum likelihood, the comparison between the complete model (Model 1 - Major gene with additive and dominance effects + polygenes with additive and dominance effects) and Model 2 (Major gene with additive and dominance effects + polygenes with additive effects) was significant for both traits under study (Table 3), showing that the complete model should be adopted for verifying the presence of the effect of the major gene and of the polygenes. The comparison of Model 1 with Model 5 (Polygenes with additive and dominance effects) was also significant ($p < 0.05$) by the chi-squared test, showing the presence of a major gene with additive and dominance effects in the genetic control of the two traits (Table 3). Also, in order to detect the involvement of polygenes, a comparison was made between Models 1 and 7 (Major gene with additive and dominance effects), which was significant for both traits, indicating the presence of polygenes with both additive and dominance effects (Table 3).

Zhang *et al*. (2010), saw a similar result to that found in the present work when studying acidity in the melon. These authors concluded that two genes of major effect and polygenes are involved in the inheritance of this trait. In addition, the effect of polygenes is greater than that of major genes. Lee and Kim (2006) saw complex inheritance for total acidity and pH, with dominance for increasing acidity and the presence of polygenes.

The results generated by the two statistical methods used in this work provide information that is complementary and consistent with the inheritance of pH and titratable acidity. In both analyses it could be seen that the inheritance is complex, and that several loci are involved. It should be noted that the number of loci in this work is underestimated due to the premisses required by the method used and the number of non-segregating loci in the parents for each trait (RAMALHO *et al*., 2012). It is therefore reasonable to consider that more genes are involved in the genetic control of both traits. This would confirm several reports found in the literature

Table 3 - Hypothesis tests of hierarchical genetic models obtained in the study of the inheritance of hydrogen potential (pH) and titratable acidity (g/100 mL juice) in the pulp of melon fruit

Models under test	pH		Titratable acidity	
	df	χ^2_c	df	χ^2_c
1 vs 2	3	8.97*	3	8.37*
1 vs 3	1	7.57*	1	60.91**
1 vs 4	4	17.68**	4	116.64**
1 vs 5	2	7.57*	2	60.39**
1 vs 6	5	17.22**	5	116.63**
1 vs 7	5	21.58**	5	14.31*
1 vs 8	6	20.45**	6	161.64*
1 vs 9	7	21.58**	7	279.69**

Continuation table 3

A	-31.42	122.63
D	-22.80	-99.32
[a]	-3.55	-335.32
[d]	52.72	-32.75
V_A	195.36	1772.72
V_D	70.84	1377.44
S_{AD}	184.12	-1134.02
$\int^2$	766.50	2359.60

**, *: significant at 1 and 5% probability by Chi-square test. A - additive effect of a gene of major effect; D - dominance effect of the gene of major effect; [a] - additive polygenic component; [d] - dominance polygenic component; VA - additive variance; VD - variance attributed to the dominance deviations of the polygenic effects; SAD - variation component relative to the products of the additive polygenic effects and the dominance polygenic effects; $\int^2$ - environmental variance

concerning the complexity of acidity in melon fruit (BURGER *et al*., 2003; COHEN *et al*., 2012; OBANDO *et al*., 2008; SINCLAIR *et al*., 2006; ZHANG *et al*., 2016).

From a practical point of view, it should be noted that the presence of a gene of major effect with dominance facilitates the selection of individuals of greater acidity. Nevertheless, considering the presence of polygenes, one possible strategy is recurrent selection to continuously increase the frequency of favourable alleles until reaching a satisfactory level of acidity (or pH). This strategy was also suggested by Zhang *et al.* (2010), to increase acidity in the pulp of melon fruit. It should also be noted that efforts have been made to obtain melon cultivars with more acidic and/or sweet fruit, especially by research groups in Israel (BURGER *et al*., 2003; COHEN *et al*., 2014; GUR *et al*., 2017) and Asia (ZHANG *et al*., 2010; ZHANG *et al*., 2016; ZHU *et al*., 2013; LEE; KIM, 2006). With greater demand from the consumer market, and a tendency towards diversifying the types of melon fruit, the development of more-acidic melon cultivars, maintaining the current levels of sugars, is promising, as it would result in fruit with more-flavourful pulp, which is determined by the ratio of soluble solids to titratable acidity.

CONCLUSION

The inheritance of hydrogen potential and titratable acidity in the pulp of melon fruit is complex, and involves a major gene with additive and dominance effects associated with polygenes with additive and dominance effects.

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