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Genetic dissimilarity, selection index and correlation estimation in a melon germplasm

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ABSTRACT

The success of breeding programs depends on genetic variability. Individuals selected based on a few traits may be a limitation. One alternative is the use of nonparametric indices. However, there is no information on the use of selection indices in melon germplasms. The present study aimed to estimate genetic dissimilarity in a melon germplasm and select potential parent plants for future breeding programs. The genetic material consisted of 37 melon accessions. The traits assessed were fruit diameter and length, diameter and length of the fruit cavity and total soluble solids. Genetic dissimilarity was assessed by multivariate analyses (UPGMA and Tocher). Selection gain estimates were analyzed by comparing the classic Smith-Hazel and sum of ranks indices. Genetic diversity was observed between accessions. The variable that contributed most to genetic dissimilarity was fruit cavity length. Simultaneous selection for the traits assessed based on the sum of ranks index is better suited to melon germplasm assessment. The best accessions for the five variables simultaneously were UFU07, UFU23, UFU09, UFU21, UFU28 and UFU30.

Keywords: *Cucumis melo*, plant breeding, multivariate analysis, nonparametric indices, selection gain.

RESUMO

Estimativas de dissimilaridade genética, índices de seleção e correlações em germoplasma de meloeiro

O sucesso dos programas de melhoramento depende da variabilidade genética. Indivíduos selecionados com base em poucas características pode ser uma limitação. Uma alternativa é o uso de índices não paramétricos. No entanto, não há informações sobre uso de índices de seleção em germoplasmas de melão. Nesse estudo objetivou-se estimar a dissimilaridade genética em um germoplasma de melão e selecionar potenciais genitores para fomentar futuros programas de melhoramento genético. O material genético consistiu de 37 acessos de melão sendo avaliado o diâmetro e comprimento do fruto, diâmetro e comprimento da cavidade do fruto e sólidos solúveis totais. A dissimilaridade genética foi avaliada por análises multivariadas (UPGMA e Tocher). Para as estimativas de ganho de seleção comparou-se o índice clássico e o da soma de *ranks*. Foi observada diversidade genética entre os acessos. A variável de maior contribuição foi o comprimento da cavidade do fruto. A seleção simultânea para os caracteres com base no índice da soma de *ranks* foi mais adequada para avaliação do germoplasma de melão. Os melhores acessos para as cinco variáveis simultaneamente foram UFU07, UFU23, UFU09, UFU21, UFU28 e UFU30.

Palavras-chave: *Cucumis melo*, melhoramento genético, análise multivariada, índices não paramétricos, ganho de seleção.

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The melon (*Cucumis melo*) is one of the main fruits in Brazil (Charlo *et al.*, 2011). In 2018, the cultivated area was approximately 23,000 hectares, with production of 581,000 tons (FAO, 2018). The species *C. melo inodorus* and *C. melo cantaloupensis* are the most produced, especially the yellow, orange flesh and frog skin melons, which together account for 84.0% of melon

exports (Nunes *et al.*, 2011).

The National Cultivar Registry (RNC) lists more than 720 cultivars; however, most of those available to producers are imported (RNC, 2020), making it important to develop new cultivars under the tropical conditions of Brazil. The success of breeding programs depends on genetic variability, which is maximized by interbreeding

contrasting genotypes, associated with the selection of morphological and physiological traits of interest. Research on genetic diversity traits provides knowledge about the best crosses for these traits (Costa *et al.*, 2018).

Several multivariate techniques can be applied to quantify genetic dissimilarity, including principal component analysis (PCA), canonic

variables, hierarchical clustering and optimization methods. The method is chosen depending on its applicability, the accuracy desired and data collection technique. Selecting individuals based on one or a few traits of interest may be a limitation in breeding programs because finding genotypes with favorable alleles for all the characters is extremely difficult. In addition, selection for a certain trait may have positive or negative consequences on the others (Cruz *et al.*, 2014). One alternative to overcome this limitation is the use of nonparametric indices.

Nonparametric indices enable simultaneous trait selection. Thus, using selection indices may increase the efficacy of breeding programs, allowing a combination of the largest possible number of traits of interest to farmers and consumers. The choice of the most adequate index depends on the crop and desired traits (Smiderle *et al.*, 2019); however, there is no information on the use of selection indices in melon germplasms.

Correlation estimates can be used to obtain faster genetic gains. This technique allows the indirect selection of a main trait, characterized by low heritability and/or difficult assessment (Cruz *et al.*, 2014), which contributes to determining which traits should be selected (Olawuyi *et al.*, 2014). Therefore, the aim of this study was to estimate genetic dissimilarity in a melon germplasm and select potential parent plants for future breeding programs.

MATERIAL AND METHODS

The experiment was conducted at the Experimental Station of Vegetables, Monte Carmelo-MG, Brazil (18°42'43"S, 47°29'55"W, altitude 873 m), in clay soil classified as a red latosol. Soil samples were collected at a depth between 0 and 20 cm and analyzed at the Soil Fertility Laboratory. Physicochemical analysis exhibited clay texture (>50%), pH in CaCl₂ = 4.9, OM = 3.9 dag kg⁻¹, P (rem) = 79.1 mg dm⁻³, K = 0.29 cmolc dm⁻³, Ca = 3.3 cmolc dm⁻³, Mg = 1.3 cmolc dm⁻³, H + Al = 4.9 cmolc dm⁻³, SB = 4.90

cmolc dm⁻³, CEC = 9.80 cmolc dm⁻³, BS% = 50. The soil was fertilized according to recommendations for the crop (Filgueira, 2013).

The germplasm consists of 37 yellow melon accessions belonging to generation F4, from the germplasm bank of the melon breeding program and were obtained from four successive self-fertilizations of open market cultivars. Planting occurred in polystyrene trays (128 cells) on August 18, 2019 using coconut fiber-based commercial substrate. The seedlings were transplanted to the field 20 days after planting, using 1.0 m spacing between rows and 0.6 m between plants.

Throughout the experiment, crop traits, pest and disease control and weed management were conducted according to melon crop recommendations (Filgueira, 2013). A localized irrigation system was used to meet the water requirements, consisting of rubber hoses installed along the rows of plants with drippers spaced 0.6 m apart, and two days between irrigations.

The fruits obtained commercially were cut and then submitted to agronomic analyses to determine the following traits: fruit diameter (FD), fruit length (FL), cavity diameter (CD) and cavity length (CL). These measurements were taken with a 30-cm ruler. Total soluble solid (TSS) content was quantified using a portable digital refractometer (Atago PAL-1 3810).

A randomized block design (RBD) was used, with 37 treatments and two repetitions. Each plot contained 20 plants. The data were submitted to Analysis of Variance using the F-test ($p < 0.05$) and the measures compared by the Scott-Knott test ($p < 0.05$). Next, multivariate analysis of genetic dissimilarity was carried out using the Mahalanobis distance. Dissimilarity was represented by the unweighted pair-group method with arithmetic mean (UPGMA) dendrogram and Tocher's optimization procedure. The relative contribution of the quantitative traits was calculated according to criterion of Singh (1981).

For selection gains estimation, six accessions were chosen using direct and

indirect selection methodologies (Cruz *et al.*, 2014), namely the classic index proposed by Smith (1936) and Hazel (1943) (SH) and sum of ranks index proposed by Mulamba & Mock (1978) (MM). The selection criteria used were to reduce CL and CD, and increase FL, FD and TSS. The respective coefficients of genetic variation for each trait were adopted as economic weights. Genes software was used for data analysis (Cruz, 2016). The correlations were obtained using the "qgraph" package (Epskamp *et al.*, 2012), processed in R software version 3.6.3 (R Core Team, 2020).

RESULTS AND DISCUSSION

The highest variance values were observed for fruit length (7.60), total soluble solids (4.98), fruit diameter (4.55) and fruit cavity length (4.55), indicating high genetic diversity for these traits among the accessions under study. Fruit diameters varied between 8.00 and 17.70 cm, with an average of 12.95 cm. Aroucha *et al.* (2018) evaluated the influence of plant biostimulant application on the quality and shelf-life of yellow melon cultivars 'Iracema' and 'Goldex' and obtained fruit diameters of 14.08 and 14.46 cm, respectively.

The UFU18 accession exhibited the longest fruit (21.3 cm), with an average length of 16.05 cm. Chikh-Rouhou *et al.* (2019) characterized melon genotypes and observed average values similar to those of the present study, with fruit length ranging between 12.46 and 21.01 cm.

For cavity length and diameter, UFU09 and UFU14 obtained the highest averages, with 14.9 and 9.1 cm, respectively. By contrast, lower average values were found in genotypes UFU18 (6.0 cm) and UFU32 (2.0 cm). According to Dalastra *et al.* (2016), the smaller the cavity diameter, the greater the fruit resistance during handling and transport. Moreover, fruits with a smaller cavity are more visually pleasing and better accepted by consumers. In their studies, the authors assessed melon production and quality,

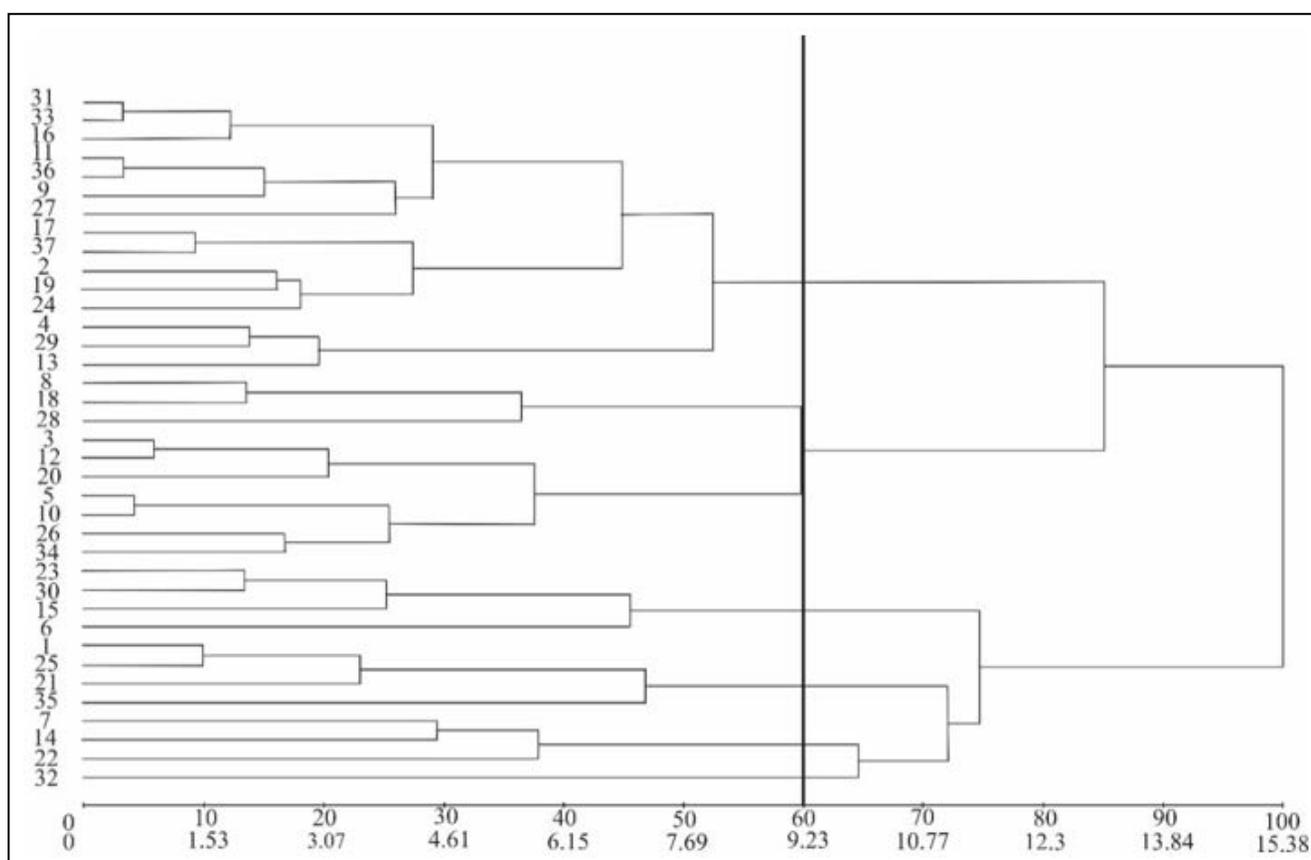


Figure 1. UPGMA genetic divergence dendrogram between 37 melon genotypes. Numbers indicate the UFU genotypes. Monte Carmelo, UFU, 2020.

Table 1. Selection gain (%SG) estimation for five variables in 37 melon accessions obtained by the classic Smith-Hazel index (SH) and Mulamba and Mock’s (MM) sum of ranks index with the respective indication of the six superior genotypes for each selection index. Monte Carmelo, UFU, 2020.

Variables	SH	MM
FD	82.58	38.72
FL	41.38	50.05
CD	-11.49	-21.47
CL	30.94	-28.62
TSS	19.75	40.97
%SG Total	163.16	79.65
Selected Genotypes	UFU07 UFU28 UFU21 UFU12 UFU24 UFU10	UFU07 UFU23 UFU09 UFU21 UFU28 UFU30

FD: fruit diameter (cm); FL: fruit length (cm); CD: cavity diameter (cm); CL: cavity length (cm) and TSS: total soluble solids (°Brix).

varying the number of fruits per plant, and obtained an average cavity length and diameter of 8.25 and 4.27 cm, respectively, corroborating the values recorded in the present study.

In regard to total soluble solids, an important trait for commercial melons, values varied between 2.5 (UFU30) and 12.3°Brix (UFU03). The TSS content is used as an acceptance criterion in countries that commercialize fruit. Fruits with TSS between 12 and 15°Brix are considered of excellent quality, approximately 9°Brix acceptable and below this value, not suitable for foreign markets (Monge-Pérez, 2016). Macedo *et al.* (2017) evaluated the effect of strobilurins and boscalid on the physical-chemical quality of melons and found TSS values between 8.7 and 10.7°Brix.

In addition to comparisons of individual performance, separating the genotypes into groups using dissimilarity measures helps breeders select parent plants in breeding programs (Araujo *et al.*, 2016). Genetic

dissimilarity measures estimated by the Mahalanobis distance (D_{ii}^2) ranged from 0.49 (UFU31 and UFU33) to 41.08 (UFU21 and UFU28) (data not shown), demonstrating the genetic diversity of the accessions under study.

The UPGMA dendrogram (Figure 1) with a 60% cutoff point, established at the point of sudden change in the dendrogram branches (Cruz *et al.*, 2014), resulted in the formation of six clusters. The first group consisted of fifteen accessions, accounting for 40.54% of the total, followed by group II, with ten (27.03%), groups III and IV with four each (21.62%), group V with three (8.11%) and group VI with the genotype UFU32 (2.70%). Thus, the use of accession UFU32 as one of the parent plants is viable, due to its divergence from the others.

The study of genetic diversity using clustering techniques such as UPGMA can be applied to different crops. In a study carried out by Maciel *et al.* (2018), in cherry tomato genotypes, 42 accessions were evaluated resulting

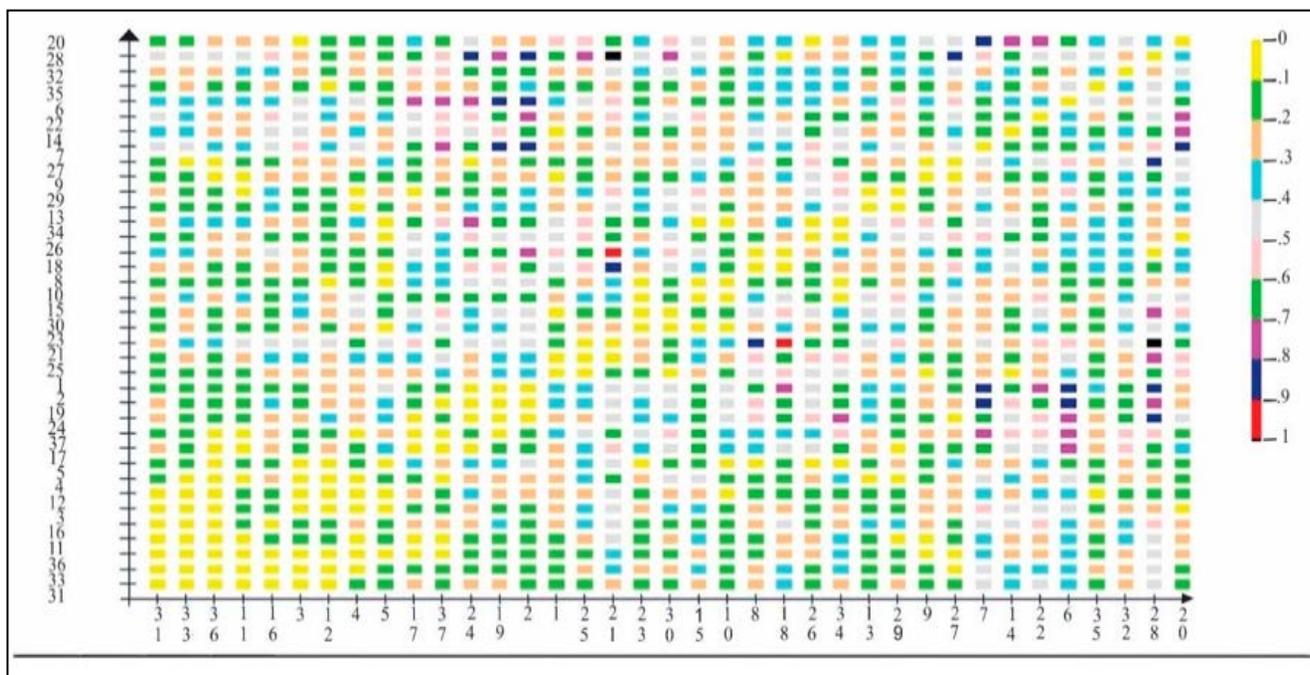


Figure 2. Tocher's graphical method based on the Mahalanobis distance (D_{ii}) in 37 melon accessions. Numbers indicate the accessions. The colors in the graph represent variability between 0 and 1, the latter being the highest genetic divergence. Monte Carmelo, UFU, 2020.

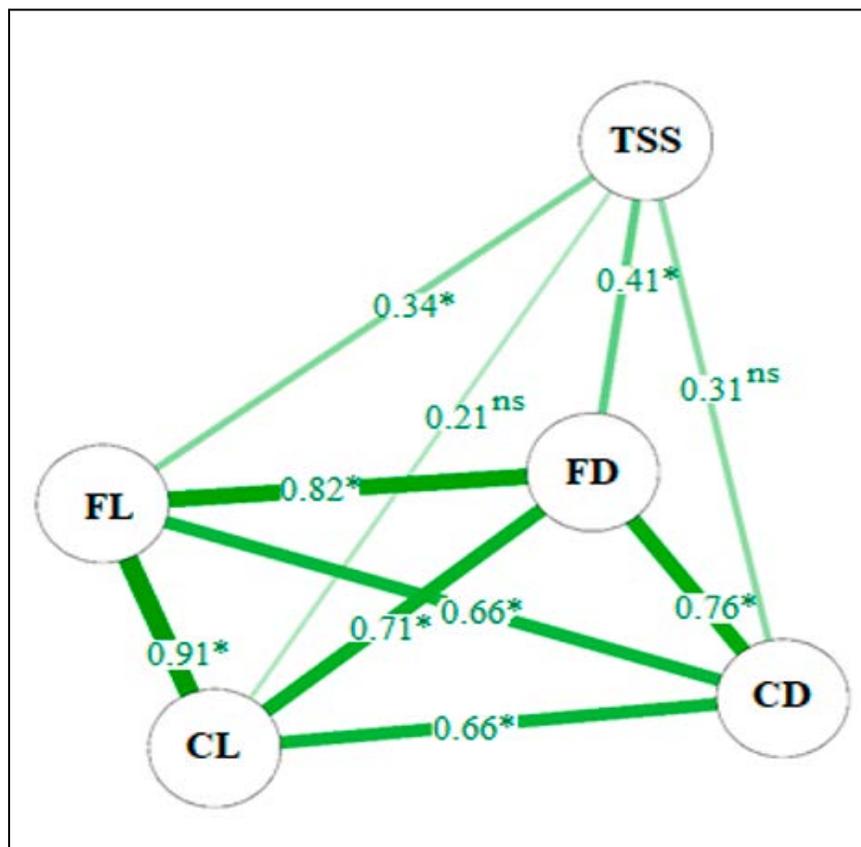


Figure 3. Genotype correlations of melon traits. Green lines represent positive correlations. Line thickness is proportional to the magnitude of the correlation. CL: cavity length; FD: fruit diameter; FL: fruit length; TSS: total soluble solids and CD: cavity diameter. Monte Carmelo, UFU, 2020.

in the creation of four groups, being that 93.0% were concentrated in only one group. In the present study, fewer than 50% of the genotypes were in the same group, indicating balanced genetic variability.

The use of different clustering methods results in greater efficiency in determining genetic diversity (Valadares *et al.*, 2018). Thus, a third methodology was applied in order to guarantee genetic variability between melon accessions (Figure 2). Tocher's optimization clustering method is used to determine minor genetic differences between two genotypes. In this methodology, values near zero (yellow) and one (black) indicate greater genetic similarity and dissimilarity, respectively. The results obtained by Tocher's optimization show substantial genetic variability.

Analysis of the relative contribution of traits using Singh's method (1981) considers that the most variable traits are essential, making it possible to exclude traits that contributed little to dissimilarity, reducing the work, time and additional costs involved in data collection (Alves *et al.*, 2003; Valadares *et al.*, 2018).

All the assessed traits contributed to determining the genetic divergence between accessions, to a greater or lesser degree. The most important descriptor to explain divergence was cavity length (26.69%), followed by fruit diameter (19.61%), fruit length (19.36%), total soluble solids (17.83%) and cavity diameter (16.50%). Among the traits studied, cavity diameter contributed least to the genetic divergence between melon genotypes. Nevertheless, it was considered a relevant attribute and cannot be eliminated because this would change group distribution.

Valadares *et al.* (2018) studied genetic divergence in melon accessions belonging to the Momordica group and found that TSS was one of the traits that accounted most for the divergence (17.60%), corroborating with results presented.

Superior melon genotypes should be selected based on several traits simultaneously, in order to achieve genetic gains for the largest possible number of attributes (Vasconcelos *et al.*, 2010; Rezende *et al.*, 2014). Thus, the use of selection indices is a promising method for simultaneous selection, since it promotes favorable genetic combinations (Figueiredo *et al.*, 2012; Cruz *et al.*, 2014).

The Mulamba & Mock (MM) and Smith-Hazel (SH) selection indices made it possible to presume total selection gains (SG) of 79.65% and 163.16% respectively (Table 1). Considering the traits assessed in the present study, except fruit diameter, the highest selection gain estimates were observed in the MM index for fruit length (50.05%) and total soluble solids (40.97%) and greater declines in cavity diameter (-21.47%) and cavity length (-28.62%).

Based on the estimates recorded, satisfactory and better distributed gains were obtained for the traits in question when the MM selection index was used. Once the index that provides the best genetic gain estimates was determined, the genotypes with agronomic potential were selected. The following genotypes were selected by the MM index: UFU07, UFU23, UFU09, UFU21, UFU28 and UFU30 (Table 1). Confirming these

results, research that analyzes selection indices reported that MM achieved the best results for açai (Teixeira *et al.*, 2012); soybean (Bizari *et al.*, 2017) and tomato (Finzi *et al.*, 2020) crops.

Genetic correlations were positive in all combinations between the studied traits (Figure 3), demonstrating that changes caused by selecting a trait will result in comparable changes in the correlated trait. Greater genetic correlation occurred between the FL x CL (0.91), FL x FD (0.82), FD x CD (0.76), CL x FD (0.71), FL x CD (0.66) and CL x CD (0.66). By contrast, CL x TSS, CD x TSS, FL x TSS and FD x TSS exhibited the lowest genetic correlation estimates with 0.21, 0.31, 0.34 and 0.41, respectively. The increase in TSS cannot be attributed to variations in CL and CD since the correlations between these traits were not significant.

Valadares *et al.* (2017) estimated genetic parameters and correlations between the following traits: peduncle diameter, size of pistil scar, fruit width, fruit length, pulp thickness, fruit fresh weight, total soluble solids, and number of days from male and female flowering to fruiting of Momordica melons, obtaining positive correlations for all the characteristics. This result corroborates the findings obtained here.

The present study emphasized the importance of genotype clustering and the use of selection indices for melon breeding. Clustering guides cross-breeding in order to achieve a greater heterotic effect. The practical usefulness of selection gain makes it possible to adopt more elaborate criteria for selecting superior genotypes, given the simultaneous selection of several traits (Cruz *et al.*, 2014). These measures significantly reduce the time and resources needed to select potential genotypes for breeding programs (Teixeira *et al.*, 2012). Thus, estimations of genetic dissimilarity, selection indices and character correlation are essential strategies in melon breeding programs.

Therefore, the germplasm assessed exhibits genetic variability, with fruit cavity length the trait with the greatest contribution. The Mulamba and Mock index provides the best balance and highest selection gain values in melon

genotypes. The genetic correlations were positive for all the combinations of the traits under study. The genotypes of melons UFU07, UFU23, UFU09, UFU21, UFU28 and UFU30 are promising for breeding programs.

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