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Morpho-agronomic diversity and botanical identification of melon accessions from northeastern Brazil

Diversidade morfoagronômica e identificação botânica de acessos de melão do nordeste brasileiro

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ABSTRACT - Melon (*Cucumis melo* L.) crops are grown in the Semiarid region of Brazil by small, medium, and large farmers, focused on domestic and international markets. However, melon is also grown by family farmers using their own seeds, which are important germplasm for melon breeding programs. Samples of these seeds were collected and stored in the Active Germplasm Bank of Cucurbitaceae from the Northeast Region at the Brazilian Agricultural Research Corporation (Embrapa Semiarid), and require more thorough studies for a better understanding of the existing variability. Thus, the objective of this work was to characterize sub-accessions and their respective endogamic progenies to assess the genetic variability between and among these accessions. Two experiments were conducted in a randomized complete block design, with three replications, using 11 quantitative and 8 qualitative descriptors: the first using seeds from 17 accessions from natural pollination, and the second using seeds from S_1 progenies. Morphological data were used for comparisons between generations. The 17 accessions evaluated originated 24 sub-accessions, denoting variability between and among accessions and sub-accessions. A dendrogram developed based on the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) showed the existing variability and, according to the newest melon classification, the groups identified were: *makuwa*, subgroup *nashi-uri*; and *momordica* and *cantalupensis*, subgroup *prescott*. The results showed a probable existence of introgression of alleles between different botanical groups, and some sub-accessions were not identified regarding their group by presenting variations in morphological characteristics, indicating the presence of new botanical groups.

Keywords: *Cucumis melo* L. Taxonomy. Phenotyping. Genetics.

RESUMO - O cultivo do melão (*Cucumis melo* L.) no Semiárido brasileiro é realizado por pequenos, médios e grandes agricultores, visando o mercado interno e externo. Contudo, o meloeiro também é cultivado por agricultores familiares que utilizam sementes próprias, as quais constituem germoplasma de grande importância para o melhoramento genético do melão. Amostras destes materiais foram coletadas e estão armazenadas no Banco Ativo de Germoplasma de Cucurbitáceas para o Nordeste Brasileiro, localizado na Embrapa Semiárido, necessitando de estudos mais aprofundados para melhor conhecimento da variabilidade existente. Assim, objetivou-se com este trabalho, estudar subacessos e suas respectivas progênies endogâmicas para aprofundar o conhecimento da variabilidade genética entre e dentro dos acessos. Foram conduzidos dois experimentos em blocos casualizados completos, com três repetições, usando 11 descritores quantitativos e oito qualitativos. O primeiro utilizou sementes de 17 acessos provenientes de polinização livre e, no segundo, sementes de progênies S_1. A partir dos dados morfológicos comparou-se as gerações e observou-se que os 17 acessos avaliados deram origem a 24 subacessos, inferindo variabilidade entre e dentro dos acessos e subacessos. O dendrograma feito a partir do método UPGMA constatou a variabilidade existente, e usando a mais nova classificação dos tipos de melões foram identificados os grupos *makuwa* subgrupo *nashi-uri*, *momordica* e *cantalupensis* subgrupo *prescott*. Provavelmente existe introgressão de alelos entre diferentes grupos botânicos, e alguns subacessos não foram identificados quanto ao seu grupo por apresentar variações em suas características morfológicas, podendo indicar a presença de novos grupos botânicos.

Palavras-chave: *Cucumis melo* L. Taxonomia. Fenotipagem. Genética.

Conflict of interest: The authors declare no conflict of interest related to the publication of this manuscript.

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INTRODUCTION

Melon (*Cucumis melo* L.) is a Cucurbitaceae species from the genus *Cucumis* (BURGER et al., 2010) that has a high economic importance in the world (GUIMARÃES; ARAGÃO, 2019). The Northeast region of Brazil is responsible for 96.84% of the Brazilian production (IBGE, 2020); the yellow melon type is the most grown for commercial purposes, using cultivars that had already been improved through breeding processes (SALVIANO et al., 2017) and present homogeneity and high productivity.

This species has been grown over several generations by family farmers in the Northeast region of Brazil, mainly within the traditional agriculture of the state of Maranhão, where it presents high genetic variability, considering the several natural and artificial selection processes that it underwent over time (QUEIRÓZ; BARBIERI; SILVA, 2015). Thus, melon samples from this region were collected and then stored in the Active Germplasm Bank of Cucurbitaceae from the Northeast Region at the Brazilian Agricultural Research Corporation

(Embrapa Semiarid), in Petrolina, state of Pernambuco, Brazil, which contains approximately 150 accessions of this species and is the holder of very important genes for breeding programs (SILVA et al., 2010).

However, despite the Northeast region is rich in melon genetic variability, thorough studies with accessions from traditional agriculture are still scarce and require, firstly, actions for taxonomic identification, characterization, evaluation, and conservation. Torres Filho et al. (2009) and Aragão et al. (2013) are among the few works carried out with samples of this germplasm; they conducted morphological and molecular characterizations of melon accessions and confirmed the existence of a wide genetic variability. However, these works did not estimate variations within accessions and used a classification that establishes only seven and six botanical groups, respectively, based on only one generation.

More recently, Amorim et al. (2016) and Macêdo et al. (2017) evaluated two sequential generations of a sample from accessions of the Active Germplasm Bank of Cucurbitaceae from the Northeast Region of Brazil and established the concept of sub-accessions to term the variation within accessions, and used the classification of Pitrat, Hanelt, and Hammer (2000), which considers that the species *C. melo* is composed of two subspecies (*agrestis* and *melo*) and botanical varieties. Amorim et al. (2016) evaluated 15 accessions which unfolded into 26 sub-accessions, and Macêdo et al. (2017) also evaluated 15 accessions and subdivided them into 25 sub-accessions; both studies described the two subspecies and their respective botanical varieties: *agrestis* (*momordica, conomon* and *makuwa*) and *melo* (*chandalak* and *cantalupensis*).

In addition, Pitrat (2016) conducted a new botanical systematization for melon, considering the previous classification (PITRAT; HANELT; HAMMER, 2000) inconsistent, as the pilosity in the ovary presents variation within a same group, thus, proposing a new classification with 19 botanical groups, and subgroups when required, to represent the variations found within groups.

Therefore, following the new melon classification, the objective of this work was to define botanical groups and subgroups, identify possible sub-accessions, and quantify the morpho-agronomic variability between and among sub-accessions from the Active Germplasm Bank of Cucurbitaceae from the Northeast Region of Brazil.

MATERIAL AND METHODS

Seventeen melon accessions from traditional agriculture in the states of Piaui (1 accession), Bahia (3 accessions), and Maranhão (13 accessions), collected from 1991 to 1998, were evaluated (Table 1). These accessions were at the Active Germplasm Bank of Cucurbitaceae from the Northeast Region at the Brazilian Agricultural Research Corporation (Embrapa Semiarid), in Petrolina, state of Pernambuco, Brazil, stored in a cold chamber at temperature of 10 °C and relative air humidity of 40%.

Two experiments were conducted during 2018 and 2019, at the Experimental Field and Laboratory of Molecular Biology of the Department of Technology and Social Sciences of the Bahia State University, in Juazeiro, BA, Brazil (09°25'04.92271"S, 40°29'04.73710"W, and altitude of 351.893 meters).

Table 1. Passport data of melon (*Cucumis melo*) accessions from the Active Germplasm Bank of Cucurbitaceae from the Northeast Region at the Brazilian Agricultural Research Corporation (Embrapa Semiarid), used in the study in 2018 and 2019.

Accession	Municipality - State	Town hall coordinates	Collection year
BGMEL 20	Nova Iorque - MA	06°37'49"S 43°57'38"W	1991
BGMEL 22	Pastos Bons - MA	06°35'59"S 44°04'21"W	1991
BGMEL 23	Ibipeba - BA	11°38'29"S 42°00'45"W	1991
BGMEL 27	Jacobina - BA	11°11'08"S 40°32'10"W	1992
BGMEL 28	Jacobina - BA	11°11'08"S 40°32'10"W	1992
BGMEL 30	Altos - PI	05°02'24"S 42°27'41"W	1992
BGMEL 42	São Luiz Gonzaga do Maranhão - MA	04°22'51"S 44°22'51"W	1995
BGMEL 71	Brejo - MA	03°41'07"S 42°45'04"W	1996
BGMEL 74	Barra do Corda - MA	05°30'21"S 45°14'06"W	1997
BGMEL 104	Coroatá - MA	04°07'31"S 44°07'49"W	1997
BGMEL 113	Arari - MA	03°27'38"S 44°46'56"W	1996
BGMEL 114	Arari - MA	03°27'38"S 44°46'56"W	1996
BGMEL 116	São Vicente Ferrer (Distrito Santa Rosa) - MA	02°53'44"S 44°52'53"W	1998
BGMEL 117	São Vicente Ferrer (Distrito Santa Rosa) - MA	02°53'44"S 44°52'53"W	1998
BGMEL 156	MA	*	*
T5COD5	MA	*	*
T6COD98	MA	*	*

MA = Maranhão; BA = Bahia; PI - Piaui. *Without information on the municipality and collection date.

The first experiment started in April 2018, using seeds from accessions from natural pollination; and the second in January 2019, using seeds from the S_1 generation (endogamic progenies). Twenty seeds from each accession were sown in polyethylene trays filled with a commercial substrate (Plantmax®) in a greenhouse covered with a 50% screen shade, and irrigated twice a day.

The seedlings were transplanted to the experimental field at 20 days after sowing. The soil was previously prepared with plowing, harrowing, furrowing, and soil fertilizer application, carried out based on the soil analysis and recommendations for growing melon crops in the Northeast region of Brazil. Both the experiments were conducted in a randomized complete block design, with three replications, five plants per plot, spacings of 2.5 m between rows and 0.8 m between plants, under surface irrigation (infiltration furrows) in the first experiment, and localized irrigation (drip irrigation) in the second. Cultural and phytosanitary practices were carried out according to the recommendations for melon crops in the region. Parental and S_1 generations were obtained by subjecting, on average, nine plants of each accession to the self-fertilizing process.

The fruits were harvested between 30 and 45 days after the self-fertilizing process and characterized based on 11 quantitative and 8 qualitative descriptors (4 binary and 4 multicategory, using the list of descriptors of the IPGRI (2003). The quantitative descriptors evaluated were: fruit weight (kg); pulp thickness on the right, left, upper, and lower sides of the fruit (cm); fruit length and diameter (cm); fruit cavity length and diameter (cm); and total soluble solids in the lateral part of the fruit and in a composite pulp sample (° Brix). The qualitative descriptors evaluated were: fruit shape (globular, flat, elliptical, piriform, oval, elongated, ball, and poor-formation); epidermis color (yellow, intense yellow, orange, cream, light-green, dark-green, greenish-yellow); grooves (absent, light, medium, deep); cracks in the epidermis (absent, present); pulp color (white, cream, orange, greenish); peduncle dehiscence (absent, present); pilosity in the ovary and in young fruits (short or long trichomes); and sexual expression (monoecious or andromonoecious).

Focused on reaching a better representativeness, systematized photographs of fruits of each accession of the two generations (paternal and S_1) were developed to assess the segregation between generations and, thus, identify variations within accessions and identify sub-accessions, as described by Amorim et al. (2016) and Macêdo et al. (2017).

Regarding the statistical analyses, the quantitative data were firstly subjected to descriptive statistics. Normality and homogeneity tests were then applied, followed by a multivariate analysis based on the quantitative and qualitative descriptors. A dissimilarity matrix between accessions and sub-accessions for each type of data was developed, in which quantitative data were obtained through the Mahalanobis distance, and qualitative data were obtained using the index described by Cruz (2013), which represents the mean Euclidean distance:

$$\sqrt{\left(\frac{1}{v}\right)\sum(b+c)/(a+b+c+d)}$$

where: a = the number of type 1-1 agreements for the j-th variable; b = number of type 1-0 disagreements for the j-th variable; c = number of type 0-1 disagreements for the j-th variable; and d = number of type 0-0 agreement for the j-th variable.

These matrices were then summed, forming a sum matrix. Joint of the distance and dissimilarity matrices was carried out, firstly, by the standardization of the d and D^2 values, obtaining $(D^2)'$ and d' values, followed by simple sum. The sum dissimilarity matrix was used for the clustering analysis, using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA), and the cut point was based on the method of Mojena (1977). The coefficient of cophenetic correlation (CCC) (SOKAL; ROLF, 1962) was estimated to validate the groups generated by the UPGMA based on the Pearson's coefficient of correlation between the distance matrix and the cophenetic matrix (CRUZ; CARNEIRO, 2003). All procedures were carried out using the Genes (CRUZ, 2013) and R (R DEVELOPMENT CORE TEAM, 2019) programs.

RESULTS AND DISCUSSION

The plant and fruit phenotypic data found for the two generations (parental and S_1) and the classification of Pitrat (2016) was used to reclassify the 17 accessions firstly characterized in 24 sub-accessions (Table 2). This new classification differs from classifications previously conceived by Pitrat, Hanelt, and Hammer (2000), which are based on subspecies and varieties and use the descriptors pilosity in flower ovary and in new fruits as a differentiation factor. However, this differentiation is not consistent, as flower ovaries with short, long, or intermediate trichomes are commonly found within a same botanical group (PITRAT, 2016), as seen in the groups *momordica* and *makuwa*, subgroup *nashi-uri,* which present short ovary trichomes according to the classification; however, in the present work, they showed presence of long trichomes (BGMEL22.0, 28.1, 42.1, 74.1, 114.0, 156.0) (Table 2). Thus, this character should not be used as a classificatory factor in studies for identification of botanical groups.

Table 2. Morphological characterization of melon (*Cucumis melo*) accessions from the Active Germplasm Bank of Cucurbitaceae from the Northeast Region at the Brazilian Agricultural Research Corporation (Embrapa Semiarid), in parental (P) and S_1 generations (G), with identification and classification of sub-accessions and their respective botanical group (BG) and subgroup (SG), in study carried out in 2018 and 2019.

Accession	BG/SG	G	SE	PO	EC	GG	CE	PC	PD
BGMEL20.0	*momordica*	P	M	C	1	0	1	1	0 1
		S_1	M	C	1 2	0	1	1 2 3	0 1
BGMEL22.0	*makuwa/nashi-uri*	P	A M	C L	4	0	0	2	1
		S_1	A M	C L	4	0	0	1 2	1
BGMEL23.0	ND	P	M	C L	1	0	0	2	0
		S_1	M	C L	1 3	0	0	2 3	0
BGMEL27.1	ND	P	M	L	1	0	1	1	0
		S_1	M	L	1	0	0 1	1 2 3	0 1
BGMEL27.2	*momordica*	P	M	C	1	0	1	1	0 1
		S_1	M	C	1	0	1	1 2 3	0 1
BGMEL28.1	*momordica*	P	M	C	1	0	1	2	0 1
		S_1	M	C L	1	0	1	2 3	0 1
BGMEL28.2	ND	P	M	L	1	1	0	2	1
		S_1	M	L C	1	1	0	2 3	0 1
BGMEL30.0	*cantalupensis/ prescott*	P	M	L	3	2 3	0	3	1
		S_1	M	L	3	2	0	3	1
BGMEL42.1	*momordica*	P	M	L	1	0	1	2	1
		S_1	M	C	1	0	1	2	1
BGMEL42.2	*cantalupensis/ prescott*	P	M	L	3	3	0	3	1
		S_1	M	L	3	3	0	3	1
BGMEL71.1	ND	P	A	L	1	0	1	4	0
		S_1	A M	L C	1	0	0	3 4	0 1
BGMEL71.2	ND	P	A	L	5	1	0	4	0
		S_1	A M	L	5	1	0	4	0
BGMEL74.1	*momordica*	P	M	L	1	0	1	2	0 1
		S_1	M	L	1	0	1	3	0 1
BGMEL74.2	ND	P	M	L	7	0	0	4	1
		S_1	A M	C L	5	0	0	4	0
BGMEL104.0	*makuwa/nashi-uri*	P	A M	C	4	0	0	2	1
		S_1	A M	C	4	0	0	2	1
BGMEL113.0	*makuwa/nashi-uri*	P	A M	C	4	0	0	2	1
		S_1	A M	C	4	0	0	2	1
BGMEL114.0	*makuwa/nashi-uri*	P	A M	C	4	0	0	2	1
		S_1	A M	C L	4	0	0	2	1
BGMEL116.0	*makuwa/nashi-uri*	P	A M	C	4	0	0	2	1
		S_1	A	C	4	0	0	2	1
BGMEL117.0	*makuwa/nashi-uri*	P	A M	C	4	0	0	2	1
		S_1	A	C	4	0	0	2	1
BGMEL156.0	*makuwa/nashi-uri*	P	A M	C L	4	0	0	2	1
		S_1	A	C L	4	0	0	2	1
T5 COD5.1	ND	P	M	L	6	1	0	4	0
		S_1	M	L	5	0 1	0	4	0
T5 COD5.2	ND	P	M	L	1	0	1	2	0
		S_1	A M	C L	1	0	0	2	0 1
T6 COD98.1	*momordica*	P	M	C	1	0	1	1	0 1
		S_1	M	C	1	0	1	2	0 1
T6 COD98.2	ND	P	M	C	1	0	0	2	0
		S_1	A M	C L	1	0 1	0	2 3	0 1

ND = botanical group not defined; [0]no variation within accession; [1,2]segregation within each accession; SE = sexual expression: M = monoicous; A = andromonoecious; PO = Pilosity in ovary (C: short; L: long); EC = epidermis color (yellow – 1, intense yellow – 2, orange – 3, cream – 4, light-green – 5, dark -green – 6, greenish-yellow – 7); GG = grooves (absent – 0, light – 1, medium – 2, deep – 3); CE = cracks in the epidermis (absent – 0, present – 1); PC = pulp color (white – 1, cream – 2, orange – 3, greenish – 4); PD = peduncle dehiscence (absent – 0, present – 1).

The data of morpho-agronomic descriptors found for the two generations enabled to identify the variability within the accessions evaluated, and the multivariate analysis enabled to separate groups with morphological similarities. The dendrogram (Figure 1) showed a coefficient of cophenetic correlation (CCC) of 0.86 for the parental generation and 0.88 for the generation S_1 (Figure 2), denoting a good representativeness (CRUZ; CARNEIRO, 2003). The parental generation (Figure 1) showed the formation of three main groups: the first dendrogram included the accessions BGMEL 22, 16, 156, 104, 117, 113, and 114; the second included the accessions BGMEL 23, 71, T5COD5, 74, 30, and 42; and the third included the accessions BGMEL28, T6COD98, 20, and 27. The generation S_1 formed three main groups: the first included only one sub-accession (BGMEL 42.2); the second included the sub-accessions BGMEL 22.0, 113.0, 114.0, 117.0, 156.0, 104.0, and 116.0; and the third included the sub-accessions BGMEL 30.0, 71.2, 74.2, 28.1, T6COD98.1, 20.0, 27.2, T5COD5.1, 71.1, 42.1, T5COD5.2, 27.1, 74.1, T6COD98.2, 23.0, and 28.2.

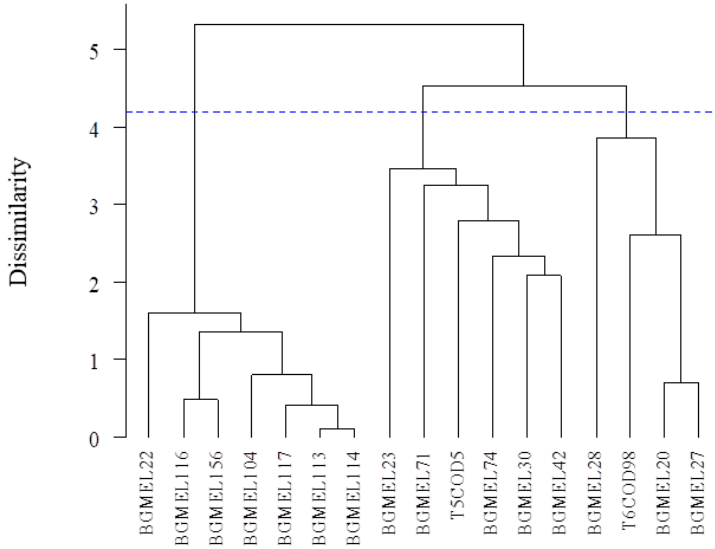

Figure 1. Dendrogram of parental generation of melon (*Cucumis melo*) accessions, generated by joint analysis of quantitative and qualitative data, using UPGMA.

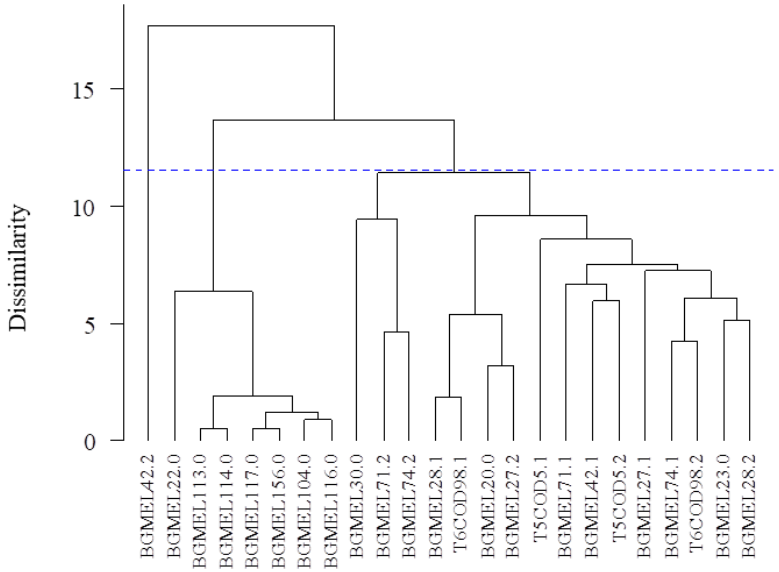

Figure 2. Dendrogram of generation S_1 of melon (*Cucumis melo*) accessions, generated by joint analysis of quantitative and qualitative data, using UPGMA method.

The morpho-agronomic data of the two generations and the comparison of them showed the formation of three data sets, in which group I was formed by nine accessions (Figure 3, Table 2), with fruits presenting the same phenotype, in both generations, for flower and fruit characters, in addition to present characters that enable to identify botanical groups and subgroups, namely: *mormordica* (BGMEL20.0) (Figure 3A), *makuwa* subgroup *nashi-uri* (BGMEL22.0, 104.0, 113.0, 114.0, 116.0, 117.0, and 156.0) (Figures 3B the 3H), and the group *cantalupensis* subgroup *prescott* (BGMEL30.0) (Figure 3I). These accessions presented no variations within accessions from one generation to another and, thus, were identified with zero in their identification code from the Active Germplasm Bank of Cucurbitaceae from the Northeast Region of Brazil, as described by Amorim et al. (2016).

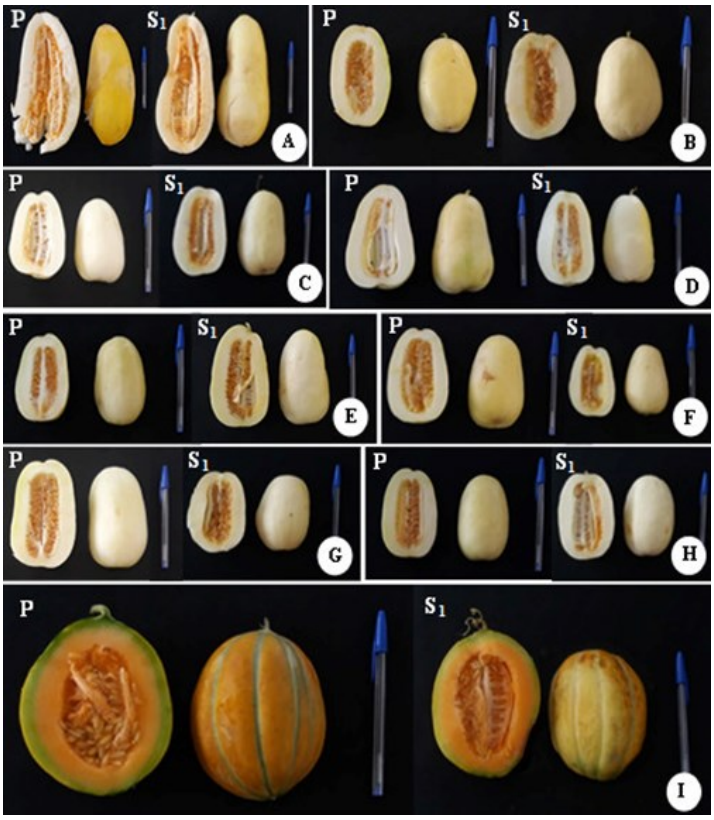

Figure 3. Melon (*Cucumis melo*) accessions of group I that presented the same phenotype for flower and fruit characteristics in the two generations (P and S_1) studied. (A) BGMEL20.0; (B) BGMEL22.0 (C) BGMEL104.0 (D) BGMEL113.0 (E) BGMEL114.0 (F) BGMEL116.0 (G) BGMEL117.0 (H) BGMEL156.0 (I) BGMEL30.0. Photos: BARBOSA, BLR 2018 (P) / 2019 (S_1).

The correlation of the results found for group I with the multivariate analysis showed that the groups in the dendrograms reinforced this separation and the respective botanical identifications, as the parental (Figure 1) and S_1 (Figure 2) generations showed approximations of sub-accessions of the botanical group *makuwa* subgroup *nashi-uri*, and indicated that *momordica* and *cantalupensis* subgroup *prescott* remained close to other sub-accessions (BGMEL71.2, 74.2, 28.1, T6COD98.1, 27.2, T5COD5.1, 71.1, 42.1, T5COD5.2, 27.1, 74.1, T6COD98.2, 23.0, and 28.2) with similar morpho-agronomic characteristics.

According the new systematization for melon (PITRAT, 2016), the subgroup *prescott* of the group *cantalupensis* is characterized by presenting deep grooves on the fruit surface; however, the sub-accession BGMEL30.0 presented a variation, with grooves varying from medium to deep (Table 2). This character is controlled by a recessive gene (DOGIMONT, 2011), and the gradual variation observed in the present work may have been originated from introgression of alleles that are responsible for expression of different types of fruit surfaces in melon genotypes that are grown by family farmers in the Northeast region of Brazil (MACÊDO et al., 2017).

Group II was composed of six sub-accessions (Figure 4, Table 2), with the parental generation presenting variation within the accessions evaluated. Thus, these accessions with variations were separated and grown in the field to be analyzed (generation S_1) and compared to data of the parental generation. The analysis showed that the two generations expressed the same characteristics previously presented, with no segregation for flower and fruit descriptors (PITRAT, 2016). Thus, this uniformity allowed for the identification of botanical groups and subgroup: *momordica* (BGMEL27.2, 28.1, 42.1, 74.1, and T6COD98.1) (Figures 4A to 4D), and *cantalupensis* subgroup *prescott* (BGMEL42.2) (Figure 4F).

Figure 4. Sub-accessions of melon (*Cucumis melo*) of group II that presented variation within the accessions evaluated and, after comparison with data of generation S_1, expressed the same characteristics of the paternal generation (P). (A) BGMEL27.2 (B) BGMEL28.1 (C) BGMEL42.1 (D) BGMEL74.1 (E) T6COD98.1 (F) BGMEL42.2. Photos: BARBOSA, BLR, 2018 (P) / 2019 (S_1).

The multivariate analysis (Figures 1 and 2) grouped closely the sub-accessions identified as *momordica*. The sub-accession BGMEL42.2 (*cantalupensis*) in generation S_1 was isolated in the dendrogram (Figure 2) in relation to BGMEL30.0, which was also identified for the same botanical group. It was probably because, in addition to qualitative, quantitative characters were analyzed, such as fruit weight (BGMEL42.2: 2.290 kg; BGMEL30.0: 0.700 kg), fruit length and diameter (BGMEL42.2: 21.95 cm and 16.25 cm, respectively; BGMEL30.0: 13.50 cm and 10.90 cm, respectively), fruit cavity length and diameter (BGMEL42.2: 16.45 cm and 9.85 cm, respectively; BGMEL30.0: 9.90 cm and 5.40 cm, respectively) and pulp thickness (EPD - BGMEL42.2: 2.80 cm and BGMEL30.0: 2.60 cm; EPE - BGMEL42.2: 3.30 cm and BGMEL30.0: 2.0 cm; EPS: BGMEL42.2: 3.45 cm and BGMEL30.0: 1.90 cm; EPI - BGMEL42.2: 2.10 cm and BGMEL30.0: 1.70 cm), which showed higher values and may have caused this separation,

The variations found for color of pulp (white, cream, and orange) and epidermis (yellow, yellow-intense) in the *momordica* group (Table 2) are consistent with the group description presented by Pitrat (2016), i.e., pulp colors from light-green, sometimes white, that may reach orange. This variation is also expressed in the epidermis color, which may present uniform color or spots and stripes (PITRAT, 2016). Melon pulp color is controlled by two genes that involve the colors green, orange, and white; this species may present variations in epidermis color according to the different combinations of three main pigments: chlorophyll; carotenoids; and naringenin chalcone, which is a flavonoid pigment responsible for yellow colors in mature fruits (DOGIMONT, 2011). Therefore, crossed forms of alleles may result in different colors for botanical groups.

The sub-accessions BGMEL42.1 and 42.2 (Table 2, Figures 4C and 4F) were previously from the same accession; however, after analyzed for variations in the two generations, they were separated as different botanical groups (*momordica* and *cantalupensis* subgroup *prescott*, respectively). This variation factor was probably caused by seed exchanges between family farmers, which is common practice; in addition, simultaneous handling of seeds from different melon groups occurs within the sites where these accessions were collected, which probably led to mixtures of germplasms from different botanical groups (AMORIM et al., 2016).

The botanical identification carried out for the two first groups showed that the characteristics found in the present study are consistent with results found in other works (MANOHAR; MURTHY, 2012; MALIK et al., 2014), defining marked characteristics for the group *momordica.* The fruits presented shapes varying from elliptical to elongated, weights reaching 2.380 kg, and cracks in the epidermis when mature, which is not a satisfactory morphological trait, as decreases in post-harvest durability hinder the fruit marketing; the plants were monoecious, with a smooth fruit peel, floury pulp with white, creme, or orange colors, and low sugar contents (Table 2). The group *momordica* is highly marketed in street markets in the Northeast region of Brazil, where it is popularly known as melão-de-cheiro, pepino, or caxixi (MACÊDO et al., 2017).

The characteristics presented by the botanical group *makuwa* are also consistent with results of other works (BURGER et al., 2010; XIAO-HANG et al., 2014) and denote that their fruits usually present low weight (fruits had weights of up to 0.100 g in the present study). However, variations in this characteristic may be found within the group, reaching higher weights (fruits with up to 0.900 g were found in the

present work). In addition, the fruits presented elliptical to oval shapes, epidermis with cream color, and fruit pulp with crisp texture, cream color, and high sugar contents, reaching 10.2 °Brix, which is considered sweet, and small seeds (Table 2).

Studies on fruits of the group *cantalupensis* found in the literature have classified them as medium-sized fruits, which is true for most of them. However, variations in this character may be found, with fruits classified as large (IPGRI, 2003), as the fruit weight in the present work reached 2.870 kg. The *cantalupensis* fruits presented peduncle dehiscence, elliptical shape, and light-orange pulp with a juicy smooth texture; fruits with green pulp were not found. In addition, the fruits were aromatic when mature, confirming the findings of other works (PITRAT, 2016; VALADARES et al., 2018).

The groups *makuwa* and *cantalupensis* present subgroups, including *nashi-uri* and *prescott*, respectively, as identified in the present work; *nashi-uri* is characterized by presenting uniform cream to white epidermis color and no presence of grooves, whereas the subgroup *prescott* is characterized by presenting deep grooves, pulp exclusively orange, and being monoecious (PITRAT, 2016), as found in the present work.

Group III was composed of nine sub-accessions (BGMEL23.0, 27.1, 28.2, 71.1, 71.2, 74.2, T5COD5.1, T5COD5.2, and T6COD98.2) (Figure 5), for which botanical groups and subgroups were not possible to identify, as they presented introgression of characters or characteristics different from those present in groups and subgroups already defined, making it difficult to separate them based on Pitrat (2016) (Table 2). The sub-accession BGMEL23.0 (Figure 5A) presented uniform flower and fruit characteristics in the two generations studied; however, classifying it into a group based on the classification of Pitrat (2016) was not possible, which denotes that it is probable from a new subgroup, or even from a new botanical group. This sub-accession presented, in the two generations, fruits with a piriform shape; yellow to orange epidermis color; no stripes; no grooves; no cracks in the epidermis; no reticulated peel; no roughness; cream to orange pulp color; no peduncle dehiscence; and monoecious flowers (Table 2).

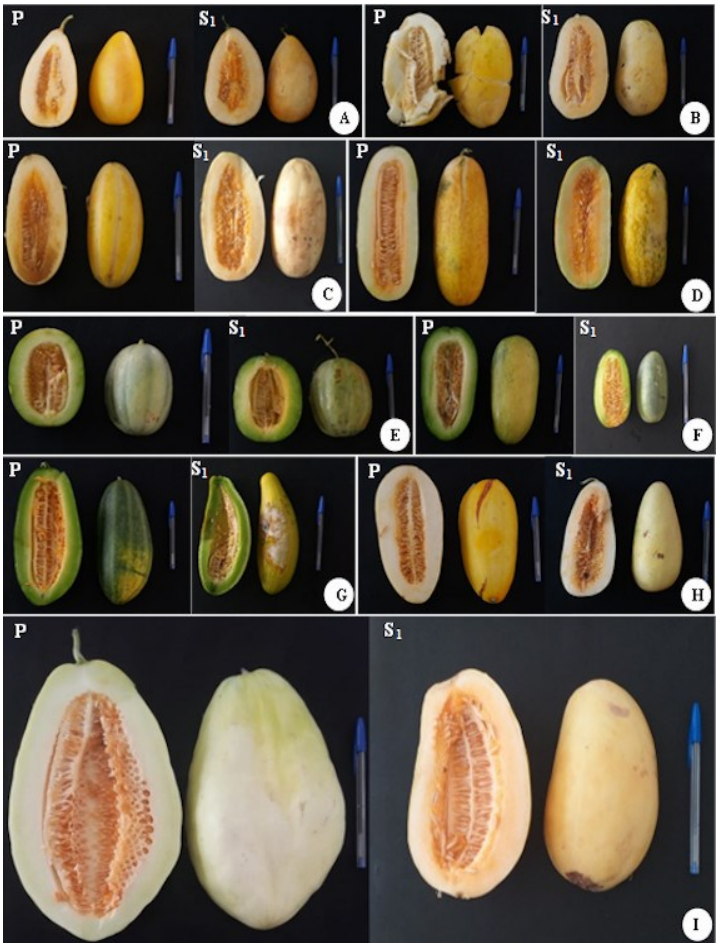

Figure 5. Sub-accessions of melon (*Cucumis melo*) of group III that presented introgression of characters between botanical groups, or descriptors that were not possible to identify regarding their botanical group in the parental (P) and S_1 generations. (A) BGMEL23.0 (B) BGMEL27.1 (C) BGMEL28.2 (D) BGMEL71.1 (E) BGMEL71.2 (F) BGMEL74.2 (G) T5COD5.1 (H) T5COD5.2 (I) T6COD98.2. Photos: BARBOSA, BLR, 2018 (P) / 2019 (S_1).

The sub-accessions BGMEL27.1, T5COD5.2, and T6COD98.2 (Figures 5B, 5H and 5I) presented similar characteristics to those of the *momordica* group, but with no cracks in the fruit epidermis, which is a marked character of fruits of this group when mature. In addition, T5COD5.2 and T6COD98.2 (Figures 5H and 5I) presented andromonoecious flowers (Table 2), diverging from the classification of Pitrat (2016), which characterize these flowers as monoecious. Dhillon et al. (2015) confirmed the existence of cracks in the epidermis or only a peeling in *momordica* fruits, which makes it a characteristic for identification of the group. Thus, the different characteristics that make them segregating were considered as introgression of characters between botanical groups in the present work, thus hindering the definition of the groups.

The sub-accession BGMEL28.2 (Figure 5C) did not express the character cracks in the epidermis, presenting light grooves in the epidermis (Table 2), which is not consistent with *momordica*, which usually presents a smooth surface with no grooves (PITRAT, 2016). This also denotes introgression of characters between *momordica* and, probably, *cantalupensis,* which has grooves. The sub-accession BGMEL71.2 (Figure 5E) presented superficial grooves and green epidermis and pulp, which are characteristics of the group *cantalupensis*; however, it was not possible to identify it, as it presented non-dehiscent peduncle in the two generations studied, which also is a characteristic of the group *cantalupensis*.

Regarding these sub-accessions that were not identified, the dendrogram of generation S_1 (Figure 2) showed the formation of a main cluster with all genotypes identified as *momordica* and *cantalupensis* subgroup *prescott*, in addition to grouping all sub-accessions that were not identified but were morphologically similar to *cantalupensis* or *momordica*, denoting an introgression of characters that may have easily occurred, as there are no barriers for the occurrence of cross-pollination between different botanical groups (VALADARES et al., 2017) and the management of farmers facilitates this process between neighboring crops with different botanical groups.

The findings of the present work are consistent with those of Burger et al. (2010), who reported that *C. melo* exhibits high diversity for fruit characteristics, varying in size, shape, external color, aroma, sugar contents, pulp color, and other characters, which often hinders the intraspecific classification that has been carried out since the first half of the nineteenth century (PITRAT, HANELT; HAMMER, 2000). However, despite all existing variation found in the present work, 62.50% of the sub-accessions were identified regarding their group and respective subgroup (Table 2, Figure 6). Similarly, Trimech et al. (2013) had not succeeded in identifying some groups when studying variability in melon, which may be attributed to the high heterogeneity and introgression of characters that did not allow for a clear identification of groups.

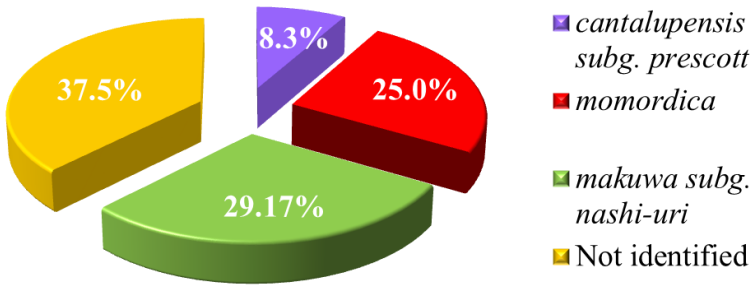

Figure 6. Percentage of identified and non-identified botanical groups and subgroups of melon (*Cucumis melo*) accessions from the Active Germplasm Bank of Cucurbitaceae from the Northeast Region at the Brazilian Agricultural Research Corporation (Embrapa Semiarid), in the study carried out in 2018 and 2019.

The morpho-agronomic data found showed the existence of a high genetic variability and denoted the importance of knowing the existing variation in melon species and how it is distributed through a throughout study of variations between and among accessions and sub-accessions. It was also shown in other studies evaluating melon germplasm from family farmers in the Northeast region of Brazil (TORRES FILHO et al., 2009; DANTAS; HOLANDA; 2015; AMORIM et al., 2016; MACÊDO et al., 2017; ANDRADE et al., 2019), which confirms the existence of high variability, denoting the wealth present in farming production units, which has been rescued and stored in the Active Germplasm Bank of Cucurbitaceae from the Northeast Region of Brazil. Although these throughout analysis had been carried out with botanical classifications different from those used in the present study, they are very important by presenting detailed information that can be used in future breeding programs for these melon types studied, as the

samples evaluated present potential for selection of useful alleles responsible for several factors related to fruit quality and production.

Thus, studies on botanical classification are also important because they rescue genetic variability and denote the need for starting documentation processes for these samples through passport data, in which the botanical identification process is one of the first steps for the management of active germplasm banks, contributing to studies with their accessions that can be useful for melon breeding programs (DANTAS, et al, 2012; PITRAT, 2016).

In addition, the botanical groups identified in the present study already showed satisfactory performance regarding resistance to several diseases and pests; the group *momordica*, for example, has resistance to viruses, powdery mildew, mildew, and *Aphis gossypii*; and the group *makuwa* has resistance to viruses, withering by *Fusarium* sp. Races 1 and 2, and *A. gossypii*; and the group *cantalupensis* has resistance to *Fusarium oxysporum* races 0 and 2 (PITRAT, 2013; PITRAT, 2016; DOGIMONT, 2011). Thus, their preservation in the short-, medium-, and long-terms is essential to maintain the genetic variability, avoiding genetic erosion and enable their use by future generations.

CONCLUSION

The melon germplasm from traditional agriculture in the Northeast region of Brazil presents different botanical groups (*makuwa* subgroup *nashi-uri*, *momordica,* and *cantalupensis* subgroup *prescott*), confirming the genetic variability between and among accessions and sub-accessions evaluated, which are stored in the Active Germplasm Bank of Cucurbitaceae from the Northeast Region at the Brazilian Agricultural Research Corporation (Embrapa Semiarid).

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