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Genetic parameters in melon sub-accessions from traditional agriculture

Parâmetros genéticos em subacessos de melão da agricultura tradicional

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ABSTRACT - Family farming in Brazil holds a high diversity of melon germplasm, composing an important source of alleles for breeding programs. Thus, the objective of this study was to estimate genetic parameters and select genotypes from a population of melon sub-accessions from different botanical varieties grown by family farmers, based on morphological parameters. Two experiments were conducted, one in 2019 and another in 2020, in a complete randomized block design, with three replications and five plants per plot, using 27 melon sub-accessions (generation S_2) from family farmers, and a commercial variety. Nine quantitative descriptors were evaluated. Assumptions of ANOVA were tested, followed by individual and joint analyses of variance. Significant differences were found among sub-accessions for all descriptors evaluated, with heritabilities higher than 83% and significant genotype-environment interactions for 88.8% of the characteristics evaluated. Thus, genetic variability was found among sub-accessions, with predominance of genetic effects over environmental effects, denoting the possibility to obtain genetic gains by the improvement of several characteristics of agronomic interest. The sub-accessions BGMEL66.0, BGMEL111.0, and BGMEL112.0 are recommended for inclusion in breeding programs focused on obtaining good prolificacy and small fruits with high soluble solid contents. BGMEL sub-accessions (108.3 and 108.5) can generate progenies with high prolificacy, and sub-accessions of the variety *momordica* can be used for generation of progenies focused on shortening the crop cycle and increasing fruit size.

Keywords: *Cucumis melo*. Diversity. Heritability. Genetic gain.

RESUMO - A agricultura familiar possui uma grande diversidade de germoplasma de melão, constituindo-se em uma importante fonte de alelos para uso em programas de melhoramento. Assim, o presente estudo objetivou estimar parâmetros genéticos e selecionar genótipos de uma população de subacessos de melão da agricultura familiar pertencentes a diferentes variedades botânicas, com base em caracteres morfológicos. Foram realizados dois experimentos (2019 e 2020), utilizando 27 subacessos de melão (geração S_2) provenientes da agricultura familiar e uma variedade comercial, em Delineamento em Blocos Casualizados (DBC) com três repetições e cinco plantas por parcela. Para avaliação foram utilizados nove descritores quantitativos. Inicialmente testou-se as pressuposições da ANOVA e, em seguida, realizou-se a análise de variância individual e a análise conjunta. Com isso, constatou-se diferença significativa entre os subacessos para todos os descritores avaliados, com herdabilidades superiores a 83% e iteração G x A significativa para 88,8% das características avaliadas. Assim, percebeu-se a existência de variabilidade genética entre os subacessos, com predominância dos efeitos genéticos sobre os ambientais, sendo possível obter ganhos genéticos para o melhoramento de várias características de interesse agronômico. Indica-se os subacessos BGMEL66.0, BGMEL111.0 e BGMEL112.0 para serem inseridos em programas de melhoramento visando obter frutos pequenos, com uma boa prolificidade e elevado teor de sólidos solúveis. Já os subacessos BGMEL (108.3 e 108.5) podem fornecer progênies de elevada prolificidade e os subacessos da variedade *momordica* podem ser utilizados para extração de progênies que visem diminuir o ciclo da cultura e aumentar o tamanho do fruto.

Palavras chaves: *Cucumis melo*. Diversidade. Herdabilidade. Ganho genético.

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. Cucurbitaceae) is a species that presents centers of diversity in Africa and Asia (PITRAT, 2013). However, it has great economic expression in Brazil, mainly those from the *inodorus* and *cantalupensis* groups; the Northeast region is responsible for 96.84% of the Brazilian melon production (IBGE, 2020). However, creole varieties have been grown in small rural properties, where farmers use their own seeds for new crops (QUEIRÓZ; BARBIERI; SILVA, 2015), resulting in a high variability.

Previous studies using melon germplasm from family farming showed the existence of high variability among melon accessions (DANTAS et al., 2012; ARAGÃO et al., 2013; AMORIM et al., 2016; MACÊDO et al., 2017; ANDRADE et al., 2019). However, some important characters for the improvement of melon were not emphasized in these studies, mainly regarding characteristics of some botanical varieties (PITRAT; HANELT; HAMMER, 2000), which are believed to be important factors and, therefore, should be considered.

Information on genetic factors is essential for any breeding program to identify and maintain favorable alleles; thus, obtaining estimates of genetic parameters is essential to identify the action of alleles involved in controlling characters and estimate genetic gains by selection. (CRUZ; CARNEIRO; REGAZI, 2014).

Melons from traditional agriculture are an important source of alleles for breeding programs. Although several studies have shown variability among melon accessions (AMORIM et al., 2016; MACÊDO et al., 2017), there is no study on this germplasm, focused on generating information for selection of genotypes. It denotes the need for studies using melon germplasm from family farmers for morphological characterization of different botanical varieties based on genetic parameters, focused on selecting superior genotypes.

Thus, the objective of this study was to estimate genetic parameters and select genotypes from a population of melon sub-accessions from different botanical varieties grown by family farmers, based on morphological parameters.

MATERIAL AND METHODS

Two experiments were conducted, one in 2019 and another in 2020, at the Experimental Field of the Department of Technology and Social Sciences of the Bahia State University (DTCS/UNEB), in Juazeiro, Bahia, Brazil (09°25'04.92271"S and 40°29'04.73710"W, and altitude of approximately 352 meters). Twenty-seven melon sub-accessions (AMORIM et al., 2016) (S_2 generation) from the botanical varieties *momordica*, *cantalupensis*, and *makuwa* and some accessions not identified were evaluated. These accessions were from the traditional agriculture of the state of Maranhão, Brazil (Table 1) that were stored in the Active Germplasm Bank of Cucurbitaceae from the Northeast Region at the Brazilian Agricultural Research Corporation (Embrapa Semiarid), in Petrolina, Pernambuco. A commercial variety (Melao Amarelo) was used as control.

Table 1. Passport data of sub-accessions of *Cucumis melo* from the Active Germplasm Bank of Cucurbitaceae from the Northeast Region at the Brazilian Agricultural Research Corporation (Embrapa Semiarid), evaluated in 2019 and 2020.

Sub-accession	Variety*	Municipality of collection	Municipality coordinates
BGMEL 10.0	*momordica*	São João of Patos	6°29'43"S, 43°42'10"W
BGMEL 66.0	*makuwa*	Colinas	7°6'59"S, 46°15'26"W
BGMEL 67.0	*makuwa*	Colinas	7°6'59"S, 46°15'26"W
BGMEL 68.1	*momordica*	Colinas	7°6'59"S, 46°15'26"W
BGMEL 68.2	ND	Colinas	7°6'59"S, 46°15'26"W
BGMEL 68.3	ND	Colinas	7°6'59"S, 46°15'26"W
BGMEL 77.1	*momordica*	Coroatá	4°7'31"S, 44°7'49"W
BGMEL 77.3	ND	Coroatá	4°7'31"S, 44°7'49"W
BGMEL 78.0	*cantalupensis*	Codó	4°27'18"S, 43°52'44"W
BGMEL 82.2	*cantalupensis*	Itapecuru Mirim	3°23'42"S, 44°21'36"W
BGMEL 83.1	ND	Itapecuru Mirim	3°23'42"S, 44°21'36"W
BGMEL 83.2	ND	Itapecuru Mirim	3°23'42"S, 44°21'36"W
BGMEL 86.1	*cantalupensis*	Codó	4°27'18"S, 43°52'44"W
BGMEL 86.2	ND	Codó	4°27'18"S, 43°52'44"W
BGMEL 86.3	ND	Codó	4°27'18"S, 43°52'44"W
BGMEL 87.1	*momordica*	São Luís Gonzaga	4°22'51"S, 44°40'14"W
BGMEL 87.2	*cantalupensis*	São Luís Gonzaga	4°22'51"S, 44°40'14"W
BGMEL 87.3	ND	São Luís Gonzaga	4°22'51"S, 44°40'14"W
BGMEL 97.1	*cantalupensis*	Caxias	4°52′29"S, 43°20′49"W
BGMEL 98.0	ND	Caxias	4°52′29"S, 43°20′49"W
BGMEL 108.3	ND	Caxias	4°52′29"S, 43°20′49"W
BGMEL 108.4	ND	Caxias	4°52′29"S, 43°20′49"W
BGMEL 108.5	ND	Caxias	4°52′29"S, 43°20′49"W
BGMEL 109.2	ND	Caxias	4°52′29"S, 43°20′49"W
BGMEL 111.0	*makuwa*	Colinas	7°6′59″S, 46°15′26″W
BGMEL 112.0	*makuwa*	Colinas	7°6′59″S, 46°15′26″W
BGMEL 115.0	*makuwa*	São Vicente Ferrer	2°53'44"S, 44°52'53"W

*Botanical classification according to Amorim et al. (2016); ND = botanical variety not defined.

Thirty seeds of each sub-accession were sown in plastic trays filled with a commercial substrate, in a greenhouse covered with a 50% shade screen, and irrigated daily. The seedlings were transplanted to soils previously prepared with plowing and harrowing 15 days after sowing.

The experiments were conducted in a complete randomized block design, with three replications, five plants per plot, and spacings of 2.5 m between rows and 0.8 m between plants, under localized drip irrigation.

The experiments were conducted approximately in the same period (January to April) in 2019 and 2020. Weeding and plant health status monitoring were carried out; the natural soil fertility was adopted, since this system is commonly used under traditional agriculture.

The evaluations were carried out using the following quantitative descriptors (IPGRI, 2003; PITRAT; HANELT; HAMMER, 2000): fruit weight (kg); fruit diameter and length (cm); fruit cavity diameter and length (cm); pulp thickness (cm); soluble solid contents (ºBrix) in pulp composite samples homogenized in a kitchen food processor; earliness (number of days from transplanting to harvest), and prolificacy (number of fruits per plant, counted at the end of the crop cycle).

Regarding the statistical analyses, firstly, the assumptions of ANOVA were tested, transforming the variables when necessary. Individual analysis of variance was then performed for each growing year to assess whether the sub-accessions differed from each other. Subsequently, test of homogeneity of variances was applied (Fmax: ratio between the highest and lowest residual mean square for each descriptor). Joint analysis (A×B simple factorial) was carried out using the model: $Y_{ijk} = \mu + G_i + A_j + GA_{ij} + B/A_{jk} + \varepsilon_{ijk}$, where μ = overall mean; G_i = effect of the i-th genotype; A_j = effect of the j-th environment; GA_{ij} = effect of the interaction of the i-th genotype with the j-th environment; B/A_{jk} = effect of the k-th block inside the j-th environment; and εijk = random error and effects: G (random) and A (fixed) (CRUZ; REGAZI; CARNEIRO, 2012). All genetic and statistical analyses were processed using the program Genes (CRUZ, 2013).

RESULTS AND DISCUSSION

The data of analysis of variance showed significant differences among melon sub-accessions for all characteristics evaluated (Table 2), denoting the existence of genetic variability among sub-accessions. Similar results were found in previous studies on melon accessions from traditional agriculture (AMORIM et al., 2016; MACÊDO et al., 2017; ANDRADE et al., 2019), supporting those found in the present study and, therefore, denoting the possibility of selecting agronomically superior accessions for the characteristics analyzed (CRUZ; REGAZI; CARNEIRO, 2012).

Table 2. Test of means for nine characters of melon sub-accessions from family farmers of the state of Maranhão, Brazil, evaluated in 2019 and 2020.

SUB	EARL		PROL		FW		FD		FL	
	19	20	19	20	19	20	19	20	19	20
10.0 ^{mo}	49.9dA	53.5bA	3.2cA	3.8cA	1.1aA	1.3cA	11.3cA	11.5cA	24.1bA	26.0bA
68.1 ^{mo}	51.7dA	53.6bA	2.7cB	6.6bA	1.1aA	1.3cA	11.2cA	12.2cA	24.9bA	24.5cA
77.1 ^{mo}	50.3dA	52.1bA	4.3cA	3.6cA	1.3aA	1.4cA	11.6cA	11.7cA	27.9aA	28.5aA
87.1 ^{mo}	58.8cA	56.0bA	1.8cA	2.2cA	0.9bB	2.1bA	11.0cA	12.6bA	19.6dB	29.9aA
Mean ^{mo}	52.73	53.83	3.03	4.09	1.17	1.56	11.31	12.05	24.16	27.24
66.0 ^{mk}	54.6dA	55.0bA	3.0cB	6.7bA	0.3cA	0.4fA	8.0eA	8.6dA	11.6eA	12.6fA
67.0 ^{mk}	55.4cA	53.3bA	2.3cA	4.1cA	0.5cA	0.4fA	9.3dA	8.6dA	13.2eA	12.1fA
111.0 ^{mk}	54.0dA	54.0bA	1.8cB	7.7bA	0.3cA	0.3fA	8.1eA	7.6eA	11.5eA	10.3fA
112.0 ^{mk}	55.7cA	54.2bA	3.4cA	5.9bA	0.3cA	0.2fA	8.0eA	7.5eA	11.6eA	10.1fA
115.0 ^{mk}	56.1cA	55.4bA	2.0cB	5.5bA	0.4cA	0.5eA	8.3eA	9.2dA	12.3eA	13.7eA
Mean ^{mk}	55.19	54.40	2.51	6.02	0.42	0.41	8.38	8.35	12.09	11.79

Means followed by same lowercase letter in the columns, or uppercase letter in the rows, are not statistically different from each other by the Scott Knott test at 5% significance. SUB = sub-accession; 19 and 20 = evaluation years of 2019 and 2020; FW = fruit weight (Kg); EARL: earliness (number of days from transplanting to harvest); PROL: prolificacy (number of fruits per plants, counted at the end of the crop cycle); FD and FL= fruit diameter and length, respectively (cm); FCD and FCL = fruit cavity diameter and length, respectively (cm); PT = pulp thickness (cm); SS: soluble solid contents (°Brix); Min and Max refer to the individual values and show the variation within the sub-accession; Fc = Snedecor's F distribution. ** = significant at 1%; CV(%) = coefficient of variation; Ama = commercial variety Melao Amarelo; and mo, mk, c, and nd = varieties *momordica*, *makuwa*, *cantalupensis*, and not defined, respectively.

Table 2. Continuation.

SUB	EARL		PROL		FW		FD		FL	
	19	20	19	20	19	20	19	20	19	20
78.0 ^{c}	65.8bA	59.6aB	1.6cA	2.5cA	1.1aA	1.5cA	10.6cA	10.8cA	20.6cB	24.1cA
82.2 ^{c}	63.1bA	55.1bB	1.1cA	3.3cA	0.2cB	0.7eA	7.6eB	9.8dA	7.4fA	14.4eA
86.1 ^{c}	63.0bA	55.0bB	1.0cA	2.3cA	0.5cA	0.8eA	9.2dA	10.6cA	14.0eA	15.9eA
87.2 ^{c}	67.6bA	61.0aB	0.5cA	1.0cA	1.4aB	1.9bA	11.7cB	13.7bA	18.8dB	21.9dA
97.1 ^{c}	71.3aA	59.3aB	0.4cA	1.1cA	0.8bA	0.8eA	11.8cA	10.7cA	14.4eA	15.9eA
Mean ^{c}	66.22	60.17	0.96	2.06	0.86	1.16	10.22	11.13	15.10	18.47
68.2 nd	54.1dA	55.1bA	2.6cA	4.2cA	0.8bA	0.8eA	10.8cA	11.1cA	17.8dA	16.5eA
68.3 nd	62.4bA	55.0bB	1.5cA	1.9cA	0.5cB	1.0dA	8.1eA	9.0dA	18.4dB	25.6bA
77.3 nd	66.8bA	58.6aB	1.9cA	0.9cA	1.4aA	1.0dB	13.2bA	10.4cB	21.8cA	20.2dA
83.1 nd	57.6cA	55.0bA	1.5cA	3.6cA	1.3aA	1.0dA	14.8aA	13.3bA	14.4eA	14.6eA
83.2 nd	71.6aA	55.3bB	0.5cA	1.2cA	0.3cB	0.7eA	8.7dB	11.3cA	10.4fA	11.5fA
86.2 nd	56.3cA	57.0bA	1.2cB	5.1bA	0.4cB	0.8eA	9.4dB	11.3cA	8.9fA	11.5fA
86.3 nd	59.6cA	56.0bA	0.5cA	1.6cA	0.5cA	0.6eA	9.2dA	9.9dA	12.3eA	13.3fA
87.3 nd	58.5cA	58.5aA	1.5cA	2.1cA	1.5aB	3.1aA	12.7bB	15.6aA	22.3cB	27.1bA
98.0 nd	72.0aA	61.0aB	0.7cA	2.0cA	0.3cB	0.7eA	7.8eB	10.4cA	10.8fB	14.3eA
108.3 nd	54.3dA	51.0bA	11.5aA	10.9aA	0.3cA	0.3fA	7.7eA	7.6eA	11.4eA	12.5fA
108.4 nd	61.1cA	56.5bA	5.2cA	6.9bA	0.5cA	0.6eA	9.1dA	9.5dA	14.0eA	14.4eA
108.5 nd	52.5dA	51.3bA	8.0bA	10.8aA	0.2cA	0.3fA	7.2eA	7.7eA	8.2fA	9.8fA
109.2 nd	59.0cA	52.8bB	3.2cA	3.8cA	0.2cA	0.4fA	7.0eA	7.9eA	10.7fA	12.8fA
Mean nd	60.48	55.64	3.10	4.26	0.68	0.92	9.72	10.43	14.01	15.75
Ama	72.3aA	61.0aB	0.6cA	2.1cA	0.5cB	0.9dA	8.9dB	10.6cA	13.8eA	16.6eA
Min	45.0	49.0	0.2	0.4	0.44	0.25	6.73	7.27	7.1	9.0
Max	76.0	61.0	15.8	16.0	1.52	3.34	15.15	16.7	29.98	32.8
Mean	59.88	55.77	2.51	4.08	0.81	0.96	9.77	10.42	15.30	17.20
Fc	**	**	**	**	**	**	**	**	**	**
CV%	6.60	3.53	75.87	45.99	12.81	22.50	11.16	8.04	11.04	11.29

SUB	FCD		FCL		PT		SS	
	19	20	19	20	19	20	19	20
10.0 ^{mo}	5.9bA	6.1aA	20.0bA	21.3bA	2.3bA	2.4bA	4.4dA	3.7dA
68.1 ^{mo}	5.7bA	6.4aA	20.5bA	20.0bA	2.4bA	2.6bA	4.3dA	3.7dA
77.1 ^{mo}	6.4bA	6.2aA	23.7aA	24.1aA	2.5aA	2.6bA	4.4dA	4.2dA
87.1 ^{mo}	5.0cB	6.4aA	16.8cB	24.8aA	2.1bB	3.0bA	4.8dA	3.8dA
Mean ^{mo}	5.81	6.31	20.28	22.60	2.38	2.71	4.48	3.85
66.0 ^{mk}	4.4cA	5.0bA	9.1eA	10.1eA	1.4cA	1.8cA	8.6aA	8.1aA
67.0 ^{mk}	5.0cA	4.8bA	9.9eA	9.7eA	1.7cA	1.7dA	7.5bA	6.7aA
111.0 ^{mk}	4.6cA	4.4bA	9.0eA	8.2eA	1.4cA	1.4dA	9.5aA	7.7aB
112.0 ^{mk}	4.4cA	4.7bA	9.0eA	8.2eA	1.5cA	1.3dA	9.2aA	7.7aB
115.0 ^{mk}	4.6cA	5.0bA	9.6eA	11.5dA	1.5cB	2.0cA	7.5bA	5.8bB
Mean ^{mk}	4.63	4.84	9.36	9.56	1.53	1.67	8.46	7.20

Means followed by same lowercase letter in the columns, or uppercase letter in the rows, are not statistically different from each other by the Scott Knott test at 5% significance. SUB = sub-accession; 19 and 20 = evaluation years of 2019 and 2020; FW = fruit weight (Kg); EARL: earliness (number of days from transplanting to harvest); PROL: prolificacy (number of fruits per plants, counted at the end of the crop cycle); FD and FL= fruit diameter and length, respectively (cm); FCD and FCL = fruit cavity diameter and length, respectively (cm); PT = pulp thickness (cm); SS: soluble solid contents (°Brix); Min and Max refer to the individual values and show the variation within the sub-accession; Fc = Snedecor's F distribution. ** = significant at 1%; CV(%) = coefficient of variation; Ama = commercial variety Melao Amarelo; and mo, mk, c, and nd = varieties *momordica*, *makuwa*, *cantalupensis*, and not defined, respectively.

Table 2. Continuation.

SUB	FCD		FCL		PT		SS	
	19	20	19	20	19	20	19	20
78.0^{c}	5.2cA	4.9bA	15.6dB	19.8bA	2.6aA	2.7bA	6.0cA	4.3dB
82.2^{c}	4.3cA	4.6bA	5.2fB	11.0dA	1.5cB	2.5bA	7.4bA	5.1cB
86.1^{c}	4.8cA	5.6aA	10.0eA	10.9dA	2.1bA	2.3cA	6.4cA	5.8dA
87.2^{c}	4.6cA	5.2bA	13.7dB	16.9cA	3.1aB	4.1aA	6.0cA	5.7bA
97.1^{c}	7.3aA	5.9aB	11.0eA	12.1dA	1.9cA	2.0cA	4.7dA	4.2dA
Mean^{c}	5.29	5.29	11.14	14.18	2.27	2.76	6.10	5.02
68.2nd	6.0bA	6.1aA	14.4dA	12.9dA	2.1bB	3.0bA	6.1cA	4.6dB
68.3nd	3.8cA	4.2bA	15.5dB	21.6bA	1.7cA	2.2cA	4.1dA	5.0cA
77.3nd	8.1aA	6.3aB	17.2cA	15.8cA	2.3bA	1.9cA	5.8cA	4.4dB
83.1nd	8.4aA	7.1aB	9.9eA	9.9eA	2.8aA	2.7bA	5.8cA	5.3cA
83.2nd	4.4cB	5.8aA	6.4fA	7.7eA	1.9cB	2.5bA	6.0cA	6.9aA
86.2nd	5.2cA	5.6aA	6.2fA	8.6eA	1.7cB	2.6bA	4.2dA	5.3cA
86.3nd	5.4cA	6.0aA	8.9eA	10.1eA	1.7cA	1.8cA	5.4cA	5.9bA
87.3nd	6.1bA	7.0aA	17.4cB	21.1bA	2.7aB	4.2aA	4.7dA	3.4dB
98.0nd	5.0cA	6.1aA	8.0eB	11.3dA	1.4cB	2.1cA	6.1cA	4.3dB
108.3nd	4.3cA	3.7bA	8.7eA	8.7eA	1.6cA	1.9cA	3.8dA	3.8dA
108.4nd	4.5cA	5.1bA	10.5eA	11.3dA	2.0bA	2.1cA	5.9cA	5.3cA
108.5nd	3.9cA	4.3bA	6.1fA	7.7eA	1.3cA	1.6dA	6.4cA	4.2dB
109.2nd	3.7cA	4.0bA	7.8eA	9.5eA	1.4cA	1.8cA	7.2bA	6.8aA
Meannd	5.33	5.51	10.58	12.05	1.94	2.36	5.50	5.02
Ama	4.50cA	4.81bA	9.75eA	12.00dA	2.11bB	2.78bA	5.6cA	4.4dA
Min	3.37	3.47	5.0	6.7	1.2	1.2	2.93	2.87
Max	10.15	8.0	24.85	27.2	4.06	4.45	10.4	9.2
Mean	5.23	5.43	11.82	13.49	1.9	2.37	6.03	5.24
Fc	**	**	**	**	**	**	**	**
CV%	8.77	9.23	3.41	6.97	7.28	14.17	13.82	14.40

Means followed by same lowercase letter in the columns, or uppercase letter in the rows, are not statistically different from each other by the Scott Knott test at 5% significance. SUB = sub-accession; 19 and 20 = evaluation years of 2019 and 2020; FW = fruit weight (Kg); EARL: earliness (number of days from transplanting to harvest); PROL: prolificacy (number of fruits per plants, counted at the end of the crop cycle); FD and FL= fruit diameter and length, respectively (cm); FCD and FCL = fruit cavity diameter and length, respectively (cm); PT = pulp thickness (cm); SS: soluble solid contents (°Brix); Min and Max refer to the individual values and show the variation within the sub-accession; Fc = Snedecor's F distribution. ** = significant at 1%; CV(%) = coefficient of variation; Ama = commercial variety Melao Amarelo; and mo, mk, c, and nd = varieties *momordica*, *makuwa*, *cantalupensis*, and not defined, respectively.

Regarding the homogeneity of sub-accessions in the different growing years, the test of means (Table 2) showed that 22.2% of the sub-accessions (BGMEL10.0, BGMEL77.1, BGMEL67.0, BGMEL86.3, BGMEL108.3, and BGMEL108.4) presented no difference to each other for the characters evaluated. However, 25.9% of the sub-accessions (BGMEL77.3, BGMEL82.2, BGMEL83.2, BGMEL87.1, BGMEL87.2, BGMEL87.3, and BGMEL98.0) presented variations higher than 55.5%; the highest variations were found for earliness (37%), soluble solid contents (37%), fruit weight (33.3%), and pulp thickness (33.3%).

The earliness in the different growing years presented variations in for 37% of the sub-accessions: five from the variety *cantalupensis* (BGMEL78.0, BGMEL82.2, BGMEL 86.1, BGMEL 87.2, and BGMEL97.1), five from botanical varieties not identified (BGMEL68.3, BGMEL77.3, BGMEL83.2, BGMEL98.0, and BGMEL109.2), and the control. According to the means of the melon varieties, the highest means were found in the growing year I (2019), except for *momordica*. The lowest means were found for *momordica* and the highest for the commercial variety (Melao Amarelo) (Table 2), denoting the potential of the variety *momordica* for selection focused on increasing earliness.

Prolificacy and fruit cavity diameter presented only 18.5% variation, highlighting the variety *makuwa* and botanical varieties not defined (ND), respectively. Regarding the other characteristics, the highest variations were found for sub-accessions of ND varieties (Table 2); these variations are probably because of the high variability among plants within the sub-accessions, which is due to the introgression of alleles among different botanical varieties (MACÊDO et al., 2017; AMORIM et al., 2016).

All characteristics were, in general, favored in the growing year II (2020), except soluble solid contents. Sub-accessions from *momordica* stood out for earliness and characteristics related to fruit size (fruit weight, fruit diameter and length, fruit cavity diameter and length, and pulp thickness). In addition, they presented a good prolificacy (Table 2), denoting that this botanical variety is important for selection processes focused on improving these characteristics.

Sub-accessions from ND varieties presented the highest prolificacy (Table 2), mainly the sub-accessions BGMEL108.3 and BGMEL 108.5, however they presented small fruits with low soluble solid contents. Sub-accessions from *makuwa* also presented prolificacy and progenies with high soluble solid contents, mainly BGMEL66.0, BGMEL111.0, and BGMEL112.0, with small fruits and good prolificacy, which can be a novelty in the market. The control (commercial variety) presented low prolificacy and medium-sized fruits with low solid soluble contents, under the same crop conditions. The commercial variety presented low performance was probably due to the use of the natural soil fertility management, which is common for traditional agricultural crops, since high chemical fertilizer rates are applied to soils for commercial crops.

The joint analysis of variance (Table 3) showed coefficients of variation varying from 5.40 (earliness) to 57.38 (prolificacy). Joint analysis is recommended only for environments with homogeneous residual variances. According to Cruz, Regazi and Carneiro (2012), several tests can be used to evaluate the homogeneity of residual variances, however, they have limitations or restrictions of use; thus, a practical criterion that can be adopted for grouping experiments to proceed joint analysis is to combine trials whose residual mean squares do not exceed the approximate ratio of 7:1 in the same group. In the present study, the ratios between the highest and lowest variances were between 1.03 and 4.01 for all characteristics evaluated (Table 3), which allowed to proceed the joint analysis and assess the genotype-environment interaction. The high variability found among sub-accessions is partially due to existing differences among plants within each sub-accession. Studies on melon germplasm showed a high variation among accessions (DANTAS et al., 2012; ARAGÃO et al., 2013; TRIMECH et al., 2013; YILDIZ ; AKGUL; SENSOY, 2014; ANDRADE et al., 2019) and among plants within accessions (AMORIM et al., 2016; MACÊDO et al., 2017).

Table 3. Joint analysis of variance among melon sub-accessions from family farmers of the state of Maranhão, Brazil, evaluated in 2019 and 2020.

SV	DF	Mean square								
		EARL	FW	FD	FL	FCD	FCL	PT	SS	PROL
G	27	12.99**	32.90**	22.70**	57.90**	12.00**	57.12**	19.64**	17.51**	10.18**
E	1	7.85ns	3.99ns	2.38ns	4.84ns	2.02ns	5.56ns	9.38ns	14.68ns	6.69*
G×E	27	3.71**	5.33**	2.72**	3.52**	1.80*	2.97**	3.06**	2.04**	1.04ns
RES		9.77	0.04	0.94	3.31	0.48	2.64	0.09	0.63	3.58
CV		5.40	25.41	9.63	11.20	13.08	12.83	13.91	14.11	57.38
Mean		57.82	0.84	10.09	16.25	5.33	12.65	2.18	5.64	3.29
Fmax		4.01	1.03	1.68	1.31	2.87	1.97	1.57	1.21	1.03

SV = source of variation; DF = degrees of freedom; EARL = earliness; FW = fruit weight; FD = fruit diameter; FL = fruit length; FCD = fruit cavity diameter; FCL = fruit cavity length;; PT = pulp thickness; SS = soluble solid contents (°Brix); PROL = prolificacy; G = genotype; E = environment; G×E = genotype-environment interaction; RES = residue; CV = coefficient of variation; Fmax = ratio between the highest and lowest residual mean square; **, * = significant at 1% and 5% significance, respectively; ns = not significant.

The joint analysis of variance (Table 3) showed that the genotype effect was highly significant ($p \leq 0.01$) for all variables, whereas the environmental effect was not significant, except for prolificacy. The genotype-environment interaction was significant for all variables, except prolificacy.

The predominance of estimates of genetic effects over environmental effects indicates that the genetic factors had a greater effect on the observed phenotype. However, the significant interaction for 88.8% of the variables denotes that the relative performance of the sub-accessions (BORÉM; MIRANDA, FRITSCHE-NETO, 2017) varied in the two growing years for all variables evaluated, except prolificacy. However, the temperature data were similar in the two growing years: mean temperatures varied from 27.46 to 28.03 °C (2019) and from 26.56 to 27.28 °C (2020). Rainfall data showed a small difference between growing years: 0.26 to 5.27 mm (2019) and 1.19 to 9.15 mm (2020) (AGRITEMPO, 2021).

High heritability was found for the genetic parameters, with estimates higher than 83% for all characters evaluated (Table 4), mainly for some characteristics related to fruit size (fruit length, cavity length, and fruit weight). These results denote a great potential for successful selection focused on these characters, as the observed phenotype was mostly affected by the genetic factor. The sub-accessions BGMEL 77.1 and BGMEL 87.1 (variety *momordica*) and BGMEL 87.3 (variety not defined) stood out for these characteristics (Table 2), showing to be promising for selection processes focused on increasing fruit size.

Lower results were found by Valadares et al. (2017) for fruit weight (86.00%) and length (93.00%) when evaluating heritability of 23 melon accessions from the *momordica* group. However, this difference can be attributed to the use of another set of genotypes in the experiment conducted under greenhouse conditions, which allows for more control of environmental effects. Aragão, Nunes and Queiróz (2015) evaluated melon families and found lower heritabilities than those found in the present study, for all characters evaluated.

The estimated genetic, phenotypic, and environmental variations (Table 4) indicated that the genetic variation (σ^2_G) was higher than the environmental variation (σ^2_E) for all characters evaluated. Thus, it can be said that genetic effects predominate in the expression of the phenotype, indicating greater reliability and greater genetic gains in phenotypic selection. However, more significant variations between growing years were found for earliness, prolificacy, fruit length, and fruit cavity length.

Table 4. Genetic parameters for characters of melon sub-accessions from family farmers of the state of Maranhão, Brazil, evaluated in 2019 and 2020.

		Genetic parameters						
Character	Year	σ^2_F	σ^2_E	σ^2_G	h^2(%)	CV_g(%)	CV_e(%)	(CV_g/CV_e)
EARL	19	46.45	5.22	41.23	88.76	10.72	6.61	1.62
	20	0.03	0.005	0.02	83.31	2.24	1.73	1.29
PROL	19	0.26	0.03	0.22	85.54	26.88	19.2	1.40
	20	7.50	1.17	6.33	84.34	61.64	46.00	1.34
FW	19	0.02	0.001	0.02	93.07	11.75	5.56	2.11
	20	0.04	0.001	0.04	95.97	14.73	5.22	2.82
FD	19	4.01	0.39	3.61	90.11	19.45	11.17	1.74
	20	4.01	0.23	3.77	94.15	18.63	8.06	2.31
FL	19	29.56	0.95	28.61	96.77	34.93	11.05	3.16
	20	38.32	1.25	37.06	96.71	35.39	11.29	3.13
FCD	19	0.05	0.008	0.04	83.86	8.38	6.39	1.31
	20	0.81	0.08	0.72	89.63	15.67	9.27	1.69
FCL	19	23.57	0.59	22.98	97.48	40.55	11.29	3.59
	20	0.46	0.01	0.44	95.79	17.75	6.45	2.75
PT	19	0.23	0.02	0.21	89.93	23.15	13.45	1.72
	20	0.03	0.002	0.02	92.45	9.35	4.62	2.02
SS	19	2.35	0.23	2.12	90.12	24.12	13.86	1.74
	20	1.78	0.19	1.59	89.29	24.03	14.47	1.66

σ^2_F = phenotypic variation; σ^2_E = environmental variation; σ^2_G = genetic variation; h^2(%) = heritability; CV_g(%) = coefficient of genetic variation; CV_e(%) = coefficient of environmental variation; (CV_g/CV_e) = CV_g to CV_e ratio; FW = fruit weight (kg); EARL = earliness; PROL = prolificacy; FD = fruit diameter (cm); FL = fruit length (cm); FCD = fruit cavity diameter (cm); FCL = fruit cavity length (cm); PT= pulp thickness; and SS = soluble solid contents (°Brix).

The coefficients of genetic variation (CV_g) found varied from 2.24% to 61.64% (Table 4) and were higher than the coefficients of environmental variation (CV_e) for all characters evaluated. The lowest CV_g were found for earliness and the highest for prolificacy, fruit cavity length, fruit length, and soluble solids. However, the highest CV_e were also found for prolificacy and soluble solid contents, indicating that these characteristics were highly affected by environmental factors. Valadares et al. (2017) evaluated melon accessions from the variety *momordica* and found the highest CV_g for pistil scar size (72.04) and soluble solid contents (55.34). Ferreira et al. (2016) evaluated pumpkin accessions and found the highest CV_g for fruit weight and prolificacy, which denotes a greater effect of genetic factors on the expression of the phenotype and reinforces the existence of high variability in the germplasm.

The CV_g to CV_e ratio (CV_g/CV_e) presented values >1 for all characters (Table 4). CV_g/CV_e equal to or higher than 1 and heritability higher than 80% are favorable conditions for selection (CRUZ; REGAZI; CARNEIRO, 2012), which were found for all characteristics evaluated, denoting great potential for a successful selection.

CONCLUSIONS

The melon sub-accessions evaluated present genetic variability, with predominance of genetic effects over environmental effects, denoting the possibility of obtaining genetic gains by improving several characteristics of agronomic interest. The sub-accessions BGMEL 66.0, BGMEL111.0, and BGMEL112.0 from the variety *makuwa* are an important source of germplasm for the obtaining of good prolificacy and small fruits with high soluble solid contents. However, the sub-accessions BGMEL 108.3 and BGMEL 108.5, from botanical varieties not defined, can generate progenies with a high prolificacy; whereas sub-accessions from the variety *momordica* can be used for generation of progenies focused on shortening the crop cycle and increasing fruit size.

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