horticultura brasileira

Scientific communication

VALADARES, RN; MELO, RA; SARINHO, IVF; OLIVEIRA, NS; ROCHA, FAT; SILVA, JW; MENEZES, D. 2018. Genetic diversity in accessions of melon belonging to *momordica* group. *Horticultura Brasileira* 36: 253-258. DOI: http://dx.doi.org/10.1590/S0102-053620180218

Genetic diversity in accessions of melon belonging to *momordica* group

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ABSTRACT

The genetic divergence of melon genotypes belonging to *momordica* group, collected in five Brazilian States, was estimated, and the relative contribution of the morphological characters was determined for the genetic variability. The experimental design was randomized blocks, with four replicates. We evaluated 19 accessions of melon, *momordica* group, two accessions of *cantaloupensis* group and two commercial cultivars of *inodorus* group. These genotypes were characterized by 42 morphological descriptors. The data were submitted to Tocher and UPGMA grouping methods using the genetic dissimilarity matrix, using Mahalanobis' distance. Singh criterion was used to identify the relative contribution of each character to the genetic divergence. Four groups of similarity were obtained in both multivariate techniques, with agreement between hierarchical UPGMA and Tocher grouping methods. The characters: pistil scar size, soluble solid content, seed length, fruit length and cotyledon length contributed with approximately 53.86% to genetic divergence among genotypes.

Keywords: *Cucumis melo* var. *momordica*, genetic variability, snow melon, papoco melon.

RESUMO

Divergência genética em acessos de melão do grupo *momordica*

A divergência genética de genótipos de melão do grupo *momordica* foi estimada, coletados em cinco estados brasileiros, e determinada a contribuição relativa dos caracteres morfológicos avaliados para a variabilidade genética. Foi adotado o delineamento de blocos casualizados com quatro repetições. Nesse estudo, foram utilizados 19 acessos de melão do grupo *momordica*, dois acessos do grupo *cantaloupensis* e duas cultivares comerciais do grupo *inodorus*. Esses genótipos foram caracterizados por meio de 42 descritores morfológicos. Os dados foram submetidos aos métodos de agrupamento de Tocher e UPGMA a partir da matriz de dissimilaridade genética de Mahalanobis (D^2). Foi utilizado o critério de Singh, para identificar a contribuição relativa de cada caráter para a divergência genética. Obtiveram-se quatro grupos de similaridade em ambas as técnicas multivariadas utilizadas, havendo concordância entre os métodos hierárquicos UPGMA e de agrupamento de Tocher. Os caracteres, tamanho da cicatriz do pistilo, teor de sólidos solúveis, comprimento da semente, comprimento de fruto e comprimento do cotilédone contribuíram com aproximadamente 53,86% para a divergência genética entre os genótipos.

Palavras-chaves: *Cucumis melo* var. *momordica*, variabilidade genética, melão de neve, melão papoco.

Received on March 30, 2016; accepted on November 14, 2017

Melon (*Cucumis melo*), belonging to *Cucurbitaceae* family, is one of the species presenting great genetic variability for several characters, mainly with respect to fruits. Due to this fact, some intraspecific classifications of *C. melo* have been suggested, over time, by Cogniaux & Harms (1924), Pangalo (1933), Filov (1960), Whitaker & Davis (1962), Grebenščikov (1986), Munger & Robinson (1991) and Pitrat *et al*. (2000) cited by Aragão (2011).

One of the most recent classification, and widely used in literature, proposed to divide the species into six botanical groups: *cantaloupensis*, *inodorus*, *conomon*, *dudaim*, *flexuosus* and *momordica* (Robinson & Decker-Walters, 1997). Many of these groups are economically important in developed countries and they were based on their culinary attributes (Staub *et al*., 2000). We highlight that different botanic groups can be crossed among each other, without any incompatibility barriers (Aragão, 2011).

The botanical groups *inodorus* and *cantaloupensis* are considered the most important ones considering the commercial value, and in these groups we can also find the most commonly grown and widely marketed varieties in Brazil, yellow melon and piel de sapo melon (Aragão, 2011). The yellow melon is Brazil's most exported melon fruit, followed by orange flesh and piel de sapo, with 60, 15 and 9% of exportations, respectively (Nunes *et al.*, 2011).

On the other hand, in the national market, the local or native cultivars have been dividing space with the commercial

cultivars in some areas of Brazil. These cultivars are adapted to several soil and climatic conditions (Torres Filho *et al.*, 2009) and have been grown over time by family farmers, and can be used as parents in melon breeding programs.

The melons belonging to *momordica* group are known by different names in the countries where they are found. In tropical and subtropical regions of India, the melons are vulgarly known as "*phut"* or *"snapmelon*". In some Brazilian regions, they are known as papoco melon, meloite, snow melon and vitamin melon. Among the most striking characteristics is the rupture of the fruit when it reaches ripeness, low total soluble solid content, besides exhaling a soft aroma similar to melons of the *cantaloupensis* group. Because having a flavor of naturally tasteless pulp, they are consumed *in natura* with sugar, honey or other sweeteners, besides being used for the preparation of soft drinks, salads and pickles when ripe or cooked when immature (Valadares, 2014; Dhillon *et al*., 2007).

Accessions of *momordica* group melons with genetic resistance to several diseases were observed. Among these diseases can be related the ones caused by the fungus *Fusarium oxysporium, Podosphaera xanthii*, *Myrothecium roridum* (Nascimento *et al.*, 2012), by the nematode *Meloidogyne incognita,* by PRSV virus (*Papaya Ring Spot Vírus*) (Dhillon *et al*., 2007), and some pests like the leafminer *Liriomyza trifolii* and aphid *Aphis gossypii* (Fergany *et al*., 2011).

In order to use the genetic variability of Brazilian melon populations belonging to *momordica* group, some collections of traditional varieties in the main producer regions are necessary, as well as the characterization using morphological descriptors available in literature aiming to identify favorable characters and characters of interest for the breeding program of this vegetable.

The aim of this study was to estimate genetic divergence of melon genotypes of *momordica* group, collected in five Brazilian States, and determine the relative contributions of the evaluated morphological characters.

MATERIAL AND METHODS

The experiment was installed in the Department of Agronomy, at the Area of Phytotechnology at Universidade Federal Rural of Pernambuco, Campus Dois Irmãos, Recife, from April to July, 2013. The plants were conducted in hydroponic system in a greenhouse, arch type, 30 m length, 14 m width, 3 m ceiling height, closed laterally with 50% shading screen and covered with low-density polyethylene film, 150 µm.

The experimental design was randomized blocks, with 23 treatments, four replicates and two plants per experimental plot. The authors evaluated 19 accessions of melon belonging to *momordica* group collected in the States of Pernambuco, Bahia, Minas Gerais, Paraná and Rio Grande do Sul, two accessions of *cantaloupensis* group from Maranhão and two commercial cultivars of *inodorus* group (Table 1).

Sowing was performed in expanded polystyrene trays of 128 cells, containing pine bark-based substrate for vegetable. The seedlings were transplanted into 5 L-capacity pots using coconut powder as substrate, in a spacing of 0.60 x 1.75 m, ten days after planting, after the first definitive leaf appeared.

The plants were staken vertically using plastic ribbons and wire at 1.30 m height and at the base of the plant. After the appearance of the fifth leaf, from the third leaf on, we eliminated the tertiary shoots up to the eighth leaf, conducting the plant with only one secondary stem. Both, the tertiary and secondary stems which appeared after the eighth leaf, were pruned after the second leaf.

The side screens of the greenhouse were lifted during the day in order to allow the entrance of pollinating agents. During fructification period, thinning was performed, letting just two fruits per plant in different tertiary stems in order to reduce the competition between the

Table 1. Accessionss of *C. melo* with identifications and origins. Recife, UFRPE, 2013.

Accessions/cultivars	Botanical group	Origin
A01	*momordica*	São José do Egito-PE
A02	*momordica*	Granito-PE
A03	*momordica*	Triunfo-PE
A04	*momordica*	Petrolina-PE
A05	*momordica*	São Lourenço da Mata-PE
A06	*momordica*	Ibimirim-PE
A07	*momordica*	Lagoa de Itaenga-PE
A08 and A09	*momordica*	Serra Talhada-PE
A10 and A11	*momordica*	Floresta-PE
A12	*momordica*	Arcoverde-PE
A13	*momordica*	Buíque-PE
A14	*momordica*	Belo Jardim-PE
A15	*momordica*	Mocambinho-MG
A16	*momordica*	Juazeiro-BA
A17	*momordica*	Jeremoabo-BA
A18	*momordica*	Santa Tereza do Oeste-PR
A19	*momordica*	Nova Petrópolis-RS
A20 and A21	*cantalupensis*	Chapadinha-MA
A22[1]	*inodorus*	-
A23[2]	*inodorus*	-

[1]Simple hybrid of the commercial cultivar Gold Mine from the commercial company Seminis; [2]Simple hybrid of the commercial cultivar Mandacaru from the commercial company Clause Tézier.

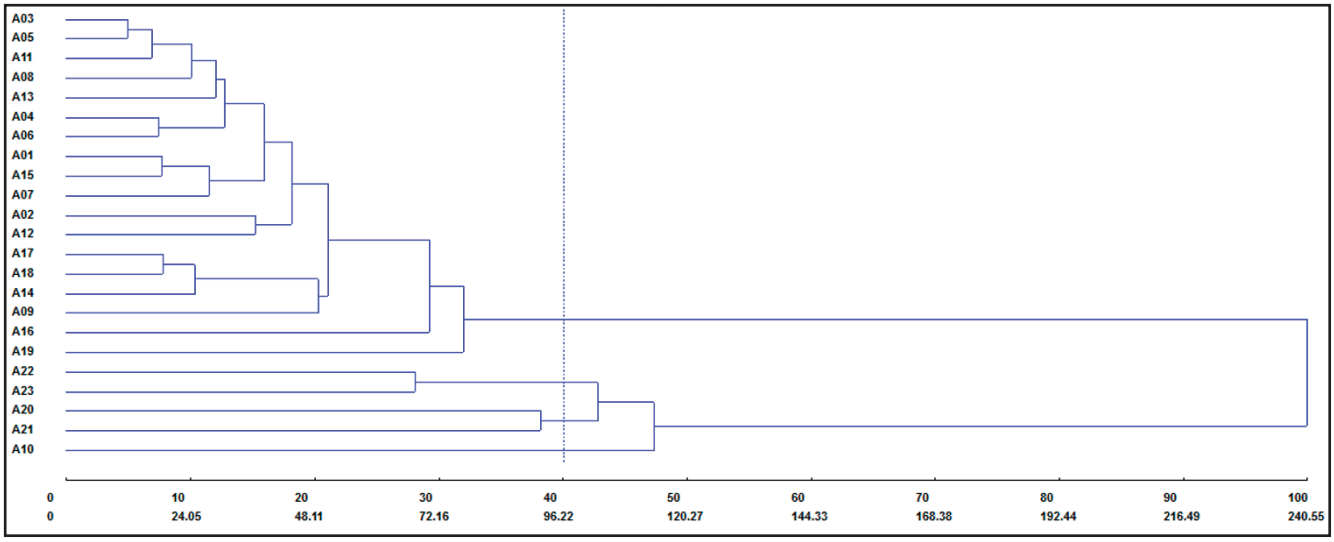

Figure 1. Dendrogram resulting from the analysis of 23 accessions of *Cucumis melo*, obtained using UPGMA grouping method, and Mahalanobis distance. Recife, UFRPE, 2013.

fruits, favoring their development and higher quality for harvest.

Mineral nutrition and need of water were supplied through balanced nutrient solution in each stage of the plant development through a drip irrigation system using an emitter flow rate of 2 L h^{-1}, two to four times a day, according to the weather conditions and water absorption by the plants. The supply of nutrient solution was suspended with the start of the drainage at the bottom of the pots.

In order to verify the genetic variability of papoco melon genotypes, some morphological evaluations were made of the seeds, plants and fruits based on the list of minimum descriptors established for melon by SNPC (National Service for Plant Variety Protection) and recommended for tests of distinctiveness, homogeneity and stability, also called test DHE, MAPA (Ministry of agriculture, livestock and food supply) (MAPA, 2008).

After obtained all data, multivariate analyses through hierarchical grouping technique, based on UPGMA, using Mahalanobis generalized distance (D^2), using the dissimilarity measure (Cruz *et al.*, 2012, 2014), were performed. The optimization was verified using Tocher method (Cruz *et al.*, 2012, 2014). In order to verify the efficiency of the hierarchical grouping method, the authors estimated the cophenetic correlation coefficient (Sokal & Rohlf, 1962). The criterion of Singh was used to identify the relative contribution of each character for genetic divergence (Cruz *et al.*, 2012, 2014). Data analysis was performed using the computer software GENES (Cruz, 2013).

RESULTS AND DISCUSSION

Dissimilarity averages between each pair of the accessions obtained using Mahalanobis generalized distance (D^2) allowed forming four similarity groups (Figure 1). Group I was formed by 94.74% of the evaluated accessions, however only the accession A19 showed the background color of the peel, intensity of the background color of the peel, peel color hue, fruit base shape, fruit apex shape and placental color different from the characters observed in the other accessions of *momordica* group, with yellow color, dark intensity, orange toned, round-based shape, flat apex, and salmon-colored placenta (Table 2).

The second group took into consideration two cultivars belonging to *inodorus* group, Gold Mine and Mandacaru, which differed only in relation to the shape of the longitudinal, circular and middle elliptical section, respectively. The third group included the accessions A20 and A21 belonging to *cantaloupensis* group, which differed in relation to the placenta color, showing salmon and orange color, respectively (Table 2). The last group was formed only by the accession A10 which stood out in relation to the other accessions of *momordica* group, since it showed soluble solid content about 5% and did not show any cracks in fruits at maturity, white peel color and yellowish white flesh color, characters which are opposite to that observed in the other accessions of *momordica* group (Table 2). Fruit rupture in accessions of *momordica* group was observed in studies carried out previously by Valadares (2014), Torres Filho *et al.* (2009) and Dhillon *et al.* (2007).

The grouping of accessions using Tocher method showed to be similar to UPGMA method considering the groups formed among the most divergent accessions (Table 3). The similarity between the two used grouping techniques can be verified by the fact that the accessions of *momordica* group belonging to groups I, Tocher group, were the same as the groupings by UPGMA method. Agronomic characters different from this first group are expected for the accessions A22, A23 (Group II), A20, A21 (Group III), due to the fact that they formed isolated groups, and the accession A10 (Group IV) has formed an isolated group, similar to the one observed using UPGMA method;

Table 2. Characterization of accessions and cultivars of melon from qualitative descriptors of the fruit. Recife, UFRPE, 2013.

Accessions/ cultivars	VFR	MCA	PDI	FSL	IFU	TCA	FBA	FAP	SUL	CSU	RSU	CPO	CPL	AIN	AEX	RFR	FRU
A01	Méd	FDe	DFl	Obo	Cla	Esb	Arr	Arr	Aus	-	Aus	Br	Lar	Pr	Pr	Pro	Alt
A02 to A09	Méd	FDe	DFl	Obo	Cla	Esb	Pon	Arr	Aus	-	Aus	Br	Lar	Pr	Pr	Pro	Alt
A10	Méd	FDe	DFl	Obo	Cla	Esb	Arr	Arr	Aus	-	Aus	BAm	Lar	Pr	Pr	Aus	
A11 and A12	Méd	FDe	DFl	Obo	Cla	Esb	Pon	Arr	Aus	-	Aus	Br	Lar	Pr	Pr	Pro	Alt
A13	Méd	FDe	DFl	Obo	Esc	Am	Pon	Arr	Aus	-	Aus	Br	Lar	Pr	Pr	Pro	Alt
A14 to A18	Méd	FDe	DFl	Obo	Cla	Esb	Pon	Arr	Aus	-	Aus	Br	Lar	Pr	Pr	Pro	Alt
A19	Méd	FDe	DFl	Obo	Esc	Ala	Arr	Pla	Aus	-	Aus	Br	Sal	Pr	Pr	Pro	Alt
A20	Esc	FDe	NCe	EAl	Esc	Ala	Pla	Pla	For	Bra	Aus	Lar	Sal	Pr	Pr	Aus	-
A21	Esc	FDe	NCe	EAl	Esc	Ala	Pla	Pla	For	Bra	Aus	Lar	Lar	Pr	Pr	Aus	-
A22	Cla	FDe	DPe	Cir	Esc	Am	Arr	Arr	Aus	-	Méd	BEs	Bra	Aus	Aus	Aus	-
A23	Cla	FDe	DPe	EMe	Esc	Am	Arr	Arr	Aus	-	Méd	BEs	Bra	Aus	Aus	Aus	-

VFR= intensity of the green color of the young fruit peel (Cla= light; Méd= medium; Esc= dark); MCA= change from the color of the young fruit peel to the ripe fruit (FDe= at the end of fruit development); PDI= position of maximum diameter (DFl= toward the flower; NCe= in the center; DPe= toward the peduncle); FSL= shape of longitudinal section (Obo= obovate; Cir= round, EAl= wide elliptic; EMe= average elliptic); IFU= intensity of the background color of the peel (Cla= light; Esc= dark); TCA= peel color hue (Esb= whitish; Am= yellowish; Ala= orange); FBA= base shape (Pon= pointed; Arr= rounded; Pla= flat); FAP= apex shape (Arr= rounded; Pla= flat); SUL= grooves (Aus= absent or very weakly expressed; For= strong); CSU= groove color (Bra= white); RSU= surface roughness (Aus= absent or very weak; Méd= medium); CPO= main color of the flesh (Br= white; BAm= yellowish white; BEs= greenish white; Lar= orange); CPL= placenta color (Lar= orange; Sal= salmon, Bra= white); AIN= aroma inside the fruit (Pr= present; Aus= absent); AEX= aroma outside of the fruit (Pr= present; Aus= absent); RFR= fruit rupture (Pro= deep; Aus= absent); FRU= fruit rupture frequency (Alt= high).

Table 3. Grouping using Tocher method and the Mahalanobis distance, for the 23 accessions of *C. melo*. Recife, UFRPE, 2013.

Groups	Accessions
I	A19, A16, A09, A14, A18, A17, A12, A02, A07, A15, A01, A06, A04, A13, A08, A11, A05 and A03
II	A22, A23
III	A20, A21
IV	A10

this fact occurs due to a specific character or a set of these characters had allowed an isolated group of the accession A10, the only accession in *momordica* group, possibly the characters of pistil scar size and soluble solid content were the most determinant for the isolation of accession A10 (Table 4).

An agreement between multivariate and grouping technique is important for the genetic diversity study, since this evaluation makes it possible to recommend crossing between more divergent parents, in order to broaden the genetic base and, consequently, to increase variability (Abreu *et al.*, 2004).The use of different grouping methods provides more efficient support for determination of divergence, since Tocher method discriminates each group and UPGMA discriminates each genotype, helping, with greater security, choose parents in breeding programs (Bertan *et al.*, 2006).

The analysis of relative contribution of each character for genetic divergence expression using Singh method considers that the most important characters express greater variability. Thus, the authors verified that all the evaluated characters contributed to determine genetic divergence among the evaluated accessions, to a greater or lesser extent. Soluble solid content (17.60%), seed length (13.41%), fruit length (11.80%), cotyledon length (11.05%) and pistil scar size (9.41%), were the descriptors which contributed the most for divergence among the 23 evaluated accessions of *C. melo*, which explains 53.86% of total dissimilarity (Table 4). On the other hand, the character which contributed the least was fruit shape index (0.31%), shown in Table 4.

In the genetic divergence study from Paiva (2002) using lines of melons belonging to *cantaloupensis*, *inodorus* and *momordica* groups, and by Rizzo & Braz (2002) studying genetic divergence among five genotypes of net melon, soluble solid content was also one of the characters which most contributed to genetic variability.

According to Alves *et al.* (2003), evaluating the relative importance of the characters, it is interesting due to the possibility of discarding the characters which little contribute to discriminate the evaluated genotypes, reducing labor, time and cost spent on experiments.

Cophenetic correlation coefficient (r) was 0.89 showing that good adjustment

Table 4. Relative contribution (S.j) of 22 quantitative descriptors for the genetic divergence among accessions, using Singh's method. Recife, UFRPE, 2013.

Characteristic	S.j	S.j (%)
DPEN	255.426	1.043
TCPI	2305.021	9.419
CFRU	2887.636	11.800
LFRU	802.719	3.280
IFOR	88.832	0.363
EPOL	273.630	1.118
TSSO	4307.231	17.601
MMFR	905.294	3.699
CSEM	3282.439	13.414
LSEM	613.904	2.508
RSEM	295.180	1.206
CCOT	2704.718	11.053
LCOT	795.368	3.250
RCOT	861.740	3.521
CPEC	632.156	2.583
CFOL	605.498	2.474
LFOL	331.796	1.355
RFOL	352.413	1.440
CLTE	250.295	1.022
FMAS	322.122	1.316
FFEM	481.85	1.969
MATU	1114.919	4.556
Total		100

DPEN= peduncle diameter; TCPI= pistil scar size; CFRU= fruit length; LFRU= fruit width; IFOR= fruit length/width ratio; EPOL= pulp thickness; TSSO= soluble solid content; MMFR= average fruit mass; CSEM= seed length; LSEM= seed width; RSEM= seed C/L ratio; CCOT= cotyledon length, LCOT= cotyledon width, RCOT= cotyledon C/L ratio; CPEC= petiole length; CFOL= leaf length, LFOL= leaf width, RFOL= leaf C/L ratio; CLTE= terminal lobe length, FMAS= number of days for male flowering; FFEM= number of days for female flowering; MATU= number of days for maturation.

between graphical representation of distances and its original matrix could be noticed. The adjustment of cophenetic correlation coefficient is considered good when it shows values equal or superior to (r) 0.70 (Sokal & Rohlf, 1962). Cophenetic correlation coefficient enables visual inferences (dendogram) and the higher its estimate, the lower the grouping distortion, presenting a good adjustment between the matrix and the formed dendrogram (Cruz *et al.*, 2012).

Given the results, the authors verified an agreement between hierarchical UPGMA and Tocher grouping methods. The characters that permitted the visualization of genetic variability among 23 evaluated accessions, evaluated through four distinct groups, were soluble solid content, seed length, fruit length, cotyledon length and pistil scar size. These characters were the ones which most contributed to genetic divergence among the accessions. Due to this fact, the evaluated accessions may constitute a potential to be used in breeding programs, in order to obtain good materials for *in natura* consumption or for industrialization.

ACKOWLEDGEMENTS

This research is part of the MSc thesis of the first author, presented at UFRPE.

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