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

Ricardo N Valadares¹; Roberto A Melo¹; Isabel VF Sarinho¹; Natália S Oliveira²; Fernando AT Rocha¹; José W Silva¹; Dimas Menezes¹

¹Universidade Federal Rural de Pernambuco (UFRPE), Recife-PE, Brazil; rnvaladares@yahoo.com.br (corresponding author); robertoagronomo@yahoo.com.br; isabelsarinho@gmail.com; fernandortrecife@hotmail.com; jwsamaral@hotmail.com; dimasmenezes@superig.com.b; ²Universidade Federal de Lavras (UFLA), Lavras-MG, Brazil; natalia.agro@yahoo.com.br

### 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

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 (D²). 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*, *dudaaim*, *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 botanical 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. When they are consumed having a flavor of naturally tasteless of the fruit when it reaches ripeness, besides being used for the preparation of soft drinks, salads and pickles when ripe 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., 2007), by the nematode *Meloidogyne incognita*, by the PRSV virus (*Papaya Ring Spot Virus*) (Dhillon et al., 2007), and some pests like the leafminer *Liriomyza trifoli* 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).

<table>
<thead>
<tr>
<th>Accessions/cultivars</th>
<th>Botanical group</th>
<th>Origin</th>
</tr>
</thead>
<tbody>
<tr>
<td>A01</td>
<td><em>momordica</em></td>
<td>São José do Egito-PE</td>
</tr>
<tr>
<td>A02</td>
<td><em>momordica</em></td>
<td>Granito-PE</td>
</tr>
<tr>
<td>A03</td>
<td><em>momordica</em></td>
<td>Triunfo-PE</td>
</tr>
<tr>
<td>A04</td>
<td><em>momordica</em></td>
<td>Petrolina-PE</td>
</tr>
<tr>
<td>A05</td>
<td><em>momordica</em></td>
<td>São Lourenço da Mata-PE</td>
</tr>
<tr>
<td>A06</td>
<td><em>momordica</em></td>
<td>Ibimirim-PE</td>
</tr>
<tr>
<td>A07</td>
<td><em>momordica</em></td>
<td>Lagoa de Itaenga-PE</td>
</tr>
<tr>
<td>A08 and A09</td>
<td><em>momordica</em></td>
<td>Serra Talhada-PE</td>
</tr>
<tr>
<td>A10 and A11</td>
<td><em>momordica</em></td>
<td>Floresta-PE</td>
</tr>
<tr>
<td>A12</td>
<td><em>momordica</em></td>
<td>Arcuverde-PE</td>
</tr>
<tr>
<td>A13</td>
<td><em>momordica</em></td>
<td>Buique-PE</td>
</tr>
<tr>
<td>A14</td>
<td><em>momordica</em></td>
<td>Belo Jardim-PE</td>
</tr>
<tr>
<td>A15</td>
<td><em>momordica</em></td>
<td>Mocambinho-MG</td>
</tr>
<tr>
<td>A16</td>
<td><em>momordica</em></td>
<td>Juazeiro-BA</td>
</tr>
<tr>
<td>A17</td>
<td><em>momordica</em></td>
<td>Jeremoabo-BA</td>
</tr>
<tr>
<td>A18</td>
<td><em>momordica</em></td>
<td>Santa Tereza do Oeste-PR</td>
</tr>
<tr>
<td>A19</td>
<td><em>momordica</em></td>
<td>Nova Petrópolis-PR</td>
</tr>
<tr>
<td>A20 and A21</td>
<td><em>cantaloupensis</em></td>
<td>Chapadinha-MA</td>
</tr>
<tr>
<td>A22</td>
<td><em>inodorus</em></td>
<td>-</td>
</tr>
<tr>
<td>A23</td>
<td><em>inodorus</em></td>
<td>-</td>
</tr>
</tbody>
</table>

1Simple hybrid of the commercial cultivar Gold Mine from the commercial company Seminis; 2Simple hybrid of the commercial cultivar Mandacaru from the commercial company Clause Tézier.
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 (D²), 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 (D²) 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;
RN Valadares et al.

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

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

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; Al= 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 weakly expressed; 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>
<thead>
<tr>
<th>Groups</th>
<th>Accessions</th>
</tr>
</thead>
<tbody>
<tr>
<td>I</td>
<td>A19, A16, A09, A14, A18, A17, A12, A02, A07, A15, A01, A06, A04, A13, A08, A11, A05 and A03</td>
</tr>
<tr>
<td>II</td>
<td>A22, A23</td>
</tr>
<tr>
<td>III</td>
<td>A20, A21</td>
</tr>
<tr>
<td>IV</td>
<td>A10</td>
</tr>
</tbody>
</table>

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 cantaloupe, 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
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 (dendrogram) and the higher its estimate, the lower the grouping distortion, presenting a good adjustment between graphical representation (dendogram) 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.

ACKNOWLEDGEMENTS

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

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

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>S.j</th>
<th>S.j (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>DPEN</td>
<td>255.426</td>
<td>1.043</td>
</tr>
<tr>
<td>TCPI</td>
<td>2305.021</td>
<td>9.419</td>
</tr>
<tr>
<td>CFRU</td>
<td>2887.636</td>
<td>11.800</td>
</tr>
<tr>
<td>LFRU</td>
<td>802.719</td>
<td>3.280</td>
</tr>
<tr>
<td>IFOR</td>
<td>88.832</td>
<td>0.363</td>
</tr>
<tr>
<td>EPOL</td>
<td>273.630</td>
<td>1.118</td>
</tr>
<tr>
<td>LSSO</td>
<td>4307.231</td>
<td>17.601</td>
</tr>
<tr>
<td>MMFR</td>
<td>905.294</td>
<td>3.699</td>
</tr>
<tr>
<td>CSEM</td>
<td>3282.439</td>
<td>13.414</td>
</tr>
<tr>
<td>LSEM</td>
<td>613.904</td>
<td>2.508</td>
</tr>
<tr>
<td>RSEM</td>
<td>295.180</td>
<td>1.206</td>
</tr>
<tr>
<td>CCOT</td>
<td>2704.718</td>
<td>11.053</td>
</tr>
<tr>
<td>LCOT</td>
<td>795.368</td>
<td>3.250</td>
</tr>
<tr>
<td>RCOT</td>
<td>861.740</td>
<td>3.521</td>
</tr>
<tr>
<td>CPEC</td>
<td>632.156</td>
<td>2.583</td>
</tr>
<tr>
<td>CFOL</td>
<td>605.498</td>
<td>2.474</td>
</tr>
<tr>
<td>LFOL</td>
<td>331.796</td>
<td>1.355</td>
</tr>
<tr>
<td>CFU</td>
<td>352.413</td>
<td>1.440</td>
</tr>
<tr>
<td>CLL</td>
<td>250.295</td>
<td>1.022</td>
</tr>
<tr>
<td>FMAS</td>
<td>322.122</td>
<td>1.316</td>
</tr>
<tr>
<td>FSEM</td>
<td>481.85</td>
<td>1.969</td>
</tr>
<tr>
<td>MATU</td>
<td>1114.919</td>
<td>4.556</td>
</tr>
</tbody>
</table>

Total 100

REFERENCES

ABREU, FB; LEAL, NR; RODRIGUES, R; AMARAL, J; R; SILVA, DJH. 2004. Divergência genética entre acessos de feijão-de-vagem de crescimento indeterminado. Horticultura Brasileira 22: 547-552.


ARAGÃO, FAS. 2011. Divergência genética de acessos e interação genótipo x ambiente de famílias de meloeiro. Mossoró: UFRN.

BERTAN, I; CARVALHO, FIF; OLIVEIRA, AC; VIEIRA, EA; HARTWIG, I; SILVA, JAG; SHIMIDT, DAM; VALÉRIO, IP; BUSATO, CC; RIBEIRO, G. 2006. Comparação de métodos de agrupamento na representação da distância morfológica entre genótipos de trigo. Revista Brasileira de Agrociência 12: 79-286.


DHILON, NPS; RANJANA, R; SINGH, K; EDUARDO, I; MONFORTE, AJ; PITRAT, M; DHILON, NL; SINGH, PP. 2007. Diversity among landraces of Indian snapmelon (Cucumis melo var. momordica). Genetics Resources Crop Evolution 54: 1267-1283.

FERGANY, M; KAUR, B; MONFORTE, AJ; PITRAT, M; RYS, C; LECQO, H; DHILLON, NPS; DHALIWAL, SS. 2011. Variation in melon (Cucumis melo) landraces adapted to the humid tropic of southern India. Genetic Resources Crop Evolution 58: 225-243.


NUNES, GHS; FILHO, JHC; SILVA, DJH; CARNEIRO, PCS; DANTAS, MSA. 2011. Divergência genética entre linhagens de melão pele de sapo. Ciência Agropecuária 42: 765-773.


RN Valadares et al.