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Morphoagronomic genetic diversity of Brazilian melon accessions based on fruit traits

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ABSTRACT

Morphoagronomic characterization and genetic diversity analysis of fruit quality traits and production were performed in 42 Brazilian melon accessions and four commercial reference cultivars. The experiment was undertaken in three distinct environments in the Northeast Region, Brazil, which is the most productive culturing state. Analysis of variance (ANOVA) indicated significant differences among the locations for all evaluated traits, indicating that the locations were different from each other and influence the phenotypic gain. However, significant interactions among genotypes and locations were detected only in six of the studied characteristics, demonstrating that the edafoclimatic conditions quantitatively influenced the expression of important descriptors for fruit quality and production. The ANOVA performed for the variation in each location showed significant effect in all descriptors, suggesting wide variability among accessions and commercial cultivars, focusing on the Brazilian genetic resource. Differences in quantitative behavior characteristics and, consequently, in the groupings of genotypes of each accession and cultivars, in relation to the locations was found by Scott-Knott grouping test. Genetic diversity inferred by the Ward-Modified Location Model (Ward-MLM) multivariate analysis, allowed the detection of genetic divergence among accessions with the distribution of the germplasm analyzed in distinct canonical groups. The differences between the average quantitative characteristics, observed in the genotypes of the same accessions in different locations, influenced the grouping of these genotypes. Among the four groups formed from the Ward-MLM analysis, only the commercial cultivars were clustered together, suggesting that these cultivars differ from the other accessions, but have close characteristics introgreded during the process of genetic improvement. An association between these groups and the botanical classification of accessions was also observed, indicating genotypic conservation for some descriptor expression. The soluble solids content contributed was the most relevant fruit trait to contributed for multivariate clustering formation. The genetic variability detected in these accessions should be further used for breeding, to obtain more prolific cultivars, with high productivity that are adapted to the different production regions.

1. Introduction

Melon (*Cucumis melo* L.) is a cultivated domesticated plant that is grown in many regions worldwide (Akashi, 2001), including Brazil where this crop has great economic importance and accounts for the highest production and largest fruit export from this country. In 2016, 224.669 thousand tons of melon were exported from Brazil, generating a revenue of US$148,741,470 (Anuário brasileiro da fruticultura, 2018). In Brazil, the production of melon is concentrated in the Northeast Region, accounting for more than 95% of the national production, which is represented mainly by the States of Ceará and Rio Grande do Norte (Nunes et al., 2011; Anuário brasileiro da fruticultura, 2018). The production of hybrid cultivars between *C. melo* and fruit of the commercial yellow variety belonging to the botanical group Inodorus is one of the most important breeding strategy for fruit quality and yield (Nunes et al., 2011; Aragão et al., 2015).

The species *C. melo* L. is the most polymorphic taxon of *Cucumis* genus (Luan et al., 2010), displaying variability in fruit type and quality, with variations in shape, size, color, texture, flavor, and chemical composition (Esteras et al., 2013). *C. melo* is divided into two subspecies: *melo* and *agrestis* (Jeffrey, 1980; Kirkbride, 1993). Naudin (1859) was the first to group the cultivars by subdividing the species

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Table 1
Traditional melon accessions of the Northeast Region, Brazil, and the qualitative trait for fruit quality.

Accessions	Botanical group*	RC	FC	Accessions	Botanical group*	RC	FC
A1	*Cantaloupensis*	Gr	Sa	A24	*Cantaloupensis*	Ye	Sa
A2	*Cantaloupensis*	Ye	Wh	A25	*Cantaloupensis*	Ye	Sa
A3	*Cantaloupensis*	Gr	WG	A26	*N/D*	Wh	Wh
A4	*Cantaloupensis*	Ye	Sa	A27	*N/D*	Wh	Sa
A5	*N/D*	Gr	Wh	A28	*Cantaloupensis*	Gr	Sa
A6	*Cantaloupensis*	Ye	Sa	A29	*Cantaloupensis*	Gr	WG
A7	*Cantaloupensis*	Ye	Sa	A30	*Momordica*	Wh	Wh
A8	*N/D*	Wh	Wh	A31	*Cantaloupensis*	Ye	Gr
A9	*Conomon*	Ye	Wh	A32	*Momordica*	Sp	Wh
A10	*Cantaloupensis*	Ye	WG	A33	*N/D*	Ye	Wh
A11	*Conomon*	Wh	Wh	A34	*Cantaloupensis*	Ye	Sa
A12	*N/D*	Ye	Wh	A35	*N/D*	Gr	Sa
A13	*Cantaloupensis*	Gr	Gr	A36	*Cantaloupensis*	Gr	Wh
A14	*Cantaloupensis*	Ye	WG	A37	*Momordica*	Wh	Wh
A15	*Momordica*	Wh	Wh	A38	*Momordica*	Gr	Wh
A16	*Conomon*	Ye	Wh	A39	*Cantaloupensis*	Cr	Wh
A17	*Conomon*	Ye	Wh	A40	*Momordica*	Wh	Wh
A18	*Cantaloupensis*	Ye	Wh	A41	*Cantaloupensis*	Wh	Wh
A19	*N/D*	Wh	Wh	A42	*Momordica*	Wh	Wh
A20	*Momordica*	Wh	Wh	Vedrantais	*Cantaloupensis*	Gr	Sa
A21	*Conomon*	Ye	WG	Vereda	*Inodorus*	Ye	Wh
A22	*Cantaloupensis*	Gr	Gr	Hy Mark	*Cantaloupensis*	Gr	Sa
A23	*Momordica*	Wh	Wh	Sancho	*Inodorus*	Gr	Wh

(RC) rind fruit color, (FC) flesh color, (N/D) not defined, (Gr) Green, (Am) yellow, (Sa) Salmon, (Br) white, (Bv) white greenish, (Rj) Spotted, (Cr) Cream, (RC) rind color, (*) taxonomic classification previously established by Torres Filho et al. (2009).

into nine cultivated varieties and one wild variety. This pioneering study became the basis for subsequent classifications that used the terms botanical groups or botanical varieties for each of the members of the two subspecies (Pitrat et al., 2000; Pitrat, 2008; Burger et al., 2010; Pitrat, 2013). In the most recent classification, Hammer and Gladis (2014) cited 17 botanical groups distributed among the 2 subspecies as follows: the subspecies *melo* includes the groups Flexuosus, Inodorus, Cantalupensis, Reticulatus, Adana, Ameri, Chandalak, and Tibish, and the subspecies *agrestis* includes the groups Acidulus, Agrestis, Chate, Chito, Conomom, Dudaim, Momordica, Texanuse, and Makuwa. The commercially most important botanical groups or varieties in Brazil are Cantalupensis and Inodorus, among which are classified the different "types" of melons, including Canary, Santa Claus, Cantaloupe, Galia, and Charentais.

The history of the origin of the species is controversial in the scientific world. Some researchers argue that this species originated in Africa because it possesses the same number of chromosomes as many African species of *C. silvestres* (Kerje and Grum, 2000; Dhillon et al., 2007). Other authors suggest that the origin occurred in Asia, due to the indication that Australian *C. picrocarpus* and *C. melo* are sister species and are likely wild progenitors of *C. trigonus* and *C. callosus*, which are both Asian species (Sebastian et al., 2010; John, 2012). Melon diversity is widespread within its primary and secondary diversification centers, with primary centers located in south central Asia (Tzitzikas et al., 2009) and secondary centers comprising East Asian and Mediterranean regions (Monforte et al., 2004; Lopez-Sese et al., 2003; Blanca et al., 2012). From these primary and secondary centers, the melon was disseminated separately from the gene pool of wild melons located in these continents (Giardi and Dogimont, 2012), which favored the emergence of significant genetic variability in local populations from different regions worldwide (Feyzian et al., 2007; Neitzke et al., 2009; Nhi et al., 2010; Soltani et al., 2010; Fergany et al., 2011; Nasrabadi et al., 2012; Ajuru and Okoli, 2013; Aragão et al., 2013a,b; Trimech et al., 2013; Ali-Shtayeh et al., 2015; Dantas et al., 2015; Macêdo et al., 2017).

In Brazil, the *C. melo* genetic variability was considerably increased by the introduction of accessions along the Brazilian coast, mainly in the Northeast Region, by African slaves and European immigrants during the 16th century. Since their introduction, the genetic material has moved through an intense selection process and crosses that have resulted in many local cultivars adapted to various soil and climatic conditions, which are grown in different regions of the country under different Brazilian subsistence agricultural systems (Delwing et al., 2007). The main melon producing regions display differences in climatic and environment conditions, which cause phenotypic variation in the plants, mainly in productivity and fruit quality traits (Aragão et al., 2015; Guimarães et al., 2016). However, little is known about the influence of the genotype-environment interaction on the genetic diversity expression of these accessions because this is inadequately addressed in genetic diversity studies owing to the expense of evaluating accessions that are located in more than one experimental location.

Morphological characterization and quantification of genetic variability are crucial in studies of pre- and post-improvement populations to understand the diversity and also to selection of plant groups. Multivariate analysis methods are ideal for genetic diversity descriptions and can be performed with analysis of qualitative descriptors, quantitative descriptors, and binary data obtained via molecular information (Aragão et al., 2013a,b). The Ward-Modified Location Model (Ward-MLM) multivariate technique, proposed by Franco et al. (1998), is a reliable strategy to quantify variability using quantitative and qualitative variables simultaneously. This procedure has been applied in cultures of different species to analyze genetic diversity, provide an indication of the descriptors that contribute the most to the formation of groups, and recommend the germplasm with the potential for genetic improvement (Brasileiro et al., 2013; Paiva et al., 2014; Melo et al., 2015; Rodrigues et al., 2016). In a previous study, the Ward-MLM technique distinguished the highly promising progenies of *Passiflora* for the advancement of generations in breeding programs for ornamental use (Melo et al., 2015). However, to date, the use of this methodology has not been reported in studies involving melon traits.

The objective of this study was to analyze the variability and genetic diversity of Brazilian melon germplasm using qualitative and quantitative data for descriptors related to yield and fruit quality. Additionally, the environmental experimentation influence on genotype clustering was also evaluated, to reflect the genotype x environment interaction on the expression of fruit traits quality.