



Genetic dissimilarity of 'yellow' and 'sleep' passion fruit accessions based on the fruits physical-chemical characteristics

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Received 25 March 2009

Accepted 15 June 2009

ABSTRACT - The intra- and inter-specific genetic dissimilarity between 14 'yellow' passion fruit plants and eight 'sleep' passion fruit plants were evaluated through nine physical-chemical descriptors, whose measured values were submitted to descriptive (average, standard deviation and variation coefficient) and inferential [univariate (ANOVA, averages and correlations tests) and multivariate (Mahalanobis distance, hierarchical clustering, Singh coefficient and Mantel test)] statistics. Intra- and, especially, inter-specific variability were found among the passion fruit plants ($p < 0.001$). The total soluble solid, equatorial diameter, total titratable acidity, and fruit weight descriptors presented the highest percentage of relative contribution, totaling 85.2% of the observed divergence. Preferential crossings among genotypes with physical-chemical characteristics of desirable fruits and useful genetic dissimilarity in divergent and convergent crossings were identified.

Key words: Diversity, multivariate analysis, *Passiflora edulis* Sims, *Passiflora setacea* DC, variability.

INTRODUCTION

The Passifloraceae family originated from tropical America and is comprised of about 530 species, of which approximately 150 are distributed in Brazilian territory (Bernacci et al. 2005). Among these species, the 'yellow' passion fruit (*Passiflora edulis* Sims) is highlighted for being cultivated in a great majority of the Brazilian fields used for the production of passion fruit (Meletti et al. 2005), significantly contributing to Brazil's position as the world's largest passion fruit producer and exporter (Ferreira et al. 2005). However, the average productivity of the passion fruit plants in Brazil is considered low (Pimentel et al. 2008).

Among the factors that contribute to the low productivity are: occurrence of pests and pathogens, inadequate techniques of cultivation, heterogeneity of the orchards and the reduced number of improved genotypes available to the producers (Meletti et al. 2000, Pimentel et al. 2008). Several wild species of the *Passiflora* genus present potential characteristics for genetic breeding of the passion fruit culture; for example, resistance to pathogens, longevity, self-compatibility, better adaptation to adverse edafo-climatic conditions, increased period of flowering and presents physical-chemical characteristics of desirable fruits to the market (Meletti et al. 2005). The 'sleep' passion fruit (*P. setacea* DC) is among those species

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which presents both a resistance to pathogens and the physical-chemical characteristics of desirable fruits for genetic breeding (Cardoso-Silva et al. 2007).

However, even though Brazil has the largest center of geographical distribution of the *Passiflora* species (Meletti et al. 2000) the effective use of this inter-specific variability in genetic breeding programs of the culture is still considered an open field (Nascimento et al. 2003), having few available results. In this sense, a growth in the number of works, including recent characterizations of genetic diversity of *Passiflora* through molecular markers (Bellon et al. 2007, Junqueira et al. 2008) and agronomic descriptors (Araújo et al. 2008, Negreiros et al. 2008) are observed. There are few publications, such as the ones by Cardoso-Silva et al. (2007) and Godoy et al. (2007), whose evaluation of genetic dissimilarity is based on physical-chemical descriptors which are intimately associated with the quality of the fruit, a major objective in the genetic breeding of fruit plants.

For species unrelated to the *Passiflora* genus, for example, the umbu-caja fruit (*Spondias* sp) and cassava (*Manihot esculenta*), diversity characterizations through morphologic and physical-chemical descriptors were already carried out in order to expand the selection of genotypes for hybridization (Ritzinger et al. 2008, Fonseca et al. 2008, Nick et al. 2008).

In order to guarantee and increase the productivity and quality of the 'yellow' passion fruit from hybridizations with wild species which present resistance to diseases, accompanied with the high organoleptic potential of fruits, the present work aimed (i) to quantify the intra- and inter-specific genetic dissimilarities among genotypes of 'yellow' passion fruit plants and 'sleep' passion fruit plants through the evaluation of physical-chemical descriptors of fruits; (ii) to estimate, under multivariate analysis, the relative contribution of each of the measured descriptors, and (iii) to identify preferential crosses which can contribute to the genetic breeding of physical-chemical attributes of these species.

MATERIAL AND METHODS

An amount of the 22 genotypes of passion fruit plants, originating from natural pollination and belonging to the Active Collection of *Passiflora* Work Germplasm from the Universidade Estadual do Sudoeste da Bahia (CAGT-*Passiflora*/UESB), Vitória da Conquista

campus, Bahia (14° 53' 20" S and 40° 47' 54" W, alt. 900 m asl; average annual precipitation 700-800 mm, concentrated between November and March, average annual temperature 20-22°C) (Instituto Nacional de Meteorologia/Ministério da Agricultura e Abastecimento) were used. Of these genotypes, 14 are 'yellow' passion fruit (UESB-*Pef*-G1 a -G14), originating from the germination of seeds of fruits collected in Vitória da Conquista street markets and characterized for the reaction to the *Cowpea aphid-borne mosaic virus* (Cerqueira-Silva et al. 2008), as well as possessing genotypes previously identified for the high (UESB-*Pef*-G11 and -G13) and low (UESB-*Pef*-G3 and -G5) prolificity, e.g., production of fruits. The other eight genotypes are 'sleep' passion fruit (UESB-*Ps*-G1 to -G8), prospected in native areas of Vitória da Conquista, presenting no pests or diseases.

The passion fruit were randomly collected during the months of October and November of 2008, only those that were ripe and had fallen on the ground with a yellowish peel were harvested, solely in the case of the 'yellow' passion fruit. Soil differences and climate variability possibly existing in the area were not considered. After harvest, the fruits, from 4 to 13 for genotype/species, were evaluated in the Laboratory of Molecular Biology of UESB - Vitória da Conquista, for nine physical-chemical descriptors: fruit weight (FW), equatorial diameter (ED), longitudinal diameter (LD), pulp weight with seeds (PWS), peel weight (PW), peel thickness (PT), pH, total soluble solids (TSS) expressed in °Brix and total titratable acidity (TTA). The fruit conformity index [CI=ED/LD] and pulp yield (PY) [PY (%) = (FW-PW/FW) x 100] were also calculated.

For physical characterizations, the fruits and the pulp were weighed with a 0.01g precision. The diameter measurements and peel thickness were obtained with a digital pachymeter Starrett® 727, with 0.01 mm precision. LD was determined measuring the distance taken between the poles of the fruit, while ED was calculated from the larger equatorial dimension area of the fruit. For chemical characterizations, the pH was calculated employing Quimis® benchtop pHmeter. TSS contents were determined with a manual benchtop refractometer (Abbe model, ATAGO) with direct reading and corrected for 20° C. Titratable acidity was determined collecting an aliquot of 10 mL of the pulp, followed by titration with NaOH to 0.1N in pHmetro until pH 8.2; according to Carvalho (1990).

The statistical analyses used were (i) descriptive type (average, standard deviation and variation coefficient of each descriptor); (ii) univariate [analysis of variance (ANOVA), followed by a mean comparison test (Tukey)] and (iii) multivariate analyses [(iii.a) estimates of dissimilarity among the genotypes through Mahalanobis generalized distance; (iii.b) clustering of the genotypes through hierarchical methods (Ward, Gower, More Distant Neighbor, Closer Neighbor, and the unweighted pair-group method using arithmetic averages); (iii.c) clustering selection for two-dimensional representation (dendrogram) based on the values of cophenetic correlation coefficient, distortion and stress; (iii.d) estimates of the relative contribution of each one of the descriptors, adopting the Singh criterion (1981), and (iii.e) determination of the correlation values among the descriptors which more or less contribute to the divergence of the

genotypes, obtained by Spearman test]. Data normality was verified through the Lilliefors test.

For the analyses 'i', 'ii', 'iii.e' and the normality test, BioEstat 5.0 software was used (Ayres et al. 2005), and Genes software was adopted for analyses 'iii.a-d' (Cruz 2001).

RESULTS AND DISCUSSION

The average results of the physical-chemical characteristics of fruits presented statistical differences both between the 'yellow' passion fruit plants and between 'sleep' passion fruit plants ($p < 0.001$) (Table 1), which certifies the existence of intra-specific genetic variability. Another indication regarding the intra-specific variability of these species is the percentage of the variation coefficient (VC) checked among the genotypes for each one of the physical-chemical

Table 1. Averages, variation coefficients (VC) and results of the Tukey test ($\alpha = 0.05$) regarding nine physical-chemical descriptors [fruit weight (FW), equatorial diameter (ED), longitudinal diameter (LD), pulp weight with seeds (PWS), peel weight (PW), peel thickness (PT), pH, total soluble solids (TSS) in °Brix and total titratable acidity (TTA)], evaluated in fruits of 14 'yellow' passion fruit (UESB-Pef-G1 a -G14), superior part of the Table, and eight 'sleep' passion fruit (UESB-Ps-G1 a -G8), inferior part of the Table

Genotype	Physical-chemical descriptors of fruits								
	FW(g)	ED(mm)	LD(mm)	PWS(g)	PW(g)	PT(mm)	pH	TSS	TTA
UESB-Pef-G1	142.3a	76.1a	83.1ab	58.6a	83.6a	8.3a	3.3bc	9.4ab	8.6bcd
UESB-Pef-G2	100.7bc	64.2bcd	68.9bcd	41.4bcd	59.2bc	9.4ab	3.3bc	8.5abcd	10.7abc
UESB-Pef-G3	124.0bc	68.5bcd	74.1bcd	50.7abcd	73.2ab	11.4a	3.4bc	5.3bcdefgh	12.0a
UESB-Pef-G4	127.2ab	68.7bc	82.2ab	54.4ab	74.5ab	10.6ab	3.3bc	10.7a	9.0abcd
UESB-Pef-G5	157.3a	72.1ab	88.3a	65.5a	91.8a	8.1ab	3.4bc	8.6abcd	6.7bcde
UESB-Pef-G6	108.9bc	64.5bcde	69.7bcd	45.4abcd	63.4abc	8.9ab	3.3bc	9.5abc	8.9abcd
UESB-Pef-G7	99.3bcde	62.5bcde	69.9bcd	38.2bcde	61.1bc	8.3b	3.3bc	7.8bcde	7.6bcd
UESB-Pef-G8	117.5b	68.1bc	74.9b	52.6ab	64.8ab	9.5ab	3.9ab	5.1bcdefgh	3.6bcdef
UESB-Pef-G9	108.0bcde	66.4bcd	77.3bc	44.6bcd	63.3bc	10.2ab	4.1a	3.8bcdefgh	4.7bcde
UESB-Pef-G10	98.3bcd	65.3bcd	75.1bc	41.2bcde	57.1bc	9.6ab	3.8bc	5.1bcdefgh	5.4bcdef
UESB-Pef-G11	77.8bcde	58.2bcde	64.2bcd	30.6bcde	47.1bc	10.4ab	3.9b	4.8bcdefgh	4.3bcdef
UESB-Pef-G12	101.3bcd	64.2bcde	71.1bcd	40.7bcde	60.5bc	10.8a	3.5bc	6.3bcdefgh	6.3bcde
UESB-Pef-G13	90.2bcde	62.9bcde	65.2bcd	31.8bcde	58.4bc	11.2a	3.8bc	4.7bcdefgh	3.7bcdef
UESB-Pef-G14	137.6b	66.0bcd	78.7ab	57.2abc	80.3ab	10.4ab	3.3bc	6.7bcdef	7.1bcd
CV(%)	19.3	6.5	9.3	21.9	18.0	11.0	8.1	31.4	36.6
UESB-Ps-G1	54.4a	44.1a	52.0bc	32.1ab	22.4a	2.8a	3.2a	18.1ab	2.2bc
UESB-Ps-G2	33.6abc	35.7bcdef	43.2bcd	22.7bc	10.8bc	1.6bc	3.0bcd	17.0bc	2.9ab
UESB-Ps-G3	50.5abc	38.7bcde	56.4ab	32.4abc	17.7bc	2.4bcd	3.2ab	17.2bc	1.9bc
UESB-Ps-G4	53.9a	40.7bc	56.4ab	32.1a	21.8a	3.0a	3.0abc	18.2ab	2.3bc
UESB-Ps-G5	51.4bc	41.2bcd	54.0a	33.4ab	17.9ab	2.5a	2.9bcd	17.4ab	3.1a
UESB-Ps-G6	33.4abc	33.1bcdef	48.4bcd	24.0bc	9.4bc	1.5bc	3.1abc	17.3ab	2.6abc
UESB-Ps-G7	40.9fab	39.0bcde	46.4bcd	24.9bc	16.0bc	2.8bc	3.1abc	19.4a	1.9bc
UESB-Ps-G8	50.9bc	38.7bcde	59.7a	35.1bc	15.7bc	1.9bc	3.0bcd	18.5ab	2.2bc
CV(%)	19.0	8.6	10.8	16.4	28.1	24.4	3.3	4.5	18.6

descriptors evaluated (Table 1). Except for the percentage of VC checked for TSS and TTA descriptors, the other VCs checked for 'yellow' passion fruit plants (between 6.5 and 21.9 %) and 'sleep' passion fruit plants (between 3.3 and 28.1%) are similar to the ones described by Nascimento et al. (2003) when characterizing 'yellow' passion fruit progenies. When considering the 22 genotypes of passion fruit plants jointly, the VC percentiles (19% to 57%) are quite superior to those observed inside each one of the two species (between 6.5 and 36.6% and 3.3 and 28.1% for 'yellow' passion fruit and 'sleep' passion fruit plants, respectively), attesting that the inter-specific dissimilarity is higher than the intra-specific ones.

The magnitude of the average physical-chemical characteristics (Table 1) and the relative importance of them is the aggregate value on the commercialization of 'yellow' passion fruit plants and 'sleep' passion fruit plants which makes it able to foresee the useful genotypes to be used in intra-and inter-specific hybridizations, since the observed values in this work are, as discussed below, similar or higher than those observed in the literature.

Higher levels of TSS superior to °Brix 13 are desired by the juice industry (Meletti et al. 2000, Fortaleza et al. 2005). We observed an average result for 'sleep' passion fruit (TSS = 17.9) superior to the average found in 'yellow' passion fruit for Meletti et al. (2000), Nascimento et al. (2003), Godoy et al. (2007) and Negreiros et al. (2008) (TSS = 16, 16.2, 13.1, and 15.7; respectively). In this work the UESB-Ps-G7 genotype stands out and was prominent with a TSS °Brix of 19.4.

Average percentages of PY used by the industry (PY around or superior to 45%) were partly detected in the 'yellow' passion fruit and 'sleep' passion fruit (PY of 41 and 61%, respectively) evaluated. These percentages observed were superior to those reported by Ruggiero et al. (1996) of 19.00 to 38.00% and by Ritzinger et al. (1989) of 34.67% to 35.74% and around the average value observed by Godoy et al. (2007) (52.8%) for 'yellow' passion fruit. Attention was drawn to the average results checked in the fruits of the UESB-Pef-G8 (45%) and UESB-Ps-G6 (72%) genotypes.

In relation, it was possible to observe at the CI 1.1 for 'yellow' passion fruit and 1.3 for 'sleep' passion fruit. Similar values were found by Fortaleza et al. (2005) for 'yellow' passion fruit (between 1.05 and 1.22). In this work the results checked for UESB-Pef-G5 (1.2) and UESB-Ps-G1, -G2 and -G7 (1.2) genotypes stand out.

These values are desirable for the juice industry, considering that the oblong fruits present a superior yield, in up to 10%, in relation to those found in round fruits (Fortaleza et al. 2005).

Although a screening of genotypes in pre-breeding and preliminary characterizations of natural populations is of great importance, the differences observed between the values obtained for the different physical-chemical descriptors of fruits may vary, in part, due to the influence of uncontrolled soil and climatic factors (Nascimento et al. 2003, Vianna-Silva et al. 2008).

Genetic dissimilarity among the genotypes was estimated from the 484 pairs of passion fruit plants, and revealed considerable genetic variability among the genotypes of passion fruit (Table 2). The average genetic distances (D^2) were of 24.5 ($3.4 \leq D^2 \leq 72.8$) and 7.2 ($2.4 \leq D^2 \leq 16.6$) for the 196 pairs and 64 pairs of 'yellow' passion fruit and 'sleep' passion fruit genotypes, respectively. Inter-specific genotypes pairs with higher and lower distances [UESB-Pef-G3 vs. UESB-Ps-G8 ($D^2 = 369.9$) and UESB-Pef-G4 vs. UESB-Ps-G5 ($D^2 = 150.1$), respectively] were identified in the dissimilarity matrix (Table 2). These pairs of genotypes can be explored in divergent (with higher dissimilarity) and convergent (with lower dissimilarity) crossings. Inter-specific characterizations have not been reported so far, being that this is the first work evaluating inter-specific genetic diversity through physical-chemical descriptors of fruits among species of passion fruit plants.

The highest diversity values observed among the genotypes of 'yellow' passion fruit plants in relation to the 'sleep' passion fruit plants can be explained as the consequence of coming from different places, considering that the seeds that resulted from the 'yellow' passion fruit plants have been obtained from fruits bought in different production fields, when compared with the origin of a duplicate area of the 'sleep' passion fruit seeds. Regarding high intra-specific variability, Junqueira et al. (2005), in studies carried out on 'suspiro' passion fruit (*P. nitida*) accessions, it was observed that accessions of different origins present a variability superior to those from the same origin.

Besides, the 'yellow' passion fruit genotypes were previously selected from a working population that presented genotypes with high and low productivity and prolificity of the fruits. This contrast could have contributed to the verified value for the D^2 average in 'yellow' passion fruit genotypes evaluated.

Table 2. Measurements of intra and interspecific dissimilarity of the Mahalanobis generalized distance (D^2) between pairs of genotypes of *Passiflora* [‘yellow’ passion fruit (UESB-*Pef*-G1 a -G14) and ‘sleep’ passion fruit (UESB-*Ps*-G1 a G8)] through physical-chemical characterization of fruits

Genótipos	<i>Pef1</i>	<i>Pef2</i>	<i>Pef3</i>	<i>Pef4</i>	<i>Pef5</i>	<i>Pef6</i>	<i>Pef7</i>	<i>Pef8</i>	<i>Pef9</i>	<i>Pef10</i>	<i>Pef11</i>	<i>Pef12</i>	<i>Pef13</i>	<i>Pef14</i>	<i>Ps1</i>	<i>Ps2</i>	<i>Ps3</i>	<i>Ps4</i>	<i>Ps5</i>	<i>Ps6</i>	<i>Ps7</i>	<i>Ps8</i>	
UESB- <i>Pef</i> -G1	0																						
UESB- <i>Pef</i> -G2	11.5	0																					
UESB- <i>Pef</i> -G3	37.8	14.6	0																				
UESB- <i>Pef</i> -G4	19.4	30.8	6.6	0																			
UESB- <i>Pef</i> -G5	10.5	24.2	5.0	2.7	0																		
UESB- <i>Pef</i> -G6	7.2	4.3	3.1	2.9	1.3	0																	
UESB- <i>Pef</i> -G7	11.1	6.7	2.6	3.0	1.2	3.6	0																
UESB- <i>Pef</i> -G8	3.6	3.0	4.9	6.0	2.5	3.1	2.1	0															
UESB- <i>Pef</i> -G9	4.6	3.9	4.0	6.8	3.8	4.0	2.1	6.1	0														
UESB- <i>Pef</i> -G10	2.7	2.3	3.2	4.9	2.4	2.3	1.2	6.5	4.7	0													
UESB- <i>Pef</i> -G11	4.3	2.9	4.1	6.2	3.4	2.8	1.6	8.1	5.9	5.3	0												
UESB- <i>Pef</i> -G12	2.1	1.3	2.4	3.8	1.8	1.2	6.0	9.4	10.9	3.9	5.5	0											
UESB- <i>Pef</i> -G13	4.9	3.8	4.7	7.2	4.1	3.5	2.2	9.2	10.1	9.2	3.4	8.6	0										
UESB- <i>Pef</i> -G14	1.6	1.2	2.6	3.0	1.7	0.9	5.0	1.7	2.3	1.2	1.6	5.3	2.2	0									
UESB- <i>Ps</i> -G1	1.8	2.1	3.2	6.2	1.6	1.6	1.7	2.1	2.6	2.3	2.0	2.1	2.3	1.9	0								
UESB- <i>Ps</i> -G2	1.9	2.0	3.2	1.7	1.7	1.6	1.7	2.2	2.6	2.3	2.1	2.1	2.3	1.9	0								
UESB- <i>Ps</i> -G3	1.9	2.1	3.3	1.7	1.6	1.7	1.8	2.2	2.6	2.3	2.2	2.1	2.3	1.9	0								
UESB- <i>Ps</i> -G4	1.9	2.3	3.5	1.7	1.7	1.7	1.9	2.3	2.8	2.5	2.3	2.2	2.3	1.9	0								
UESB- <i>Ps</i> -G5	1.6	1.9	3.1	1.5	1.5	1.4	1.6	2.1	2.5	2.2	2.1	2.0	2.2	1.8	0								
UESB- <i>Ps</i> -G6	2.1	2.3	3.5	1.8	1.8	1.8	1.9	2.4	2.8	2.6	2.3	2.3	2.5	1.9	0								
UESB- <i>Ps</i> -G7	2.3	2.6	3.9	2.1	2.1	2.1	2.2	2.8	3.3	2.9	2.8	2.7	2.9	2.5	0								
UESB- <i>Ps</i> -G8	2.1	2.4	3.6	1.8	1.8	1.9	2.1	2.5	3.0	2.6	2.5	2.4	2.7	2.1	0								

From the clustering analysis carried out through the data of the Mahalanobis generalized distance, clear inter-specific separations were detected between the 'yellow' passion fruit and the 'sleep' passion fruit plants (Figure 1). This clustering was obtained from the unweighted pair-group method using arithmetic averages (UPGMA) that exhibited the best projection coefficients (cophenetic correlation, distortion and stress of 0.94, 4.8, 21.9, respectively), in relation to the other tested methods. Similar results were also obtained by Cerqueira-Silva et al. (2009) to the evaluate different statistical methods to characterize the genetic diversity of *Passiflora*.

The separation of the species into different groups in the dendrogram (Figure 1), is derived from the fact that the largest D^2 observed was found in inter-specific pairs that presented a D^2 average of 197.2 and corroborates the intra- and inter-specific VC values previously discussed (Table 1). A higher inter-specific variability was also found when characterizing the access variability of 'yellow' passion fruit plants and

related species of *Passiflora* (Viana et al. 2003). In the present work, the genotypes that differentiated both to a lesser and greater degree were "UESB-*Ps*-G7 with UESB-*Pef*-G3" ($D^2=399.3$) and "UESB-*Ps*-G5 with UESB-*Pef*-G4 and UESB-*Pef*-G6" ($D^2=150$), respectively.

The relative contributions, individual and accumulative, of the analyzed descriptors for the genetic divergence were identified (Table 3). The characteristics that contributed significantly more to genetic diversity were TSS (43.6%), ED (20.1%), TTA (11.9%), and FW (9.6%) which, together, represented 85.2% of the variability that is existent among the genotypes. These results reinforce the existent relationship for the differences in VC values among the passion fruit plants concerning these physical-chemical characteristics (Table 1). It is noteworthy that those descriptors with a greater contribution for divergence of the genotypes are considered decisive in the characterization of the fruits as being appropriate for consumption *in natura* or for the production of industrialized juices (Fortaleza et al. 2005).

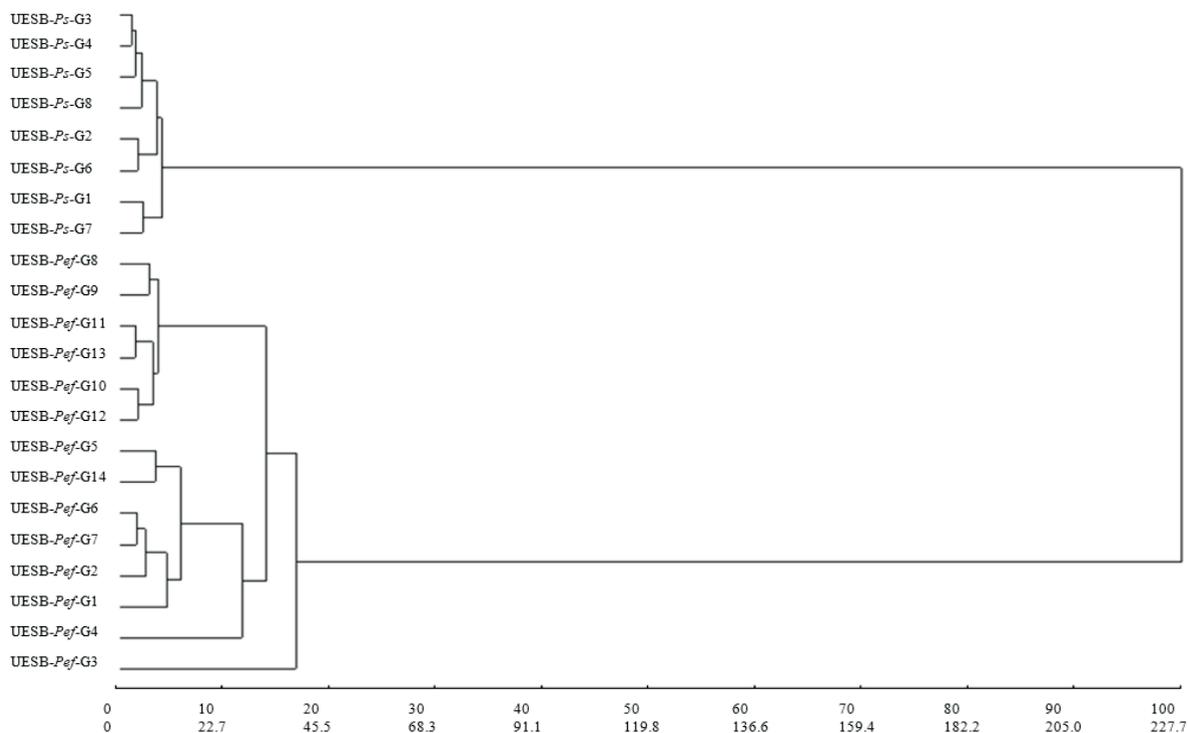


Figure 1. Clustering analysis of 'yellow' passion fruit (UESB-*Pef*-G1 a -G14) and 'sleep' passion fruit (UESB-*Ps*-G1 a -G8) genotypes, pertaining to the CAGT-*Passiflora*/UESB (*Coleção Ativa de Germoplasma de Trabalho de Passiflora da Universidade Estadual do Sudoeste da Bahia*, in Vitória da Conquista, Bahia, Brazil) carried out by the UPGMA method, based on the Mahalanobis generalized distance and using nine physical-chemical descriptors of fruits

Table 3. Estimates of the relative contribution (S_j) of each physical-chemical descriptor of fruits for the genetic divergence between ‘yellow’ passion fruit and ‘sleep’ passion fruit plants, based on the Mahalanobis generalized distance (D²)

Descriptors	Relative contribution		
	S _j	Value (%)	Accumulated (%)
Total soluble solids	15,098.2	43.6	43.6
Equatorial diameter	6,965.1	20.1	63.8
Total titratable acidity	4,101.5	11.9	75.6
Fruit weight	3,333.6	9.6	85.2
Peel thickness	2,382.3	6.9	92.1
Pulp weight with seeds	13,20.9	3.8	95.9
pH	569.8	1.6	97.6
Peel weight	487.4	1.4	99.0
Longitudinal diameter	350.3	1.0	100.0

The correlation values existent among the descriptors that contribute to a greater and lesser degree to genetic divergence were high and significant ($r \geq 0.78$; $p < 0.01$) (Table 4). This high correlation among descriptors, associated with their values of relative contribution (Table 3), indicate that the descriptors of lower relative contribution for divergence (LD, PWS, PW, PT, and pH) highlight the same variation in descriptors of higher importance (TSS, ED, TTA, and FW). From these results, considering the Singh (1981) criterion, the descriptors with a lower contribution can be considered redundant and disregarded for the purpose of evaluation of new populations of plants, at least in the evaluated species. In studies of the genetic characterization of ‘scrub’ passion fruit (*P. cincinnata*) the variables LD, PWS, PW, PT, and pH also presented a lower relative contribution (Araújo et al. 2008).

All the physical-chemical descriptors present statistical differences among the ‘passion’ fruit plants and contribute to genetic divergence, standing out due to the elevated values of VC and percentages of relative

contribution in the descriptors TSS, ED, TTA, and FW. The observed variability can be explored in divergent (UESB-*Pef*-G3 vs. UESB-*Ps*-G7) and convergent (UESB-*Pef*-G4 vs. UESB-*Ps*-G5) inter-specific crossings, as well as in crossings aimed at the growth in TSS (UESB-*Pef*-G4 vs. UESB-*Pef*-G7), pulp yield (UESB-*Pef*-G8 vs. UESB-*Ps*-G6) and conformity index (UESB-*Pef*-G5 vs. UESB-*Ps*-G7) content. In addition to the genetic improvement of the physical-chemical characteristics, the execution of inter-specific hybridizations between these species may allow the selection of hybrid genotypes of backcrossings between ‘yellow’ passion fruit and ‘sleep’ passion fruit plants, endowed with resistance genes from the ‘sleep’ passion fruit. Since the resistance this species is known for is for diseases that attack the passion fruit culture (Cardoso-Silva et al. 2007, Meletti et al. 2005).

Table 4. Correlation coefficients between the descriptors of higher importance (in the horizontal) and those of less importance (in the vertical), for the nine physical-chemical descriptors of the analyzed fruits

Descriptor**	FW (g)	ED (mm)	TSS	TTA
LD (mm)	0.969	0.937	-0.767	0.691
PWS (g)	0.948	0.837	-0.568	0.663
PW (g)	0.991	0.979	-0.827	0.772
PT (mm)	0.824	0.920	-0.952	0.708
pH	0.503	0.653	-0.855	0.183

**The correlations presented values of $p < 0.01$; The acronyms are as presented in Table 1

ACKNOWLEDGEMENTS

To CNPq (*Conselho Nacional de Desenvolvimento Científico e Tecnológico*) and FAPESB (*Fundação de Amparo à Pesquisa do Estado da Bahia*) for the Master’s degree and Scientific Initiation scholarships granted to the first two authors, respectively.

Dissimilaridade genética de acessos de maracujazeiros ‘amarelo’ e ‘do-sono’ com base em características físico-químicas de frutos

RESUMO - A dissimilaridade genética intra e interespecífica entre 14 e oito genótipos de maracujazeiro ‘amarelo’ e o ‘do-sono’, foi avaliada por meio de nove descritores físico-químicos, cujos valores mensurados foram submetidos à estatísticas descritiva (média, desvio padrão e coeficiente de variação) e inferencial [univariada (ANOVA, teste de médias e correlações)

e multivariada (distância de Mahalanobis, agrupamentos hierárquicos, coeficiente de Singh e teste de Mantel)]. Foi encontrada variabilidade intra e, especialmente, interespecífica entre os maracujazeiros ($p < 0,001$). Os descritores sólidos solúveis totais, diâmetro equatorial, acidez titulável total e peso dos frutos apresentaram os maiores percentuais de contribuição relativa, totalizando 85,2% da divergência observada. Cruzamentos preferenciais entre genótipos com características físico-químicas de frutos desejáveis e dissimilaridade genética útil em cruzamentos divergentes e convergentes foram identificados.

Palavras-chave: Análise multivariada, diversidade, variabilidade, *Passiflora edulis* Sims, *Passiflora setacea* DC.

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