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Characterization of a segregating population of passion fruit with resistance to *Cowpea aphid-borne mosaic virus* through morpho-agronomic descriptors

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ABSTRACT. In passion-fruit breeding programs, characterizing genotypes developed through morpho-agronomic descriptors helps quantify genetic diversity and identify individuals with desirable qualities. We examined the discriminatory ability of passion-fruit descriptors and determined their relative importance in the characterization of 91 genotypes from a breeding program for resistance to *Cowpea aphid-borne mosaic virus*. Twenty-four quantitative and 14 multi-category qualitative descriptors related to plant, leaf, flower, and fruit characteristics were used. The quantitative descriptors were subjected to correlation and principal-component analyses and selected based on direct selection and the Singh method. The traits were used to obtain a distance matrix, based on Gower's algorithm, and a comparative clustering between the dendrograms for the morpho-agronomic variables was obtained using the unweighted pair group method with arithmetic mean procedure. Based on the principal components method, the traits that most contributed to genetic variability were number of seeds (23.241%), petiole length (19.438%), and petal width (10.440%). In its turn by the Singh method, the traits androgynophore length (6.68%),

followed by flower length (5.47%), area under the disease progress curve (5.27%), and peduncle length (5.17%) were those which most contributed to the differentiation of genotypes. Although seven descriptors (leaf length, bract width, corona long filament length, sepal length, fruit width, fruit mass, and mass of fruit pulp) showed little contribution to the characterization of genotypes, their discard is not suggested, as they significantly contribute to the discrimination of genetic divergence in the population. Comparative analysis between the dendrogram containing all descriptors and the dendrogram containing only flower, leaf, or fruit descriptors evidenced the need for using a large number of descriptors in the characterization of genetic diversity in *Passiflora*. The use of all 38 descriptors increased the efficiency in the discrimination of groups.

Key words: *Passiflora edulis*; CABMV; Principal components; Canonical variables

INTRODUCTION

Brazil is one of the main centers of genetic diversity of genus *Passiflora*, with 147 species of which 86 are endemic (Flora do Brasil, 2020). Because of its inter- and intraspecific variability, the interest in the genus goes further, given its ornamental potential, medicinal properties, and production of fresh fruit for consumption (Sanchéz-Zapata et al., 2011; Santos et al., 2012). The main commercially cultivated species of the genus is *Passiflora edulis*, thanks to its quality, vigor, and juice yield (Silva et al., 2014). The country is among the biggest world producers of this fruit crop, having generated 554,598 t in 2017 (IBGE, 2017).

Phytosanitary problems such as the fruit woodiness (hardening) disease, caused by *Cowpea aphid-borne mosaic virus* (CABMV) and considered one of the most economically important diseases affecting the passion fruit crop in Brazil, limit its production. As a result, considerable production losses occur and the cultivated area is markedly reduced, since there are no cultivars of commercial species resistant to it (Cerqueira-Silva et al., 2014).

Research has been conducted on the development of resistance through interspecific hybridization (Di Piero et al., 2010; Correa et al., 2015; Freitas et al., 2015). The State University of Northern Rio de Janeiro (UENF) stands out in this scenario for having a well-structured passion-fruit breeding program - the only one in the Brazil -, which in the last 10 years has focused on obtaining varieties resistant to the disease with desirable agronomic traits (Santos et al., 2015).

UENF's program aimed at resistance to CABMV started in 2010, with crossed between commercial species *P. edulis* and the wild species *P. setacea*. Interspecific hybrids with great potential for morpho-agronomic traits and resistant to the virus were selected (Santos et al., 2015). Later, Freitas et al. (2015) developed studies on inheritance of resistance with the first-backcross population and concluded that resistance is complex, discarding the hypothesis of polygenic inheritance. In this regard, the morphological and agronomic characterization of this backcross population of passion fruit using descriptors is

essential, in the breeding program, to aid in the selection of genotypes that meet the interest of the breeder and to direct future crosses.

The term "descriptor" refers to an attribute or characteristic that allows for the discrimination of genotypes. However, even descriptors of great importance such as those related to the fruit, for instance, may become redundant if they are correlated with other selected traits (Castro el al., 2012). Thus, many descriptors are deemed unnecessary because their contribution to the total variability is small when compared with the work and cost incurred in data collection (Oliveira et al., 2012).

Castro et al. (2012) evaluated the discriminatory ability of 20 quantitative and eight qualitative descriptors in *P. edulis* varieties subjected to principal component analysis and the method of Singh and showed that six descriptors could be discarded (four quantitative and two qualitative) without information losses occurring after their elimination. Oliveira et al. (2012) conducted a study to define the minimum number of descriptors to distinguish papaya genotypes, and after subjecting the 21 descriptors to principal component analysis using the direct selection and the method of Singh, they concluded that eight descriptors could be discarded with no information loss.

Principal component analysis, the method of Singh, and correlation estimates stand out among the methodologies available for the determination of the importance of descriptors in the characterization of a population. Sousa et al. (2012) developed a study to characterize and quantify the genetic diversity of accessions of *P. edulis* and *P. cincinnata*. They obtained estimates of genetic correlations between fruit traits and also used the Singh method to estimate the relative contribution of these traits to the expression of genetic diversity in the accessions. Alves et al. (2012) undertook an experiment to evaluate the relationships between physical and chemical components of *Passiflora alata* fruits in which they subjected the data to Pearson's correlations and obtained significant correlations between most evaluated traits.

The objectives of this study were to generate information on the discriminatory ability of 38 morpho-agronomic descriptors used in segregating populations of passion fruit developed for resistance to CABMV; associate quantitative and qualitative descriptors for the formation of groups; and determine their relative importance in the characterization of 91 genotypes derived from interspecific crosses from the breeding program developed at UENF.

MATERIAL AND METHODS

Plant material

Ninety-one individuals were analyzed, consisting of one *P. setacea* genotype, four *P. edulis* genotypes, 14 interspecific hybrids from the cross between *P. setacea* and *P. edulis*, and 72 genotypes from the first backcross generation (BC_1). This population originates from the passion-fruit breeding program aimed at resistance to CABMV developed by UENF, whose goal is to obtain passion fruit varieties with greater resistance to the fruit woodiness disease caused by CABMV, higher productivity, and which produce fruit with higher physicochemical quality.

Experimental settings

The genotypes were planted in September 2015, in the experimental area of the Antônio Sarlo State Agricultural Technical School, northern region of Rio de Janeiro State, Brazil (21º45' S, 41º20' W, 11 m altitude), in a randomized block design with four replicates. Plants were trained in the field using vertical stakes with 2.5-m-high fence posts spaced 4 m apart, with 12-gauge wire at 1.80 m from the soil. The distance between planting rows and between furrows was 3.5 m and 2 m, respectively. The cultivation practices applied were those recommended for the passion fruit crop (Abreu, 2011).

Twenty-four quantitative and 14 multi-category qualitative traits related to plant, leaf, flower, and fruit characteristics were evaluated (Table 1). Of these, 37 were part of the list of descriptors proposed for the passion-fruit crop by the Brazilian Ministry of Agriculture, Livestock, and Food Supply (MAPA, 2019).

Table 1. Quantitative and qualitative descriptors used to assess the 91 genotypes of *Passiflora* including parental, interspecific hybrids and first generation of backcross (BC_1) of the breeding program for resistance to *Cowpea aphid-borne mosaic virus*.

Descriptors	Nature of the descriptor	Descriptor	Abbreviation
Plant	Qualitative	Color of the branch	CBR
Plant	Quantitative	Stem diameter	SD
Plant	Quantitative	Area under the disease progress curve	AUDPC
Leaf	Qualitative	Depth of the sinus	DES
Leaf	Qualitative	Position of leaf gland	PLG
Leaf	Qualitative	Leaf blade pilosity	LIH
Leaf	Quantitative	Leaf length	LL
Leaf	Quantitative	Leaf width	LW
Leaf	Quantitative	Petiole length	PEL
Flower	Qualitative	Pollen	PO
Flower	Qualitative	Hypanthium shape	HIS
Flower	Qualitative	Color of the perianth	COP
Flower	Qualitative	Corona color	COC
Flower	Qualitative	Corona filament banding	CFB
Flower	Qualitative	Number of colored rings	NCR
Flower	Qualitative	Long corona filaments	LCL
Flower	Quantitative	Flower length	FL
Flower	Quantitative	Flower peduncle length	FPL
Flower	Quantitative	Petal length	PL
Flower	Quantitative	Petal width	PW
Flower	Quantitative	Sepal length	SL
Flower	Quantitative	Sepal width	SW
Flower	Quantitative	Bract length	BL
Flower	Quantitative	Bract width	BW
Flower	Quantitative	Corona diameter	CD
Flower	Quantitative	Corona long filament length	CLFL
Flower	Quantitative	Androgynophore length	AL
Fruit	Qualitative	Fruit shape	FRS
Fruit	Qualitative	Fruit skin color	FRSC
Fruit	Qualitative	Fruit pulp color	FPC
Fruit	Quantitative	Fruit length	FRL
Fruit	Quantitative	Fruit width	FRW
Fruit	Quantitative	Fruit mass	FRM
Fruit	Quantitative	Mass of fruit pulp	MFP
Fruit	Quantitative	Peel thickness	PT
Fruit	Quantitative	Total soluble solids	TSS
Fruit	Quantitative	Seed size	SS
Fruit	Quantitative	Number of seeds	NS

Statistical analysis

The descriptors were evaluated based on principal component analysis and based on the average of the measurements taken from each descriptor, from the correlation matrix, using the Genes software (Cruz, 2013). For the suggestion of which least informative quantitative descriptors to discard, we followed a method based on the relative importance of the traits (Singh, 1981) and another based on direct selection (Jolliffe, 1973). Any descriptor with a higher weighting coefficient in absolute value (eigenvector) in the principal component of lowest eigenvalue was indicated for discard, starting from the last component until the one whose eigenvalue did not exceed 0.70.

Pearson's correlation was used to determine the efficiency of discard, since the discarded traits must be correlated with other selected traits. The significance of the correlation coefficient was checked by the t test. All statistical analyses were performed using Genes software (Cruz, 2013). Linear correlation (Pearson) analyses were based on the significance of their coefficients. The correlation intensity for $P \leq 0.05$ is classified as follows: very strong ($r \pm 0.91$ to ± 1.00), strong ($r \pm 0.71$ to ± 0.9), moderate ($r \pm 0.51$ a ± 0.70), and weak ($r \pm 0.31$ to ± 0.50) (Carvalho et al., 2004).

Multivariate analyses were carried out to obtain estimates of genetic divergence of the genotypes based on the Gower distance (Gower, 1971), for the 38 morpho-agronomic variables evaluated in the trials. Based on the generated distance matrix, the individuals were grouped by the UPGMA method (Unweighted Pair Group Method with Arithmetic Mean). In addition to the matrix with the 38 variables, matrices containing only the flower, fruit, and leaf variables were obtained. These distance matrices with fewer variables were compared with the matrix containing the 38 variables using the Dendextend package in R software (http://www.r-project.org).

RESULTS

The accumulated variance in the 24 quantitative descriptors did not indicate a distribution concentrated in the first components. Only from the eighth principal component was it possible to accumulate a satisfactory percentage, with 81.23% of the total genotypic variability (Table 2).

Based on the principle that the importance or variance of principal components declines from the first to the last component, the last components explain a very small fraction of the total variance. Thus, the variable with the highest coefficient in the component of lowest eigenvalue should be the least important to explain the total variance, thereby allowing for the discard of morphological descriptors that contribute little to the study of divergence (Cruz et al., 2014).

The first three components explain 53.12% of total variation (first: 23.24%; second: 19.44%; and third: 10.44%) (Table 2). Despite similar, this result differs from that reported by Castro et al. (2012), who characterized accessions of *P. edulis* using 20 morpho-agronomic descriptors and found 67.17% of the total variation in the first three components. Silveira et al. (2016), in turn, quantified the relative contribution of 30 flower and fruit traits in *Passiflora* and showed that the first and second variables explained 22.45% and 16.81% of the variation, respectively, and 52.11% of the total variation was explained by the first three variables.

Table 2. Eigenvalues, variance and cumulative variance obtained from 24 quantitative morphoagronomic descriptors assess in 91 genotypes of *Passiflora* including parents, interspecific hybrids and first generation of backcross (RC_1) of the breeding program aiming resistance to *Cowpea aphid-borne mosaic virus.*

Descriptor	Eigenvalue	Variance (%)	Cumulative variance (%)
NSE	5.578	23.241	23.241
PEL	4.665	19.438	42.679
PW	2.506	10.440	53.119
PL	2.051	8.544	61.664
LW	1.613	6.721	68.385
TSS	1.157	4.823	73.208
CD	1.007	4.195	77.403
FPL	0.920	3.830	81.233
PT	0.815	3.397	84.631
BL	0.644	2.682	87.313
SD	0.566	2.357	89.670
SS	0.531	2.210	91.880
AUDPC	0.423	1.760	93.641
FL	0.323	1.346	94.987
FRL	0.261	1.086	96.073
SW	0.207	0.863	96.936
AL	0.175	0.728	97.664
FRW	0.158	0.656	98.320
LL	0.124	0.515	98.836
BW	0.115	0.478	99.313
CLFL	0.065	0.270	99.583
SL	0.057	0.236	99.819
FRM	0.023	0.095	99.915
MFP	0.020	0.085	100.0

NSE = number of seeds, PEL = petiole length, PW = petal width, PL = petal length, LW= leaf width, TSS = total soluble solids, CD = corona diameter, FPL = flower peduncle length, PT = peel thickness, BL = bract length, SD = stem diameter, SS = seed size, AUDPC = area under the disease progress curve, FL = flower length, FRL = fruit length, SW = sepal width, AL = androgynophore length, FRW = fruit width, LL = leaf length, BW = bract width, CLFL = corona long filament length, SL = sepal length, FRM = fruit mass e MFP = mass of fruit pulp.

By adopting the methodology proposed by Jolliffe (1973), which establishes the elimination of descriptors whose association between eigenvectors and eigenvalues is lower than 0.7, seven morpho-agronomic descriptors could be discarded: one related to the leaf (LL), three related to the flower (BW, CLFL, and LS), and three related to the fruit (FRW, FRM, and MFP). This methodology suggests that 29% of the morpho-agronomic descriptors used contributed little to the characterization of the evaluated population.

According to the method proposed by Singh (1981), however, which is used to evaluate the relative contribution of the 24 quantitative traits, 10 of these traits contributed with 52.24% to genetic diversity, while the other 14 contributed with 47.76% (Table 3).

The analysis of the relative contribution of the traits to genetic dissimilarity shows that, for the evaluated genotypes, the contribution values of the 24 descriptors used were similar, ranging from 2.14 to 6.68%. The traits androgynophore length (6.68%), followed by flower length (5.47%), area under the disease progress curve (5.27%), and peduncle length (5.17%) were those which most contributed to the differentiation of genotypes. The descriptors length of the long filament of the corona (2.29%), corona diameter (2.17%), and seed size (2.14%) had the lowest contributions. Therefore, according to this criterion, it can be stated that all selected descriptors are important in the characterization of the evaluated *Passiflora* genotypes, as they provide important contributions (greater than 1.0% of the total variation) in the discrimination of divergence.

Table 3. Relative contribution of 24 quantitative morphogronomics descriptors of *Passiflora* to genetic divergence by the Singh method.

Variable	S.j	Value (%)	Variable	S.j	Value (%)
AL	526.378	6.682	LL	349.377	4.435
FL	430.838	5.469	PW	343.510	4.3610
AUDPC	415.311	5.272	LW	291.874	3.705
FPL	407.101	5.168	PT	284.761	3.615
FRW	398.836	5.063	BL	267.817	3.4
PL	393.469	4.995	NS	254.545	3.231
SL	392.841	4.987	MFP	247.342	3.140
SW	386.952	4.912	FRM	239.532	3.041
BW	385.015	4.888	SD	235.392	2.988
FRL	378.242	4.802	CLFL	180.627	2.293
TSS	368.139	4.674	CD	171.358	2.175
PEL	359.333	4.562	SS	168.440	2.138

AL = androgynophore length, FL = flower length, AUDPC = area under the disease progress curve, FPL = flower peduncle length, FRW = fruit width, PL = petal length, SL = sepal length, SW = sepal width, BW = bract width, FRL = fruit length, TSS = total soluble solids, PEL = petiole length, LL= Leaf length, PW= Petal width, LW= Leaf width, PT= Peel thickness, BL= Bract length, NS= Number of seeds, MFP= Mass of fruit pulp, FRM= Fruit mass, SD= Stem diameter, CLFL= Long corona filaments, CD= Corona diameter, SS= Seed size. S.j = Relative contribution of characters evaluated for diversity.

Different results were reported by Sousa et al. (2012), who characterized and quantified genetic diversity in accessions of *P. edulis* based on physical and chemical fruit traits and obtained higher values than those reported here for the relative contributions of fruit width (15.94%) and peel thickness (5.38%). On the other hand, soluble solids content (2.93%), number of seeds (2.52%), and fruit weight (3.04%) had lower contributions to the genetic divergence of passion fruit genotypes as compared with this study.

The estimates of phenotypic correlation values, obtained from the evaluation of the 91 genotypes, are described in Table 4.

Table 4. Linear correlation matrix (Pearson) between passion fruit traits obtained from passion fruit genotypes including parents, interspecific hybrids and first generation backcrossing (BC_1) of the breeding program aiming at resistance to *Cowpea aphid-borne mosaic virus*.

	FRW	FRM	MFP	NSE	LL	LW	PL	PW	SL	SW	BL	BW	CD	AL
FRM	0.874**													
MFP	0.745**	0.924**												
NSE	0.716**	0.881**	0.952**											
LL	0.058^{ns}	0.123^{ns}	0.078^{ns}	0.048^{ns}										
LW	0.097^{ns}	0.056^{ns}	-0.026^{ns}	-0.069^{ns}	0.776**									
PL	-0.073^{ns}	-0.110^{ns}	-0.214*	-0.256*	0.223*	0.209*								
PW	0.307**	0.295**	0.188^{ns}	0.144^{ns}	-0.176^{ns}	0.008^{ns}	-0.018^{ns}							
SL	-0.041^{ns}	-0.099^{ns}	-0.172^{ns}	-0.186^{ns}	0.269**	0.226*	0.875**	-0.238*						
SW	0.145^{ns}	0.108^{ns}	0.053^{ns}	0.037^{ns}	-0.103^{ns}	-0.030^{ns}	-0.038^{ns}	0.738**	-0.263*					
BL	0.058^{ns}	-0.044^{ns}	-0.097^{ns}	-0.146^{ns}	0.310**	0.278**	0.377**	0.013^{ns}	0.348**	0.143^{ns}				
BW	0.033^{ns}	-0.038^{ns}	-0.102^{ns}	-0.128^{ns}	0.307**	0.319**	0.421**	0.148^{ns}	0.385**	0.290**	0.792**			
CD	-0.057^{ns}	-0.057^{ns}	-0.113^{ns}	-0.197^{ns}	0.015^{ns}	0.074^{ns}	0.365**	0.244*	0.127^{ns}	0.159^{ns}	0.152^{ns}	0.043^{ns}		
AL	-0.159^{ns}	-0.243*	-0.249*	-0.220*	0.349**	0.217*	0.584**	-0.45**	0.752**	-0.428**	0.365**	0.318**	0.027^{ns}	
CLFL	-0.051^{ns}	-0.061^{ns}	-0.084^{ns}	-0.135^{ns}	0.161^{ns}	0.199^{ns}	0.448**	-0.263*	0.297**	-0.062^{ns}	0.258*	0.066^{ns}	0.860**	0.291**

FRW = fruit width, FRM = fruit mass, MFP = mass of fruit pulp, NSE = number of seeds, LL = leaf length, LW= leaf width, PL = petal length, PW = petal width, SL = sepal length, SW = sepal width, BL = bract length, BW = bract width, CD = corona diameter, AL = androgynophore length e CLFL = corona long filament length. (**) and (*) significant at 1 and 5% probability by the t test, respectively. ns not significant.

These correlation estimates make it possible to predict the response of a trait when selection is performed on another correlated trait. In other words, for instance, it allows for selection on an easily measurable trait to obtain gains in one that is difficult to measure (Oliveira et al., 2011).

To explain the relationship between the traits of economic importance, correlation estimates should be considered satisfactory; i.e., r >±0.50 (Greco et al., 2014). Fruit width showed to be highly correlated with fruit weight (0.874), pulp weight (0.745), and number of seeds (0.716) (Table 4). Greco et al. (2014) evaluated physical and physicochemical traits of 32 genotypes of passion fruit and also found high and positive correlations between fruit width and weight (0.870). However, the correlation coefficients between fruit width and pulp weight and number of seeds diverged (0.063 from 0.297, respectively) from those obtained in the current experiment.

Fruit weight was highly correlated with number of seeds (0.881) and with pulp weight (0.924), which in turn was highly correlated with number of seeds (0.952) (Table 4). These correlations with fruit weight were expected, since they indicate that genotypes with heavier fruits typically produce wider fruits, with consequent higher pulp weight and number of seeds. According to Sousa et al. (2012), in the direct selection of passion-fruit genotypes, these are among the most relevant traits.

The correlation between leaf length and leaf width was strong (0.776), and so were the correlations between bract width and bract length (0.792) and between sepal width and petal width (0.738). Further, there was a positive and strong correlation between corona diameter and the length of the long filament of the corona (0.860) (Table 4).

In the cluster analysis of the 91 genotypes, the UPGMA method resulted in five distinct groups formed when all 38 morpho-agronomic descriptors were used (Figure 1).

The objective of cluster analysis is to gather the genotypes into groups such that there is homogeneity within the group and heterogeneity between groups (Cruz; Regazzi, 2004). Group I was formed by 1 genotype; groups II, III, IV, and V, by 12, 6, 57, and 15 genotypes, respectively. Parents *P. setacea* and *P. edulis* and the interspecific hybrids were clustered into three distinct groups (groups I, III, and V, respectively), whereas the backcross genotypes were clustered into groups II and IV, the latter of which contained 65% of the individuals (Figure 1).

Comparative analysis between the dendrogram containing all descriptors and the dendrogram containing only flower, leaf, or fruit descriptors evidenced the need for using different descriptors in the characterization of genetic diversity in *Passiflora*, since neither the number of groups nor the arrangement between genotypes remained the same. The entanglement rate, which measures the correspondence of genotypes between distinct dendrograms, ranging from 0 to 1 (0 = dendrograms with full correspondence; 1 = dendrograms with no correspondence), was 0.51 for the dendrogram with fruit descriptors, demonstrating divergence in the distribution of genotypes between the dendrograms (Figure 1).

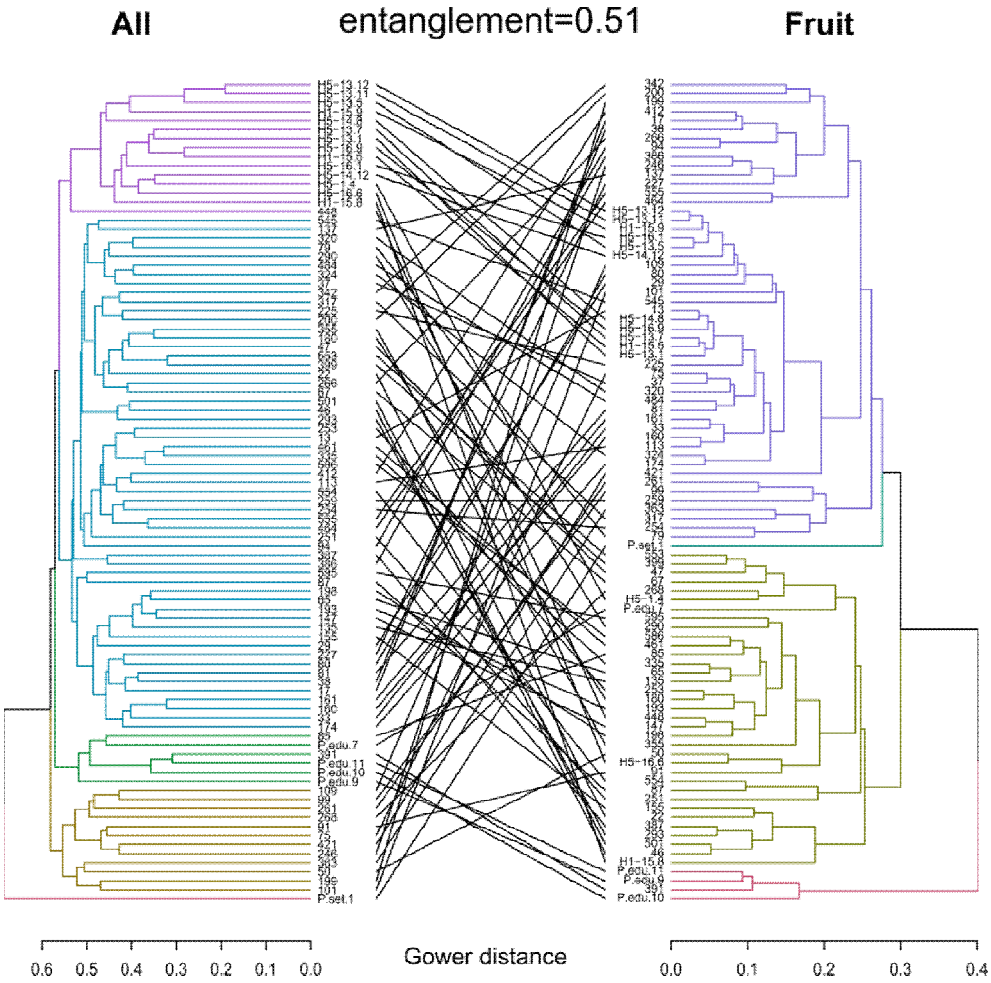

Figure 1. Relationships among 91 Passiflora genotypes including parents, interspecific hybrids and first generation backcross (BC_1) of the breeding program aiming at resistance to *Cowpea aphid-borne mosaic virus*, obtained by the Dendextend package, based on Gower distance considering the morphoagronomic variables of fruit, flower and leaf, and only fruit.

Unlike the dendrogram with all descriptors, the dendrogram that contained only fruit descriptors had the genotypes clustered into four groups, with no distinction between parents and backcross individuals. Group I was formed by 4 genotypes (3 *P. edulis* and 1 backcross); group II contained 35 genotypes (1 *P. edulis*, 3 interspecific hybrids, and 31 backcrosses); group III only had the *P. setacea* genotype; and group IV was formed by 51 genotypes (11 interspecific hybrids and 40 backcrosses). Individuals 254, 259, and 113 had the fewest changes across clusters, and despite the change in position of parent *P. setacea*, it was not grouped with another genotype.

The dendrogram containing only flower descriptors had an entanglement rate of 0.44 (Figure 2).

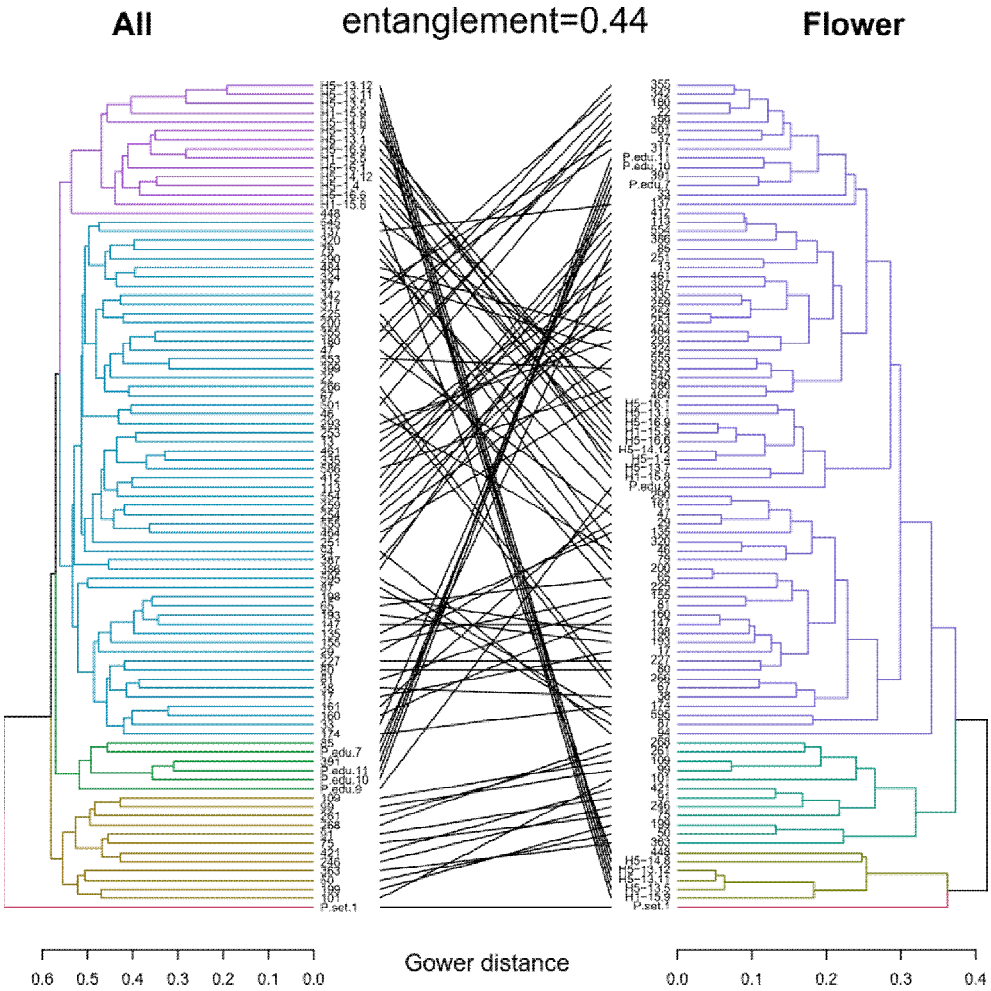

Figure 2. Relationships among 91 *Passiflora* genotypes including parents, interspecific hybrids and first generation backcross (BC_1) of the breeding program aiming at resistance to *Cowpea aphid-borne mosaic virus*, obtained by the Dendextend package, based on Gower distance considering the morphoagronomic variables of fruit, flower and leaf, and only of flower.

Four groups were also formed. Group I had one individual (*P. setacea*); group II contained six individuals (five interspecific hybrids and one backcross); group III included 12 backcrosses; and group IV had 72 individuals (nine interspecific hybrids, four *P. edulis*, and 59 backcrosses), or 79% of the evaluated genotypes. Individuals 80, 227, 553, and *P. setacea* had the fewest changes across clusters. The dendrogram containing the leaf descriptors, in turn, had the least entanglement (0.43) (Figure 3).

Six groups were formed, containing one (*P. setacea*), one (backcross), four (two interspecific hybrids and two backcrosses), 26 (seven interspecific hybrids and 19 backcrosses), 18 (one *P. edulis* and 17 backcrosses), and 41 individuals (five interspecific hybrids, three *P. edulis*, and 33 backcrosses), respectively. Parents and backcross individuals were not allocated to distinct groups; however, just as in all other dendrograms,

the parent *P. setacea* was not grouped with any other genotype. Individuals 261, 399, 553, and 225 had the fewest changes across clusters.

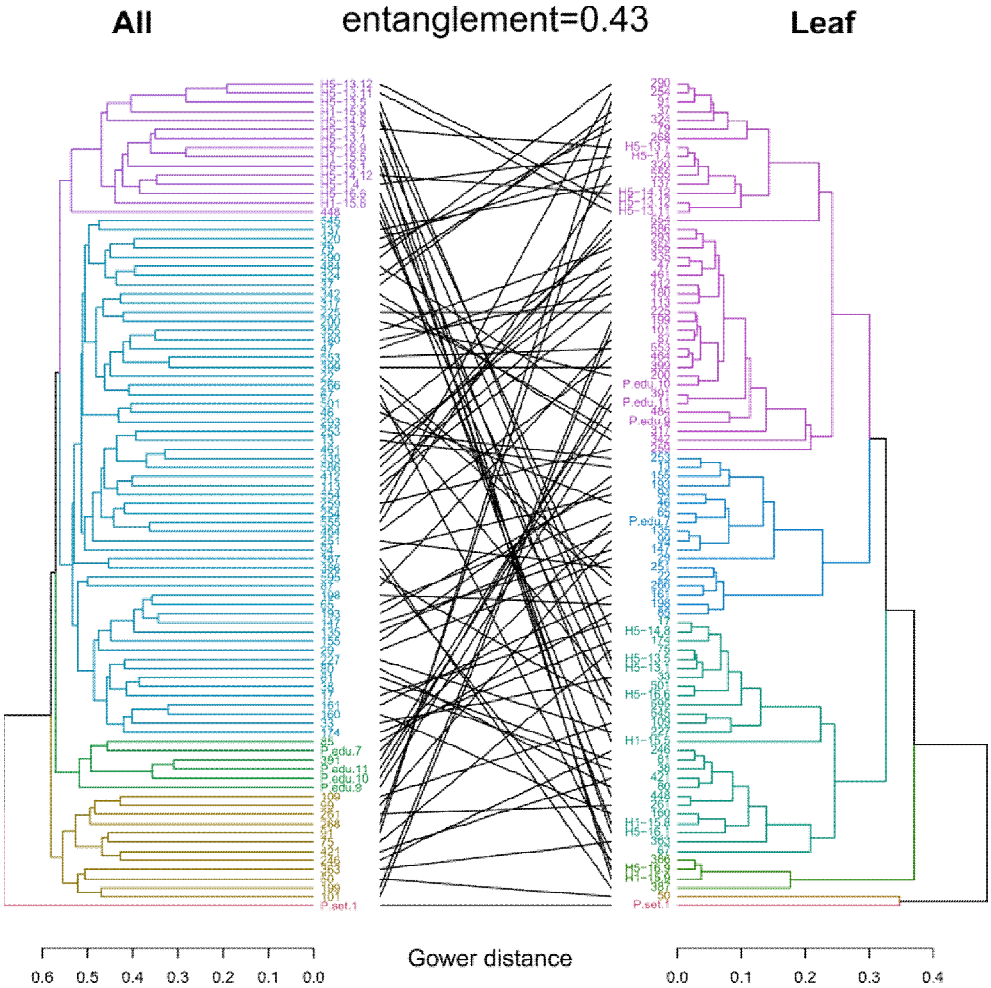

Figure 3. Relationships among 91 *Passiflora* genotypes including parents, interspecific hybrids and first generation backcross (BC_1) of the breeding program aimed at resistance to *Cowpea aphid-borne mosaic virus*, obtained by the Dendextend package, based on Gower distance considering the morphoagronomic variables of fruit, flower and leaf, and only of leaf.

CONCLUSIONS

The traits that contributed most to genetic variability in the population were number of seeds, petiole length, and petal width. However, along with the leaf, flower and resistance descriptors, fruit related descriptors aid in the discrimination and selection of genotypes.

Although seven descriptors (LL, BW, CLFL, LS, FRW, FRM, and MFP) showed little contribution to the characterization of genotypes, their discard is not suggested, as they strongly contribute to the discrimination of genetic divergence in the breeding population.

Comparative analysis of dendrograms showed that the use of the 38 descriptors provided greater efficiency in the discrimination of groups.

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REFERENCES

Abreu SPM (2011). Cultivo de maracujá-azedo. Dossiê Técnico. Centro de Apoio ao Desenvolvimento Tecnológico - CDT/UnB. Available at: [http://www.respostatecnica.org.br/dossie-tecnico/downloadsDT/NTY4Mw==].

Alves RR, Carlos LCC, Salomão C, Siqueira DL, et al. (2012). Relações entre características físicas e químicas de frutos de maracujazeiro-doce sweet passion fruit cultivated in Viçosa, *Rev. Bras. Frutic.* 34: 619–623.

Carvalho FIF, Lorencetti C and Benin G (2004). Estimativas e implicações da correlação no melhoramento vegetal. Pelotas: Editora e Gráfica Universitária – UFPel, Pelotas.

Castro JÁ, Neves CG, Jesus ON and Oliveira EJ (2012). Definition of morphoagronomic descriptors for the characterization of yellow passion fruit. *Sci Hortic*. 145: 17-22.

Cerqueira-Silva CBM, Jesus ON, Santos ESL, Corrêa RX, et al. (2014). Genetic breeding and diversity of the genus *Passiflora*: progress and perspectives in molecular and genetic studies. *Int. J. Mol. Sci.*15: 14122-14152.

Correa MF, Pinto APC, Rezende JAM, Harakava R, et al. (2015). Genetic transformation of sweet passion fruit (*Passiflora alata*) and reactions of the transgenic plants to Cowpea aphid borne mosaic virus. *Eur. J. Plant Pathol.* 143: 813-821.

Cruz CD (2013). GENES - a software package for analysis in experimental statistics and quantitative genetics. *Acta Sci. Agron*. 35: 271-276.

Cruz CD and Regazzi AJ (2004). Modelos biométricos aplicados ao melhoramento genético. Viçosa-MG: UFV.

Di Piero RM, Novaes QS and Pascholati SF (2010). Effect of *Agaricus brasiliensis* and *Lentinula edodes* Mushrooms on the Infection of Passionflower with *Cowpea aphid-borne mosaic virus*. *Braz. arch. biol. technol*. 53: 269-278.

Fávero LP, Belfiore P, Silva FL and Chan BL (2009). Análise de dados**:** modelagem multivariada para tomada de decisões. Rio de Janeiro: Campus/Elsevier.

Flora do Brasil 2020. Jardim Botânico do Rio de Janeiro. Available: <http://floradobrasil.jbrj.gov.br/reflora/floradobrasil/FB12506>. Accessed: 2 May 2019.

Freitas JCO, Viana AP, Santos EA, Silva FHL, et al. (2015). Genetic basis of the resistance of a passion fruit segregant population to *Cowpea aphid-borne mosaic virus* (CABMV). *Trop. Plant Pathol*. 40: 291-297.

Gower JCA (1971). General coefficient of similarity and some of its properties. *Biometrics*. 27: 857-874.

Greco SML, Peixoto JR and Ferreira LM (2014). Avaliação física, físico-química e estimativas de parâmetros genéticos de 32 genótipos de maracujazeiro-azedo cultivados no Distrito Federal. *Biosc. J*. 30: 360-370.

IBGE (2017). Banco de dados agregados: produção agrícola municipal. Sistema IBGE de recuperação automática – SIDRA. Available: <https://sidra.ibge.gov.br/> Accessed 02/05/2019.

Jolliffe IT (1973). Discarding variables in a principal component analysis. II. Real data. *App. Stat*. 21(1): 21-31.

Junqueira NTV, Braga MF, Faleiro, FG, Peixoto JR, et al. (2005). Maracujá: germoplasma e melhoramento genético. In: Potencial de espécies silvestres de maracujazeiro como fonte de resistência a doenças (Faleiro FG, Junqueira NTV, Braga MF eds.). Embrapa Cerrados, Planaltina, DF.

MAPA (2019). Ministério da Agricultura, Pecuária e Abastecimento. Anexo IX Formulário para Inscrição de Cultivares no Registro Nacional de Cultivares. Available at: http://www.agricultura.gov.br/assuntos/insumos-agropecuarios/insumos-agricolas/sementes-e-mudas/registro-nacional-de-cultivares-2013-rnc-1/formularios-para-registro-de-cultivares.

Negreiros JS, Alexandre RS, Álvares VS, Bruckner CH, et al. (2008). Divergência genética entre progênies de maracujazeiro-amarelo com base em características das plântulas, *Rev. Bras. Frutic.* 30: 197-201.

Oliveira EJ, Dias NLP and Dantas JLL (2012). Selection of morpho-agronomic descriptors for characterization of papaya cultivars. *Euphytica*. 185: 253–265.

Oliveira EJ, Santos VS, Lima DS, Machado MD, et al. (2011). Estimativas de correlações genotípicas e fenotípicas em germoplasma de maracujazeiro. *Bragantia*. 70: 255-261.

Pereira AV, Vencovsky R and Cruz CD (1992). Selection of botanical and agronomical descriptors for the characterization of cassava (*Manihot esculenta* Crantz.) germplasm, SP. *Braz. J. Genet.* 15: 115-124.

R development core team (2011). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL http://www.R-project.org/. 2011.

Sanchéz-Zapata E, Fernandéz-Lopez J, Peñaranda M, Fuentes-Zaragoza E, et al. (2011). Technological properties of date paste obtained from date by-products and its effect on the quality of a cooked meat product. *Food Res. Int.* 44: 2401 – 2407.

Santos EA, Souza MM, Abreu PP, Conceição LDHCS, et al. (2012). Confirmation and characterization of interspecific hybrids of *Passiflora* L. (Passifloraceae) for ornamental use. *Euphytica*. 184: 389–399.

Santos EA, Viana AP, Freitas JCO, Silva FHL, et al. (2015). Resistance to *Cowpea aphid-borne mosaic virus* in species and hybrids of Passiflora: advances for the control of the passion fruit woodiness disease in Brazil. *Eur. J. Plant Pathol.*143: 85-98.

Silva FHL, Viana AP, Ferreira RT, Freitas JCO, et al. (2014). Measurement of genetic diversity in progenies of sour passion fruit by Ward-MLM methodology: a strategy for heterotic group formation. *Ciênc. Agrotec*. 38: 1234–1239.

Silveira GF, Rossi AAB, Varella TL, Carvalho MLS, et al. (2016). Genetic divergence among *Passiflora cristalina* Vanderpl & Zappi. Genotypes based on flower and fruit characteristics. *Rev. Bras. Frutic*. 38: e491.

Sousa LB, Silva EM, Gomes RLF, Lopes ACA, et al. (2012). Caracterização e divergência genética de acessos de *Passiflora edulis* e *P. cincinnata* com base em características físicas e químicas de frutos, SP. *Rev. Bras. Frutic.* 34: 832-8393.