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Genetics and plant breeding

Characterization and selection of "Maracujá-do-mato" (*Passiflora cincinnata* mast) morphoagronomic descriptors

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Abstract - The present study consists of the *in situ* characterization and selection of minimal morphoagronomic descriptors in *Passiflora cincinnata* genotypes. Forty-one quantitative morphoagronomic descriptors were used, divided in "Plant and Leaf", "Floral" and "Fruit". Principal component analysis were used to eliminate descriptors that were less important in the study of multivariate dissimilarity among genotypes. The formation of groups was carried out using Ward's hierarchical grouping method. The importance of the characters was estimated through the participation of the components by Singh's method (1981) in order to verify the similarity between lower participation variables in the components. For the set of descriptors "Plant and Leaf" the characteristics that presented the greatest relative contributions were: maximum leaf width 76.1% and leaf blade length 17.2%. For the set of descriptors "Floral" the characteristics that presented the greatest relative contributions were: pedicel length 42.1%, corona tip diameter 32.6% and petal length 11.8%. For the set of descriptors "Fruit" the characteristic that presented the greatest relative contribution was: number of seeds per fruit 89.2%. From the results obtained, we can infer that from the 41 descriptors, only 15 were relevant for the evaluation of the genetic diversity among the individuals of the population. These descriptors were: titratable acidity, bract length, leaf blade length, petal length, sepal length, pedicel length, corona filament ring length, corona tip diameter, fruit longitudinal diameter, sepal width, maximum leaf width, number of fruits, number of seeds per fruit, bark weight and fruit mass.
Index terms: Principal components, hierarchical grouping, Singh's method.

Caracterização e seleção de descritores morfoagronômicos de "Maracujá-do-mato" (*Passiflora cincinnata* mast)

Resumo - O presente estudo consiste na caracterização e na seleção de descritores morfoagronômicos mínimos em genótipos de Passiflora cincinnata in situ. Foram utilizados 41 descritores morfoagronômicos quantitativos, divididos em "Planta e Folha", "Floral" e "Fruto". Utilizou-se a análise de componentes principais com o objetivo de eliminar descritores que tivessem menor importância no estudo de dissimilaridade multivariada entre genótipos. Foi realizada a formação de grupos por meio do método de agrupamento hierárquico de Ward. Foi estimada a importância dos caracteres por meio da participação dos componentes pelo método de Singh (1981), com o intuito de verificar a similaridade entre variáveis de menor participação dos componentes. Para o grupo de descritores "Planta e Folha", as características que apresentaram as maiores contribuições relativas foram: largura máxima da folha (76,1%) e comprimento da lâmina foliar (17,2%). Para o grupo de descritores "Floral", as características que apresentaram as maiores contribuições relativas foram: comprimento do pedicelo (42,1%), diâmetro da ponta da corona (32,6%) e comprimento da pétala (11,8%). Para o grupo de descritores "Fruto", a característica que apresentou a maior contribuição relativa foi: número de sementes por fruto (89,2%). A partir dos resultados obtidos, pode-se inferir que, dos 41 descritores, apenas 15 se mostraram relevantes para a avaliação da diversidade genética entre os indivíduos da população. Estes descritores foram: acidez titulável, comprimento da bráctea, comprimento da lâmina foliar, comprimento da pétala, comprimento da sépala, comprimento do pedicelo, comprimento dos anéis dos filamentos corona, diâmetro da ponta da corona, diâmetro longitudinal do fruto, largura da sépala, largura máxima da folha, número de frutos, número de sementes por fruto, peso da casca e massa do fruto.
Termos para indexação: Componentes principais, agrupamento hierárquico, método de Singh.

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Introduction

There is a great variety of fruit plants that occur in the Caatinga biome and/or adapted to the dry conditions, of exotic flavors, which attend to the current trends of natural products consumption, that reinforces the initiatives of collection, characterization and cultivation in commercial scale of these fruit trees (Kiill *et al*., 2008). There are only about 70 effectively edible *Passiflora* species (Cunha *et al*., 2002). Among them, the wild species *Passiflora cincinnata* Mast, popularly known in Brazil as "Maracujá-do-Mato" or "Maracujá-de-Boi" (Nunes & Queiroz, 2006) stands out. Among *P. cincinnata* populations, there are vigorous and very diverse plants, showing variation in flower color, fruit size, juice color and taste (Oliveira & Ruggiero, 2005).

This wild *Passiflora* species is used in large scale in fruit extractivism, which generates seasonal employment and income in the countryside (Junior *et al.*, 2010; Pereira *et al.*, 2012), and it is characterized by its resistance to long periods of drought (Pereira *et al*., 2012). This characteristic, allied to the general rusticity in field conditions, could be incorporated to commercial passion fruit (Junqueira *et al*., 2005).

The main prerequisite for initiating a genetic breeding program for a particular plant species is the genetic variability characterization (Faleiro *et al*., 2006a; Lopes & Carvalho, 2008). This can be done by using genetically inherited descriptors: physiological, biochemical, molecular or morphological (Machado *et al*., 2006).

Morphoagronomic descriptors are important for conservation programs, germplasm use, genetic improvement of plants, registration and protection of cultivars, besides being a valuable means of characterizing plants and *Passiflora* species, and quantifying the existing variability (Jesus et al. al., 2017). The genetic variability characterization and quantification of *P. cincinnata* using morphoagronomic descriptors do not count on *in situ* studies.

The characterization of *Passiflora cincinnata* using morphoagronomic descriptors has not been accompanied by a list of minimum descriptors. The importance of identifying them exist due to the demand to discern which ones are necessary and which can be discarded (Beale et al., 1967). Discarding variables that do not provide extra information is critical, because it will reduce time and costs in future reviews, without considerable loss of information (Barbosa et al., 2005).

The evaluation of genotypes of this passion fruit species through the use of morphoagronomic descriptors, aiming at identifying, among the descriptors, redundant variables do not count on *in situ* studies.

The present work deals with the *in situ* identification of minimal morphoagronomic descriptors in *Passiflora cincinnata* genotypes.

Material and methods

Plant genetic material. A total of 53 individuals of passion fruit (*P. cincinnata*) were sampled, under non-irrigated *in situ* conditions, on a 50 km road adjacent to the municipalities of Vitória da Conquista and Belo Campo, both located in the state of Bahia, Brazil, at an altitude from 840 to 892m above sea level, with latitude between 14 ° 95 '38.7'S and 15 ° 01' 59.6'S, longitude between 40 ° 97'97.8'W and 41 ° 17 ' 21.1'W, Cwa climate (mesothermal with dry winter, commonly named *tropical de altitude*) with annual average rainfall of 712 mm (CLIMATE-DATA.ORG, 2018).

The area where the collections took place was determined through prospective trips and also through contacts with residents of the region who work with "Maracujá-do-Mato" extraction and whose commercialization takes place in the Central de Abastecimento de Vitória da Conquista (CEASA).

In the area where the collections took place, a perimeter of at least 30m between each selected plant was delimited in order to define which plants would be part of the research, and to avoid selecting plants that were very close.

Morphoagronomic descriptors. We used 41 quantitative morphoagronomic descriptors (Table 1), divided in "Plant and Leaf", "Floral" and "Fruit" described by Jesus *et al*. (2017). In order to evaluate all the characteristics, it was necessary to go to the field twice, once in September and again in the month of November, 2017. In the first trip to the field, we selected all the plants that had mature fruits and in the second trip, all plants that had completely open flowers. Therefore, not all the descriptors were evaluated for the same genotypes.

Methods and analyzes. For each group of descriptors, the genetic diversity among genotypes was evaluated by group formation using Ward's hierarchical grouping method (Ward, 1963), with Euclidean distance as a measure of dissimilarity. With the same group of descriptors, principal component analysis (PCA) was used to eliminate descriptors that are less important in the study of multivariate dissimilarity between genotypes, having as main criterion the maintenance of descriptors with higher eigenvector in the first components and the removal of higher eigenvector descriptors in the final components until the first two main components accounted for at least 70% of the data variation. After discarding of variables, new PCAs and hierarchical grouping were carried out with the purpose of graphically evaluating the maintenance of the groups of genotypes obtained.

In addition, the relative importance of the characters was estimated through the participation of the Mahalanobis (D^2) generalized distance components, relative to each characteristic, in the total dissimilarity observed (Singh, 1981). This methodology was used

in order to verify similarity between variables of lesser participation of the D² components and the variables discarded by principal components analysis. The analyzes were performed with the aid of software R (R Core Team, 2014), mainly using the packages biotools (da Silva et al, 2017), dplyr (Wickham et al, 2018) and dendextend (Galili, 2015).

Results and discussion

The set of descriptors denominated "Plant and Leaf" was evaluated in 35 individuals; for "Floral" was evaluated 16 individuals; for "Fruit" was evaluated 29 individuals.

We initially estimated the variance of the values measured between the genotypes for each of the 41 descriptors and the degree of multicollinearity in the matrix of variance and covariance between all the descriptors. Three descriptors belonging to the "Floral" group were devoid of variance (NRCF, NFPN and NSN) and, therefore, were discarded from the ACP.

Then, the remaining 38 morphoagronomic descriptors were submitted to multivariate dissimilarity analysis among the individuals. The variables were discarded until the first two components in the eigenvector matrix explained more than 70% of the total variance. In this procedure, 24 less important descriptors were eliminated (Tables 2, 3 and 4).

This high number of discard of less important descriptors may have occurred because the 41 descriptors were not applied in the 53 genotypes. Flower descriptors, for example, were applied in only 16 genotypes.

The descriptors PEL, NFN and NPN were discarded for the group "Plant and Leaf"; for the group "Floral" the descriptors ANGL, ANTL, OVL, CCED, OVD, CCID, ANTW, SEW and NBN; for the "Fruit" group the descriptors SLD, FTD, STD, BT, ST, SW, pH, PW, PPR, RLT, SS and SS/TA.

In the three groups of descriptors of "Plant and Leaf", "Floral" and "Fruit", after the discard of the variables mentioned above, the first two main components accumulate 97.8%, 80.5% and 82.0%, respectively, of all available variation (Table 5).

The analysis of the results suggests that the remaining descriptors (LCFR, BRL, LBL, PEDL, PETL, SEL, FLD, CTD, MLW, SEW, FM, NFR, NSF, BW and TA) are the minimum descriptors to morphoagronomic genetic diversity among passion fruit trees. And, additionally, the 26 descriptors eliminated constitute redundant morphoagronomic aspects that would not aid in the study of genetic diversity and would make data collection and analysis more laborious.

Similar results were found by Santos *et al*. (2011), in the study to estimate genetic parameters by multivariate analysis of two species of *Passiflora* and their hybrids, considered ornamental potential, based on morphological characteristics, in which, through principal component analysis, they reduced the 14 descriptors for two main components which explained 84% of the total variance. Component 1 explained 48.9% of the total variance and component 2 explained 35.12%.

The correct discard of the 26 redundant descriptors and selection of the 15 minimum descriptors were validated by the hierarchical cluster analysis of Ward. When comparing the pairs of dendrograms generated by this analysis, for each group of descriptors, before and after the discard of the descriptors, the maintenance of the groups formed for two of the three groups of descriptors is verified. Only, except for the descriptors of "Plant and Leaf", where there was a subtle difference in the grouping, since genotypes 1, 5 and 8 that were initially in the third group, after the discarding were reallocated in the first group (Figures 1, 2 and 3). That is, this result indicates that the discard of variables through the use of PCA was effective, since the grouping continued the same, not harming the classification of the genotypes within the groups.

Similar results were found by Campos *et al*. (2015), in the study to obtain the minimum efficient descriptors for mango (*Mangifera indica* L.), also used the Ward's method to verify the groupings before and after the discard of variables. And from the comparison between the groupings, they concluded that the use of only 34 fruit characteristics was sufficient to distinguish the genotypes evaluated in this study, optimized the 64 descriptors recommended for the characterization of this fruit tree.

The analysis of the relative contribution of the morphoagronomic descriptors, estimated by Singh's methodology (1981), used to evaluate the importance of the 41 descriptors, determined the characteristics that contributed the most to the genetic divergence between the genotypes in each group of descriptors (Tables 6, 7 and 8).

The correct discard of the 26 redundant descriptors and selection of the 15 minimum descriptors were revalidated by the relative contribution analysis of the descriptors estimated according to Singh (1981). The redundant descriptors in the PCA presented little relative contribution for all groups of descriptors.

For the set of descriptors "Plant and Leaf" the characteristics that presented the greatest relative contributions were: maximum leaf width 76.1% and leaf blade length 17.2%. For the group of descriptors "Floral" the characteristics that presented the greatest relative contributions were: pedicel length 42.1%, corona tip diameter 32.6% and petal length 11.8%. For the group of descriptors "Fruit" the characteristic that presented the greatest relative contribution was: number of seeds per fruit 89.2%.

Similar results were found by Fonseca *et al*. (2017), in his work to validate the morphoagronomic

descriptors used in the protection processes of plant cultivars in Brazil, characterizing six ornamental passion fruit cultivars, in which they identified maximum leaf width (approximately 34%) and petal length (26,17%) as the descriptors that contributed the most to the differentiation of the analyzed cultivars. Lawinscky *et al*. (2014), in the work of morphological characterization and genetic diversity in *Passiflora alata* Curtis and *P. cincinnata* Mast, for the 16 morphological descriptors measured, the corona diameter with 43.46%, the petal width with 9.81% and pedicel length with 7.49% were the main contributors to the divergence between the two species.

The results of Sousa *et al*. (2012) and Araújo *et al*. (2008), related to the relative contribution of the number of seeds per fruit were of 2.52% and 1.65% respectively. It differs from the results obtained here, since in the present work the number of seeds per fruit was the descriptor that contributed the most to the genetic divergence among the studied genotypes.

From the results obtained, we can infer that of the 41 descriptors, only 15 were relevant for the evaluation of the genetic diversity among the individuals of the population. These descriptors were: titratable acidity, bract length, leaf blade length, petal length, sepal length, pedicel length, corona filament ring length, corona tip diameter, fruit longitudinal diameter, sepal width, maximum leaf width, number of fruits, number of seeds per fruit, bark weight and fruit mass.

The genotypes sampled in Vitória da Conquista and Belo Campo represent a small genetic variability of the species. Thus, discarded descriptors for this group of genotypes may not be discarded for other groups.

However, this reduced list of morphoagronomic descriptors should represent an important working tool for research focused on the genetic and phenotypic variability of "Maracujá-do-Mato" populations, *in situ* or not, since the discarding of redundant variables allows saving time and material resources without loss information.

Table 1 - Quantitative morphoagronomic descriptors evaluated in passion fruit trees (Passiflora cincinnata Mast) grouped between plant parts.

PLANT AND LEAF DESCRIPTORS			
LBL	Leaf blade length	**NFR**	Number of fruits
MLW	Maximum leaf width	**NPN**	Number of petiole nectaries
NFN	Number of foliar nectaries	**PEL**	Petiole length
FLORAL DESCRIPTORS			
ANGL	Androgynophore length	**NFPN**	Number of flowers per node
ANTL	Anther length	**NRCF**	Number of colored rings on corona filaments
ANTW	Anther width	**NSN**	Number of sepal nectaries
BRL	Bract length	**OVD**	Ovary diameter
CCED	Corona cavity external diameter	**OVL**	Ovary length
CCID	Corona cavity internal diameter	**PEDL**	Pedicel length
CTD	Corona tip diameter	**PETL**	Petal length
LCFR	Length of corona filament rings	**SEL**	Sepal length
NBN	Number of bract nectaries	**SEW**	Sepal width
FRUIT DESCRIPTORS			
BT	Bark thickness	**RLT**	Relation between longitudinal and transverse fruit diameter
BW	Bark weight	**SLD**	Seed longitudinal diameter
FM	Fruit mass	**SS**	Soluble solids
FLD	Fruit longitudinal diameter	**SS/TA**	Ratio
FTD	Fruit transverse diameter	**ST**	Seed thickness
NSF	Number of seeds per fruit	**STD**	Seed transverse diameter
pH	Hydrogenionic potential	**SW**	Seed weight
PPR	Pulp production	**TA**	Titratable acidity
PW	Pulp weight		

Table 2 - Coefficients of the six Principal Components (eigenvectors) of the "Plant and Leaf" morphoagronomic descriptors.

Descriptors	Coefficients					
	PC1	PC2	PC3	PC4	PC5	PC6
LBL	0.567	0.053	-0.105	0.056	0.249	0.774
MLW	0.549	0.072	-0.129	0.019	0.556	-0.606
NFN	-0.209	0.607	-0.427	-0.623	0.117	0.061
NFR	-0.174	0.696	0.108	0.682	0.097	0.013
NPN	0.241	0.310	0.835	-0.373	-0.098	-0.025
PEL	0.495	0.209	-0.284	0.071	-0.772	-0.172

LBL: leaf blade length; MLW: maximum leaf width; NFN: number of foliar nectaries; NFR: number of fruits; NPN: number of petiole nectaries; PEL: petiole length; PC: principal components.

Tabela 3 - Coefficients of the fifteen Principal Components (eigenvectors) of the "Floral" morphoagronomic descriptors.

Descriptors	Coefficients							
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
ANGL	-0.030	0.449	0.189	0.267	-0.217	0.043	-0.014	0.632
ANTL	-0.307	0.057	0.193	-0.079	-0.492	-0.252	0.444	-0.183
ANTW	-0.105	0.315	0.332	-0.448	-0.003	0.146	-0.401	-0.137
BRL	-0.213	-0.216	0.345	-0.356	-0.120	-0.211	-0.076	0.193
CCED	-0.032	0.000	0.482	0.336	-0.075	0.319	0.183	-0.506
CCID	-0.091	-0.125	0.393	0.552	0.149	-0.149	-0.234	0.210
CTD	-0.427	-0.092	-0.055	-0.114	0.010	-0.076	-0.044	0.066
LCFR	0.037	0.449	-0.284	0.068	0.136	-0.235	0.380	-0.028
NBN	0.250	-0.358	-0.065	-0.025	-0.394	-0.394	-0.132	0.087
OVD	-0.287	-0.143	-0.345	0.160	-0.069	0.256	-0.375	-0.064
OVL	-0.339	-0.185	-0.147	0.326	0.027	-0.315	-0.031	-0.177
PEDL	0.016	-0.458	0.022	-0.080	-0.009	0.501	0.449	0.361
PETL	-0.421	0.064	0.012	-0.064	0.191	-0.045	0.128	0.178
SEL	-0.406	-0.024	-0.044	-0.078	0.345	0.042	0.095	0.022
SEW	-0.235	0.164	-0.282	0.103	-0.578	0.331	-0.125	0.000

Descriptors	Coefficients						
	PC9	PC10	PC11	PC12	PC13	PC14	PC15
ANGL	-0.099	0.309	-0.106	0.333	-0.014	-0.050	0.107
ANTL	0.209	0.086	0.109	-0.022	0.322	-0.326	-0.223
ANTW	0.019	-0.163	0.160	0.326	0.138	0.266	-0.360
BRL	-0.569	0.043	-0.244	-0.378	0.024	0.100	0.146
CCED	-0.197	0.233	0.039	0.050	-0.348	0.171	0.094
CCID	0.108	-0.308	0.328	-0.305	0.182	0.037	-0.178
CTD	-0.119	-0.256	0.501	0.286	-0.401	-0.300	0.344
LCFR	-0.466	-0.092	0.324	-0.140	-0.040	0.289	-0.239
NBN	0.133	0.298	0.294	0.133	-0.261	0.420	-0.122
OVD	-0.309	0.423	0.118	-0.087	0.068	-0.260	-0.412
OVL	-0.169	-0.214	-0.424	0.501	0.171	0.236	-0.037
PEDL	-0.117	-0.182	0.102	0.208	0.117	0.156	-0.249
PETL	0.346	0.036	-0.293	-0.186	-0.565	0.107	-0.395
SEL	0.231	0.444	0.221	-0.047	0.353	0.390	0.344
SEW	0.112	-0.317	-0.039	-0.294	0.001	0.345	0.223

ANGL: androgynophore length; ANTL: anther length; ANTW: anther width; BRL: bract length; CCED: corona cavity external diameter; CCID: corona cavity internal diameter; CTD: corona tip diameter; LCFR: length of corona filament rings; NBN: number of bract nectaries; NFPN: number of flowers per node; NRCF: number of colored rings on corona filaments; NSN: number of sepal nectaries; OVD: ovary diameter; OVL: ovary length; PEDL: pedicel length; PETL: petal length; SEL: sepal length; SEW: sepal width; PC: principal components.

Tabela 4 - Coefficients of the seventeen Principal Components (eigenvectors) of the "Fruit" morphoagronomic descriptors.

Descriptors	Coefficients								
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
BT	0.169	-0.367	-0.387	-0.085	0.029	0.084	-0.072	-0.054	0.120
BW	0.347	-0.094	-0.138	-0.095	-0.154	0.263	-0.123	0.084	-0.357
FLD	0.351	-0.017	-0.033	-0.271	0.121	-0.143	-0.281	0.068	0.129
FM	0.375	0.106	-0.023	0.046	-0.107	0.102	-0.135	0.088	-0.310
FTD	0.333	0.137	-0.104	0.089	-0.304	0.174	-0.175	-0.196	0.113
NSF	0.234	0.331	-0.094	-0.262	-0.183	-0.162	0.406	-0.175	0.361
pH	-0.224	-0.022	0.288	-0.299	-0.272	-0.312	-0.100	-0.308	-0.313
PPR	-0.027	0.427	0.273	0.324	0.216	-0.153	-0.249	0.190	0.112
PW	0.286	0.325	0.152	0.228	-0.009	-0.075	-0.203	0.089	-0.203
RLT	0.179	-0.137	0.047	-0.443	0.428	-0.361	-0.232	0.268	0.112
SLD	0.220	-0.293	0.161	0.171	0.132	-0.391	0.125	-0.393	-0.394
SS	-0.153	0.116	-0.552	0.163	0.104	-0.224	-0.032	0.103	-0.173
SS/TA	-0.141	-0.040	-0.400	0.207	-0.333	-0.485	-0.091	0.251	-0.063
ST	0.206	-0.287	0.168	0.263	0.169	0.038	0.526	0.407	-0.083
STD	0.146	-0.352	0.087	0.464	-0.027	-0.135	-0.262	-0.300	0.465
SW	0.321	0.209	-0.054	0.026	-0.068	-0.326	0.383	-0.051	0.068
TA	-0.014	0.241	-0.312	0.074	0.588	0.123	0.059	-0.460	-0.145

Descriptors	Coefficients							
	PC10	PC11	PC12	PC13	PC14	PC15	PC16	PC17
FLD	-0.076	-0.190	-0.044	0.059	0.012	-0.156	-0.771	-0.002
SLD	-0.368	0.156	0.289	0.265	-0.007	-0.045	-0.002	0.000
FTD	-0.071	-0.251	0.015	0.184	0.237	-0.622	0.319	0.000
STD	0.161	-0.036	-0.367	0.004	-0.131	0.239	0.039	0.000
BT	0.460	0.340	0.533	-0.164	0.088	-0.059	0.004	0.000
ST	0.349	-0.287	-0.091	0.176	0.169	-0.148	-0.063	0.000
FM	0.088	0.039	-0.082	-0.046	-0.079	0.227	0.060	-0.789
NSF	0.118	0.021	0.092	0.454	0.046	0.375	0.031	0.000
BW	0.060	-0.136	-0.069	0.134	-0.501	0.217	0.108	0.496
SW	-0.010	0.133	-0.144	-0.609	-0.325	-0.253	0.027	0.070
pH	0.592	-0.134	-0.134	0.003	0.008	-0.129	-0.028	0.000
PW	0.112	0.250	-0.058	-0.169	0.587	0.250	-0.029	0.356
PPR	0.243	0.008	0.420	0.193	-0.404	-0.141	0.029	0.000
RLT	-0.034	-0.051	-0.132	0.018	0.070	0.006	0.523	0.001
SS	0.121	0.378	-0.419	0.373	-0.049	-0.226	-0.064	0.000
SS/TA	-0.093	-0.478	0.238	-0.117	0.085	0.196	0.029	0.000
TA	0.150	-0.430	0.001	-0.138	0.060	0.106	0.019	0.000

BT: bark thickness; BW: bark weight; FM: fruit mass; FLD: fruit longitudinal diameter; FTD: fruit transverse diameter; NSF: number of seeds per fruit; pH: hydrogenionic potential; PPR: pulp production; PW: pulp weight; RLT: relation between longitudinal and transverse fruit diameter; SLD: seed longitudinal diameter; SS: soluble solids; SS/TA: ratio; ST: seed thickness; STD: seed transverse diameter; SW: seed weight; TA: titratable acidity; PC: principal components.

Table 5 - Estimates of the variances (eigenvalue) and accumulated variance (%) of the minimum morphoagronomic descriptors of the "Plant and Leaf", "Floral" and "Fruit" groups obtained for passion fruit of the bush (*Passiflora cincinnata* Mast).

Plant and Leaf						
Components	Before Discard			After the Discard		
	Standard Deviation	Variance	Accumulated Proportion	Standard Deviation	Variance	Accumulated Proportion
PC1	1.705	0.484	0.484	1.422	0.674	0.674
PC2	1.120	0.209	0.693	0.955	0.304	0.978
PC3	0.944	0.149	0.842	0.256	0.022	1.000
Floral						
Components	Before Discard			After the Discard		
	Standard Deviation	Variance	Accumulated Proportion	Standard Deviation	Variance	Accumulated Proportion
PC1	2.213	0.327	0.327	1.751	0.511	0.511
PC2	1.659	0.184	0.510	1.327	0.294	0.805
PC3	1.589	0.168	0.679	0.795	0.105	0.910
Fruit						
Components	Before Discard			After the Discard		
	Standard Deviation	Variance	Accumulated Proportion	Standard Deviation	Variance	Accumulated Proportion
PC1	2.527	0.376	0.376	1.745	0.609	0.609
PC2	1.654	0.161	0.536	1.027	0.211	0.820
PC3	1.460	0.125	0.662	0.764	0.117	0.936

PC: principal components.

Table 6 - Relative contribution of the descriptors "Plant and Leaf", evaluated in passion fruit trees (*Passiflora cincinnata* Mast), by the method proposed by Singh (1981).

Descriptors	Plant and Leaf		
	S.j	Proportion	Accumulated Proportion
MLW	189942900.000	0.761	76.1%
LBL	42857320.000	0.172	93.3%
PEL	16051370.000	0.064	99.7%
NFR	513406.900	0.002	99.9%
NFN	172507.200	0.001	100%
NPN	3420.479	0.000	100%

LBL: leaf blade length; MLW: maximum leaf width; NFN: number of foliar nectaries; NFR: number of fruits; NPN: number of petiole nectaries; PEL: petiole length; S.j: Singh's analysis.

Table 7 - Relative contribution of the descriptors "Floral", evaluated in passion fruit trees (*Passiflora cincinnata* Mast), by the method proposed by Singh (1981).

Descriptors	Floral		
	S.j	Proportion	Accumulated Proportion
PEDL	1039896.000	0.422	42.2%
CTD	801724.400	0.326	74.8%
PETL	290660.500	0.118	86.6%
SEL	149597.600	0.061	92.7%
LCFR	73179.780	0.030	95.6%
BRL	57749.280	0.023	98.0%
ANTL	14667.280	0.006	98.6%
SEW	11995.110	0.005	99.1%
ANGL	8605.322	0.003	99.4%
OVL	6488.218	0.003	99.7%
OVD	2819.501	0.001	99.8%
ANTW	2714.684	0.001	99.9%
CCED	1161.347	0.000	100%
NBN	800.209	0.000	100%
CCID	365.866	0.000	100%

ANGL: androgynophore length; ANTL: anther length; ANTW: anther width; BRL: bract length; CCED: corona cavity external diameter; CCID: corona cavity internal diameter; CTD: corona tip diameter; LCFR: length of corona filament rings; NBN: number of bract nectaries; NFPN: number of flowers per node; NRCF: number of colored rings on corona filaments; NSN: number of sepal nectaries; OVD: ovary diameter; OVL: ovary length; PEDL: pedicel length; PETL: petal length; SEL: sepal length; SEW: sepal width; S.j: Singh's analysis.

Table 8 - Relative contribution of the descriptors "Fruit", evaluated in passion fruit trees (*Passiflora cincinnata* Mast), by the method proposed by Singh (1981).

Descriptors	Fruit		
	S.j	Proportion	Accumulated Proportion
NSF	1779174000.000	0.892	89.2%
FM	129498500.000	0.065	95.7%
BW	33522820.000	0.017	97.4%
PW	20647430.000	0.010	98.5%
FLD	15375360.000	0.008	99.2%
FTD	7748771.000	0.004	99.6%
TA	6088972.000	0.003	99.9%
SW	1484393.000	0.001	100%
SS	153372.900	0.000	100%
BT	22186.300	0.000	100%
SLD	4256.817	0.000	100%
STD	3515.067	0.000	100%
pH	1132.761	0.000	100%
ST	1054.558	0.000	100%
RLT	472.513	0.000	100%
PPR	157.854	0.000	100%
SS/TA	33.164	0.000	100%

BT: bark thickness; BW: bark weight; FM: fruit mass; FLD: fruit longitudinal diameter; FTD: fruit transverse diameter; NSF: number of seeds per fruit; pH: hydrogenionic potential; PPR: pulp production; PW: pulp weight; RLT: relation between longitudinal and transverse fruit diameter; SLD: seed longitudinal diameter; SS: soluble solids; SS/TA: ratio; ST: seed thickness; STD: seed transverse diameter; SW: seed weight; TA: titratable acidity; S.j: Singh's analysis.

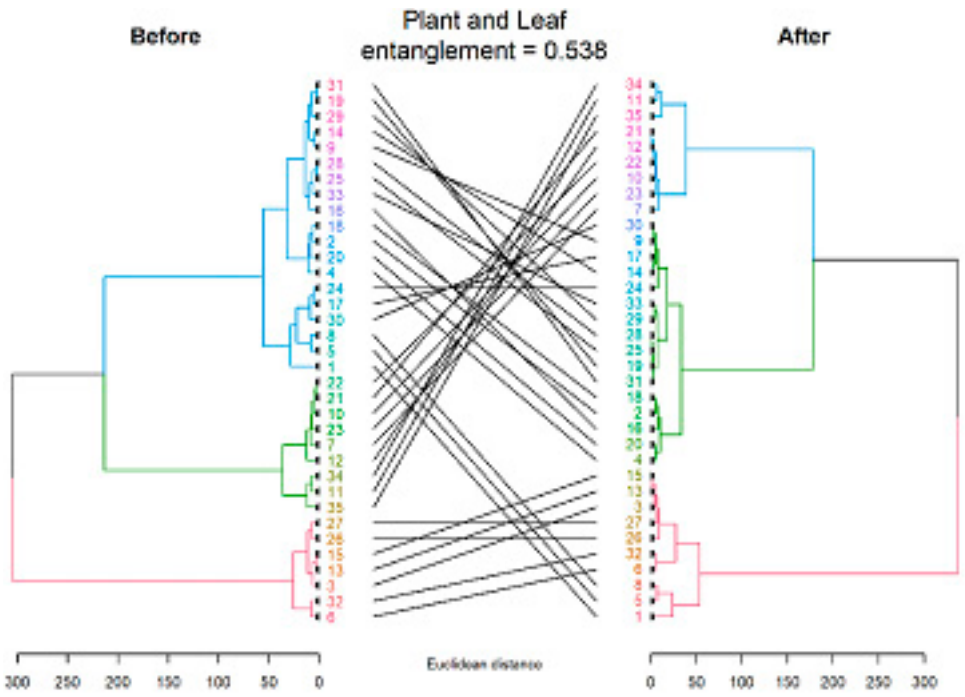

Figure 1 - Dendrogram of the dissimilarity pattern obtained by Ward's method, based on Euclidian distance for *Passiflora cincinnata*, Mast using descriptors for "Plant and Leaf" before and after of variables.

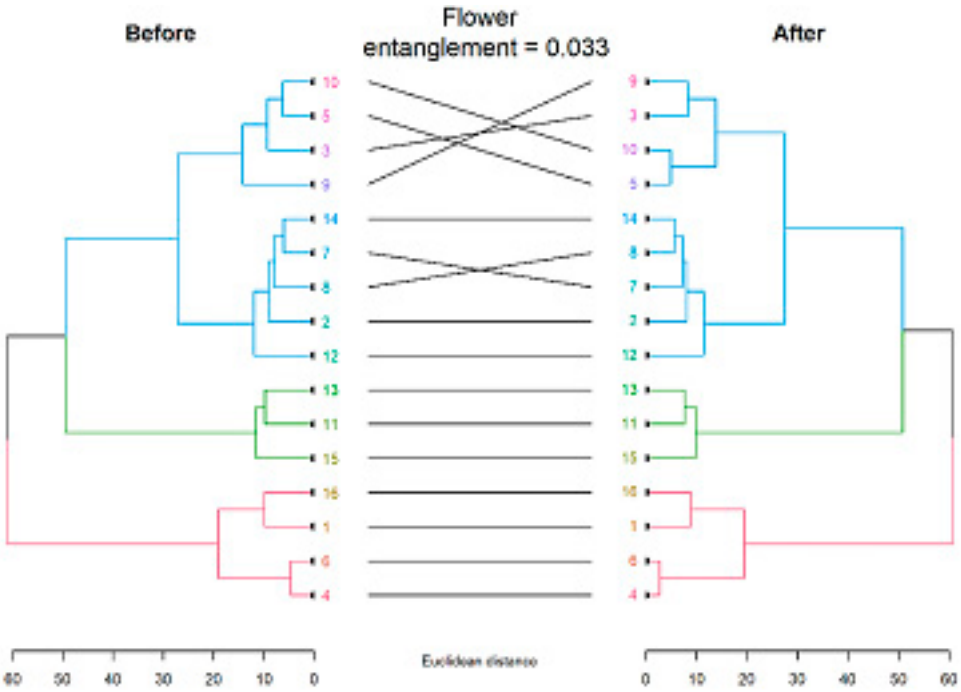

Figure 2 - Dendrogram of the dissimilarity pattern obtained by Ward's method, based on Euclidian distance for *Passiflora cincinnata,* Mast using descriptors for "Floral" before and after of variables.

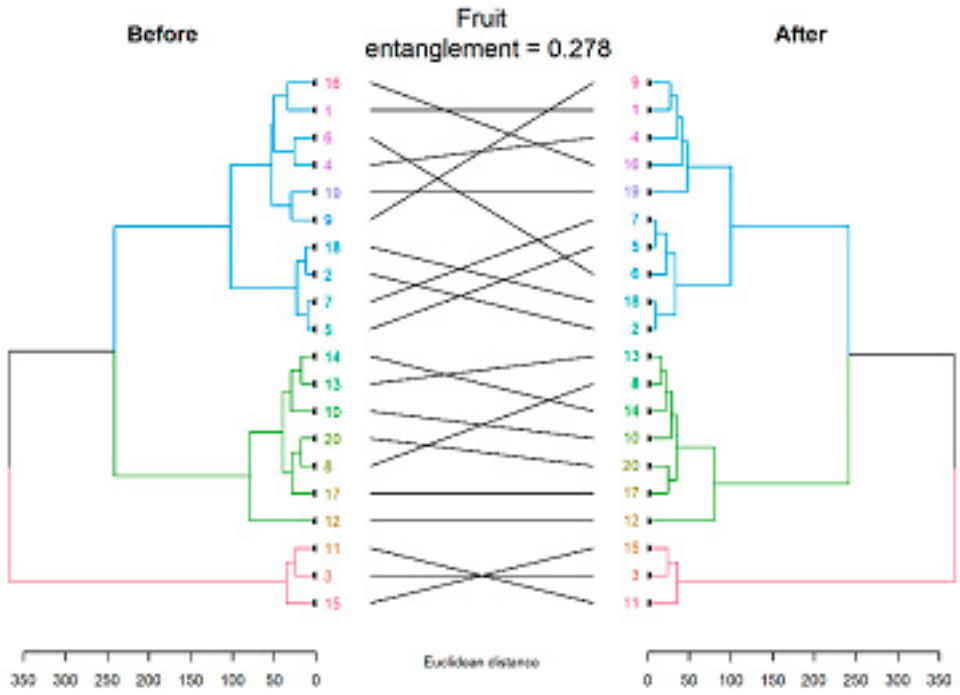

Figure 3 - Dendrogram of the dissimilarity pattern obtained by Ward's method, based on Euclidian distance for *Passiflora cincinnata,* Mast using descriptors for "Fruit" before and after of variables.

Conclusions

Based on the results obtained, it was possible to identify and discard redundant variables of morphoagronomic descriptors through the analysis of main components and validated by Ward's (1963) and Singh's (1981) methods, without prejudice to diversity estimation and genotyping, to propose a reduced list of morphoagronomic descriptors. These descriptors were: titratable acidity, bract length, leaf blade length, petal length, sepal length, pedicel length, corona filament ring length, corona tip diameter, fruit longitudinal diameter, sepal width, maximum leaf width, number of fruits, number of seeds per fruit, bark weight and fruit mass. The genotypes sampled in Vitória da Conquista and Belo Campo represent a small genetic variability of the species. Thus, discarded descriptors for this group of genotypes may not be discarded for other groups.

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