

Genetic divergence between *bocaiuva acrocomia aculeata (jacq.) lodd. ex mart.* genotypes through fruit morphometry

This research aimed to analyze the genetic divergence between genotypes of *Acrocomia aculeata* (Jacq.) Lodd. Ex Mart collected in natural vegetation in the municipality of Cáceres-Mato Grosso based on morphological characters of fruits and seeds. Bocaiuva fruits were collected at three points of natural occurrence: point 1 - Sítio Peniel dos Sonhos - Barreiro Vermelho Community (15°53'53"S, 57°30'49"W), point 2 - Chácara Boa Esperança (16°05'57"S, 57°39'03"W) point 3 - Santana Community-Morraria Region (15°55'36"S, 57°26'50"W). To estimate the genetic divergence between the bocaiuva genotypes through the morphometry of the fruits and seeds, 420 fruits of 21 genotypes were collected and the following characteristics were evaluated: Horizontal diameter of the fruit, Vertical diameter of the fruit, Total weight of the fruit, Total weight of fresh mesocarp (pulp), Horizontal diameter of almonds, Vertical diameter of almonds and Weight of fresh almond. To estimate the genetic divergence between the genotypes, the standardized Average Euclidean Distance was used as a measure of dissimilarity. Based on this matrix, the Tcher optimization clustering methods and the Hierarchical Clustering Average Between Groups (UPGMA) method were used. The criterion of Singh (1981) was also used to quantify the relative contribution of traits in the estimation of genetic divergence. All analyses were performed using the computational resources of the Genes software. Through the results obtained, it was possible to verify the greatest dissimilarity between genotypes 3 and 8. The groupings by the Tcher method and the Hierarchical Average Grouping Between Groups (UPGMA) were partially similar in the groupings of genotypes and the characteristics of total fruit weight, followed by characteristic total weight of fresh pasta were the ones that most contributed to estimate the genetic divergence of the evaluated genotypes. The use of multivariate analyzes was efficient in estimating the genetic divergence in which the genotypes evaluated in the present research present genetic divergence and can be used in future pre-genetic improvement research.

Keywords: Genetic variation; Multivariate analysis; Macaúba.

Divergência genética entre *bocaiuva acrocomia aculeata (jacq.) lodd. ex-mart.* genótipos através da morfometria de frutas

Esta pesquisa teve como o objetivo analisar a divergência genética entre genótipos de *Acrocomia aculeata* (Jacq.) Lodd. Ex Mart coletados em vegetação natural no município de Cáceres-Mato Grosso com base em caracteres morfológicos dos frutos e sementes. Os frutos de *Acrocomia aculeata*, foram coletados em três pontos de ocorrência natural, sendo: ponto 1 - Sítio Peniel dos Sonhos - Comunidade Barreiro Vermelho (15°53'53"S, 57°30'49"W), ponto 2 - Chácara Boa Esperança (16°05'57"S, 57°39'03"W) ponto 3 - Santana Community-Morraria Region (15°55'36"S, 57°26'50"W). Para realizar a estimativa da divergência genética entre os genótipos de bocaiuva por meio da morfometria dos frutos e sementes, foram coletados 420 frutos de 21 genótipos sendo avaliados as seguintes características: Diâmetro horizontal do fruto, Diâmetro vertical fruto, Peso total do fruto, Peso total da massa fresca mesocarpo (pulpa), Diâmetro horizontal das amêndoas, Diâmetro vertical amêndoas e Peso da amêndoa fresca. Para estimar a divergência genética entre os genótipos foi utilizado a Distância Euclidiana Média padronizada como medida de dissimilaridade. Com base nesta matriz, foram empregados os métodos de agrupamentos de otimização de Tcher e método Hierárquico de Agrupamento Médio Entre Grupos (UPGMA). Utilizou-se, também, o critério de Singh (1981) para quantificar a contribuição relativa das características na estimativa da divergência genética. Todas as análises foram realizadas utilizando os recursos computacionais do software Genes. Por meio dos resultados obtidos foi possível verificar a maior dissimilaridade entre os genótipos 3 e 8. Os agrupamentos pelo método de Tcher e Hierárquico de Agrupamento Médio Entre Grupos (UPGMA) foram parcialmente similares nos agrupamentos dos genótipos e as características peso total do fruto, seguido da característica peso total da massa Fresca foram as que mais contribuíram para estimar a divergências genética dos genótipos avaliados. O emprego das análises multivariadas foi eficiente na estimativa da divergência genética em que os genótipos avaliados na presente pesquisa apresentam divergência genéticas e podem ser utilizados em futuras pesquisas de pré-melhoramento genético.

Palavras-chave: Macaúba; Análise multivariada; Variação genética.

Topic: Genética Vegetal

Received: 04/09/2023

Approved: 09/09/2023

Reviewed anonymously in the process of blind peer.

Valvenarg Pereira da Silva 

Universidade do Estado de Mato Grosso, Brasil
<http://lattes.cnpq.br/4699841326689779>
<https://orcid.org/0000-0001-8450-3016>
silvabiologo@hotmail.com

Deise Parabás de Oliveira 

Universidade do Estado de Mato Grosso, Brasil
<http://lattes.cnpq.br/1385342709931892>
<https://orcid.org/0000-0002-7067-3070>
deise6457@gmail.com

Andressa Juliana da Silva 

Instituto Federal Mato Grosso, Brasil
<http://lattes.cnpq.br/3211540140112041>
<https://orcid.org/0000-0001-6233-3706>
andressajuly@hotmail.com

Joari Costa de Arruda 

Universidade do Estado de Mato Grosso, Brasil
<http://lattes.cnpq.br/7417323137885131>
<https://orcid.org/0000-0001-8813-983X>
arrudajcbio@gmail.com

Marco Antonio Aparecido Barelli 

Universidade do Estado de Mato Grosso, Brasil
<http://lattes.cnpq.br/3692696368567512>
<https://orcid.org/0000-0002-6385-6733>
mbarelli@unemat.br

Flávio Valadares Pereira Borges 

Universidade do Estado de Mato Grosso, Brasil
<http://lattes.cnpq.br/0941748574705928>
<https://orcid.org/0000-0002-2205-0688>
flavinhovb@hotmail.com

Rafael Felipin Azevedo 

Universidade do Estado de Mato Grosso, Brasil
<http://lattes.cnpq.br/4478780017449638>
<https://orcid.org/0000-0002-4490-0823>
rafaelfelipin@gmail.com

Laura Letícia Monteiro Catelan 

Universidade do Estado de Mato Grosso, Brasil
<http://lattes.cnpq.br/5689742119308733>
<https://orcid.org/0009-0009-8867-7457>
proflauracatelan@outlook.com

Nilo Leal Sander 

Universidade do Estado de Mato Grosso, Brasil
<http://lattes.cnpq.br/6241511798904038>
<https://orcid.org/0000-0001-9856-6819>
nilosander@gmail.com



DOI: 10.6008/CBPC2318-2881.2022.004.0002

Referencing this:

SILVA, V. P.; OLIVEIRA, D. P.; SILVA, A. J.; ARRUDA, J. C.; BARELLI, M. A. A.; BORGES, F. V. P.; AZEVEDO, R. F. F.; CATELAN, L. L. M.; SANDER, N. L.. Genetic divergence between bocaiuva acrocomia aculeata (jacq.) lodd. ex mart. genotypes through fruit morphometry. *Nature and Conservation*, v.15, n.4, p.14-21, 2022. DOI: <http://doi.org/10.6008/CBPC2318-2881.2022.004.0002>

INTRODUCTION

The Cerrado Biome has several fruit species, among them the *Acrocomia aculeata* (Jacq) species. Lodd and ex Mart., a very heat resistant palm that has enormous economic and cultural potential and is popularly known as bocaiuva or macaúba (MOOZ et al., 2012). In Brazil, this palm tree is found in several Brazilian states such as Mato Grosso, Mato Grosso do Sul, Pará, Goiás, Distrito Federal, São Paulo, Minas Gerais and Paraná (LORENZI, 2006).

This thorny palm with an average height of 10 to 15 meters, native to Tropical America and distributed in tropical and subtropical regions from Mexico to Argentina, is the most dispersed palm tree in Brazil with occurrence of natural stands in almost the entire National Territory (CARDOSO et al., 2020). Its fruits are usually spherical or slightly flattened, with a color ranging from yellow to orange and a diameter ranging from 2.5 to 5.0 cm (LORENZI, 2006).

It has a fibrous mesocarp with a slightly sweet flavor and an endocarp strongly adhered to the pulp. Usually its fruits have a seed (almond) that is surrounded by a hard and dark endocarp with approximately 3 mm of thickness, its fruiting occurs mainly between the months of September and January (LORENZI et al., 2006).

It has a wide geographic distribution throughout the Brazilian territory, its fruits have a peculiar taste with a fibrous mesocarp with a slightly sweet flavor, an endocarp strongly adhered to the pulp and a seed (almond) that produces an oil of great quality, equivalent to olive oil and that contribute to the economy for many communities (LORENZI et al., 2006).

Kopper (2009) considers that the pulp and almonds of bocaiuva are consumed in natura by the local population and/or in regional cuisine preparations, such as ice cream, cakes, paçoca, sweet and cocada, helping to enrich the diet as complementary source of essential nutrients. The stem of this palm tree is still used for rural constructions, its heart of palm is edible with a sweet flavor, and its leaves are used for making hammocks and covering the house.

Bocaiuva is also important from an ecological point of view, as it serves as a food resource for different species of fauna and colonizes degraded areas (NEGRELLE, 2013). In this way, knowledge about the genetic diversity of this species and its potential for use makes it possible to infer about its importance and commercial advantages as well as conservationist attitudes (SILVA et al., 2001).

Due to the great variety of uses and its ecological and cultural importance, it is extremely important to know to preserve the genetic diversity present in the bocaiuvas genotypes. There are numerous tools to assess genetic divergence between plants, with emphasis on the use of multivariate analyzes (CRUZ et al., 2003). The use of these to estimate genetic divergence has become common and used by several researchers for different plant species (LOURENÇO et al., 2013).

Due to the scarcity of research related to the characterization and genetic divergence of bocaiuva fruits in the State of Mato Grosso-Brazil, this research aimed to analyze the genetic divergence between

bocaiuva genotypes collected in natural vegetation in the municipality of Cáceres, state of Mato Grosso with based on morphological characters of fruits and seeds.

METHODOLOGY

Study area – The fruits of *A. aculeata* were collected at three points of natural occurrence, as follows: point 1 - Sítio Peniel dos Sonhos - Barreiro Vermelho Community ($15^{\circ}53'53"S, 57^{\circ}30'49"W$), point 2 - Chácara Boa Esperança ($16^{\circ}05'57"S, 57^{\circ}39'03"W$) point 3 - Santana Community, Morraria Region ($15^{\circ}55'36"S, 57^{\circ}26'50"W$).

Data collection and samples – To estimate the genetic divergence between the bocaiuva genotypes through fruit and seed morphometry, 420 fruits of 21 genotypes (20 fruits of each genotype) were collected between November and December 2021 (Table 1). For each collection, the minimum distance of 150 meters between each genotype was respected, this condition is necessary to reduce the possibility of specimens coming from common parents, which would reduce genetic variability.

Tabela 1: Order, Collection Point of the Bocaiuva Genotypes collected in three Points in the region of Cáceres, Mato Grosso.

Genotype	Collect point
Genotype 1	Point: 1 Sítio Peniel dos Sonhos
Genotype 2	Point: 1 Sítio Peniel dos Sonhos
Genotype 3	Point: 2 Chácara Boa Esperança
Genotype 4	Point: 2 Chácara Boa Esperança
Genotype 5	Point: 2 Chácara Boa Esperança
Genotype 6	Point: 2 Chácara Boa Esperança
Genotype 7	Point: 2 Chácara Boa Esperança
Genotype 8	Point: 3 Comunidade Santana
Genotype 9	Point: 3 Comunidade Santana
Genotype 10	Point: 3 Comunidade Santana
Genotype 11	Point: 3 Comunidade Santana
Genotype 12	Point: 3 Comunidade Santana
Genotype 13	Point: 3 Comunidade Santana
Genotype 14	Point: 3 Comunidade Santana
Genotype 15	Point: 3 Comunidade Santana
Genotype 16	Point: 3 Comunidade Santana
Genotype 17	Point: 3 Comunidade Santana
Genotype 18	Point: 3 Comunidade Santana
Genotype 19	Point: 3 Comunidade Santana
Genotype 20	Point: 3 Comunidade Santana
Genotype 21	Point: 3 Comunidade Santana

The fruits were collected using the following criteria: color of the pericarp that presented 50% of the fruits in the stage of maturation, that is, totally yellow fruits without whitish punctuations as recommended by Amaral et al. (2011).

After harvesting the fruits, they were separated and stored in polypropylene bags, identified and packed in cardboard boxes to avoid dehydration during transport. The collections remained under refrigeration in the Laboratory of Genetic Resources and Biotechnology located at the University of the State of Mato Grosso-UNEMAT, campus of Cáceres.

The measured characteristics of the fruits were: Horizontal diameter of the fruit (DHF) in mm, Vertical diameter of the fruit (DVF) in mm, Total weight of the fruit (PTF) in g, Total Weight of Fresh Mesocarp Mass (pulp) (PMF) in g, Horizontal diameter of kernels (DHA) in mm, Vertical diameter of kernels (DVA) in mm and Weight of fresh kernels (PAF) in g. All fruit and seed measurements were measured using a 0.01 mm precision digital caliper (Stainless Hardened model) and the weight was measured using a digital scale (Shimadzu Model AUY220), expressed in millimeters and kilograms, respectively.

Statistical analysis - To estimate the genetic divergence between the genotypes, multivariate analyzes were performed, using the standardized Average Euclidean Distance as a measure of dissimilarity. Based on this matrix, the Tocher optimization clustering methods and the Hierarchical Clustering Average Between Groups (UPGMA) method were used. The criterion of Singh (1981) was also used to quantify the relative contribution of traits in the estimation of genetic divergence. All analyzes were performed using the computational resources of the Genes software (CRUZ, 2013).

RESULTS

Based on the dissimilarity matrix estimated from the Average Euclidean Distance, it was found that genotypes 3 and 8 were the most dissimilar genotypes (Table 2). These dissimilarities between these genotypes may be related to the following factors: the fruits of genotype eight had the highest total fruit weight of 84.23g and the fresh almond weight of 28.53g, on the other hand, genotype three had the lowest values for total fruit weight 22.50g and fresh almond weight of 6.85g (Table 3). Another factor that may be linked to this dissimilarity is due to the geographic location, since genotype eight was collected in Comunidade Santana and genotype three was collected in Chácara Boa Esperança. Regarding similarity, genotypes six and seven were the most similar, this fact is due to the fact that both genotypes were collected in the same area, presenting fruits with similar values for the evaluated characteristics.

Regarding the genotypes with higher averages with possibilities of use in future genetic pre-improvement programs as well as subsequent technological use in the agroindustry, genotypes 16, 8, 15, 14, 20, 13, 9 and 12 stood out with average values above of 30 g for Total weight of fresh mesocarp (pulp) mass. Junqueira et al. (2019), points out that with technological advances and genetic improvement, macaúba may surpass traditional agro-energy crops such as sugarcane and palm oil. In this way, fruits with greater weight of fresh mass should be preferred. Nunes (2015) considers that the oil extracted from the mesocarp (pulp) has uses in the food industry, cosmetics, and the energy sector, offering great potential to produce biodiesel.

Table 2: Genetic dissimilarity measures, among 21 Bocaiuva Genotypes, in relation to seven fruit characters, Cáceres, Mato Grosso.

Genotypes	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	
1	0	0,64 73	1,00 75	0,55 34	0,43 07	0,58 42	0,61 23	1,60 97	0,75 76	0,80 88	0,95 68	0,74 21	1,38 42	1,3 3	0,87 98	1,54 3	0,43 09	0,42 05	0,55 05	1,23 89	0,64 54	
2		0 26	1,43 1,02 1	1,06 78	0,97 98	1,11 29	1,17 61	0,71 88	0,50 14	0,66 15	0,44 65	0,91 24	0,96 01	0,53 72	1,17 51	0,65 92	0,46 01	0,39 73	0,76 91	0,22 45		
3			0 52	0,47 88	0,61 64	0,44 53	0,47 65	2,51 17	1,71 92	1,74 5	1,90 66	1,57 54	2,29 27	2,24 89	1,75 04	2,45 61	0,83 45	1,37 65	1,48 88	2,13 43	1,47	
4				0 32	0,22 15	0,12 89	0,20 08	2,10 84	1,27 29	1,30 11	1,46 81	1,18 81	1,86 68	1,80 03	1,35 26	2,04 65	0,42 88	0,92 62	1,04 95	1,71 65	1,04	
5					0 28	0,18 22	0,19 79	1,98 66	1,11 08	1,19 24	1,34 53	1,07 61	1,76 72	1,67 52	1,23 15	1,92 21	0,43 9	0,79 92	0,92 96	1,62 06	0,97 35	
6						0 61	0,10 19	2,12 01	1,28 01	1,33 01	1,48 81	1,19 65	1,89 34	1,82 56	1,36 56	2,06 05	0,46 8	0,94 8	1,06 96	1,75 06	1,08 35	
7							0 5	2,14 26	1,28 35	1,34 31	1,50 01	1,23 6	1,91 12	1,83 26	1,39 72	2,08 75	0,50 65	0,96 94	1,08 1	1,78 12	1,11	

8					0	0,98 42	0,90 08	0,69 77	0,95 37	0,38 1	0,47 45	0,77 46	0,25 69	1,74 58	1,20 83	1,09 0,38	0,44 82	1,11 19
9					0	0,38 95	0,36 45	0,48 89	0,81 67	0,63 62	0,42 9	0,92 39	0,92 39	1,00 84	0,38 84	0,36 82	0,72 86	0,60 02
10					0	0,25 91	0,48 49	0,61 15	0,54 11	0,40 16	0,92 07	0,96 07	0,43 84	0,29 33	0,54 4	0,38 1		
11					0	0,47 17	0,48 62	0,36 01	0,32 21	0,68 81	1,13 71	0,55 44	0,43 29	0,39 62	0,39 76			
12					0	0,80 42	0,78 1	0,20 23	0,89 04	0,85 79	0,40 57	0,35 57	0,61 31	0,41 25				
13					0	0,30 61	0,62 53	0,53 85	1,49 95	0,99 25	0,85 53	0,27 36	0,84 55					
14					0	0,59 78	0,55 46	1,46 09	0,89 53	0,77 96	0,41 78	0,84 22						
15					0	0,72 72	1,01 69	0,49 43	0,40 09	0,44 09	0,47 87							
16					0	1,71 91	1,15 36	1,06 48	0,49 49	1,12 27								
17					0	0,64 04	0,72 84	1,36 36	0,65 91									
18										0,18 79	0,85 63	0,36 63						
19										0	0,71 85	0,29 84						
20										0	0,72 84							
21										0								

Table 3: Avearges values of the characteristics DHF= Horizontal diameter of the fruit, DVF= Vertical diameter of the fruit, TFP= Total weight of the fruit, PTMF= Total weight of the fresh mesocarp (pulp), DHA= Horizontal diameter of the kernels, DVA= Vertical diameter almonds and PAF= Weight of fresh almonds evaluated from 21 Genotypes of *A. aculeata* collected in the region of Cáceres, Mato Grosso.

Genotypes	Features evaluated						
	DHF (mm)	DVF (mm)	PTF (g)	PTMF (g)	DHA (mm)	DVA (mm)	PAF (g)
Genotype 1	41,85	46,83	40,31	19,63	26,35	28,55	12,32
Genotype 2	47,57	44,00	47,60	20,73	33,16	28,95	20,55
Genotype 3	35,91	35,94	22,50	10,80	22,10	21,00	6,85
Genotype 4	38,15	40,68	28,91	13,32	24,90	25,07	9,45
Genotype 5	38,58	45,05	32,76	16,74	24,47	25,22	9,45
Genotype 6	37,55	42,23	29,70	14,57	24,48	24,04	9,12
Genotype 7	36,65	44,20	28,57	14,15	24,14	23,76	9,43
Genotype 8	53,53	55,25	84,23	41,40	38,23	33,30	28,53
Genotype 9	46,25	57,44	60,25	30,12	30,59	30,51	17,06
Genotype 10	47,48	53,97	58,08	22,28	33,23	31,33	21,52
Genotype 11	48,44	54,83	68,85	28,46	32,88	31,78	22,16
Genotype 12	47,76	47,78	64,31	31,04	32,47	28,10	18,45
Genotype 13	52,37	55,06	71,66	30,47	37,63	32,84	28,71
Genotype 14	49,47	59,27	73,97	31,86	35,17	33,11	26,66
Genotype 15	49,01	50,79	66,65	31,97	33,79	29,15	19,73
Genotype 16	54,01	54,11	86,23	45,48	35,59	33,19	25,34
Genotype 17	39,39	42,38	38,03	15,22	29,57	25,99	14,77
Genotype 18	44,25	50,31	52,60	24,98	29,98	29,62	16,07
Genotype 19	46,19	51,01	57,47	22,29	31,09	29,67	17,80
Genotype 20	52,61	51,06	76,04	30,51	36,30	32,12	24,9
Genotype 21	44,76	47,01	52,65	21,46	33,34	29,36	21,39

Regarding the cluster analysis generated by the Tocher method, in which the 21 genotypes were separated into seven distinct groups (Table 4). Group I grouped genotypes 6, 7, 4 and 5 and group IV also grouped four genotypes 13,20,14 and 11 representing 19% of the evaluated genotypes each of these groups.

Group II brought together the largest number of genotypes, represented by genotypes 18,19, 21, 2,10,12 and 15. The largest number of genotypes in this group may be linked to the fact that the genotypes mentioned have median values for all traits evaluated.

Table 4: Clustering of 21 Bocaiuva Genotypes by Tocher's optimization method, based on the Average Euclidean Distance, estimated from seven quantitative characters of fruits and seeds.

Groups	Genotypes	% de Genotypes
I	6, 7, 4, 5	19,0
II	18, 19, 21, 2, 10, 12, 15	33,3
III	8 e 16	9,5
IV	13, 20, 14, 11	19,0

V	1 e 17	9.5
VI	9	4.8
VII	3	4.8
Total	21	100 %

Group III was formed by genotypes 8 and 16, both from Santana Community. Group V was also composed of two genotypes, genotypes 1 and 17, however, these genotypes were collected in different locations.

Groups VI and VII were formed by one genotype each, being from group VI, genotype 9, coming from Santana Community, and from group VII, genotype 3 Chácara Boa Esperança (Table 3). The results obtained by the Tocher method are indicative of which genotypes should be used in crosses in future breeding programs for this species. It is recommended to choose genotypes from different groups for these crosses, as considered by Bispo et al. (2014) who emphasize that discriminating the most dissimilar individuals is important for future breeding programs of the species and that the combination of individuals allocated in different groups can provide individuals with greater variability and better performance in segregating generations.

According to Figure 1, with the cut at 60%, it is noted that the UPGMA hierarchical clustering method, based on the dissimilarity matrix, presented the formation of three groups. The cophenetic correlation coefficient (CCC) presented a significant value with $r=0.78^{**}$, demonstrating good reliability in the relationship between the dissimilarity matrix and the dendrogram. Monteiro et al. (2010), reports that the closer to the value 1.0, the better the representation of the similarity matrix in the form of a dendrogram.

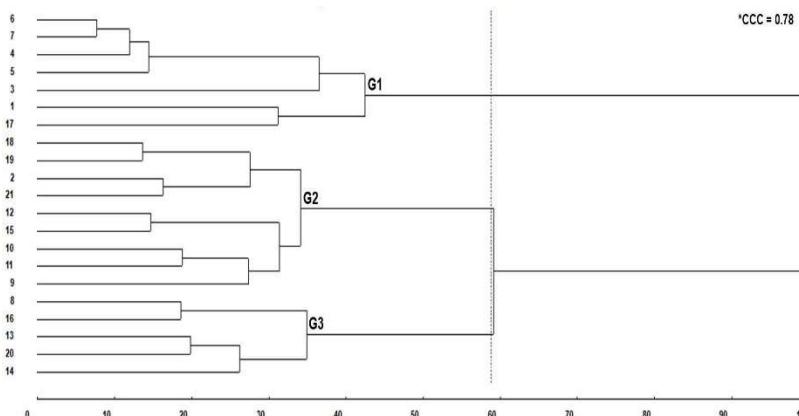


Figure 1: Dendrogram of cluster analysis of 21 Bocaiuva Genotypes, collected by the Average Linkage Grouping between Groups (UPGMA) method based on the standardized Average Euclidean Distance, estimated from 7 quantitative characters of bocaiuva fruit. *CCC = Cophenetic Correlation Coefficient 0.78.

When comparing the clustering methods, the Tocher method formed more clusters than the UPGMA method. However, the UPGMA method offered a more detailed presentation, enabling the visualization of distances within a given group. This is because the UPGMA uses arithmetic means, that is, unweighted means of dissimilarity, which avoids characterizing dissimilarity by extreme values (maximum and minimum) between genotypes (CRUZ et al., 2003).

To evaluate the contribution of each trait evaluated on the total variation available between the evaluated genotypes, the methodology of Singh (1981) was used, in which the traits Total Fruit Weight,

followed by the trait Total Fresh Mass Weight with 61.07 and 14.00%, respectively, contributed the most (Table 5). These characteristics are essential in breeding programs since they are directly linked to the productivity of bocaiuva. The characteristic that least contributed to estimate the genetic divergence was the horizontal diameter of the beans 2.03%, however this characteristic should not be discarded in further studies since it is closely linked with the productivity of bocaiuva.

Table 5: Relative contribution of seven fruit characters of 21 Bocaiuva Genotypes in estimating the genetic divergence collected in Cáceres, Mato Grosso. 1/DHF= Horizontal diameter of the fruit, DVF= Vertical diameter of the fruit, TFP= Total weight of the fruit, TMF= Total weight of the fresh mesocarp (pulp), DHA= Horizontal diameter of the kernels, DVA= Vertical diameter of the kernels and PAF= Weight of the fresh kernel.

Evaluated Features ^{1/}	Contribution (%)
DHF	5.4374
DVF	6.1416
PTF	61.0783
PTMF	14.0034
DHA	3.787
DVA	2.0324
PAF	7.5199

Correa et al. (2012) report that the relative contribution of each character to estimate genetic divergence is of great importance to identify the characters with the greatest contribution and also to help discard those that contribute little to the discrimination of genotypes.

CONCLUSIONS

According to the results obtained in the present research, it was possible to verify the existence of genetic diversity among the bocaiuva genotypes evaluated in the present research with greater genetic dissimilarity between genotypes 3 and 8. The use of multivariate analyzes were efficient and help breeders to identify genotypes with agronomic interest to be used.

REFERÊNCIAS

- AMARAL, F. P.; BROETTO, F.; BATISTELA, C. B.; JORGE, S. M. A.. Extração e caracterização qualitativa de óleos de polpa e amêndoas de frutos de macaúba [*Acrocomia aculeata* (Jacq) Lo dd. ex Mart] coletados na região de Botucatu. **Revista Energia na Agricultura**, São Paulo, v.26, p.12-20, 2011.
- BISPO, R. B.; DARDENGO, J. F. E.; BISPO, R. B.; BISPO, R. B.; ROSSI, A. A. B.. Divergência genética entre Genotypes de Mauritia Flexuosa L. f. por meio de morfometria de frutos e sementes. **Nativa**, v.8, n.4, p.585-590, 2020. DOI: <http://doi.org/10.31413/nativa.v8i4.8622>
- BISPO, R. B.; ROSSI, A. A. B.; BISPO, R. B.; BISPO, R. B.; DARDENGO, J. F. E.. Análise da divergência genética de tamarindeiros cultivados em quintais no município de Alta floresta, MT por meio de diferentes métodos de agrupamento. **Enciclopédia Biosfera**, Goiânia, v.10, n.19, p.1978-1987, 2014.
- CARDOSO, N. A.; SANTOS, S. G.; FAVARO, P. S.; DINIZ, B. C.; SOUZA, U. H.. Extrativismo da macaúba na região do Cariri Cearense: comercialização e oportunidades. **Braz. J. of Develop**, Curitiba, v.6, n.5, p.25261-25279, 2020.
- CORREA, A. M.; GONÇALVES, M. C.. Divergência genética em Genotypes de feijão comum cultivados em Mato Grosso do Sul. **Revista Ceres**, v. 59, n.2, p.206-212, 2012.
- CRUZ, C. D.; CARNEIRO, P. C. S.. Modelo Biométricos aplicados ao melhoramento genético. **EdUFV**, Viçosa, v.2, n.6, p.357-434, 2003.
- CRUZ, C. D.. GENES: a software package for analysis in experimental statistics and quantitative genetics. **Acta Scientiarum**, v.35, n.3, p.271-276, 2013.
- DOMICIANO, G. P.; ALVES, A. A.; LAVIOLA, B. G.; CONCEICAO, L. D. H. C. S.. Parâmetros genéticos e diversidade em progênies de Macaúba com base em características morfológicas e fisiológicas. **Ciência Rural Santa Maria**, v.45, n.9, p.1599-1605, 2015. DOI: <https://doi.org/10.1590/0103-8478cr20140909>
- JUNQUEIRA, N. T. V.; CONCEIÇÃO, L. D. H. C. S.; ANTONIASSI, R.; BRAGA, M. F; MALAQUIAS, J. V.. **Caracterização de**

populações naturais de macaúba e avaliação do potencial produtivo. Planaltina: Embrapa Cerrados, 2019.

KOPPER, A. C.. **Bebida simbiótica elaborada com farinha de Bocaiúva (Acrocomiaaculeata) e Lactobacillusacidophilus incorporados ao extrato hidrossolúvel de soja.** Dissertação (Especialização em Tecnologia de Alimentos) - Universidade Federal do Paraná, 2009.

LORENZI, G. M. A. C.. **Acrocomiaaculeata (Jacq.) Lodd. ex Mart. Arecaceae: bases para o extrativismo sustentável.** Dissertação (Mestrado em Agronomia) - Universidade Federal do Paraná, Curitiba, 2006.

LOURENÇO, I. P.; FIGUEIREDO, R. W.; ALVES, R. E.; ARAGÃO F. A. S.; MOURA, C. F. H.. Caracterização de frutos de Genotypes de muricizeiros cultivados no litoral cearense. **Revista Ciência Agronômica**, v.44, n.3, p.499-504, 2013.

MONTEIRO, E. R.; BASTOS, E. M.; LOPES, Â. C. de A.; GOMES, R. L. F.; NUNES, J. A. R.. Diversidade genética entre acessos de espécies cultivadas de pimentas. **Ciência Rural**, v.40, n.2, p.288-293, 2010.

MOOZ, E. D.; CASTELUCCI, A. C. L.; SPOTO, M. H.. Potencial tecnológico e alimentício de frutos de macaúba Acrocomiaaculeata (Jacq.) Lodd. **Revista Brasileira de Pesquisa em Alimentos**, Campo Mourão, v.3, n.2, p.86-89, 2012.

MOTOIKE, S. Y.; CARVALHO, M.; PIMENTEL, L. D.; KUKI, K. N.; PAES, J. M. V.; DIAS, H. C. T.; SATO, A. Y.. **A cultura da macaúba: implantação e manejo de cultivos racionais.** Viçosa: EdUFV, 2013.

NEGRELLE, R. R. B.. Composição e estrutura do componente arbóreo de remanescente de Floresta Estacional Semidecidual Aluvial no Pantanal Mato-Grossense, Brasil. **Revista Árvore**, v.37, p.989-999, 2013.

NUNES, A. P.. **Estudo da macaúba (Acrocomiaaculeata) como fonte de energia sustentável e obtenção de insumo**

para o setor farmacêutico. Dissertação (Mestrado em Agroenergia) – Universidade Federal do Tocantins, Palmas, 2015

OLIVEIRA, T. C.; BARELLI, M. A. A.; AZEVEDO, R. F.; GONÇALVES, D. L.; SANTOS, P. R. J.; SILVA, V. P.; OLIVEIRA, A. J.; TARDIN, F. D.; PARRELLA, R. A. C.. Genetic divergence of sweet sorghum genotypes based on morphoagronomic characters by multivariate techniques. **International Journal of Development Research**, v.10, n.10, p.41084-41088, 2020. DOI: <https://doi.org/10.37118/ijdr.20145.10.2020>

SANDER, N. L.; SILVA, C. J.; DUARTE, A. VM.; ZAGO, B. W.; GALBIATI, C.; VIANA, I. G.; ARRUDA, J. C.; DARDENGO, J. E.; POLETINE, J. P.; LEITE, M. H. S.; SOUZA, M. HS.; OLIVEIRA, R. F.; GUIMARÃES, T.; SILVA, V. P.; BARRELLI, M. A. A.. The Influence of Environmental Features on the Morphometric Variation in Mauritia flexuosa L.f. Fruits and Seeds. **Plants. Publisher of Open Access Journals**, v.9, 2020. DOI: <https://doi.org/10.3390/plants9101304>

SILVA, D. B.; SILVA, J. A.; JUNQUEIRA, N. T. V.; ANDRADE, L. R. M.. **Frutas do cerrado.** Embrapa Informação Tecnológica, Brasília, 2001.

SILVA, V. P.; VITAL, A. H. A.; LIRA, J. P. E. ; POLETINE, J. P. .; MORAIS, L. H. P. ; OLIVEIRA, A. J. de ; FELIPIN-AZEVEDO, R.; BARELLI, M. A. A. . Analysis of genetic divergence in safflower genotypes through morphological characters. **Society and Development**. v.10, n.5, p.e40610514596, 2021. DOI: <https://doi.org/10.33448/rsd-v10i5.14596>

SINGH, D.. The relative importance of characters affecting genetics divergence. **The Indian Journal of Genetics & Plant Breeding**, v.41. p.237-245. 1981.

VILELA, M. F.; AQUINO, F. G.; JUNQUEIRA, N. T. V.; CONCEIÇÃO, L. D. H. C. S.. Maciços naturais de macaúba (Acrocomiaaculeata): mapeamento e análise do potencial para produção de biodiesel. In: Embrapa Cerrados-Artigo em anais de congresso (ALICE). In: CONGRESSO INTERNACIONAL DE BIOENERGIA, 9. **Anais**. Paraná: Porths Eventos, 2014.