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Special Supplement: *Cerrado* **[Brazilian Savanna]**

Selection of *Hancornia speciosa* germplasm accessions based on the FAI-BLUP index[1]

Gabriella Queiroz de Almeida[2], João Romero Amaral Santos de Carvalho Rocha[3],
Herika Paula Pessoa[2], Flávia Maria Alves[2], Lázaro José Chaves[4]

ABSTRACT

Hancornia speciosa Gomes is one of the native fruit species most frequent in the Brazilian Savanna. Studies on the genetic variability of quantitative traits for this species are scarce and the identification of accessions with the best agronomic traits may support strategies for conservation and breeding programs. This study aimed to estimate the genetic diversity of accessions from the *H. speciosa* germplasm collection of the Universidade Federal de Goiás (Goiânia, Goiás state, Brazil) and rank them based on a selection index combining eleven agronomic traits. A total of 192 individual accessions from 57 progenies, from 29 natural populations, were evaluated. The data were subjected to multivariate analysis and the individuals and progenies evaluated using the FAI-BLUP selection index. The Tocher cluster analysis allowed grouping the progenies into ten divergent clusters and the individuals into 18 divergent clusters. The simultaneous selection of traits based on the FAI-BLUP index may be recommended while maintaining the potential variability in the population resulting from the recombination. The individual selection proved to be more effective than the selection based on progenies means, because it exploits the genetic variation among and within progenies.

KEYWORDS: Brazilian Savanna, native fruit, mangaba.

RESUMO

Seleção de acessos de germoplasma de *Hancornia speciosa* com base no índice FAI-BLUP

Hancornia speciosa Gomes é uma das espécies frutíferas nativas mais frequentes no Cerrado. Estudos sobre a variabilidade genética de caracteres quantitativos para essa espécie são escassos e a identificação de acessos com as melhores características agronômicas pode subsidiar estratégias de programas de conservação e melhoramento genético. Objetivou-se estimar a diversidade genética de acessos da coleção de germoplasma de *H. speciosa* da Universidade Federal de Goiás e classificá-los com base em um índice de seleção combinando onze características agronômicas. Foram avaliados 192 acessos individuais de 57 progênies, de 29 populações naturais. Os dados foram submetidos a análise multivariada e os indivíduos e progênies avaliados pelo índice de seleção FAI-BLUP. A análise de agrupamento de Tocher permitiu agrupar as progênies em dez agrupamentos divergentes e os indivíduos em 18 agrupamentos divergentes. A seleção simultânea de caracteres com base no índice FAI-BLUP pode ser recomendada, mantendo-se a variabilidade potencial na população resultante da recombinação. A seleção individual mostrou-se mais eficaz do que a seleção baseada em médias de progênies, por explorar a variação genética entre e dentro das progênies.

PALAVRAS-CHAVE: Cerrado, fruteira nativa, mangaba.

INTRODUCTION

Mangaba (*Hancornia speciosa* Gomes) is a Brazilian fruit species native from the Brazilian Savanna and coastal areas of the Northeast and Northern regions of Brazil. A phytosociology study identified this species in at least 50 % of 98 sampled areas of cerrado *stricto sensu* and was one of the most frequent among the 1,534 tree species found in this biome (Ribeiro & Walter 1998).

H. speciosa fruits are aromatic, delicate, tasty and nutritious, with higher vitamins and minerals contents, if compared to the majority of fruit species (Ferreira et al. 2007). Due to its characteristics and pleasant flavor, the fruit may be consumed *in natura* or processed as candies, ice cream, jelly, liqueur and pulp. The fruit is low calorie, iron-rich and also a good source of vitamin C (Soares et al. 2000). This plant also produces latex, which has potential commercial and medicinal applications.

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[2] Universidade Federal de Viçosa, Departamento de Fitotecnia, Viçosa, MG, Brasil.
E-mail/ORCID: gabriellaqueirozalmeida@hotmail.com/0000-0002-0340-7346; herikapaulapessoa@gmail.com/0000-0001-5284-684X; flaviamarialves@gmail.com/0000-0001-5679-3255.
[3] Universidade Federal de Viçosa, Departamento de Genética e Melhoramento, Viçosa, MG, Brasil.
E-mail/ORCID: joaoascrocha@gmail.com/0000-0002-0976-0917.
[4] Universidade Federal de Goiás, Escola de Agronomia, Goiânia, GO, Brasil. *E-mail/ORCID*: lchaves@ufg.br/0000-0002-4678-9014.

Such potential economic value could be improved by breeding programs.

H. speciosa is a self-incompatible allogamous species (Darrault & Schlindwein 2005, Collevatti et al. 2016). Its seeds are recalcitrant and its micropropagation and *in vitro* conservation are difficult and expensive. Thus, up to now, *H. speciosa* germplasm must be preserved *in vivo*, both in *ex situ* collections and *in situ* natural populations (Pereira et al. 2010).

The correct characterization and evaluation of a germplasm collection greatly simplify a subsequent plant breeding (Valls 2007). One of the assumptions for successful breeding programs is genetic variability in the breeding population. This variability may be natural or generated by recombination of divergent materials. Some studies have identified genetic variability among *H. speciosa* populations using molecular and biochemical markers, as well as agronomic traits (Ganga et al. 2009, Ganga et al. 2010, Collevatti et al. 2016, Costa et al. 2017, Santos et al. 2017, Collevatti et al. 2018, Flores et al. 2018, Almeida et al. 2019, Chaves et al. 2020).

Selection indices are often used in breeding programs to simultaneously select and promote the improvement of several traits. This study aimed to estimate the genetic diversity among *H. speciosa* accessions from the Universidade Federal de Goiás germplasm collection, as well as to rank them based on a selection index, combining multiple agronomic traits.

MATERIAL AND METHODS

Maternal progenies from the *H. speciosa* germplasm collection of the Universidade Federal de Goiás (Goiânia, Goiás state, Brazil) (16º35’39”S, 49º17’26”W and altitude of 720 m), assumed as half-sib families, were evaluated.

According to the Köppen classification, the climate in the region is Aw, tropical, with a rainy season from October to April and a dry season from May to September (Brasil 1992). The soil of the experimental area is a medium texture Dark Red Latosol (Embrapa 2013), which corresponds to a Ferralsol in the international soil classification system (Prado 2021). The original vegetation was a transitional tropical forest to the Brazilian Savanna. Soil correction or artificial fertilization was not performed in the area.

The germplasm collection was installed in the field in December 2005, in a randomized complete block design, with 57 treatments and four replications with one plant per plot, with spacing of 6 x 5 m (Ganga et al. 2009). The treatments (progenies) represented 29 subpopulations from different provenances of the Brazilian Savanna and four botanical varieties (*H. speciosa* var. *pubescens*, *H. speciosa* var. *gardneri*, *H. speciosa* var. *speciosa* and *H. speciosa* var. *cuyabensis*). With time, some plants (individual accessions) died, and it was only possible to evaluate192 individuals (Table 1). Further details on the origin of accessions and previous evaluations of the germplasm collection can be found in Ganga et al. (2009 and 2010) and Almeida et al. (2019).

The individual accessions were characterized for agronomical quantitative traits that included plant height, canopy diameter, stem circumference up to 10 cm from the soil surface and below the lower branch, lower branching height and primary branching number. At the time of production, the fruit diameter and fruit length were determined in five fruits per plant directly on the trees. Five to ten fruits were collected per accession (according to availability), and data were collected on the fruit mass, number of seeds per fruit and seed mass per fruit. The number of fruits per plant was also evaluated every three days by counting the number of fruits fallen per accession and removing them from the area. Fruit data were taken from September to December 2013, the period of greatest yield.

The mixed model methodology was adopted for statistical analyses via restricted maximum likelihood/best linear unbiased prediction (REML/BLUP) to estimate the genetic values of individual and progeny accessions genetic values. The statistical model was denoted by $y = Xb + Zv + Ws + Ti + e$, where y is the vector of data; b the vector of block effects (assumed as fixed) added to the overall mean; v the vector of varieties effects [assumed as random; $v \sim N(0, \sigma_v^2)$]; s the vector of subpopulation effects within varieties [random; $s \sim N(0, \sigma_s^2)$]; i the vector of progeny effects within subpopulation, within variety, within a block or vector of individual effect [random; $i \sim N(0, \sigma_i^2)$]; e the vector of errors [random; $e \sim N(0, \sigma_e^2)$]; X, Z, W and T are the incidence matrices for these effects; σ_v^2 is the variance component associated with varieties effect; σ_s^2 the variance component associated with the subpopulations effect within varieties; σ_i^2 the variance component associated with individual effect; and σ_e^2 the variance component associated with the error effects.

Predicted genetic values (BLUPs) were used in multivariate methods to estimate the genetic dissimilarities between individuals and progenies, using the standardized average Euclidean distance. This distance was then used in the clustering analysis of the Tocher optimization (Rao 1952). According to this methodology, the average intragroup distance should be smaller than the mean intergroup distance. The clustering criterion was given by the highest dissimilarity measured value (θ) found in the clustering of the smallest distances involving each pair of individuals (Rao 1952).

In addition to the genetic diversity study, BLUPs were used for the simultaneous selection of the best individual accessions and progenies using the FAI-BLUP index, with a selection intensity of approximately 20 % (ten superior progenies and 40 superior individuals). FAI-BLUP uses the exploratory factor analysis combined with the construction of ideotypes (confirmatory factor analysis). In this way, the index exploits the correlations among the evaluated traits (Rocha et al. 2018).

In the FAI-BLUP index, the number of ideotypes is defined based on the combination of desirable and undesirable factors for the selection objective. The number of ideotypes is given by the following equation: $NI = 2^n$, where NI is the number of ideotypes and n the number of factors.

After the ideotypes determination, the distances from each genotype according to ideotypes (genotype-ideotype distance) were estimated and converted into spatial probability, enabling the genotype ranking. For that, the following equation was used:

$$P_{ij} = \frac{\frac{1}{d_{ij}}}{\sum_{i=1;\,j=1}^{i=n;\,j=m} \frac{1}{d_{ij}}}$$

where P_{ij} is the probability of the ith genotype ($i = 1, 2, ..., n$) to be similar to the jth ideotype ($j = 1, 2, ..., m$), and d_{ij} is the genotype-ideotype distance from the ith genotype to the jth ideotype - based on standardized average Euclidean distance.

The R software (R Core Team 2017) was used to obtain the BLUPs, with the sommer package (Covarrubias-Pazaran 2016), and the routine provided by Rocha et al. (2018) for the FAI-BLUP index. Genetic diversity analyses were performed with the Genes software (Cruz 2013).

RESULTS AND DISCUSSION

The Tocher cluster analysis allowed grouping the 57 progenies into ten divergent clusters. Cluster 1 was the largest group with 34 progenies, cluster 2 grouped four progenies, cluster 3 seven progenies, cluster 4 four progenies, clusters 5 and 6 two progenies each, and the other four clusters included only one progeny each (Table 1).

The individual accessions were grouped into 18 divergent clusters, based on the individual BLUPs. Cluster 1 was the largest and grouped 142 individuals. Cluster 2 grouped 11 individuals, clusters 3 and 4 grouped five individuals each, cluster 5 grouped three individuals, cluster 6 grouped four individuals,

Table 1. Tocher clustering of 57 *Hancornia speciosa* progenies from the germplasm collection of the Universidade Federal de Goiás (Goiânia, Goiás state, Brazil), based on 11 agronomic traits.

Clusters	Progenies
1	15 23 37 57 31 4 49 14 21 55 29 2 24 8 22 9 56 16 27 10 6 53 18 12 25 46 20 34 30 48 33 39 42 26
2	11 44 54 45
3	1 51 3 35 32 47 17
4	7 19 36 52
5	13 28
6	41 50
7	5
8	38
9	43
10	40

cluster 7 grouped two individuals, and the other 11 clusters included only one individual each (Table 2). Individuals from *H. speciosa* var. *pubescens* (30 out of 31 accessions) and *H. speciosa* var. *speciosa* (13 out of 14 accessions) tended to cluster in group 1. Accessions from *H. speciosa* var. *gardneri* and *H. speciosa* var. *cuyabensis* were distributed over several groups, with many accessions in isolated groups, what suggests a greater genetic diversity among the accessions of these two botanical varieties.

Selection based on individual accessions showed a greater expected genetic gain for most traits. This indicates that the selection including the genetic variability within half-sib families is more advantageous than the selection among families only (Table 3). Individuals from progenies 10 and 13 did not take part in the selection of individual accessions (Table 4). This result was expected because they belong to the *H. speciosa* var. *speciosa*, which did not adapt well to the environmental conditions of the experimental area. Progenies from clusters 1 and 2 were included in the progenie's selection index. Individuals from the clusters 1; 2; 3; 4; 6; 7; 8; 9; and 14 were included in the individuals selection index.

Several studies on the genetic diversity of *H. speciosa* using both morphological and molecular markers have shown that this species has a higher variability within populations than among populations (Moura et al. 2011, Silva et al. 2011, Martins et al. 2012, Collevatti et al. 2018). The clusters found in this study characterize the genetic divergence among accessions belonging to different subpopulations and botanical varieties. This allows several recombination alternatives to increase the genetic variability and the frequency of favorable alleles.

Due to its economic importance and natural distribution, *H. speciosa* is under intense anthropic pressure. Genetic diversity within and among populations is being lost and the populations are becoming smaller and even disappearing. This reinforces the need to explore the diversity conserved in germplasm collections in targeted crosses to

Table 2. Tocher clustering of 192 *Hancornia speciosa* individuals from the germplasm collection of the Universidade Federal de Goiás (Goiânia, Goiás state, Brazil), based on 11 agronomic traits.

Cluster	Individual accessions															
1	22	65	67	1	71	26	190	91	3	66	78	109	36	181	161	108
	56	55	23	50	42	58	9	17	39	59	192	167	18	41	37	130
	100	102	29	90	148	34	154	53	24	178	47	75	82	19	157	143
	99	20	142	40	191	62	124	5	134	98	30	11	139	156	105	84
	95	186	112	64	151	31	150	25	45	92	10	79	57	83	35	104
	117	81	80	68	146	63	187	113	4	76	70	7	85	123	101	174
	54	49	72	110	12	46	127	153	6	138	162	27	69	172	60	184
	38	122	137	163	73	114	32	166	159	188	61	169	33	43	21	116
	93	176	165	74	173	97	158	28	77	13	119	164	185	15	115	86
	170	144	171	179	52	180	94									
2	44	152	118	149	8	106	168	120	2	155	96					
3	140	141	133	182	189											
4	107	145	183	135	175											
5	51	87	147													
6	14	128	111	125												
7	48	121														
8	136															
9	131															
10	103															
11	88															
12	126															
13	160															
14	177															
15	132															
16	89															
17	16															
18	129															

Table 3. Predicted genetic gain based on the FAI-BLUP index for *Hancornia speciosa* half-sib progenies and individual accessions from the germplasm collection of the Universidade Federal de Goiás (Goiânia, Goiás state, Brazil).

Traits	Ideotype		Progenies (57)		Individuals (192)	
	Desirable	Undesirable	Factor	Gain (%)	Factor	Gain (%)
FL	Mean	Minimum	1	0.1584	1	0.5167
FD	Mean	Minimum	1	0.1448	1	-0.4920
FM	Mean	Minimum	1	-0.2098	1	-0.0757
FN	Maximum	Minimum	2	1.4524	2	6.5693
CD	Maximum	Minimum	2	0.8126	2	0.4099
SC	Maximum	Minimum	2	0.0998	2	1.3623
BN	Maximum	Minimum	2	1.8892	3	0.6480
BH	Maximum	Minimum	3	0.4655	4	1.2476
PH	Minimum	Maximum	3	0.5307	3	0.7136
NS	Minimum	Maximum	4	-0.8049	4	-0.2443
SM	Minimum	Maximum	4	-0.7781	4	2.2705

FL: fruit length; FD: fruit diameter; FM: fruit mass; FN: number of fruits per plant; CD: canopy diameter; SC: stem circumference; BN: primary branching number; BH: lower branching height; PH: plant height; NS: number of seeds per fruit; SM: seed mass.

Table 4. Selection of the 20 % best individual accessions of *Hancornia speciosa* from the germplasm collection of the Universidade Federal de Goiás (Goiânia, Goiás state, Brazil), based on the FAI-BLUP index, from 11 agronomic traits.

Accession code	Progeny	Population/State	FAI-BLUP index	Ranking
140	46	Coxim/MS	0.06681	1
145	47	Coxim/MS	0.06632	2
141	46	Coxim/MS	0.06460	3
97	34	General Carneiro/MT	0.06427	4
177	56	Caçu/GO	0.06116	5
175	55	Caçu/GO	0.06072	6
173	55	Caçu/GO	0.06040	7
115	39	Jaciara/MT	0.05972	8
162	51	Alcinópolis/MS	0.05832	9
107	37	Chapada dos Guimarães/MT	0.05817	10
136	44	Sonora/MS	0.05751	11
146	47	Coxim/MS	0.05743	12
180	56	Caçu/GO	0.05637	13
6	2	Barro Alto/GO	0.05586	14
86	32	Barra do Garças/MT	0.05555	15
32	16	Alexânia/GO	0.05546	16
169	53	Chapadão do Sul/MS	0.05517	17
155	50	Alcinópolis/MS	0.05493	18
14	5	Porangatu/GO	0.05475	19
48	20	Silvânia/GO	0.05456	20
121	40	Rondonópolis/MT	0.05347	21
179	56	Caçu/GO	0.05275	22
13	5	Porangatu/GO	0.05252	23
188	58	Niquelândia/GO	0.05250	24
111	38	Chapada dos Guimarães/MT	0.05109	25
109	37	Chapada dos Guimarães/MT	0.05104	26
161	51	Alcinópolis/MS	0.05101	27
153	49	Alcinópolis/MS	0.05086	28
168	53	Chapadão do Sul/MS	0.05086	29
127	42	Rondonópolis/MT	0.05047	30
129	42	Rondonópolis/MT	0.05045	31
7	2	Barro Alto/GO	0.05031	32
131	43	Sonora/MS	0.05031	33
119	40	Rondonópolis/MT	0.04978	34
80	29	Piranhas/GO	0.04909	35
138	45	Sonora/MS	0.04894	36
106	37	Chapada dos Guimarães/MT	0.04883	37
2	1	Barro Alto/GO	0.04883	38

increase variability for selection programs (Costa et al. 2015).

The formation of several clusters was observed in these subpopulations, what is a sign of structured genetic diversity. However, many clusters were formed by only one accession, demonstrating that the genetic diversity is poorly represented. In this situation, the loss of one genotype may influence the population variability. This observation led to the need to amplify the genetic base of the evaluated germplasm collection. In view of this, new expeditions to collect subpopulations that are poorly represented in the collection would be useful.

The analysis of genetic divergence greatly simplifies the treatment of the population structure, what facilitates the germplasm use by breeders (Resende 2002). The breeding process should emphasize the crossing of genotypes within clusters when the objective is to maintain the homogeneity or uniformity of the traits, and the crossing of genotypes among clusters when the objective is to create more variability and/or promote heterosis in offspring. As this study aimed to explore the genetic variability of the *H. speciosa* germplasm collection to improve agronomic traits, the most appropriate procedure is the recombination of accessions from different clusters based on the selection index.

In a study carried out for the same germplasm collection (Almeida et al. 2019), significant variances and moderate to low genotypic correlation were verified among the 11 agronomic traits evaluated in the present study. This suggests that it is not satisfactory to improve one trait by indirect selection. Thus, the use of a selection index combining all the agronomic traits of interest is recommended.

The ideotypes were previously defined on the basis of the desired commercial fruit, such as in cultivated citrus species, considering the importance of medium-sized fruits with few seeds, large crowns, strong stems and low and branched plants. Some negative gains observed in the selection index, such as fruit mass, were expected, because a positive genetic correlation between the number of seeds and fruit mass was observed. Thus, reducing the number of seeds should also reduce the fruit mass (Almeida et al. 2019). A fruit tree yield potential is traditionally obtained multiplying the number of fruits by their mass. However, the correlation analysis showed that the yield of the *H. speciosa* tree is more related to the size of its crown than to the mass of its fruits (Almeida et al. 2019).

The FAI-BLUP selection index proposed by Rocha et al. (2018) is advantageous, because it can be used with unbalanced data, does not require weight assignment to the different traits and does not present a problem with multicollinearity. The index was satisfactory for the purpose of this study. In addition, the procedure allows the selection of genotypes by means of predicted genetic values, what excludes environmental effects.

The selection and recombination of genotypes of different clusters with high genetic values and high selective accuracy allow satisfactory gains and the consequent improvement of the desired agronomic traits (Resende 2002). Therefore, for the purpose of recurrent selection, it is recommended to collect open pollinated seeds from the best individuals (Table 4), which represent individual selection in female parents only. The evaluation of clones from the best individuals could be recommended to accelerate the development of uniform cultivars. Another alternative could be to clone the best individuals to form an indoor orchard, in order to perform directional crosses.

The predicted gains from selection, as percentage of the mean, were relatively low for most traits. This was because the simultaneous selection of several traits tends to reduce the genetic gain per trait. Furthermore, for some traits, the ideotypes were defined to maintain an average performance. The higher predicted genetic gain for individual accessions for most traits, in comparison with family selection, was expected. In half-sib families, the genetic variability among family means is equivalent to one-quarter of the additive genetic variance only, while the variability within families is equivalent to three-quarters of the additive genetic variance plus the dominance variance. In addition, the reduced number of remaining plants in many progenies decreases the accuracy of the progeny means. The highest genetic gain at the individual level occurred for number of fruits per plant (6.7 %), which is the main yield component in *H. speciosa* (Almeida et al. 2019). Because the accessions were planted in individual plots, the genetic variance within families is confounded with environmental effects of blocks and plots within blocks.

CONCLUSION

The *H. speciosa* germplasm collection of the Universidade Federal de Goiás shows a genetic diversity to be explored in selection programs, based on the formation of several divergent groups in the cluster analysis, and the FAI-BLUP index is effective to explore the genetic variability among its individual accessions.

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REFERENCES

ALMEIDA, G. Q.; VIEIRA, M. C.; GANGA, R. M. D.; CHAVES, L. J. Agronomic evaluation of a *Hancornia speciosa* Gomes germplasm collection from the Brazilian Cerrado. *Crop Breeding and Applied Biotechnology*, v. 19, n. 1, p. 8-14, 2019.

BRASIL. *Normais climatológicas*: 1960-1991. Brasília, DF: Ministério da Agricultura e Reforma Agrária, 1992.

CHAVES, L. J.; GANGA, R. M. D.; GUIMARÃES, R. A.; CALDEIRA, A. J. R. Quantitative and molecular genetic variation among botanical varieties and subpopulations of *Hancornia speciosa* Gomes (Apocynaceae). *Tree Genetics & Genomes*, v. 16, n. 50, p. 1-11, 2020.

COLLEVATTI, R. G.; OLIVATTI, A. M.; TELLES, M. P. C.; CHAVES, L. J. Gene flow among *Hancornia speciosa* (Apocynaceae) varieties and hybrid fitness. *Tree Genetis & Genomes*, v. 12, n. 1, p. 74-85, 2016.

COLLEVATTI, R. G.; RODRIGUES, E. E.; VITORINO, L. C.; LIMA-RIBEIRO, M. S.; CHAVES, L. J.; TELLES, M. P. C. Unravelling the genetic differentiation among varieties of the tropical Savanna tree *Hancornia speciosa* Gomes. *Annals of Botany*, v. 122, n. 6, p. 973-984, 2018.

COSTA, C. F.; COLLEVATTI, R. G.; CHAVES, L. J.; LIMA, J. S.; SOARES, T. N.; TELLES, M. P. C. Genetic diversity and fine-scale genetic structure in *Hancornia speciosa* Gomes (Apocynaceae). *Biochemical Systematics and Ecology*, v. 72, n. 1, p. 63-67, 2017.

COSTA, D. F. D.; VIEIRA, F. D. A.; FAJARDO, C. G. CHAGAS, K. P. T. D. Genetic diversity and ISSR initiators selection in a natural population of mangaba (*Hancornia speciosa* Gomes) (Apocynaceae). *Revista Brasileira de Fruticultura*, v. 37, n. 4, p. 970-976, 2015.

COVARRUBIAS-PAZARAN, G. Genome-assisted prediction of quantitative traits using the R package sommer. *PLoS One*, v. 11, n. 6, e0156744, 2016.

CRUZ, C. D. Genes: a software package for analysis in experimental statistics and quantitative genetics. *Acta Scientiarum Agronomy*, v. 35, n. 3, p. 271-276, 2013.

DARRAULT, R. O.; SCHLINDWEIN, C. Limited fruit production in *Hancornia speciosa* (Apocynaceae) and pollination by nocturnal and diurnal insects. *Biotropica*, v. 37, n. 3, p. 381-388, 2005.

EMPRESA BRASILEIRA DE PESQUISA AGROPECUÁRIA (Embrapa). *Sistema brasileiro de classificação de solos*. Rio de Janeiro: Centro Nacional de Pesquisa de Solos, 2013.

FERREIRA, M. E.; MORETZSOHN, M. C.; BUSO G. S. C. Fundamentos de caracterização molecular de germoplasma vegetal. *In*: NASS, L. L. *Recursos genéticos vegetais*. Brasília, DF: Embrapa Recursos Genéticos e Biotecnologia, 2007. p. 377-420.

FLORES, I. S.; SILVA, A. K.; FURQUIM, L. C.; CASTRO, C. F. S.; CHAVES, L. J.; COLLEVATTI, R. G.; LIÃO, L. M. HR-MAS NMR allied to chemometric on *Hancornia speciosa* varieties differentiation. *Journal of the Brazilian Chemical Society*, v. 29, n. 4, p. 708-714, 2018.

GANGA, R. M. D.; CHAVES, L. J.; NAVES, R. V. Parâmetros genéticos em *Hancornia speciosa* Gomes do Cerrado. *Scientia Forestalis*, v. 37, n. 84, p. 395-404, 2009.

GANGA, R. M. D.; FERREIRA, G. A.; CHAVES, L. J.; NAVES, R. V.; NASCIMENTO, J. L. Caracterização de fruto e árvores de populações naturais de *Hancornia speciosa* Gomes do Cerrado. *Revista Brasileira de Fruticultura*, v. 32, n. 1, p. 101-113, 2010.

MARTINS, G. V.; MARTINS, L. S. S.; VEASEY, E. A.; LEDERMAN, I. E.; SILVA, E. F. Diversity and genetic structure in natural populations of *Hancornia speciosa* var. *speciosa* Gomes in Northeastern Brazil. *Revista Brasileira de Fruticultura*, v. 34, n. 4, p. 1143-1153, 2012.

MOURA, N. F.; CHAVES, L. J.; VENCOVSKY, R.; NAVES, R. V.; AGUIAR, A. V.; MOURA, M. F. Genetic structure of mangaba (*Hancornia speciosa* Gomes) populations in the Cerrado region of central Brazil. *Bioscience Journal*, v. 27, n. 3, p. 473-481, 2011.

PEREIRA, A. V.; PEREIRA, E. B. C.; SILVA JUNIOR, J. F.; SILVA, D. B. Mangaba. *In*: VIEIRA, R. F.; AGOSTINI-

COSTA, T. S.; SILVA, D. B.; SANO, S. M.; FERREIRA, F. R. *Frutas nativas da região Centro-Oeste do Brasil*. Brasília, DF: Embrapa Informação Tecnológica, 2010. p.188-213.

PRADO, H. *Classificação dos solos*. 2021. Available at: http://www.pedologiafacil.com.br/classificacao.php. Access on: 06 July 2021.

R CORE TEAM. *R*: a language and environment for statistical computing. Vienna: R Foundation for Statistical Computing, 2017.

RAO, C. R. *Advanced statistical methods in biometric research*. New York: John Wiley & Sons, 1952.

RESENDE, M. D. V. *SELEGEN-REML/BLUP*: seleção genética computadorizada: manual do usuário. Colombo: Embrapa-CNPF, 2002.

RIBEIRO, J. F.; WALTER, B. M. Fitosionomias do bioma Cerrado. *In*: SANO, S. M.; ALMEIDA, S. P. *Cerrado*: ambiente e flora. Planaltina, DF: Embrapa Cerrados, 1998. p. 87-166.

ROCHA, J. R. A. S. C.; MACHADO, J. C.; CARNEIRO, P. C. S. Multitrait index based on factor analysis and ideotype-design: proposal and application on grass breeding for bioenergy. *GCB Bioenergy*, v. 10, n. 1, p. 52-60, 2018.

SANTOS, P. S.; FREITAS, L. S.; SANTANA, J. G. S.; MUNIZ, E. M.; RABBANI, A. R. C.; SILVA, A. V. C. Genetic diversity and the quality of mangaba tree fruits (*Hancornia speciosa* Gomes - Apocynaceae), a native species from Brazil. *Scientia Horticulturae*, v. 226, n. 1, p. 372-378, 2017.

SILVA, A. V. C.; SANTOS, A. R. F.; WICKERT, E.; SILVA JÚNIOR, J. F.; COSTA, T. S. Divergência genética entre acessos de mangaba tree (*Hancornia speciosa* Gomes). *Revista Brasileira de Ciências Agrárias*, v. 6, n. 4, p. 572-578, 2011.

SOARES, F. P.; PAIVA, R.; NOGUEIRA, R. C.; OLIVEIRA, L. M.; SILVA, D. R. G.; PAIVA, P. D. O. *Cultura da mangaba (Hancornia speciosa Gomes)*. Lavras: Boletim Agropecuário, 2000.

VALLS, J. F. Caracterização de recursos genéticos vegetais. *In*: NASS, L. L. *Recursos genéticos vegetais*. Brasília, DF: Embrapa Recursos Genéticos e Biotecnologia, 2007. p. 281-306.